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PROTEOMIC INVESTIGATION ON NASU-HAKOLA DISEASE: SHEDDING LIGHT ON FRONTOTEMPORAL TREM2-BASED DEMENTIA

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Alla mia famiglia

Tieni un capo del filo,
con l'altro capo in mano
io correrò nel mondo.
E se dovessi perdermi, tu, tira.

SOMMARIO

La malattia di Nasu-Hakola (NHD), nota anche come osteodisplasia lipomembranosa policistica con leucoencefalopatia sclerosante (PLOSL), è una patologia sistemica ereditaria recessiva caratterizzata da demenza presenile frontotemporale e lesioni ossee. Le basi genetiche che determinano la patologia sono correlate ad un difetto strutturale di due geni, TREM2 e DAP12, che codificano per due subunità del recettore transmembrana di un complesso di segnalazione espresso dalle cellule della microglia e dagli osteoclasti. Ad oggi, studi molecolari o proteomici di questa malattia sono assenti o scarsi, infatti in letteratura sono riportati solo studi cognitivo-comportamentali e genetici di singoli pazienti. Con l'obiettivo di ottenere maggiori informazioni circa l'insorgenza e/o la progressione dell'NHD, lo scopo di questo progetto di dottorato è stato quello di caratterizzare il proteoma linfoblastoide di un'intera famiglia in cui due membri hanno manifestato un fenotipo NHD.

Il progetto è stato focalizzato sull'analisi proteomica della linea cellulare linfoblastoide (LCL) ottenuta da 7 soggetti: due omozigoti (Ho), quattro eterozigoti (He) ed un wildtype (Wt). L'approccio proteomico utilizzato è gel-free e basato sulla tecnologia MudPIT (Multidimensional Protein Identification Technology) che si avvale della combinazione di micro-cromatografia liquida bidimensionale e spettrometria di massa tandem ad alta risoluzione. L'identificazione delle sequenze peptidiche e delle relative proteine è stata ottenuta tramite un software (Bioworks) basato sull'algoritmo SEQUEST per l'interpretazione degli spettri di massa acquisiti. Le liste proteiche sono state sottoposte all'analisi bioinformatica mediante software sviluppati in laboratorio (MAProMa, Multidimensional Algorithm Protein Map) e/o disponibili in rete, allo scopo di evidenziare gli andamenti di espressione proteica e le vie metaboliche coinvolte nell'insorgenza e/o progressione dell'NHD. Lo studio ha permesso di identificare circa 3000 proteine distinte all'interno dei tre gruppi analizzati e circa 400 proteine sono state identificate come peculiari di ciascuna categoria (Ho, He, Wt). In particolare, i dati hanno evidenziato la presenza di proteine differenzialmente espresse associate a processi correlabili alla neurodegenerazione. Inoltre, le reti proteiche hanno messo in rilievo alcune via molecolari che potrebbero essere coinvolte nell'insorgenza o nella progressione di questo raro disordine frontotemporale. Pertanto, la piattaforma MudPIT, completamente automatizzata, ha dimostrato la sua efficacia nello studio dei profili di espressione proteica di pazienti affetti da NHD e si può candidare come valida piattaforma per lo studio di altre demenze frontotemporali legate a TREM2. Infatti, questo approccio ha consentito di generare, per la prima volta, il profilo proteico più completo delle cellule linfoblastoidi appartenenti a soggetti Nasu-Hakola e di caratterizzare le vie metaboliche coinvolte nelle alterazioni funzionali di questa patologia.

ABSTRACT

Nasu-Hakola Disease (NHD), also known as Polycystic Lipomembranous Osteodysplasia with Sclerosing Leukoencephalopathy (PLOSL), is a recessively inherited systemic leucodystrophy disorder characterized by a combination of frontotemporal presenile dementia and lytic bone lesions. It is known that NHD is genetically related to a structural defect of TREM2 and DAP12 genes that encode for different subunits of the membrane receptor signalling complex expressed by microglia and osteoclast cells. To date, molecular or proteomic studies about this disorder are absent or scarce, and only case reports based on neuropsychological and genetic tests have been reported. In light of this, to obtain in depth knowledges about the onset and/or progression of the NHD, the aim of this PhD project was to characterize the Lymphoblastoid proteome of an entire family in which two members manifested a NHD phenotype, through an innovative proteomic approach.

The project was focused on the proteomic analysis of Lymphoblastoid cell lines (LCLs) obtained from 7 kin subjects: two homozygote (Ho), four heterozygote (He) and one wild type (Wt). Gel-free proteomic approach, based on MudPIT (Multidimensional Protein Identification Technology), was applied for the analysis of the whole protein extract. The identification of peptide sequences and their assigned proteins was obtained through an automated protein discovery software (Bioworks) based on SEQUEST algorithm for data handling of mass spectra. Protein lists were submitted to bioinformatics analysis by means of a home-made software (MAProMa, Multidimensional Algorithm Protein Map) and available on-line tools, in order to highlight the protein expression trends and the most involved pathways in the NHD onset and/or progression.

The application of a gel-free proteomic approach on NHD subjects allowed to identify about 3000 distinct proteins within the three analysed groups and about 400 proteins were identified as peculiar of each category (Ho, He, Wt). Of note, data showed the presence of differentially expressed proteins associated to neurodegenerative processes. Moreover, the protein networks highlighted some molecular pathways that could be involved in the onset or progression of this rare frontotemporal disorder. Therefore, the fully automated MudPIT platform has demonstrated its effectiveness in the study of the protein expression profiles of NHD patients and could be a valid platform for the investigation of other TREM2-based frontotemporal dementias. This approach allowed to generate, for the first time, the whole protein profile of Lymphoblastoid cells from Nasu-Hakola subjects and to characterize the metabolic pathways involved in functional alterations of this pathology.

INDEX

ABBREVIATIONS

1-DE	Mono-Dimensional Gel Electrophoresis
1D-LC	Mono-Dimensional Liquid Chromatography
2-DE	Two-Dimensional Gel Electrophoresis
2D-LC	Two-Dimensional Liquid Chromatography
AD	Alzheimer’s Disease
ALS	Amyotrophic Lateral Sclerosis
aSpC	Average Spectral Count
BSA	Bovine Serum Albumin
CHAPS	3-[(3-Cholamidopropyl)Dimethylammonio]-1-Propanesulfonate
CID	Collision-Induced Dissociation
CNS	Central Nervous System
CSF	Cerebrospinal Fluid
CT	Computed Tomography
C-trap	Curved Linear Trap
DAP12	DNAX-Activating Protein 12
DAve	Differential Average
DCI	Differential Control Index
DEP	Differentially Expressed Proteins
DTT	Dithiothreitol
EBV	Epstein-Barr Virus
ECL	Enhanced Chemiluminescence
EIC	Extracted Ion Chromatogram Peak
emPAI	Exponentially Modified PAI
ESI	Electrospray Ionization
ESI–MS	Electrospray Ionization Coupled Mass Spectrometry
FDR	False Discovery Rates
FFE	Free-Flow Fractionation
FFT	Fast Fourier Transformation
FT	Fourier Transformation
FTD	Frontotemporal Dementia
FWHM	Full Width At Half Maximum
HCD	Higher-Energy Collisional Dissociation
HD	Huntington’s Disease
He	Heterozygote Subjects

HIC	HYDROPHOBIC CHROMATOGRAPHY
Ho	HOMOZYGOTE SUBJECTS
HPLC	HIGH-PRESSURE LIQUID CHROMATOGRAPHY
ICR	ION CYCLOTRON RESONANCE TRAP
iPSC	INDUCED PLURIPOTENT STEM CELLS
KAW	KNUT AND ALICE WALLENBERG FOUNDATION
LC	LIQUID CHROMATOGRAPHY
LCLs	LYMPHOBLASTOID B-CELLS LINE
LC-MS/MS	LIQUID CHROMATOGRAPHY TANDEM MASS SPECTROMETRY
LDA	LINEAR DISCRIMINANT ANALYSIS
LDA-SP	LDA SIGNIFICANT PROTEINS
LIT	LINEAR ION TRAP
L-svPPA	LEFT-PREDOMINANT ATROPHY
m/z	MASS-TO-CHARGE RATIO
MALDI	MATRIX-ASSISTED LASER DESORPTION/IONIZATION
MALDI–MS	MATRIX-ASSISTED LASER DESORPTION/IONIZATION COUPLED MASS SPECTROMETRY
MAProMA	MULTIDIMENSIONALALGORITHM PROTEIN MAP
MRI	MAGNETIC RESONANCE IMAGING
MRM	MULTIPLE ION MONITORING
MS/MS	TANDEM MASS SPECTROMETRY
MS	MASS SPECTROMETRY
MS1	FIRST MASS ANALYZER
MS2	SECOND MASS ANALYZER
MudPIT	MULTIDIMENSIONAL PROTEIN IDENTIFICATION TECHNOLOGY
MW	MOLECULAR WEIGHT
NCBI	NATIONAL CENTER FOR BIOTECHNOLOGY INFORMATION
NDs	NEURODEGENERATIVE DISEASES
NHD	NASU-HAKOLA DISEASE
OCs	OSTEOCLASTS
PAI	PROTEIN ABUNDANCE INDEX
PCR	POLYMERASE CHAIN REACTION
PD	PARKINSON'S DISEASE
pI	ISOELECTRIC POINT
PLOSL	POLYCYSTIC LIPOMEMBRANOUS OSTEODYSPLASIA WITH SCLEROSING LEUKOENCEPHALOPATHY
PMF	PEPTIDE-MASS FINGERPRINTING

PMSS	PROTEIN/PEPTIDE MATCH SCORE SUMMATION
PPI	PROTEIN-PROTEIN INTERACTION
PTMs	POST-TRANSLATIONAL MODIFICATIONS
p-value	PROBABILITY VALUE
PVDF	POLYVINYLIDENE DIFLUORIDE
RAID	REDUNDANT ARRAY OF INDEPENDENT DISKS
RF	RADIO FREQUENCY
RMS	ROOT-MEAN- SQUARE
RPC	REVERSE-PHASE CHROMATOGRAPHY
R-svPPA	RIGHT-PREDOMINANT ATROPHY
SAX	STRONG ANION-EXCHANGE RESIN
SCX	STRONG CATION-EXCHANGE RESIN
SDS	SODIUM DODECYL SULPHATE
SDS-PAGE	SODIUM DODECYL SULPHATE - POLYACRYLAMIDE GEL ELECTROPHORESIS
SpC	SPECTRAL COUNTING
TBST	TRIS-BUFFERED SALINE
TOF	TIME-OF-FLIGHT
TQ	TRIPLE QUADRUPOLE
TREM2	TRIGGERING RECEPTOR EXPRESSED ON MYELOID CELLS 2
UniProt	UNIVERSAL PROTEIN
Wt	WILD TYPE OR CONTROL SUBJECTS
XCorr	CORRELATION COEFFICIENT
XIC	EXTRACTED ION CURRENTS
μ2DC-MS/MS	MICRO TWO DIMENSIONAL LIQUID CHROMATOGRAPHY TANDEM MASS SPECTROMETRY

FIGURES

TABLES

1. INTRODUCTION

1.1. Neurodegenerative Diseases

Neurodegenerative diseases (NDs) are characterized by slow progressive loss of one or more functions of the Central Nervous System (CNS). Worldwide, the number of people affected by anatomical and functional deterioration of the nervous system is dramatically high and the social impact is upsetting. While being a heterogeneous group of diseases, most of these pathologies manifest similar clinical features and illness progression, thus making their diagnosis elusive [1]. Moreover, despite the extensive research carried out in the recent years, the current pathophysiological notions about the onset, the progression and the treatments of NDs are largely unknown [2]. In addition, neurodegenerative diseases are classified as multifactorial pathologies, characterized by several molecular and clinical features, including the most common abnormal protein accumulation [3], inflammatory events with neuronal loss [4–6], and latest microbiota homeostasis involvement [2]. From this panel of possible illness causes, several studies demonstrated that proteins with altered physicochemical properties deposit in the human brain and represent the fundamental phenomenon in most NDs [7]. On the basis of the major protein showing depositions in the CNS, NDs are classified as tauopathies, α-synucleinopathies, TDP-43 proteinopathies, FUS/FET proteinopathies, prion diseases, trinucleotide repeat diseases, neuroserpinopathy, ferritinopathy, and cerebral amyloidosis [8]. The anatomical location of protein deposits differs for each NDs (Figure 1) and it does not necessarily coincide with the area affected by neuronal loss.

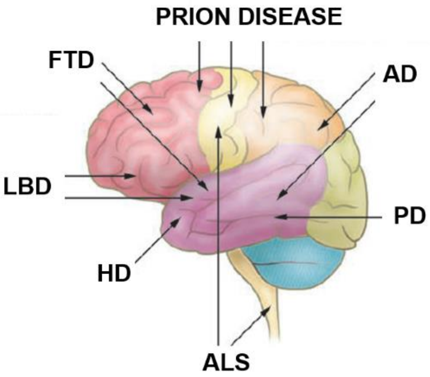


Figure 1. Overview about the major NDs.
Anatomical location of the major NDs (modified from Bertram et al. [9]) FTD: Frontotemporal Disease; LBD: Lewy Body Dementia; HD: Huntington's Disease; ALS: Amyotrophic Lateral Sclerosis; PD: Parkinson's Disease; AD: Alzheimer's Disease.

Nevertheless, neurodegeneration can manifests through the alteration of a single gene that does not necessarily lead to an abnormal accumulation/aggregation of disease-specific proteins. For example, the activation of innate immune signaling pathways by aberrant host proteins may be a common step in the development of several neurodegenerative disorders [10]. As previously mentioned, most of the literature concerns the inflammation events in the context of Alzheimer's disease [4], but a role for the innate immune activation in the pathogenesis of many neurodegenerative diseases, including Parkinson's disease (PD), amyotrophic lateral sclerosis (ALS), Huntington's disease (HD) and frontotemporal dementia (FTD) is also emerging. Several cellular actors of immune system, such as microglia or astrocytes, mediate the release of pro- and anti-inflammatory molecules and the up- or down-expression of them may result in neuro-inflammation, disease onset and progression. Despite different triggering events that characterize NDs, a common feature is the chronic immune activation, in particular of microglia, the resident macrophages of the CNS [11]. Sure enough, microglia represent the major cellular component of the innate immune system of the brain, thus possible mutation carriage of proteins expressed by these cells, could be implicated into neuronal damage. Currently, key data demonstrated that inflammation may be involved in neurodegenerative dementia. Other findings highlighted the importance of inflammation events in onset or progression of FTD, too [12, 13]. A 2001 Swedish study suggested that autoimmunity and inflammation could be part of the pathophysiological mechanisms of FTD because increased serum levels of antibodies were found in FTD patients [14]. In addition, a subsequent research found evidence for increased levels of the inflammatory cytokines in the CSF of FTD patients compared with controls. Although these changes are not specific for FTD, they suggest that inflammatory mechanisms take part in the processes that triggers frontotemporal dementia. In light of the central role that inflammatory and immune mediators play in the neurodegeneration processes, could be overall considered a potential source of biomarkers for several NDs, including FTD.

1.1.1. Frontotemporal Dementia

Frontotemporal dementia (FTD) includes a heterogeneous spectrum of neurodegenerative disorders characterized by premature death of specific neuron populations belonging to frontal and/or anterior temporal lobes of the brain. These regions of CNS influence human personality, motivation, attention, executive function, emotions, social capability, and language [15]. On the basis of early predominant clinical features, FTDs are classified into three major subtypes: behavioral variant FTD, non-fluent variant primary progressive aphasia, and semantic variant of primary progressive aphasia (left- or right-predominant atrophy, l-svPPA or r-svPPA, respectively) [16, 17]. FTD represents a common cause of dementia in subjects with less than 65 years. The age of onset is typically in the range of 45–65 years, with a mean average in the 50s, and the prevalence is equal among men and women [18]. Currently, several genes have been identified as FTD triggers: microtubule-associated protein Tau (MAPT), progranulin (GRN), valosin-containing protein (VCP), chromatin modifying protein 2B (CHMP2B), transactivator regulatory DNA binding protein 43 (TARDP), chromosome 9 open reading frame 72 (C9orf72), and triggering receptor expressed on myeloid cells 2 (TREM2). In this PhD thesis, the attention will be focused on TREM2 protein, the main responsible of the rare investigated frontotemporal dementia. Mutations in TREM2 may prevent the cell from making any TREM2 protein, or result in the production of an abnormally short and/or non-functional version of the protein. In all cases, impairment of the normal maturation of the protein interferes with phagocytosis and may therefore contribute to the pathogenesis of neurodegenerative diseases [19, 20]. A rare case of homozygous loss-of-function mutation in TREM2, have been associated with an autosomal recessive form of early-onset dementia, presenting bone cysts, too. This peculiar pathology, called Polycystic Lipomembranous Osteodysplasia with Sclerosing Leukoencephalopathy (PLOSL), or simply Nasu-Hakola Disease (NHD) [21] is the focus of this PhD dissertation.

1.1.1.1. Nasu-Hakola Disease (NHD)

Nasu-Hakola Disease (NHD) is a rare systemic disorder based on autosomal recessive transmission of inheritance, which is phenotypically manifested as a combination of neurological and bone symptoms. NHD is also popular under the name of Polycystic Lipomembranous Osteodysplasia with Sclerosing Leukoencephalopathy, or simply PLOSL (MIM 221770), according to its major clinical features. It takes the name from its first pioneers, the Japanese Nasu T. [22] and the Finnish Hakola H.P. [23]. In particular, the first ones that concurrently reported a case study of an unknown syndrome were Järvi et al [24] in Finland and Terayama et al [25] in Japan in 1961. But the phenothypic features were described in 1970 by

Hakola et al [26] studying some Finnish families. Few years later, Nasu et al [22, 27] reported the same disorder in Japanese patients. In the past decades, about 200 cases were reported worldwide, despite NHD is endemic in Japan [28–50] and Finland [51–62], it is also present in: Sweden [63], Norway [64], USA [65, 66], Colombia [67], South Africa [68], Austria [69], Turkey [70–73], Belgium [74], Tunisia [75], Germany [76–79], Lebanon [80], Iran [81], Greece [82] and Bolivia [66, 83]. The NHD incidence is higher in Finland ($2x10^{-7}$/years), whereas in Japan and in other nations is unknown [23].

- *Clinical aspects*

The pathogenesis of NHD is unknown, but the clinical history of patients is defined and consists of four sequential stages, identified as: i) latent ii) osseous iii) early neurological and iv) late neurological stages [84]. The latent phase is asymptomatic and begin during the adolescent period. NHD usually manifests the first symptoms approximately at the age of 20 years with the first bone swelling and pain, at level of body extremities. Before age 30 years, commonly, the patients manifest the first bone fractures, after minimal trauma; the breaks are due to development of cyst-like cavities filled with inhomogeneous content, among which lipid material and fat cells, at level of wrists, hands, ankles and feet, in addition to trabecular bone loss in the distal and of the long tubular bones. These fractures can be treated and heal well. In the fourth decade of the life (30-40 years), the NHD patients develop a full-blown picture of the frontal lobe dementia, with the first changes of personality. In particular, progressive loss of judgment and social inhibitions arise, concurrently to disturbances of concentration and mood (euphoria, moria, tendency to joke, depression), lack of insight and hallucinations. Moreover, faint loss of memory started; the first signs of motor neuron involvement (such as spasticity and Babinki’s sign) and disturbances of cortical functions (aphasia, agraphia and apraxia) add up. Urinary incontinence and impotence complete the clinical manifestations. The late neurological stage culminates with deep dementia, inability to walk and carry out the primitive reflexes. Death usually occurs by 45 years of age (Figure 2).

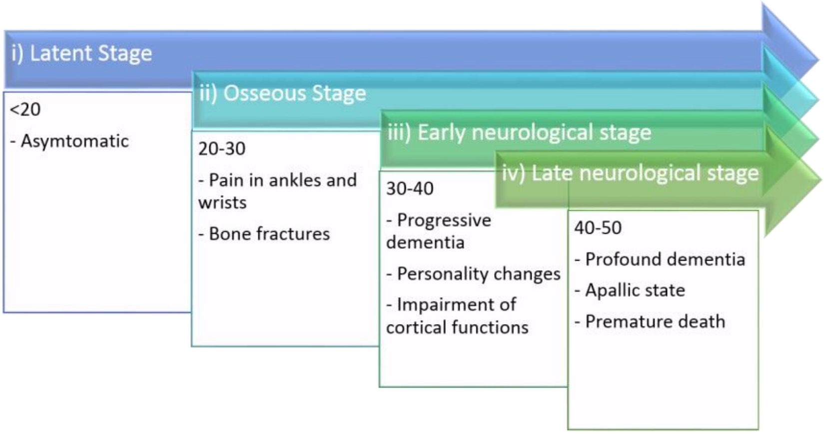


Figure 2. Natural course of Nasu-Hakola Disease.
NHD progression consists of four sequential stages i) latent ii) osseous iii) early neurological and iv) late neurological stages.

- *Genetic bases*

The genetic bases of NHD are related to several mutations arranged on two genes encoding different subunits of the same membrane receptor signaling complex (Figure 3a): the DNAX-activating protein 12 (DAP12, also named TYROBP) on the chromosome 19q13.12 and the Triggering Receptor Expressed on Myeloid cell 2 (TREM2) gene on the chromosome 6p21.1 [78]. According to the literature [66], different mutations occurring on these two components of the same receptor complex result in an identical disease phenotype and clinically identical symptoms of pathology. Of note, NHD shows its symptoms only in homozygous arrangement.

TREM2 is located in a cluster of TREM-immunoglobulin superfamily genes that also includes TREM1, TREML1 (TREM-like 1), TREML2, and TREML4 [85, 86]. TREM2 consists of 230 amino acid (aa) (~40 kDa) splitted into four domains: a 13-aa signal peptide followed by a 154-aa extracellular domain with two cysteine involved in an intra-chain disulfide bridge and a 33-aa transmembrane domain followed by a short 30-aa cytoplasmic segment. [87]. The majority of TREM2 mutations are found in the extracellular domain, suggesting that these mutations may affect the interaction between TREM2 and its ligands [88]. In the brain, TREM2 is exclusively expressed by microglia cells [89] where interacts with DAP12 to promote microglia activation and survival [90, 91] or phagocytosis [19, 92, 93]. The interaction between TREM2 and an unspecified anionic ligand (Gram-negative and -positive bacteria, heparin, dextran sulphate, HSP60, Plexin-A1, Semaphorin 6D, apoptotic cells Lypopolysaccharide (LPS) or Tumor necrosis factor (TNF)) [94–100] results in the phosphorylation of the intracellular tyrosin-based activation domain (ITAM) of his co-receptor DAP12 and subsequent cellular activation. However, the relevance of these ligands in the context of NHD or other neurodegenerative diseases is unclear. Studies in human and mouse cells demonstrated that the ITAM domain recruits Syk and/or ZAP-70 kinases to transduce downstream signals through the extracellular signal-regulated kinases (ERK), phosphoinositide3-kinase (PI3K), intracellular Ca^{2+} signaling, and actin reorganization pathways, leading to cellular activities including promotion of phagocytosis and NFAT (nuclear factor of activated T cells)-dependent transcriptional activation [101]. The list of human variants and the disease-linked mutations of TREM2 are reported in Table 1.

Mutation	Amino Acid Change	Disease	Type of mutation	ref
Gln33stop	Q33X	NHD	Nonsense	[71, 72, 102, 103]
Glu14stop	E14X	NHD	Nonsense	[80, 104]
Tyr38Cys	Y38C	NHD	Missense	[71, 72, 105]
Arg47His	R47H	AD/FTD/PD/ALS/PPA	Missense	[103, 105–111]
Arg62His	R62H	AD	Missense	[112]
Asp86Val	D86V	FTD/NHD	Missense	[71]
Asp87Asn	D87N	AD/FTD	Missense	[74, 105]
Thr96Lys	T96K	AD/FTD/PPA	Missense	[108]
Arg136Gln-Trp	R136Q-W	AD	Missense	[112]
Trp198stop	W198X	FTD/NHD	Nonsense	[67]
Leu211Pro	L211P	FTD/PPA	Missense	[108]
Leu205Pro	L205P	AD	Missense	[113]
Arg52His	R52H	AD	Missense	[112]
Gly58Ala	G58A	AD	Missense	[74]
Thr66Met	T66M	FTD	Missense	[72, 103, 105]
Trp78Stop	W78X	NHD	Nonsense	[66]
Frame shift	G90X	NHD	Deletion	[78]
Arg98Trp	R98W	AD	Missense	[105]
Frame shift	/	NHD	Deletion	[66]
Ala105Thr	A105T	PPA	Missense	[108]
Gly115Ser	G115S	AD	Missense	[114]
Ser116Cys	S116C	PPA	Missense	[103]
Val126Gly	V126G	NHD	Missense	[78]
Asp134Gly	D134G	NHD	Missense	[66]
His157Tyr	H157Y	AD/FTD	Missense	[74, 105]
Lys186Asn	K186N	NHD	Missense	[66]
Trp191stop	W191X	AD	Nonsense	[112]
Glu202Asp	E202D	AD	Missense	[112]
His215Gln	H215Q	AD	Missense	[112]
Gly219Cys	G219C	AD	Missense	[113]
Thr223Ile	T223I	AD	Missense	[112]
Ala28Val	A28V	PPA	Missense	[108]
Asp39Gly	D39G	AD	Missense	[74]
Asp39Glu	D39E	AD	Missense	[74]
Trp44Stop	W44X	NHD/FTD	Nonsense	[66]
Frame shift	/	NHD	Deletion	[78]

Table 1. List of TREM2's mutations.
NHD: Nasu-Hakola Disease; AD: Alzheimer's Disease; ALS: Amyotrophic Lateral Sclerosis; FTD: Frontotemporal Dementia; PD: Parkinson's disease; PPA: Primary Progressive Aphasia. (modified from Dardiotis et al. [82])

DAP12 is a 113 amino acidic protein consisting of a small extracellular region with a cysteine residue, a negatively charged transmembrane segment and a cytoplasmic ITAM domain [115]. DAP12 is expressed principally on immune cells, such as macrophages, monocytes and osteoclasts [95]. To date, several variants of DAP12 were identified as NHD-related mutations. Many of these alterations were associated to the reduction or complete loss of DAP12 function, but the mechanism that induces microglia dysfunction in NHD remains unclear.

TREM2-DAP12 co-expression is observed in different human tissues: Central Nervous System (CNS), microglia, pre-osteoclast and immune system, including natural killer (NK) cells, lymphocytes, macrophages and dendritic cells. Nevertheless, TREM2-DAP12 are expressed principally in myeloid cells; this cellular distribution of co-receptor indicated a role in microglia and osteoclasts, both specialized myeloid-derived cell types [116–118]. The data reported by Colonna et al. [119] demonstrate that TREM2 function is essential for normal osteoclastogenesis. TREM2-deficient mouse/human shown in vitro defect of osteoclast formation and accelerated osteoclastogenesis suggesting the inability of fusing into multinucleated osteoclast endowed with bone resorptive activity. As reported by Sessa et al. [118], in both human and mouse cerebral cortex, TREM2-DAP12 proteins, are strongly expressed by microglia and in a fraction of neurons, but they are not present in astrocytes and oligodendrocytes. Furthermore, in both neurons and microglia, the protein complex appeared to be located mostly intracellularly, above all in proximity of Golgi complex or inside it. Recently, Colonna et al [120] reported that TREM2 binds negatively charged lipid ligands, probably through the positively charged arginine residues (R+) that are present in its extracellular domain. Upon ligand binding, the DAP12 is tyrosine phosphorylated by the protein kinase SRC and recruits the tyrosine protein kinase SYK. SYK phosphorylates the adaptors LAT (linker for activation of T-cells family member 1) and/or LAT2, which in turn recruit various signalling mediators and adaptors, including phospholipase Cγ (PLCγ) (which degrades phosphatidylinositol-3,4,5-trisphosphate (PIP3) into inositol trisphosphate (IP3) and diacylglycerol (DAG)), lymphocyte cytosolic protein 2 (LCP2; also known as SLP76), protooncogene vav (VAV1), growth factor receptor-bound protein 2 (GRB2) and members of the son of sevenless homologue (SOS) family. Ultimately, these pathways lead to Ca2+ mobilization, activation of protein kinase Cθ (PKCθ), activation of the RAS–ERK pathway and actin remodeling (Figure 3b).

It is undeniable that the combination of dementia and cyst-like osseous lesions is truly unique. From a genetic point of view, although the different DAP12-TREM2 mutations of NHD patients are well known [66], the precise molecular mechanism and the relationship between neuro- and bone-involvement in NHD progression are not yet understood.

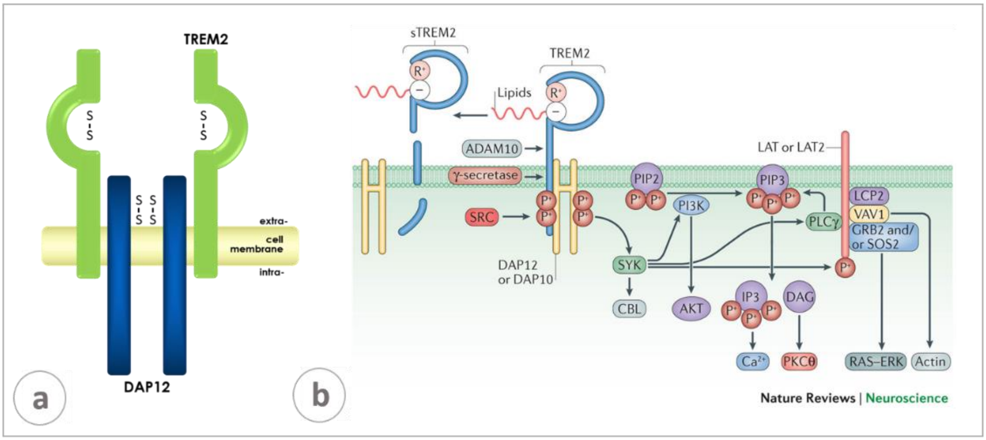


Figure 3 TREM2-DAP12 co-receptor.
a) TREM2-DAP12 membrane receptor signaling complex. b) TREM2-DAP12 signaling pathway. TREM2 binds negatively charged lipid ligands that are present in its extracellular domain. Upon ligand binding, DAP12 is tyrosine phosphorylated by the protein kinase SRC and recruits the tyrosine protein kinase SYK. SYK phosphorylates the adaptors LAT and/or LAT2, which in turn recruit various signalling mediators and adaptors, including PLCγ, LCP2; VAV1, GRB2 and members of the SOS family. These pathways lead to Ca2+ mobilization, activation of protein kinase Cθ (PKCθ), activation of the RAS–ERK pathway and actin remodeling. (Modified from Colonna et al. [120]).

- *Phenotypic expression of NHD*

Nasu-Hakola Disease is phenotypically characterized by simultaneous impairment of nervous and skeletal systems. Although the localization of the cells involved in this pathology is very different (brain and bones), they share a common myeloid-lineage progenitors. The etiology of the NHD must be investigated starting by microglia and osteoclast cells.

Microglia represent the resident innate immune cells of the Central Nervous System (CNS). Microglia are professional phagocytes of the brain guided by “eat-me” and “don’t-eat-me” signals. In particular, phagocytosis events are triggered by receptors such as TLRs, which recognizes the microbial pathogens, and TREM2 which binds apoptotic debris [121]. The expression levels of TREM2 in microglial cells were found to differ not only from region to region but also within each region [122] likely due to the capacity of the microenvironment to induce specific microglial phenotypes. These findings could explain the reason for which microglia is activated only at the level of fronto-temporal lobe in FTDs. The result of microglia activation is the production and secretion of cytokines that include ILs, interferons, tumor necrosis factors (TNFs), CSFs and TGFs, principally involved in cellular communication and growth, regulating inflammation, immune responses, survival and differentiation. In Nasu-Hakola Disease, microglia are strictly related to the inhibition of the apoptotic neuron clearance. It is possible to speculate that in NHD, amyloid stimulated TLR activation is disinhibited, with consequent excessive microglial activation and reduced ability to phagocytize amyloid deposits or apoptotic neurons [121].

Osteoclasts (OCs) are the co-protagonists of the medical NHD history. They play a role in bone-resorbing processes, making and secreting digestive enzymes that break up or dissolve/absorb the damaged bone tissue. As reported above, OCs also express the TREM2-DAP12 co-receptor. In NHD, mutations associated to this receptor lead to excessive osteoclast activity, loss of trabecular bone tissue and fracture development. To determine the potential role of the TREM-2/DAP12 complex in osteoclast function, studies were performed in human TREM-2- and DAP12-deficient osteoclasts in vitro and in DAP12- deficient mice both in vitro and in vivo [123, 124]. In culture conditions, blood monocyte derived from TREM2- or DAP12-deficient patients were unable of fusing into multinucleated osteoclasts endowed with bone resorptive activity [65, 104]. Humphrey et al [124] showed the role of TREM2/DAP12 signaling in OCs differentiation and function by direct stimulation or blockage of TREM2. The results indicated that TREM2 is necessary for OCs formation in vitro, and it regulates both OCs resorption and migration. Taken together, these data suggest that TREM2 is required for successful osteoclastogenesis.

Unfortunately, the reasons that lead to an involvement of these specific cells, also through the mediation of other cellular types expressing the same co-receptor, is still unclear.

- *Diagnosis and therapy*

Actually, the diagnosis of NHD consists of neuroradiological and neuropathological examinations. If the family pedigree is unknown, genetic investigation is performed successively to appearance of the first symptoms.

Kenechi Nwawka et al [125] described the radiographic, Computed Tomography (CT), Magnetic resonance imaging (MRI), and histopathologic skeletal findings that occurs in a case of membranous lipodystrophy. The authors highlighted the importance of brain and bone imaging for an appropriate clinical management of NHD manifestations, because the identification of abnormalities in this districts allowed to fulfill an appropriate clinical care and genetic counseling to the patients.

Ohtani et al [126] reported a case in which NHD was diagnosed through X-ray of the body extremities of the subject. The author asserted that X-ray is a very useful tool for diagnosing NHD, even in patients without obvious bone symptoms. Obtaining X-rays of the both extremities may help to diagnose early-onset frontotemporal dementia.

To investigate the personality disorders of NHD patients, Ilonen et al [127] tried to apply Rorschach protocols for NHD diagnosis. The personality profile of the eight analyzed NHD patients was similar to frontal personality disturbance, and was in line with clinical findings. The data presented by Ilonen et al confirmed the previous study of Stuss et al. [128] who reported that frontal lobe disturbances tend to have repercussions throughout the behaviour.

Pre-mortem molecular diagnosis of NHD requires genetic analysis of both DAP12 and TREM2, in which 20 distinct NHD-causing mutations have been reported. Due to genetic heterogeneity, it is often difficult to identify the exact mutation responsible for NHD. Recently, the next-generation sequencing (NGS) technology was evaluated as approach for the diagnosis of several Mendelian pathology, including NHD [129], but this tool results too much expensive and time-consuming.

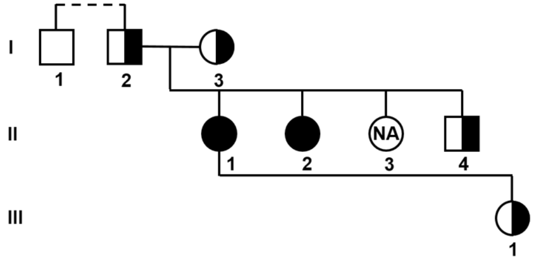
Currently, no therapy that can stop illness progression is applicable. Orthopedic ankle surgery as well as supportive orthopedic devices may be of value in individual cases. Symptomatic medication can be useful to control abnormal behaviour and the use of appropriate antiepileptic medication is important since epileptic seizures may worsen the patient’s condition [130]. In light of this, a deeper investigation of the molecular mechanisms involved in the disease progress is mandatory to develop a personalized therapy.

- *The Italian cases*

Up to now, only 7 reports of NHD cases are reported in Italian families, with accurate clinical and instrumental descriptions [20, 66, 102, 130–139]. These subjects belong to only 3 families principally localized in the northern Italy.

The Italian family considered in this proteomic investigation is composed by two NHD patients (Ho, II1-II2), four healthy carriers with heterozygous mutation (He, I2,I3,II4,III1) and one healthy subject (Wt, I1) (Figure 4).

Disease subjects expressed a homozygous C to T loss-of-function mutation at position 97 in the exon 2 of the TREM2 gene. The complete medical picture of this family was reported by Soragna et al. [102, 137].



SUBJECTS	GENDER	AGE (years)	NHD PHENOTYPE
I1	M	n/a	no
I2	M	73	no
I3	F	70	no
II1	F	45	yes
II2	F	33	yes
II4	M	43	no
III1	F	21	no

Figure 4. Pedigree of the Italian family affected by Nasu-Hakola Disease.
Black symbols denote mutant homozygote subjects (Ho), white symbols denote wild type homozygote individuals (Wt) and half black symbols denote the heterozygote subjects (He). NA: not available; I, II, III: three generations chart.

1.1.2. Choice of biological sample

A crucial step in the study of a rare pathology is represented by the availability, the choice, the quality, and the extraction procedure of the starting material (Figure 5). Although several tissues or body fluids are suitable for investigations of neurodegenerative diseases, the biomaterial of election should reflect CNS processes, minimize variability and invasiveness, and improve diagnostic accuracy [1]. Being the implication of insoluble protein aggregates in the majority of neurodegenerative diseases [140], brain tissue is expected to be the optimal source to investigate these neuro-pathologies. Of course, practical and ethical issues of ante-mortem brain biopsies restrict the collection of brain specimens to postmortem tissues. This latter procedure, implies the impossibility to investigate early aetiologies, the possible impairment of proteins for degradation and the increased medical case complexity for the presence of comorbidities (see cases of tissue donation). A valid alternative to brain specimens is represented by cerebrospinal fluid (CSF), thanks to its brain proximity and direct contact with CNS. A not negligible disadvantage for CSF sampling is the invasiveness of sample collection that requires a lumbar puncture, only feasible by medical personnel, with patient discomfort and some health risks. Moreover, blood contamination, as well as physiological variables related to circadian variation, changes with age/gender and alteration by medications, have a great impact on the CSF composition [141]. Urine is another body fluid very useful because it can be obtained in great quantity and, being its collection not invasive, it does not require a medical staff. At the contrary, urine contains a low quantity of brain-related proteins and a high amount of salts, requiring a desalting steps [142, 143]. Given the high vascularization of salivary glands and the high content of proteins derived from blood, also saliva recently gained attention for CNS studies [144]. Recently, several facts supported the notion of a “brain-skin axis” in which biochemical changes in the brain are mirrored in peripheral tissues such as skin [145]. Since 1997, Idoate Gastearena et al used skin biopsies to diagnose NDs [146], but the development of skin fibroblast-based assays for NDs remains an active research area [147]. To bypass direct human sampling, animal models have been considered, although these can be unsatisfactory because they may only partially reflect the complexity of human condition [143]. Nevertheless, blood and its subcomponents are the most commonly used biological materials, easier and safer to obtain than other sample sources. Thus they are considered a valid alternative to brain tissue for the study of NDs [148]. Taking into account the latter aspect, together with the rarity and the impossibility of frequent sampling of NHD patients, a sub-group of cells derived from blood were selected and immortalized to be investigated in this PhD work for the first comprehensive NHD proteomic study. In particular, Lymphoblastoid B-cells were chosen, considering their advantages and growing popularity in personalized medicine research [149].

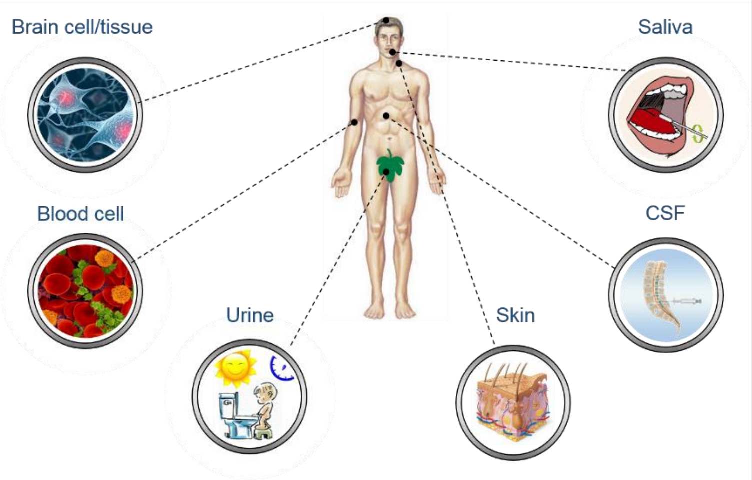


Figure 5. Overview of biological sample sources for NDs studies.
Several tissues or body fluids are suitable for investigations of neurodegenerative diseases, such as brain tissue, blood and its subcomponents, urine, skin, CSF and saliva.

Lymphoblastoid B-cells lines (LCLs) were obtained by in vitro EBV-immortalization of Lymphocite B-cell [139]. In spite of Nasu-Hakola Disease manifests its symptoms through the microglia and the bone cells, LCLs represent a valid alternative to them. As previously described in our work [139], the reasons to utilize LCLs were the following i) the possibility of having sufficient biomaterials for multiple LC-MS/MS analyses; ii) avoid the need of patient resampling, especially when the subjects death; iii) identification of TREM2 mutation in LCLs by PCR analysis; iv) the setup of a non-invasive method for diagnostic or research purpose, because the access to central nervous tissue is practically not available. Thus, despite some inherent limitations, LCLs are increasingly recognized as important resource for genetic and functional research of neurological disorders. Recently, Mori et al investigated TREM2 expression level in leukocytes of patients with AD and schizophrenia, founding an increase in both neuropathologies [150].

1.1.3. Limitations of the study

It is probably fair to say that a limitation of the present study is the sample size of individuals examined. It is important to note that the NHD spread in Europe (as by the Orphanet Report Series, Rare Disease Collection, dated November 2013 - http://www.orpha.net) is of 0.15/100.000. The prevalence in Japan and Finland, the two countries in which the majority of patients is confined, is of 0.2/100.000 and 1/100.000, respectively. The fact that no more than 200 cases have been identified worldwide, points to NHD as a very rare disease. By a systematic survey of the literature, only three families (one of which decided to preserve its incognito) have been diagnosed for this disorder in Italy [138]. Thus, patients analyzed in this study, while being around 3% of total cases in the world, represent more than 50% of all Italian cases described so far. Moreover, this study involved the largest NHD family ever investigated and the only one for which genetic and radiological analyses of all components have been performed. In addition, the fact that all of patients originate from the same family, no matter how large the cohort is, makes this set of samples very uniform and represents a strength of the work although, of course, it is clear that more evidences will have to be produced. Moreover, as previously mentioned, another limitation of this study is the choice of Lymphocite B-cells to investigate a pathology that manifests its symptoms in districts very different from blood (brain and bones). But, as stated before, given the rarity of the pathology, the difficulty to recruit patients and to withdraw samples from subjects with advanced states of disease, the choice of the starting material is often obligated. Nevertheless, it’s important to note that together with human induced pluripotent stem cell (iPSC)-derived neurons, human lymphoblastoid cell lines (LCLs) are employed in biomedical research for decades and they are increasingly being adopted as in vitro research tool on personalized medicine in brain diseases [137]. Surely their use brings both advantages and limitations. The preparation of human LCLs is simple, inexpensive and very reliable and could derive from a large number of peripheral blood lymphocytes, resulting in a polyclonal nature of cell lines. In fact, they can be maintained in continuous in vitro growth over many months and their genome remain stable during subsequent cell divisions. Moreover, the EBV genome used for LCL generation remains in the cytosol without incorporation into the germ-line genome of the cell. On the basis of these properties, LCLs are considered the best research tools for comparing cohorts from diseased vs healthy, including their proteome and in vitro phenotype, allowing new insights into disease pathophysiology and providing consistent data at lower research costs. In addition, the very reproducible findings obtained with their employment make it possible biomarker discovery even with smaller cohorts, impossibility of frequent sampling of NHD patients and when funds are limited. On the other hand, a pitfall is due to the fact that these cells have a B-lymphocyte phenotype. Based on these premises, the decision to utilize LCLs was guided on the hand by the interest of developing a non-invasive sampling method for neurodegenerative studies, on the other by the proof that LCLs express the homozygous mutation on the TREM2 gene (Figure 6), as reported by Giuliano et al [139].

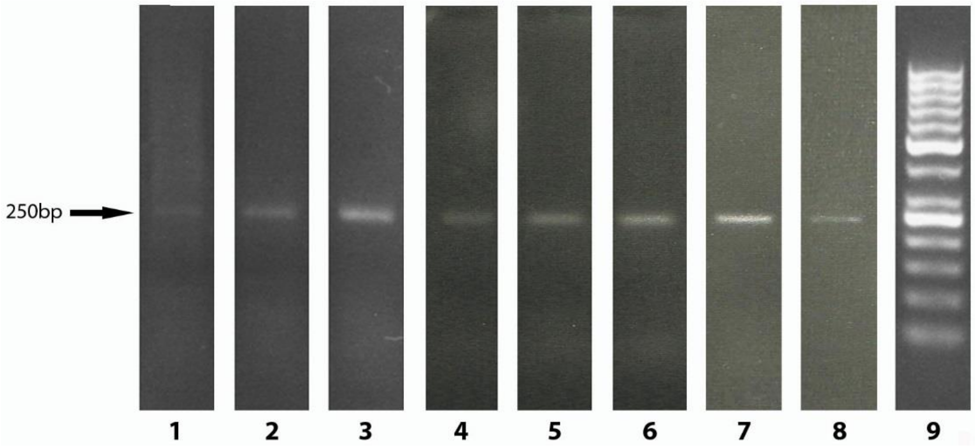


Figure 6. PCR amplification of TREM2 gene.
PCR amplification of cDNA from Hela cells (lane 1, positive control); wild type homozygote (lane 2); all patients considered in Giuliano et al. study (lane 3→8) and 250 bp DNA ladder (lane 9). The arrow indicates the position of TREM2 [139].

1.2. Proteomics

At the end of the last century, a new term was publicly announced during a small meeting held in Italy by the PhD student Marc R. Wilkins: “proteome”. The term was coined to explain with a single word the definition “PROTEin complement of the genOME”. As is common knowledge, the proteome of a living system is a dynamic entity that changes during the organism development (including post-translational modifications and alternative splicing) and under the influence of environmental conditions, thus increasing its complexity. It can be defined as a “snapshot” of the biochemical phenotype of an organism.

The complex of advanced technologies applied to investigate the proteome takes the name of “Proteomics”. Despite Genomics, it represents a different way to deal with biological complexity, because genes are only the "recipes" of the cell, while proteins are the functional players that drive both normal and disease physiology. Proteomics is a large-scale comprehensive study of a specific proteome, including information on protein abundances, their variations and modifications, along with their interacting partners and networks in order to deepen the knowledge of cellular processes.

Proteomics is a relatively young discipline [151]. It is having a tremendous impact on modern life sciences and biomedicine, also because more than other global -omics approaches, it allows to investigate the molecular mechanisms underlying physio- and/or pathological states. Sure enough, the impact of proteomics does not affect only technological aspect, but it also involves the approach itself to biological studies, because it has paved the way for new strategies that identify proteins as potential therapeutic agents and biomarkers of diseases and stress due to external stimuli at much reduced time and cost [152].

Actually, the proteomic studies are mainly focused on three main areas:

1. Expression Proteomics, that includes the qualitative and quantitative analysis of the protein expression levels concerning the homeostasis cellular changes (e.g. cellular stress, pathological conditions, different growth states, etc.) in a cell, tissue or biofluid.

   Expression proteomics can in turn be divided into Systemic or Post-Translational Modification Proteomics and Differential Proteomics. The first one concerns the identification and the study of post-translational modified proteins, notably that those undergo phosphorylation (phosphoproteomics), methylation (methylproteomics) or glycosylation (glycoproteomics). The second one deals with the quantification of the protein expression levels under different physiological states (e.g. healthy versus diseased subjects, or drug- and toxin-treated subjects).
2. Functional Proteomics, that includes the study of the protein functions, the signaling pathways and the protein interaction networks.
3. Structural Proteomics, that consists of a study of 3D structures and dynamics of proteins complexes.

1.2.1. Expression Proteomic

Early traditional expression proteomic studies began developing and cataloging lists of the entire cellular protein repertoire. The research that underpinned the start of the exploration of the whole human proteome started in 2003 by the non-profit organization Knut and Alice Wallenberg Foundation (KAW) [153]. It began “the Human Protein Atlas program”. In 2005, the first version of the Human Protein Atlas (www.proteinatlas.org) was released with protein profile data based on immunohistochemistry on tissue microarrays covering 48 different human tissues and organs, including kidney, liver, heart, brain and pancreas [154]. An important objective of the project was to integrate this database with other -omics databases covering genomics, transcriptomic, proteomics and metabolomics data. In particular, data from several proteomic platforms, including yeast two-hybrid screens, mass spectrometry, peptide/protein arrays, immunohistochemistry, western blots, co-immunoprecipitation and fluorescence microscopy–type experiments (with a total of >1.8 million peptides and >4 million MS/MS-spectra deposited) contributed to increase the knowledges [155]. This large-scale analysis of the protein expression profiles of human proteome is a classic example of expression proteomics. Certainly, the expression proteomics is not limited to this, but it includes even more applications. Primarily, can be mentioned the comparison of the protein expression levels of a biological system under different conditions: physiological or pathological states, disease stages, drugs treatment, etc. Moreover, the application of proteomics in clinical diagnostics is steadily increasing, with the aim to discover disease biomarkers that can be used to improve the accuracy and the rapidity of the diagnosis.

1.2.2. Mass Spectrometry for Proteomics

The “proteomic revolution” would not have been possible without the technological improvements achieved in the last decade mainly in the fields of separation and identification techniques and bioinformatics tools. Among them, certainly a decisive role has been played by the employment and advancement of Mass spectrometry (MS).

Mass spectrometry is the most comprehensive and versatile tool used in large-scale proteomics [156]. Nowadays, on the base of its power and versatility, it is considered a complete “biochemical laboratory” at the disposal of chemists and biologists [157]. In fact, simultaneously with the availability and development of technical options, increasingly proteomics applications came to light (Figure 7).

Figure 7. Timeline showing important advances in mass spectrometry over the last century.

Instrument developments are marked in blue, applications of mass spectrometry are reported in gray and general scientific achievements in green [158].

It can be inferred that the wide field of protein identification strategies to be applied. Fundamentally, the main proteomics strategies can be classified into two big branches: “Peptide-centric or Bottom-up” and “Protein-centric or Top-down” strategies (Figure 8). The first one is considered the most popular method for the analysis of high-complex samples. This approach consists of proteolytic digestion of proteins into its peptides before mass spectrometry analysis; peptide masses and/or the ion signals of their corresponding sequences are used to identify related proteins by means of database search. These measurements can be based on several approaches:

- Peptide-mass fingerprinting, in which a protein is digested with a protease to a unique set of peptides. The molecular mass of each peptide is accurately determined. All entries in a protein database are virtually treated with the same protease to provide a list of theoretical peptide masses. The matching between the measured mass of a peptide with the theoretical peptide masses in the database will identify the protein that was the precursor of the target peptide.

- Peptide sequence tags is similar to peptide-mass fingerprinting but with a fundamental difference: the observed fragment ion pattern is matched with the predicted patterns of fragment ions of peptides derived from all protein entries in the database. An example of peptide sequence tags is represented by multidimensional protein identification technology (MudPIT). Briefly, the entire proteome is tryptic digested and analyzed directly with an online 2D-LC–ESI–MS/MS system to obtain the molecular mass and amino acid sequence ions pattern of the eluting peptides. The sequence ions data are correlated with the simulated fragment ions pattern obtained from *in-silico* tryptic digestion of all protein entries in a protein database or of all translated protein entries in a given database. For further details, see Paragraph 1.2.4 – “Multidimensional Protein Identification Technology (MudPIT)“.

- Accurate mass tags can be obtained with FT-ICR instruments, because high degree of mass accuracy is needed. In particular, the mass of a peptide fragment is measured with <1 ppm accuracy, therefore the mass of a single unique peptide becomes a unique identifier of the protein. It is applied to *de-novo* peptide sequencing, too.

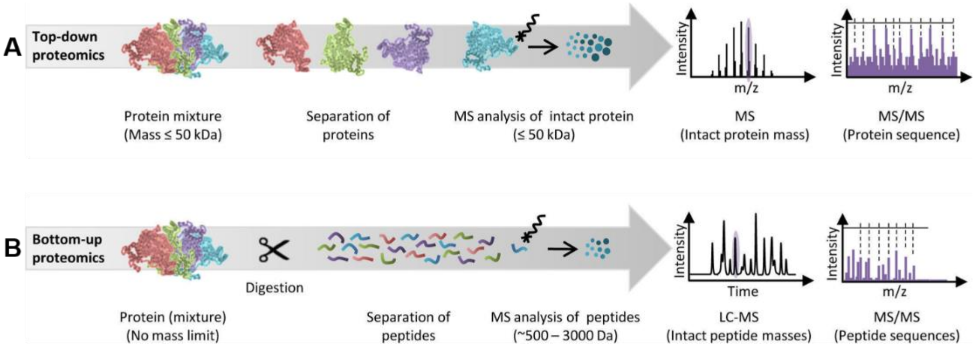


Figure 8. “Peptide-centric or Bottom-up” and “Protein-centric or Top-down” strategies in MS-based proteomics (modified from Switzar et al. [159]***).***

Top-down or protein-centric strategies, instead, are based on the analysis of undigested biomolecules. Usually, the sample is directly injected into the mass spectrometer and, based on the sample preparation procedures, it is possible to obtain information about conformation and shape of analyzed protein; about the protein isoforms or the post-translational modifications (PTMs). For these reasons, the choice to prefer one strategy to another, depends on the purpose of the proteomics study.

1.2.3. Shotgun Proteomics

The concept of proteome analysis is simple, but its execution is challenging, primarily owing to the complexity of any given proteome. For this reason, most of proteomic studies employ the coupling of multiple analytical methods that are able to reduce biospecimen complexity (separative techniques) and identify them (identification techniques).

In fact, a typical protocol for proteome analysis (Figure 9) usually follows these essential steps: (1) sample preparation, (2) proteins cleavage, (3) complex mixture separation, (4) mass spectrometry analysis and (5) database searching.

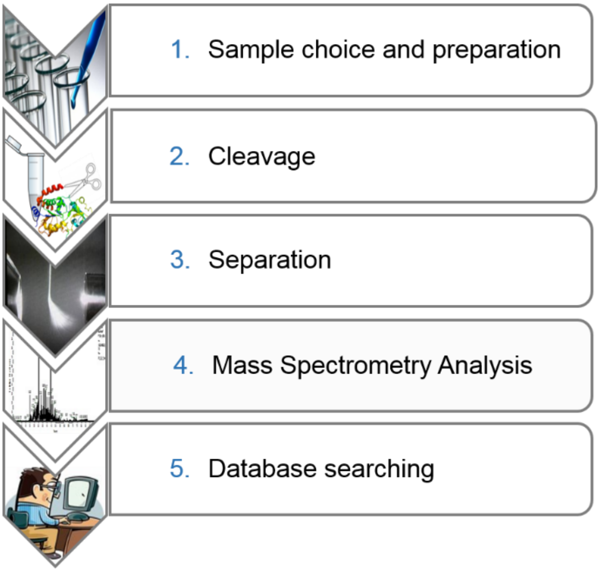
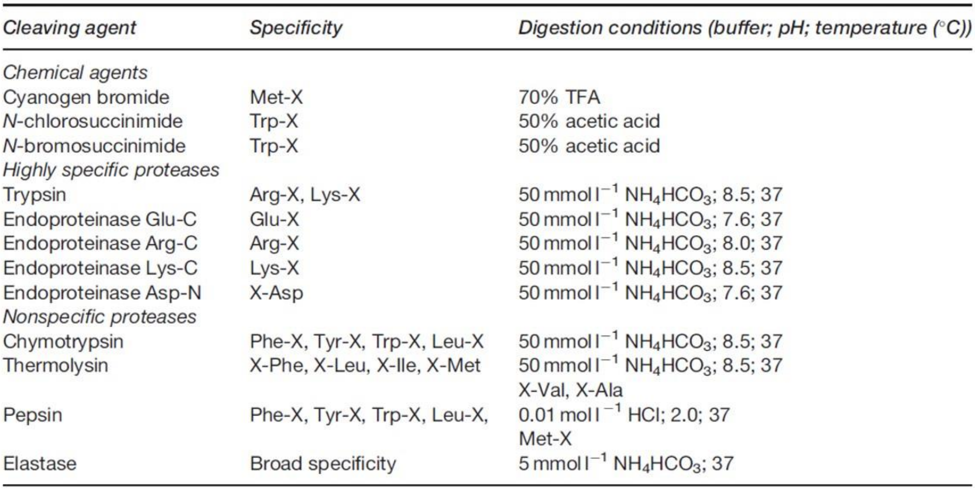


Figure 9. Typical Proteomics Workflow.
Protocol for proteome analysis consist of five main steps: sample preparation, cleavage of proteins, separation of a complex mixture, mass spectrometry analysis, and database searching.

<u>Sample preparation.</u> Briefly, the biological sample must be processed so that proteins can be extracted with high efficiency; to this end, to solubilize membrane proteins, sample is treated with suitable lysis buffer that contains detergents (e.g., SDS, CHAPS, Tween, MS-compatible detergent Rapigest®); to disrupt protein–protein interactions denaturing agents (urea or acids) are used; to reduce disulfide bonds, sample is treated with reducing agents (2-mercaptoethanol or dithiothreitol, DTT); to digest nucleic acids, carbohydrates and lipids, several enzymes (DNase, RNase) can be added;

protease inhibitors cocktails can be used to prevent proteolysis of proteins. Moreover, clean-up passages are indispensable to remove MS-incompatible detergents, buffers or salts. The choice of the best protocol depends on the kind of sample and technology that will be chosen. Often, protein enrichment can be necessary in order to isolate specific subclasses of proteins. To enrich low-abundance proteins, fractionation of the whole lysate into distinct organelles (e.g., nuclear membrane, mitochondria, cytoplasm, etc.) by differential centrifugation, density gradient centrifugation or pre-fractionation of the sample with free-flow fractionation (FFE) can be applied [160, 161].

Protein Cleavage. The cutting of proteins into smaller peptides is a necessary step because current mass spectrometry instruments are equipped for the analysis of small peptides with respect to accuracy, sensitivity, and tandem MS capability. With current instruments, the useable data can be obtained from peptides with a chain length of 6–20 amino acids. A diverse collection of chemical reagents (to hydrolyze) and endo-proteases (to digest) with broad specificity is available for protein cleavage (Table 2).



Cleaving agent	*Specificity*	*Digestion conditions (buffer; pH; temperature (°C))*
Chemical agents		
Cyanogen bromide	Met-X	70% TFA
N-chlorosuccinimide	Trp-X	50% acetic acid
N-bromosuccinimide	Trp-X	50% acetic acid
Highly specific proteases		
Trypsin	Arg-X, Lys-X	50 mmol l^{-1} NH_4HCO_3; 8.5; 37
Endoproteinase Glu-C	Glu-X	50 mmol l^{-1} NH_4HCO_3; 7.6; 37
Endoproteinase Arg-C	Arg-X	50 mmol l^{-1} NH_4HCO_3; 8.0; 37
Endoproteinase Lys-C	Lys-X	50 mmol l^{-1} NH_4HCO_3; 8.5; 37
Endoproteinase Asp-N	X-Asp	50 mmol l^{-1} NH_4HCO_3; 7.6; 37
Nonspecific proteases		
Chymotrypsin	Phe-X, Tyr-X, Trp-X, Leu-X	50 mmol l^{-1} NH_4HCO_3; 8.5; 37
Thermolysin	X-Phe, X-Leu, X-Ile, X-Met	50 mmol l^{-1} NH_4HCO_3; 8.5; 37 X-Val, X-Ala
Pepsin	Phe-X, Tyr-X, Trp-X, Leu-X,	0.01 mol l^{-1} HCl; 2.0; 37 Met-X
Elastase	Broad specificity	5 mmol l^{-1} NH_4HCO_3; 37

Table 2. List of protein cleaving reagents [152]***.***

Trypsin is more or less a universal choice for most applications. It cuts an amide bond on the C-terminal side of lysine and arginine residues and produces smaller peptides that contain a basic residue at the C-terminus, except for the C-terminus of the protein. This aspect is especially useful for the Electrospray Ionization (ESI) process and for subsequent sequencing by tandem mass spectrometry [162].

Separation techniques. Proteomic analysis involves the study of complex protein or peptide mixtures and therefore a separation step prior to MS analysis is advantageous to simplify the mixtures and to identify its components. Moreover, the identification of low-abundance species is tightly linked to a better separation technique, because these molecules would be overshadowed by higher abundance signals. Several properties of proteins/peptides, such as shape, charge, hydrophobicity, and affinities for other molecules, are exploited to achieve optimal separation. The separation techniques widely used in proteomics are mainly *gel-based* or *gel-free*: mono-dimensional gel electrophoresis (1-DE), two-dimensional gel electrophoresis (2-DE) for the first approach and mono-dimensional liquid chromatography (1D-LC) and two-dimensional liquid chromatography (2D-LC) for the second one. *Gel-based* electrophoretic methods, introduced by O'Farrell and J.Klose in 1975 [163, 164], represent the traditional approach used in proteomics studies [165]. *Gel-based* approach appears to be a powerful method for the analysis of complex protein mixtures, but conceal some limitations. The main issues are primarily represented by i) the (low) reproducibility of the gels; ii) the low resolution power that leads to a difficult separation of hydrophobic membrane-bound proteins and pI extreme proteins; III) low dynamic range and staining sensitivity (detection limit of about 100 ng). In light of this, *gel-based* approach, while being useful for small-scale research investigations, is not adequate for projects that involve screening of a large number of samples. To overcome the limitations of 1- or

2-DE technology, *gel-free* liquid chromatography–based approaches have taken hold. In particular, liquid chromatography is practiced in the following formats:

- Adsorption chromatography, in which the stationary phase consists of a high-surface-area solid adsorbent; the solutes physically adsorb on the stationary phase, while the liquid mobile phase allows the elution of them. The adsorption can be based on different properties of the molecules. As example, in hydrophobic chromatography (HIC), the reversible adsorption of biomolecules is carried out according to their hydrophobicity. This separation, also named Reverse-Phase Chromatography (RPC), consists of a stationary hydrophobic phase with a strong affinity for hydrophobic molecules in the mobile phase, which bind (or "adsorb") to the column. The hydrophilic molecules pass through the column and are eluted first. Increasing the polarity of the mobile phase, molecules linked to the column can be eluted.
- Partition chromatography that involves the distribution of the solutes between a liquid stationary phase and a liquid mobile phase.
- Ion-exchange chromatography, used for ionic solutes, involves competition for solute ions between immobilized ionic sites on the stationary phase (strong anion- or cation-exchange resin, SAX or SCX) and liquid mobile phase.
- Size-exclusion chromatography that consists on the separation of the solutes on the basis of their size. The stationary phase is a polymer matrix of various pore sizes and solutes are separated according to their ability to penetrate the polymer matrix.
- Affinity chromatography, based on specific interaction between one type of solute molecule and a second complementary type of molecule that is immobilized on a solid support.

The most commonly types of LC materials used in Mass Spectrometry-based proteomics are: reverse phase, ion-exchange, hydrophilic interaction and affinity chromatography. Of note, these formats can be coupled in order to increase the loading capacity and to gain a superior fractionating power. These combinations take the name of “multidimensional” separation technologies [166] (see paragraph 1.2.4 – “Multidimensional Protein Identification Technology (MudPIT)”).

Independently from the chromatographic method adopted, the eluted species were acquired and analyzed by the selected identification tool, in most cases represented by MS, as stated before.

Mass Spectrometry Analysis. MS is an analytical technique that measures the mass-to-charge ratio (*m/z*) of individual compounds and atoms by converting them into charged gas-phase ions. Three basic steps are involved in a mass spectrometric analysis:

1. *Ionization*. Analyte molecules or atoms are converted into gas-phase ionic species, using the removal or addition of an electron or proton;
2. *Isolation.* Under high vacuum, molecular ions and their charged fragments are isolated in turn and mass analyzed on the basis of their *m/z* ratios;
3. *Measurement.* The ion current due to these mass-separated ions is measured, amplified, and displayed in the form of a mass spectrum.

Briefly, what is the “itinerary” of the analytes? Afterwards the separation of the complex mixture by liquid chromatography, the analytes are transformed into gaseous ions in the ion source. After ionization, the charged analytes are transferred into the high vacuum regions of mass spectrometer; at this point, the ions pass through several electric and/or magnetic fields, which allow them to be mass-selected, activated and separated from the remaining neutral molecules. At the end of the way, the *m/z* ratios of the analytes are measured by a mass analyzer and recorded by a detector.

The development of electrospray ionization (ESI) [167] and matrix-assisted laser desorption/ionization (MALDI) [168], two ionization sources capable of ionizing peptides or proteins, allowed a revolution in the MS-based protein analysis. Both MALDI and ESI are soft ionization techniques in which ions are created with low internal energies and thus undergo little fragmentation in source.

In MALDI, samples are co-crystallized with an organic matrix on a metal target. A pulsed laser is used to excite the matrix, which causes rapid thermal heating of the molecules and eventually desorption of ions into the gas phase. Because of the usage of a pulsed laser, MALDI produces packets of ions rather than a continuous beam.

Unlike MALDI, the ESI source produces ions from solution, so it can easily be interfaced with liquid separation methods. ESI is based on spraying an electrically generated fine mist of ions into the inlet of a mass spectrometer at atmospheric pressure. Electrospray ionization mass spectrometry (ESI-MS) is a technique that uses high voltage (2-6 kV), applied between an emitter and inlet system of mass spectrometer, in order to generate ions from an aerosol of charged liquid droplets (Taylor cone). Traditionally, commercial ESI mass spectrometers utilize flow rates from tens of microliters-per-minute (10 μL/min) to milliliters-per-minute (1 mL/min). Because of the relatively large volume of liquid exiting from the emitter, aerosol formation must be assisted by pneumatic nebulization and/or by thermal heating in the effort to obtain a stable spray. This requirement is especially pronounced for highly aqueous liquids. An important advance in the application of ESI techniques was the reduction in the flow rate of the liquid used to create the electrospray, leading to more efficient creation of ions, i.e., nanoelectrospray [169, 170].

Nanospray-ESI is a development of ESI that improves the method's sensitivity, spraying very low amounts of very low concentrated samples (nmol/mL). This increased performance is the result of lowering the inner diameter of the spray needle and reducing potentials normally applied in ESI. When the flow rate is reduced to nanoliters-per-minute (nL/min), droplet formation occurs more readily, requiring only the applied voltage to generate spray. No sheath gas or additional heat is required. Consequently, the stability of spray, and therefore signal, at the lower flow rates is typically improved for aqueous or "salty" mobile phases. Moreover, the efficiency of ionization improves as the flow rate is lowered because less volume of mobile phase passes through the emitter, producing smaller aerosol droplets. Furthermore, the advent of nanospray-ESI allows the coupling of the mass spectrometers with nanoLC separation methods, decreasing the amount of required sample and enhancing the sensitivity.

After ionization, under high vacuum, the molecular ions and their charged fragments are separated and mass analyzed on the basis of their *m/z* ratios. This task is performed by different kind of mass analyzers. The choice of the best mass analyzer take place on the basis of mass resolving power, accuracy and scan speed required. For further details, see Paragraph 1.2.5 - "MS Instrumentation".

Database searching. A final step in the proteome analysis consist of database search with the acquired MS and MS/MS data. The molecular masses and fragment ions of peptides acquired in the experimental procedure are matched against the theoretical ones created by *in-silico* digestion of each protein entry in the database with the specific protease that was used in the experimental procedure (e.g. Trypsin). Several free or commercial algorithms that automatically perform this matching between MS/MS sequence ion data and protein sequences have been developed: SEQUEST, MASCOT, ProFound, MS-Tag, PeptideSearch, X1Tandem, OMSSA, Parallax, DBDigger, GlobalLynx, and Spectrum Mill [171]. More details will be discussed in Chapter 1.3 "Bioinformatics Tools".

1.2.4. Multidimensional Protein Identification Technology (MudPIT)

As mentioned in the previous paragraph, the possibility of relying on liquid chromatographic separation or not is a very critical point when the peptide mixtures are very complex. Moreover, in the 90's, thanks to the improvement in separation strategies, mainly represented by the advent of multidimensional chromatography, a several-fold increase in dynamic range separation was achieved. In fact, in 1997 Opiteck et al. [172] first reported the combination of multidimensional separation approach with mass spectrometry to separate *Escherichia coli* proteins. During the following years, different approaches were developed to combine these separation methods with new “soft” ionization techniques for mass spectrometry, such as MALDI and ESI. In particular, nanospray ionization in combination with one-dimensional or two-dimensional chromatography methods has been the forefront of proteomic research.

Multidimensional Protein Identification Technology (MudPIT) provides the possibility for rapid and large-scale proteome analysis and it is now widely implemented for the analyses of whole cellular lysates [173], tissue extracts [174], subcellular fractions, and other subproteomes [175].

MudPIT is an automated *gel-free* bottom-up approach in which the complexity problem is addressed at the peptide level [176]. It is based on two-dimensional chromatography coupled to tandem mass spectrometry (2DC-MS/MS). MudPIT represents a technology that simultaneously allows separation of digested peptides, their sequencing and the identification of the corresponding proteins (Figure 10). In this way, it is possible to characterize quantitatively the protein mixtures in wide pI and MW range, as well as membrane proteins. In details, in the original configuration, following enzymatic digestion of a total protein mixture, peptides are separated by liquid chromatography system, consisting of different phases packed in the same column, e.g. a strong cation exchange (SCX) as initial phase, followed by a reversed-phase (RP) material. They are then delivered online to a tandem mass spectrometer, and MS/MS spectra are automatically acquired and used to query protein sequence databases. Peptides are eluted from SCX using different steps of increasing salt concentration and subsequently peptides are eluted from hydrophobic column by means of acetonitrile gradient.

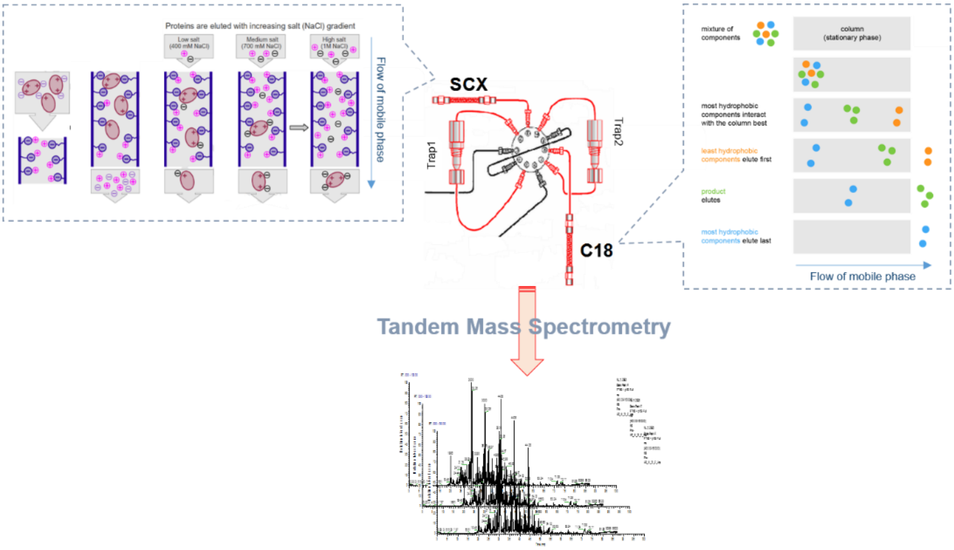


Figure 10. Multi-dimensional protein identification technology (MudPIT).
MudPIT combines ion-exchange with reversed-phase chromatography of peptide mixtures obtained from direct digestion of a protein extracts. In particular, peptides are first loaded onto a strong cation exchange (SCX) column and then separated using different steps of increasing salt concentration. After this, the peptides are captured onto C18-traps (Trap1 and Trap2) and subsequently loaded into reverse phase C18 column. The peptides are eluted from hydrophobic column by means of acetonitrile gradient and the eluate is analyzed by high-resolution mass spectrometer (2DC-MS/MS).

Commercially developed variants of the MudPIT platforms often use separate columns for SCX and RP. In this set-up, the SCX column is combined with the RP column off-line or by means of a 10-port valve.

Sometimes, there is a multiplexing of RP columns to increase throughput [177]. While MS detection is performed on the peptides eluting from the RP column, the salt elution step from SCX onto the second RP column can proceed with an exhaustive washing step. The second column is ready for gradient separation once the first RP run finishes. In this manner, the whole experiment can be fully automated and, more importantly, idle time on the most expensive part of the system, the MS, is kept to a minimum.

1.2.5. MS Instrumentation

In the last decades, many and new proteomic applications based on MS emerged, inviting the design and the development of numerous type of mass spectrometers. For this reason, it is difficult speak about a single specific instrumental platform that is suitable for all type of biomolecular studies.

The essential components of a mass spectrometer are (Figure 11):

a. An <u>inlet system</u> that transfers a sample into the ion source.
b. An <u>ion source</u> that converts the neutral sample molecules into gas-phase ions.
c. A <u>mass analyzer</u> that separates ionized analytes on the basis of *m/z*. Magnetic and/or electric fields are used in mass analyzers to control the motion of ions.
d. A <u>detector</u> that records and amplifies the ion current of resolved ions.
e. A <u>data system</u> that records, processes, stores, and displays data in a form that a human eye can easily recognize.
f. A <u>vacuum system</u> that maintains a very low pressure in the mass spectrometer. The ion source region is usually maintained at a pressure of 10^{-4} to 10^{-8} torr; the mass analyzer region requires a lower pressure of 10^{-8} torr.

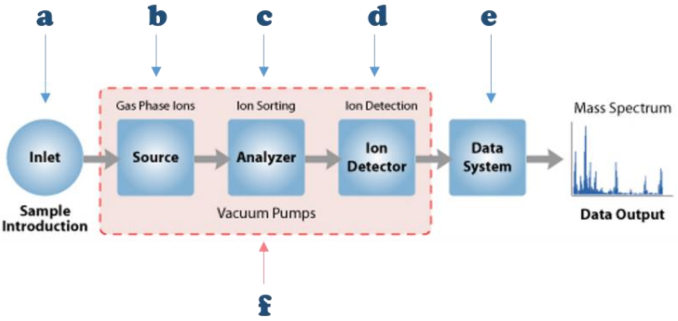
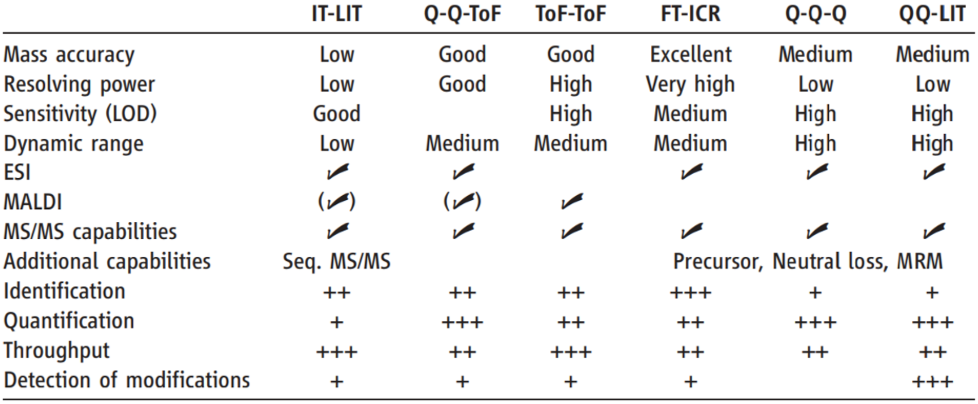


Figure 11. Basic components of a mass spectrometer.
a) Inlet system b) ion source c) mass analyzer d) detector e) data system f) vacuum system. [Modified from http://www.premierbiosoft.com]

The most common instruments used in proteomics are summarized in Table 3.

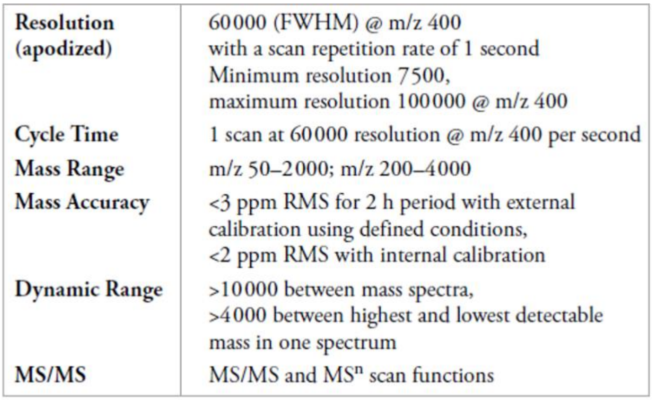


	IT-LIT	Q-Q-ToF	ToF-ToF	FT-ICR	Q-Q-Q	QQ-LIT
Mass accuracy	Low	Good	Good	Excellent	Medium	Medium
Resolving power	Low	Good	High	Very high	Low	Low
Sensitivity (LOD)	Good		High	Medium	High	High
Dynamic range	Low	Medium	Medium	Medium	High	High
ESI	✓	✓		✓	✓	✓
MALDI	(✓)	(✓)	✓			
MS/MS capabilities	✓	✓	✓	✓	✓	✓
Additional capabilities	Seq. MS/MS				Precursor, Neutral loss, MRM	
Identification	++	++	++	+++	+	+
Quantification	+	+++	++	++	+++	+++
Throughput	+++	++	+++	++	++	++
Detection of modifications	+	+	+	+		+++

Table 3. Comparison of the main features of the most common Mass Spectrometers.
Characteristics and performances of commonly used types of Mass Spectrometers. Check marks indicate available, check marks in parentheses indicate optional. +, ++, and +++ indicate possible or moderate, good or high, and excellent or very high, respectively. Seq.: sequential [178].

1.2.5.1. LTQ-Orbitrap

Certainly among several hybrid mass spectrometers and the new generation of instrument applied to proteomics, LTQ-Orbitrap deserves a special mention, also because it is the MS instrument used in this PhD project. The new Orbitrap mass analizer was invented by Makarov in 1999 and was reported as a tool for proteomics research in 2005 by Hu et al. [179]. LTQ-Orbitrap consists of a Linear Ion Trap mass analyzer coupled to an Orbitrap through a C-Trap. It combines the robustness, sensitivity, and fast scanning capabilities of the LTQ with a very high mass accuracy and resolution offered by the Orbitrap, and has become a powerful tool in proteomics. It can operate in a parallel fashion: the Orbitrap acquires MS full scans while the LTQ carries out fragmentation reactions. The instrument is capable of a high mass resolution up to 100000 and mass measurement accuracies of 2 ppm for the analysis of complex peptide mixtures. The main features of LTQ-Orbitrap are reported in Table 4.



Resolution (apodized)	60000 (FWHM) @ m/z 400 with a scan repetition rate of 1 second Minimum resolution 7500, maximum resolution 100000 @ m/z 400
Cycle Time	1 scan at 60000 resolution @ m/z 400 per second
Mass Range	m/z 50–2000; m/z 200–4000
Mass Accuracy	<3 ppm RMS for 2 h period with external calibration using defined conditions, <2 ppm RMS with internal calibration
Dynamic Range	>10000 between mass spectra, >4000 between highest and lowest detectable mass in one spectrum
MS/MS	MS/MS and MS^n scan functions

Table 4. Principal properties of LTQ-Orbitrap instrument.
FWHM: Full Width at Half Maximum; RMS: Root mean square. [modified from Thermo Fischer Scientific, LTQ Orbitrap XL Hardware Manual].

The LTQ-Orbitrap (Figure 12) consists of four main components:

1. A linear ion trap for sample ionization, selection and fragmentation
2. An intermediate storage device (curved linear trap) that is required for short pulse injection and/or HCD fragmentation.
3. An Orbitrap analyzer for Fourier transformation based analysis.
4. A collision cell for performing higher energy CID experiments.

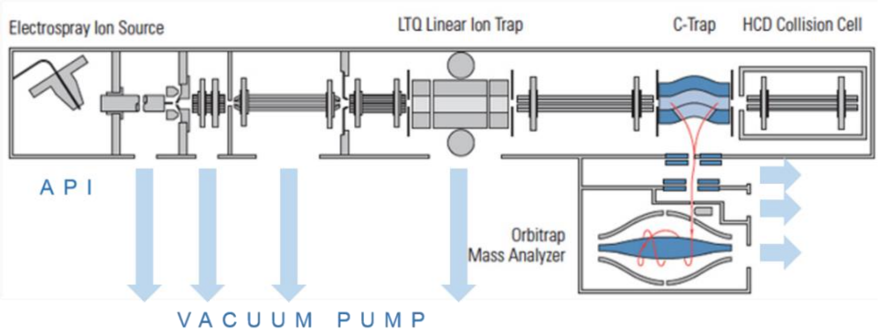


__Figure 12. Schematic overview of the linear ion trap-orbitrap hybryd instrument by Thermo Fischer Scientific (LTQ-Orbitrap).__
API: Atmospheric pressure ionization; CID: Collision-induced dissociation.

In particular, Orbitrap mass analyzer is composed of a spindle-like central electrode and a barrel-like outer electrode. In the Orbitrap, ions are trapped and they orbit around a central spindle-like electrode and oscillate harmonically along its axis with a frequency characteristic of their *m/z* values, inducing an image current in the outer electrodes that is Fourier transformed into the time domain producing mass spectra. Stable ion trajectories involve both orbiting motion around the central electrode (r) and simultaneous oscillations in the z-direction. (Figure 13) [180]. The Orbitrap employs electric fields to capture and confine ions.

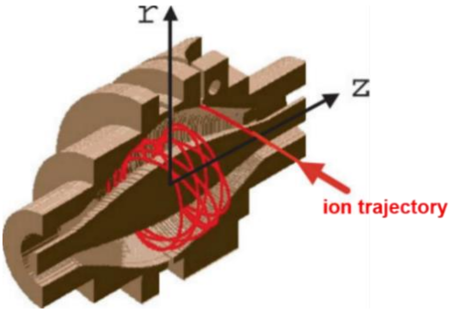


__Figure 13. Cutaway view of the Orbitrap mass analyzer.__
Ions orbit around a central electrode and oscillate in the axial direction. r and z are cylindrical coordinates (modified from Hu Q et al. [179]).

In the mass analyzer, stable ion trajectories rotate around an axial central electrode with harmonic oscillations along it. The frequency ω of these harmonic oscillations along the z-axis (Equation 1) depends only on the ion *mass-to-charge* ratio *m/q* and the instrumental constant k:

Equation 1.

$$\omega = \sqrt{\frac{q}{m} \cdot k}$$

Two split halves of the outer electrode of the Orbitrap detect the image current produced by the oscillating ions. By Fast Fourier Transformation (FFT) of the image current, the instrument obtains the frequencies of these axial oscillations and therefore the *mass-to-charge* ratios of the ions.

On their way from the linear trap to the Orbitrap, ions move through the gas-free RF octapole into the gas-filled curved linear trap (C-Trap). Ions in the C-Trap are returned by the trap electrode. Upon their passage, the ions loose enough kinetic energy to prevent them from leaving the C-Trap through the gate. The N_2 collision gas is used for dissipating the kinetic energy of ions injected from the linear ion trap and for cooling them down to the axis of the curved linear trap. For ion extraction, the C-Trap is switched off and extracting voltage pulses are applied to the electrodes, pushing ions orthogonally to the curved axis through a slot in the inner hyperbolic electrode. Because of the initial curvature of the curved trap and the subsequent lenses, the ion beam converges on the entrance into the Orbitrap. Owing to the fast pulsing of ions from the curved trap, ions of each *mass-to-charge* ratio arrive at the entrance of the Orbitrap as short packets only a few millimeters long. For each mass/charge population, this corresponds to a spread of flight times of only a few hundred nanoseconds for *mass-to-charge* ratios of a few hundred Daltons/charge. When ions are injected into the Orbitrap at a position offset from its equator, these packets start coherent axial oscillations without the need for any additional excitation cycle. When the injected ions approach the opposite electrode for the first time, the increased electric field contracts the radius of the ion cloud by a few percent. A further increase of the field continues to squeeze the trajectory closer to the axis, meanwhile allowing for newly arriving ions (normally, with higher *m/q*) to enter the trap as well. After ions of all *m/q* have entered the Orbitrap and moved far enough from the outer electrodes, the voltage on the central electrode is kept constant and image current detection takes place. The image current is amplified and then undergoes analog-to-digital conversion before processing using the fast Fourier transform algorithm.

1.2.5.2. Fragmentation Techniques

To determine the aminoacid sequence of a specific peptide, tandem mass spectrometry (MS/MS) is commonly applied. To date, different types of MS/MS are feasible (Figure 14).

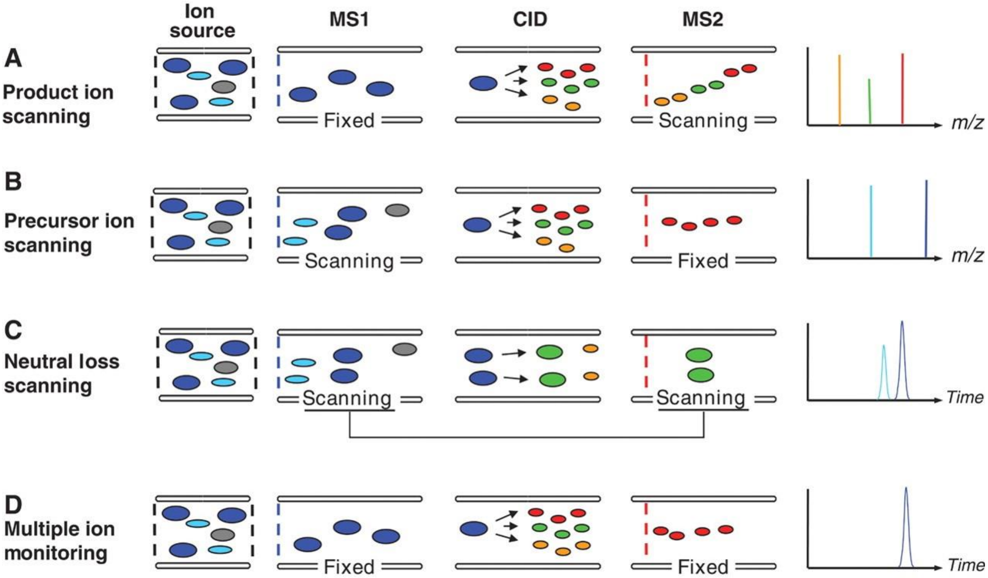


Figure 14. Schematic MS/MS mode of operation.
Schematic representation of various types of tandem mass spectrometry experiments. (A) Product ion scanning (B) Precursor ion scanning (C) Neutral loss scanning. (D) Multiple ion monitoring (MRM) [178].

Product ion scanning (Figure 14A) represents the most common type of MS/MS experiment in proteomics to identify the peptide sequence. The first analyzer (MS1) is set to a value that selects one specific precursor ion at a time. The selected ion undergoes collision-induced dissociation (CID) in the collision cell, and the resulting fragments are analyzed by the second analyzer (MS2). This process is repeated for different precursors.

Precursor ion scanning (Figure 14B) is typically used to detect a subset of peptides in a sample that contain a specific functional group. This method provides for the selection of only one specific fragment ion in the second mass analyzer (MS2), transmitting to the detector. In the first mass analyzer (MS1) all the precursor ions that generate this fragment are scanned.

Neutral loss scanning (Figure 14C) is used for the detection of peptides phosphorylated at serine or threonine residues due a loss of phosphoric acid. In this method both analyzers scan in a synchronized manner, so that the mass difference of ions passing through MS1 and MS2 remains constant. The mass difference corresponds to a neutral fragment that is lost from a peptide ion in the collision cell.

Multiple ion monitoring (Figure 14D), or MRM, is used for the detection of a specific analyte with known fragmentation properties in complex samples. MRM consists of a series of short experiments in which one precursor ion and one specific fragment characteristic for that precursor are selected by MS1 and MS2, respectively.

As reported above, all of these methods, based its fragmentation technique on the collision-induced dissociation (CID), the most widely used in proteomics research.

During a CID event, gas-phase peptide/protein cations are internally heated by multiple collisions with rare gas atoms. This leads to peptide backbone fragmentation of the C-N bond resulting in a series of *b*-fragment and *y*-fragment ions. Because of the slow-heating, the internal fragmentation and neutral-losses of H2O, NH3, and labile PTMs are common. This also results in limited sequence information for large peptides (>15 amino acids) and intact proteins. All information necessary to rebuild the primary sequence of a peptide is comprised in the MS/MS spectrum of the precursor peptide ion. There are three different types of bonds that can fragment along the amino acid backbone: the NH-CH, CH-CO, and CO-NH bonds. Each bond cleavage gives rise to two species, one neutral and the other one charged, and only the charged species are monitored by the mass spectrometer. The charge can stay on either of the two fragments depending on the chemistry and relative proton affinity of the two species. Hence there are six possible fragment ions for each amino acid residue and these are labelled with the *a*, *b*, and *c* ions having the charge retained on the N-terminal fragment, and the *x*, *y*, and *z* ions having the charge retained on the C-terminal fragment (Figure 15).

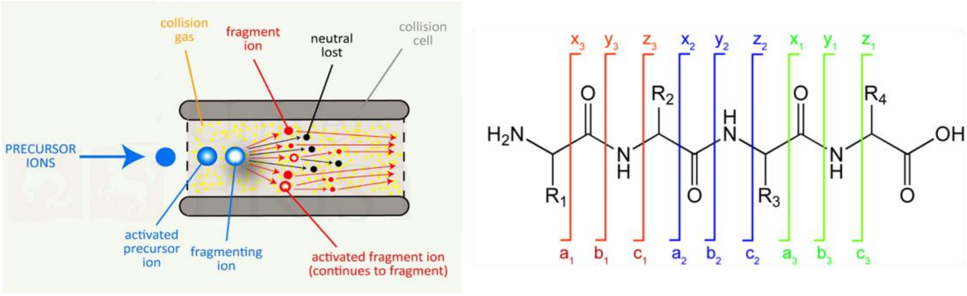


Figure 15. Collision-induced dissociation (CID).
CID consist of fragmentation of molecular ions in the gas phase. The molecular ions (activated precursor ion, blue) are accelerated by some electrical potential (inside of the collision cell) to high kinetic energy and then allowed to collide with neutral molecules. In the collision some of the kinetic energy is converted into internal energy which results in bond breakage and the fragmentation of the molecular ion (fragmenting ion, white-blue) into smaller fragments (fragment ions, red). These fragment ions can be analyzed by a tandem mass spectrometry or can be submitted to other fragmentation (activated fragment ion, white-red).

Using low energy fragmentations, the most common cleavage sites are at the CO-NH bonds which give rise to the *b* and/or the *y* ions. The mass difference between two adjacent *b* ions, or *y* ions, is indicative of a particular amino acid residue. A consequence of the low energy involved during fragmentation is the detection of fewer types of side-chain fragments. Immonium ions are formed by losing a molecule of CO, and they appear in the very low *m/z* range of the MS/MS spectrum. Each amino acid residue leads to a diagnostic immonium ion, with the exception of the two pairs leucine (L) and iso-leucine (I), and lysine (K) and glutamine (Q), which produces immonium ions with the same *m/z* ratio. Immonium ions are useful for detecting and confirming many of the amino acid residues in a peptide, although no information regarding the position of these amino acid residues in the peptide sequence can be ascertained from the immonium ions. Varying amounts of sequence information can be gleaned from each fragmentation spectrum, and the spectra need to be interpreted carefully. Manual interpretation of an MS/MS spectrum is a very time and energy consuming process; because of this, much powerful software have been introduced with the aim to automate the data processing and protein identification against databases. These software (SEQUEST, Mascot, Spectrum Mill), starting from the unprocessed analyses, rebuild the amino acid sequence and search against the whole databases identifying statistically the target protein.

1.2.6. Quantitative Proteomics

The mere identification of a protein expressed in a biological system is not sufficient to answer most biological questions because quantitative answers are even more required in order to provide a snapshot of the protein expression state of a cell in response to biological perturbations. It should also be considered that the complexity of the proteome is related to the variable abundance of the various proteins expressed by an organism in a certain moment (e.g. Interleukin 6 ~ 2pg/ml [181] and Albumin ~ 50 mg/ml [182]). This requires sensitive and accurate assays for identifying proteins in complex mixtures and correctly quantifying their abundances. To this aim, several strategies have been developed to allow an accurate quantification of the protein expression profile of cells, tissues and fluids. A summary of the main quantitative approaches is reported in Figure 16, in which is possible to distinguish the two principal applicable strategies: absolute or relative/semi-quantitative quantification. For both methods could be adopted *label* or *label-free* techniques.

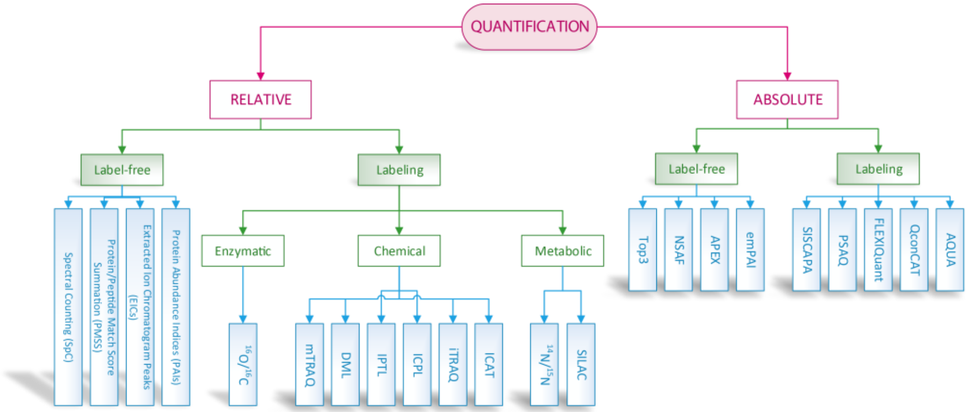


Figure 16. Quantitative proteomic approaches.
Mass spectrometry (MS)-based quantification can be achieved either by relative or absolute quantification. Both of them can be further classified into labeled and label-free quantification, each of which can be performed by several approaches.

This PhD thesis is based on relative *label-free* quantification strategy, therefore an excursus on these methods will be discussed in detail. *Label-free* approaches do not use labeling and stable isotopes to obtain a semi-quantitative information. Literature proposes different parameters which can be derived from raw MS and /or MS/MS data to measure protein relative abundances.

A first strategy is based on Protein/Peptide Match Score Summation (PMSS) [183] in order to obtain protein abundance, expressed in terms of score value. The method is based on the assumption that a protein score is a sum of identification scores of its peptides and that a high protein score is correlated with a higher abundance, thus yielding semi-quantitative information. The main limitation of protein score depends on its tendency to saturation: each protein sequence shows a limited number of tryptic peptides suitable for mass spectrometry detectability. Therefore, a limit in the increase of protein score exists for each protein.

Another *label-free* index, named Spectral Counting (SpC), compares the number of MS/MS spectra assigned to each protein. The spectral counting is the sum of all MS/MS observed for any peptide in a given protein, including redundant spectra for ion charge states. An advantage of spectral counting is that relative abundances of different proteins can in principle be measured.

Protein Abundance Indices (PAIs) represent another way to perform *label-free* quantitation in which the number of peptides identifying a protein growth with the increase of protein amount. As a larger protein will statistically generate more measurable peptides than a smaller one, a simple PAI can be derived by normalizing the number of observed peptides with the number of observable peptides for the protein under consideration [184, 185]. Ishihama and colleagues have described an exponentially modified PAI (emPAI) by observing a logarithmic relationship between the number of observed peptides and the protein amount within a given sample [186].

Ion intensity *label-free* method offers another example of quantitation based on the integration of Extracted Ion Chromatogram peaks (EICs). They rely on the observation that the peak intensity (or better: peak volume or peptide area) in most cases is proportional to the concentration of the peptide in the sample [187–190]. Unfortunately, it is not possible to predict the MS detect or response to a particular peptide because of unknown extraction and peptide ionization properties and, therefore, extracted ion currents (XICs or EICs) from different peptides of the same protein are also very different even if they are present at the same concentration. These sources of error do not occur when comparing the same peptide in different chromatographic runs using identical experimental conditions. Thus, two proteomes can be compared when analyzed one after the other and in exactly the same way [191, 192]. A clear advantage of such method is the absence of any labelling and the applicability to any type of instrument. Clear disadvantages are the multiple occasions for quantification error that occur during parallel sample processing, analysis and the need for very accurate and reproducible LC and MS runs. Measurements of mass spectral peak intensities and spectral counts are probably most promising methods for quantifying protein relative abundance changes in a complex sample. Overall spectral counting proved to be a more sensitive method for detecting proteins that undergo changes in abundance, whereas peak area intensity measurements yielded more accurate estimates of protein ratios [193].

1.3. Bioinformatics Tools

The high-throughput nature of mass spectrometry-based proteomic studies allows to generate a huge amount of data from complex biological samples. The raw information obtained from MS/MS experiments must be stored and elaborated, converting the data to biologically interpretable results and functional outcomes. The processing of raw spectra involves computational procedures, database searching, protein identification and their quantitation, as well as models of protein interaction.

Currently, different bioinformatic platforms are available for functional analysis and data mining of MS-generated proteomic data, as well as several software to communicate and monitor all connected instrumentations. A briefly description about the principal bioinformatics tools employed in this PhD project will be discussed below.

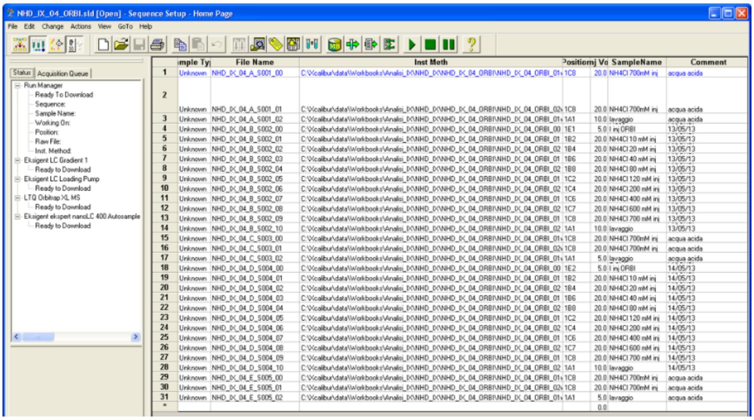
The MudPIT approach is fully automated and managed by dedicated softwares, for both the chromatographic and mass spectrometry systems. This allows to improve the efficiency, the sensitivity and the accuracy of the data acquisition, a crucial requirement for the analysis of complex biological samples.

Xcalibur™ software (Thermo Fisher Scientific™) provides method setup, data acquisition, data processing and reporting of LC-MS/MS instrumentation. In particular, Xcalibur allow:

- To manage the chromatographic system and the mass spectrometer;
- To setup a method for both systems;
- To create and manage an analysis sequence with the right instrument method, injection volume, vial position and file name for each sample;
- To open the raw files;
- To display chromatograms, spectra, and maps of the data;
- To choose spectra from chromatograms;

- To optimize a chromatogram peak's spectrum by change the average scans;
- To determine the elemental composition of the peaks in the spectrum;
- To create and save layouts, add text and graphics, apply filters, amplify regions, and print the resulting graphic.

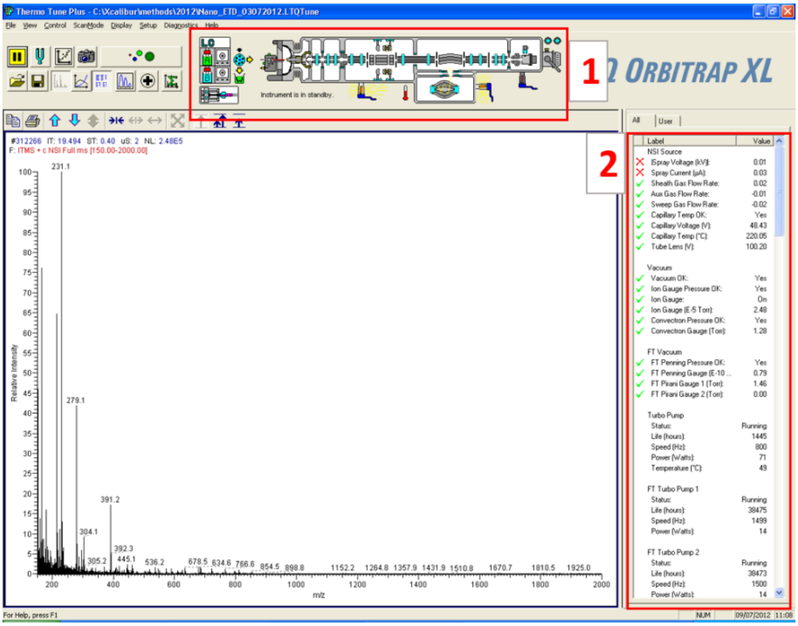
A typical graphic view of Xcalibur software is reported in Figure 17.



	mple Ty	File Name	Inst Meth	Positio	nj Vo	SampleName	Comment
1	Unknown	NHD_IX_04_A_S001_00	C:\Xcalibur\data\Workbooks\Analisi_IX\NHD_IX\NHD_IX_04_ORBI\NHD_IX_04_ORBI_01	1C8	20.0	NH4Cl 700mM inj	acqua acida
2	Unknown	NHD_IX_04_A_S001_01	C:\Xcalibur\data\Workbooks\Analisi_IX\NHD_IX\NHD_IX_04_ORBI\NHD_IX_04_ORBI_02	1C8	20.0	NH4Cl 700mM inj	acqua acida
3	Unknown	NHD_IX_04_A_S001_02	C:\Xcalibur\data\Workbooks\Analisi_IX\NHD_IX\NHD_IX_04_ORBI\NHD_IX_04_ORBI_01	1A1	10.0	lavaggio	acqua acida
4	Unknown	NHD_IX_04_B_S002_00	C:\Xcalibur\data\Workbooks\Analisi_IX\NHD_IX\NHD_IX_04_ORBI\NHD_IX_04_ORBI_00	1E1	5.0	I inj ORBI	13/05/13
5	Unknown	NHD_IX_04_B_S002_01	C:\Xcalibur\data\Workbooks\Analisi_IX\NHD_IX\NHD_IX_04_ORBI\NHD_IX_04_ORBI_01	1B2	20.0	NH4Cl 10 mM inj	13/05/13
6	Unknown	NHD_IX_04_B_S002_02	C:\Xcalibur\data\Workbooks\Analisi_IX\NHD_IX\NHD_IX_04_ORBI\NHD_IX_04_ORBI_02	1B4	20.0	NH4Cl 20 mM inj	13/05/13
7	Unknown	NHD_IX_04_B_S002_03	C:\Xcalibur\data\Workbooks\Analisi_IX\NHD_IX\NHD_IX_04_ORBI\NHD_IX_04_ORBI_01	1B6	20.0	NH4Cl 40 mM inj	13/05/13
8	Unknown	NHD_IX_04_B_S002_04	C:\Xcalibur\data\Workbooks\Analisi_IX\NHD_IX\NHD_IX_04_ORBI\NHD_IX_04_ORBI_02	1B8	20.0	NH4Cl 80 mM inj	13/05/13
9	Unknown	NHD_IX_04_B_S002_05	C:\Xcalibur\data\Workbooks\Analisi_IX\NHD_IX\NHD_IX_04_ORBI\NHD_IX_04_ORBI_01	1C2	20.0	NH4Cl 120 mM inj	13/05/13
10	Unknown	NHD_IX_04_B_S002_06	C:\Xcalibur\data\Workbooks\Analisi_IX\NHD_IX\NHD_IX_04_ORBI\NHD_IX_04_ORBI_02	1C4	20.0	NH4Cl 200 mM inj	13/05/13
11	Unknown	NHD_IX_04_B_S002_07	C:\Xcalibur\data\Workbooks\Analisi_IX\NHD_IX\NHD_IX_04_ORBI\NHD_IX_04_ORBI_01	1C6	20.0	NH4Cl 400 mM inj	13/05/13
12	Unknown	NHD_IX_04_B_S002_08	C:\Xcalibur\data\Workbooks\Analisi_IX\NHD_IX\NHD_IX_04_ORBI\NHD_IX_04_ORBI_02	1C7	20.0	NH4Cl 600 mM inj	13/05/13
13	Unknown	NHD_IX_04_B_S002_09	C:\Xcalibur\data\Workbooks\Analisi_IX\NHD_IX\NHD_IX_04_ORBI\NHD_IX_04_ORBI_01	1C8	20.0	NH4Cl 700 mM inj	13/05/13
14	Unknown	NHD_IX_04_B_S002_10	C:\Xcalibur\data\Workbooks\Analisi_IX\NHD_IX\NHD_IX_04_ORBI\NHD_IX_04_ORBI_02	1A1	10.0	lavaggio	13/05/13
15	Unknown	NHD_IX_04_C_S003_00	C:\Xcalibur\data\Workbooks\Analisi_IX\NHD_IX\NHD_IX_04_ORBI\NHD_IX_04_ORBI_01	1C8	20.0	NH4Cl 700mM inj	acqua acida
16	Unknown	NHD_IX_04_C_S003_01	C:\Xcalibur\data\Workbooks\Analisi_IX\NHD_IX\NHD_IX_04_ORBI\NHD_IX_04_ORBI_02	1C8	20.0	NH4Cl 700mM inj	acqua acida
17	Unknown	NHD_IX_04_C_S003_02	C:\Xcalibur\data\Workbooks\Analisi_IX\NHD_IX\NHD_IX_04_ORBI\NHD_IX_04_ORBI_01	1A1	5.0	lavaggio	acqua acida
18	Unknown	NHD_IX_04_D_S004_00	C:\Xcalibur\data\Workbooks\Analisi_IX\NHD_IX\NHD_IX_04_ORBI\NHD_IX_04_ORBI_00	1E2	5.0	I inj ORBI	14/05/13
19	Unknown	NHD_IX_04_D_S004_01	C:\Xcalibur\data\Workbooks\Analisi_IX\NHD_IX\NHD_IX_04_ORBI\NHD_IX_04_ORBI_01	1B2	20.0	NH4Cl 10 mM inj	14/05/13
20	Unknown	NHD_IX_04_D_S004_02	C:\Xcalibur\data\Workbooks\Analisi_IX\NHD_IX\NHD_IX_04_ORBI\NHD_IX_04_ORBI_02	1B4	20.0	NH4Cl 20 mM inj	14/05/13
21	Unknown	NHD_IX_04_D_S004_03	C:\Xcalibur\data\Workbooks\Analisi_IX\NHD_IX\NHD_IX_04_ORBI\NHD_IX_04_ORBI_01	1B6	20.0	NH4Cl 40 mM inj	14/05/13
22	Unknown	NHD_IX_04_D_S004_04	C:\Xcalibur\data\Workbooks\Analisi_IX\NHD_IX\NHD_IX_04_ORBI\NHD_IX_04_ORBI_02	1B8	20.0	NH4Cl 80 mM inj	14/05/13
23	Unknown	NHD_IX_04_D_S004_05	C:\Xcalibur\data\Workbooks\Analisi_IX\NHD_IX\NHD_IX_04_ORBI\NHD_IX_04_ORBI_01	1C2	20.0	NH4Cl 120 mM inj	14/05/13
24	Unknown	NHD_IX_04_D_S004_06	C:\Xcalibur\data\Workbooks\Analisi_IX\NHD_IX\NHD_IX_04_ORBI\NHD_IX_04_ORBI_02	1C4	20.0	NH4Cl 200 mM inj	14/05/13
25	Unknown	NHD_IX_04_D_S004_07	C:\Xcalibur\data\Workbooks\Analisi_IX\NHD_IX\NHD_IX_04_ORBI\NHD_IX_04_ORBI_01	1C6	20.0	NH4Cl 400 mM inj	14/05/13
26	Unknown	NHD_IX_04_D_S004_08	C:\Xcalibur\data\Workbooks\Analisi_IX\NHD_IX\NHD_IX_04_ORBI\NHD_IX_04_ORBI_02	1C7	20.0	NH4Cl 600 mM inj	14/05/13
27	Unknown	NHD_IX_04_D_S004_09	C:\Xcalibur\data\Workbooks\Analisi_IX\NHD_IX\NHD_IX_04_ORBI\NHD_IX_04_ORBI_01	1C8	20.0	NH4Cl 700 mM inj	14/05/13
28	Unknown	NHD_IX_04_D_S004_10	C:\Xcalibur\data\Workbooks\Analisi_IX\NHD_IX\NHD_IX_04_ORBI\NHD_IX_04_ORBI_02	1A1	10.0	lavaggio	14/05/13
29	Unknown	NHD_IX_04_E_S005_00	C:\Xcalibur\data\Workbooks\Analisi_IX\NHD_IX\NHD_IX_04_ORBI\NHD_IX_04_ORBI_01	1C8	20.0	NH4Cl 700mM inj	acqua acida
30	Unknown	NHD_IX_04_E_S005_01	C:\Xcalibur\data\Workbooks\Analisi_IX\NHD_IX\NHD_IX_04_ORBI\NHD_IX_04_ORBI_02	1C8	20.0	NH4Cl 700mM inj	acqua acida
31	Unknown	NHD_IX_04_E_S005_02	C:\Xcalibur\data\Workbooks\Analisi_IX\NHD_IX\NHD_IX_04_ORBI\NHD_IX_04_ORBI_01	1A1	5.0	lavaggio	acqua acida
*					0.0		

Figure 17. Xcalibur software principal view.
An example of sequence for NHD analysis. It is possible to see the different columns: File name, Istrument method, position of the vials in MicroAS, Injection Volume, Sample description and comment.

Tune Plus (Thermo Fisher Scientific™) allows to show the schematic view of the mass spectrometer, displaying real-time ion trap or FT mass spectra depending on the analyzer type selected (Figure 18).



Thermo Tune Plus - C:\Xcalibur\methods\2012\Nano_ETD_03072012.LTQTune

Instrument is in standby.

#312266 IT: 19.494 ST: 0.40 uS: 2 NL: 2.48E5
F: ITMS + c NSI Full ms [150.00-2000.00]

	Label	Value
	NSI Source	
✗	|Spray Voltage (kV)|:	0.01
✗	Spray Current (µA):	0.03
✓	Sheath Gas Flow Rate:	0.02
✓	Aux Gas Flow Rate:	-0.01
✓	Sweep Gas Flow Rate:	-0.02
✓	Capillary Temp OK:	Yes
✓	Capillary Voltage (V):	48.43
✓	Capillary Temp (°C):	220.05
✓	Tube Lens (V):	100.20
	Vacuum	
✓	Vacuum OK:	Yes
✓	Ion Gauge Pressure OK:	Yes
✓	Ion Gauge:	On
✓	Ion Gauge (E-5 Torr):	2.48
✓	Convectron Pressure OK:	Yes
✓	Convectron Gauge (Torr):	1.28
	FT Vacuum	
✓	FT Penning Pressure OK:	Yes
✓	FT Penning Gauge (E-10 ...	0.79
✓	FT Pirani Gauge 1 (Torr):	1.46
✓	FT Pirani Gauge 2 (Torr):	0.00
	Turbo Pump	
	Status:	Running
	Life (hours):	1445
	Speed (Hz):	800
	Power (Watts):	71
	Temperature (°C):	49
	FT Turbo Pump 1	
	Status:	Running
	Life (hours):	38475
	Speed (Hz):	1499
	Power (Watts):	14
	FT Turbo Pump 2	
	Status:	Running
	Life (hours):	38473
	Speed (Hz):	1500
	Power (Watts):	14

Figure 18. Principal window of Tune Plus.
Red square (1) shows the several elements of HPLC and mass spectrometer; red square (2) displays the real-time status information about the parameters of the mass spectrometer.

From these screens it is possible to manage data generated during calibration, tuning, and diagnostic tests in real-time; it is possible to set the parameters related to each element of HPLC system (MicroAS injection and wash, pump system, etc.) and mass spectrometer (divert valve, ion source, ion optics, temperature monitor, mass analyzer, vacuum, etc.).

Storage RAID System. To manage the enormous amount of data produced by MudPIT analysis, at both experimental and processing levels, it is necessary to employ a data storage system fitted of a great computing power. For this aim, it is necessary to use a multi-node PC cluster [194] capable to process the different chromatographic steps of MudPIT in parallel, drastically reducing the protein search times in the databases. Therefore, these *Redundant Array of Independent Disks* (RAID) combine multiple physical disk drive components into a single logical unit to improve the analysis performance and speed. The results from each node or disk are automatically integrated to generate a single output file.

Database resources. A hallmark of bottom-up proteomics is the identification of proteins by database searching methods. The experimental masses of the parent peptides and their fragments (MS/MS) are compared with those generated *in-silico*, based on the available genomic/proteomic sequences, annotated in spectral libraries. In this way, peptide sequences are characterized and assembled back into the corresponding proteins. This step is possible thanks to on-line free database resources. Protein databases are a collection of sequences from several sources, including information about function, subcellular localization, PTMs, structure, etc. The main sources to download a protein database of interest are UniProt and NCBI. UniProt (Universal Protein, www.uniprot.org) is the largest bioinformatic database for protein sequences of all living organisms and viruses. It provides a stable, comprehensive, freely accessible, central resource on protein sequences and functional annotation [195]. NCBI (National Center for Biotechnology Information, www.ncbi.nlm.nih.gov) is a collection of databases of nucleotide sequence (GenBank), protein and genomic sequence (RefSeq), human gene (Omin), biomedic literature (PubMed), etc. Actually, UniProt is preferred to NCBI because are much controlled and contain less redundant information.

Computing Algorithms. Manual interpretation of an MS/MS spectrum is a very time and energy consuming process. Moreover, the abundance and complexity of raw data led to develop computing algorithms to compare results with above specified protein databases in order to identify the protein components of the biological mixture. For these reasons, powerful software have been developed with the aim to process data and identify proteins against databases. Among the plethora of search algorithms (MASCOT, SEQUEST, ProFound, MS-Tag, PeptideSearch, X!Tandem, X!Hunter, OMSSA, Parallax, DBDigger, GlobalLynx, Paragon, Spectrum Mill, SpectraST, Bonanza, BiblioSpec, and more) that have been created to these functions, MASCOT, SEQUEST and X!Tandem are the leading ones. MASCOT and SEQUEST are commercial software, whereas X!Tandem is an open source algorithms. These software starting from the unprocessed analyses, rebuild the amino acid sequence, and search against the whole databases identifying statistically the target protein. Usually, these algorithms are an integral parts of software, such as BioWorks (Thermo Fisher Scientific^{TM}) that convert the MS output in a much comprehensive information and add statistical functions.

BioWorks© software (www.thermo.com/bioworks; University of Washington, licensed to ThermoFinnigan Corp., San Jose, CA, USA) is a configurable software package for peptide and protein analyses based on mass spectrometry. As previous mentioned, BioWorks features SEQUEST® protein search engine for label and label-free quantitative analysis of peptides. In detail, SEQUEST algorithm (University of Washington, USA, licensed to ThermoFinningan Corp.) follows this procedure: first, the algorithm selects a peptide ion and simplifies its acquired MS/MS spectrum. Next, it identifies all possible peptide sequences in the database that with their "*in-silico*" signals may fit with the experimental ions of this selected peptide spectrum. The algorithm then predicts the similarity score of theoretical sequence ions patterns of all those peptides. SEQUEST is well-known and popular algorithm in MS-based proteomics, because it allows:

- To calculate the correlation coefficient (XCorr) to define the quality of the peptide match;
- To evaluate the probability index (p-value);
- To manage and change the stringency of filter settings and parameters.

MAProMa. The output data obtained from SEQUEST algorithm can be treated with the MultidimensionalAlgorithm Protein Map (MAProMa), in-house software developed at the Institute of Biomedical Technologies (ITB-CNR, Milan) [196]. MAProMa software permits the presentation of results in a usual form for biologists such as two dimensional virtual maps in which it is possible to assign a pI value and a MW to each identified protein. Moreover, using a color-shape index, it is possible to associate to each protein a confidence of the identification on the basis of its Sequest-score. MAProMa software allows to perform the Sequest score-based label-free differential analysis utilizing two semi-quantitative parameters for the evaluation of the relative protein expression within compared biological samples: the DAve (Differential Average) and DCI (Differential Control Index) algorithms.

DAve evaluated how many time the expression of a protein changed between two samples, i.e. one patient and one control, applying the formula (X-Y)/(X+Y)/0.5 where X is the Sequest score of the protein in the patient protein-list and Y is the Sequest score of the same protein in the control protein-list. DAve values ranged from -2 to +2. A DAve value equal to +2 corresponds to a protein present only in the patients. For example: X =130, Y = 0, DAve = (130-0)/ (130+0)/0.5 = +2. On the contrary, a DAve value equal to -2 corresponds to a protein present only in control. For example X = 0, Y = 130, DAve = (0-130)/ (0+130)/0.5 = -2. If DAve value is equal to 0 the protein shows the same score in patients and controls and its expression may be considered unchanged. Positive DAve values correspond to proteins having a Sequest score greater in patient than in control suggesting that the protein may be more expressed in patient than in control; moreover, if the value is closer to +2, the protein is much expressed in patient. Negative DAve values correspond to proteins with a score greater in control than in patient suggesting that the protein may be more expressed in control than in patient;

moreover, a value closer to -2 , means that the protein is much expressed in controls.

DCI is an index to evaluate the confidence of the differential expression indicated by the DAve. It is obtained by applying the formula (X+Y)*(X-Y)/2 at the same Sequest score value described previously: the greater is its value, the greater is the probability that the protein is really differentially expressed. For example: if X = 80 and Y = 0, DAve has a value equal to +2 and DCI a value of 3200. On the contrary, if X =8 and Y = 0 DAve has a value equal to +2 exactly as in the previous example but DCI showed a value of 32. The probability that the protein is really present only in patient in the second example is lower than in the first example because X in the second example (X = 8) is greatly lower than in the first example (X = 80) suggesting the fact that a major number of peptides was attributed to the protein in first example than in the second. The lower value of DCI in the second example with respect to the first demonstrates this fact.

Cluster analysis. Hierarchical clustering provides a good tool to visualize the similarities between samples in relation to the differences between classes of samples. In particular, heat maps can provide an estimation of multiple peptides that display similar quantitative behaviour within the dataset. It is expected that multiple peptides per protein will display very similar quantitative behaviour, and will end in the same clusters. Protein lists of patients and controls can be processed using multivariate analysis in order to extract information about the similarity of their protein profiles. The aim of this statistical approach is the research of a preliminary rationale to support a successive accurate label-free differential analysis having the aim to identify putative biomarkers and to obtain information about the altered metabolic pathways.

Network analysis. In order to integrate the high-throughput expression data with biomolecular interaction networks in a unique graphical and informational view, it is possible to use several software, among which Cytoscape (http://www.cytoscape.org), a software originally designed for biological research. Cytoscape is an open source platform for visualizing molecular interaction networks and biological pathways and integrating these networks with annotations, gene expression profiles and other state data. Cytoscape is the most powerful platform for large databases of protein–protein, protein–DNA and genetic interactions [197]. The main window of Cytoscape is reported in Figure 19. Cytoscape allows to visualize and evaluate the dysregulated protein pathways in the different compared states (i.e. patient vs healthy; drug treatment vs control) using specific customized plug-in, designed to highlight the several features of interested proteins.

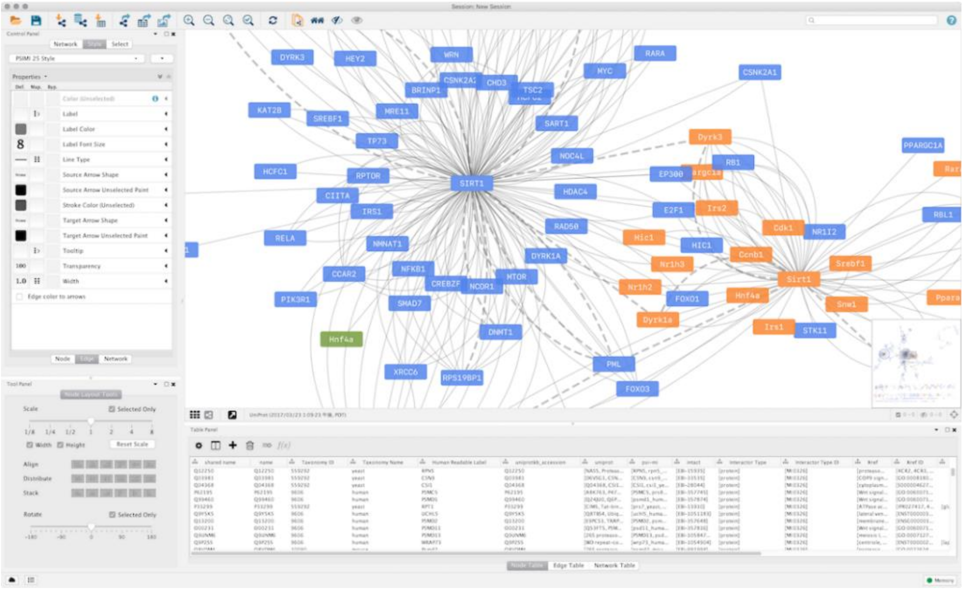


Figure 19. Main window of Cytoscape software.

1.4. Clinical Proteomics

A sub-discipline of proteomics that involves the application of proteomic technologies on clinical specimens takes the name of “Clinical proteomics”. The main purposes of this discipline are to provide clinicians with tools to accurately diagnose and treat patients in a personalized manner, focusing on the discovery of diagnostic and prognostic biomarkers, as well as novel drug targets. Biomarker identification is aiming at the selection of those cellular components that are consistently correlated with a particular physiological states like development or disease. Biomarker discovery essentially comes down to detect consistent differences within a large number of samples mainly following the trend of protein expression. In fact, recently proteomics has been used to develop new serological biomarkers for early diagnosis of chronic diseases.

On this assumption, proteomics has been applied to investigate Nasu-Hakola Disease by Multidimensional Protein Identification Technologies (MudPIT) analysis of Lymphocyte cells. A brief overview of the fields in which MudPIT was successfully applied to biomarker discovery is reported below. Literature is rich of MudPIT applications in clinical investigation, in which it has been used to probe various disease-related samples with the aim to identify differentially expressed proteins (up- or down-regulated proteins), candidates as putative biomarkers of disease.

A great number of MudPIT-based studies were performed in cardiovascular disorders. One experiment identified over 7000 unique proteins from left ventricular tissue. This study formed the basis for a public database of human cardiac tissue [198]. Moreover, Kline et al. [199] proposed methods for optimizing each analytic step for unfractionated human heart tissue proteome characterization including tissue homogenization and preparation, MudPIT set up, and data mining.

The MudPIT approach has been applied to cancer investigation with the aim to identify candidate biomarkers [200]. For example, investigations of proteins released from pancreatic cancer cells allowed identification of some differentially expressed proteins involved in extracellular matrix degradation, invasion, metastasis and angiogenesis [201]. Sodek et al. [202] reported that MudPIT analyses of ovarian cancer cells could be used for grouping cell lines in relation to their motility/ invasive capacity. About 200 proteins, including actin cytoskeleton and extracellular matrix, were identified to be up-regulated in cancer cell lines with high motility. Other authors applied MudPIT to characterize proteomic profiles in pathological conditions that affect various organs such as reproductive organs [203], lung [204], and breast [205].

Concerning neurological diseases, Hilder et al. [206] have been successfully applied MudPIT to the study of cerebral cavernous malformations (CCM), due to vascular lesions of the central nervous system. Liao et al. [207] studied the changes in synaptic proteins due to the transcriptional silencing of fmr1, a gene involved in a form of mental retardation called fragile X syndrome. More than 100 proteins were identified in this study as being up- or down-regulated. The MudPIT approach has been used for identifying actin-associated proteins in central nervous system synapses. Many proteins were identified as being involved in synaptic vesicle formation and movement, and maintenance of synaptic structure [208, 209]. However, up to now, in literature there are no data about the application of MudPIT to FTDs or in particular to Nasu-Hakola Disease studies.

In all cases mentioned above, the MudPIT approach increased both the quantity and quality of information when compared with other approaches, thanks to enormous improvement of Liquid Chromatography- Tandem-Mass Spectrometry (LC-MS/MS) technologies, verified in the last decade.

2. PURPOSE

The aim of my PhD project was to realize a significant improvement in the knowledge of the molecular pathways involved in the onset and development of Nasu-Hakola Disease. In order to provide a correlation between pathophysiology and protein expression profile of this neuropathy, Lymphoblastoid cells coming from all components of an Italian family were analyzed. The study is aimed to get a deeper understanding of biological processes unexpectedly implicated in so divergent clinical presentations: bone degeneration and neuronal death. In addition, the comparative analysis of healthy *vs* sick allowed the identification of proteins that could be candidates as potential biomarkers for the diagnosis and the treatment of the pathology. Not least, the know-how derived from an increased knowledge of the signaling pathways involved in Nasu-Hakola Disease, could be taken as model for the study of other TREM2-based FTDs. To this end, the application of an innovative proteomic approach proved to be a promising choice. This study contributed to an improvement in Nasu-Hakola Disease investigations, because in literature there are no studies about the application of any fully automated technology to identify protein expression profiles of NHD patients. This project allowed to generate, for the first time, the most complete protein profile of Lymphoblastoid cells from Nasu-Hakola subjects and to characterize the metabolic pathways involved in functional alterations caused by this pathology. Furthermore, the possibility to adopt a *label-free* strategy and specific bioinformatics tools, permitted a semi-quantitative evaluation of the differentially expressed proteins between healthy *vs* NHD subjects. After that, it was possible to realize a protein-protein interaction network in order to highlight the dysregulated pathways and to evaluate the possible proteins involved in functional alterations of this pathology. In light of this, this work allowed to find new insights in NHD pathogeneses, opening the way to the discovery of new biomarkers of TREM2-based dementias.

3. MATERIALS AND METHODS

3.1. Subjects

The project was focused on an Italian family consisting of seven individuals that present a homozygous C to T loss-of-function mutation at position 97 in the exon 2 of the TREM2 gene. The family (Figure 4) originated from a restricted area of northern Italy and it is composed by two homozygote NHD patients (Ho), four healthy carriers with heterozygous mutation (He) and one healthy subject (Wt, control). It is possible to exclude the consanguinity in the last five generations. During the early 2000s, still alive subjects, were submitted to a battery of neuropsychological tests covering a wide range of cognitive functions. The complete medical case was reported by Soragna et al. [102, 137]. Ethics Committee of the Neurological Institute ‘‘C.Mondino’’, Pavia and the ‘‘Laura Fossati Foundation’’, Montesegale, Pavia, who reviewed and authorized studies on these patients.

3.2. Lymphoblastoid B-cell line preparation

All seven subjects were submitted to a blood withdrawal. An aliquot (10 mL) was used to isolate the B-lymphocytes that were immortalized by treatment with Epstein - Barr virus (EBV) as described in detail by Giuliano et al. [139]. In particular, the Lymphoblastoid cell lines (LCLs) were maintained in suspension culture in RPMI 1640 medium supplemented with 10% fetal bovine serum, 4 mM glutamine, streptomycin, and penicillin. Cells were harvested by centrifugation (1300 g for 5 min at 4°C) and freezed.

3.3. PCR amplification

As described by Giuliano et al [139], the total lymphoblastoid B-cell RNA was purified by using the RNeasy mini kit (Qiagen, Manchester, UK), and quantified by determining the optical density at 260 nm. Total cellular RNA was reverse-transcripted by means of the RNA PCR Core Kit (Applied

Biosystems, Foster City, CA, USA). The resulting complementary DNA (cDNA, 200 ng) was submitted to conventional PCR amplification in a 25 ml reaction volume on a PCR SPRINT Thermal Cycler (Thermo Electron Corporation, MA, USA). The parameters used for PCR amplification were the following: i) initial DNA denaturation at 94°C for 3 min followed by 35 cycles of denaturation at 94°C for 30 s; ii) primer annealing at 57°C for 30 s, and elongation at 72°C for 30 s; iii) extension at 72°C for 3 min. Detection of the PCR amplification products was performed using the PCR 59-TCT TTG TCA CAG AGC TGT CC-39 (sense) and 59-AGG GTA TCG TCT GTG ATG GC-39 (antisense) primers (PRIMM Co. Ltd, Milan, Italy). An aliquot (10 ml) of each PCR reaction sample was submitted to 1.5% agarose gel electrophoresis to visualize the products by staining with ethidium bromide.

3.4. Protein extraction protocol

For each subject, about 30x10^6 Lymphoblastic B-cells were used. Cells were resuspended into 100 µL of 0.1 M NH_4HCO_3 pH 8.0 and homogenized. The pellets were treated with 0.25 % MS compatible detergent (Rapigest^{TM}, Waters) and incubated for 20 min at 100°C. After centrifugation (2,2g for 10 min at room temperature) the supernatant was recovered. Protein concentration was performed with SPN^{TM}-Protein assay (Biosciences$^{®}$) kit. Each sample was digested overnight with sequencing grade Trypsin (Promega, Madison, WI, USA) in ratio 1:100, at 37°C. Prior to analysis, the resulting peptide mixtures were desalted with PepClean (Pierce) C-18 spin columns.

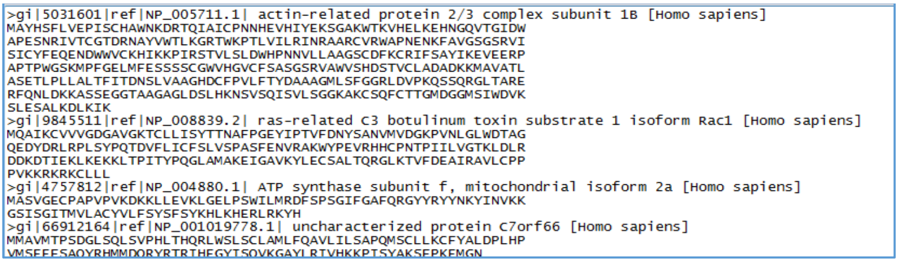
3.5. 2DC-MS/MS Analysis

The µ2DC-MS/MS method was applied for the analysis of the whole lymphoblastic proteome. In MudPIT technology, the peptide mixture (5 µg) was loaded onto a strong cation exchange (PolyLC-SCX column 0.3 i.d. x 100mm, 5µm, 300 Å, PolyLC) column, eluted stepwise with salt injections of increasing molarity (10, 20, 40, 80, 120, 200, 400, 600, 700 mM) and captured onto peptide traps for concentration and desalting prior to final separation by reverse phase C18 column (Biobasic-C18, 0.18 i.d. x 100 mm, 5µm, 300 Å, Thermo Fischer). The peptides, gradually eluted from C18 column (3 min of column conditioning followed by 65 min gradient of 5-95% CH_3CN/0.1% HCOOH, flow rate of 130 µL/min splitted to reach a final flow of 2 µL/min at the end of the column), were MS and MS/MS analyzed by a mass spectrometer equipped with a NSI-ESI ion source and a linear ion trap combined to an Orbitrap benchtop mass analyzer (LTQ-OrbitrapXL, Thermo Fisher Scientific). The spray capillary voltage was set at 2.4 kV and the ion transfer capillary temperature was held at 220°C. For each step of peptides eluted from C18 column high resolution full MS spectra were recorded over a 400–1600 *m/z* range in positive ion mode, followed by five MS/MS events sequentially generated in a data-dependent manner on the Top 5 ions selected from the full MS spectrum (at 35% collision energy), using dynamic exclusion of 0.5 min for MS/MS analysis. System MudPIT management was performed by Xcalibur data system v.1.4 (Thermo Fisher Scientific, San Josè, CA, USA).

3.6. Data Mining

3.6.1. Database

The experimental MS/MS spectra were correlated to tryptic peptide sequences by comparison with the theoretical mass spectra obtained by *in-silico* digestion of the *Homo sapiens* protein database (about 228763 entries), downloaded January 2013 from the National Centre for Biotechnology Information (NCBI) website (http://www.ncbi.nlm.nih.gov). This database contains all the known proteins of the human organism, reported in terms of sequence. An extract of *Homo sapiens* database is reported in Figure 20.



```
>gi|5031601|ref|NP_005711.1| actin-related protein 2/3 complex subunit 1B [Homo sapiens]
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APESNRIVTCGTDRNAYVWTLKGRTWKPTLVILRINRAARCVRWAPNENKFAVGSGSRVI
SICYFEQENDWWVCKHIKKPIRSTVLSLDWHPNNVLLAAGSCDFKCRIFSAYIKEVEERP
APTPWGSKMPFGELMFESSSSCGWVHGVCFSASGSRVAWVSHDSTVCLADADKKMAVATL
ASETLPLLALTFITDNSLVAAGHDCFPVLFTYDAAAGMLSFGGRLDVPKQSSQRGLTARE
RFQNLDKKASSEGGTAAGAGLDSLHKNSVSQISVLSGGKAKCSQFCTTGMDGGMSIWDVK
SLESALKDLKIK
>gi|9845511|ref|NP_008839.2| ras-related C3 botulinum toxin substrate 1 isoform Rac1 [Homo sapiens]
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QEDYDRLRPLSYPQTDVFLICFSLVSPASFENVRAKWYPEVRHHCPNTPIILVGTKLDLR
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PVKKRKRKCLLL
>gi|4757812|ref|NP_004880.1| ATP synthase subunit f, mitochondrial isoform 2a [Homo sapiens]
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GSISGITMVLACYVLFSYSFSYKHLKHERLRKYH
>gi|66912164|ref|NP_001019778.1| uncharacterized protein C7orf66 [Homo sapiens]
MMAVMTPSDGLSQLSVPHLTHQRLWSLSCLAMLFQAVLILSAPQMSCLLKCFYALDPLHP
VMSEEESAQYRHMMDQRYRTRTHEGYISQVKGAYLRIVHKKPISYAKSEPKEMGN
```

Figure 20. Extract of NCBI Homo sapiens protein database.

3.6.2. Bioworks

Data handling were performed using the 3.3.1 Bioworks version, based on SEQUEST algorithm (Thermo Fisher Scientific, San Jose, CA, USA), that correlate the experimental MS/MS spectra (i.e., .raw data) to tryptic peptide sequences by comparison with the above mentioned *Homo sapiens* protein database. The following criteria were applied for the identification of peptide sequences and related proteins: Trypsin as enzyme; three missed cleavages per peptide were allowed; a mass tolerance of 50 ppm for precursor ions (threshold) and 0.8 Da for fragment ions were used. Validation based on separate target and decoy searches and subsequent calculation of classical score-based false discovery rates (FDR) were used for assessing the statistical significance of the identifications (FDR ≤ 1%). Finally, to assign a final score to proteins, the SEQUEST output data were filtered as follows: 1,5; 2.0; 2.25 and 2.5 were chosen as minimum values of correlation score (Xcorr) for single-; double-; triple- and quadrupole-charged ions, respectively. A total of 7 big protein lists for each sample was obtained by averaging of the technical replicates.

3.6.3. Protein quantitation and differential analysis

As previously reported, to improve the identification of differentially expressed proteins, in this study it was adopted two different approaches respectively based on Linear Discriminant Analysis (LDA) and DAve and DCI indices inserted in MAProMa software [210].

3.6.4. Linear Discriminant Analysis

To perform the reduction of data dimensions, protein lists obtained by MudPIT replicate analyses were aligned by MAProMa, normalized by means of the Total Signal normalization methods [211] and processed by means of Linear Discriminant Analysis [212]. Specifically, a matrix *mxn* consisting of 3458 proteins and 19 replicates grouped into three subgroups (Ho, He, Wt), was considered. LDA was applied by using a common covariance matrix for all groups and the Mahalanobis distance [213] from each point to each group's multivariate mean. In order to select proteins that distinguished the analyzed subgroups, we considered those F ratio≥4 and p-value ≤0.05; RapidMiner software was used.

3.6.5. DAve and DCI indices

Protein lists obtained by MudPIT replicate analyses were aligned and, for each protein, it was calculated the average spectral count (aSpC) corresponding to each analyzed condition (Ho, He, Wt). Based on a direct correlation between the SpC (or SEQUEST-based score) and the relative abundance of the identified proteins [201], the three subgroups were pairwise compared (He *vs* Ho; He *vs* Wt; Wt *vs* Ho) by DAve (Differential Average) and DCI (Differential Confidence Index) indexes of the homemade Multidimensional Algorithm Protein Map (MAProMa) software [214]. Specifically, DAve, which evaluates changes in protein expression, is defined as (X-Y)/(X+Y)/0.5, while DCI, that evaluates the confidence of differential expression, is defined as (X+Y)*(X-Y)/2, where the X and Y terms represent the SpC of a given protein in two compared samples. To select differentially expressed proteins, a threshold of 0.4 and 15 was applied to DAve and DCI, respectively.

3.6.6. Hierarchical Clustering

Biological and technical replicates were evaluated by means of an unsupervised learning method, such as hierarchical clustering [213] using an in-house R-scripts, which was based on the XlsReadWrite, clue and clValid libraries. In particular, the Euclidean distance metric was applied, and an agglomerative coefficient was calculated.

3.6.7. In-house Python Script

To convert the NCBI Accession code of the identified proteins into Gene Name, an in-house script was realized in Python programming language.

3.6.8. Network Analysis

A human protein-protein interaction (PPI) network was retrieved by Cytoscape [197] plugin PESCA [215]. This network was built by combining data retrieved from major interactomic repositories, including HPRD, MINT, BioGrid, IntAct, DIP, BIND and Pathway Commons online database. In addition, it was complemented by in-house manually curated data derived from literature. The combined dataset included only manually curated PPI binary interactions inferred by two to six independent methods. Functional, protein-DNA, protein-RNA, protein-metabolite and protein-drug interactions, as well as, duplicates and self-interactions were removed.

The human PPI network retrieved by PESCA plugin was matched to all differentially expressed proteins and a subnetwork of 469 nodes and 5628 interactions was obtained. This network was evaluated at topological and functional level to identify topological and functional modules/clusters. In particular, Cytoscape plugin MCODE [216] was used to find highly interconnected regions in the network, while Cytoscape plugin BINGO 2.44 [217] was used to evaluate the most represented GO terms; *Homo sapiens* organism, hypergeometric test, Benjamini & Hochberg FDR correction and a significance level ≤ 0.001 were applied.

3.7. Protein validation by Western Blot

During writing this thesis, Western Blotting analysis is taking place in order to validate the up- and down-regulated TREM2-interactor proteins (RAC1, PLCG2 and VAV2). The analysis will be achieve starting from 50 micrograms of protein extracted from Lymphoblastoid cells of Wt, He and Ho. Separated proteins on mini-PROTEAN TGX Stain-free Precast gel for SDS-PAGE (8-16% gradient) will be transfer onto PVDF membrane using a Trans-Blot Turbo Transfer System (Bio-Rad) applying a current of 1.3 A up to 2.5 V for 7 minutes. After 1h incubation in 5 % of BSA (10 ml) diluted in TBS and three additional washes with TBST (0,1% Tween in 10 ml), the membrane will be incubate overnight (4°C), with anti-RAC1, anti- PLCG2 and anti-VAV2 (Thermo Fischer) at a dilution 1:1000, 1:1500 and 1:500 respectively in 1% BSA. After washing the membrane three times with TBST (10ml), incubation with second antibody will be perform for 1h at room temperature with polyclonal anti- rabbit immunoglobulin diluted 1:15000 (Cell Signaling Technology) for each western blotting, in 1% TBST. The membranes will be finally washed three times with TBS and incubated in ECL Prime Solution (GE, Healthcare) and the immunoblots will be acquire with the ImageQuant LAS 4000 analyzer (GE Healthcare).

4. RESULTS

In the present PhD thesis a *gel-free* proteomic platform, based on a bi-dimensional µliquid-chromatographic system (also known as MudPIT) combined to an Orbitrap mass spectrometer, was applied to the analysis of Lymphoblastoid cell lines (LCLs) obtained from seven subjects of an Italian family suffering for Nasu-Hakola Disease. The considered family, previously investigated for the genetic and neuropsychological profiles by Soragna et al. [102], included: two mutant homozygote subjects (Ho); four heterozygotes (He) and one wild type individual (Wt).

4.1. Protein profiling

MudPIT analysis of LCLs from NHD family identified 10253 unique peptides and 3458 distinct proteins from a total of 19 protein lists, including technical and biological replicates (6 lists for He and Ho groups; 7 lists for Wt group). The complete list of identified proteins for each subject is reported in Appendix 1.

All proteins showed a SEQUEST score average, calculated by dividing the sum of protein scores in samples vs. the identification frequency (IF, i.e. in how many samples the protein was identified), greater than 10. This means that the protein has been successfully identified in at least one sample with at least one peptide that exceed the stringent thresholds of the SEQUEST search (i.e.: Xcorr greater than 1.5, 2.0 and 2.5 for single, double and triple charge ions, respectively; peptide/protein probability to 10−3, protein consuensus score greater than 10).

Comparing all lists, 1478 proteins were shared among the three groups, while 10-13% of proteins were specific of each group; specifically, 335, 452 and 448 proteins resulted specific for He, Ho and Wt groups, respectively (Figure 21). Moreover, the number of common proteins between healthy carriers (He) and diseased subject (Ho) resulted higher (n=425) in comparison to the common proteins between heterozygote (He) and healthy subjects (Wt) (n=115) or diseased subject (Ho) (n=205).

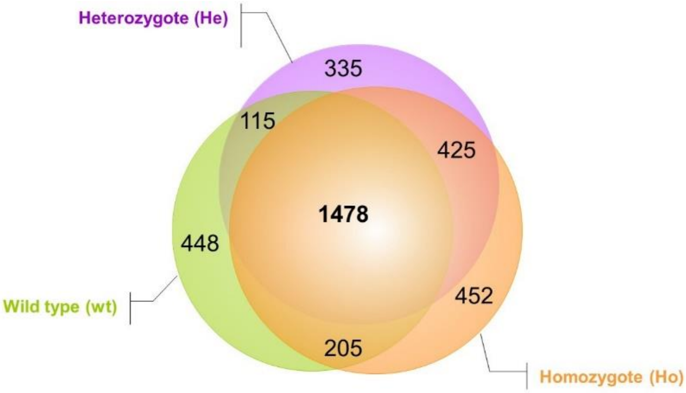

Figure 21. Venn Diagram.
The figure shows the distribution of all identified proteins within three investigated categories (heterozygote, He, violet circle; wild type, Wt, green circle; homozygote, Ho, orange circle). About 1400 proteins were shared between the three groups of subjects and approximately 400 proteins were identified as peculiar of each category.

The reproducibility of the mass spectrometry data acquired is an essential starting point to develop reliable differential analysis based on *label-free* approach. More samples are complex and more the reproducibility is difficult to be controlled and monitored. In this study, to verify the repeatability of the data and the efficiency of our procedure, all samples have been over-analyzed in order to obtain a comparable number of technical replicates. In particular, due to the absence of other members of the NHD family, each group (Wt, Ho and He) was submitted to six and seven runs, respectively. To evaluate the reproducibility of the experimental MudPIT data, the SpC of each identified protein in the first technical replicate were plotted *vs* the SpC in the second technical replicate. The same procedure was applied to two different subjects of the same group (biological replicates). Nearly optimal linear correlation (R2 value ≥ 0.95) and slope (y =1.08 ± 0.15) close to theoretical value (1.00) were obtained. Figure 22 showed that there is a good linear correlation between the two replicate assuring a good reproducibility of the 2D-LC-MS/MS analyses of samples.

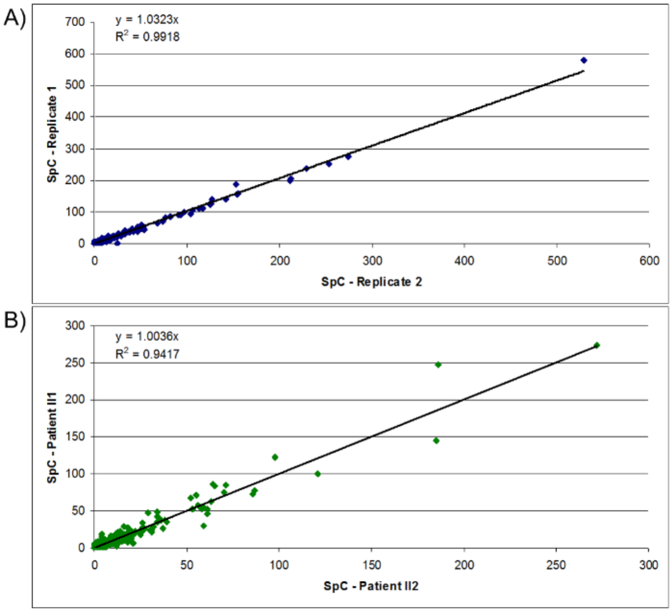

Figure 22. MudPIT Technical and Biological Repeatability.
Linear regression analysis obtained by considering SpC values of proteins identified into two technical replicates (A, blue) and two Homozygote subjects (B, green) of MudPIT analysis. R^2 and slope (y) are close to theoretical value of 1.00.

All identified proteins showed a score ≥ 10 (or Spc>2) and an IF ≥ major than 2. Of note, this approach allowed to identify many proteins usually difficult to be detected, as shown in 2D virtual maps (Figure 23) where all the identified proteins were plotted according to their theoretical molecular weight (MW) and isoelectric point (pI). It is interesting to note that a significant number of proteins with extreme MW and pI value was characterized. For example, about 100 proteins with MW <10 kDa or MW >200 kDa, were identified. Among proteins with very acidic (about 10 proteins had pI< 4), or very basic pI (about 100 proteins had pI> 10), such as acidic leucine-rich nuclear phosphoprotein 32 (pI = 3.5) and several ribosomal and histone proteins (pI = 11-12), respectively, were identified.

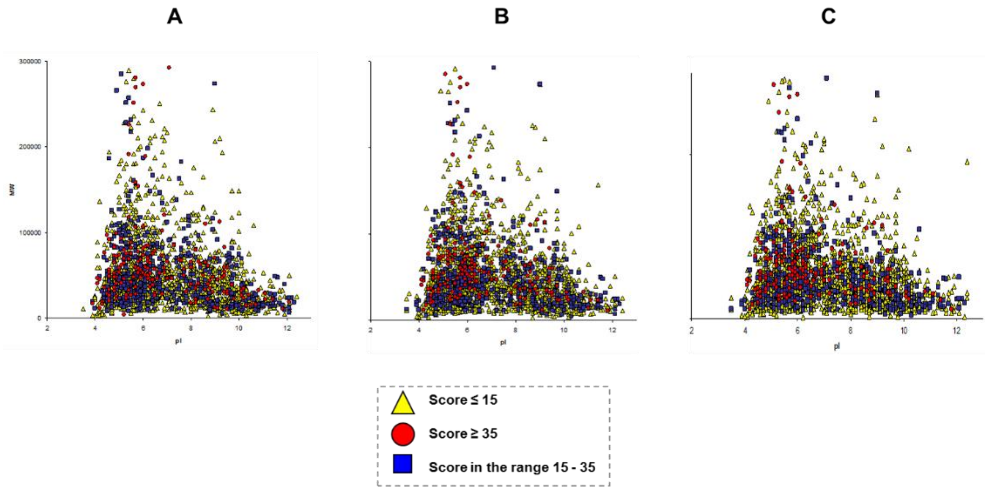

Figure 23. Virtual 2D map of Wt (A), He (B) and Ho (C) subjects plotted by MaProMa software.

Identified proteins were plotted according to their theoretical pI and MW. For each protein, a color/shape code was used according to the frequency of identification among the samples. Proteins with score ≤15 were reported as yellow triangle; proteins with score ≥35 were reported as red circle and proteins with a score in the range 15-35 were plotted as blue squares.

4.2. Clustering & Differential Analysis

All normalized lists (n= 19) of identified proteins were compared using MAProMa platform and performing a hierarchical clustering. As reported in Figure 24, the seven subjects resulted correctly grouped into the three corresponding categories (Ho, He, Wt). In particular, two main branches were reported: the first one contained the protein lists from wild type subjects (Wt) only, the second one, instead, included healthy carriers (He) and patients (Ho). In addition, He and Ho subjects resulted correctly sub-grouped, too.

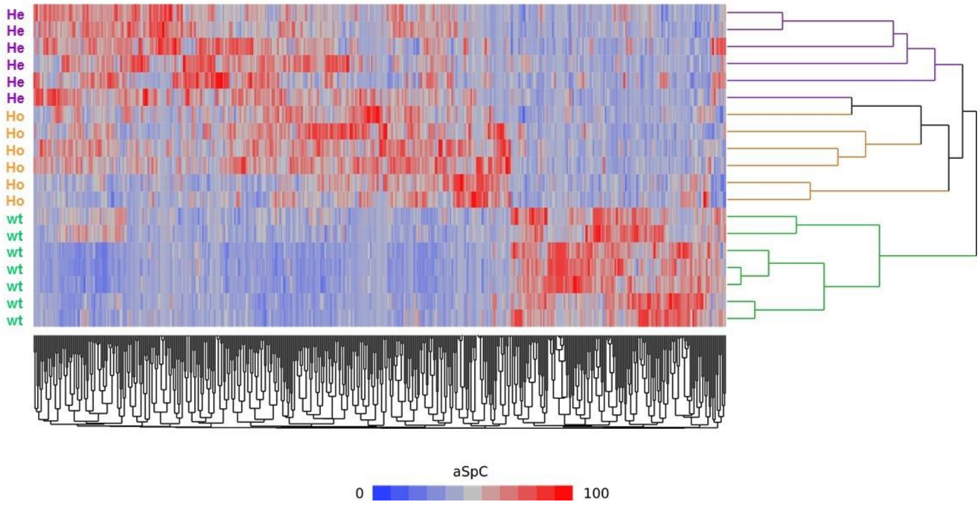

Figure 24. Hierarchical Clustering.
Dendogram of protein lists from 7 Nasu-Hakola's subjects and their technical replicates. Clustering performed by computing the average spectral count (aSpC) value of proteins selected by Linear Discriminant Analysis (LDA); Euclidean's distance metric and Ward 's method were applied. Categories were reported in different colours: He subjects in violet, Ho subjects in orange and Wt subjects in green.

The average lists from each category (Wt: 2246; He: 2353; Ho: 2560 identified proteins) were obtained and compared one-to-one, applying DAve (Differential Average) and DCI (Differential Coefficient Index) algorithms of MAProMa Software. Using stringent filters on SpC for both DAve and DCI indexes (0.4 and 15, respectively), it was possible to extract 272 differentially expressed proteins (DEP) (Appendix 2): 116 distinct proteins resulted differentially expressed comparing Wt and Ho subjects (77 down-represented in Ho and 39 up-regulated in Wt); 133 distinct proteins resulted differentially represented in He and Wt (38 down-regulated in Wt and 95 up-regulated in He). Of note, only 23 distinct proteins (7 down-represented in Ho and 16 up-represented in He) distinguished the protein profiles of heterozygote (He) from homozygote (Ho). This minimal difference was in agreement with the cluster analysis shown in Figure 24 and highlights the homology of protein expression profiles between heterozygote, He, and homozygote, Ho, subjects. The complete list of the up- and down-expressed proteins into the different categories is reported in Appendix 2.

Finally, about 500 proteins were extracted as discriminants from the total identified proteins by means of Linear Discriminant Analysis (LDA) applying a p<0.01. Of note, these selected LDA Significant Proteins (LDA-SP) include all 272 DEP reported above (Figure 25, Appendix 2).

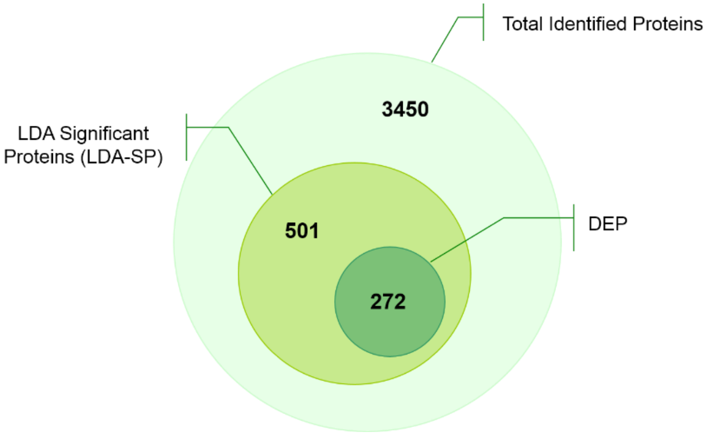

Figure 25. Diagram.
The figure shown the portion of LDA Significant Proteins (LDA-SP) and differentially expressed proteins (DEP) compared to the total identified distinct proteins in all processed samples and replicates.

The subcellular localization of these selected proteins was realized using data deposited in UniPROT database. We observed that 35% of them were cytoplasmic proteins; 20% were nuclear and 10% mitochondrial proteins; while 8% of them corresponded to membrane proteins. This subcellular distribution was conserved in the total identified proteins (Figure 26).

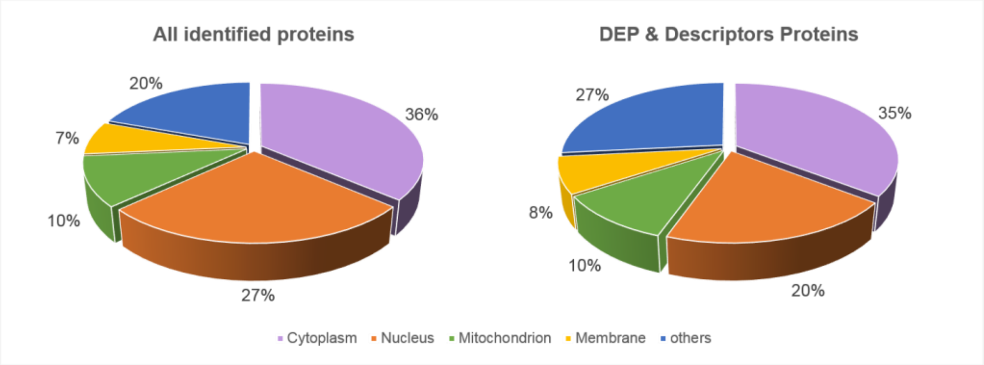

Figure 26. Subcellular Localization.
The subcellular localization was obtained using data deposited in UniPROT. The protein distribution of DEP and LDA-SP matched with the total identified proteins allocation.

4.3. Network Analysis: Systems Biology evaluation

The identification of a very large number of proteins and the availability of a *Homo Sapiens* network dataset constituted the premise to investigate the functional relationships between groups identified in this proteomic analyses (Wt, He, Ho). In this context, the differentially expressed proteins (DEP) and LDA Significant Proteins (LDA-SP), were plotted onto the protein-protein onteraction (PPI) network by means of Cytoscape and its plug-in. In this way, it was possible to identify four principal sub-networks: (i) Energetic metabolism (Glycolysis, Krebs Cycle and Electron Transport Chain); (ii) Cell cycle (Jak-STAT cascade, Chromatin assembly and Proteasome); (iii) Protein synthesis (Translation factors and mRNA splicing) and (iv) Cytoskeleton (Figure 28). Moreover, focusing on the possible comparisons (He *vs* Ho; He *vs* Wt; Wt *vs* Ho, Figures 29 - 31), many interesting pathways characterized by up- or down-regulated proteins were highlighted: JAK-STAT cascade, ER, Vescicle-mediated transport, extracellular region, T- and B-cell activations, etc. In particular, concerning energetic metabolism, pathways related to Glycolysis and Krebs Cycle were identified, confirming and increasing the identified differentially expressed proteins (DEP) identified by Giuliano et al [139] (Figure 27).

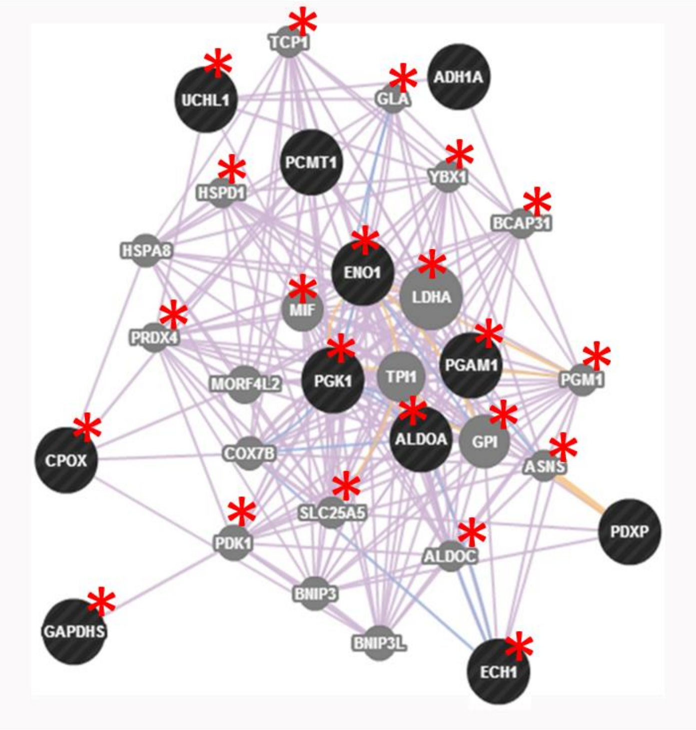

Figure 27. Glycolysis Network.
Identified proteins by Giuliano et al [139] reported in black circle. Red asterisk indicates the proteins identified in this work.

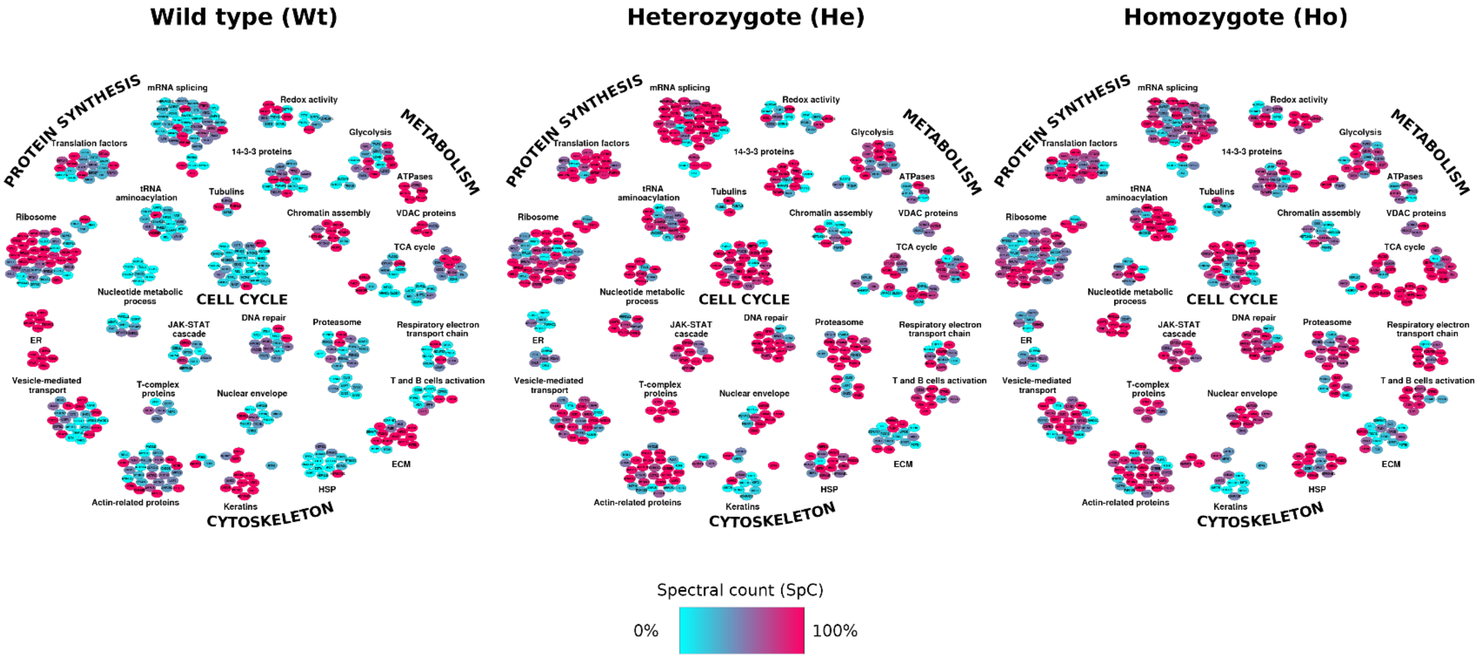

Figure 28. Protein-Protein Interaction (PPI) Network of Wt, He and Ho subjects.
The protein expression trend in Wildtype (Wt), Heterozygote (He) and Homozygote (Ho) subjects based on average Spectral Count (aSpC) by means of Cytoscape and its plug-in. Red circle: proteins up-regulated; blue circle: proteins down-regulated.

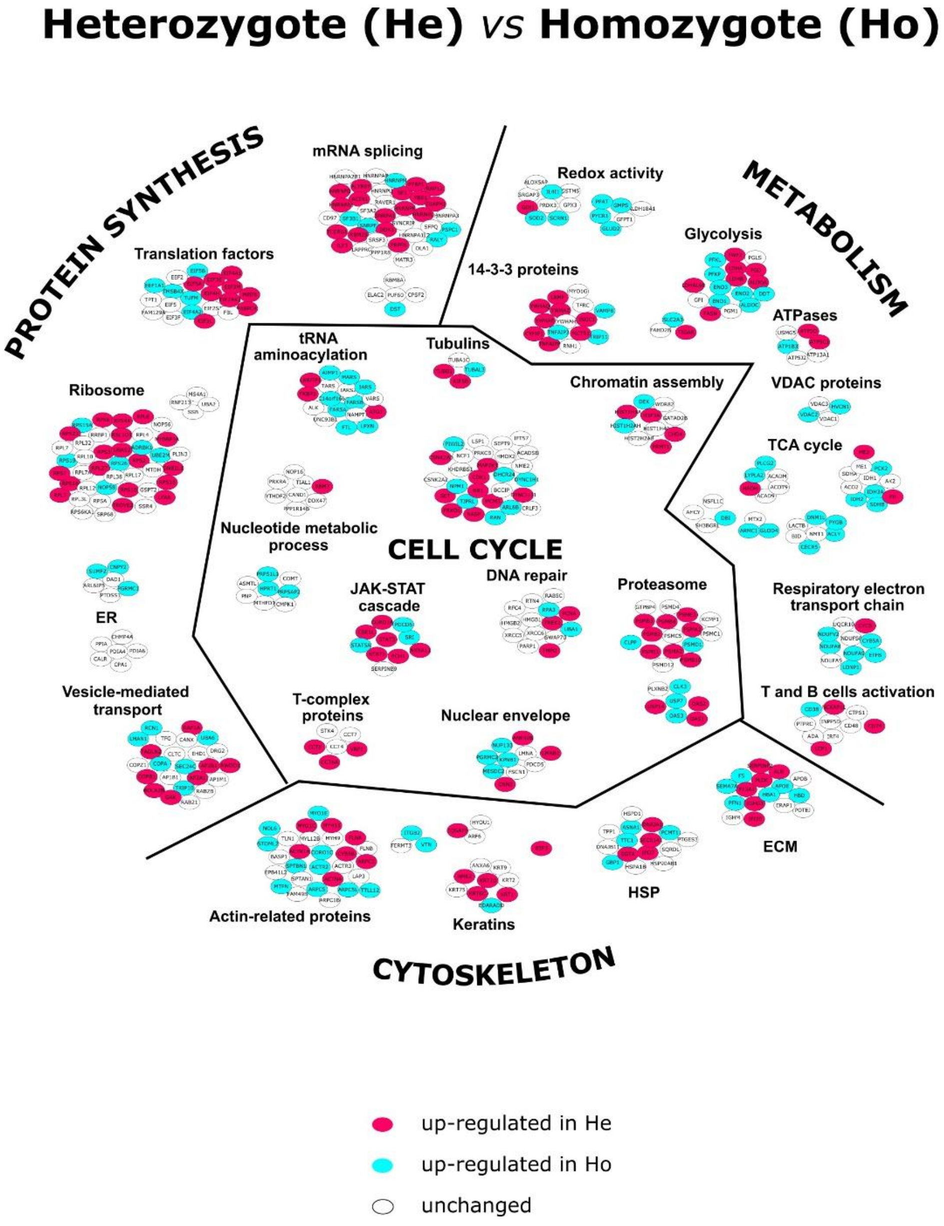

Figure 29. Protein-Protein Interaction (PPI) Network1.

The differentially expressed proteins between Heterozygote (He) and Homozygote (Ho) subjects, selected by LDA, plotted on protein-protein interaction Network by means of Cytoscape and its plug-in. Red circle: proteins up-regulated in He; blue circle: proteins up-regulated in Ho; white circle: unchanged proteins.

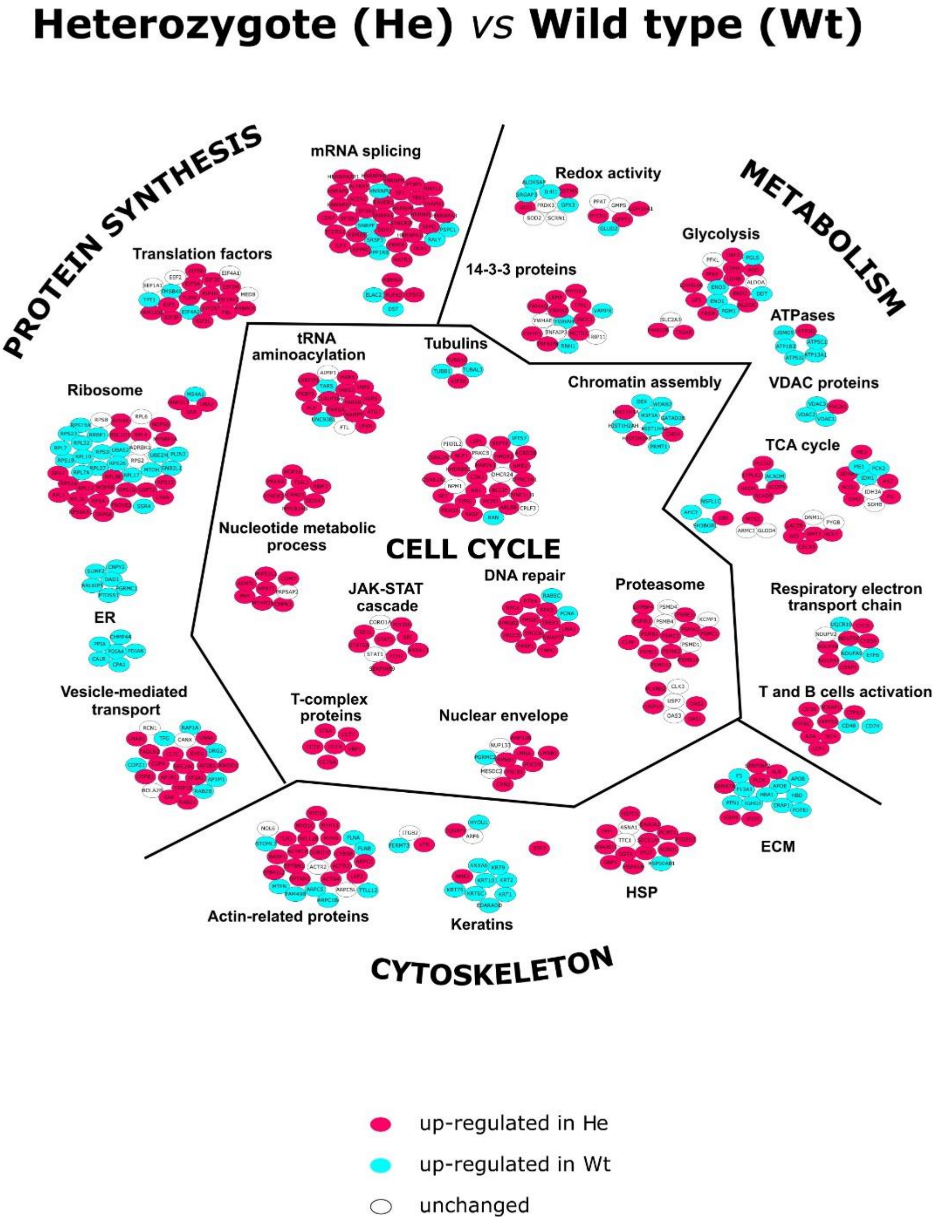

Figure 30. Protein-Protein Interaction (PPI) Network2.
The differentially expressed proteins between Heterozygote (He) and Wild Type (Wt) subjects, selected by LDA, plotted on protein-protein interaction Network by means of Cytoscape and its plug-in. Red circle: proteins up-regulated in He; blue circle: proteins up-regulated in Wt; white circle: unchanged proteins.

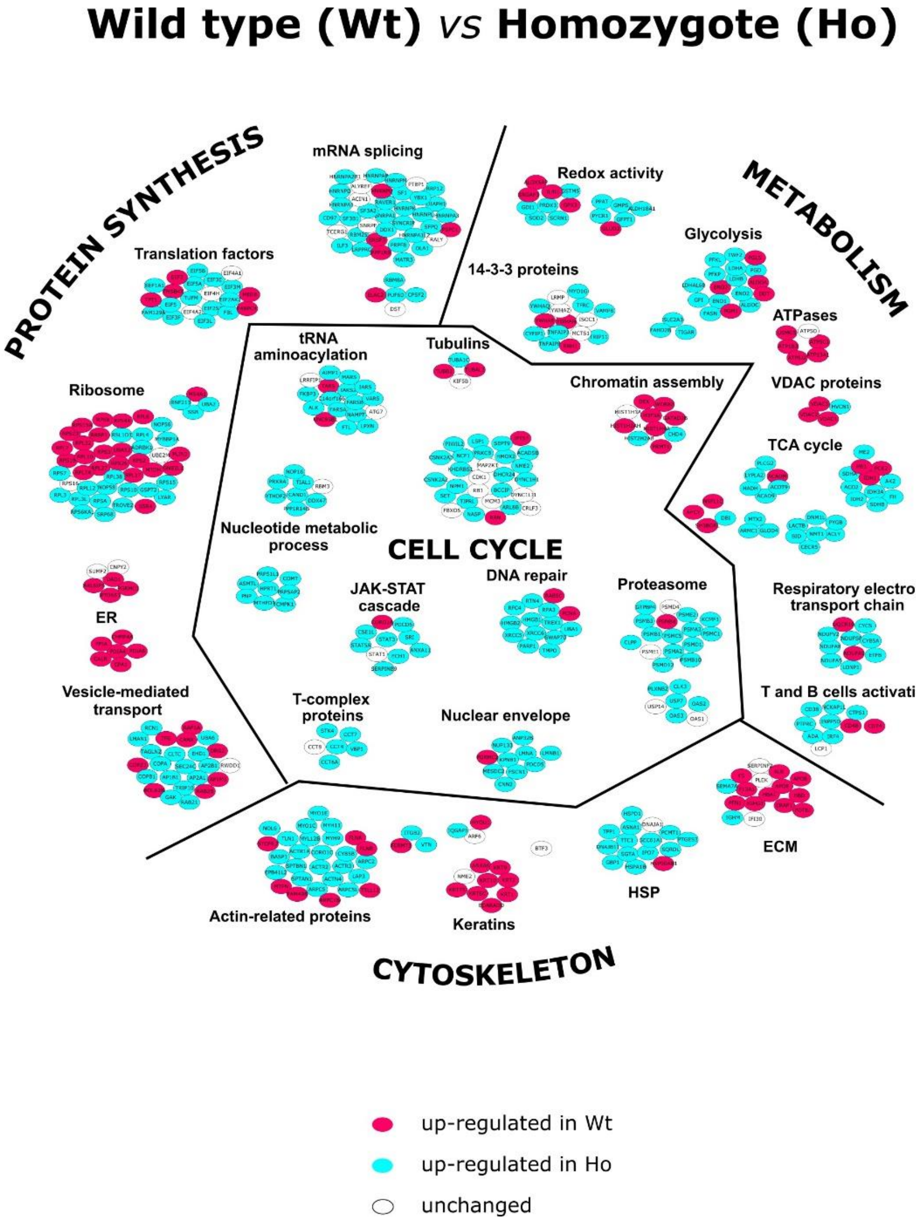

Figure 31. Protein-Protein Interaction (PPI) Network3.
The differentially expressed proteins between Wild Type(Wt) and Homozygote (Ho) subjects, selected by LDA, plotted on protein-protein interaction Network by means of Cytoscape and its plug-in. Red circle: proteins up-regulated in Wt; blue circle: proteins up-regulated in Ho; white circle: unchanged proteins.

Considering the importance of TREM2 receptor for Nasu-Hakola Disease, it was decided to deeply investigate its protein networking, even if TREM2 was unidentified in the proteomic analysis. The study allowed to identify 3 specific proteins that interacts with TREM2 (Figure 32): Ras-related C3 botulinum toxin substrate 1 (RAC1), Guanine nucleotide exchange factor (VAV2) and 1-Phosphatidylinositol 4,5-Bisphosphate Phosphodiesterase Gamma-2 (PLCG2). In particular, these TREM2 interactor proteins resulted down-regulated in healthy subjects (Wt) while they presented similar expression levels in both disease (Ho) and carriers (He). An alternative method to validate these data (Western Blot analysis), is ongoing during the writing of this thesis.

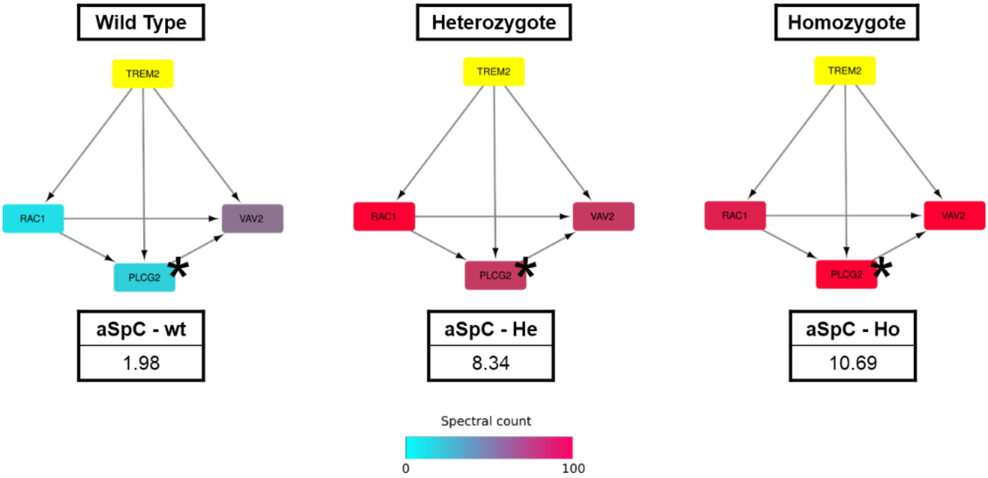

Figure 32. TREM2-interactor proteins.
Three different proteins associated to TREM2 network were highlighted: RAC1, PLCG2 and VAV2. These interactor proteins resulted up-regulated in NHD patients (Ho) in comparison with healthy subjects (Wt). (*) statistically significant value.

At last, the co-receptor of TREM2, DAP12, was not detected in our analysis, but it was possible to identify its protein interactor Sialic acid-binding Ig-like lectin 14 (SIGLEC14).

5. DISCUSSION

Our innovative proteomic approach is aimed to better understand the driving mechanisms of NHD as well as identify key protein markers useful for the diagnosis and/or treatment of this TREM2-based disease. Previously, NHD has been investigated using myeloid cells, but the Lymphoblastoid cells line (LCL) may be a precious alternative (as previously stated in paragraph 1.1.3. – “IntroductionLimitations of the study”), because it present the TREM2 expression and its mutation, as evidenced by Giuliano et al [139].

It is known that transcript levels do not completely correlate with protein expression levels, so proteomic analysis is needed to supplement genomic and transcriptomic analysis. Sure enough, in literature proteomic studies on NHD were lacking and recently Giuliano et al. applied traditional 2Dgel-electrophoresis for a preliminary proteomics investigation of NHD [139]. In the present PhD work, for the first time has been performed the analysis of more complete proteome of LCLs obtained from seven subjects of an entire family carrier of TREM2 mutation, including 2 homozygotes, manifesting dementia, and 4 heterozygotes subjects. Specifically, using MudPIT approach, based on *gel-* and *label-free* strategy, about 3500 distinct proteins were identified, 100-fold higher than those identified by 2-DE [139], including a very large dynamic range in terms of isoelectric point (pI) and molecular weight (MW); in addition, subsets of proteins were associated to each specific group (Ho, He or Wt).

To gather the biological message of this work, a Protein-Protein Interaction (PPI) Network was built. Based on the total human protein network, the most significant proteins (LDA-SP) were grouped into four principal sub-networks: (i) Energetic Metabolism (ii) Cell Proliferation; (iii) Protein synthesis and (iv) Cytoskeleton.

Although the phenotype of He is healthy, both cluster and differential analyses evidenced that the protein profile of heterozygote results more similar to homozygote than wildtype. The 90% of proteins that shown a specific behavior in Wt subjects, then appeared to own completely opposite trend in He and Ho, with different expression levels. This observation is well highlighted in Figure 28, in which it is clear the similar expression trend between He and Ho: the majority of proteins down-represented in sub-networks of Wt subjects (reported in blue), resulted up-represented in He and Ho subjects (reported in red).

On the basis of the previous considerations, we focused our attention on proteins emerging from the Heterozygote (He) *vs* Homozygote (Ho) comparison.

5.1. Focus on Energetic Metabolism.

The µ2DC-MS/MS method allowed to confirm the differential trend of identified proteins by Giuliano et al. [139] and, at the same time, to identify additional proteins belonging to the Glycolysis Network (Figure 27).

Glycolysis sub-group includes: PFKL, PFKP, ENO1, ENO2, ENO3, ALDOC, DDT and SLC2A3 (up-regulated in Ho); TWF2, LDHA, LDHB, PGD, ALDOA, LDHAL6B, FASN and TIGAR (up-regulated in He) (Figure 33). In particular, ALDOC and ENO1 previously have been already associated to psychiatric disorders [218–220]. ALDOC is a brain-specific glycolytic enzyme that we found up-regulated in disease subjects; this agrees with what has been pointed out by previous studies about mood disorders [221, 222].

These findings allow to validate the hypothesis advanced by Giuliano et al. [139] about the alteration of energy metabolism in NHD patients. They proposed that the impaired glucose metabolism could be a result of the accumulation of glycolytic intermediates. In particular, this fact supports the idea that the general decrease of energy metabolism due to the reduced metabolic rate of glucose may be a feature of NHD, at least as far as the neurodegenerative aspect is concerned. Sure enough, it is known that, to maintain its functions, brain needs an enormous amount of energy compared with another tissues, to maintain its functions. Moreover, the majority of glycolysis proteins resulted up-regulated in homozygote, while proteins related to redox activity, TCA and Respiratory electron transport chain resulted down-regulated in heterozygote. In particular, redox activity sub-network up-represented in disease subjects, includes: IL4I1, SOD2, SCRN1, PPAT, GMPS, PYCR1 and GLUD2. TCA sub-network is formed by: PLCG2, LYPLA2, PCK2, IDH3A, IDH2, SDHB, DBI, ARMC1, GLOD4, DNM1L, PYGB, ACLY and CECR5 up-regulated in Ho; ME2, FH and HADH up-represented in He. A particular mention deserves PLCG2 proteins because directly connected to TREM2 protein (for details see Chapter 5.5 – “Focus on TREM2 network”). Respiratory electron transport chain sub-group includes: NDUFV2, NDUFA8, NDUFA9, CYB5A, ETFB and LONP1 up-regulated proteins in homozygote and CYCS protein with opposite trend.

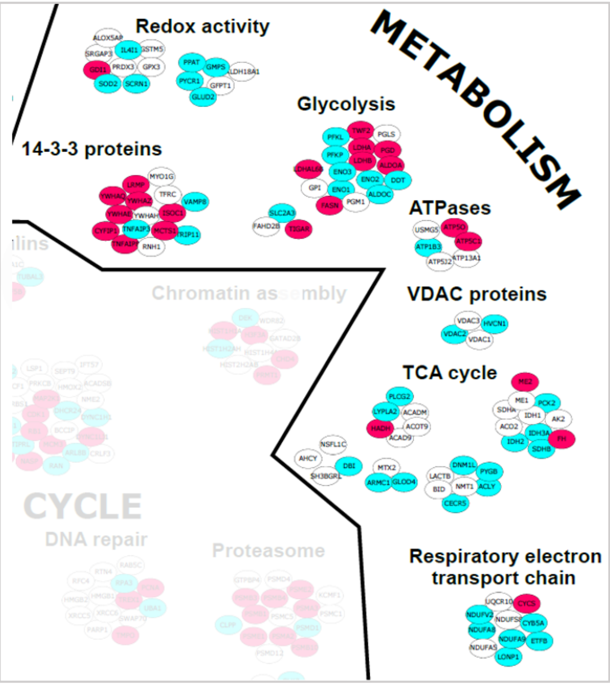

Figure 33. Zoom on Energetic Metabolism Network.
Protein up-regulated in He are reported in red; Protein up-regulated in Ho are reported in blue.

Among the Energetic Metabolism sub-groups, 14-3-3 proteins represent the only proteins expressing an opposite trend. In details, the majority of its components are up-regulated in heterozygote subjects: LRMP, YWHAQ, YWHAZ, YWHAE, ISOC1, CYFIP1, MCTS1 and TNFAIP8.

5.2. Focus on Cell Proliferation and Cytoskeleton.

Our data confirmed the effects of TREM2-mutations on cell proliferation [223–225]; sure enough, proteomics data evidenced the up-regulation of the proteins implicated in cell cycle, JAK-STAT cascade [226], DNA repair and proteasome in both Heterozygote (He) and Homozygote (Ho) (Figure 28); these findings are coherent with the observed down-regulation of chromatin assembly sub-network and the activation of actin-related proteins and HSP processes. In particular, the sub-network of heat shock proteins (HSP) resulted completely down-expressed by healthy subjects in comparison with heterozygote and/or homozygote. This observation agrees with results reported by Stefano and co-worker [96] about the importance of HSP60 (called HSPD1, also) as activation agonist of TREM2, as it induces all critical processes governed by the receptor in myeloid cells, osteoclast and microglia (phagocytosis, proliferation, activation and migration, apoptosis phenomenons). In addition, Koh et al. [227] published a proteomic work about the implication of HSP60 in osteoclast bone resorption, identifying this protein as up-regulated. Recently, Ferrari et al [228] reported a co-expression network of FTD-cluster-genes that revealed a specific enrichment for DNA metabolism (i.e. transcription regulation, chromatin remodeling), immune processes and protein meta/catabolism, supporting our data.

5.3. Focus on Immune System

As previously mentioned, the recognition of a role of innate immune activation in the pathogenesis of many neurodegenerative diseases, including Parkinson’s disease (PD), amyotrophic lateral sclerosis (ALS), Huntington’s disease (HD) and frontotemporal dementia (FTD) is growing. It is interesting to note that TREM2 gene is allocated on chromosome 6, where are organized hundred genes codifying for immunological system. In this context, the sub-network related to T- and B-cell activation resulted strangely up-regulated in Heterozygote subjects (Figure 34). In particular, in the comparison He *vs* Ho NCKAP1L, CD74 and LCP1 are up-regulated in the first term of comparison, while only CD38 is up-regulated in disease subjects. An increase of CD74 protein, a chaperone involved in antigen presentation during immune response, was associated to an increase of neurodegeneration process. Furthermore, in diabetes studies CD74 was identified as a microglial activation marker, too [229, 230]. Given the role of CD38 in neuroinflammation and repair processes, Blacher et al. investigated the effect of CD38 deletion on AD pathology [231]. The authors demonstrated that CD38$^{-/-}$ mice exhibited significant reductions in Aβ plaque in AD, according with our data.

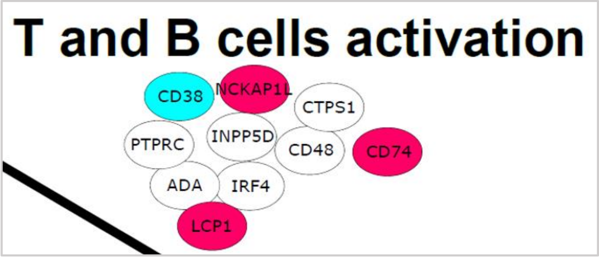

Figure 34. Zoom on T- and B-cell activation Network.
Protein up- regulated in He are reported in red; Protein up-regulated in Ho are reported in blue.

The data reported until now support the hypothesis that events occurring in LCLs could be the mirror of what happens into the districts where the pathology is localized, i.e. microglia and osteoclast cells.

5.4. Focus on Protein Synthesis.

Regarding the Protein Synthesis sub-network (Figure 35), it resulted overall up-regulated in Heterozygote individuals, including: HNRNPD, HNRNPA1, HNRNPK, HNRNPL, ALVREF, ACIN1, SF1, PTBP1, RRP12, YBX1, DIAPH1, SNRPA1, DDX1, PRPF8, RBM25, TCERG1 and ILF3 (mRNA splicing events); EIF4A1, EIF3E, EIF5A, EIF4H, EIF3M, EIF2AK2, EIF3L, MED8 and PABPC4 (translation factors); RPS2, RPS3, RPS8, RPS4X, RPS7, RPS10, RPS15, RPS16, RPS23, RPL3, RPL6, RPL27, TROVE2, LYAR, GNB2L1, UBA52, MYBBP1A and RSL1D1 (ribosome proteins); RAP1A, TAGLN2, COPB1, BOLA2B, GAK, AP2A1, AP2B1 and RWDD1 (vescicle-mediated transport). These data support the importance of heterozygous profile in FTDs and accordingly in NHD, too.

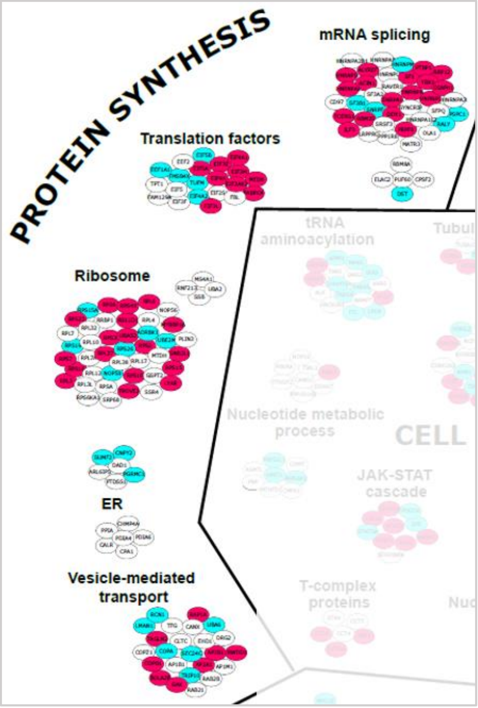

Figure 35. Zoom on Protein Synthesis Network.
Protein up- regulated in He are reported in red; Protein up-regulated in Ho are reported in blue.

5.5. Focus on TREM2 network

Finally, in order to evaluate the behavior of TREM2's activation way, in disease state compared to healthy condition, the investigation was focused on TREM2's protein network, identifying some dysregulated proteins involved in TREM2 activation among the investigated groups (Ho, He, Wt). Despite TREM2 was unidentified in this proteomics analysis, three proteins associated to TREM2 network were identified at very low levels: Ras-related C3 botulinum toxin substrate 1 (RAC1), Guanine nucleotide exchange factor (VAV2) and 1-Phosphatidylinositol 4,5-Bisphosphate Phosphodiesterase Gamma-2 (PLCG2). In particular, PLCG2 is a crucial enzyme in transmembrane signaling, and in osteoclasts, it forms a complex with the regulatory adapter molecule GAB2, modulating GAB2 recruitment to RANK and inducing osteoclastogenesis [232]. It is interesting to note that the 3 identified proteins resulted to show a positive trend, increasing their expression at similar levels in both heterozygote (He) and homozygote (Ho). However, NHD is expressed in Ho, only. This may be considered a confirmation that PLCG2, RAC1 and VAV2 were not correlated to disease. Co-receptor of TREM2, DAP12, was not detected in our analysis, but it was possible to identify one of its interactors, Sialic acid-binding Ig-like lectin 14 (SIGLEC14), an additional protein linked to chaperonine pathway.

6. CONCLUSIONS

Nasu-Hakola Disease is a very peculiar pathology, but for its features can be considered a good model for a deeper understanding of Frontotemporal TREM2-based diseases. Given the absence of reports dealing with the application of shotgun proteomics to NHD investigation, this PhD work represents a proof of principle in this field. In fact, here, an extensive protein profile of Lymphoblastoid cells from NHD subjects has been performed and it was useful to tentative characterize metabolic pathways involved in functional alterations of this pathology.

Despite this, it is fair to point out that a limitation of the present study is the sample size of individuals examined. However, the apparently low number of subjects enrolled in this study (n=7; 2/7 kin NHD subjects), considering the rare pathology they are suffering, is however a strength in comparison with the individual cases discussed in literature. Sure enough, for the first time, a more complete set of expressed proteins by LCLs belonged to kin NHD subjects was investigated.

It is interesting to note that proteomic clustering confirmed the clinical classification of the subjects, proving the efficiency of MudPIT approach on NDs studies. Moreover, our data highlighted that the proteomic profiles of He and Ho were more similar to what one could expect from their phenotype. This is a very interesting point because opens the way to new investigations aimed to unravel the reasons for the difference between healthy carriers and sick subjects. By means of network analysis, possible metabolic pathways involved in functional alterations caused by NHD were widely characterized. In addition, our study may help to set up new experiments targeted to identify possible circulating biomarkers.

This work contributed to obtain a widest vision about the protein perturbations involved in NHD, being a starting point for the discovery of new biomarkers of TREM2-based dementias. Given the similarity with other FTDs, our approach could significantly contribute, in the future, to manage these diseases. In fact, this approach could represent a new non-invasive early diagnostic method to investigate neurodegenerative diseases, for which only post-mortem analysis are feasible.

Of course, more investigations are needed to confirm the correlation of the described pathways with TREM2-related loss of functions disease, including frontotemporal dementia. Sure enough, the interactor proteins of TREM2 and pathways involved in NHD will be validated and characterized by alternative methods. Moreover, additional studies on a new Italian family affected by NHD are ongoing and will be capable to validate and to extend these preliminary results. Of note, the data presented here are so promising that could support a continuation of the project on TREM2-KO mouse model. This new phase of the work will permit to obtain the proteomic profile of microglia and osteoclast cells and will highlight the molecular mechanisms triggered by TREM2 silencing.

7. BIBLIOGRAPHY

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8. APPENDIX

Appendix 1. Complete list of identified protein expressed by the seven subjects of the Italian family affected by NHD.

For each protein are reported: GI Accession Number, Gene Name, Reference, pI, MW, Hits and Score of each subject.

#	Accession	Gene Name	Reference	pI	MW	Subject Wt - I1		Subject He - I2		Subject He - I3		Subject He - III1		Subject He - II4		Subject Ho - II2		Subject Ho - II1	
						Hits	**Score**	**Hits**	**Score**	**Hits**	**Score**	**Hits**	**Score**	**Hits**	**Score**	**Hits**	**Score**	**Hits**	**Score**
1	1000704	NNT	NAD(P) transhydrogenase	8,0	113948	1	11,1	0	0,0	0	0,0	0	0,0	0	0,0	1	9,4	1	9,7
2	10047313	RNF213	KIAA1618 protein	5,6	160273	2	15,9	2	15,1	1	8,7	4	18,8	0	0,0	1	9,0	1	9,7
3	10047337	DHTKD1	KIAA1630 protein	6,3	101086	1	9,7	1	10,1	1	8,7	1	9,4	0	0,0	2	11,7	1	7,9
4	1008089	PSMD2	55.11 protein	5,0	99316	4	32,2	4	19,9	4	31,8	2	18,8	2	12,2	5	36,2	4	25,1
5	100816392	FUBP3	far upstream element-binding protein 3	8,4	61622	0	0,0	1	10,3	1	9,9	1	9,4	0	0,0	0	0,0	2	7,9
6	1009337	RANBP2	RanBP2 (Ran-binding protein 2)	5,8	358170	1	11,7	0	0,0	1	9,3	0	0,0	0	0,0	1	9,6	1	7,9
7	1017757	PRKDC	DNA-PK, partial	6,5	105853	1	9,7	1	10,0	2	9,3	1	9,4	2	12,2	3	8,0	0	0,0
8	10197646	TRMT11	AF182423_1 MDS024	6,4	29193	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
9	1020315	GPD2	glycerol-3-phosphate dehydrogenase	7,3	80834	1	10,8	1	9,7	0	0,0	1	9,5	0	0,0	1	8,0	0	0,0
10	102469694	LGALS9	galectin-9 isoform short	8,1	35889	2	15,5	1	9,7	0	0,0	4	26,2	0	0,0	0	0,0	1	9,7
11	10334541	IGHG3	immunoglobulin heavy chain	7,9	41302	1	11,7	1	10,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
12	10337595	PPM1A	protein phosphatase 1A isoform 1	5,1	42449	1	10,9	2	19,3	1	9,9	0	0,0	0	0,0	1	9,1	2	13,6
13	10346135	MAPRE2	microtubule-associated protein RP/EB family member	5,3	37013	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	1	8,7	2	9,7
14	103471987	ISOC1	isochorismatase domain-containing protein 1	7,2	32218	0	0,0	2	10,1	1	9,8	1	9,5	0	0,0	0	0,0	0	0,0
15	1037164	PSMD8	26S proteasome subunit p31	7,2	30006	2	10,5	3	10,0	2	9,3	1	9,5	2	12,2	1	8,9	2	9,7
16	1040689	SEPT2	Human Diff6,H5,CDC10 homologue	7,0	46586	5	45,8	3	24,6	8	49,5	8	46,8	9	72,3	6	38,5	6	51,1
17	1042034	PIP4K2A	1-phosphatidylinositol-4-phosphate 5-kinase isoform C	6,9	46060	1	9,7	1	9,7	1	9,2	1	9,4	0	0,0	1	8,0	2	15,7
18	10432591	LARS	unnamed protein product	7,0	50091	1	11,7	0	0,0	1	9,9	0	0,0	2	12,2	4	19,4	1	8,0
19	10433597	NAT10	unnamed protein product	8,3	115748	1	9,7	1	9,7	1	9,8	4	28,1	0	0,0	1	8,9	0	0,0
20	10433717	TUBB6	unnamed protein product	4,6	49844	1	11,2	0	0,0	1	17,7	4	28,1	5	24,3	1	14,2	2	17,4
21	10433885	H2AFY2	unnamed protein product	10,5	29898	0	0,0	1	10,3	1	9,9	0	0,0	0	0,0	0	0,0	0	0,0
22	10433909	PRRC2C	unnamed protein product	9,5	65579	1	11,6	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
23	10434033	ACAD9	unnamed protein product	7,8	55084	0	0,0	1	10,0	1	8,7	0	0,0	2	12,2	0	0,0	1	7,9
24	10434042	USP25	unnamed protein product	5,1	85843	0	0,0	0	0,0	0	0,0	1	9,4	0	0,0	0	0,0	0	0,0
25	10434055	CHD9	unnamed protein product	8,5	84016	0	0,0	0	0,0	0	0,0	0	0,0	2	12,2	0	0,0	0	0,0
26	10434343	DARS2	unnamed protein product	6,1	52640	1	11,1	0	0,0	1	8,7	0	0,0	0	0,0	1	9,4	1	13,6
27	10434384	WDR12	unnamed protein product	5,6	47544	1	13,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
28	10434632	SMG9	unnamed protein product	6,2	54788	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
29	10434704	VPS26A	unnamed protein product	6,3	38199	1	12,4	2	19,9	0	0,0	2	18,8	0	0,0	0	0,0	0	0,0
30	10435148	ARHGAP17	unnamed protein product	6,4	78623	1	12,0	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
31	10435325	NAA15	unnamed protein product	8,1	61603	1	11,2	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	1	8,8
32	10435327	KCMF1	unnamed protein product	5,4	41874	1	9,7	0	0,0	1	9,3	1	9,5	2	12,2	1	9,1	1	9,7
33	10435335	H2AFY	unnamed protein product	10,2	39592	3	17,9	2	19,3	4	14,2	1	9,5	2	12,2	3	13,3	4	16,1
34	10435519	RARS2	unnamed protein product	8,2	65488	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	1	8,0	0	0,0
35	10436017	NELFCD	unnamed protein product	4,8	66220	0	0,0	0	0,0	1	8,6	0	0,0	2	12,2	0	0,0	0	0,0
36	10436199	CIZ1	unnamed protein product	5,6	93675	0	0,0	0	0,0	1	8,6	0	0,0	0	0,0	0	0,0	0	0,0
37	10436325	MRPL44	unnamed protein product	8,7	37506	0	0,0	0	0,0	1	8,6	0	0,0	0	0,0	1	9,3	1	7,9
38	10436857	EEF1D	unnamed protein product	6,2	71418	6	39,1	1	10,0	6	37,3	6	37,4	11	60,3	5	36,3	5	31,4
39	10437006	WDR26	unnamed protein product	5,4	41840	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,8	0	0,0
40	10437129	ABCF3	unnamed protein product	7,4	45090	1	11,2	0	0,0	0	0,0	1	9,4	0	0,0	0	0,0	0	0,0
41	10437984	ESYT1	unnamed protein product	5,3	97131	2	22,0	2	14,8	1	9,2	6	37,4	8	60,3	2	13,7	2	14,9
42	10438128	INTS3	unnamed protein product	5,4	50943	0	0,0	1	10,3	1	9,3	0	0,0	0	0,0	0	0,0	0	0,0
43	10438183	NOL6	unnamed protein product	6,4	45977	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	1	9,8	1	9,6
44	10438313	PIP4K2C	unnamed protein product	5,8	25000	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
45	10438469	APMAP	unnamed protein product	6,1	25123	0	0,0	2	10,1	1	8,7	0	0,0	0	0,0	0	0,0	0	0,0
46	10438576	RNF213	unnamed protein product	7,7	104444	2	15,9	2	14,8	2	17,2	1	9,4	0	0,0	1	11,7	1	13,4
47	10438756	NUP210	unnamed protein product	5,5	50363	1	12,5	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
48	10438851	RBM25	unnamed protein product	10,0	51398	0	0,0	1	9,9	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
49	10438892	MFF	unnamed protein product	7,4	32974	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,8
50	10439439	HINT1	unnamed protein product	6,0	13804	2	14,3	5	30,7	5	13,6	4	18,9	3	12,2	4	12,9	7	19,2
51	10439794	SLC12A8	unnamed protein product	5,8	34758	0	0,0	0	0,0	1	9,8	0	0,0	0	0,0	0	0,0	0	0,0
52	10439926	ATL2	unnamed protein product	5,6	66160	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	0	0,0
53	10440119	PPP1R12C	unnamed protein product	5,8	66269	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9

54	10440375	MRPS25	FLJ00023 protein	9,5	21910	0	0,0	1	10,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
55	10440462	UNC13D	FLJ00067 protein	6,2	63335	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,1	0	0,0
56	10444289	KSR2	MYG1 homolog	6,3	42446	1	9,6	2	14,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
57	1049104	DST	dystonin isoform 1, partial	5,4	53873	1	12,4	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
58	1050527	SARS	seryl-tRNA synthetase	6,0	58751	2	20,0	4	24,7	1	9,9	5	28,1	2	12,3	3	26,4	6	43,5
59	10635153	SRC	v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene ho	7,8	60570	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
60	10637168	IGKV1	immunoglobulin kappa chain variable region	7,9	8951	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,6
61	10637309	IGKV1	immunoglobulin kappa chain variable region	8,8	9126	0	0,0	2	10,0	1	15,5	0	0,0	0	0,0	0	0,0	0	0,0
62	10637404	IGKV2D	immunoglobulin kappa chain variable region	7,0	9288	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7	0	0,0
63	10645195	HIST1H2AB	histone H2A type 1-B/E	11,5	14136	41	28,6	45	19,9	63	18,5	36	9,5	71	24,3	52	18,0	68	19,3
64	1066082	UBE2V1	DNA-binding protein	8,4	25798	1	11,5	2	10,0	0	0,0	2	18,8	0	0,0	2	8,0	0	0,0
65	106897261	IGHV5	circulating B cell antibody heavy chain variable reg	6,5	13079	0	0,0	0	0,0	1	9,9	0	0,0	0	0,0	0	0,0	0	0,0
66	10800412	MAPRE3	microtubule-associated protein RP/EB family member	5,2	31964	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,6
67	10801139	HLA	MHC class II antigen	6,1	10868	2	12,0	2	10,0	4	9,3	1	9,4	2	12,2	5	14,8	5	9,7
68	10801345	EIF3K	eukaryotic translation initiation factor 3 subunit	4,7	25042	1	9,7	0	0,0	1	8,7	1	9,5	0	0,0	0	0,0	0	0,0
69	1082034	PTK2B	focal adhesion kinase	5,8	115816	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	1	8,7	1	9,7
70	10835063	NPM1	nucleophosmin isoform 1	4,5	32576	9	11,5	7	10,1	7	9,3	5	9,5	8	12,3	8	9,1	12	9,7
71	10835121	PKLR	pyruvate kinase isozymes R/L isoform 1	7,6	61812	4	11,4	3	10,0	6	9,8	7	9,4	6	12,2	4	9,0	3	8,8
72	10835256	PYCARD	apoptosis-associated speck-like protein containing	5,9	21609	1	10,4	0	0,0	1	8,7	1	9,5	2	12,3	1	8,0	1	7,9
73	10863945	XRCC5	X-ray repair cross-complementing protein 5	5,5	82686	12	68,9	20	88,9	24	67,8	20	84,1	20	96,4	19	83,1	18	72,8
74	10863955	PSAT1	phosphoserine aminotransferase isoform 2	6,2	35170	1	14,6	0	0,0	2	13,5	0	0,0	0	0,0	0	0,0	1	9,6
75	10863977	LSM2	U6 snRNA-associated Sm-like protein LSm2	6,1	10816	1	12,1	0	0,0	0	0,0	1	9,5	0	0,0	0	0,0	0	0,0
76	10863997	PTBP2	polypyrimidine tract-binding protein 2	9,0	57472	1	11,2	0	0,0	1	9,8	1	9,4	0	0,0	0	0,0	0	0,0
77	10864011	SQRDL	sulfide:quinone oxidoreductase, mitochondrial	9,4	49942	1	14,0	3	25,0	5	32,4	1	9,5	2	12,2	4	28,8	2	19,2
78	10864017	ENOPH1	enolase-phosphatase E1	4,5	28933	0	0,0	0	0,0	1	9,9	1	9,5	0	0,0	1	8,1	1	8,0
79	108796056	TROVE2	60 kDa SS-A/Ro ribonucleoprotein isoform 1	8,5	59252	1	10,6	3	19,9	3	17,9	1	9,4	2	12,2	2	16,9	2	12,3
80	10880989	RAB18	ras-related protein Rab-18 isoform 1	5,0	22959	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
81	108936958	DCAF7	DDB1- and CUL4-associated factor 7	5,2	38927	0	0,0	1	10,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
82	109134349	COPG2	coatomer subunit gamma-2	5,5	97623	1	11,2	2	15,1	2	9,3	0	0,0	3	24,2	2	8,9	0	0,0
83	109150416	PXDN	peroxidasin homolog precursor	6,8	165275	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
84	10933784	RNPEP	aminopeptidase B	5,4	72624	2	18,3	2	19,3	1	9,3	1	9,5	0	0,0	1	9,0	1	10,6
85	109389365	G6PD	glucose-6-phosphate 1-dehydrogenase isoform a	8,0	62450	3	34,1	4	34,5	3	22,1	1	9,5	3	24,2	2	21,1	5	30,2
86	109693027	HLA	MHC class I antigen	6,4	20914	0	0,0	0	0,0	0	0,0	0	15,1	2	12,2	1	9,8	1	8,9
87	109693166	ENSG00000228325	immunoglobulin light chain variable region	8,2	11729	0	0,0	0	0,0	1	9,9	0	0,0	0	0,0	0	0,0	0	0,0
88	109715854	CARHSP1	calcium-regulated heat stable protein 1	8,2	15874	0	0,0	0	0,0	0	0,0	1	9,5	0	0,0	1	8,0	0	0,0
89	109730545	MANF	Arginine-rich, mutated in early stage tumors	9,1	21126	3	24,4	2	10,0	2	13,6	1	9,5	0	0,0	2	11,7	3	21,4
90	109731245	CASP5	Caspase 5, apoptosis-related cysteine peptidase	9,2	47757	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
91	109731503	TRIP12	TRIP12 protein	8,7	225520	0	0,0	0	0,0	1	9,8	0	0,0	0	0,0	0	0,0	0	0,0
92	110227601	COASY	bifunctional coenzyme A synthase isoform a prec	6,5	62310	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7	0	0,0
93	110347418	SMC2	structural maintenance of chromosomes protein 2	8,6	135637	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
94	11034845	RPRD1B	regulation of nuclear pre-mRNA domain-containing pr	5,6	36881	1	11,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
95	110349738	STK24	serine/threonine-protein kinase 24 isoform b	5,2	47895	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
96	110349786	ALMS1	Alstrom syndrome protein 1	5,8	461189	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
97	1103842	STOM	band 7.2b stomatin	8,0	32594	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
98	11038643	AP2S1	AP-2 complex subunit sigma isoform AP17delta	5,5	12399	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
99	11056044	HEL	inorganic pyrophosphatase	5,5	32661	0	0,0	0	0,0	1	9,2	0	0,0	2	12,2	1	8,7	1	9,7
100	110611218	RRBP1	ribosome-binding protein 1	5,3	108656	1	16,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
101	11067747	CDC5L	cell division cycle 5-like protein	8,3	92251	1	12,5	0	0,0	0	0,0	1	9,5	0	0,0	0	0,0	1	7,9
102	1107696	CHD4	Mi-2 protein	5,5	217990	2	13,5	7	39,9	7	39,8	7	37,5	2	12,2	2	14,9	5	22,4
103	11095441	ALDH6A1	methylmalonate-semialdehyde dehydrogenase	8,6	57821	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
104	111052651	G6PD	glucose-6-phosphate dehydrogenase	7,4	8166	1	12,1	0	0,0	1	8,6	0	0,0	0	0,0	1	8,6	0	0,0
105	111052653	G6PD	glucose-6-phosphate dehydrogenase	7,8	7187	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
106	111118981	FDXR	NADPH:adrenodoxin oxidoreductase, mitochondrial is	8,4	53818	1	10,4	5	24,7	2	13,5	0	0,0	0	0,0	3	18,5	5	32,6
107	11121196	DDX47	DEAD box protein	9,3	50636	0	0,0	1	10,0	0	0,0	0	0,0	0	0,0	1	8,9	1	9,7
108	11125770	AIMP2	aminoacyl tRNA synthase complex-interacting multifu	8,2	35331	1	11,9	2	9,7	1	9,2	1	9,4	2	12,1	1	9,7	1	10,5
109	11128019	CYCS	cytochrome c	10,0	11750	1	9,7	3	19,9	3	22,7	2	18,8	2	12,2	3	26,9	1	9,8
110	111305821	HEL	Valosin-containing protein	5,1	89344	7	32,9	3	19,8	2	13,5	5	28,2	3	24,2	2	17,5	2	16,0
111	111306395	MORF4L1	MORF4L1 protein	9,5	26880	0	0,0	1	9,8	1	9,9	1	9,5	0	0,0	1	8,1	1	7,9
112	111494085	HNRPR	HNRPR protein	9,1	67861	0	0,0	0	0,0	1	9,9	1	9,5	0	0,0	0	0,0	1	9,8
113	1122278	USP5	de-ubiquitinase	4,8	95745	3	25,6	6	39,6	3	17,9	4	9,5	2	12,2	3	17,4	3	15,5
114	11225260	TOP1	DNA topoisomerase 1	9,7	90726	1	10,8	0	0,0	1	8,7	0	0,0	0	0,0	1	8,7	1	10,6
115	11225591	TAPBP	AF314222_1 tapasin	6,5	43886	5	9,7	2	15,1	6	13,6	1	9,4	2	12,2	2	8,9	4	13,6
116	112293277	DNAJC8	dnaJ homolog subfamily C member 8	9,5	29842	1	10,5	2	10,1	1	9,9	0	0,0	2	12,2	1	8,9	1	8,0

117	112382214	SEC24B	protein transport protein Sec24B isoform b	7,0	133610	1	11,9	1	10,0	0	0,0	1	9,4	0	0,0	2	15,9	1	11,4
118	112692538	IGHV3	immunoglobulin heavy chain variable region	8,5	10796	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
119	112695499	IGHV3	immunoglobulin heavy chain variable region	8,0	10964	0	0,0	0	0,0	0	0,0	1	9,4	0	0,0	1	8,0	0	0,0
120	112696692	IGHV3	immunoglobulin heavy chain variable region	9,3	10851	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
121	112698031	IGHV3	immunoglobulin heavy chain variable region	6,5	10809	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
122	112699767	ENSG00000223931	immunoglobulin heavy chain variable region	8,9	10822	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
123	112700762	ENSG00000223931	immunoglobulin heavy chain variable region	8,9	10707	1	10,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
124	112701523	IGHV3	immunoglobulin heavy chain variable region	8,5	11004	0	0,0	0	0,0	0	0,0	1	9,4	0	0,0	0	0,0	0	0,0
125	112789526	STAG2	cohesin subunit SA-2 isoform a	5,2	145752	0	0,0	1	9,7	1	8,7	0	0,0	0	0,0	0	0,0	1	9,7
126	11321583	SUCLA2	succinyl-CoA ligase [ADP-forming] subunit beta, mithocondrial	7,2	50299	0	0,0	1	10,3	0	0,0	0	0,0	0	0,0	1	8,0	2	13,6
127	11321601	PFKP	6-phosphofructokinase type C isoform 1	7,3	85578	2	27,2	5	35,1	6	45,8	6	46,8	3	24,2	8	64,1	6	45,5
128	11321634	CD2AP	CD2-associated protein	6,0	71452	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	1	7,9
129	113374156	VTI1A	vesicle transport through interaction with t-SNARE	6,0	25200	0	0,0	0	0,0	1	9,3	0	0,0	0	0,0	0	0,0	0	0,0
130	113413200	POTEJ	PREDICTED: POTE ankyrin domain family member J	5,6	117371	1	10,9	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
131	113415686	PROB1	PREDICTED: uncharacterized protein LOC285556	9,3	193648	1	10,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
132	11342680	ACTR1B	beta-centractin	6,0	42294	1	11,2	2	10,1	0	0,0	0	0,0	0	0,0	2	13,3	2	19,4
133	11345462	SPCS3	signal peptidase complex subunit 3	9,1	20314	1	11,8	1	10,3	0	0,0	1	9,5	2	12,2	1	12,2	1	7,9
134	1136430	PDCD11	KIAA0185	9,2	210045	1	11,6	1	10,3	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
135	11386183	WASF2	wiskott-Aldrich syndrome protein family member 2 is	5,2	54266	1	12,0	2	20,5	1	8,8	1	16,9	0	0,0	1	8,9	1	9,7
136	11414808	VASP	vasodilator-stimulated phosphoprotein	9,3	39593	2	13,0	3	15,1	5	18,4	1	9,5	2	12,2	2	17,4	4	34,6
137	11414998	POR	NADPH-cytochrome P-450 reductase	5,3	76638	0	0,0	1	9,7	0	0,0	0	0,0	2	12,2	0	0,0	0	0,0
138	11415026	RPL18A	60S ribosomal protein L18a	11,1	20763	1	14,1	2	10,0	2	13,6	0	0,0	0	0,0	1	12,8	2	21,0
139	11415028	TCL1A	T-cell leukemia/lymphoma protein 1A	4,8	13460	0	0,0	0	0,0	2	8,7	1	9,4	2	12,2	1	13,3	1	7,9
140	114225276	HLA	MHC class I antigen	5,7	31633	1	12,2	1	10,3	1	8,7	0	0,0	0	0,0	0	0,0	0	0,0
141	114306762	TC4	TC4 protein	9,7	12230	4	16,0	4	15,1	6	17,9	4	9,5	2	12,2	6	14,7	9	16,1
142	114306796	HLA	HLA-B protein	5,8	40522	3	12,9	4	16,0	5	13,0	5	18,9	6	19,5	3	12,7	5	18,0
143	114319027	JCHAIN	immunoglobulin J chain	5,1	19603	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,9	1	7,9
144	114796646	RCC1	regulator of chromosome condensation isoform b	8,0	46735	1	9,6	3	14,8	1	8,6	0	0,0	0	0,0	1	9,3	1	9,7
145	11493441	QARS	AF130117_26 PRO2195	6,7	69344	2	16,3	2	19,6	2	17,2	0	0,0	2	12,2	2	15,9	1	8,8
146	11493496	USP39	AF130117_55 PRO2855	8,8	34656	0	0,0	1	10,3	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
147	11493524	CCT2	AF130117_69 PRO1633	5,6	19523	1	13,7	3	20,5	2	13,6	6	37,4	2	12,2	3	14,9	2	16,1
148	11527773	OAS3	2'-5' oligoadenylate synthetase 3	8,3	121236	1	10,8	1	10,2	1	9,9	1	9,4	0	0,0	2	14,7	3	25,3
149	115298668	SNRNP40	U5 small nuclear ribonucleoprotein 40 kDa protein	8,0	39292	2	10,5	1	10,1	1	9,9	0	0,0	0	0,0	1	8,7	1	8,0
150	115298678	HEL	complement C3 precursor	6,0	187148	2	16,1	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
151	115298682	PRRC2C	protein PRRC2C	9,5	308605	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
152	115334682	SRCIN1	SRC kinase signaling inhibitor 1	9,7	127105	0	0,0	0	0,0	0	0,0	1	9,4	0	0,0	1	8,0	0	0,0
153	115387094	SDHB	succinate dehydrogenase [ubiquinone] iron-sulfur s	8,8	31612	1	12,1	1	10,3	1	8,7	0	0,0	0	0,0	1	14,7	2	19,8
154	115430108	RHOBTB3	rho-related BTB domain-containing protein 3	7,4	69395	1	12,5	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
155	115430112	REEP5	receptor expression-enhancing protein 5	8,2	21475	0	0,0	0	0,0	1	9,8	0	0,0	0	0,0	0	0,0	0	0,0
156	115430241	SCYL1	N-terminal kinase-like protein isoform A	5,9	89613	1	12,5	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
157	11544639	IPO7	importin7	4,6	116379	0	0,0	2	15,1	3	25,8	2	18,8	0	0,0	1	9,8	1	9,7
158	11545863	MCCC2	methylcrotonoyl-CoA carboxylase beta chain, mitocho	7,5	61315	0	0,0	0	0,0	1	8,6	1	9,4	0	0,0	0	0,0	0	0,0
159	115501316	NSUN2	putative 5-methycytoisine methyltransferase	6,4	86480	1	13,4	4	29,4	2	17,2	0	0,0	0	0,0	0	0,0	2	12,3
160	115527973	ADAM33	ADAM33 protein	6,7	75271	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
161	115583663	SERPINF2	alpha-2-antiplasmin isoform a precursor	5,8	54547	0	0,0	1	10,0	2	9,3	2	9,5	2	12,2	0	0,0	0	0,0
162	11559923	EIF4H	eukaryotic translation initiation factor 4H isoform	7,2	27367	1	11,2	2	10,0	2	9,3	0	0,0	2	12,3	1	8,7	1	11,4
163	11559927	MRPS14	28S ribosomal protein S14, mitochondrial	11,9	15121	1	10,5	1	9,7	0	0,0	1	9,4	0	0,0	1	9,3	1	10,6
164	116063573	FLNA	filamin-A isoform 1	5,6	280017	1	10,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
165	116089337	IQGAP2	ras GTPase-activating-like protein IQGAP2	5,3	180560	1	11,2	1	10,1	1	8,7	0	0,0	0	0,0	1	8,0	0	0,0
166	1160945	HLA	MHC class II HLA-DQ-beta-1, partial	8,2	27039	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
167	11610605	PABPC3	AF132026_1 testis-specific poly(A)-binding protein	10,1	70098	2	15,1	0	0,0	4	19,0	4	28,1	6	36,2	2	9,8	1	12,9
168	116283262	CPNE3	CPNE3 protein	8,1	30017	1	10,5	2	14,8	0	0,0	0	0,0	0	0,0	1	9,3	1	9,7
169	116283280	IQGAP1	IQGAP1 protein	5,6	35359	2	11,6	4	25,0	4	22,8	8	37,5	5	24,3	5	21,7	4	25,0
170	116283348	TRIM22	Tripartite motif-containing 22	7,7	56947	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	0	0,0
171	116283434	MNDA	MNDA protein	10,3	34982	0	0,0	0	0,0	2	8,7	0	0,0	0	0,0	0	0,0	0	0,0
172	116283481	PSMA7	PSMA7 protein	9,2	26714	1	11,5	1	10,0	1	8,7	1	9,4	3	12,2	1	9,0	1	10,5
173	116283591	NDUFB5	NDUFB5 protein	5,1	6228	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	1	9,7
174	116283609	HCFC1	HCFC1 protein	9,2	59036	1	9,7	0	0,0	1	8,6	0	0,0	0	0,0	1	8,1	1	7,9
175	116283809	ALPK3	C1orf167 protein	10,9	59162	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
176	116283979	UBTF	UBTF protein	9,5	37234	0	0,0	1	10,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
177	116284350	UNC93B1	UNC93B1 protein	7,7	56551	2	10,9	1	9,7	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
178	116284394	N/A	myosin-14 isoform 2	5,4	227870	0	13,4	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
179	11640560	CDK5RAP3	AF110322_1 MSTP016	4,4	46351	1	10,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0

180	116534937	IFIT1	interferon-induced protein with tetratricopeptide	6,8	55342	2	15,2	1	10,3	0	0,0	4	18,8	5	24,2	0	0,0	1	13,4
181	116734696	RBM23	probable RNA-binding protein 23 isoform 1	10,2	48712	0	0,0	0	0,0	0	0,0	1	9,5	0	0,0	0	0,0	0	0,0
182	11693132	UPF2	regulator of nonsense transcripts 2	5,4	147810	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
183	117190174	HNRNPC	heterogeneous nuclear ribonucleoproteins C1/C2 iso	4,8	32319	11	60,3	7	39,6	8	58,4	11	37,5	14	60,3	9	44,7	15	50,5
184	117306169	PRCP	lysosomal Pro-X carboxypeptidase isoform 2 preprop	7,0	58081	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	2	8,1	0	0,0
185	117320531	NFKB2	nuclear factor NF-kappa-B p100 subunit isoform	5,8	96730	2	14,6	1	10,1	1	8,8	4	18,9	0	0,0	4	23,9	3	16,2
186	1173867	ITGAD	beta-2 integrin alphaD subunit, partial	4,2	3449	1	12,5	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
187	1173905	SF3B2	spliceosome associated protein	5,4	97657	1	11,0	1	10,0	2	18,4	1	9,4	0	0,0	1	13,3	2	12,9
188	1174149	RAB7A	small GTP binding protein Rab7	6,6	23463	4	31,2	3	15,0	3	26,9	5	37,4	0	0,0	5	36,0	3	26,1
189	117553580	AP3D1	AP-3 complex subunit delta-1 isoform 2	8,5	130139	1	11,7	1	10,0	0	0,0	0	0,0	0	0,0	0	0,0	1	11,4
190	117553608	SLC39A7	zinc transporter SLC39A7 precursor	6,4	50119	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	0	0,0
191	117553627	ASMTL	N-acetylserotonin O-methyltransferase-like protein	5,7	68838	0	0,0	1	10,0	1	9,3	1	9,5	2	12,2	2	12,9	2	13,6
192	11761619	GMPPB	mannose-1-phosphate guanyltransferase beta isoform	6,0	42631	1	10,9	1	10,1	2	13,5	0	0,0	0	0,0	0	0,0	1	11,5
193	117938314	MZB1	plasma cell-induced resident endoplasmic reticulum	5,3	20676	3	11,9	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
194	117938762	GNAS	protein GNAS isoform f	5,5	45752	0	0,0	2	10,0	0	0,0	0	0,0	0	0,0	1	9,8	1	7,9
195	117938801	ERLIN2	ERLIN2 protein	7,8	38890	1	10,4	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
196	117938814	BXDC2	BXDC2 protein	10,3	39171	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
197	117938815	STAT2	STAT2 protein	8,0	66565	1	11,1	0	0,0	0	0,0	0	0,0	0	0,0	1	9,4	0	0,0
198	118026927	NUDT18	nucleoside diphosphate-linked moiety X motif 18	5,8	35483	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
199	118084547	AIP	aryl hydrocarbon receptor interacting protein	5,7	37648	1	12,5	0	0,0	0	0,0	1	9,4	0	0,0	2	15,9	2	15,7
200	118142816	MRPL1	MRPL1 protein	9,8	34447	1	11,6	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
201	118142858	CCDC186	C10orf118 protein	8,4	26253	2	10,9	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
202	118341393	PLXNB2	PLXNB2 protein	6,1	56277	0	0,0	1	10,3	0	0,0	0	0,0	0	0,0	1	8,0	1	7,9
203	118406098	IGHV5	immunoglobulin heavy chain variable region	9,1	13956	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
204	1184537	TXNRD1	thioredoxin reductase	6,0	54420	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
205	118498343	ATP2C2	calcium-transporting ATPase type 2C member 2	5,4	103169	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
206	118498359	RSL1D1	ribosomal L1 domain-containing protein 1	10,6	54954	1	11,7	3	14,8	3	17,8	6	28,1	3	24,2	4	21,6	3	22,4
207	118498362	KTN1	kinectin isoform b	5,5	150352	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	1	9,3	2	16,2
208	118599857	ATP5H	ATP5H protein	10,2	11486	3	18,0	2	10,0	3	18,4	2	18,8	3	12,2	1	12,3	3	12,3
209	118601081	HNRNPUL2	heterogeneous nuclear ribonucleoprotein U-like	4,7	85086	3	26,0	4	30,1	3	22,1	6	37,5	0	0,0	3	26,5	3	24,4
210	118722349	RBM12B	RNA-binding protein 12B	6,3	118103	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7	0	0,0
211	11875211	SPAST	spastin isoform 1	10,1	67198	1	11,6	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
212	119395709	F13A1	coagulation factor XIII A chain precursor	5,6	83250	1	12,5	0	0,0	0	0,0	1	9,4	0	0,0	0	0,0	0	0,0
213	119395750	KRT1	keratin, type II cytoskeletal 1	8,3	66039	15	100,9	1	10,0	3	14,2	1	9,5	8	60,3	2	15,3	1	9,7
214	119567961	TTBK2	hCG1643231, isoform CRA_b	8,3	35300	1	13,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
215	119568030	RBMS2	hCG2036917	9,2	13590	0	0,0	0	0,0	1	8,6	0	0,0	0	0,0	0	0,0	0	0,0
216	119568094	RPL27A	hCG21078	11,6	16623	1	10,5	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
217	119568173	PCMT1	protein-L-isoaspartate (D-aspartate) O-methyltransfe	5,0	17691	0	0,0	0	0,0	0	0,0	1	9,5	0	0,0	0	0,0	0	0,0
218	119568393	RPS12	ribosomal protein S12, isoform CRA_a	5,8	10529	1	12,1	0	0,0	0	0,0	1	9,4	0	0,0	1	9,3	0	0,0
219	119568484	SOGA3	hCG2030443, isoform CRA_a	6,4	104595	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
220	119569069	RPL23A	hCG2040303	10,7	13041	1	11,7	1	9,7	0	0,0	0	0,0	0	0,0	1	13,2	1	11,4
221	119569224	CES5A	hCG2031213, isoform CRA_a	8,9	45635	0	0,0	0	0,0	1	9,8	0	0,0	0	0,0	0	0,0	0	0,0
222	119569230	LMNB1	lamin B1, isoform CRA_a	5,1	37582	4	10,5	11	10,2	11	9,4	4	9,5	6	12,4	4	9,1	5	9,8
223	119569295	HSD17B4	hydroxysteroid (17-beta) dehydrogenase 4, isoform CR	8,9	64575	0	0,0	1	9,7	0	0,0	0	0,0	2	12,2	1	9,0	0	0,0
224	119569298	TNFAIP8	tumor necrosis factor, alpha-induced protein 8, isof	8,0	19472	2	11,5	4	10,0	4	9,3	4	9,5	5	12,2	3	9,1	3	9,7
225	119569329	RPS25	hCG1640785, isoform CRA_a	10,5	13616	2	17,6	1	10,3	2	9,2	6	28,1	2	12,2	1	9,0	1	8,8
226	119569337	AP3S1	adaptor-related protein complex 3, sigma 1 subunit,	9,0	32126	1	13,1	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
227	119569338	AP3S1	adaptor-related protein complex 3, sigma 1 subunit,	4,6	19084	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
228	119569439	FER	fer (fps/fes related) tyrosine kinase (phosphoprotei	9,7	17586	1	11,1	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
229	119569538	GLRX3	thioredoxin-like 2, isoform CRA_b	5,6	35666	2	15,0	2	10,0	2	8,7	1	9,5	2	12,2	1	8,9	1	9,7
230	119569541	N/A	hCG1648656, isoform CRA_a	8,9	11739	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
231	119569757	SEC23IP	SEC23 interacting protein, isoform CRA_b	5,2	111059	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	1	9,7
232	119569772	TIAL1	TIA1 cytotoxic granule-associated RNA binding protei	8,2	37204	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	1	9,8	1	9,7
233	119570063	ARL3	ADP-ribosylation factor-like 3	7,1	20325	1	11,0	0	0,0	1	9,9	1	9,4	0	0,0	1	8,7	0	0,0
234	119570072	ACTR1A	ARP1 actin-related protein 1 homolog A, centractin a	6,4	42154	0	0,0	2	14,9	4	28,2	0	0,0	3	24,3	1	12,9	1	9,7
235	119570172	SFXN3	sideroflexin 3	9,1	35980	1	11,4	2	10,0	1	9,2	0	0,0	2	12,1	1	9,0	1	7,9
236	119570597	FIS1	fission 1 (mitochondrial outer membrane) homolog (ye	8,8	20819	1	11,2	0	0,0	1	9,8	0	0,0	0	0,0	0	0,0	0	0,0
237	119570735	RAB1B	hCG2036720	8,2	11566	1	11,5	0	0,0	1	8,7	0	0,0	2	12,1	0	0,0	1	9,7
238	119570872	RPS8	hCG1988775	10,3	24213	1	11,2	1	10,3	1	9,8	1	9,4	0	0,0	2	9,5	0	0,0
239	119570878	EIF3C	eukaryotic translation initiation factor 3, subunit	6,2	69249	1	12,1	0	0,0	1	9,3	0	0,0	2	12,2	0	0,0	1	11,4
240	119571367	SDHA	succinate dehydrogenase complex, subunit A, flavopro	6,9	45197	1	9,7	1	10,0	1	9,8	1	9,5	0	0,0	0	0,0	1	9,6
241	119571504	SUPT6H	suppressor of Ty 6 homolog (S. cerevisiae), isoform	4,6	193856	1	12,5	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
242	119571896	CAPRIN2	hCG2041782	11,8	7018	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7

243	119571920	FMNL1	formin-like 1, isoform CRA_b	5,6	126869	1	10,4	1	9,8	0	0,0	0	0,0	2	12,1	1	8,9	0	0,0
244	119571922	FMNL1	formin-like 1, isoform CRA_d	5,1	65016	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,8	0	0,0
245	119572070	MDH1	hCG1643466, isoform CRA_a	5,3	17727	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
246	119572166	NECAP2	NECAP endocytosis associated 2, isoform CRA_b	6,2	19401	1	11,6	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	1	9,7
247	119572383	TUFM	Tu translation elongation factor, mitochondrial, iso	6,1	37438	3	27,1	3	14,8	5	31,2	2	18,8	3	24,2	5	36,5	6	44,1
248	119572468	EIF4A1	hCG28210	4,4	17690	1	11,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
249	119572480	ANAPC1	anaphase promoting complex subunit 1	5,6	106644	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	0	0,0
250	119572887	NOSIP	nitric oxide synthase interacting protein, isoform C	10,2	23817	1	12,4	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
251	119573062	F11R	F11 receptor, isoform CRA_a	6,9	32228	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,4	0	0,0
252	119573386	MEX3A	hCG17179	7,7	36389	0	0,0	0	0,0	0	0,0	0	0,0	2	12,1	0	0,0	0	0,0
253	119573666	INTS3	integrator complex subunit 3, isoform CRA_c	5,6	124956	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	2	9,7
254	119573998	DLG1	discs, large homolog 1 (Drosophila), isoform CRA_c	11,5	12864	1	11,1	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
255	119574116	ARPP19	hCG18385	10,0	12338	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
256	119574189	CANX	calnexin, isoform CRA_b	4,4	37308	3	11,5	3	10,0	4	9,3	2	9,5	3	12,2	2	12,3	4	15,5
257	119574284	BCLAF1	hCG1795985	10,3	100140	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	0	0,0
258	119574690	DDX21	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21, isoform C	9,3	22555	1	11,5	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,8
259	119574769	HEL	pyrophosphatase (inorganic) 1, isoform CRA_b	5,5	27378	6	51,3	15	49,5	13	36,7	13	46,8	11	48,3	10	34,9	9	37,2
260	119575342	PSMC1	hCG2002932, isoform CRA_a	5,0	46669	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
261	119575548	GLRX3	hCG1978918	4,6	17469	1	11,9	0	0,0	1	9,8	0	0,0	0	0,0	1	9,7	0	0,0
262	119575634	EEF1E1	hCG15559, isoform CRA_d	8,5	16687	2	13,7	1	9,7	0	0,0	1	9,4	2	12,2	1	8,7	1	8,8
263	119575807	DEK	DEK oncogene (DNA binding), isoform CRA_b	8,9	43230	1	13,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	2	20,1
264	119576060	FLII	flightless I homolog (Drosophila), isoform CRA_d	5,8	142315	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7	0	0,0
265	119576126	MPRIP	myosin phosphatase-Rho interacting protein, isoform	4,9	159715	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
266	119576203	PRKCB	protein kinase C, beta 1, isoform CRA_c	5,6	62403	1	13,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
267	119576324	SPEF2	KPL2 protein, isoform CRA_a	4,8	122632	0	0,0	0	0,0	0	0,0	1	9,4	0	0,0	0	0,0	0	0,0
268	119576516	RER1	RER1 retention in endoplasmic reticulum 1 homolog (S	8,7	21006	1	11,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
269	119577050	ATP1A1	ATPase, Na+/K+ transporting, alpha 1 polypeptide, is	5,7	83719	3	22,0	3	10,1	3	18,4	4	9,5	0	0,0	3	17,8	4	25,6
270	119577088	WDR3	WD repeat domain 3, isoform CRA_a	6,2	105149	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
271	119577215	ACTN4	actinin, alpha 4, isoform CRA_c	5,1	104165	2	18,3	4	34,8	2	18,4	6	37,5	0	0,0	2	18,4	3	22,3
272	119577252	SARS2	seryl-tRNA synthetase 2, isoform CRA_d	8,2	58164	1	11,1	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
273	119577296	RPS16	ribosomal protein S16, isoform CRA_a	10,6	14420	3	19,2	2	15,1	2	14,1	2	18,8	3	24,2	2	13,7	1	9,6
274	119577707	TOMM40	translocase of outer mitochondrial membrane 40 homol	7,5	28511	1	11,7	1	10,3	1	8,7	0	0,0	0	0,0	2	12,6	1	9,7
275	119577796	SYMPK	symplekin, isoform CRA_c	5,7	72925	1	10,9	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
276	119577797	SYMPK	symplekin, isoform CRA_d	5,5	78070	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	1	7,9
277	119577893	NAPA	N-ethylmaleimide-sensitive factor attachment protein	5,8	19379	0	0,0	0	0,0	1	8,7	2	18,8	2	12,2	1	8,9	0	0,0
278	119577898	NAPA	N-ethylmaleimide-sensitive factor attachment protein	7,1	10728	1	11,5	1	10,0	1	9,3	1	9,4	0	0,0	1	8,9	2	9,7
279	119577902	NAPA	N-ethylmaleimide-sensitive factor attachment protein	5,6	21796	1	12,4	0	0,0	1	9,8	0	0,0	0	0,0	1	9,7	1	9,6
280	119578414	DDX23	DEAD (Asp-Glu-Ala-Asp) box polypeptide 23, isoform C	9,2	73189	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	2	15,3
281	119578676	RAB1C	hCG2011109	5,1	22018	1	11,3	0	0,0	1	9,9	1	9,5	0	0,0	1	9,1	1	9,8
282	119578899	NOL6	nucleolar protein family 6 (RNA-associated), isoform	6,5	102394	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,8	1	7,9
283	119579143	GLDC	glycine dehydrogenase (decarboxylating; glycine deca	7,5	94600	0	0,0	2	20,4	1	9,8	0	0,0	0	0,0	1	8,1	2	13,6
284	119579272	NANS	N-acetylneuraminic acid synthase (sialic acid syntha	6,1	30676	2	16,2	1	10,3	2	13,6	0	0,0	0	0,0	1	12,2	2	12,9
285	119580147	PITPNB	phosphatidylinositol transfer protein, beta, isoform	6,2	31682	1	11,1	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
286	119580296	STAP2	hCG2041789	9,9	10284	1	10,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
287	119580378	DRG1	developmentally regulated GTP binding protein 1, iso	9,7	25436	1	11,0	0	0,0	0	0,0	0	0,0	2	12,2	1	9,5	0	0,0
288	119580379	DRG1	developmentally regulated GTP binding protein 1, iso	8,5	38523	0	0,0	1	10,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,8
289	119580405	YWHAH	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase	4,6	26688	1	12,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	1	9,7
290	119580409	RPS17L	hCG2010544	10,0	15603	3	25,0	2	17,9	3	17,6	1	16,9	2	21,8	4	19,4	1	15,8
291	119580514	EIF3D	eukaryotic translation initiation factor 3, subunit	5,9	63709	1	16,5	1	10,0	1	9,3	0	0,0	0	0,0	1	8,7	1	8,8
292	119580759	UQCRFS1P1	hCG1641472	9,2	29681	1	16,9	1	10,3	1	8,6	0	0,0	0	0,0	0	0,0	1	14,1
293	119580781	ADSL	adenylosuccinate lyase, isoform CRA_c	7,6	46608	1	9,7	2	20,5	0	0,0	2	18,8	0	0,0	1	8,9	1	8,8
294	119580915	MRPL45	mitochondrial ribosomal protein L45	8,5	15784	2	10,4	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
295	119581678	SSB	hCG1982987, isoform CRA_a	9,8	11922	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	2	9,3	1	9,7
296	119581910	FBLL1	hCG1641252	9,4	26349	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
297	119581951	ATP10B	hCG1979529, isoform CRA_b	8,4	57466	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,6
298	119582091	ANXA6	annexin A6, isoform CRA_c	5,3	75277	1	11,2	1	10,3	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
299	119582537	ETF1	eukaryotic translation termination factor 1, isoform	9,0	38962	0	0,0	0	0,0	0	0,0	2	18,8	0	0,0	0	0,0	1	7,9
300	119582796	SLC12A2	solute carrier family 12 (sodium/potassium/chloride	5,7	124573	1	13,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
301	119582831	HDGFRP3	hepatoma-derived growth factor, related protein 3, i	5,2	19290	0	0,0	1	10,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
302	119582899	MAMDC2	MAM domain containing 2, isoform CRA_c	7,3	36052	1	12,5	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
303	119582952	ANXA1	annexin A1, isoform CRA_c	7,8	40083	0	0,0	0	0,0	1	9,2	0	0,0	0	0,0	0	0,0	0	0,0
304	119583133	RPS29	hCG1820564	10,0	6708	1	12,5	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
305	119583356	ACAA2	acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3	7,8	42557	4	30,5	3	20,1	3	27,5	2	18,8	2	12,2	4	20,6	4	26,2

306	119583361	N/A	hCG2045172	8,0	5195	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
307	119583453	NARS	asparaginyl-tRNA synthetase, isoform CRA_b	5,9	62853	1	11,1	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
308	119583493	SEC11C	SEC11-like 3 (S. cerevisiae), isoform CRA_a	9,4	17386	1	11,9	3	24,7	3	22,7	2	18,8	0	0,0	1	11,7	3	17,5
309	119583621	VDAC3	voltage-dependent anion channel 3, isoform CRA_a	9,4	13819	3	25,7	3	14,8	3	19,1	0	0,0	0	0,0	1	15,2	2	17,3
310	119583623	VDAC3	voltage-dependent anion channel 3, isoform CRA_c	8,6	20175	1	15,0	1	10,1	0	0,0	1	9,5	2	12,2	1	11,7	1	8,8
311	119583846	HEL	glutathione reductase, isoform CRA_a	8,4	56487	1	12,5	0	0,0	1	8,7	0	0,0	0	0,0	3	16,0	2	13,6
312	119584289	TRNT1	tRNA nucleotidyl transferase, CCA-adding, 1, isoform	10,4	7773	0	0,0	0	0,0	0	0,0	0	0,0	2	12,2	0	0,0	0	0,0
313	119584354	SRGAP3	SLIT-ROBO Rho GTPase activating protein 3, isoform C	6,0	107162	1	12,4	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
314	119584450	EMC3	hCG1996542, isoform CRA_a	8,4	34128	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
315	119584819	STT3B	STT3, subunit of the oligosaccharyltransferase compl	8,6	49532	1	11,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,4	1	9,7
316	119584968	TTC21A	tetratricopeptide repeat domain 21A, isoform CRA_c	6,9	150868	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
317	119585114	ZNF852	hCG1643112, isoform CRA_b	8,0	56780	0	0,0	1	10,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
318	119585350	IMPDH2	hCG2002013, isoform CRA_a	8,4	63586	4	19,7	0	0,0	2	14,2	1	9,5	3	24,3	4	24,1	3	21,3
319	119585401	APEH	N-acylaminoacyl-peptide hydrolase, isoform CRA_c	5,8	61336	1	11,1	0	0,0	1	9,8	0	0,0	0	0,0	1	8,0	1	7,9
320	119585428	UBA7	ubiquitin-activating enzyme E1-like, isoform CRA_b	5,9	70212	2	15,3	1	10,0	3	23,3	4	18,8	2	12,2	1	8,0	2	16,1
321	119585747	PDE12	2'-phosphodiesterase, isoform CRA_b	5,4	48763	0	0,0	0	0,0	0	0,0	0	0,0	2	12,2	0	0,0	0	0,0
322	119586050	ERO1A	ERO1-like (S. cerevisiae), isoform CRA_a	5,1	29772	0	0,0	0	0,0	1	8,6	0	0,0	0	0,0	1	8,6	1	9,6
323	119586051	ERO1L	ERO1-like (S. cerevisiae), isoform CRA_b	5,5	54000	2	13,1	4	39,9	3	25,8	2	18,8	0	0,0	3	23,1	2	16,6
324	119586310	RPL12	hCG21173, isoform CRA_a	10,5	10124	2	13,3	1	10,0	0	0,0	0	0,0	2	12,2	1	9,3	0	0,0
325	119586537	AP1G2	hCG2014408, isoform CRA_b	5,5	37068	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7	0	0,0
326	119587211	ZFPM1	zinc finger protein, multitype 1, isoform CRA_b	7,9	16266	1	11,2	0	0,0	1	9,8	0	0,0	0	0,0	0	0,0	0	0,0
327	119587420	RPS6	hCG1642882	10,7	20143	1	12,5	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
328	119587681	APOA1	apolipoprotein A-I, isoform CRA_b	5,3	23469	1	11,2	2	10,0	3	9,3	2	9,5	0	0,0	3	9,0	3	9,7
329	119588171	TCEB2	hCG2041310	5,0	13158	1	12,5	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
330	119588314	CELF1	CUG triplet repeat, RNA binding protein 1, isoform C	8,4	55124	0	0,0	1	10,3	0	0,0	0	0,0	0	0,0	1	8,0	1	9,6
331	119588388	ARHGAP1	Rho GTPase activating protein 1, isoform CRA_a	9,5	22920	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,9	1	7,9
332	119588586	CAPRIN1	GPI-anchored membrane protein 1, isoform CRA_d	4,8	70335	0	0,0	1	10,1	0	0,0	2	18,8	0	0,0	1	8,0	0	0,0
333	119588747	HTATIP2	HIV-1 Tat interactive protein 2, 30kDa, isoform CRA_	8,8	30181	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
334	119588787	TSG101	tumor susceptibility gene 101, isoform CRA_a	5,0	29002	1	11,1	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
335	119588851	RPS2	hCG1992539, isoform CRA_d	10,4	29961	0	0,0	0	0,0	1	9,8	0	0,0	2	12,2	1	9,7	1	9,7
336	119588892	RRAS2	related RAS viral (r-ras) oncogene homolog 2, isofor	5,1	21736	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	1	7,9
337	119588990	SWAP70	SWAP-70 protein, isoform CRA_b	5,7	62034	2	10,5	2	15,2	3	13,2	4	18,8	3	12,3	2	14,4	4	16,8
338	119588991	SWAP70	SWAP-70 protein, isoform CRA_c	5,8	57384	0	0,0	5	39,7	2	17,2	0	0,0	0	0,0	4	29,2	2	13,6
339	119589327	HNRNPM	heterogeneous nuclear ribonucleoprotein M, isoform C	9,1	77629	1	11,1	1	10,0	3	19,0	5	18,8	3	12,2	2	14,9	2	21,4
340	119589356	ELAVL1	ELAV (embryonic lethal, abnormal vision, Drosophila)	12,1	50460	2	14,2	2	10,1	3	22,3	1	9,5	2	12,2	2	18,0	2	12,3
341	119589411	FCER2	Fc fragment of IgE, low affinity II, receptor for (C	5,2	36481	1	10,2	0	0,0	0	0,0	1	9,5	0	0,0	0	0,0	1	9,7
342	119589464	VAV1	vav 1 oncogene, isoform CRA_b	6,7	97879	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
343	119589514	NCKAP5L	hCG2004878, isoform CRA_a	11,9	25833	1	10,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
344	119589669	MAP2K2	mitogen-activated protein kinase kinase 2, isoform C	6,3	33863	0	0,0	0	0,0	1	9,9	0	0,0	0	0,0	1	9,1	0	0,0
345	119589787	TIMM13	translocase of inner mitochondrial membrane 13 homol	8,2	8876	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	1	8,7	1	9,7
346	119589816	N/A	DOT1-like, histone H3 methyltransferase (S. cerevisi	9,8	156744	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	13,0	0	0,0
347	119589968	ABCA7	ATP-binding cassette, sub-family A (ABC1), member 7,	7,1	163880	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
348	119590265	GUK1	guanylate kinase 1, isoform CRA_g	8,5	12696	0	0,0	0	0,0	1	9,8	0	0,0	0	0,0	0	0,0	0	0,0
349	119590315	GALNT2	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-ace	7,4	60776	1	10,4	1	10,0	0	0,0	0	0,0	0	0,0	2	13,3	3	19,3
350	119590453	EDARADD	EDAR-associated death domain, isoform CRA_a	5,6	42323	3	19,7	0	0,0	2	8,7	1	9,4	0	0,0	1	9,5	2	12,2
351	119590499	FH	fumarate hydratase, isoform CRA_d	7,0	46414	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
352	119590557	HSPD1	heat shock 60kDa protein 1 (chaperonin), isoform CRA	4,9	40903	36	83,2	89	103,9	32	91,5	40	84,1	31	108,5	53	106,6	52	86,1
353	119590563	HSPE1	heat shock 10kDa protein 1 (chaperonin 10), isoform	7,0	7523	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
354	119590930	HEL	5-aminoimidazole-4-carboxamide ribonucleotide formyl	8,0	55516	0	0,0	1	10,0	0	0,0	0	0,0	0	0,0	2	8,9	0	0,0
355	119590977	RPL37A	ribosomal protein L37a, isoform CRA_c	10,4	7606	1	12,1	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
356	119591127	TUBA4B	tubulin, alpha 4, isoform CRA_b	8,5	27575	1	10,2	2	10,3	1	9,8	4	9,4	2	12,2	0	0,0	1	11,4
357	119591238	DOCK10	dedicator of cytokinesis 10, isoform CRA_a	5,5	67435	1	11,6	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	1	9,7
358	119591240	DOCK10	dedicator of cytokinesis 10, isoform CRA_c	7,0	165545	0	0,0	0	0,0	2	9,3	1	9,5	0	0,0	1	8,0	1	7,9
359	119591241	DOCK10	dedicator of cytokinesis 10, isoform CRA_d	6,4	176618	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
360	119591651	PPP1R7	protein phosphatase 1, regulatory subunit 7, isoform	5,7	19778	2	11,5	2	10,1	1	9,2	0	0,0	3	12,3	1	9,1	1	9,7
361	119591925	RPL22	ribosomal protein L22, isoform CRA_b	7,2	11169	2	22,9	1	10,3	3	19,6	1	9,5	3	24,2	2	18,4	1	13,6
362	119592082	SRM	spermidine synthase, isoform CRA_b	5,2	34941	1	15,5	1	10,3	0	0,0	1	9,4	0	0,0	2	15,9	1	8,8
363	119592142	RPL10	hCG1644589	10,4	16299	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
364	119592215	NEK4	hCG2040539	9,0	13469	0	0,0	0	0,0	1	8,6	0	0,0	0	0,0	1	8,0	1	11,4
365	119592808	U2AF2	U2 (RNU2) small nuclear RNA auxiliary factor 2, isof	10,1	41949	2	10,9	1	9,7	2	14,1	1	9,5	2	12,2	1	9,0	1	9,7
366	119593011	TRIM28	tripartite motif-containing 28, isoform CRA_a	5,5	75830	2	18,5	1	10,4	3	18,4	2	18,8	2	12,2	2	16,2	3	21,3
367	119593174	HCFC1	host cell factor C1 (VP16-accessory protein), isofor	6,8	198344	0	0,0	0	0,0	0	0,0	0	0,0	2	12,2	0	0,0	0	0,0
368	119593417	RPL7	hCG31916	11,1	29326	8	51,5	2	18,9	6	31,8	5	28,1	2	12,2	3	23,1	7	26,1

369	119593584	SEPT15	15 kDa selenoprotein	4,3	7361	1	12,4	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
370	119593933	PLXNB2	hCG1988148	5,9	126896	0	0,0	1	10,0	1	9,3	0	0,0	0	0,0	0	0,0	0	0,0
371	119594145	SLC43A3	hCG39762, isoform CRA_a	8,0	67853	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
372	119594164	UBE2L6	ubiquitin-conjugating enzyme E2L 6, isoform CRA_d	8,8	18867	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
373	119594296	MS4A1	membrane-spanning 4-domains, subfamily A, member 1,	4,9	33002	3	30,4	0	0,0	1	9,2	0	0,0	3	24,2	1	9,3	1	7,9
374	119594310	PRPF19	PRP19/PSO4 pre-mRNA processing factor 19 homolog (S.	6,6	45713	1	11,5	0	0,0	0	0,0	2	18,8	0	0,0	1	9,3	1	9,7
375	119594471	UBXN1	unknown protein LOC51035, isoform CRA_d	5,3	31447	1	11,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
376	119594593	OTUB1	OTU domain, ubiquitin aldehyde binding 1, isoform CR	4,7	22720	4	14,3	2	15,1	2	9,3	4	9,5	3	12,2	3	9,1	2	9,7
377	119594594	OTUB1	OTU domain, ubiquitin aldehyde binding 1, isoform CR	8,5	35267	2	19,6	1	9,7	2	13,5	0	0,0	2	12,1	1	8,9	1	12,7
378	119594596	OTUB1	OTU domain, ubiquitin aldehyde binding 1, isoform CR	4,8	20317	1	11,5	0	0,0	0	0,0	0	0,0	0	0,0	1	9,4	0	0,0
379	119594603	STIP1	stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organiz	7,6	68062	5	33,5	4	24,7	5	44,6	5	37,4	9	72,3	4	39,0	7	68,1
380	119594606	FERMT3	UNC-112 related protein 2, isoform CRA_b	7,8	26724	1	10,4	0	0,0	2	8,7	0	0,0	0	0,0	2	8,0	0	0,0
381	119594632	PPP1R14B	protein phosphatase 1, regulatory (inhibitor) subuni	5,0	20946	0	0,0	1	10,0	2	8,7	1	9,4	0	0,0	1	8,0	1	11,4
382	119594659	TRMT112	hypothetical protein HSPC152, isoform CRA_b	5,2	11791	1	11,2	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	1	8,8
383	119594723	EHD1	EH-domain containing 1, isoform CRA_a	6,3	61909	2	22,1	7	34,6	10	55,6	7	37,5	3	24,2	10	71,3	8	55,2
384	119594987	ADRBK1	adrenergic, beta, receptor kinase 1, isoform CRA_a	6,8	75070	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
385	119595112	LRP5	low density lipoprotein receptor-related protein 5,	5,0	180457	1	13,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
386	119595133	MRPL21	mitochondrial ribosomal protein L21, isoform CRA_c	8,8	16594	1	12,4	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
387	119595581	PRPF6	chromosome 20 open reading frame 14, isoform CRA_b	8,4	59636	2	17,9	2	15,0	0	0,0	0	0,0	0	0,0	1	8,7	1	9,7
388	119595582	PRPF6	chromosome 20 open reading frame 14, isoform CRA_c	8,2	102410	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
389	119595805	PSMA7	hCG41772, isoform CRA_c	8,6	18255	2	19,3	2	10,1	1	13,2	1	17,0	2	12,2	1	13,8	1	9,7
390	119596081	ARPC3	hCG1786148	8,3	23771	0	0,0	0	0,0	1	8,6	0	0,0	0	0,0	0	0,0	0	0,0
391	119596675	DYNLRB1	hCG38498, isoform CRA_c	10,1	15369	1	10,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
392	119597080	PDAP1	PDGFA associated protein 1, isoform CRA_a	9,4	20605	0	0,0	0	0,0	1	9,8	0	0,0	0	0,0	0	0,0	0	0,0
393	119597384	HNRNPA1	hCG2023776	9,6	33912	3	13,5	2	15,9	4	16,7	2	13,2	3	17,0	3	16,5	3	15,8
394	119597733	BLOC1S6	hCG2001986, isoform CRA_f	4,0	8600	0	0,0	0	0,0	0	0,0	0	0,0	2	12,2	0	0,0	0	0,0
395	119597834	TMOD2	tropomodulin 2 (neuronal), isoform CRA_a	6,5	34474	1	11,3	1	9,7	0	0,0	0	0,0	0	0,0	1	8,0	1	10,5
396	119598010	VPS13C	vacuolar protein sorting 13C (yeast), isoform CRA_f	6,2	341434	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
397	119598044	LACTB	lactamase, beta, isoform CRA_b	8,5	60694	0	0,0	3	15,1	1	9,3	1	9,5	0	0,0	2	11,7	2	7,9
398	119598172	MAP2K1	mitogen-activated protein kinase kinase 1, isoform C	6,0	40746	1	10,8	2	19,9	2	17,2	1	9,4	0	0,0	1	9,3	1	9,7
399	119598503	CCT6A	hCG1644127, isoform CRA_a	4,7	7419	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
400	119598985	PDCD10	programmed cell death 10, isoform CRA_b	9,6	17516	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	15,6
401	119599019	RPL23A	hCG16001, isoform CRA_a	10,9	17708	2	16,7	2	10,0	2	14,1	4	18,8	3	12,2	2	17,9	1	13,4
402	119599272	COMMD2	COMM domain containing 2, isoform CRA_a	8,2	25969	1	11,2	0	0,0	0	0,0	1	9,5	0	0,0	0	0,0	0	0,0
403	119599446	COPB2	coatomer protein complex, subunit beta 2 (beta prime	4,9	99027	4	36,9	6	39,6	2	17,9	4	28,1	3	24,2	2	16,8	3	25,6
404	119599582	CDV3	CDV3 homolog (mouse), isoform CRA_a	9,9	28600	1	14,3	1	9,8	3	22,7	0	0,0	2	12,2	2	12,2	3	18,7
405	119599627	GSTO1	hCG1646871	5,3	29141	0	0,0	0	0,0	1	8,6	0	0,0	0	0,0	0	0,0	0	0,0
406	119599675	COPG1	coatomer protein complex, subunit gamma, isoform CRA	5,5	97609	0	0,0	2	19,3	0	0,0	2	18,8	2	12,2	0	0,0	1	10,6
407	119599876	PARP14	poly (ADP-ribose) polymerase family, member 14, isof	8,2	170582	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	1	8,0	1	7,9
408	119599878	PARP14	hCG1779993	4,6	16314	1	11,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
409	119599882	DTX3L	deltex 3-like (Drosophila)	7,9	83527	1	11,2	1	9,7	1	8,7	0	0,0	2	12,2	1	9,0	1	9,7
410	119600020	QTRTD1	queuine tRNA-ribosyltransferase domain containing 1,	6,4	46891	1	12,5	0	0,0	0	0,0	1	9,4	0	0,0	0	0,0	0	0,0
411	119600033	ATP6V1A	ATPase, H+ transporting, lysosomal 70kDa, V1 subunit	5,8	53459	2	24,0	2	19,9	2	18,4	1	9,4	0	0,0	2	14,3	1	10,6
412	119600195	RPS18	hCG1777176, isoform CRA_b	11,3	17665	1	11,0	0	0,0	0	0,0	1	9,4	2	12,2	1	9,3	0	0,0
413	119600315	CORO1A	coronin, actin binding protein, 1A, isoform CRA_b	6,0	39687	13	10,5	15	10,0	9	9,3	13	9,5	8	12,3	9	9,1	6	9,7
414	119600392	MVP	major vault protein, isoform CRA_e	5,2	74325	2	19,2	7	49,5	4	32,4	0	0,0	2	12,2	4	38,8	2	21,3
415	119600393	MVP	major vault protein, isoform CRA_f	5,7	53356	0	0,0	1	9,7	1	9,8	0	0,0	2	12,2	1	8,0	0	0,0
416	119600644	PAF1	chromosome 17 open reading frame 75	4,8	44579	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
417	119601073	UBE2L3	hCG1789329, isoform CRA_b	9,6	14135	5	16,8	4	9,8	1	8,7	0	0,0	0	0,0	2	9,0	3	8,0
418	119601114	SLC35F4	hCG22486, isoform CRA_a	8,9	67959	1	11,3	0	0,0	1	9,8	0	0,0	0	0,0	0	0,0	0	0,0
419	119601356	RDH11	retinol dehydrogenase 11 (all-trans and 9-cis), isof	8,8	33985	1	11,1	0	0,0	0	0,0	0	0,0	0	0,0	1	8,7	1	7,9
420	119601698	AHSA1	AHA1, activator of heat shock 90kDa protein ATPase h	5,4	20053	1	14,8	1	10,0	1	9,8	0	0,0	2	12,2	1	9,5	1	9,7
421	119601710	SLIRP	chromosome 14 open reading frame 156, isoform CRA_b	10,6	11876	1	13,0	2	19,9	1	8,6	1	9,4	0	0,0	1	9,3	1	7,9
422	119601889	CPSF2	cleavage and polyadenylation specific factor 2, 100k	4,8	77875	0	0,0	1	10,0	1	8,7	0	0,0	2	12,2	1	9,7	0	0,0
423	119602166	DYNC1H1	dynein, cytoplasmic 1, heavy chain 1, isoform CRA_b	6,0	525453	2	21,6	5	19,6	7	45,8	1	9,5	0	0,0	5	40,6	7	40,5
424	119602169	DYNC1H1	dynein, cytoplasmic 1, heavy chain 1, isoform CRA_e	6,0	403291	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
425	119602227	HEL	creatine kinase, brain, isoform CRA_b	5,7	44903	0	0,0	0	0,0	0	0,0	1	9,5	0	0,0	1	8,9	0	0,0
426	119602762	GMPS	hCG1640714, isoform CRA_b	6,4	65046	1	10,9	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
427	119602776	GRPEL1	GrpE-like 1, mitochondrial (E. coli), isoform CRA_a	6,3	19570	1	11,1	1	10,3	1	9,3	0	0,0	0	0,0	1	9,7	1	9,7
428	119602881	HTT	huntingtin (Huntington disease), isoform CRA_b	5,7	333281	1	13,1	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
429	119603008	CTBP1	C-terminal binding protein 1, isoform CRA_c	6,3	47604	1	11,1	0	0,0	0	0,0	1	9,4	0	0,0	1	9,7	2	9,8
430	119603139	CAMTA2	hCG2040968	10,2	5917	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
431	119603872	NPM1	hCG1642933, isoform CRA_a	4,7	20911	2	24,7	10	26,9	7	24,0	6	24,5	6	34,0	16	25,8	29	24,4

432	119604262	NUP205	nucleoporin 205kDa, isoform CRA_b	5,8	228147	1	9,7	2	10,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
433	119604464	PIN1	protein (peptidylprolyl cis/trans isomerase) NIMA-in	9,3	19575	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,8
434	119604561	CARM1	coactivator-associated arginine methyltransferase 1,	7,5	24228	1	10,4	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
435	119604803	KIN27	protein kinase, cAMP-dependent, catalytic, alpha, is	9,6	19258	0	0,0	0	0,0	0	0,0	0	0,0	2	12,1	1	9,8	0	0,0
436	119605019	PGLS	6-phosphogluconolactonase, isoform CRA_a	5,4	20191	1	13,7	1	10,1	1	9,9	0	0,0	0	0,0	1	9,4	1	9,8
437	119605144	UPF1	UPF1 regulator of nonsense transcripts homolog (yeas	6,2	124326	1	11,6	1	10,1	1	8,7	0	0,0	0	0,0	1	8,9	2	13,6
438	119605254	ATP13A1	ATPase type 13A1, isoform CRA_b	6,8	66484	1	10,4	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
439	119605879	TCEB2	transcription elongation factor B (SIII), polypeptid	4,7	12509	1	12,5	0	0,0	1	9,3	0	0,0	0	0,0	0	0,0	1	7,9
440	119606033	MRPS34	mitochondrial ribosomal protein S34, isoform CRA_a	10,2	28682	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	1	11,4
441	119606382	KIF5B	kinesin family member 5B, isoform CRA_a	6,1	109639	1	11,0	2	15,1	0	0,0	1	9,4	0	0,0	1	8,0	1	7,9
442	119606609	NRG1	hCG2017501	10,0	14141	1	12,5	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
443	119606726	NUDT5	nudix (nucleoside diphosphate linked moiety X)-type	4,8	24080	2	14,3	2	10,0	2	8,7	0	0,0	0	0,0	2	9,0	3	8,8
444	119606784	ITIH2	inter-alpha (globulin) inhibitor H2, isoform CRA_b	6,4	106418	1	12,1	0	0,0	1	9,2	1	9,5	2	12,2	1	9,7	0	0,0
445	119607048	ALOX5	arachidonate 5-lipoxygenase, isoform CRA_a	5,3	60736	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
446	119607088	PRKDC	protein kinase, DNA-activated, catalytic polypeptide	6,7	468967	4	39,7	5	39,6	3	22,7	11	74,7	3	24,3	6	46,9	6	49,3
447	119607149	LYPLA1	lysophospholipase I, isoform CRA_b	7,1	19752	1	11,0	0	0,0	1	8,7	0	0,0	0	0,0	1	9,3	0	0,0
448	119607152	LYPLA1	lysophospholipase I, isoform CRA_d	7,0	15140	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
449	119607490	ZNF704	hCG1764572	5,0	26511	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	11,4
450	119607594	MGC11257	hypothetical protein MGC11257, isoform CRA_a	9,6	18493	1	11,1	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
451	119608006	RPL35	ribosomal protein L35, isoform CRA_a	10,7	17775	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
452	119608139	DHRS13	family with sequence similarity 102, member A, isofo	9,8	14674	1	11,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
453	119608226	SET	SET translocation (myeloid leukemia-associated), iso	5,7	28827	4	19,3	8	39,6	7	41,0	10	37,5	6	36,3	4	23,7	8	31,5
454	119608326	GPR107	G protein-coupled receptor 107, isoform CRA_a	8,1	49192	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
455	119608696	PHPT1	phosphohistidine phosphatase 1, isoform CRA_b	7,2	13354	1	11,1	0	0,0	2	9,3	0	0,0	2	12,2	1	9,5	1	9,7
456	119609105	PHB2	prohibitin 2	10,1	32283	11	51,5	15	59,6	12	55,0	13	56,1	11	60,3	14	49,0	9	37,8
457	119609437	PITPNC1	phosphatidylinositol transfer protein, cytoplasmic 1	5,5	31743	1	11,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
458	119609470	PRKAR1A	protein kinase, cAMP-dependent, regulatory, type I,	4,8	28784	1	12,0	1	10,3	0	0,0	1	9,4	0	0,0	1	8,7	1	7,9
459	119609678	GRB2	growth factor receptor-bound protein 2, isoform CRA_	6,4	23537	2	15,2	3	19,8	1	8,7	1	9,5	0	0,0	2	15,9	2	17,5
460	119609744	MRPL38	mitochondrial ribosomal protein L38, isoform CRA_a	5,6	19079	0	0,0	0	0,0	0	0,0	0	0,0	2	12,2	0	0,0	0	0,0
461	119609755	ACOX1	acyl-Coenzyme A oxidase 1, palmitoyl, isoform CRA_a	8,1	74423	1	11,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
462	119610004	RNF213	chromosome 17 open reading frame 27, isoform CRA_c	5,7	100542	1	11,2	2	20,2	2	13,6	1	9,5	0	0,0	1	12,9	3	23,5
463	119610091	FAM195B	hCG1818442, isoform CRA_a	10,0	12951	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
464	119610105	ALYREF	THO complex 4	11,3	24794	1	10,5	3	19,9	1	8,7	2	9,4	0	0,0	1	8,0	1	9,6
465	119610138	DCXR	dicarbonyl/L-xylulose reductase, isoform CRA_a	9,6	24685	1	11,1	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
466	119610151	FASN	fatty acid synthase	6,0	273425	7	60,9	14	64,5	13	73,9	6	46,8	8	48,3	7	35,5	8	62,1
467	119610485	AURKB	aurora kinase B, isoform CRA_e	9,9	25216	0	0,0	1	10,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
468	119610535	DNAH2	dynein heavy chain domain 3, isoform CRA_a	8,4	90448	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
469	119610615	ACAP1	centaurin, beta 1, isoform CRA_a	8,0	54564	1	11,2	2	10,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
470	119610741	C1QBP	complement component 1, q subcomponent binding prote	3,9	20116	3	15,9	4	14,8	4	27,6	4	28,1	3	24,3	3	20,6	4	21,9
471	119610743	C1QBP	complement component 1, q subcomponent binding prote	4,7	35862	3	11,5	4	10,0	3	13,6	2	18,8	6	12,2	4	12,1	3	19,2
472	119610747	NUP88	nucleoporin 88kDa, isoform CRA_b	8,2	32683	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
473	119610788	PFN1	profilin 1, isoform CRA_b	9,5	11391	69	50,8	20	29,7	34	27,6	35	37,4	22	48,3	34	30,1	49	28,8
474	119610832	PELP1	proline, glutamic acid and leucine rich protein 1, i	6,5	84599	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7	0	0,0
475	119611166	RECK	hCG2036737, isoform CRA_a	9,0	6428	0	0,0	0	0,0	0	0,0	1	9,4	0	0,0	0	0,0	0	0,0
476	119611543	DHX9	DEAH (Asp-Glu-Ala-His) box polypeptide 9, isoform CR	5,8	114099	3	17,4	4	19,9	3	8,7	2	18,8	2	12,2	2	21,0	5	21,8
477	119611741	CACNA1S	calcium channel, voltage-dependent, L type, alpha 1S	6,2	212355	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
478	119611781	IPO9	importin 9, isoform CRA_a	4,7	111818	1	11,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
479	119611783	IPO9	importin 9, isoform CRA_c	4,6	117110	0	0,0	0	0,0	1	9,9	0	0,0	2	12,2	0	0,0	0	0,0
480	119612049	CPNE3	copine III, isoform CRA_b	5,9	33695	1	11,0	1	10,0	0	0,0	0	0,0	0	0,0	1	8,7	1	8,8
481	119612068	DECR1	2,4-dienoyl CoA reductase 1, mitochondrial, isoform	7,9	21216	1	11,7	0	0,0	1	9,3	0	0,0	0	0,0	1	8,7	2	13,6
482	119612175	RPL30	ribosomal protein L30, isoform CRA_a	9,7	9557	2	10,7	2	10,0	1	9,3	5	18,8	2	12,2	3	8,0	2	7,9
483	119612225	PABPC1	poly(A) binding protein, cytoplasmic 1, isoform CRA_	9,8	70320	2	9,7	2	10,0	0	0,0	1	9,5	0	0,0	1	8,9	1	7,9
484	119612264	NPM1	hCG2041218	5,0	15449	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
485	119612312	TAGLN2	hCG2008737	5,1	14619	0	0,0	0	0,0	1	9,9	1	9,5	2	12,3	0	0,0	0	0,0
486	119612416	HAS2	hyaluronan synthase 2	8,2	50208	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
487	119612457	FAM91A1	family with sequence similarity 91, member A1, isofo	9,1	25817	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	0	0,0
488	119613555	SMC1A	SMC1 structural maintenance of chromosomes 1-like 1	5,5	63078	1	11,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
489	119613565	HSD17B10	hydroxyacyl-Coenzyme A dehydrogenase, type II, isofo	5,1	14569	3	16,3	6	10,1	5	18,5	5	18,8	11	12,3	4	14,8	3	9,7
490	119614196	ABCE1	hCG2010034	5,1	22658	3	10,5	7	10,1	2	9,3	1	9,5	0	0,0	4	8,1	2	9,7
491	119614244	HNRPA2B1	heterogeneous nuclear ribonucleoprotein A2/B1, isofo	9,4	31144	19	68,5	24	78,1	13	48,3	16	54,2	17	60,3	16	63,9	14	62,1
492	119614465	SEPT7	septin 7, isoform CRA_a	8,3	44843	3	17,5	4	19,9	4	22,1	6	28,2	5	24,3	4	17,9	4	28,2
493	119614577	BLVRA	biliverdin reductase A	5,7	31032	2	15,7	3	19,9	5	27,6	1	9,4	5	36,3	3	18,1	2	18,6
494	119614841	IGBP1	hCG1642624, isoform CRA_a	5,5	39175	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0

495	119614863	SET	hCG1795875, isoform CRA_b	5,8	24982	2	17,0	2	14,8	1	9,3	2	18,8	5	36,3	1	15,5	2	18,1
496	119615085	EIF4E	hCG1777996	6,0	25127	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	1	7,9
497	119615217	NPEPPS	aminopeptidase puromycin sensitive, isoform CRA_a	5,1	92841	4	37,5	6	44,4	5	37,3	4	28,2	3	24,2	5	39,0	5	41,6
498	119615294	CAPZB	capping protein (actin filament) muscle Z-line, beta	6,5	29277	4	36,6	5	29,8	6	41,0	5	28,1	6	48,3	5	33,2	4	34,6
499	119615330	CAMK2N1	calcium/calmodulin-dependent protein kinase II inhib	10,6	12509	1	10,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
500	119615389	RAP1GAP	RAP1, GTPase activating protein 1, isoform CRA_d	6,2	68193	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
501	119615439	KDM1A	amine oxidase (flavin containing) domain 2, isoform	5,9	55941	1	10,8	0	0,0	0	0,0	0	0,0	0	0,0	1	8,1	1	11,5
502	119615548	CLIC4	chloride intracellular channel 4, isoform CRA_a	6,0	24160	1	11,1	0	0,0	1	8,6	0	0,0	0	0,0	0	0,0	1	11,4
503	119615762	UGGT1	UDP-glucose ceramide glucosyltransferase-like 1	5,4	142273	2	16,7	1	10,3	1	9,3	0	0,0	0	0,0	3	29,7	2	13,5
504	119615877	USP10	ubiquitin specific peptidase 10, isoform CRA_b	5,7	98084	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	1	8,1	1	7,9
505	119616019	RPL18	hCG1979897, isoform CRA_b	11,2	16626	0	18,8	0	0,0	1	9,8	0	0,0	2	12,2	0	0,0	0	0,0
506	119616098	MCCC2	methylcrotonoyl-Coenzyme A carboxylase 2 (beta), iso	7,2	47098	3	24,5	3	24,7	1	8,7	1	9,5	2	12,2	2	14,3	1	7,9
507	119616180	SNRPC	hCG1758872	10,3	16912	0	0,0	0	0,0	0	0,0	1	9,5	0	0,0	1	9,8	1	9,7
508	119616214	RPL7	hCG2015956	11,2	30509	5	11,5	3	10,0	3	9,3	1	9,5	5	12,2	3	9,1	2	9,7
509	119616745	ARHGDIB	Rho GDP dissociation inhibitor (GDI) beta, isoform C	4,6	20685	10	47,4	12	39,7	9	36,8	10	46,8	8	36,4	8	41,5	7	27,7
510	119616848	GOLT1B	golgi transport 1 homolog B (S. cerevisiae), isoform	11,0	16143	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
511	119617192	NCKAP1L	NCK-associated protein 1-like, isoform CRA_a	6,4	129116	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
512	119617484	TSFM	Ts translation elongation factor, mitochondrial, iso	6,3	29915	1	11,4	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
513	119617679	TBC1D15	TBC1 domain family, member 15, isoform CRA_a	5,3	66444	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
514	119617914	SUCLG2	hCG1791842, isoform CRA_a	5,1	46491	1	11,1	0	0,0	0	0,0	0	0,0	0	0,0	1	9,4	1	9,7
515	119617945	METAP2	methionyl aminopeptidase 2, isoform CRA_c	5,0	35973	1	11,1	1	10,3	0	0,0	0	0,0	0	0,0	0	0,0	1	9,8
516	119617955	SNRPF	small nuclear ribonucleoprotein polypeptide F, isofo	4,2	7702	1	11,9	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	1	9,7
517	119617981	CFAP54	FLJ44112 protein	8,3	88439	0	0,0	1	10,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
518	119618062	UTP20	UTP20, small subunit (SSU) processome component, hom	7,0	318380	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
519	119618222	SART3	squamous cell carcinoma antigen recognised by T cell	8,3	65112	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,4	0	0,0
520	119618308	ATP2A2	ATPase, Ca++ transporting, cardiac muscle, slow twit	5,7	100674	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	1	11,4
521	119618319	ARPC3	actin related protein 2/3 complex, subunit 3, 21kDa,	8,7	18931	1	12,8	2	15,0	2	13,5	4	18,8	3	24,2	2	17,9	3	17,2
522	119618398	HEL	endoplasmic reticulum protein 29, isoform CRA_b	9,6	29411	3	29,7	2	14,8	0	0,0	1	9,4	2	12,2	1	8,7	1	13,4
523	119618619	MLEC	KIAA0152, isoform CRA_b	5,8	40091	1	11,1	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,9
524	119618620	MLEC	KIAA0152, isoform CRA_c	5,4	28580	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	1	9,8	0	0,0
525	119618923	RAN	RAN, member RAS oncogene family, isoform CRA_c	6,6	26206	3	11,4	2	10,0	2	9,3	1	9,4	3	12,2	2	9,0	3	9,7
526	119618985	SH3BGRL	SH3 domain binding glutamic acid-rich protein like,	5,1	12685	2	11,6	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
527	119619008	HEL	phosphoglycerate kinase 1, isoform CRA_a	9,5	28434	18	42,2	21	39,6	20	41,0	19	46,8	20	60,3	27	44,6	26	44,1
528	119619048	RLIM	hCG1811491	6,7	15527	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	1	9,7
529	119619063	USMG5	hCG1820685	10,3	6618	1	11,4	1	10,0	0	0,0	0	0,0	0	0,0	1	8,0	1	7,9
530	119619270	MOSPD2	motile sperm domain containing 2, isoform CRA_a	5,2	11053	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
531	119619403	ACOT9	acyl-CoA thioesterase 9, isoform CRA_a	6,7	43189	0	0,0	1	10,0	0	0,0	0	0,0	0	0,0	1	13,2	1	13,6
532	119619705	SCAMP2	secretory carrier membrane protein 2, isoform CRA_a	8,4	20132	0	0,0	0	0,0	1	8,8	0	0,0	0	0,0	1	9,9	0	0,0
533	119619920	MAT2A	methionine adenosyltransferase II, alpha, isoform CR	5,6	39692	2	17,6	0	0,0	3	19,6	1	9,5	3	24,2	1	9,8	2	13,5
534	119620359	UGP2	UDP-glucose pyrophosphorylase 2, isoform CRA_a	9,1	16979	1	11,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
535	119620360	UGP2	UDP-glucose pyrophosphorylase 2, isoform CRA_b	7,4	38747	1	13,5	0	0,0	1	8,7	1	9,4	2	12,2	0	0,0	0	0,0
536	119620368	HEL	malate dehydrogenase 1, NAD (soluble), isoform CRA_d	7,8	31694	7	56,6	7	29,8	8	36,7	10	46,8	12	60,3	8	41,5	7	41,0
537	119620369	MDH1	malate dehydrogenase 1, NAD (soluble), isoform CRA_e	5,5	7766	0	0,0	1	9,8	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
538	119620390	CCT4	chaperonin containing TCP1, subunit 4 (delta), isofo	6,7	52484	4	38,1	5	19,9	7	37,3	8	37,4	9	36,3	7	44,3	6	27,6
539	119620393	CCT4	chaperonin containing TCP1, subunit 4 (delta), isofo	7,8	58092	0	0,0	1	10,0	0	0,0	0	0,0	0	0,0	1	9,8	0	0,0
540	119620401	XPO1	exportin 1 (CRM1 homolog, yeast), isoform CRA_b	9,8	17449	2	11,5	3	14,8	2	13,5	1	9,4	0	0,0	2	14,7	2	15,4
541	119620768	SRSF7	splicing factor, arginine/serine-rich 7, 35kDa, isof	10,0	15745	2	10,6	1	9,7	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
542	119620869	DPY30	dpy-30-like protein, isoform CRA_b	7,4	13867	1	10,4	0	0,0	0	0,0	1	9,5	2	12,2	2	8,9	0	0,0
543	119620880	AK2	hCG1988320, isoform CRA_a	7,7	14118	0	0,0	1	10,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
544	119621095	SELI	selenoprotein I	6,3	43994	0	0,0	0	0,0	1	8,7	1	9,5	0	0,0	1	9,0	1	7,9
545	119621106	HADHB	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coen	10,2	40396	2	22,8	0	0,0	2	18,4	0	0,0	0	0,0	2	25,9	1	14,8
546	119621213	LDAH	hypothetical protein FLJ21820, isoform CRA_c	9,1	18663	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
547	119621373	RRM2	hCG23833, isoform CRA_b	6,1	51078	1	11,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
548	119621875	HEL	hCG23783, isoform CRA_a	10,2	23417	22	77,6	6	30,0	13	60,4	7	28,2	11	48,3	14	62,5	11	43,6
549	119622098	SMCHD1	hCG2041207	8,1	13132	1	11,1	1	10,3	1	8,6	1	9,4	0	0,0	1	8,0	1	7,9
550	119622352	WDR73	WD repeat domain 73, isoform CRA_c	6,3	44570	1	10,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	11,4
551	119622403	MRPL46	mitochondrial ribosomal protein L46, isoform CRA_d	8,2	19151	0	0,0	1	10,1	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
552	119623224	CSTF2	cleavage stimulation factor, 3' pre-RNA, subunit 2,	8,6	51103	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	1	9,7
553	119623396	RANBP1	RAN binding protein 1, isoform CRA_e	10,4	7711	1	11,6	1	10,0	1	9,2	1	9,4	2	12,2	1	8,0	0	0,0
554	119623603	RPS17L	hCG1644208	8,8	12319	2	15,5	2	10,0	1	8,7	2	9,5	2	12,2	1	8,7	1	9,7
555	119623678	TRIM26	tripartite motif-containing 26, isoform CRA_b	8,0	36057	1	11,2	0	0,0	0	0,0	1	9,5	0	0,0	0	0,0	0	0,0
556	119624101	RPS18	ribosomal protein S18, isoform CRA_c	10,7	15030	3	27,8	1	10,3	2	18,4	1	9,5	2	12,2	2	18,4	3	24,8
557	119624172	HMGA1	high mobility group AT-hook 1, isoform CRA_f	10,9	11529	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0

558	119624337	FGD2	FYVE, RhoGEF and PH domain containing 2, isoform CRA	6,1	43191	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
559	119624496	BCLAF1	transcriptional regulating factor 1, isoform CRA_c	11,8	10474	0	0,0	0	0,0	0	0,0	1	9,4	0	0,0	0	0,0	0	0,0
560	119624647	MRPL14	mitochondrial ribosomal protein L14, isoform CRA_a	10,0	22612	1	10,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
561	119624862	DST	dystonin, isoform CRA_b	5,9	314122	1	11,6	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
562	119625468	N/A	hCG2026271	6,0	8877	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
563	119625602	HSPA4L	heat shock 70kDa protein 4-like, isoform CRA_a	5,9	80212	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,1	0	0,0
564	119625804	HEL70	moesin, isoform CRA_b	5,8	66606	6	46,4	6	34,7	7	38,0	8	56,2	11	48,4	8	47,0	7	45,1
565	119626153	G3BP2	Ras-GTPase activating protein SH3 domain-binding pro	4,5	30011	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
566	119626554	CISD2	similar to RIKEN cDNA 1500009M05 gene, isoform CRA_b	10,4	17245	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
567	119626608	AIMP1	small inducible cytokine subfamily E, member 1 (endo	9,1	35953	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	13,3	2	19,3
568	119627154	CTNND2	chromosome 1 open reading frame 123, isoform CRA_a	4,5	14529	1	11,1	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
569	119627229	EPS15	epidermal growth factor receptor pathway substrate 1	4,4	97079	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,4	0	0,0
570	119627553	YBX1	Y box binding protein 1, isoform CRA_a	10,3	14714	2	11,4	4	20,0	4	22,8	4	18,9	8	12,3	2	12,3	4	26,3
571	119627645	CAP1	CAP, adenylate cyclase-associated protein 1 (yeast),	7,7	51086	1	11,2	0	0,0	5	8,7	0	0,0	0	0,0	2	9,3	4	22,6
572	119627697	MYCBP	c-myc binding protein, isoform CRA_c	5,6	14040	1	11,2	1	10,0	1	9,9	0	0,0	0	0,0	1	8,1	1	9,7
573	119627737	N/A	hCG2041179	10,7	9204	1	12,4	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
574	119627942	MARCKSL1	MARCKS-like 1, isoform CRA_a	4,4	17185	1	11,3	0	0,0	1	9,9	0	0,0	0	0,0	1	9,4	0	0,0
575	119627980	KHDRBS1	KH domain containing, RNA binding, signal transducti	6,0	38664	3	18,4	5	19,9	5	18,4	6	18,8	3	24,2	5	18,0	7	19,3
576	119628218	RPL17	hCG20217	10,1	20141	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	2	9,3	0	0,0
577	119628393	PHKG1	hCG18830, isoform CRA_b	5,1	29927	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
578	119628455	DNAH5	dynein, axonemal, heavy polypeptide 5	5,7	528984	1	11,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
579	119628511	NSUN2	NOL1/NOP2/Sun domain family, member 2, isoform CRA_b	6,1	59365	1	12,5	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
580	119628710	N/A	hCG1774379	9,9	9566	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
581	119628806	RPL21	ribosomal protein L21, isoform CRA_f	10,7	9887	4	20,3	5	19,9	3	18,4	5	18,8	3	12,3	3	21,1	3	15,5
582	119629071	VWA8	KIAA0564 protein, isoform CRA_b	9,2	54432	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
583	119629147	COG3	component of oligomeric golgi complex 3, isoform CRA	5,2	97008	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
584	119629465	METTL21C	OTTHUMP00000018663, isoform CRA_a	4,8	31747	1	12,5	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
585	119629468	N/A	hCG2011852	9,1	784999	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	15,5
586	119629883	HEL	hCG401289, isoform CRA_d	7,5	42389	1	11,1	0	0,0	2	13,5	0	0,0	0	0,0	1	8,0	0	0,0
587	119630377	ATP5J	ATP synthase, H+ transporting, mitochondrial F0 comp	9,5	13170	0	0,0	0	0,0	0	0,0	1	9,4	0	0,0	0	0,0	0	0,0
588	119630439	BTF3L4	hCG2008008	5,5	18241	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	1	7,9
589	119630558	NAPB	N-ethylmaleimide-sensitive factor attachment protein	5,2	33899	0	0,0	1	10,0	1	8,7	1	9,5	0	0,0	1	8,7	2	13,6
590	119630667	MGME1	chromosome 20 open reading frame 72, isoform CRA_b	8,2	28175	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
591	119630887	MAVS	virus-induced signaling adapter, isoform CRA_b	5,0	51139	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,4	1	9,7
592	119630948	DDRGK1	chromosome 20 open reading frame 116, isoform CRA_a	5,0	35235	1	15,2	0	0,0	0	0,0	0	0,0	0	0,0	1	9,8	0	0,0
593	119631258	STAT1	signal transducer and activator of transcription 1,	6,0	81842	22	116,2	27	97,5	26	96,4	26	95,3	32	132,5	20	88,1	20	91,2
594	119631259	STAT1	signal transducer and activator of transcription 1,	5,7	86485	4	19,4	3	15,1	6	18,4	2	9,4	5	12,2	3	14,9	5	16,6
595	119631275	INPP1	inositol polyphosphate-1-phosphatase, isoform CRA_b	4,7	13520	0	0,0	0	0,0	1	9,8	0	0,0	0	0,0	0	0,0	0	0,0
596	119631468	HNRNPA3	heterogeneous nuclear ribonucleoprotein A3, isoform	8,4	37011	1	16,5	6	49,4	6	31,9	7	37,4	9	48,4	7	43,1	4	27,6
597	119631540	WIPF1	Wiskott-Aldrich syndrome protein interacting protein	11,9	51978	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
598	119631661	SSB	Sjogren syndrome antigen B (autoantigen La), isoform	9,4	39474	1	10,6	1	10,3	3	17,8	1	9,4	2	12,2	1	8,9	2	18,6
599	119631662	SSB	Sjogren syndrome antigen B (autoantigen La), isoform	8,6	30818	0	0,0	0	0,0	1	9,9	1	9,5	0	0,0	1	9,5	1	9,7
600	119631889	PRPF40A	hCG1811743, isoform CRA_f	9,2	104943	0	0,0	0	0,0	1	9,9	0	0,0	0	0,0	0	0,0	0	0,0
601	119632042	RAB3GAP1	RAB3 GTPase activating protein subunit 1 (catalytic)	5,7	99116	1	9,8	0	0,0	1	8,7	1	9,5	0	0,0	1	9,8	2	15,7
602	119632119	RPS4Y2	hCG38986, isoform CRA_b	10,3	27203	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
603	119632165	HPRT1	hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyha	6,0	24126	1	16,4	1	10,0	3	27,5	2	18,8	3	24,2	3	23,9	3	25,0
604	119703746	ETFDH	electron transfer flavoprotein-ubiquinone oxidored	7,3	68477	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
605	1197210	ADA	adenosine deaminase	5,5	35130	1	11,2	3	24,7	3	17,8	2	9,5	2	12,2	3	21,1	2	9,7
606	119874207	OCIAD1	OCIA domain-containing protein 1 isoform 2	6,6	21574	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
607	11990422	UBA6	MOP-4	5,7	117998	0	0,0	2	14,8	2	8,7	0	0,0	0	0,0	2	15,9	2	15,5
608	11991864	OR52D1	odorant receptor HOR3'beta2	8,6	31441	1	10,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
609	1200067	ENSG00000223931	immunoglobulin heavy chain	9,2	12684	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
610	1200072	KRT7	keratin	5,3	51335	2	13,1	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
611	1200089	ORF	ORF	8,6	59966	0	0,0	0	0,0	0	0,0	1	9,4	0	0,0	0	0,0	0	0,0
612	1203796	STK3	MST2	5,0	56262	1	11,2	1	10,0	0	0,0	0	0,0	0	0,0	1	9,3	1	9,7
613	120433593	DBI	acyl-CoA-binding protein isoform 2	6,2	10126	4	23,5	12	19,9	10	13,6	8	28,1	12	36,3	13	17,8	21	19,3
614	12043565	PGM1	phosphoglucomutase 1	4,8	16271	1	12,2	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
615	12052750	NCALD	hypothetical protein	5,2	22216	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
616	12052810	ECI2	hypothetical protein	9,2	43602	1	10,8	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
617	12052812	UBQLN1	hypothetical protein	4,9	62490	1	12,5	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
618	12052814	PHP14	hypothetical protein	5,6	13823	1	11,0	1	10,1	1	9,3	1	9,5	2	12,2	1	12,2	2	9,7
619	12052826	RAB10	hypothetical protein	8,8	22470	2	11,5	2	10,0	2	13,5	2	9,5	3	12,2	2	9,0	2	12,3
620	12052854	MRPL15	hypothetical protein	10,3	33497	1	12,5	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0

621	12052938	ABI3	hypothetical protein	4,8	38948	3	11,2	1	10,0	0	0,0	0	0,0	0	0,0	1	8,0	1	7,9
622	12052955	HEL	hypothetical protein	9,0	12802	6	35,8	4	29,8	2	9,3	2	18,8	3	24,3	2	18,0	1	11,8
623	12053161	USP44	hypothetical protein	7,7	81156	0	0,0	0	0,0	0	0,0	1	9,4	0	0,0	0	0,0	0	0,0
624	12053245	NEURL4	hypothetical protein	5,5	163091	1	12,5	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
625	12053339	CLPX	hypothetical protein	8,7	58096	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
626	12054072	IGHG1	immunoglobulin heavy chain constant region gamma 1	8,2	36134	29	48,6	8	25,0	17	37,3	6	18,8	2	12,2	1	8,7	2	13,5
627	12056479	UTS2	urotensin-2 isoform a preproprotein	7,2	16030	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7	0	0,0
628	12056568	SCAPER	AF119814_1 MSTP063	6,2	130800	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
629	120659964	CNTN5	CNTN5 protein	5,9	120700	0	0,0	0	0,0	1	8,6	0	0,0	0	0,0	0	0,0	1	11,4
630	1208427	HEL	ER-60 protease	5,9	56797	45	176,8	29	123,3	31	137,8	35	84,1	28	132,5	32	131,2	29	121,6
631	121488441	ENSG00000223931	immunoglobulin heavy chain variable region	8,8	15300	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
632	1217959	HLA	human leukocyte antigen-DQ beta chain	7,8	29766	2	11,5	0	0,0	2	9,3	1	9,5	2	12,2	2	9,0	2	9,7
633	122114654	METTL16	methyltransferase-like protein 16	7,7	63622	0	0,0	0	0,0	0	0,0	1	9,4	0	0,0	1	8,0	0	0,0
634	12224880	MRPS35	hypothetical protein	7,2	31952	1	11,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
635	12224953	SAR1B	hypothetical protein	5,1	14830	1	11,8	0	0,0	1	8,6	0	0,0	0	0,0	0	0,0	1	9,7
636	12225000	VPS35	hypothetical protein	5,1	56898	1	9,7	3	14,8	2	13,6	0	0,0	0	0,0	1	8,7	2	16,7
637	12232385	COPS7B	COP9 signalosome complex subunit 7b	5,8	29623	1	10,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
638	12232625	HLA	MHC class I antigen	5,2	21054	3	22,9	1	12,1	1	13,8	0	0,0	3	21,9	2	15,1	2	12,4
639	12276066	MCCC1	AF310339_1 3-methylcrotonyl-CoA carboxylase alpha sub	7,6	80414	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,8
640	1228045	NUP160	nuclear pore protein	5,3	148829	1	11,2	0	0,0	1	8,7	0	0,0	0	0,0	1	8,0	0	0,0
641	122937211	KIAA0368	proteasome-associated protein ECM29 homolog	8,8	223674	0	0,0	0	0,0	2	9,3	0	0,0	0	0,0	0	0,0	0	0,0
642	1230564	DDX21	Gu protein, partial	9,7	89251	2	14,4	1	10,1	2	9,3	1	17,0	3	12,3	1	8,9	2	9,7
643	1232077	MCM2	huMCM2	5,3	100886	1	11,7	0	0,0	1	8,7	2	9,5	0	0,0	1	9,4	2	9,7
644	1232079	MCM5	huMCM5	8,4	81833	1	11,7	0	0,0	1	9,2	0	0,0	0	0,0	1	9,8	1	13,7
645	12330685	MRPL37	AF325707_1 ribosomal protein L2	8,7	48102	1	12,5	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	1	9,7
646	1235522	UFM1	ORF	9,3	8702	1	12,1	0	0,0	1	8,6	0	0,0	0	0,0	0	0,0	1	9,7
647	1235727	PRMT1	unnamed protein product	5,4	40518	4	25,6	1	9,7	0	0,0	0	0,0	2	12,2	0	0,0	1	9,7
648	12408675	PFDN2	prefoldin subunit 2	6,2	16649	0	0,0	0	0,0	0	0,0	1	9,4	0	0,0	1	9,8	0	0,0
649	12408677	PFDN4	prefoldin subunit 4	4,3	15315	0	0,0	0	0,0	0	0,0	0	0,0	2	12,2	1	9,8	0	0,0
650	124244088	BROX	BRO1 domain-containing protein BROX	7,5	46458	1	10,4	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
651	124297989	TRIP11	C5orf51 protein	4,3	16962	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,0	1	8,0
652	124494254	PA2G4	proliferation-associated protein 2G4	6,1	43769	3	30,5	4	24,7	4	33,0	7	46,8	6	48,2	4	35,6	3	22,4
653	124504669	MAPRE1	MAPRE1 protein	9,6	19409	1	13,0	3	29,5	2	17,3	1	9,5	2	12,2	1	9,1	2	13,4
654	1245398	CAMK2D	CaMK-II, delta	4,9	12846	1	12,0	1	10,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
655	1255255	IRF5	interferon regulatory factor 5	5,4	56669	0	0,0	0	0,0	1	9,3	1	9,4	0	0,0	1	8,9	1	7,9
656	12620919	PSMA6	prosomal P27K protein	9,3	6201	2	19,1	3	14,8	2	14,1	4	18,8	3	24,2	3	14,7	2	15,5
657	1262583	PABPC4	polyadenylate binding protein II	9,4	21988	1	10,7	0	0,0	1	8,7	0	0,0	0	0,0	1	9,5	0	0,0
658	126362971	STK10	serine/threonine-protein kinase 10	6,5	112136	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7	1	9,8
659	126507399	HLA	MHC class I antigen	5,6	20971	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	2	8,7	0	0,0
660	126507451	CSE1L	cellular apoptosis susceptibility protein variant 2	5,7	103890	2	10,5	5	39,9	7	27,7	4	28,1	3	24,3	3	19,6	2	18,6
661	12653465	SUCLG1	SUCLG1 protein	9,1	35048	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
662	12653475	PSMB7	Proteasome (prosome, macropain) subunit, beta type, 7	7,6	29919	1	11,2	0	0,0	0	0,0	1	9,5	2	12,1	0	0,0	0	0,0
663	12653493	BASP1	Brain abundant, membrane attached signal protein 1	4,5	22603	3	23,9	9	44,8	8	41,0	0	0,0	5	24,4	4	21,1	10	45,4
664	12653523	EIF3S8	EIF3C protein	7,5	37681	3	22,2	1	9,7	1	9,3	0	0,0	0	0,0	2	13,7	2	15,7
665	12654031	CCBL2	CCBL2 protein	8,4	33230	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
666	12654253	IPO5	IPO5 protein	4,6	35486	0	0,0	1	9,7	1	9,8	1	9,6	0	0,0	1	9,7	1	9,7
667	12654285	NGLY1	Similar to peptide N-glycanase homolog (S.cerevisiae)	8,0	71993	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
668	12654399	GNL3	Guanine nucleotide binding protein-like 3 (nucleolar)	9,5	61979	1	10,8	1	10,0	1	8,7	0	0,0	0	0,0	1	8,7	1	8,8
669	12654453	RECQL	RecQ protein-like (DNA helicase Q1-like)	8,0	73438	3	22,0	3	19,9	0	0,0	1	9,5	2	12,2	1	9,0	3	15,7
670	12654713	HS6ST1	Similar to heparan sulfate 6-O-sulfotransferase, part	8,7	20705	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
671	12655017	IFI35	Interferon-induced protein 35	5,7	31745	1	10,4	1	9,7	2	9,3	1	9,5	0	0,0	1	9,8	3	7,9
672	12667788	MYH9	myosin-9	5,4	226532	11	38,7	8	19,9	7	22,7	11	28,2	11	48,3	7	30,1	7	25,1
673	126723060	ZC3H4	zinc finger CCCH domain-containing protein 4	5,8	140238	1	11,1	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
674	12697901	SPHKAP	KIAA1678 protein	5,0	142123	1	12,5	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
675	12698013	UBE2O	KIAA1734 protein	4,9	143477	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
676	12698051	UNK	KIAA1753 protein	6,5	89042	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
677	12698057	SYNE1	KIAA1756 protein	5,8	116741	0	0,0	0	0,0	0	0,0	0	0,0	2	12,1	0	0,0	0	0,0
678	1272662	RPS4X	ribosomal protein S4	12,1	6901	5	15,2	7	19,9	3	13,6	2	18,8	0	0,0	2	11,7	2	13,6
679	127798841	HEL	ATP synthase, H+ transporting, mitochondrial F1 comp	9,4	59689	31	70,7	23	63,4	31	83,0	28	65,5	35	84,4	30	59,4	24	54,2
680	127801388	PGM1	Phosphoglucomutase 1	6,4	61440	2	18,5	1	10,3	1	9,8	1	9,4	2	12,2	1	9,0	1	7,9
681	12803713	MMS19	MMS19 protein	6,3	75913	1	10,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
682	12803939	NCF1	Neutrophil cytosolic factor 1	9,4	44683	1	14,6	5	29,5	18	96,3	7	37,5	9	48,3	13	74,0	6	63,2
683	12804019	AKR1E2	AKR1CL2 protein	7,2	34934	1	13,1	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0

684	12804119	FBXL15	FBXL15 protein	7,5	32544	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
685	12804225	HEL	Unknown (protein for IMAGE:3543711), partial	5,3	59450	1	12,8	2	10,4	1	8,7	1	9,5	2	12,2	1	9,3	2	15,7
686	12804243	SCRN2	Ses2 protein, partial	5,8	43531	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,8	0	0,0
687	12804481	WDR18	WD repeat domain 18	6,2	47436	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	1	10,6
688	12804709	LSP1	Lymphocyte-specific protein 1	4,5	37222	3	22,4	11	44,7	5	32,5	11	37,5	5	36,3	8	38,3	8	39,0
689	1296664	SEC23A	Sec23 protein	6,6	86147	1	11,3	0	0,0	2	17,2	0	0,0	0	0,0	1	14,2	1	13,7
690	1296666	SEC23B	Sec23 protein	6,4	86471	2	19,3	3	19,9	2	13,6	0	0,0	0	0,0	2	8,9	2	18,1
691	1304314	ALDH18A1	pyrroline 5-carboxylate synthetase	6,6	87280	3	21,8	10	39,6	11	59,9	5	28,1	5	24,2	9	47,5	6	42,4
692	13097156	NDUFA9	Similar to NADH dehydrogenase (ubiquinone) 1 alpha su	10,1	38423	4	27,3	3	19,9	1	8,7	1	9,4	0	0,0	2	14,7	2	18,6
693	13124873	CBFB	core-binding factor subunit beta isoform 2	6,2	21490	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
694	13124879	MYH11	myosin-11 isoform SM1A	5,3	227339	2	16,3	6	20,0	7	41,0	7	28,2	9	60,4	4	23,7	4	30,8
695	13129006	DDX50	ATP-dependent RNA helicase DDX50	9,5	82565	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
696	13129018	GGCT	gamma-glutamylcyclotransferase isoform 1	4,9	20990	0	0,0	0	0,0	0	0,0	1	9,5	0	0,0	1	8,1	0	0,0
697	13129068	NOC4L	nucleolar complex protein 4 homolog	7,1	58468	0	0,0	0	0,0	1	9,3	0	0,0	0	0,0	0	0,0	1	7,9
698	13129100	DCTPP1	dCTP pyrophosphatase 1	4,8	18682	0	0,0	2	19,3	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
699	13129104	CCDC86	coiled-coil domain-containing protein 86	10,8	40217	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,4	1	9,8
700	13129110	WDR77	methylosome protein 50	4,9	36725	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
701	13172068	IGHV5	AF235866_1 immunoglobulin heavy chain variable region	5,4	9676	0	0,0	1	9,7	1	9,8	0	0,0	2	12,2	0	0,0	0	0,0
702	13172120	ENSG00000223931	AF235892_1 immunoglobulin heavy chain variable region	6,5	7713	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
703	1322019	UROD	uroporphyrinogen decarboxylase	5,7	40804	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
704	13236495	CRYZ	quinone oxidoreductase isoform a	8,6	35207	5	24,2	5	14,8	9	27,0	0	0,0	2	12,2	4	14,3	8	25,6
705	13236516	DERL1	derlin-1 isoform a	9,7	28802	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
706	13236577	THTPA	thiamine-triphosphatase isoform 1	4,6	25567	1	10,5	1	10,0	1	9,3	0	0,0	0	0,0	1	8,0	1	7,9
707	13236587	TMEM43	transmembrane protein 43	8,4	44876	1	11,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
708	1326108	MTX1	metaxin	5,9	35778	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
709	13272562	MT-ATP6	ATP synthase 6	10,5	24788	2	12,4	0	0,0	1	9,8	0	0,0	0	0,0	1	8,9	1	7,9
710	13276641	NCLN	hypothetical protein	7,1	61788	2	11,4	0	0,0	2	13,5	0	0,0	0	0,0	1	8,9	3	23,5
711	13277564	KIAA1068	NudC domain containing 3	5,1	24726	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
712	13279065	CSRP1	Similar to cysteine and glycine-rich protein 1, parti	8,7	17804	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	2	15,7
713	13279239	ENO1	ENO1 protein, partial	5,5	29884	5	11,9	14	10,0	17	9,3	17	9,5	8	12,2	59	9,1	30	9,7
714	13279281	PMPCA	PMPCA protein, partial	9,2	16197	1	11,3	1	10,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
715	1335134	N/A	unnamed protein product	5,8	11592	1	11,5	6	10,0	3	9,3	6	9,5	9	12,2	6	9,0	5	9,7
716	1335344	F2	unnamed protein product	5,4	69286	3	11,7	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	1	9,7
717	13375618	DHCR24	delta(24)-sterol reductase precursor	8,1	60083	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	1	8,8
718	13375746	ARMT1	UPF0364 protein C6orf211	5,4	51173	0	0,0	1	10,3	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
719	13375789	PANK3	pantothenate kinase 3	6,1	41095	0	0,0	1	10,2	1	9,8	0	0,0	0	0,0	1	9,7	0	0,0
720	13376181	TUBAL3	tubulin alpha chain-like 3 isoform 1	5,6	49890	14	18,2	2	14,8	1	9,9	2	9,4	5	24,3	4	17,4	2	14,9
721	13376331	L2HGDH	L-2-hydroxyglutarate dehydrogenase, mitochondrial p	8,1	50298	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
722	13376840	WDR61	WD repeat-containing protein 61	5,1	33581	1	10,7	2	14,8	1	9,9	1	9,4	5	24,2	2	16,6	1	9,7
723	133777825	PBRM1	PB1 protein	6,3	184656	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
724	13378137	TRADD	tumor necrosis factor receptor type 1-associated DE	5,9	34229	0	0,0	0	0,0	1	8,6	1	9,4	0	0,0	3	17,7	1	7,9
725	13386490	LIMD2	LIM domain-containing protein 2	9,2	14071	1	9,6	1	10,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
726	133925811	TNPO1	transportin-1 isoform 1	4,7	102355	1	11,3	2	19,3	1	9,3	1	9,5	2	12,2	1	9,0	1	9,7
727	13399304	APOBEC3G	DNA dC->dU-editing enzyme APOBEC-3G	7,9	46409	1	11,1	2	19,9	1	8,7	0	0,0	0	0,0	1	12,6	2	15,4
728	13436086	DOK3	DOK3 protein	7,8	23203	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
729	13436305	GADD45GIP1	GADD45GIP1 protein, partial	10,4	25024	1	11,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
730	13436308	HNRNPA1L2	Unknown (protein for IMAGE:3615335), partial	9,5	31734	9	51,4	13	76,1	15	71,2	14	37,5	18	94,0	14	66,6	12	56,8
731	13436335	ATPIF1	ATPIF1 protein	9,2	10208	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	1	11,4
732	13477137	PITRM1	Pitrilysin metallopeptidase 1	6,6	117497	1	9,7	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	1	7,9
733	13477169	VTN	Vitronectin	5,5	54336	2	10,6	1	10,3	4	9,3	1	9,5	3	12,2	4	9,1	3	9,7
734	13477237	ZNF607	ZNF607 protein	5,2	16921	0	0,0	0	0,0	1	9,9	0	0,0	0	0,0	1	9,8	0	0,0
735	13489087	HEL57	leukocyte elastase inhibitor	5,9	42743	0	0,0	2	19,3	3	18,4	0	0,0	0	0,0	1	8,0	1	7,9
736	13528729	HYOU1	HYOU1 protein	10,3	16668	8	28,5	2	10,0	2	14,1	1	9,4	0	0,0	2	17,9	2	13,6
737	13528888	MRE11A	MRE11A protein	5,0	23145	0	0,0	1	10,3	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
738	1353386	ADK	adenosine kinase	6,1	37513	1	11,4	1	10,3	2	17,3	1	9,5	0	0,0	2	8,0	2	13,6
739	13540192	IDI1	AF291755_1 isopentenyl pyrophosphate isomerase 1	5,9	26432	1	16,4	0	0,0	1	8,7	1	9,4	2	12,2	2	19,4	0	0,0
740	13540477	WNT3	proto-oncogene Wnt-3 precursor	7,2	39646	1	13,1	0	0,0	1	9,8	0	0,0	0	0,0	1	8,0	0	0,0
741	13542987	RPS8	Similar to ribosomal protein S8, partial	10,2	9265	2	11,1	1	10,0	2	9,2	4	9,4	3	12,2	1	8,0	2	9,6
742	13543307	PLIN3	Mannose-6-phosphate receptor binding protein 1	5,2	47029	3	27,4	0	0,0	1	9,3	2	18,9	2	12,3	2	14,9	2	8,0
743	13543317	PDXK	PDXK protein	5,6	31809	2	20,7	1	10,0	3	23,3	2	18,8	3	24,2	1	12,3	2	21,8
744	13543489	BLVRA	Biliverdin reductase A	6,0	33433	1	12,5	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
745	13543875	TDP1	TDP1 protein	6,4	33647	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	1	9,7
746	13559170	NUBP1	C447E6.1 (nucleotide binding protein 1 (E.coli MinD	5,9	28204	2	10,7	2	10,1	1	9,4	0	0,0	2	12,3	2	12,3	1	9,8

747	13562114	TUBB1	tubulin beta-1 chain	4,9	50328	2	10,8	0	0,0	0	0,0	1	9,5	0	0,0	0	0,0	0	0,0
748	13569848	TBRG4	protein TBRG4 isoform 2	6,6	58443	1	11,2	2	10,0	0	0,0	0	0,0	0	0,0	1	8,0	1	9,7
749	13569879	ANP32E	acidic leucine-rich nuclear phosphoprotein 32 famil	3,6	30674	0	0,0	0	0,0	0	0,0	1	9,4	0	0,0	0	0,0	0	0,0
750	13569901	TSC22D4	TSC22 domain family protein 4	6,8	41027	0	0,0	1	9,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
751	13569956	ARPC5L	actin-related protein 2/3 complex subunit 5-like pr	6,2	16923	1	14,2	0	0,0	0	0,0	0	0,0	2	12,2	1	15,2	2	15,5
752	13620885	MRPS6	mitochondrial ribosomal protein S6	9,9	18360	0	0,0	0	0,0	2	8,7	0	0,0	0	0,0	0	0,0	0	0,0
753	13623421	MBOAT7	MBOAT7 protein	8,9	38437	1	11,2	1	10,0	1	8,7	1	9,5	0	0,0	1	8,0	1	7,9
754	13623609	PFKL	Phosphofructokinase, liver	7,7	90204	5	32,1	7	34,9	5	13,6	7	37,4	3	24,2	8	41,9	8	41,7
755	13623693	U2SURP	Unknown (protein for IMAGE:2820942), partial	8,7	118085	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
756	13699256	PPP1R8	nuclear inhibitor of protein phosphatase 1 isoform	7,0	38460	1	12,4	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
757	1373146	PICALM	CALM	7,4	70696	1	12,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
758	13774112	ENSG00000223931	anti TNF-alpha antibody heavy-chain Fab fragment	8,8	23424	1	12,5	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
759	13775198	SH3BGRL3	SH3 domain-binding glutamic acid-rich-like protein	4,7	10420	2	13,5	1	10,0	0	0,0	1	9,4	0	0,0	1	9,0	1	9,7
760	13775200	SF3B5	splicing factor 3B subunit 5	5,9	10136	2	11,0	2	10,0	1	9,8	1	9,5	0	0,0	1	13,3	1	9,7
761	13775228	DOHH	deoxyhypusine hydroxylase	4,6	32905	0	0,0	0	0,0	0	0,0	0	0,0	2	12,2	0	0,0	0	0,0
762	13785574	EIF6	p27BBP protein	4,4	26350	3	16,6	3	14,8	2	14,2	2	9,5	3	24,3	2	13,7	2	15,5
763	13810206	PARVG	hypothetical protein	4,8	31043	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
764	1381027	PRPSAP1	phosphoribosypyrophosphate synthetase-associated prot	6,8	39462	1	11,2	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
765	13938613	OSTF1	OSTF1 protein	5,2	24065	1	11,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
766	13940245	ARHGAP17	RICH1B protein	6,8	25761	2	10,5	1	9,8	1	8,7	0	0,0	3	12,2	1	9,8	2	9,7
767	13994151	HEL	PDZ and LIM domain protein 1	6,6	36072	1	15,3	3	19,9	1	9,3	5	37,5	2	12,3	2	17,9	2	18,4
768	13994242	SH3KBP1	SH3 domain-containing kinase-binding protein 1 isof	6,2	73108	1	12,4	0	0,0	1	9,8	0	0,0	0	0,0	0	0,0	1	11,4
769	13994259	MRPS5	28S ribosomal protein S5, mitochondrial	10,3	47988	0	0,0	0	0,0	1	8,6	0	0,0	0	0,0	0	0,0	0	0,0
770	14016	COX2	cytochrome C oxidase II subunit	4,5	20995	3	17,4	2	10,1	3	9,3	5	18,8	6	12,3	3	9,1	2	12,3
771	14017799	CDK13	KIAA1791 protein	5,7	71740	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
772	14017877	TMX3	KIAA1830 protein	4,7	55204	1	10,5	0	0,0	1	9,3	1	9,5	0	0,0	1	8,7	1	8,8
773	14017887	RANGAP1	KIAA1835 protein	4,5	67334	2	17,7	0	0,0	0	0,0	0	0,0	0	0,0	1	8,1	1	7,9
774	14028397	MRPS23	mitochondrial ribosomal protein S23	9,8	2537	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	11,4
775	14030609	RGS10	AF368902_1 regulator of G protein signaling 10	5,2	20218	1	13,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
776	14041905	QKI	unnamed protein product	9,1	35596	1	13,1	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
777	14041924	SRP68	unnamed protein product	5,8	37217	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
778	14041927	SRP68	unnamed protein product	5,9	38225	0	0,0	1	10,0	1	9,3	1	9,4	0	0,0	2	12,3	1	8,8
779	14042261	OLA1	unnamed protein product	7,8	44716	3	16,1	4	14,8	7	36,1	1	9,5	8	12,2	6	20,5	5	19,3
780	14042447	SEPT11	unnamed protein product	8,1	30612	1	11,3	2	14,8	0	0,0	0	0,0	0	0,0	2	9,4	1	9,7
781	14042449	CIRH1A	unnamed protein product	9,0	76923	1	10,5	2	10,0	1	8,7	1	9,4	0	0,0	1	8,7	1	9,6
782	14042717	CAND1	unnamed protein product	5,4	45512	0	0,0	2	9,7	1	8,7	0	0,0	0	0,0	2	17,4	1	11,4
783	14042722	CCDC47	unnamed protein product	4,5	55319	2	20,7	1	10,0	1	9,8	2	18,8	0	0,0	1	9,6	1	8,8
784	14042728	STT3B	unnamed protein product	9,9	33410	1	9,7	1	9,7	2	9,3	1	9,4	2	12,2	3	8,0	1	9,7
785	14042741	SCOC	unnamed protein product	4,5	13895	0	0,0	0	0,0	1	9,8	1	9,4	0	0,0	0	0,0	0	0,0
786	14042761	LACTB	unnamed protein product	8,0	41153	0	0,0	1	9,7	1	9,9	0	0,0	0	0,0	1	8,1	1	7,9
787	14042776	ACSS1	unnamed protein product	5,8	24259	1	12,4	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
788	14042792	TMEM43	unnamed protein product	8,5	25452	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	1	8,1	2	7,9
789	14042816	PRPF38A	unnamed protein product	10,7	28733	0	0,0	1	9,8	2	17,2	0	0,0	0	0,0	0	0,0	1	7,9
790	14042861	IPO4	unnamed protein product	4,5	46992	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0
791	14043026	VAMP8	vesicle-associated membrane protein 8	7,3	11420	1	11,9	0	0,0	0	0,0	0	0,0	0	0,0	1	9,5	2	12,7
792	14043107	FSCN1	FSCN1 protein	6,9	55136	3	29,0	7	39,3	9	50,7	8	46,8	12	48,4	10	51,4	6	44,7
793	14043145	LASP1	LASP1 protein	8,6	36015	1	9,7	0	0,0	1	9,8	0	0,0	0	0,0	1	9,3	1	9,7
794	14043155	PLCG2	PLCG2 protein	6,3	147937	2	16,1	7	54,3	9	72,1	5	37,4	0	0,0	9	58,3	9	56,9
795	14043165	FBF1	FBF1 protein, partial	6,3	74324	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
796	14043273	SAPS1	SAPS1 protein, partial	4,0	24560	1	12,5	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
797	14043628	EIF4G1	EIF4G1 protein	5,9	72201	1	10,6	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
798	14043666	ATAD3A	ATAD3A protein	9,5	66277	1	14,5	0	0,0	2	8,7	1	9,4	0	0,0	0	0,0	0	0,0
799	14043943	FASN	FASN protein	5,3	48348	7	31,1	12	34,6	11	36,1	4	28,2	5	24,4	7	23,4	6	25,0
800	14044088	CALM3	CALM1 protein	4,0	12877	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
801	14110407	HNRNPDL	heterogeneous nuclear ribonucleoprotein D-like isof	9,9	46419	2	14,8	3	10,0	4	29,3	5	37,4	3	12,2	3	8,7	1	9,7
802	14124984	CCT3	Chaperonin containing TCP1, subunit 3 (gamma)	6,1	60384	7	48,2	8	44,4	9	54,7	14	84,0	9	72,3	10	62,1	8	49,9
803	14124991	ZNF207	ZNF207 protein	10,3	41560	1	11,1	0	0,0	0	0,0	0	0,0	0	0,0	1	9,4	0	0,0
804	14141166	PCBP2	poly(rC)-binding protein 2 isoform b	6,4	38203	2	20,2	1	10,3	2	13,6	2	18,8	2	12,1	2	13,8	2	17,5
805	14141170	MTA2	metastasis-associated protein MTA2	10,0	75024	8	25,6	2	14,8	1	9,8	0	0,0	0	0,0	1	9,3	1	13,6
806	14141193	RPS9	40S ribosomal protein S9	11,1	22592	6	37,7	6	34,5	6	36,6	7	37,4	8	48,2	5	26,4	5	24,4
807	14149627	USP15	ubiquitin carboxyl-terminal hydrolase 15 isoform 2	4,9	109278	1	16,4	1	10,0	2	17,2	2	9,5	0	0,0	1	12,9	1	7,9
808	14149777	HEL	haloacid dehalogenase-like hydrolase domain-contain	5,8	28518	1	12,5	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
809	14150017	TMEM126A	transmembrane protein 126A isoform 1	9,6	21509	1	11,0	0	0,0	0	0,0	0	0,0	0	0,0	2	9,3	1	9,7

810	14150171	THOC3	THO complex subunit 3	5,7	38772	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
811	141515930	HLA	MHC class I antigen, partial	5,9	31726	1	13,9	2	13,0	1	9,9	0	9,4	0	14,6	0	9,5	1	11,6
812	141516249	N/A	MHC class I antigen, partial	5,8	20979	0	0,0	0	13,5	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
813	14165258	CYLD	ubiquitin carboxyl-terminal hydrolase CYLD isoform	5,3	107297	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	0	0,0
814	14165270	MRPL13	39S ribosomal protein L13, mitochondrial	9,5	20674	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
815	141797011	IQGAP1	IQ motif containing GTPase activating protein 1	6,1	189261	5	50,2	7	54,3	8	56,1	7	46,8	17	96,4	6	44,3	8	56,5
816	1418772	HLA	MHC Class II HLA-DRB3	6,1	9809	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,7	0	0,0
817	1419567	DCTN1	dynactin	5,4	139960	1	10,9	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
818	1419581	ENSG00000228325	immunoglobulin kappa light chain	9,3	11907	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,1	0	0,0
819	14198113	POLR1C	POLR1C protein, partial	5,3	38463	1	12,5	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
820	14198272	PGAM5	Phosphoglycerate mutase family member 5	6,9	27988	0	0,0	1	10,3	1	8,7	0	0,0	0	0,0	0	0,0	1	9,7
821	14211889	DPY30	protein dpy-30 homolog	4,7	11251	2	10,4	3	10,0	2	9,3	0	0,0	0	0,0	1	9,8	1	11,4
822	14211923	HINT2	histidine triad nucleotide-binding protein 2, mitoc	9,6	17144	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,4	0	0,0
823	14249348	TXNDC17	thioredoxin domain-containing protein 17	5,3	13923	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
824	14249821	SH3BP1	SH3BP1 protein	5,6	66666	0	0,0	1	9,7	1	8,7	0	0,0	0	0,0	1	8,0	1	7,9
825	14249932	XPO5	Unknown (protein for IMAGE:3532513), partial	5,6	68980	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	1	8,0	0	0,0
826	14250108	DPM1	Dolichyl-phosphate mannosyltransferase polypeptide 1,	9,9	29604	1	11,2	1	10,3	1	9,3	0	0,0	0	0,0	1	8,9	1	7,9
827	14250401	PS1TP5BP1	actin, beta, partial	5,5	41006	94	22,9	62	20,0	76	18,5	48	18,9	57	24,3	64	18,1	86	19,3
828	14250528	MAP4	MAP4 protein	5,2	102906	1	16,5	0	0,0	1	9,3	0	0,0	0	0,0	2	12,6	1	10,6
829	14250542	ASNS	Asparagine synthetase	6,3	64400	1	13,8	2	14,8	2	13,6	1	9,5	0	0,0	2	11,7	2	20,7
830	14250587	PCMT1	Protein-L-isoaspartate (D-aspartate) O-methyltransfer	6,8	24632	1	12,5	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
831	14250672	YBX3	Cold shock domain protein A	10,1	40061	1	11,1	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
832	14269586	MRPS26	28S ribosomal protein S26, mitochondrial	10,8	24194	1	9,6	1	9,7	1	8,7	0	0,0	0	0,0	0	0,0	0	0,0
833	14270766	FAM82A2	putative TCPTP-interacting protein	4,6	44072	1	10,7	0	0,0	1	9,8	0	0,0	0	0,0	1	8,0	1	7,9
834	14277126	PPIL3	peptidyl-prolyl cis-trans isomerase-like 3 isoform	6,6	18609	1	11,1	2	15,1	0	0,0	0	0,0	0	0,0	1	9,5	0	0,0
835	14289076	ENSG00000223931	immunoglobulin heavy chain variable region	4,5	13822	1	12,4	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
836	14326411	HSPD1	AF380943_1 short heat shock protein 60 Hsp60s1	9,7	23612	5	14,4	15	39,6	16	32,4	17	37,5	14	48,3	12	29,7	8	25,0
837	14326412	HSPD1	AF380943_2 short heat shock protein 60 Hsp60s2	4,5	27078	7	27,6	32	49,5	17	36,7	13	28,2	11	24,3	15	26,9	17	34,6
838	14389309	TUBA1C	tubulin alpha-1C chain	4,8	49896	50	79,9	140	127,6	58	104,5	93	100,9	80	130,1	86	98,3	72	101,2
839	14424542	RPL14	RPL14 protein	11,4	23646	0	0,0	0	0,0	3	9,9	0	0,0	2	12,3	0	0,0	0	0,0
840	14495677	HDGFRP2	MGC2641 protein, partial	6,1	62858	0	0,0	1	10,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
841	14495685	CCT5	Unknown (protein for IMAGE:3534054), partial	6,1	43014	3	23,8	2	19,9	4	18,4	4	22,6	5	24,3	3	21,1	2	16,6
842	14495689	PTGES2	Unknown (protein for IMAGE:3536456), partial	9,5	41794	1	9,7	1	10,1	0	0,0	0	0,0	0	0,0	1	8,9	0	0,0
843	145312241	DEF6	differentially expressed in FDCP 6 homolog	5,7	73892	0	0,0	0	0,0	2	8,7	0	0,0	0	0,0	0	0,0	1	7,9
844	145386517	PPP1R18	phostensin	5,2	67943	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	11,4
845	145553959	ELAC2	zinc phosphodiesterase ELAC protein 2 isoform 1	7,7	92200	1	12,1	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
846	14579002	DNAJB11	AF277317_1 PWP1-interacting protein 4	5,8	40501	0	0,0	0	0,0	2	13,5	0	0,0	0	0,0	1	9,6	1	12,9
847	14579643	SART3	AF387506_1 KIAA0156 isoform	4,4	41830	1	11,2	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
848	145843637	SET	SET	4,6	26610	0	0,0	0	0,0	0	0,0	1	9,5	0	0,0	0	0,0	1	8,0
849	14586956	MMS19	AF357881_1 transcriptional coactivator MMS19	5,9	113300	0	0,0	0	0,0	0	0,0	1	9,4	0	0,0	1	9,0	1	7,9
850	14587851	ARHGAP10	Graf2	6,8	89329	1	10,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	11,4
851	14591909	RPL5	60S ribosomal protein L5	10,1	34363	6	37,4	5	24,7	5	22,7	2	9,5	6	24,2	5	27,3	5	24,4
852	145942126	IGHV3	immunoglobulin heavy chain variable region	8,5	9578	0	0,0	0	0,0	0	0,0	1	9,4	0	0,0	0	0,0	0	0,0
853	14595132	RAP1A	Raichu404X	6,5	85016	7	17,9	2	10,0	7	23,3	7	28,1	5	12,2	6	12,9	4	14,9
854	14602539	SF3B3	SF3B3 protein	6,1	30211	1	10,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
855	14602923	HLA	HLA-DPA1 protein	5,0	29336	0	0,0	1	10,0	0	0,0	1	9,4	0	0,0	2	9,3	1	9,7
856	146424330	TUBB2A	TUBB2A protein	4,6	27918	1	12,1	1	10,0	1	8,7	1	9,4	0	0,0	0	0,0	1	9,7
857	14670394	DEDD	death effector domain-containing protein	9,0	36776	1	11,9	1	9,7	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
858	1469171	BOP1	KIAA0124	6,0	76950	0	0,0	0	0,0	1	9,3	0	0,0	0	0,0	1	8,0	1	8,8
859	1469888	TTLL12	KIAA0153	5,3	73730	3	29,8	1	10,0	0	0,0	0	0,0	0	0,0	2	11,7	2	17,5
860	14701786	CELF2	neuroplastoma apoptosis-related RNA-binding protein 2	8,9	54329	1	11,1	1	10,3	0	0,0	1	9,5	0	0,0	1	8,1	1	8,0
861	14715040	MCU	CCDC109A protein	9,0	36280	1	9,7	1	10,0	0	0,0	0	0,0	0	0,0	1	8,0	1	7,9
862	1477646	PLEC	plectin	5,5	518486	1	13,9	1	10,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
863	147904340	WDR82	WD repeat-containing protein 82	7,6	35080	1	12,5	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
864	147905700	ENTPD1	ectonucleoside triphosphate diphosphohydrolase	6,3	58688	2	11,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
865	1480279	IGHV3	Immunoglobulin heavy chain	9,2	12359	1	12,5	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
866	1480845	HLA	MHC class II antigen, partial	8,2	12514	1	9,7	1	10,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,6
867	1480869	STXBP2	Hunc-18b	6,1	66439	0	0,0	0	0,0	2	17,2	1	9,5	0	0,0	1	9,3	1	12,7
868	148233642	PPP6R1	transmembrane protein C16orf54	5,9	24361	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
869	148271063	DCD	dermcidin isoform 2	8,2	12415	1	12,4	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
870	1483131	ALK	p80 protein	6,4	75357	15	40,1	36	45,6	21	38,4	17	33,8	26	43,6	26	36,2	34	33,9
871	148491091	SLC25A24	calcium-binding mitochondrial carrier protein SCaM	6,0	53336	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
872	148536853	COPA	coatomer subunit alpha isoform 2	7,4	138346	4	33,6	6	39,3	8	50,1	5	37,4	3	24,2	7	50,5	9	59,5

873	148612816	RECQL5	ATP-dependent DNA helicase Q5 isoform 1	8,5	108840	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
874	14861834	CECR5	cat eye syndrome critical region protein 5 isoform	8,1	46303	0	0,0	0	0,0	1	8,6	0	0,0	0	0,0	2	20,4	1	15,4
875	148719679	HLA	MHC class I antigen, partial	6,2	20921	0	0,0	2	9,8	0	0,0	0	0,0	2	12,2	1	8,8	2	9,8
876	148727333	AK7	adenylate kinase 7	4,5	82659	1	11,2	0	0,0	0	0,0	0	0,0	2	12,1	0	0,0	1	9,6
877	148727341	STRAP	serine-threonine kinase receptor-associated protei	4,8	38420	1	18,6	2	14,8	2	14,1	2	18,8	0	0,0	2	14,7	2	17,5
878	148727351	CBWD3	COBW domain-containing protein 3	4,6	44039	0	0,0	0	0,0	1	9,9	0	0,0	0	0,0	0	0,0	1	7,9
879	148746218	TAOK3	serine/threonine-protein kinase TAO3	6,9	105387	0	0,0	1	10,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
880	148747351	PACSIN2	protein kinase C and casein kinase substrate in ne	4,9	55720	1	9,7	2	14,8	0	0,0	1	9,5	0	0,0	1	8,0	3	22,8
881	148747437	MOB1A	MOB kinase activator 1A	6,5	25081	1	11,1	1	10,0	1	8,7	0	0,0	0	0,0	1	9,3	1	7,9
882	148753311	RCC2	RCC2 protein	8,8	49679	2	11,5	1	10,0	1	9,9	1	9,4	2	12,2	2	9,4	1	10,6
883	14917109	AP2M1	AP-2 complex subunit mu isoform a	9,9	49655	1	10,4	2	10,0	0	0,0	0	0,0	0	0,0	1	8,0	2	9,7
884	1498227	ANP32B	PHAPI2b protein	4,0	22277	1	11,5	2	15,1	4	26,9	6	28,1	5	24,3	2	20,4	4	23,9
885	149999606	MOGS	mannosyl-oligosaccharide glucosidase isoform 1	9,1	91899	1	15,9	3	24,9	3	27,6	1	9,4	2	12,2	2	17,5	1	12,7
886	150010589	IFITM1	interferon-induced transmembrane protein 1	8,0	13920	1	10,7	0	0,0	0	0,0	1	9,5	0	0,0	1	9,6	1	13,6
887	15010550	HEL	heat shock protein gp96 precursor	4,6	90194	46	11,5	1	10,0	6	9,3	1	9,5	0	0,0	4	9,0	9	9,7
888	1504002	DOCK2	KIAA0209	6,5	213145	1	13,5	2	19,9	2	13,6	2	18,8	0	0,0	3	20,7	3	21,4
889	1504026	HMHA1	KIAA0223	5,7	127346	4	10,6	3	10,1	2	9,4	1	9,4	2	12,2	3	9,1	2	9,7
890	15042941	MAGEH1	melanoma-associated antigen H1	9,3	24441	0	0,0	0	0,0	1	9,8	0	0,0	0	0,0	0	0,0	0	0,0
891	15072342	TRIM68	GC109	6,6	37416	0	0,0	0	0,0	1	8,6	0	0,0	0	0,0	0	0,0	0	0,0
892	15072538	SLAMF1	SLAM	8,5	37222	0	0,0	1	10,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
893	15080043	BEND5	BEND5 protein	7,2	29216	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
894	15080279	CAPNS1	CAPNS1 protein	5,8	33787	2	15,2	0	0,0	1	9,9	2	18,8	2	12,3	4	26,5	2	17,6
895	15080291	DPP7	Dipeptidyl-peptidase 7	5,9	54328	0	0,0	0	0,0	2	8,7	0	0,0	0	0,0	1	8,0	0	0,0
896	15082258	CBX3	chromobox protein homolog 3	5,1	20812	2	17,7	1	10,0	2	13,6	4	28,1	2	12,2	1	9,6	1	12,3
897	15082451	ATP6V1C2	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit	5,6	43848	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7	0	0,0
898	15082470	AP2B1	Unknown (protein for IMAGE:4558274), partial	4,7	61064	0	0,0	1	10,0	0	0,0	1	9,4	2	12,2	1	8,9	1	9,7
899	15082494	SEPT1	Septin 1	5,5	41972	2	15,5	2	19,9	0	0,0	1	9,4	2	12,2	2	15,3	0	0,0
900	15088550	MZB1	AF338109_1 proapoptotic caspase adaptor protein	8,0	13048	0	0,0	0	0,0	1	9,3	0	0,0	0	0,0	1	8,7	3	9,8
901	151101292	TMX1	thioredoxin-related transmembrane protein 1 precur	4,8	31773	1	11,4	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	1	7,9
902	151101404	PTMA	prothymosin alpha isoform 2	3,5	12075	0	0,0	0	0,0	1	15,5	0	0,0	0	0,0	0	0,0	2	15,3
903	15131402	CSTF3	dJ85M6.1 (cleavage stimulation factor, 3' pre-RNA, s	8,4	82026	0	0,0	0	0,0	0	0,0	0	0,0	2	12,2	1	8,7	2	15,7
904	151333376	ND2	NADH dehydrogenase subunit 2	10,2	38932	1	11,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
905	15149476	RARS	arginine--tRNA ligase, cytoplasmic	6,2	75380	2	19,1	2	10,0	2	13,5	0	0,0	3	24,2	3	22,5	1	11,4
906	15150811	MRPS36	28S ribosomal protein S36, mitochondrial	10,4	11448	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	1	9,3	1	9,7
907	1518018	TANK	I-TRAF	5,4	47624	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
908	15208471	HLA	MHC class II antigen	8,5	29764	0	0,0	1	10,0	2	8,6	0	0,0	0	0,0	0	0,0	0	0,0
909	15214721	HDHD1	Haloacid dehalogenase-like hydrolase domain containin	5,2	23811	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	0	0,0
910	1524058	CFHR4	complement factor H-related protein 4	5,0	37326	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
911	1526426	HEL	proteasome subunit p42	7,3	44162	1	11,7	3	14,8	2	9,3	0	0,0	6	24,2	5	24,4	2	15,5
912	15281853	RAB1A	GTP binding protein Rab1a, partial	8,8	9879	3	17,1	1	9,7	3	14,2	1	9,5	3	12,2	2	11,7	2	12,9
913	153082755	IFIT2	interferon-induced protein with tetratricopeptide	6,3	54614	0	0,0	1	10,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
914	15342081	MRPL38	Mitochondrial ribosomal protein L38	6,2	40758	1	10,8	1	10,0	1	8,6	0	0,0	0	0,0	1	9,3	1	9,7
915	153791384	RPL22L1	60S ribosomal protein L22-like 1	9,8	14588	2	13,4	3	14,9	1	9,4	5	9,6	3	12,4	1	9,1	3	12,4
916	153791586	MYH2	myosin-2	5,5	223044	1	10,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
917	154090997	CCDC13	coiled-coil domain-containing protein 13	9,3	80865	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
918	15431288	RPL10A	60S ribosomal protein L10a	10,4	24832	3	19,4	3	24,7	5	22,7	4	28,1	8	36,3	5	27,3	5	27,1
919	15431293	RPL15	60S ribosomal protein L15 isoform 1	12,1	24147	5	26,4	2	19,9	6	36,7	2	9,5	5	36,3	4	35,5	4	27,6
920	15431303	RPL9	60S ribosomal protein L9	10,4	21864	4	11,6	4	19,9	2	14,1	6	37,5	0	0,0	3	17,3	1	12,7
921	154354964	IMMT	mitochondrial inner membrane protein isoform 1	6,1	83659	6	52,4	3	24,7	6	41,0	6	37,4	5	36,2	5	35,4	7	47,8
922	15451765	PML	protein PML isoform 9	6,5	90722	1	12,4	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
923	1545952	USP7	herpesvirus associated ubiquitin-specific protease (H	5,2	128253	1	9,7	0	0,0	2	17,3	0	0,0	0	0,0	1	12,3	2	18,1
924	1545982	PWP2	PWP2H protein	5,8	102451	1	11,9	1	9,7	0	0,0	0	0,0	0	0,0	1	8,6	1	7,9
925	154816184	TMEM55B	transmembrane protein 55B isoform 2	8,9	29451	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
926	15489373	TUBGCP3	TUBGCP3 protein	7,6	93886	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
927	15529978	ZNF622	zinc finger protein 622	5,8	54273	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
928	15529984	ARMC6	armadillo repeat-containing protein 6 isoform 2	5,6	51530	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
929	15530205	THOP1	Thimet oligopeptidase 1	5,7	78824	2	18,5	0	0,0	1	8,6	0	0,0	0	0,0	1	9,3	1	12,2
930	15592971	IQGAP1	AF401205_1 IQGAP1 protein	5,2	10789	0	0,0	0	0,0	1	10,0	2	18,8	2	12,3	1	12,7	1	9,8
931	155969707	IDE	insulin-degrading enzyme isoform 1	6,2	117969	1	11,2	1	10,3	1	8,7	0	0,0	0	0,0	0	0,0	1	7,9
932	156071450	NRD1	nardilysin isoform a precursor	4,8	139414	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,8
933	156104878	GLS	glutaminase kidney isoform, mitochondrial isoform	7,6	73443	3	24,5	0	0,0	4	26,9	4	28,1	2	12,2	1	12,7	2	16,0
934	156142186	CRLF3	cytokine receptor-like factor 3	4,9	49767	0	0,0	1	9,8	2	17,2	0	0,0	0	0,0	1	9,3	0	0,0
935	156151394	HNRNPR	heterogeneous nuclear ribonucleoprotein R isofo	8,2	71196	3	23,6	4	25,2	4	26,9	4	28,1	9	60,3	3	24,2	4	33,4

936	15620780	HEL	glutamate carboxypeptidase	5,7	52853	4	25,4	9	54,5	9	55,0	7	46,7	3	24,2	5	34,8	7	54,5
937	15626999	ITPA	inosine triphosphate pyrophosphatase isoform a	5,4	21428	1	12,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
938	156523968	PARP1	poly [ADP-ribose] polymerase 1	9,2	113084	6	53,0	9	64,1	15	88,0	16	82,2	6	48,3	15	88,5	13	96,2
939	156564401	NSF	vesicle-fusing ATPase	6,5	82595	1	11,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
940	156616275	POLD1	DNA polymerase delta catalytic subunit	6,6	123612	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	1	8,1	0	0,0
941	15680239	ACAA1	ACAA1 protein	8,3	34638	1	10,4	0	0,0	1	8,7	0	0,0	0	0,0	1	8,0	1	7,9
942	1568557	HIST1H2BN	histone H2B	10,8	13937	64	24,1	81	23,0	54	18,5	51	18,8	62	36,4	55	18,0	71	21,9
943	157057089	MUC5AC	mucin 5AC, oligomeric mucus/gel-forming	6,3	648782	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
944	15718687	RPS3	40S ribosomal protein S3 isoform 1	10,1	26689	15	72,3	11	49,8	11	53,0	11	46,8	15	82,0	9	58,9	9	53,6
945	15721937	MRPS24	28S ribosomal protein S24, mitochondrial precursor	9,6	18997	1	11,2	1	9,8	2	8,7	0	0,0	0	0,0	1	8,0	3	9,7
946	15722775	ENSG00000228325	immunoglobulin kappa chain variable region	8,1	9387	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
947	157311604	PDE4DIP	myomegalin isoform 1	5,2	265079	0	0,0	1	10,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
948	157364937	OTUD6B	OTU domain-containing protein 6B	6,3	37327	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	1	9,7
949	157426879	NPLOC4	nuclear protein localization protein 4 homolog	5,9	68102	1	11,9	1	9,7	2	24,1	1	9,5	2	12,2	1	11,7	1	9,7
950	157502193	PSMD13	26S proteasome non-ATPase regulatory subunit 13 is	5,5	42927	2	24,0	6	39,6	3	18,4	4	28,1	2	12,2	4	28,8	3	27,6
951	157694492	MYBBP1A	myb-binding protein 1A isoform 2	9,7	148854	1	9,7	1	10,3	4	25,8	2	18,8	3	12,2	1	11,7	2	17,5
952	157694524	PLXND1	plexin-D1 precursor	6,8	212053	1	11,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
953	157738677	THEMIS2	protein THEMIS2 isoform 3	5,7	72049	2	23,2	1	10,3	2	18,4	0	0,0	0	0,0	2	12,1	2	12,9
954	15778905	DCPS	Decapping enzyme, scavenger	5,8	38682	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	1	8,9	2	9,7
955	15809016	MYL12B	myosin regulatory light chain 12B	4,5	19780	4	27,0	11	44,7	11	50,7	13	54,2	14	72,4	13	46,2	10	38,6
956	15823636	ALS2	ALS2	5,8	183665	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	11,4
957	15823767	SRP14	signal recognition particle 14kD	10,5	14515	1	10,6	0	0,0	0	0,0	0	0,0	2	12,2	1	9,0	1	7,9
958	15824473	APOL2	AF305429_1 apolipoprotein L2	6,3	37079	1	11,6	0	0,0	2	17,2	0	0,0	2	12,2	0	0,0	1	9,7
959	158254494	CSK	unnamed protein product	6,6	50703	1	10,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
960	158254808	GNPDA1	unnamed protein product	6,5	32679	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	0	0,0
961	158254936	LYAR	unnamed protein product	10,0	43624	0	0,0	3	19,9	2	9,3	2	9,5	0	0,0	1	8,7	3	13,6
962	158254970	HEL	unnamed protein product	6,0	57477	0	0,0	1	10,3	0	0,0	1	9,5	2	12,2	2	8,9	0	0,0
963	158255130	GOT2	unnamed protein product	9,6	47517	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	1	9,8	0	0,0
964	158255138	PPIA	unnamed protein product	6,5	18014	1	9,7	0	0,0	1	9,8	0	0,0	0	0,0	0	0,0	0	0,0
965	158255538	PSMD5	unnamed protein product	5,3	56224	1	12,5	0	0,0	0	0,0	0	0,0	0	0,0	1	9,5	0	0,0
966	158255694	APMAP	unnamed protein product	6,1	46323	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,8
967	158256730	SKIV2L2	unnamed protein product	6,1	117899	1	11,0	1	10,0	2	18,4	0	0,0	0	0,0	1	8,0	0	0,0
968	158256976	G3BP2	unnamed protein product	5,1	50817	1	11,7	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	1	9,7
969	158258000	PRKACA	unnamed protein product	8,8	39881	0	0,0	1	10,3	0	0,0	0	0,0	0	0,0	1	9,3	1	7,9
970	158258078	HSPA14	unnamed protein product	5,4	54709	1	11,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
971	158258146	PABPC1	unnamed protein product	8,7	29877	1	11,4	1	10,0	1	9,8	1	9,4	0	0,0	2	9,3	2	9,7
972	158258705	EHD4	unnamed protein product	6,2	61157	1	15,5	1	10,1	0	0,0	2	18,8	0	0,0	1	9,5	1	9,7
973	158259379	PARP9	unnamed protein product	7,4	92282	0	0,0	0	0,0	0	0,0	1	9,5	0	0,0	0	0,0	0	0,0
974	158259545	PRKAR2A	unnamed protein product	4,8	45505	0	0,0	0	0,0	1	9,3	0	0,0	0	0,0	0	0,0	0	0,0
975	158259593	UGGT1	unnamed protein product	5,2	175007	1	9,7	1	10,3	1	8,7	1	9,5	0	0,0	1	8,7	0	0,0
976	158259881	HNRNPA2B1	unnamed protein product	9,2	37460	0	0,0	0	0,0	0	0,0	1	9,4	0	0,0	0	0,0	0	0,0
977	158260017	DHCR7	unnamed protein product	8,8	54470	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
978	158260067	VKORC1L1	unnamed protein product	9,3	19776	1	10,4	0	0,0	1	8,7	1	9,4	0	0,0	1	8,0	0	0,0
979	158260717	LASP1	unnamed protein product	7,1	29646	1	11,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
980	158260881	HSDL2	unnamed protein product	8,3	45323	1	10,5	0	0,0	1	8,7	1	9,5	2	12,2	1	9,1	1	9,7
981	158261923	GGH	unnamed protein product	7,2	36048	0	0,0	1	10,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
982	15866738	FN1	fibronectin	6,3	35591	0	0,0	0	0,0	0	0,0	8	37,5	0	0,0	0	0,0	0	0,0
983	159031630	HLA	MHC class I antigen	6,0	38423	2	17,0	0	15,0	3	15,8	0	13,2	0	14,6	2	13,3	1	13,8
984	15929088	HLA-DPB1	HLA-DPB1 protein	6,4	29250	0	0,0	0	0,0	0	0,0	1	9,4	0	0,0	1	8,0	1	7,9
985	15929104	MARS	MARS protein	5,8	100886	0	0,0	0	0,0	1	8,7	1	9,5	0	0,0	1	8,0	0	0,0
986	15930199	GNPDA2	Glucosamine-6-phosphate deaminase 2	6,7	30946	1	13,1	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
987	16041670	HSPA8	Unknown (protein for IMAGE:3906958), partial	4,6	29343	2	9,8	1	10,3	0	0,0	1	9,5	0	0,0	0	0,0	0	0,0
988	16041719	NDOR1	NADPH dependent diflavin oxidoreductase 1	5,9	66758	1	11,9	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7	0	0,0
989	16041819	CASP7	Caspase 7, apoptosis-related cysteine peptidase	5,7	34273	0	0,0	0	0,0	1	8,6	0	0,0	0	0,0	0	0,0	0	0,0
990	16075670	ENSG00000228325	immunoglobulin lambda chain variable region	4,4	9062	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
991	16117794	RPL36	60S ribosomal protein L36	12,1	12255	2	18,0	5	15,1	3	22,7	6	28,1	2	12,2	3	14,7	3	19,2
992	16198390	GLOD4	Glyoxalase domain containing 4	5,3	33216	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,0	1	7,9
993	16198525	TIA1	TIA1 protein	8,4	24063	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
994	1620022	RPL14	ribosomal protein L14	11,4	23804	3	15,3	1	10,3	0	0,0	1	9,5	0	0,0	0	0,0	0	0,0
995	1620398	RAD21	HR21spA	4,4	71689	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
996	1621457	IRF7	interferon regultory factor 7	5,6	54279	1	12,5	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
997	162417971	SPCS2	signal peptidase complex subunit 2	8,6	25004	1	15,8	1	10,1	3	13,6	0	0,0	0	0,0	1	9,1	2	9,7
998	162461738	GNAO1	guanine nucleotide-binding protein G(o) subunit al	5,5	40068	2	16,1	1	9,7	1	9,8	0	0,0	0	0,0	0	0,0	1	7,9

999	1628415	CUL5	vasopressin activated calcium mobilizing receptor-lik	7,9	90926	0	0,0	1	10,0	0	0,0	1	9,4	0	0,0	0	0,0	1	7,9
1000	16306492	CDK1	cyclin-dependent kinase 1 isoform 2	6,7	27504	1	10,5	2	10,1	1	8,7	1	9,5	2	12,2	1	8,1	1	7,9
1001	16306916	PSMD14	PSMD14 protein	5,7	11010	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
1002	16307468	LRPPRC	LRPPRC protein, partial	5,2	79991	4	41,1	7	39,9	11	62,7	8	56,1	9	81,9	6	29,5	8	56,6
1003	16357472	CDC42	cell division control protein 42 homolog isoform 2	5,7	21292	0	0,0	0	0,0	0	0,0	1	9,5	0	0,0	0	0,0	0	0,0
1004	16359158	PS1TP5BP1	Actin, beta	5,2	41764	1	11,3	0	0,0	2	9,3	0	0,0	0	0,0	3	9,4	2	9,8
1005	163660387	UBE2K	ubiquitin-conjugating enzyme E2 K isoform 3	6,1	16600	3	11,3	1	10,0	0	0,0	0	0,0	2	12,2	0	0,0	0	0,0
1006	163965364	NACA	nascent polypeptide-associated complex subunit	4,4	23366	2	23,4	3	19,3	1	15,5	4	35,6	5	24,3	3	22,9	1	15,8
1007	16418349	MMAB	cob(I)yrinic acid a,c-diamide adenosyltransferase,	8,7	27370	0	0,0	0	0,0	2	17,2	0	0,0	0	0,0	0	0,0	0	0,0
1008	16418425	GBP5	guanylate-binding protein 5	5,3	66618	0	0,0	2	10,1	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1009	164419743	DDX54	ATP-dependent RNA helicase DDX54 isoform 1	10,5	98647	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7	0	0,0
1010	16445421	SCAMP3	secretory carrier-associated membrane protein 3 iso	7,9	35183	1	11,7	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	0	0,0
1011	164664518	DDX6	probable ATP-dependent RNA helicase DDX6	8,8	54398	0	0,0	1	10,0	0	0,0	1	9,4	0	0,0	2	17,9	1	8,9
1012	164691151	YWHAZ	unnamed protein product	4,3	19073	6	38,4	10	29,8	12	22,8	13	37,5	11	24,3	7	20,7	8	29,4
1013	164691169	NAA50	unnamed protein product	8,7	10905	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	1	11,4
1014	164698438	TK1	thymidine kinase, cytosolic	8,5	25470	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
1015	16506263	FCRLA	AF329491_1 FCRLc2	6,1	23611	2	12,4	0	0,0	0	0,0	2	9,4	0	0,0	0	0,0	0	0,0
1016	16507237	HEL	78 kDa glucose-regulated protein precursor	4,9	72314	184	339,8	50	173,1	69	187,7	60	184,7	65	252,7	56	200,2	57	178,5
1017	16550229	DOCK7	unnamed protein product	6,3	72127	1	11,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1018	16550968	NDUFV3	unnamed protein product	9,5	49246	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
1019	16552001	CNST	unnamed protein product	4,2	79571	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
1020	16552477	SEH1L	unnamed protein product	7,7	46602	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,8
1021	16552892	TTC21B	unnamed protein product	6,2	79823	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	11,4
1022	16553656	TARSL2	unnamed protein product	6,1	50517	0	0,0	1	10,0	0	0,0	0	0,0	0	0,0	1	8,7	0	0,0
1023	16554270	LDHAL6B	unnamed protein product	8,8	41980	0	0,0	2	10,3	2	8,7	1	9,6	2	12,3	0	0,0	1	8,0
1024	16554604	MRPS23	28S ribosomal protein S23, mitochondrial	9,3	21752	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
1025	16554609	MRPS11	28S ribosomal protein S11, mitochondrial isoform a	11,3	20598	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
1026	1655596	RPL31	ribosomal protein L31	11,0	14093	1	16,6	0	0,0	1	9,3	0	0,0	2	12,2	1	9,8	2	15,4
1027	16579828	ZFP91	E3 ubiquitin-protein ligase ZFP91 isoform 1	7,0	63427	0	0,0	1	9,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1028	16596694	MRPL53	39S ribosomal protein L53, mitochondrial	9,0	12089	1	9,7	0	0,0	2	8,7	1	9,5	2	12,2	3	8,1	2	7,9
1029	16610228	TAP2	ABC-transporter	7,7	77664	0	0,0	0	0,0	1	9,9	0	0,0	0	0,0	1	9,8	0	0,0
1030	166235148	OSTF1	osteoclast-stimulating factor 1	5,3	23788	0	0,0	0	0,0	1	9,2	0	0,0	0	0,0	2	8,9	0	0,0
1031	1665723	HDAC1	RPD3 protein	5,3	55074	1	10,6	0	0,0	1	9,3	0	0,0	0	0,0	1	9,3	2	19,4
1032	1665787	SLC35D1	KIAA0260	9,6	41941	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
1033	1665789	WAPAL	KIAA0261	5,6	143624	0	0,0	0	0,0	0	0,0	0	0,0	2	12,2	0	0,0	0	0,0
1034	1666075	USP9X	ubiquitin hydrolase	5,4	289622	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	1	8,7	1	7,9
1035	166706903	GBP1	interferon-induced guanylate-binding protein 1	5,9	67912	0	0,0	0	0,0	1	9,9	0	0,0	2	12,2	1	8,9	1	11,4
1036	1669683	HLA	HLA-DRB3 major histocompatibility complex class II	6,3	9374	1	10,9	0	0,0	1	9,8	0	0,0	0	0,0	0	0,0	0	0,0
1037	167004078	METTL1	tRNA (guanine-N(7)-)-methyltransferase isoform a	7,4	31453	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1038	167234419	THRAP3	thyroid hormone receptor-associated protein 3	10,6	108647	1	9,7	2	10,0	2	17,8	1	9,4	2	12,2	3	15,9	3	17,5
1039	16740589	ORC4	Unknown (protein for IMAGE:3906697), partial	6,1	41336	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
1040	167555104	IRF4	interferon regulatory factor 4 isoform 1	6,4	51754	3	10,8	2	14,8	2	9,3	2	9,5	0	0,0	2	18,0	2	12,9
1041	16757970	FAM129A	protein Niban isoform 2	4,6	103135	0	0,0	1	10,0	1	8,7	0	0,0	2	12,2	2	8,7	1	11,4
1042	167614506	LCP1	plastin-2	5,2	70289	81	224,4	108	188,1	101	173,7	113	223,9	136	228,7	87	171,0	77	169,9
1043	167857839	IGHV1	immunoglobulin heavy chain variable region, partial	4,4	10957	0	0,0	0	0,0	0	0,0	0	0,0	2	12,2	0	0,0	0	0,0
1044	1679755	HLA	MHC class II antigen DQB1, partial	5,7	10103	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
1045	168229161	CORO7	coronin-7 isoform 1	5,4	100605	2	16,8	3	19,9	2	14,2	1	9,5	0	0,0	3	18,6	3	15,6
1046	16877108	ASAH1	ASAH1 protein	7,5	44004	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
1047	16905522	GOSR2	Golgi SNAP receptor complex member 2 isoform A	8,2	24757	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
1048	169145202	NHP2L1	NHP2 non-histone chromosome protein 2-like 1 (S. ce	8,6	14609	0	0,0	0	0,0	1	8,6	0	0,0	0	0,0	1	8,9	0	0,0
1049	16924265	ECH1	Enoyl Coenzyme A hydratase 1, peroxisomal	8,2	35740	3	18,9	12	44,7	9	27,0	7	46,8	8	24,2	8	38,0	6	29,6
1050	169790833	LAMP2	lysosome-associated membrane glycoprotein 2 iso	5,5	45152	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
1051	169790849	HCCS	cytochrome c-type heme lyase	6,3	30602	0	0,0	0	0,0	0	0,0	1	9,4	0	0,0	1	9,3	1	9,7
1052	169881252	GTF2I	general transcription factor II-I isoform 4	7,9	107951	2	19,1	1	9,7	2	13,6	4	28,1	3	24,2	1	8,7	2	17,5
1053	17016967	SYNE2	AF435011_1 NUANCE	5,1	796304	1	10,8	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	0	0,0
1054	17017967	BSND	barttin	4,1	35198	2	10,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
1055	17017988	COX5B	cytochrome c oxidase subunit 5B, mitochondrial prec	9,0	13678	1	12,0	0	0,0	1	9,9	0	0,0	0	0,0	0	0,0	1	7,9
1056	1702932	MARS	yeast methionyl-tRNA synthetase homolog	5,8	101110	1	10,2	0	0,0	0	0,0	0	0,0	0	0,0	1	12,1	1	13,6
1057	17046381	SON	AF380183_1 SON DNA binding protein isoform E	5,2	228177	1	12,1	2	15,1	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
1058	17066105	TTN	Titin	6,0	3816191	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	11,4
1059	1710248	PDIA6	protein disulfide isomerase-related protein 5	4,8	46181	2	11,6	1	10,3	1	9,3	1	9,5	2	12,2	1	9,1	1	11,5
1060	171460916	DNM1L	dynamin-1-like protein isoform 2	6,5	79442	1	9,6	0	0,0	3	19,6	0	0,0	0	0,0	3	24,8	2	20,7
1061	171460928	ADI1	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygena	5,3	21480	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	1	9,7

1062	171460997	CD226	CD226 antigen precursor	7,9	38615	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	1	9,4	0	0,0
1063	17149125	PPP2CB	protein phosphatase type 2A catalytic subunit	5,1	35613	1	17,0	1	10,0	0	0,0	1	9,4	0	0,0	0	0,0	0	0,0
1064	17158044	RPS6	40S ribosomal protein S6	11,3	28681	2	28,1	0	0,0	2	13,6	5	28,1	6	36,2	2	19,0	2	19,2
1065	17221409	BAX	bax isoform psi	5,4	19313	2	23,6	0	0,0	2	22,9	2	18,8	2	12,2	3	24,2	2	23,0
1066	1731809	PFDN5	c-myc binding protein	5,6	18643	1	9,8	0	0,0	1	9,8	1	9,5	2	12,2	1	9,0	1	8,9
1067	17389391	SCFD1	Sec1 family domain containing 1	5,8	72408	1	11,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1068	17389837	ERAP2	ERAP2 protein	6,8	40061	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	1	9,7
1069	17402871	BCCIP	BRCA2 and CDKN1A-interacting protein isoform BCCIPb	4,4	35961	0	0,0	1	9,8	1	9,3	1	9,5	2	12,3	1	9,6	1	9,8
1070	17402900	FUBP1	far upstream element-binding protein 1	7,4	67542	1	15,5	1	10,3	0	0,0	2	18,8	2	12,2	1	12,2	2	13,6
1071	17426605	F5	coagulation factor V jinjiang A2 domain	4,1	5866	1	10,4	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1072	1749794	MARK2	serine/threonine protein kinase	10,0	83205	1	10,9	0	0,0	1	8,6	0	0,0	0	0,0	0	0,0	0	0,0
1073	17529997	OSBPL1A	AF392449_1 oxysterol-binding protein-like protein OSB	6,2	50211	1	10,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1074	1770458	ILF3	M-phase phosphoprotein 4	6,4	66745	2	19,2	2	10,1	5	18,4	4	9,5	3	12,2	2	9,1	3	13,5
1075	17738287	SCAMP4	secretory carrier-associated membrane protein 4	8,9	25710	1	11,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1076	17738292	BDH1	D-beta-hydroxybutyrate dehydrogenase, mitochondrial	9,2	38139	1	12,1	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1077	178213	FDXR	adrenodoxin reductase precursor species 1	8,2	53790	0	0,0	1	10,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1078	1785635	SLC25A1	mitochondrial citrate transport protein	10,3	34769	1	11,2	2	10,0	2	9,3	0	0,0	0	0,0	2	8,7	1	8,8
1079	17865802	VPS4B	vacuolar protein sorting-associated protein 4B	6,9	49284	0	0,0	1	10,3	1	8,8	0	0,0	0	0,0	0	0,0	0	0,0
1080	17921985	COX15	cytochrome c oxidase assembly protein COX15 homolog	10,1	46012	1	11,2	1	9,7	1	8,6	0	0,0	0	0,0	1	8,0	0	0,0
1081	179318	B2M	beta-2-microglobulin	6,1	13732	2	13,0	2	10,0	2	13,5	1	9,4	2	12,2	0	0,0	2	9,6
1082	17939585	PRMT3	PRMT3 protein	7,1	61968	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
1083	17975627	STAT5A	signal transducer and activator of transcription 5A	6,0	90331	1	11,2	4	29,8	2	13,6	1	9,5	0	0,0	3	23,3	3	21,8
1084	17978512	PUF60	poly(U)-binding-splicing factor PUF60 isoform a	5,1	59857	0	0,0	1	10,2	1	9,9	1	9,4	2	12,2	1	8,0	0	0,0
1085	17980447	ENSG00000213121	unknown	10,0	149010	1	13,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1086	17986005	HLA	major histocompatibility complex, class II, DR beta	8,6	29944	2	13,1	2	10,0	3	14,1	0	0,0	2	12,2	2	13,3	2	15,5
1087	18027838	PLEKHO2	AF318373_1 unknown	4,6	30531	2	12,5	0	0,0	0	0,0	0	0,0	2	12,2	2	8,9	1	9,7
1088	18032270	RNPS1	AF274003_1 splicing-related factor RNPS1	12,4	31691	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,6
1089	18033272	DTD1	AF332356_1 histidyl-tRNA synthetase	8,8	23443	0	0,0	1	10,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1090	18041836	ENSG00000228325	immunoglobulin kappa light chain variable region	5,6	11348	0	0,0	1	10,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1091	18044582	FBL	Unknown (protein for IMAGE:4538098), partial	9,8	28431	2	16,8	6	24,7	6	32,4	2	18,8	5	24,2	3	17,3	9	34,0
1092	18044607	RPL14	RPL14 protein	11,4	23717	0	0,0	0	0,0	3	9,9	0	0,0	0	0,0	1	9,8	1	9,7
1093	1806038	ENSG00000223931	immunoglobulin heavy chain	6,5	10308	0	0,0	0	0,0	0	0,0	1	9,4	0	0,0	1	8,9	0	0,0
1094	180631	CANX	calnexin, partial	4,1	40837	14	60,3	19	64,1	13	45,3	12	46,8	15	72,4	9	42,1	16	54,3
1095	180637	PCMT1	L-isoaspartyl/D-aspartyl protein carboxyl methyltransfe	6,1	24661	1	11,2	2	10,0	2	9,3	1	9,5	0	0,0	2	12,1	2	9,7
1096	180663	ENO1	c-myc binding protein	6,8	37088	5	11,5	9	10,0	9	9,3	10	9,5	11	12,2	9	9,1	5	9,7
1097	180687	CNP	2',3'-cyclic-nucleotide 3'-phosphodiesterase (EC 3.1.4.	8,7	45080	1	10,9	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1098	1808648	PRMT1	arginine methyltransferase	5,4	39573	2	13,9	1	10,3	1	9,2	2	9,5	2	12,2	1	8,0	2	9,6
1099	18088559	PYHIN1	PYHIN1 protein	9,7	26952	3	11,2	2	9,7	0	0,0	1	9,4	2	12,2	2	8,0	1	7,9
1100	180917	SDHB	succinate-ubiquinone oxidoreductase Ip subunit precurso	8,8	29948	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,4	1	8,8
1101	18104991	PTPN6	tyrosine-protein phosphatase non-receptor type 6 is	7,6	67701	22	90,9	16	74,8	21	86,6	23	112,0	26	96,4	19	80,3	24	79,1
1102	18105007	CAD	CAD protein	6,0	242983	1	13,9	1	9,7	4	28,2	0	0,0	0	0,0	2	20,9	3	23,3
1103	18105045	HIST1H2AH	histone H2A type 1-H	11,3	13907	5	15,8	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
1104	181335	HEL	cyclophilin B	9,8	22743	15	66,8	7	39,9	10	41,0	10	46,7	5	36,2	7	41,9	5	21,8
1105	18143319	PRKDC	DNA-dependent protein kinase catalytic subunit	5,1	9101	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	0	0,0
1106	18152783	RPL10L	60S ribosomal protein L10-like	10,4	24520	1	14,7	0	0,0	2	17,8	0	0,0	2	12,2	2	18,0	2	19,3
1107	181842	MSH3	MSH3	8,1	127384	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
1108	18201905	GPI	glucose-6-phosphate isomerase isoform 2	8,4	63129	13	70,0	26	88,9	19	68,1	23	91,5	31	106,1	25	86,3	17	72,0
1109	18204653	CHERP	Calcium homeostasis endoplasmic reticulum protein	9,5	99973	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
1110	182067	EIF2S2	translational initiation factor beta subunit	5,5	38382	1	16,2	2	10,3	1	9,8	0	0,0	2	12,2	1	9,4	1	12,9
1111	182627729	MED16	mediator complex subunit MED16 variant MED16_i5	6,3	51207	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1112	182794	FH	fumarase precursor (EC 4.2.1.2)	7,5	50386	3	23,7	8	39,7	8	50,1	7	46,8	3	24,3	5	33,3	6	38,3
1113	182855	PRKCSH	80K-H protein	4,2	59297	1	11,3	2	15,1	5	32,4	2	18,8	2	12,2	3	18,5	3	19,8
1114	183056	GLUD1	glutamate dehydrogenase, partial	8,1	28696	0	0,0	0	0,0	0	13,8	1	9,4	0	0,0	0	13,8	0	0,0
1115	18375501	APEX1	DNA-(apurinic or apyrimidinic site) lyase	8,1	35536	2	23,4	2	14,8	3	22,8	0	0,0	2	12,2	2	16,0	2	17,5
1116	18375644	PTPN11	tyrosine-protein phosphatase non-receptor type 11 i	7,1	52809	0	0,0	1	10,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1117	183805	HBA1	pseudo-a-thal, partial	8,8	9079	2	15,7	5	14,9	1	9,3	6	18,8	0	0,0	3	16,9	2	9,7
1118	18390331	GFM1	elongation factor G, mitochondrial	6,6	83472	2	13,7	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	1	7,9
1119	184107	ATP4A	H,K-ATPase catalytic subunit	5,5	114091	1	15,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,8
1120	1841542	GPSM3	unknown	4,5	12905	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
1121	1842175	IRF4	ICSAT transcription factor	7,6	49805	4	10,7	7	29,8	3	9,3	7	28,2	3	24,3	5	14,3	3	16,1
1122	18482373	WDFY1	WD repeat and FYVE domain-containing protein 1	7,0	46306	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,4	0	0,0
1123	18491008	CYP2J2	cytochrome P450 2J2	8,8	57611	1	13,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1124	18491024	DPP3	dipeptidyl peptidase 3 isoform 1	4,9	82590	3	25,1	1	10,0	2	9,3	1	9,4	3	24,2	2	13,7	1	9,7

1125	1857526	TUBB4Q	beta-tubulin	5,0	48378	1	12,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1126	1857620	AGL	glycogen debranching enzyme isoform 1	6,3	174634	1	12,4	0	0,0	0	0,0	1	9,4	2	12,2	1	8,9	1	11,4
1127	18605554	IFI44	Interferon-induced protein 44	6,6	50462	1	16,5	1	9,7	0	0,0	1	9,5	0	0,0	0	0,0	1	7,9
1128	186659497	HLA	MHC class I antigen	5,5	31573	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,2	1	11,5
1129	186704290	HLA	MHC class I antigen	5,9	31616	1	13,0	3	11,0	1	10,2	0	9,5	0	12,2	3	10,5	2	9,7
1130	18676510	DOCK8	FLJ00152 protein	6,2	155596	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	1	9,4	1	9,7
1131	18676518	WDFY4	FLJ00156 protein	6,3	210612	1	12,1	2	19,3	1	8,7	0	0,0	0	0,0	1	8,0	1	8,8
1132	18676666	ATP13A1	FLJ00232 protein	9,4	35766	1	12,4	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1133	18677731	MOB3A	MOB kinase activator 3A	8,8	25465	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	1	8,0	0	0,0
1134	186928839	RDH12	retinol dehydrogenase 12 precursor	10,0	35095	1	11,6	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1135	186928854	MRPS31	28S ribosomal protein S31, mitochondrial	9,7	45300	0	0,0	0	0,0	1	9,9	0	0,0	3	12,2	1	9,8	2	9,7
1136	186972143	TPP2	tripeptidyl-peptidase 2	5,9	138350	0	0,0	1	9,7	1	8,7	0	0,0	0	0,0	0	0,0	0	0,0
1137	1869808	HSD17B4	peroxisomal multifunctional protein 2	4,5	7721	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	0	0,0
1138	1871475	RASA2	rasGTPase activating protein	8,5	47142	1	12,5	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1139	187618	HLA	HLA-A protein	5,9	40733	7	11,3	11	10,1	9	9,3	11	9,5	6	12,2	9	9,1	13	9,8
1140	187624	HLA	lymphocyte antigen	6,3	40913	0	0,0	0	16,4	0	0,0	0	0,0	0	0,0	1	9,4	1	9,7
1141	18765700	ELMO1	engulfment and cell motility protein 1 isoform 1	5,9	83811	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	1	7,9
1142	18765729	SNAP23	synaptosomal-associated protein 23 isoform SNAP23A	4,7	23336	0	0,0	0	0,0	3	19,6	0	0,0	2	12,2	1	9,4	1	8,9
1143	187744	HLA	HLA-B27 M2+, partial	5,2	31660	0	0,0	0	0,0	0	0,0	1	15,1	0	0,0	0	0,0	1	12,6
1144	187936349	MGLL	monoacylglycerol lipase isoform 2	6,4	30119	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
1145	188115	HLA	HLA DQ-beta	7,8	29915	0	0,0	0	0,0	0	0,0	1	9,4	0	0,0	0	0,0	0	0,0
1146	188219549	ANKRD32	ankyrin repeat domain-containing protein 32	8,4	121031	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
1147	188269	HLA	MHC cell surface glycoprotein	4,9	25860	29	39,4	11	29,8	10	25,9	14	37,5	6	36,4	20	20,6	18	28,8
1148	188393	HLA	MHC class II HLA-DQ beta glycoprotein, partial	7,0	11222	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,6	0	0,0
1149	188497632	HERPUD2	homocysteine-responsive endoplasmic reticulum-resi	4,8	45129	1	10,9	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1150	188497754	HK1	hexokinase-1 isoform HKI	6,4	102486	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7	0	0,0
1151	188524	HLA	SB-beta chain, partial	7,2	20424	2	11,2	2	10,0	1	9,3	2	18,8	0	0,0	2	11,7	0	0,0
1152	1888525	INPP5D	SH2 containing inositol-5-phosphatase	7,5	133319	0	0,0	2	19,3	1	9,3	1	9,4	2	12,2	1	12,1	1	16,5
1153	189027129	PDE12	2',5'-phosphodiesterase 12	6,1	67352	0	0,0	0	0,0	0	0,0	0	0,0	2	12,1	0	0,0	0	0,0
1154	189053077	UQCRB	unnamed protein product	8,9	13532	2	15,4	3	19,9	1	9,3	1	9,5	0	0,0	2	15,2	2	12,9
1155	189053208	UBL5	unnamed protein product	7,1	8549	0	0,0	0	0,0	1	8,6	0	0,0	0	0,0	0	0,0	0	0,0
1156	189053316	LSM3	unnamed protein product	4,4	11830	1	11,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
1157	189053345	HSPD1	unnamed protein product	5,7	61057	11	32,6	22	29,8	18	27,6	16	28,2	20	36,4	25	27,0	19	25,1
1158	189053380	PGM1	unnamed protein product	6,1	61397	1	12,4	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1159	189053457	PPIF	unnamed protein product	9,9	22040	1	11,3	1	10,1	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1160	189053728	RPL3L	unnamed protein product	10,9	46269	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	1	8,9	1	9,7
1161	189053823	CD38	unnamed protein product	7,3	34314	0	0,0	1	10,0	2	9,3	1	9,4	0	0,0	2	12,1	1	9,7
1162	189054023	CCDC68	unnamed protein product	9,0	38842	1	12,5	0	0,0	0	0,0	0	0,0	2	12,2	0	0,0	0	0,0
1163	189054101	CAPG	unnamed protein product	5,9	38498	1	11,7	2	19,9	2	14,1	1	9,5	0	0,0	1	9,3	2	22,4
1164	189054116	TMEM109	unnamed protein product	11,1	26195	1	11,2	0	0,0	1	9,2	0	0,0	0	0,0	1	9,5	1	8,8
1165	189054119	FKBP4	unnamed protein product	5,2	51835	2	18,9	5	24,7	3	25,8	1	9,4	0	0,0	2	17,8	2	18,1
1166	189054419	NAA15	unnamed protein product	7,1	101301	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	2	15,9	2	13,7
1167	189054433	PADI1	unnamed protein product	6,0	74694	0	0,0	0	0,0	0	0,0	0	0,0	2	12,1	0	0,0	0	0,0
1168	189054550	HEL	unnamed protein product	6,6	36045	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,1	0	0,0
1169	189065178	BANF1	unnamed protein product	5,8	10017	0	0,0	0	0,0	0	0,0	1	9,5	0	0,0	0	0,0	0	0,0
1170	189065417	HDLBP	unnamed protein product	6,4	141380	0	0,0	0	0,0	2	14,1	0	0,0	0	0,0	0	0,0	1	11,4
1171	189065517	HSD17B4	unnamed protein product	9,2	79613	1	15,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1172	189066512	KHDRBS1	unnamed protein product	8,9	48226	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	0	0,0
1173	189067218	UGP2	unnamed protein product	8,3	56907	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,0	2	10,6
1174	189069169	TUBB2A	unnamed protein product	4,6	49898	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,1	1	8,0
1175	189069230	TRIM28	unnamed protein product	5,4	88560	1	11,6	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1176	189069493	PIGS	unnamed protein product	6,0	61687	0	0,0	1	10,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1177	189083844	CTSC	dipeptidyl peptidase 1 isoform a preproprotein	6,6	51823	1	10,8	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	1	7,9
1178	189106	CYBA	p22 phagocyte b-cytochrome	9,9	20959	1	10,5	1	10,1	0	0,0	1	9,5	0	0,0	1	8,1	1	7,9
1179	18916728	GRWD1	KIAA1942 protein	4,6	49261	1	12,1	1	10,4	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1180	18916869	RAVER1	KIAA1978 protein	7,2	40492	0	0,0	0	0,0	1	8,8	0	0,0	0	0,0	1	9,0	1	9,7
1181	189181759	ETFA	electron transfer flavoprotein subunit alpha, m	8,8	30008	3	25,6	3	24,7	7	45,9	2	18,9	5	36,3	4	38,0	3	28,8
1182	189217411	PXDC1	PX domain-containing protein 1	4,8	26561	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	1	9,6
1183	189428	PPP2R1A	phosphatase 2A regulatory subunit	4,8	65224	5	35,6	7	34,9	3	22,7	5	28,2	2	12,3	3	20,9	4	25,6
1184	189502784	HSPD1	mitochondrial heat shock 60kD protein 1 variant 1	5,7	60662	10	23,6	25	37,7	14	30,7	23	35,7	14	33,9	14	22,1	23	23,8
1185	189754	PDHB	pyruvate dehydrogenase beta subunit	6,2	39250	2	13,0	0	0,0	2	13,6	1	9,4	3	24,3	2	15,5	2	15,5

1186	18999520	SAMD11	SAMD11 protein	5,9	50456	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
1187	190014586	PSIP1	PC4 and SFRS1-interacting protein isoform 1	9,6	37707	1	11,7	2	10,0	2	9,3	1	9,5	0	0,0	1	8,9	3	15,7
1188	190030	HEL	L-plastin polypeptide	5,3	63880	0	0,0	0	0,0	1	9,8	0	0,0	0	0,0	0	0,0	0	0,0
1189	190119	PML	PML-2	5,9	65007	1	14,2	0	0,0	1	8,6	0	0,0	0	0,0	1	8,0	1	9,6
1190	190167	PARP1	poly(ADP-ribose) polymerase	9,2	113083	0	0,0	0	0,0	1	9,8	1	9,4	0	0,0	1	8,9	1	7,9
1191	190194386	TM9SF3	transmembrane 9 superfamily member 3 precursor	6,8	67870	0	0,0	1	9,7	1	13,2	1	9,5	0	0,0	2	8,9	2	9,7
1192	1906048	HLA	MHC class I antigen	5,4	21077	0	0,0	0	0,0	1	9,8	0	0,0	0	0,0	1	8,0	0	0,0
1193	19070472	UBR4	AF348492_1 p600	5,6	573898	0	0,0	2	14,8	0	0,0	0	0,0	2	12,2	1	9,8	1	8,0
1194	190885499	COX5A	cytochrome c oxidase subunit 5A, mitochondrial pre	6,4	16744	4	15,9	0	0,0	2	9,3	0	0,0	2	12,2	4	18,5	2	9,7
1195	1916745	HLA	MHC class II HLA-DQ-alpha chain	4,8	27921	4	21,5	5	24,7	5	21,7	5	26,3	2	19,4	4	22,6	4	21,7
1196	1922287	ECHS1	enoyl-CoA hydratase	8,0	31372	1	11,4	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	1	8,8
1197	19262976	HLA	human leucocyte antigen A	7,3	10834	0	0,0	0	0,0	1	8,6	0	0,0	0	0,0	0	0,0	2	9,6
1198	192807332	SRRT	serrate RNA effector molecule homolog isoform c	5,7	100519	1	11,2	2	19,3	0	0,0	0	0,0	2	12,2	0	0,0	1	8,8
1199	1931577	RAB27A	Rab27a	5,1	24861	0	0,0	1	10,0	3	19,6	0	0,0	0	0,0	1	8,0	0	0,0
1200	193211616	NIPSNAP1	protein NipSnap homolog 1 isoform 1	9,6	33292	2	17,9	2	19,3	2	9,3	2	18,8	0	0,0	3	18,3	4	15,6
1201	193244921	HBB	beta globin	5,9	11489	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
1202	193248238	PTRH2	unnamed protein product	8,9	19164	1	11,5	1	9,8	1	9,3	0	0,0	0	0,0	1	9,1	1	9,7
1203	1934907	KPNA3	SRP1-like protein	4,7	57798	1	12,4	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1204	19353009	EEF2	Similar to Elongation factor 2b, partial	6,5	57482	53	119,4	35	108,7	45	106,1	39	121,4	48	156,6	39	97,6	35	90,7
1205	193784939	XPO1	unnamed protein product	5,4	82420	2	15,5	2	10,1	3	9,3	4	18,8	3	12,2	2	12,1	2	21,9
1206	193785119	DCTN4	unnamed protein product	7,4	45723	1	11,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
1207	193785624	GLRX3	unnamed protein product	5,3	37420	2	19,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1208	193785630	LAP3	unnamed protein product	6,3	52772	6	41,9	8	44,4	11	45,3	7	37,5	12	48,3	11	47,8	8	53,7
1209	193786016	CPSF2	unnamed protein product	4,7	73014	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
1210	193786457	SRBD1	unnamed protein product	8,8	111746	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	0	0,0
1211	193786611	MZB1	unnamed protein product	5,3	14338	3	21,0	2	15,1	1	9,2	1	9,4	2	12,2	2	14,7	3	18,6
1212	193786650	SCO1	unnamed protein product	10,5	20554	2	9,7	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	1	7,9
1213	193786739	TOMM70A	unnamed protein product	4,8	26480	1	10,4	0	0,0	1	9,9	0	0,0	0	0,0	1	8,0	1	9,7
1214	193786953	SLC25A12	unnamed protein product	9,4	62721	1	11,1	1	10,1	2	9,4	0	0,0	0	0,0	1	8,7	2	8,0
1215	193786980	GNB2	unnamed protein product	4,5	25932	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	1	11,4
1216	193787468	MRC2	unnamed protein product	8,1	37648	0	15,4	0	0,0	0	0,0	0	0,0	2	21,8	0	0,0	0	0,0
1217	193787507	CACYBP	unnamed protein product	9,5	23163	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1218	193787805	ARHGAP26	unnamed protein product	8,0	31816	1	11,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1219	193788236	YTHDF1	unnamed protein product	9,2	60873	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	1	11,4
1220	193788260	NPEPPS	unnamed protein product	4,9	70624	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	11,4
1221	193788434	DHX9	unnamed protein product	9,7	59948	3	18,8	4	20,4	2	8,7	4	9,5	2	12,2	2	13,3	2	13,4
1222	193788722	RTFDC1	UPF0549 protein C20orf43	8,6	33888	0	0,0	1	10,3	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
1223	19401871	BRSK1	AF479826_1 putative serine/threonine protein kinase	9,2	86735	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
1224	194272210	KARS	lysine--tRNA ligase isoform 1	6,3	71498	3	27,9	2	20,2	5	27,6	1	9,5	2	12,2	2	17,8	4	29,3
1225	194373465	TMED5	unnamed protein product	4,6	20543	1	11,2	1	10,2	0	0,0	1	9,5	0	0,0	1	9,4	1	9,7
1226	194373759	PDCD5	unnamed protein product	6,5	14998	0	0,0	0	0,0	1	9,8	0	0,0	0	0,0	0	0,0	0	0,0
1227	194373949	CSE1L	unnamed protein product	5,2	85473	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
1228	194374129	UQCRC1	unnamed protein product	5,5	40374	3	24,6	1	10,0	4	28,1	4	18,9	3	24,2	5	30,1	3	30,9
1229	194374143	ADSL	unnamed protein product	6,7	34556	1	12,4	0	0,0	1	8,7	2	9,5	0	0,0	2	8,1	1	7,9
1230	194374263	ACADVL	unnamed protein product	9,0	72928	0	0,0	0	0,0	0	0,0	0	0,0	2	12,2	1	9,7	0	0,0
1231	194374387	PABPN1	unnamed protein product	9,6	18991	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
1232	194374597	HNRNPK	unnamed protein product	5,6	48511	16	68,5	22	88,7	15	69,0	33	93,4	34	132,5	17	74,7	16	82,3
1233	194374633	AHSA1	unnamed protein product	5,4	32340	5	15,0	3	10,1	5	9,4	2	9,5	3	12,3	4	9,1	5	13,0
1234	194374755	GCDH	unnamed protein product	9,1	29522	1	9,8	1	10,3	2	9,3	1	9,6	0	0,0	0	0,0	1	9,7
1235	194375179	GPI	unnamed protein product	8,9	59991	3	9,7	0	0,0	2	8,7	1	9,5	2	12,2	3	9,1	1	11,4
1236	194375490	HADHB	unnamed protein product	9,7	49684	2	11,3	0	0,0	1	8,7	0	0,0	0	0,0	1	9,0	2	9,7
1237	194375980	PTCD3	unnamed protein product	10,0	23500	1	11,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1238	194376028	FAM162A	unnamed protein product	10,4	15930	1	12,4	1	9,7	0	0,0	0	0,0	0	0,0	1	9,0	1	8,8
1239	194376056	NIT2	unnamed protein product	5,8	16765	0	0,0	1	10,1	1	8,7	0	0,0	0	0,0	1	8,0	1	7,9
1240	194376310	ACTB	unnamed protein product	5,1	38634	7	19,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1241	194377108	PGK1	unnamed protein product	5,3	17051	7	28,9	5	29,8	9	27,6	11	28,2	9	36,3	11	32,8	13	28,8
1242	194377362	KAT7	unnamed protein product	8,4	38587	1	12,5	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1243	194377686	FEN1	unnamed protein product	8,6	38792	3	21,4	2	14,8	4	27,0	5	28,1	5	24,3	2	14,8	5	34,6
1244	194377714	CCT5	unnamed protein product	5,5	57102	0	0,0	1	9,8	0	0,0	0	0,0	0	0,0	1	9,1	0	0,0
1245	194377854	DDX39A	unnamed protein product	5,5	53697	1	10,5	1	10,0	1	9,3	1	9,5	0	0,0	1	8,9	1	7,9
1246	194378004	BLMH	unnamed protein product	5,8	42463	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
1247	194378218	CANX	unnamed protein product	4,4	71503	7	27,7	5	24,7	2	13,6	4	28,1	5	24,2	4	26,3	2	12,9
1248	194378358	APOBEC3F	unnamed protein product	8,6	22921	0	0,0	1	10,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0

1249	194378658	HSPA4L	unnamed protein product	5,7	91940	1	11,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1250	194378854	PRMT5	unnamed protein product	5,9	67644	0	0,0	0	15,5	0	0,0	0	0,0	0	0,0	1	9,8	0	0,0
1251	194378996	TM9SF4	unnamed protein product	6,2	63935	0	0,0	0	0,0	1	9,9	0	0,0	0	0,0	0	0,0	0	0,0
1252	194379046	PGK1	unnamed protein product	8,4	29993	8	14,5	9	19,9	4	18,5	4	18,9	6	24,3	7	14,9	6	15,5
1253	194379176	AK2	unnamed protein product	8,2	21637	2	15,7	5	19,9	8	18,5	4	18,8	3	24,3	4	14,8	4	12,3
1254	194379646	SASS6	unnamed protein product	6,8	71172	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
1255	194380508	SLC25A24	unnamed protein product	10,4	24997	1	12,5	0	0,0	0	0,0	2	9,5	0	0,0	1	9,8	0	0,0
1256	194380862	TOMM70A	unnamed protein product	5,6	56932	1	14,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1257	194381352	MRPS5	unnamed protein product	10,3	32010	1	11,2	1	10,0	1	8,6	0	0,0	0	0,0	1	8,0	1	9,7
1258	194381632	BASP1	unnamed protein product	4,6	17665	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	11,4
1259	194381636	YWHAE	unnamed protein product	5,5	15928	1	16,3	0	0,0	0	0,0	1	9,4	0	0,0	0	0,0	0	0,0
1260	194381652	LMNB1	unnamed protein product	4,9	43035	1	12,9	6	25,0	4	14,2	5	28,1	3	12,2	3	14,3	6	21,9
1261	194381660	CD1E	unnamed protein product	9,9	38412	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
1262	194381968	SF3A1	unnamed protein product	4,9	77407	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
1263	194382176	LDHA	unnamed protein product	8,6	33594	7	41,5	14	63,4	14	58,4	28	63,6	23	94,0	14	68,9	9	46,8
1264	194382680	UBXN1	unnamed protein product	9,5	22942	0	0,0	1	10,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1265	194383550	GOLGA5	unnamed protein product	5,3	73131	0	0,0	0	0,0	0	0,0	1	9,4	0	0,0	0	0,0	0	0,0
1266	194383554	POP4	unnamed protein product	10,3	16020	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
1267	194384032	TMED10	unnamed protein product	8,8	20060	4	22,8	2	15,1	2	18,4	2	18,8	2	12,2	2	18,0	2	15,5
1268	194385042	LAP3	unnamed protein product	9,7	39346	4	38,9	12	64,1	11	59,2	10	65,4	9	60,3	9	56,3	7	42,4
1269	194385080	ABHD14B	unnamed protein product	7,8	19757	2	15,9	2	19,9	0	0,0	0	0,0	0	0,0	1	12,8	0	0,0
1270	194385658	SSR3	unnamed protein product	10,0	22611	1	10,4	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1271	194385948	ACTN4	unnamed protein product	5,9	64161	0	0,0	0	0,0	0	0,0	2	9,5	0	0,0	0	0,0	0	0,0
1272	194386150	IFIT3	unnamed protein product	5,0	35161	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
1273	194386362	MAPRE1	unnamed protein product	5,0	26583	1	13,7	1	9,7	1	9,9	0	0,0	2	12,2	1	9,1	1	9,7
1274	194386494	RAB11A	unnamed protein product	5,1	16515	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1275	194386860	VCPIP1	unnamed protein product	7,8	86145	0	0,0	1	10,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1276	194387188	DRG2	unnamed protein product	7,5	22566	1	11,1	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1277	194388088	HSPA1A	unnamed protein product	5,3	63925	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7	0	0,0
1278	194388276	SMU1	unnamed protein product	8,2	39344	0	0,0	1	10,1	1	9,9	0	0,0	0	0,0	0	0,0	1	8,0
1279	194388772	ABCF1	unnamed protein product	5,2	59664	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	1	9,7
1280	194389264	TIMM23	unnamed protein product	6,1	17859	0	0,0	1	10,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1281	194389758	CAP1	unnamed protein product	8,8	43707	7	58,1	2	14,8	6	31,8	6	37,5	8	36,2	4	30,9	3	21,3
1282	194390062	OTUB1	unnamed protein product	5,3	35182	1	11,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1283	194390160	TBCA	unnamed protein product	9,7	15793	1	10,3	0	0,0	0	0,0	0	0,0	0	0,0	1	8,7	1	7,9
1284	194390184	CREBRF	unnamed protein product	4,7	38297	1	9,7	1	9,7	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
1285	194390560	VCL	unnamed protein product	6,0	36250	1	12,1	0	0,0	1	9,8	0	0,0	2	12,2	1	8,0	1	9,6
1286	194390946	RAB7A	unnamed protein product	7,7	21874	0	0,0	2	10,0	1	9,9	0	0,0	2	12,2	1	8,9	2	15,7
1287	194391276	ARHGAP1	unnamed protein product	6,2	52756	1	13,1	1	10,3	2	13,5	0	0,0	0	0,0	0	0,0	1	8,8
1288	194595509	SPTAN1	spectrin alpha chain, non-erythrocytic 1 isofor	5,1	285074	3	33,0	13	122,7	12	86,1	8	65,4	9	60,3	12	90,2	14	109,6
1289	194688147	PPP3CA	serine/threonine-protein phosphatase 2B catalyt	5,9	57640	1	11,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1290	19526593	AK2	adenylate kinase 2 variant AK2C	9,1	22266	3	11,5	5	19,3	5	23,3	5	18,8	2	12,2	4	9,1	6	17,3
1291	19526773	ATG3	ubiquitin-like-conjugating enzyme ATG3	4,5	35846	1	11,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	1	9,7
1292	19568094	TRIP10	truncated Cdc42 interaction protein 4	6,4	52701	0	0,0	2	19,3	0	0,0	0	0,0	2	12,2	2	12,9	2	15,5
1293	196114951	PTPN12	tyrosine-protein phosphatase non-receptor type 12	5,3	88088	1	10,4	1	10,0	1	8,7	1	9,4	0	0,0	1	8,0	0	0,0
1294	196123588	MT	NADH dehydrogenase subunit 4	9,6	51563	0	0,0	1	10,0	0	0,0	1	9,4	0	0,0	0	0,0	0	0,0
1295	197115245	ENSG00000223931	immunoglobulin heavy chain variable region	8,6	13574	1	13,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1296	197304715	VAV2	guanine nucleotide exchange factor VAV2 isoform	6,7	101270	1	11,3	1	10,0	1	8,7	1	9,5	0	0,0	2	17,9	1	9,6
1297	197692173	NPM1	nucleophosmin 1 isoform 1	4,5	32575	1	13,5	2	15,3	0	0,0	0	0,0	2	12,4	2	11,8	2	13,8
1298	19911062	TEX10	nbla10363	9,7	105688	0	0,0	0	0,0	1	9,9	0	0,0	2	12,2	1	9,4	1	11,5
1299	19911070	FACL4	Acyl-CoA synthetase 4	7,9	74423	0	0,0	2	14,8	0	0,0	0	0,0	0	0,0	2	13,3	1	8,8
1300	19913377	G6B	protein G6b isoform G6b-C precursor	8,5	23574	1	10,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1301	19913406	TOP2A	DNA topoisomerase 2-alpha	9,0	174385	0	0,0	0	0,0	1	9,8	0	0,0	0	0,0	1	8,9	0	0,0
1302	19913416	AP2A1	AP-2 complex subunit alpha-1 isoform 2	7,5	105343	1	11,1	2	15,1	2	13,6	2	18,8	2	12,2	1	12,8	2	13,6
1303	19913428	ATP6V1B2	V-type proton ATPase subunit B, brain isoform	5,5	56482	1	14,4	2	19,9	0	0,0	0	0,0	0	0,0	1	8,9	0	0,0
1304	19913485	NDEL1	NudE nuclear distribution gene E homolog (A. nidulans	5,0	38360	0	0,0	0	0,0	1	9,9	0	0,0	2	12,2	0	0,0	0	0,0
1305	19913512	FUS	Fusion (involved in t(12;16) in malignant liposarcoma	9,6	53381	2	14,1	1	9,7	1	9,3	1	9,4	2	12,2	2	9,4	3	9,7
1306	19920317	CKAP4	cytoskeleton-associated protein 4	5,6	66023	1	10,9	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	2	9,8
1307	19923142	KPNB1	importin subunit beta-1	4,5	97171	8	56,3	8	54,0	13	68,4	8	56,1	12	72,3	13	70,8	14	80,5
1308	19923193	ST13	hsc70-interacting protein	5,0	41332	1	13,6	0	0,0	1	9,9	1	9,4	2	12,2	1	9,5	0	0,0
1309	19923233	SCP2	non-specific lipid-transfer protein isoform 1 propr	6,5	58975	1	16,7	0	0,0	1	9,3	0	0,0	0	0,0	1	8,0	1	9,7
1310	19923236	SP100	nuclear autoantigen Sp-100 isoform 2	8,2	100398	2	11,1	0	0,0	1	9,8	1	9,4	0	0,0	1	9,5	1	15,4
1311	19923315	HEL	serine hydroxymethyltransferase, mitochondrial isof	8,6	55975	3	27,1	8	34,8	9	59,8	11	46,8	3	24,3	9	56,4	9	49,3

1312	19923387	NCBP2	nuclear cap-binding protein subunit 2 isoform 1	8,4	17983	1	12,5	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1313	19923613	EDC3	enhancer of mRNA-decapping protein 3	6,7	56059	0	0,0	0	0,0	0	0,0	1	9,5	0	0,0	0	0,0	0	0,0
1314	19923653	PSIP1	PC4 and SFRS1-interacting protein isoform 2	9,6	60085	0	0,0	0	0,0	0	0,0	1	9,5	0	0,0	1	9,6	1	9,7
1315	19923665	BRI3BP	BRI3-binding protein precursor	9,7	27836	0	0,0	0	0,0	0	0,0	0	0,0	2	12,2	0	0,0	0	0,0
1316	19923750	RAB3B	ras-related protein Rab-3B	4,7	24759	1	10,4	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	2	7,9
1317	19923790	RAB3GAP2	rab3 GTPase-activating protein non-catalytic subuni	5,3	155966	1	12,4	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	1	7,9
1318	19923939	KTI12	protein KTI12 homolog	6,5	38616	0	0,0	2	14,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1319	19924129	RAD50	DNA repair protein RAD50	6,5	153892	1	10,6	1	10,3	2	19,0	0	0,0	2	12,2	2	13,7	1	11,4
1320	20070125	P4HB	protein disulfide-isomerase precursor	4,6	57098	25	103,0	24	83,6	19	86,1	16	74,7	22	84,4	25	96,1	20	80,8
1321	20070130	BTF3	transcription factor BTF3 isoform B	7,8	17700	1	15,3	5	24,8	4	19,6	7	28,2	5	36,4	3	21,7	1	12,8
1322	20070220	PRMT5	protein arginine N-methyltransferase 5 isoform a	5,9	72665	1	11,2	2	10,1	0	0,0	0	0,0	0	0,0	1	9,3	2	13,6
1323	20070228	NUCB1	nucleobindin-1 precursor	5,0	53880	1	11,3	0	0,0	0	0,0	0	0,0	0	0,0	1	9,6	0	0,0
1324	20071563	SCCPDH	Saccharopine dehydrogenase (putative)	9,5	47220	1	11,0	2	10,1	1	8,7	0	0,0	0	0,0	1	9,0	1	9,7
1325	20127454	HEL	bifunctional purine biosynthesis protein PURH	6,3	64597	13	81,5	8	45,0	14	87,8	14	84,1	15	84,4	9	53,8	10	67,2
1326	20127499	SRSF6	serine/arginine-rich splicing factor 6	11,9	39568	1	16,9	0	0,0	1	8,6	1	9,4	0	0,0	0	0,0	1	7,9
1327	20127553	ANAPC5	anaphase-promoting complex subunit 5 isoform a	6,4	85058	0	0,0	0	0,0	0	0,0	1	9,5	0	0,0	0	0,0	0	0,0
1328	20127607	VIPAS39	spermatogenesis-defective protein 39 homolog isofor	7,0	56987	1	13,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1329	20143480	CDS2	phosphatidate cytidylyltransferase 2	6,7	51400	1	11,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0
1330	20147701	GNA15	AF493904_1 guanine nucleotide binding protein alpha 1	8,5	43490	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1331	20149498	FTL	ferritin light chain	5,4	20021	1	11,7	0	0,0	2	13,6	0	0,0	0	0,0	5	21,0	1	9,7
1332	20149524	SUPT5H	transcription elongation factor SPT5 isoform a	4,8	120981	0	0,0	0	0,0	1	8,6	0	0,0	0	0,0	0	0,0	0	0,0
1333	20149547	RPS6KA1	ribosomal protein S6 kinase alpha-1 isoform a	7,7	82704	0	0,0	1	10,0	1	9,3	0	0,0	2	12,2	1	8,9	1	9,7
1334	20149568	NDUFV1	NADH dehydrogenase [ubiquinone] flavoprotein 1, mithocondrial	8,1	50799	1	11,4	0	0,0	0	0,0	0	0,0	0	0,0	1	9,4	2	16,2
1335	20149675	EFHD2	EF-hand domain-containing protein D2	5,0	26679	1	11,2	0	0,0	1	9,9	0	0,0	2	12,2	1	9,8	2	7,9
1336	20270253	ASCC2	activating signal cointegrator 1 complex subunit 2	4,9	86342	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	0	0,0
1337	20271451	PEPD	PEPD protein	5,6	54583	1	10,4	1	10,0	1	9,3	0	0,0	2	12,2	1	8,0	1	7,9
1338	20357547	ATP6V1F	V-type proton ATPase subunit F isoform 1	5,2	13352	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
1339	20357568	AASDHPPT	L-aminoadipate-semialdehyde dehydrogenase-phosphopa	6,4	35758	0	0,0	1	10,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1340	20372502	ENSG00000228325	anti-acetylcholine receptor immunoglobulin kappa ligh	9,6	11879	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7	0	0,0
1341	20372922	PNPT1	polynucleotide phosphorylase-like protein	7,7	85918	0	0,0	0	0,0	1	8,6	0	0,0	0	0,0	0	0,0	0	0,0
1342	20380096	NCAPD2	Non-SMC condensin I complex, subunit D2	6,1	157150	0	0,0	1	10,3	1	8,7	0	0,0	0	0,0	0	0,0	0	0,0
1343	20380157	SEC16A	SEC16A protein	5,8	115527	1	12,0	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1344	20384693	MCM3	cervical cancer proto-oncogene 5	6,0	75788	1	11,4	1	10,0	1	9,3	1	9,5	3	24,2	1	8,9	1	12,7
1345	2052039	PGAM4	PGAM-B	5,5	8574	1	11,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1346	20521656	ARAP1	KIAA0782 protein	5,6	143933	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,1	0	0,0
1347	20521660	SNRNP200	KIAA0788 protein	5,5	231714	2	21,1	3	25,0	6	27,6	8	56,1	5	36,3	3	26,0	5	33,4
1348	20521666	DNM3	KIAA0820 protein	8,5	99950	1	10,9	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	0	0,0
1349	20521714	STK38L	KIAA0965 protein	8,4	56830	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	0	0,0
1350	20521724	CNOT1	KIAA1007 protein	6,9	206330	0	0,0	0	0,0	1	8,7	2	18,8	0	0,0	1	9,0	0	0,0
1351	20521754	TENC1	KIAA1075 protein	8,4	162870	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
1352	20521764	PRRC2C	KIAA1096 protein	10,2	207303	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
1353	20521814	ARFGEF3	KIAA1244 protein	5,5	207069	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
1354	20521858	GBF1	KIAA0248	5,5	208585	0	0,0	0	0,0	2	8,7	0	0,0	0	0,0	0	0,0	0	0,0
1355	20521876	MESDC2	KIAA0081	8,3	26206	1	10,9	1	9,7	1	8,7	0	0,0	0	0,0	1	9,1	2	12,9
1356	20521980	TNKS1BP1	KIAA1741 protein	4,6	186469	1	17,9	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1357	205277386	GFPT1	glutamine--fructose-6-phosphate aminotransferase	6,4	76741	1	14,7	2	14,8	1	9,3	2	18,8	2	12,2	1	14,1	2	13,5
1358	205362828	HLA	MHC class II antigen	5,3	10694	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
1359	206725415	GIT2	ARF GTPase-activating protein GIT2 isoform 4	6,1	52559	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	1	7,9
1360	207028494	LDHA	L-lactate dehydrogenase A chain isoform 2	6,8	30187	3	15,5	16	39,6	6	27,0	11	28,1	15	36,3	11	32,6	8	25,6
1361	2072164	TULP2	tubby related protein 2 TULP2	8,1	58641	1	11,7	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7	0	0,0
1362	2076717	HEL	glutathione S-transferase	5,3	23343	1	10,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1363	2081622	UMPS	UMP synthase	6,9	52222	1	11,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1364	20853684	RPLP0P6	BLOCK 23	5,3	34365	4	24,7	1	10,0	4	18,4	7	28,1	9	36,3	4	18,9	2	16,6
1365	209180457	TOM1	target of Myb protein 1 isoform 2	4,5	53856	0	0,0	1	10,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
1366	209553728	HLA	MHC class I antigen, partial	5,7	21176	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1367	209571584	FDPS	farnesyl pyrophosphate synthase isoform b	4,9	40514	1	12,9	2	19,6	3	22,7	2	18,8	2	12,2	2	14,9	2	16,6
1368	20975570	AKR7L	aflatoxin B1 aldehyde reductase 3	6,1	29161	2	11,7	1	9,8	1	8,7	1	9,5	0	0,0	1	8,0	1	9,7
1369	209862881	CPSF7	cleavage and polyadenylation specificity factor	8,0	52032	0	0,0	0	0,0	1	9,8	0	0,0	0	0,0	1	8,0	1	7,9
1370	20988822	CD48	CD48 protein	8,4	19430	1	10,5	1	10,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
1371	209969697	ISOC2	isochorismatase domain-containing protein 2, mi	9,4	14747	2	10,6	2	10,0	1	9,3	0	0,0	2	12,2	1	12,6	2	15,5
1372	21040386	HSPA9	HSPA9 protein	6,0	73854	20	119,6	14	94,0	26	102,4	18	100,9	22	132,5	24	110,3	20	100,2
1373	21104374	OK	cytoskeletal tropomyosin TM30	4,5	10914	2	16,4	2	10,0	2	9,3	1	9,4	0	0,0	2	12,1	2	12,9
1374	21104432	RAN	member RAS oncogene family	5,9	14732	11	19,7	6	10,0	8	9,3	4	9,5	11	24,2	9	9,1	8	13,5

1375	211827489	THEMIS2	C1orf38 protein	5,6	28987	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1376	211827908	MED8	MED8 protein	9,6	32275	1	11,5	0	0,0	0	0,0	1	9,4	2	12,2	0	0,0	0	0,0
1377	21218438	GATAD2B	transcriptional repressor p66-beta	10,1	65261	1	11,6	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1378	21237808	SMARCC2	SWI/SNF complex subunit SMARCC2 isoform b	5,3	124822	1	12,5	1	10,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1379	21245136	FCRLA	FCRLa1	5,1	39411	1	9,6	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1380	21264318	AMPD2	AMP deaminase 2 isoform 1	6,5	100688	1	10,7	1	10,0	0	0,0	1	9,4	0	0,0	1	8,0	1	7,9
1381	21264341	SMS	spermine synthase isoform 1	4,7	41269	0	0,0	0	0,0	1	8,6	0	0,0	0	0,0	0	0,0	0	0,0
1382	21264343	SAFB	scaffold attachment factor B1 isoform 3	5,2	102623	2	22,0	3	28,9	1	9,9	0	0,0	0	0,0	2	18,5	2	18,4
1383	21265093	MRPL41	39S ribosomal protein L41, mitochondrial	10,0	15365	1	11,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	2	9,7
1384	21265096	MRPL50	39S ribosomal protein L50, mitochondrial	8,0	18307	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1385	21269877	CARS	cysteine--tRNA ligase, cytoplasmic isoform a	6,6	82828	1	18,2	1	10,0	3	22,3	1	9,5	0	0,0	3	21,7	4	23,6
1386	21327701	TAF15	TATA-binding protein-associated factor 2N isoform 1	8,1	61812	1	13,0	1	9,7	0	0,0	0	0,0	2	12,2	0	0,0	0	0,0
1387	21327715	TCERG1	transcription elongation regulator 1 isoform 1	9,0	123882	1	10,8	2	15,1	0	0,0	1	9,4	2	12,2	1	9,4	1	7,9
1388	213417911	PRKRA	interferon-inducible double stranded RNA-depend	8,4	33105	0	0,0	1	10,0	1	9,3	0	0,0	0	0,0	1	8,0	1	7,9
1389	21359873	PLK1	serine/threonine-protein kinase PLK1	9,1	68236	1	13,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1390	21359945	NCAPG	condensin complex subunit 3	5,3	114334	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	2	9,7
1391	21361091	HEL	ubiquitin carboxyl-terminal hydrolase isozyme L1	5,2	24806	5	25,9	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1392	21361171	BRE	BRCA1-A complex subunit BRE isoform 1	5,7	46956	1	9,7	0	0,0	1	9,9	0	0,0	2	12,2	1	9,7	0	0,0
1393	21361320	TFG	protein TFG isoform 1	4,8	43449	2	12,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1394	21361322	TUBB4A	tubulin beta-4A chain	4,6	49586	3	15,9	3	14,9	7	36,8	6	28,2	0	0,0	4	23,4	4	25,6
1395	21361337	EIF5	eukaryotic translation initiation factor 5	5,3	49204	1	10,7	2	10,0	2	13,5	1	9,4	0	0,0	2	9,0	1	9,7
1396	21361340	GSK3B	glycogen synthase kinase-3 beta isoform 1	8,9	48015	0	0,0	1	10,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1397	21361356	TOMM34	mitochondrial import receptor subunit TOM34	9,3	34541	1	12,1	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1398	21361361	ILVBL	acetolactate synthase-like protein	8,0	67868	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
1399	21361370	PYGB	glycogen phosphorylase, brain form	6,4	96696	1	11,2	1	10,0	1	9,3	0	0,0	0	0,0	1	12,3	2	17,4
1400	21361376	SF3A2	splicing factor 3A subunit 2	10,0	49256	0	0,0	2	15,1	1	8,7	1	9,5	0	0,0	1	8,7	0	0,0
1401	21361403	TXN2	thioredoxin, mitochondrial precursor	8,4	18365	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
1402	21361535	C11orf73	protein Hikeshi	5,1	21629	1	11,0	1	9,7	0	0,0	0	0,0	0	0,0	1	9,3	1	9,7
1403	21361661	COMMD4	COMM domain-containing protein 4	7,1	21765	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1404	21361670	DBNL	drebrin-like protein isoform a	4,9	48295	4	36,2	6	29,8	3	27,0	5	37,4	3	24,2	5	35,2	4	29,4
1405	21361794	CAND1	cullin-associated NEDD8-dissociated protein 1	5,4	136357	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	1	9,3	1	8,8
1406	21361884	RAB2B	ras-related protein Rab-2B isoform 1	7,8	24196	1	11,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1407	21389447	TBC1D20	TBC1 domain family member 20	6,4	45856	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	2	8,8
1408	21396480	RALY	RNA-binding protein Raly isoform 2	10,0	30365	1	11,5	0	0,0	0	0,0	0	0,0	0	0,0	1	9,0	1	8,8
1409	21397154	HNRNPA1L2	AF517524_1 BX1	9,8	6123	2	11,5	2	10,0	1	8,7	2	9,4	3	12,2	1	8,7	1	10,6
1410	214010218	SEMA4D	semaphorin-4D isoform 1 precursor	7,8	96150	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	0	0,0
1411	214010224	RPS24	40S ribosomal protein S24 isoform f	11,4	15179	5	21,7	3	19,9	4	17,8	5	28,1	6	24,3	4	20,6	3	19,2
1412	21410970	RPL6	Ribosomal protein L6	11,0	32727	0	0,0	1	10,3	0	0,0	4	9,5	2	12,3	2	8,9	0	0,0
1413	21411235	NDUFS1	NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa	5,7	79421	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1414	21411382	PLS1	PLS1 protein	5,2	70323	2	11,5	2	10,2	4	8,6	2	9,4	5	12,1	2	9,0	3	9,6
1415	21411521	NDUFA10	NDUFA10 protein	9,1	22374	1	10,8	1	10,0	1	9,9	1	9,5	0	0,0	1	9,1	1	7,9
1416	21426922	PELP1	PELP1	4,2	136642	1	12,4	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
1417	21434741	LRBA	AF467287_1 beige-like protein	5,3	317653	1	11,0	1	10,0	1	8,7	0	0,0	0	0,0	1	13,3	1	8,8
1418	21436587	HLA	MHC class II antigen	5,8	10455	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	2	9,3	0	0,0
1419	21450846	MATK	megakaryocyte-associated tyrosine-protein kinase is	8,9	56451	0	0,0	2	9,7	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
1420	21464101	YWHAG	14-3-3 protein gamma	4,7	28303	2	26,6	5	39,6	4	21,8	2	18,8	5	24,2	4	26,3	4	32,4
1421	21464270	CSNK2A3	casein kinase II alpha subunit	8,7	45176	1	11,2	2	10,0	3	17,2	1	9,5	2	12,2	1	8,7	2	10,6
1422	2148997	FADD	Fas-associating protein	5,0	10504	0	0,0	1	9,7	0	0,0	1	9,5	0	0,0	0	0,0	1	11,4
1423	215273730	HLA	MHC class II antigen, partial	6,1	10873	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
1424	21536400	BIN1	myc box-dependent-interacting protein 1 isoform 1	4,8	64681	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,8
1425	21552762	ABHD11	AF412032_1 Williams-Beuren syndrome critical region p	12,4	10344	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1426	215598688	USP13	ubiquitin carboxyl-terminal hydrolase 13	5,2	97308	1	10,7	1	10,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1427	21591141	SPAG16	AF310672_1 PF20 variant 1a	5,8	70792	0	0,0	0	0,0	0	0,0	1	9,4	0	0,0	1	8,0	0	0,0
1428	21594340	KIF2A	Kinesin heavy chain member 2A	6,0	76956	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1429	215959387	HLA	MHC class II antigen	6,4	10867	0	0,0	4	10,0	0	0,0	1	9,4	0	0,0	0	0,0	0	0,0
1430	2160390	GPX3	glutathione peroxidase	8,2	25516	1	12,1	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1431	21618338	STAT3	signal transducer and activator of transcription 3	5,9	87962	4	27,3	9	54,3	7	50,1	8	65,5	2	12,2	7	52,9	3	25,9
1432	21618344	STAT5B	signal transducer and activator of transcription 5B	5,7	89847	0	0,0	0	0,0	3	19,6	0	0,0	0	0,0	2	19,4	0	0,0
1433	21618887	DGKA	DGKA protein	6,2	82657	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,8	0	0,0
1434	21618939	MRPL50	Mitochondrial ribosomal protein L50	8,0	18360	0	0,0	1	10,0	1	9,9	1	9,5	0	0,0	2	8,9	1	7,9
1435	21619132	BAIAP2	BAIAP2 protein	9,3	56627	1	10,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
1436	21619414	DDX39A	DDX39 protein	5,8	36578	0	0,0	0	0,0	0	0,0	1	9,4	0	0,0	0	0,0	1	9,6
1437	21619615	NAPRT	NAPRT1 protein	5,3	33200	0	0,0	0	0,0	1	8,6	0	0,0	0	0,0	1	12,6	0	0,0

1438	21624607	COTL1	coactosin-like protein	5,4	15946	2	10,6	1	10,1	1	9,8	2	9,5	3	12,3	5	16,0	2	13,4
1439	21626466	MATR3	matrin-3 isoform a	5,8	94624	3	28,3	8	25,0	8	43,8	4	28,2	9	72,3	7	39,4	8	53,6
1440	21669095	ENSG00000228325	immunoglobulin kappa light chain VLJ region	8,8	11630	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,8
1441	21669331	IGK	immunoglobulin kappa light chain VLJ region	7,6	28849	0	0,0	0	0,0	6	8,7	0	0,0	3	12,2	3	9,6	5	10,6
1442	21669337	IGK	immunoglobulin kappa light chain VLJ region	6,2	28708	1	13,0	6	19,9	4	18,1	4	18,8	2	12,3	2	19,3	2	12,8
1443	21669521	IGLL5	immunoglobulin lambda light chain VLJ region	7,9	27867	1	13,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
1444	21669631	IGL	immunoglobulin lambda light chain VLJ region	7,0	27856	2	11,5	2	10,0	2	9,3	2	9,5	2	12,2	1	9,1	2	9,7
1445	21686613	HLA	MHC class Ib antigen	5,3	39052	2	15,9	5	34,8	3	8,7	0	0,0	0	0,0	0	0,0	4	13,4
1446	21693136	NEK9	KIAA1995 protein	5,6	110399	1	13,0	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	0	0,0
1447	21706468	NUP93	Nucleoporin 93kDa	5,5	93558	2	19,4	2	10,1	0	0,0	1	9,5	2	12,2	2	15,2	2	18,4
1448	21707262	GTPBP4	GTPBP4 protein, partial	10,0	73710	0	0,0	0	0,0	1	8,7	1	9,5	0	0,0	1	13,3	1	13,6
1449	21708041	PSIP1	PSIP1 protein	9,3	5703	1	14,6	1	10,0	1	8,7	0	0,0	0	0,0	2	18,5	2	19,3
1450	21708126	PDXDC1	PDXDC1 protein	6,0	38421	0	0,0	0	0,0	1	8,7	1	9,4	0	0,0	1	9,8	1	9,8
1451	21732286	NNT	hypothetical protein	7,9	113996	2	25,1	1	9,7	3	22,7	1	9,5	0	0,0	2	12,3	1	7,9
1452	21732868	PPP1R18	hypothetical protein	4,6	35380	1	9,7	1	10,3	0	0,0	0	0,0	0	0,0	2	18,6	1	9,7
1453	217330641	IWS1	protein IWS1 homolog	4,4	91955	0	0,0	1	10,3	0	0,0	1	9,5	0	0,0	0	0,0	0	0,0
1454	21734051	XPNPEP1	hypothetical protein	5,8	73099	0	0,0	0	0,0	0	0,0	0	0,0	2	12,2	1	9,3	0	0,0
1455	21735544	MAP2K7	dual specificity mitogen-activated protein kinase k	9,5	47467	0	0,0	0	0,0	1	8,6	0	0,0	0	0,0	1	9,3	0	0,0
1456	21735596	PDCD4	programmed cell death protein 4 isoform 1	4,9	51717	2	22,6	2	19,9	1	9,9	4	28,1	0	0,0	1	12,1	1	12,9
1457	21735621	MDH2	malate dehydrogenase, mitochondrial precursor	8,8	35485	16	58,5	16	44,8	27	55,0	19	65,5	20	60,4	18	62,2	20	62,7
1458	21739272	RRBP1	hypothetical protein	6,5	87434	1	11,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1459	21739309	DNAJC11	hypothetical protein	8,7	62575	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	1	9,7
1460	21739365	FAHD2B	hypothetical protein	7,2	34213	0	0,0	0	0,0	1	9,3	0	0,0	0	0,0	1	8,7	1	9,7
1461	21739412	NUP85	hypothetical protein	5,3	75091	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
1462	21739643	CCAR2	hypothetical protein	5,0	102761	2	26,0	0	0,0	0	0,0	1	9,4	0	0,0	1	9,5	0	0,0
1463	21739834	AP5B1	hypothetical protein	5,6	55162	1	12,3	2	10,0	2	9,2	1	9,4	3	12,2	1	8,9	2	9,7
1464	21739968	ARFGAP2	hypothetical protein	8,0	56448	1	11,1	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
1465	21740024	YTHDF1	hypothetical protein	10,0	39927	0	0,0	0	0,0	1	9,8	0	0,0	0	0,0	0	0,0	0	0,0
1466	21740030	QSOX2	hypothetical protein	6,7	60874	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
1467	21740085	FMNL2	hypothetical protein	7,7	114457	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
1468	21740185	NAPB	hypothetical protein	4,9	16171	2	11,5	2	10,0	2	9,2	1	9,4	3	12,2	2	8,9	1	9,6
1469	21748590	RIN3	FLJ00372 protein	5,9	43241	0	0,0	1	9,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1470	21748624	TRAF1	FLJ00389 protein	7,5	39716	1	11,2	2	19,3	2	14,1	1	9,4	0	0,0	2	15,5	1	8,8
1471	21748660	PRRC1	FLJ00410 protein	5,3	32897	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
1472	21748877	SNRNP200	unnamed protein product	5,0	71473	1	12,4	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1473	21749550	DDX18	unnamed protein product	9,7	46644	2	15,1	4	19,9	1	8,7	6	28,2	2	12,2	3	15,9	2	13,6
1474	21749793	SRSF7	unnamed protein product	10,2	15863	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	1	7,9
1475	21749840	LARP1	unnamed protein product	7,5	90979	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7	0	0,0
1476	21750752	ZNF783	unnamed protein product	4,3	21675	0	0,0	1	10,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1477	21750956	DPYSL2	unnamed protein product	10,2	21415	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1478	21751443	CLINT1	unnamed protein product	6,0	68137	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	2	10,6
1479	21751512	MDP1	unnamed protein product	6,5	14819	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
1480	21751579	MYO1F	unnamed protein product	9,4	124635	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	1	9,7
1481	21751704	MARS	unnamed protein product	4,6	15128	0	0,0	1	10,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1482	21751732	MX1	unnamed protein product	5,9	76176	2	10,6	0	0,0	1	9,3	1	9,4	0	0,0	1	8,9	1	8,8
1483	21752044	NT5C1B	unnamed protein product	7,6	36783	1	9,6	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1484	21752174	AK8	unnamed protein product	10,6	18254	1	13,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1485	21752190	TRAP1	unnamed protein product	7,0	66047	8	69,3	7	49,5	5	35,4	10	46,8	3	21,8	4	39,7	6	41,3
1486	21752646	FERMT3	unnamed protein product	6,4	75485	10	75,3	5	39,6	8	57,6	10	65,4	8	60,3	8	62,1	7	50,9
1487	21752954	IRF3	unnamed protein product	8,7	17216	1	10,8	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
1488	21753407	THNSL1	unnamed protein product	6,1	64370	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
1489	21754039	DST	unnamed protein product	5,7	87553	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1490	21754440	ANP32E	unnamed protein product	3,5	24868	0	0,0	0	0,0	1	9,9	0	0,0	0	0,0	1	9,8	0	0,0
1491	21754454	SYNE2	unnamed protein product	5,3	110274	1	11,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1492	21754758	HMGCS1	unnamed protein product	5,1	56239	1	12,4	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1493	21755073	FAM98B	unnamed protein product	5,9	37222	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7	1	7,9
1494	21755180	RABGAP1L	unnamed protein product	5,1	92541	1	11,7	1	9,7	0	0,0	1	9,4	0	0,0	0	0,0	0	0,0
1495	21755528	ACSL1	unnamed protein product	5,4	28594	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
1496	21756043	MIA3	unnamed protein product	4,5	105868	1	11,2	1	10,3	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
1497	21756162	LONP1	unnamed protein product	6,2	100397	3	17,5	5	19,9	3	23,2	4	18,8	2	12,2	5	30,2	4	31,4
1498	21756182	PACS1	unnamed protein product	5,5	89388	1	12,5	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
1499	21756739	ANKRD44	unnamed protein product	5,9	99820	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	1	8,1	1	7,9
1500	21757045	HEL113	unnamed protein product	4,8	52439	7	63,3	3	29,7	0	0,0	12	74,7	15	84,4	5	39,4	5	31,0

1501	21757406	ATL3	unnamed protein product	5,8	63242	0	0,0	0	0,0	2	17,2	0	0,0	0	0,0	3	21,6	0	0,0
1502	21757772	DNM2	unnamed protein product	7,4	52199	1	11,2	0	0,0	0	0,0	1	9,4	0	0,0	0	0,0	1	9,7
1503	21758154	TRA2B	unnamed protein product	10,9	29202	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
1504	21758578	PNP	unnamed protein product	6,8	32552	2	17,3	5	44,4	7	41,0	5	37,4	3	24,2	5	29,7	4	36,6
1505	21758583	PRPF31	unnamed protein product	4,9	40780	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	1	9,7
1506	2181867	USP9Y	DFFRY	5,5	291117	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	1	9,3	1	9,7
1507	218456537	HLA	MHC class II antigen	5,9	10656	1	10,9	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1508	218563737	BAP18	chromatin complexes subunit BAP18 isoform 1	5,3	19943	1	10,6	0	0,0	1	9,9	0	0,0	0	0,0	1	13,3	1	9,8
1509	218751490	HLA	MHC class I antigen	5,6	31625	5	11,3	0	0,0	4	9,9	10	9,5	0	0,0	4	8,7	15	8,9
1510	21929089	GPR142	seven transmembrane helix receptor	11,4	156508	0	0,0	0	0,0	1	9,8	0	0,0	0	0,0	0	0,0	0	0,0
1511	21929208	CD97	seven transmembrane helix receptor	6,4	92059	1	11,4	3	10,0	3	9,3	5	9,5	2	12,2	4	9,1	3	9,7
1512	21951802	PDS5A	AF294791_1 SCC-112	8,0	146610	1	12,4	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	2	19,3
1513	21952248	MLL	AF512944_1 MLL/SEPTIN6 fusion protein	9,7	28788	2	16,3	1	9,9	0	0,0	2	18,9	3	24,3	2	17,9	2	19,4
1514	21952252	SEPT6	AF512946_1 MLL/SEPTIN6 fusion protein	8,0	63144	1	10,8	0	0,0	1	8,7	1	9,5	0	0,0	2	13,7	1	7,9
1515	21956484	EIF2A	AF497978_1 eukaryotic translation initiation factor 2	9,2	65042	0	0,0	0	0,0	0	0,0	1	9,4	0	0,0	0	0,0	0	0,0
1516	21956645	MTPN	myotrophin	5,2	12896	4	21,3	2	15,1	1	15,7	0	0,0	0	0,0	1	11,7	1	12,9
1517	21961605	KRT10	Keratin 10	5,0	58828	6	60,5	0	0,0	1	8,7	0	0,0	2	12,2	0	0,0	0	0,0
1518	2196872	ARHGEF1	sub1.5	5,9	97886	1	11,3	2	14,8	3	25,8	1	9,4	0	0,0	1	8,7	1	9,7
1519	219803946	WIBG	partner of Y14 and mago isoform 2	9,9	22686	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1520	219894	MARCKS	80K-L protein	4,3	31545	4	22,8	3	19,9	3	13,6	1	9,4	2	12,2	2	15,3	5	22,5
1521	219902	PTPN7	protein-tyrosine phosphatase	6,2	40574	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,4	0	0,0
1522	22028271	WDFY4	WDFY4 protein	5,2	73197	1	10,8	1	9,7	1	9,8	0	0,0	0	0,0	1	8,7	1	10,6
1523	2204213	STAG1	nuclear protein SA-1	5,3	144445	1	10,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1524	22090626	HUWE1	HECT domain protein LASU1	4,9	370175	2	14,0	2	19,6	1	9,3	1	9,5	2	12,2	3	27,8	2	16,1
1525	22095331	EMC1	ER membrane protein complex subunit 1 isoform 1 pre	7,4	111740	0	0,0	1	9,7	1	8,7	0	0,0	0	0,0	0	0,0	0	0,0
1526	221039498	ALDOC	unnamed protein product	9,5	14269	1	10,8	0	0,0	1	9,8	1	9,5	3	24,2	3	23,7	1	9,7
1527	221039576	ALDOC	unnamed protein product	6,6	22330	2	15,3	2	15,1	5	22,7	1	9,5	2	12,2	5	33,0	2	15,5
1528	221039588	RCN1	unnamed protein product	4,7	33027	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1529	221039618	ALDOC	unnamed protein product	6,7	35424	3	26,3	2	18,0	2	16,6	2	17,0	6	21,9	5	18,7	2	17,4
1530	221039872	SYNCRIP	unnamed protein product	9,4	28579	0	0,0	0	0,0	1	9,9	0	0,0	0	0,0	0	0,0	0	0,0
1531	221040010	AMPD3	unnamed protein product	6,8	63831	1	16,6	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
1532	221040116	SUCLG2	unnamed protein product	7,8	41467	1	11,2	0	0,0	1	8,6	0	0,0	0	0,0	1	9,7	0	0,0
1533	221040450	H326	unnamed protein product	4,9	84779	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1534	221040542	UQCRB	unnamed protein product	9,3	18738	1	11,2	1	10,0	0	0,0	0	0,0	0	0,0	1	8,7	1	9,7
1535	221040910	ALDH18A1	unnamed protein product	5,9	74788	1	11,7	0	0,0	1	9,9	0	0,0	2	12,2	0	0,0	1	9,7
1536	221042042	FAH	unnamed protein product	9,7	19441	0	0,0	0	0,0	1	9,9	0	0,0	2	12,2	1	9,7	0	0,0
1537	221043054	DECR1	unnamed protein product	9,2	34995	2	12,4	0	0,0	1	9,8	1	9,4	2	12,2	2	8,0	1	9,7
1538	221043412	PSMB8	unnamed protein product	6,5	16409	1	12,4	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7	0	0,0
1539	221043980	NDUFB9	unnamed protein product	9,0	20767	1	10,4	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
1540	221044014	ETF1	unnamed protein product	5,3	47477	1	11,8	1	10,1	1	8,7	2	9,5	0	0,0	1	8,0	3	15,7
1541	221044236	MTHFD1	unnamed protein product	8,6	110497	4	46,0	3	14,8	10	69,5	7	46,7	15	120,4	6	46,6	11	66,3
1542	221044840	MTM1	unnamed protein product	7,8	48119	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1543	221044958	TPP2	unnamed protein product	5,9	117965	3	18,7	2	19,9	0	0,0	1	9,4	0	0,0	0	0,0	1	11,4
1544	221316566	CHORDC1	cysteine and histidine-rich domain-containing prot	7,7	37472	0	0,0	0	0,0	1	8,7	0	0,0	2	12,2	0	0,0	1	9,7
1545	22202629	AIFM1	apoptosis-inducing factor 1, mitochondrial isoform	9,2	66276	2	24,2	1	9,7	2	13,5	5	37,4	0	0,0	2	14,4	1	13,6
1546	222080062	NDUFV2	NADH dehydrogenase [ubiquinone] flavoprotein 2, mithocondrial	8,1	27373	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	1	8,8
1547	22208850	GCC1	GRIP and coiled-coil domain-containing protein 1	5,2	87792	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
1548	22208967	HMGA1	high mobility group protein HMG-I/HMG-Y isoform a	10,8	11658	2	13,1	5	24,7	2	9,3	0	0,0	2	12,2	2	13,3	4	15,5
1549	22212931	NOL6	nucleolar protein 6 gamma isoform	7,9	77638	1	11,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
1550	222136639	MTHFD1	C-1-tetrahydrofolate synthase, cytoplasmic	6,9	101512	0	0,0	0	0,0	0	0,0	1	9,4	0	0,0	0	0,0	0	0,0
1551	222136649	DDT3	D-dopachrome decarboxylase related protein	7,2	13054	2	10,4	3	10,0	3	9,3	0	0,0	2	12,2	2	9,1	5	9,7
1552	222352151	PCBP1	poly(rC)-binding protein 1	6,7	37499	1	14,3	3	10,0	1	8,7	0	0,0	0	0,0	1	8,9	2	8,9
1553	222418587	NWD2	leucine-rich repeat and WD repeat-containing pr	5,8	197447	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1554	2224663	PFAS	KIAA0361	5,5	148051	2	18,6	2	14,8	3	14,2	1	9,5	3	24,2	2	13,7	2	15,5
1555	2224677	ECM29	KIAA0368	6,1	159478	0	0,0	0	0,0	1	9,3	0	0,0	2	12,2	1	9,8	1	11,4
1556	222476519	HSPD1	60 kDa chaperonin	8,6	19853	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	1	9,8	5	9,7
1557	223029410	TLN1	talin-1	5,7	269766	17	153,3	15	89,2	31	174,8	28	158,6	31	132,5	22	130,3	23	151,3
1558	223029430	SLC2A6	solute carrier family 2, facilitated glucose tr	9,2	48022	1	11,1	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1559	223036741	HLA	MHC class I antigen	5,7	20840	0	0,0	0	0,0	0	0,0	0	0,0	2	12,3	0	0,0	0	0,0
1560	22325356	AKAP2	PALM2-AKAP2 protein isoform 2	4,8	120630	1	10,8	0	0,0	0	0,0	0	0,0	0	0,0	1	9,4	1	9,8
1561	223278379	RRP12	RRP12-like protein isoform 1	8,9	143702	0	0,0	1	9,7	2	9,3	0	0,0	2	12,2	1	8,0	1	7,9
1562	223278403	GRID2IP	delphilin	7,1	132276	0	0,0	1	10,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1563	223462373	HEATR5B	HEAT repeat containing 5B	6,7	224276	0	0,0	1	10,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0

1564	223468564	SLC1A5	neutral amino acid transporter B(0) isoform 2	5,2	33692	1	12,4	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1565	223468571	MRPL23	39S ribosomal protein L23, mitochondrial	10,0	17763	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1566	223555917	MTDH	protein LYRIC	9,8	63837	1	13,2	0	0,0	1	8,7	2	18,8	2	12,2	1	8,0	0	0,0
1567	223555970	INTS9	integrator complex subunit 9 isoform 2	6,1	71449	0	0,0	0	0,0	1	9,9	0	0,0	0	0,0	0	0,0	0	0,0
1568	223633890	SHISA7	protein shisa-7 precursor	10,3	56214	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
1569	223890243	RPL10	60S ribosomal protein L10 isoform a	10,5	24586	2	17,1	0	0,0	0	0,0	2	18,8	0	0,0	1	9,8	1	7,9
1570	223972651	ALDH16A1	aldehyde dehydrogenase family 16 member A1 isoform	6,3	85109	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	0	0,0
1571	224451135	SCAF4	splicing factor, arginine/serine-rich 15 isofor	10,0	123624	1	12,4	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1572	224465187	SCRN1	secernin-1 isoform a	4,5	46383	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,1	1	8,8
1573	2244652	HS24	HS24/P52	8,1	52368	3	30,1	2	19,9	3	23,3	2	18,8	3	24,2	2	20,0	3	25,1
1574	224808322	ENSG00000223931	B cell antibody heavy chain variable region, partial	5,1	12807	1	11,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1575	2250701	KIAA1210	KNP-I beta protein	8,3	20124	2	10,6	2	14,8	2	13,6	0	0,0	0	0,0	2	20,6	3	21,9
1576	22531287	IFI16	interferon-inducible IFI 16	9,7	82020	4	31,0	5	39,7	3	18,4	2	18,9	3	24,3	2	18,3	5	38,6
1577	22538465	PSMB3	proteasome subunit beta type-3	6,1	22950	1	11,3	3	19,9	2	13,5	6	37,5	3	24,2	4	21,6	2	13,5
1578	225421271	HLA	MHC class I antigen	5,7	20887	0	0,0	0	0,0	0	0,0	1	9,5	0	0,0	0	0,0	0	0,0
1579	22547140	MRPL4	39S ribosomal protein L4, mitochondrial isoform b	10,5	29484	1	11,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
1580	225735593	RPAP3	RNA polymerase II-associated protein 3 isoform	7,7	71848	1	13,1	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1581	226295424	HLA	MHC class I antigen	7,2	40773	3	11,0	3	10,1	3	8,8	0	0,0	2	12,2	3	8,8	3	9,8
1582	2264346	STIM1	GOK	6,2	77493	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
1583	226530313	MICAL1	protein-methionine sulfoxide oxidase MICAL1 iso	6,0	108534	1	10,5	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1584	226821626	HLA	MHC class I antigen	7,2	21215	2	10,6	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1585	226958412	IVD	isovaleryl-CoA dehydrogenase, mitochondrial isofor	8,0	46633	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	1	11,4
1586	22749327	UBE2E2	ubiquitin-conjugating enzyme E2 E2	7,7	22256	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1587	2274968	HEL	Glucosidase II	5,7	106900	8	55,0	10	59,3	8	48,9	7	56,1	6	48,3	10	63,3	7	44,6
1588	22749694	MRPS17	MRPS17 protein, partial	10,3	15708	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
1589	22760231	ENSG00000223931	unnamed protein product	6,1	53225	2	13,6	1	10,0	2	18,4	1	9,4	0	0,0	1	15,1	2	22,9
1590	22760383	IPO4	unnamed protein product	4,3	56874	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	0	0,0
1591	22760414	JAGN1	unnamed protein product	10,0	21156	1	11,6	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1592	22760706	TRMT1L	unnamed protein product	7,6	81649	1	9,7	1	10,0	0	0,0	1	9,5	0	0,0	1	8,0	0	0,0
1593	22760762	SERBP1	unnamed protein product	9,1	44939	4	22,5	7	29,5	6	27,6	5	28,2	6	24,3	2	17,9	9	41,0
1594	22760780	TMEM214	unnamed protein product	8,2	54743	1	11,2	2	10,1	1	8,8	1	9,5	0	0,0	0	0,0	1	8,0
1595	22761168	FNDC3B	unnamed protein product	4,8	83815	1	10,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1596	22761285	TXNDC5	unnamed protein product	5,6	47658	5	29,6	2	14,8	6	32,4	7	56,1	3	24,2	5	26,9	5	29,4
1597	22761396	TMX2	unnamed protein product	8,6	42543	1	11,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1598	22761477	NUDT9	unnamed protein product	8,7	39096	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1599	22761650	SUMF2	unnamed protein product	8,2	33858	1	11,5	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	1	9,7
1600	22761762	NUP210	unnamed protein product	6,8	44684	1	10,4	1	10,0	1	8,7	1	9,5	0	0,0	1	8,7	1	8,8
1601	22796316	ACAA1	3-oxoacyl-CoA thiolase	8,6	34197	2	21,5	0	0,0	0	0,0	0	0,0	0	0,0	2	14,3	0	0,0
1602	228008291	SYNCRIP	heterogeneous nuclear ribonucleoprotein Q isoform	8,8	69584	5	33,6	7	34,9	8	42,9	8	46,8	12	89,1	8	46,8	7	44,1
1603	2285963	HMGB3	high mobility group protein 2a	8,9	22918	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
1604	22902182	RAVER1	RAVER1 protein	10,0	57656	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,8
1605	22907039	APOBEC3C	probable DNA dC->dU-editing enzyme APOBEC-3C	7,5	22808	1	10,7	1	10,3	0	0,0	1	9,5	0	0,0	1	9,3	1	10,5
1606	23065563	GSTM5	glutathione S-transferase Mu 5	7,2	25676	0	0,0	2	10,0	0	0,0	1	9,5	2	12,2	1	9,1	1	9,7
1607	23097250	TIPRL	TIP41-like protein isoform 1	5,5	31445	1	10,5	3	14,8	1	8,7	1	9,5	0	0,0	2	12,1	3	19,3
1608	23110925	PSMB6	proteasome subunit beta type-6 isoform 1 proprotein	4,7	25340	1	11,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1609	23110944	PSMA6	proteasome subunit alpha type-6	6,4	27400	3	19,8	3	15,1	1	9,3	2	18,8	5	24,2	1	9,0	1	9,7
1610	23110962	CTSS	cathepsin S isoform 1 preproprotein	8,3	37496	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
1611	23111034	SNX1	sorting nexin-1 isoform a	4,9	59070	2	16,4	0	0,0	0	0,0	0	0,0	0	0,0	2	9,3	1	8,8
1612	23242914	LSS	Lanosterol synthase (2,3-oxidosqualene-lanosterol cyc	6,2	83276	1	10,5	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
1613	2326524	ADAR	IFI-4	8,9	103670	2	23,7	3	19,9	4	31,8	1	9,5	3	24,3	2	13,8	3	30,9
1614	23270703	NPIPB3	LOC23117 protein	10,4	75739	1	10,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1615	23272068	TOR1AIP1	TOR1AIP1 protein	6,9	52436	0	0,0	1	9,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1616	23272300	CKAP5	CKAP5 protein	6,9	106966	0	0,0	0	0,0	0	0,0	0	0,0	2	12,2	1	9,4	1	7,9
1617	23308577	PHGDH	D-3-phosphoglycerate dehydrogenase	6,3	56651	2	29,1	2	10,0	3	19,0	0	0,0	0	0,0	2	18,0	3	25,0
1618	23308579	PTGES3	prostaglandin E synthase 3	4,2	18698	1	11,2	2	10,0	1	9,3	2	9,5	2	12,2	2	9,0	2	9,7
1619	23308607	HM13	minor histocompatibility antigen H13 isoform 1	6,0	41470	1	10,9	1	10,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1620	23308751	HIBADH	3-hydroxyisobutyrate dehydrogenase, mitochondrial p	8,1	35311	2	24,7	0	0,0	0	0,0	0	0,0	0	0,0	2	8,0	0	0,0
1621	23331072	FTSJ3	FtsJ homolog 3 (E. coli)	8,3	96576	1	16,6	0	0,0	0	0,0	0	0,0	2	12,3	1	9,6	1	7,9
1622	23336902	DDX46	TPA_exp: Prp5-like DEAD-box protein	9,7	117461	1	11,3	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
1623	23397678	STAT6	signal transducer and activator of transcription 6	5,8	94116	0	0,0	1	10,4	0	0,0	0	0,0	0	0,0	1	9,7	0	0,0
1624	23398599	PNPLA6	PNPLA6 protein	7,8	146819	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1625	234746	RAB8A	RAS-related protein MEL	9,7	23598	2	21,0	1	9,7	2	13,5	1	9,5	2	12,2	2	12,1	2	16,7
1626	23491733	RPS2	ribosomal protein S2	10,3	25606	2	13,5	2	10,0	4	18,4	7	28,1	3	12,2	2	11,7	2	12,3

1627	23503295	CSNK2B	casein kinase II subunit beta	5,2	24943	0	0,0	1	10,0	0	0,0	1	9,5	0	0,0	0	0,0	1	7,9
1628	23510338	UBA1	ubiquitin-like modifier-activating enzyme 1	5,4	117830	13	105,7	16	103,8	23	128,0	25	130,7	11	60,3	26	139,2	23	130,0
1629	23510451	APEH	acylamino-acid-releasing enzyme	5,2	81225	0	0,0	0	0,0	1	9,9	0	0,0	0	0,0	0	0,0	0	0,0
1630	2352814	STX16	syntaxin-16A	6,1	34619	1	11,1	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1631	2358285	KMT2D	ALR	5,6	564182	1	13,0	0	0,0	1	8,7	0	0,0	0	0,0	1	8,7	1	9,7
1632	23618867	SFXN1	sideroflexin-1	9,3	35620	1	19,1	0	0,0	2	21,4	0	0,0	0	0,0	1	19,4	1	11,8
1633	23712	SFPQ	myoblast antigen 24.1D5	6,4	45250	7	46,4	10	39,7	10	44,7	12	46,8	11	48,3	6	38,9	11	46,8
1634	237649012	EBNA1BP2	probable rRNA-processing protein EBP2 isoform 1	10,4	40666	1	12,5	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	0	0,0
1635	237681111	ATP1A1	sodium/potassium-transporting ATPase subunit al	5,0	109532	1	12,3	0	0,0	0	0,0	1	9,5	0	0,0	0	0,0	0	0,0
1636	23844	SLC25A11	2-oxoglutarate carrier	10,2	34081	0	0,0	1	10,2	0	0,0	0	0,0	0	0,0	1	9,5	0	0,0
1637	238684632	HLA	MHC class I antigen	7,4	21129	0	0,0	2	10,1	4	9,4	0	0,0	8	12,3	12	9,8	2	9,8
1638	238684658	HLA	MHC class I antigen	6,4	21045	1	12,4	0	13,0	0	0,0	0	0,0	0	12,3	0	8,1	0	0,0
1639	238684834	HLA	MHC class II antigen	7,9	10786	0	0,0	0	0,0	1	9,9	0	0,0	0	0,0	0	0,0	1	10,6
1640	238776833	ALYREF	THO complex subunit 4	11,5	27558	0	0,0	0	0,0	0	0,0	1	9,4	0	0,0	0	0,0	0	0,0
1641	239049591	GYS1	glycogen [starch] synthase, muscle isoform 2	6,1	76465	0	0,0	2	14,8	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
1642	2394332	HLA	MHC class I antigen	5,2	10582	1	10,5	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1643	23943872	SMAP2	stromal membrane-associated protein 2 isoform 1	9,1	46768	0	0,0	1	10,0	1	9,2	0	0,0	0	0,0	2	15,9	0	0,0
1644	239949265	HLA	MHC class I antigen	5,8	21177	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1645	24042327	NFS1	cysteine desulfurase	7,9	50155	0	0,0	0	0,0	1	9,3	0	0,0	0	0,0	1	8,0	1	7,9
1646	2414516	SURF4	surface 4 integral membrane protein	8,2	28516	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	10,5
1647	24234690	MRE11A	double-strand break repair protein MRE11A isoform 2	5,5	77624	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
1648	24266820	RCSD1	hypothetical protein	5,2	44484	1	11,2	1	10,0	0	0,0	0	0,0	0	0,0	1	9,4	1	9,7
1649	24307879	DYNC1I2	cytoplasmic dynein 1 intermediate chain 2 isoform 1	4,9	71438	2	10,8	1	10,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
1650	24307983	CMTR1	cap-specific mRNA (nucleoside-2'-O-)-methyltransfer	6,6	95302	1	12,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
1651	24308207	LRRC47	leucine-rich repeat-containing protein 47	8,2	63454	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
1652	24308388	TSR2	pre-rRNA-processing protein TSR2 homolog	4,1	20876	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
1653	24430137	LAGE3	L antigen family member 3	9,0	14805	1	10,9	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
1654	24430149	NUP155	nuclear pore complex protein Nup155 isoform 1	5,7	155180	1	10,8	0	0,0	0	0,0	1	9,4	0	0,0	1	9,3	0	0,0
1655	24430151	PSMC1	26S protease regulatory subunit 4	5,8	49185	1	12,9	3	20,2	3	25,6	4	28,2	2	12,2	3	26,5	2	20,1
1656	24430155	PSMC4	26S protease regulatory subunit 6B isoform 2	5,0	43490	1	11,2	1	10,0	1	9,9	0	0,0	2	12,2	4	9,8	1	10,6
1657	24431985	PIWIL2	piwi-like protein 2	9,2	109849	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	1	8,8
1658	2443580	DUT	dUTPase	9,9	26707	1	11,5	0	0,0	0	0,0	4	28,2	2	12,2	0	0,0	2	15,7
1659	24474791	SNRP116	small nuclear ribonucleoprotein component	5,6	95353	1	11,2	2	15,1	2	19,0	4	26,3	5	36,2	2	21,0	3	25,2
1660	24497603	NUP62	nuclear pore glycoprotein p62	5,1	53256	1	10,5	1	10,3	3	19,6	1	9,5	0	0,0	3	13,8	0	0,0
1661	24497614	KL	klotho precursor	7,8	116181	1	12,5	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1662	2463577	PRPF8	PRP8 protein	9,0	273784	2	21,3	9	40,2	6	17,5	4	28,1	2	12,2	5	29,4	2	14,9
1663	24660305	ARHGAP20	ARHGAP20 protein	6,2	80956	0	0,0	0	0,0	2	8,7	0	0,0	0	0,0	0	0,0	0	0,0
1664	247424380	ENSG00000223931	immunoglobulin heavy chain variable region	8,8	12828	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
1665	247425802	IGHV	immunoglobulin heavy chain variable region	9,3	13141	1	11,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
1666	24797086	IPO5	importin-5	4,7	125545	2	12,0	2	10,0	1	8,7	0	0,0	2	12,2	2	8,0	2	9,6
1667	24797097	PYCR1	pyrroline-5-carboxylate reductase 1, mitochondrial	7,4	33342	0	0,0	2	10,0	2	17,2	0	0,0	0	0,0	3	23,8	3	18,1
1668	24981047	DDX6	DDX6 protein	9,5	20427	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
1669	2506080	GAK	HsGAK	5,4	143165	0	0,0	1	9,8	2	9,3	0	0,0	2	12,2	1	8,0	1	7,9
1670	25121993	MSI2	RNA-binding protein Musashi homolog 2 isoform b	8,7	28403	0	0,0	0	0,0	1	8,6	0	0,0	0	0,0	0	0,0	0	0,0
1671	25187967	RHOT2	mitochondrial Rho 2	5,4	68027	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
1672	25282407	IRF9	interferon regulatory factor 9	5,5	43697	1	11,9	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
1673	25286703	KIAA2013	uncharacterized protein KIAA2013 precursor	8,1	69139	1	11,6	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1674	2529440	TERF2	TTAGGG repeat binding factor 2	9,6	55552	1	12,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1675	253735778	ARHGEF2	rho guanine nucleotide exchange factor 2 isofor	6,9	111453	1	10,5	0	0,0	1	8,7	0	0,0	0	0,0	1	9,4	2	10,6
1676	253970502	EWSR1	RNA-binding protein EWS isoform 3	9,5	68373	1	11,6	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	2	19,3
1677	25470890	DAZAP1	DAZ-associated protein 1 isoform a	8,3	40530	1	11,6	0	0,0	1	8,7	2	18,8	2	12,2	1	8,1	1	8,8
1678	254911007	EYA2	eyes absent homolog 2 isoform c	5,8	50534	1	11,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1679	255304946	PEO1	twinkle protein, mitochondrial isoform B	8,1	65997	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
1680	255682810	HLA	MHC class I antigen	5,1	21032	2	17,3	2	10,0	0	0,0	0	0,0	3	12,2	2	10,3	0	0,0
1681	255918129	LMF2	lipase maturation factor 2	10,4	79698	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	1	9,4	1	9,7
1682	255982614	DHX16	putative pre-mRNA-splicing factor ATP-dependent RN	6,4	119245	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1683	2570007	PGRMC2	progresterone binding protein	4,6	23819	2	13,1	1	10,0	0	0,0	0	0,0	0	0,0	2	8,7	2	10,5
1684	2576345	NDUFAB1	Acyl carrier protein, Mitochondrial (ACP) (5'partial)	4,6	17912	1	11,2	0	0,0	1	8,6	1	9,4	0	0,0	1	8,0	1	7,9
1685	25777600	PSMD1	26S proteasome non-ATPase regulatory subunit 1 isof	5,1	105818	1	13,5	2	14,8	0	0,0	0	0,0	2	12,2	3	26,3	2	17,5
1686	25777612	PSMD3	26S proteasome non-ATPase regulatory subunit 3	8,7	60959	3	31,9	2	19,8	3	22,7	1	9,4	3	24,3	3	21,6	2	19,2
1687	25777713	SKP1	S-phase kinase-associated protein 1 isoform b	4,2	18640	1	9,7	1	10,3	1	8,7	0	0,0	2	12,2	1	8,9	0	0,0
1688	25777730	ALDH1B1	aldehyde dehydrogenase X, mitochondrial precursor	6,6	57231	0	0,0	0	0,0	1	9,9	0	0,0	0	0,0	0	0,0	1	8,9
1689	25900985	APBB1IP	proline-rich protein 73	5,3	73217	1	14,8	1	10,0	0	0,0	0	0,0	0	0,0	1	9,3	1	8,8

1690	259017267	HLA	MHC class I antigen	6,1	21143	0	0,0	0	0,0	0	0,0	1	9,5	0	0,0	0	0,0	0	0,0
1691	259151157	TNFRSF13C	BAFF receptor	8,3	18907	1	11,2	1	10,0	0	0,0	0	0,0	0	0,0	1	9,3	1	7,9
1692	259155302	NFKB1	nuclear factor NF-kappa-B p105 subunit isoform	5,1	105337	1	10,8	1	9,8	1	9,4	1	9,5	2	12,3	1	8,8	2	19,3
1693	25990944	CLIC6	AF448439_1 chloride channel form B	4,1	73012	1	11,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1694	260436831	EPB41	protein 4.1 isoform 1	5,3	97017	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1695	260436864	AP1B1	AP-1 complex subunit beta-1 isoform c	4,8	101299	1	10,5	3	19,9	2	19,0	4	18,8	2	12,2	3	20,8	3	16,1
1696	26051218	CAMK2B	calcium/calmodulin-dependent protein kinase type II	7,0	50937	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	2	9,3	1	9,7
1697	26051229	MRPL28	39S ribosomal protein L28, mitochondrial	8,6	30139	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
1698	26051231	LACTB	serine beta-lactamase-like protein LACTB, mitochond	8,6	60675	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
1699	26051240	TNFAIP2	tumor necrosis factor alpha-induced protein 2	6,0	72643	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
1700	260763926	NT5C3A	cytosolic 5'-nucleotidase 3 isoform 3	5,4	32540	1	11,2	1	9,7	0	0,0	0	0,0	0	0,0	1	9,3	2	9,7
1701	262359947	FAM104B	protein FAM104B isoform 2	10,1	13210	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	10,5
1702	262474	CTH	cystathionine gamma-lyase	6,4	39532	1	12,5	1	10,0	0	0,0	0	0,0	0	0,0	1	8,1	1	13,6
1703	26251774	MAP7D3	MAP7D3 protein	10,0	101666	1	10,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1704	2627129	UBC	polyubiquitin	7,7	68492	3	11,4	0	0,0	0	0,0	1	9,5	0	0,0	1	8,0	0	0,0
1705	2632123	DDB1	Xeroderma Pigmentosum Group E Complementing protein	5,0	126893	2	15,8	5	29,8	1	9,3	5	28,2	2	12,3	3	16,9	2	9,7
1706	264657949	IGHV	immunoglobulin heavy chain variable region	8,8	10728	0	0,0	0	0,0	0	0,0	1	9,5	0	0,0	0	0,0	0	0,0
1707	2654381	HLA-DQB1	beta chain HLA-DQ molecule	8,1	10801	2	10,8	3	10,0	2	8,7	4	9,5	0	0,0	2	9,1	3	8,8
1708	2661752	PCK2	phosphoenolpyruvate carboxykinase (GTP)	7,4	70619	4	27,7	2	20,2	3	22,7	1	9,4	0	0,0	3	17,9	3	24,4
1709	2662099	RRP8	KIAA0409	9,8	51480	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	0	0,0
1710	2662291	CYB5B	cytochrome b5	4,6	16333	1	10,4	3	24,6	2	13,5	4	28,1	2	12,2	2	16,8	3	15,7
1711	2662381	GTBP	GTBP-ALT	8,2	121089	1	11,6	1	10,0	0	0,0	1	9,4	0	0,0	0	0,0	0	0,0
1712	266453278	ATXN10	ataxin-10 isoform 2	4,8	46287	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
1713	26996830	SDHA	SDHA protein	7,2	56635	1	13,6	3	24,7	3	18,4	4	18,8	3	12,2	5	24,5	3	21,3
1714	270047403	ENSG00000223931	immunoglobulin heavy chain variable region	8,4	11067	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
1715	270054526	IGHV1	immunoglobulin heavy chain variable region	9,0	13612	0	0,0	0	0,0	0	0,0	1	9,4	0	0,0	0	0,0	0	0,0
1716	27262630	NASP	nuclear autoantigenic sperm protein isoform 3	4,2	48786	2	16,6	7	15,1	5	13,6	5	28,1	8	24,3	3	9,1	4	16,7
1717	27262647	ATXN2L	ataxin-2-like protein isoform A	8,8	113374	1	10,3	0	0,0	1	9,3	0	0,0	0	0,0	1	9,1	1	8,8
1718	2737886	IDH3B	NAD+-specific isocitrate dehydrogenase beta precursor	8,6	42193	1	14,5	3	14,8	2	13,6	0	0,0	3	24,2	1	13,3	1	12,7
1719	27436889	POFUT1	GDP-fucose protein O-fucosyltransferase 1 isoform 1	8,6	43937	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
1720	27436901	MRPL12	39S ribosomal protein L12, mitochondrial	9,2	21330	0	0,0	0	0,0	3	19,6	1	9,5	2	12,2	1	12,2	1	8,8
1721	27436969	KCNAB2	voltage-gated potassium channel subunit beta-2 isof	8,8	39269	1	11,7	1	9,7	1	8,7	0	0,0	0	0,0	2	8,7	1	7,9
1722	2745883	LAMTOR5	hepatitis B virus X interacting protein	4,5	9596	1	11,1	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
1723	27462180	SPTBN1	AF327441_1 beta-spectrin 2 isoform 2	5,3	251419	2	16,6	4	34,6	5	41,0	2	18,9	5	36,3	6	47,0	9	76,2
1724	27477070	BTAF1	TATA-binding protein-associated factor 172	6,1	206868	0	0,0	0	0,0	0	0,0	1	9,5	0	0,0	0	0,0	0	0,0
1725	27477089	IL4I1	L-amino-acid oxidase isoform 2 precursor	8,6	65309	3	36,0	0	0,0	3	25,5	0	0,0	0	0,0	2	14,3	2	16,6
1726	27477109	ITCH	E3 ubiquitin-protein ligase Itchy homolog isoform 2	5,9	98657	0	0,0	1	17,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1727	27477134	NUP210	nuclear pore membrane glycoprotein 210 precursor	6,3	205092	1	11,2	0	0,0	0	0,0	0	0,0	2	12,2	1	8,9	2	15,7
1728	27502402	CD46	membrane cofactor protein isoform 1 precursor	6,3	43729	0	0,0	1	10,3	0	0,0	0	0,0	0	0,0	1	9,3	1	7,9
1729	27529720	ACIN1	KIAA0670 protein	5,8	145849	1	12,5	2	10,0	1	8,7	1	9,5	0	0,0	1	8,0	1	8,8
1730	2760483	WIPF1	SH3-domain interacting protein	11,7	50626	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
1731	27650504	ENSG00000223931	immunoglobulin heavy chain variable region	8,6	8778	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
1732	27694308	DNAJC13	DNAJC13 protein, partial	10,0	88954	0	0,0	0	0,0	1	8,7	1	9,5	0	0,0	1	8,1	1	9,7
1733	2769647	F5	coagulation factor V (proaccelerin, labile factor)	5,6	251656	5	45,6	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	1	8,8
1734	27753243	ENSG00000223931	immunoglobulin heavy chain variable region	9,3	13297	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
1735	27753455	ENSG00000223931	immunoglobulin heavy chain variable region	7,9	13207	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7	0	0,0
1736	27765085	CAST	calpastatin isoform b	4,7	74067	1	13,1	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1737	2780414	ACOT7	brain acyl-CoA hydrolase	6,9	37420	1	11,1	0	0,0	1	8,7	0	0,0	2	12,2	1	8,0	1	8,8
1738	27881506	ABCF2	ATP-binding cassette sub-family F member 2 isoform	7,0	71272	2	21,9	1	9,7	0	0,0	0	0,0	0	0,0	1	9,3	1	12,9
1739	27886529	ATP2A1	sarcoplasmic/endoplasmic reticulum calcium ATPase 1	4,9	110234	0	0,0	0	0,0	1	9,9	0	0,0	0	0,0	2	8,9	0	0,0
1740	27886568	IFIH1	interferon-induced helicase C domain-containing pro	5,3	116670	0	0,0	0	0,0	1	9,9	0	0,0	0	0,0	0	0,0	1	7,9
1741	28071028	LGMN	unnamed protein product	5,7	42008	1	9,7	1	9,7	1	9,3	0	0,0	2	12,2	1	9,7	0	0,0
1742	28071074	LGALS3	unnamed protein product	9,6	13898	1	10,5	1	10,0	2	17,2	1	9,4	0	0,0	2	12,6	1	8,8
1743	2808991	ENSG00000223931	Ig heavy chain variable region	5,6	8768	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1744	2809488	COX4I1	cytochrome c oxidase subunit IV	9,7	16863	2	22,9	2	19,3	1	9,3	5	28,1	0	0,0	1	12,1	3	15,4
1745	28173564	KRT73	keratin, type II cytoskeletal 73	7,0	58924	1	13,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1746	28178838	IDH3G	isocitrate dehydrogenase [NAD] subunit gamma, mitochondrial	9,0	41450	1	10,7	2	15,1	0	0,0	1	9,5	2	12,2	1	9,4	1	9,7
1747	28193204	ACTN1	unnamed protein product	5,9	61737	3	23,7	4	34,5	9	45,0	7	37,5	6	36,3	5	30,1	9	47,9
1748	28195394	HIST2H2AB	histone H2A type 2-B	11,3	13996	5	14,5	9	14,9	10	18,5	6	9,5	15	24,3	9	12,3	8	16,1
1749	28207879	ZC3H14	unnamed protein product	7,1	73207	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
1750	28243	FLNA	unnamed protein product	5,7	280760	21	175,4	2	19,9	0	0,0	6	46,8	29	204,6	1	11,7	2	20,1
1751	28273130	RASAL3	FLJ00412 protein	7,6	82120	2	19,3	0	0,0	0	0,0	0	0,0	0	0,0	1	8,7	2	9,7
1752	28277071	IPO5	Importin 5	4,7	125588	2	18,0	3	24,7	2	14,1	4	28,1	2	21,8	2	14,7	4	27,1

1753	28279298	EPRS	EPRS protein, partial	6,3	37179	0	0,0	1	9,7	0	0,0	1	9,5	0	0,0	1	8,1	0	0,0
1754	2832731	GSTZ1	maleylacetoacetate isomerase	8,4	24084	0	0,0	0	0,0	1	9,8	0	0,0	0	0,0	1	9,8	0	0,0
1755	28336	PS1TP5BP1	mutant beta-actin (beta'-actin)	5,1	41814	309	135,7	239	108,0	198	93,0	161	121,4	179	132,6	186	107,4	247	118,1
1756	283549153	ANKRD18A	ankyrin repeat domain-containing protein 18A	7,7	115578	1	9,6	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1757	28372509	CCDC50	coiled-coil domain-containing protein 50 short isof	6,2	35804	1	10,8	0	0,0	0	0,0	1	9,5	0	0,0	1	9,4	2	15,8
1758	28374365	CARM1	CARM1 protein, partial	6,1	42717	1	10,7	2	10,4	0	0,0	0	0,0	0	0,0	1	8,7	1	8,8
1759	28375599	DLST	unnamed protein product	8,4	29626	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
1760	28376621	SEC14L4	SEC14-like protein 4 isoform a	6,1	46644	1	11,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1761	284444053	HLA	MHC class I antigen	5,2	31591	2	11,8	1	9,7	2	8,7	0	0,0	5	12,2	2	9,3	2	10,6
1762	284795266	SRPRB	signal recognition particle receptor subunit beta	9,4	29684	2	12,4	0	0,0	0	0,0	0	0,0	2	12,2	1	8,0	0	0,0
1763	284944680	HLA	MHC class I antigen	5,6	21097	1	10,9	0	0,0	1	8,8	0	0,0	0	0,0	3	9,4	0	0,0
1764	28557709	PRPS1L1	ribose-phosphate pyrophosphokinase 3	5,9	34821	0	0,0	0	0,0	0	0,0	1	9,5	2	12,2	2	9,1	2	16,1
1765	28590	ALB	unnamed protein product	5,9	69296	0	17,7	1	15,9	0	14,8	0	15,1	0	19,4	0	13,8	0	15,4
1766	28595	ALDOA	aldolase A protein	9,1	11939	9	35,9	9	44,7	6	22,1	6	18,8	12	60,3	4	20,5	4	26,7
1767	285999	SF3B3	KIAA0017	5,1	44606	1	11,4	3	19,4	1	9,9	1	9,5	0	0,0	1	12,6	1	11,7
1768	286009	KIAA0020	KIAA0020	9,1	57509	0	0,0	1	10,3	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
1769	28703670	TTLL2	Tubulin tyrosine ligase-like family, member 2	8,9	67218	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1770	28723	ACTN1	alpha-actinin	4,9	68763	4	11,5	3	10,0	3	13,5	4	9,5	5	12,2	3	9,0	4	13,4
1771	288100	EIF4B	initation factor 4B	5,3	69225	2	15,9	1	10,1	3	22,1	2	9,5	3	12,2	4	12,9	2	7,9
1772	28827795	CHMP4B	charged multivesicular body protein 4b	4,6	24932	0	0,0	1	10,0	0	0,0	1	9,5	0	0,0	1	9,3	1	10,6
1773	28839039	MGEA5	MGEA5 protein, partial	4,6	67852	0	0,0	1	9,8	1	9,9	0	0,0	0	0,0	1	8,9	0	0,0
1774	28839044	SEC31A	SEC31A protein	6,1	56732	0	0,0	1	9,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1775	288567	TOP2B	DNA topoisomerase II	8,6	44943	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
1776	28862	YWHAH	AS1	4,9	22940	1	11,2	0	0,0	1	9,9	0	0,0	0	0,0	1	8,9	0	0,0
1777	28872725	PSMD11	26S proteasome non-ATPase regulatory subunit 11	6,1	47445	1	15,3	1	10,0	1	8,7	2	18,8	0	0,0	3	25,8	2	22,3
1778	28872734	MRPL43	39S ribosomal protein L43, mitochondrial isoform a	10,2	17835	1	10,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
1779	28872792	CDK5RAP3	CDK5 regulatory subunit-associated protein 3	4,5	56902	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
1780	28931	HEL	beta-subunit (AA 1-312)	4,8	34048	1	13,1	0	0,0	3	9,9	0	0,0	0	0,0	0	0,0	0	0,0
1781	28940	HEL	unnamed protein product	5,8	57956	63	181,2	65	172,8	59	177,6	58	158,6	63	202,2	61	167,4	46	164,0
1782	289577080	EIF4G2	eukaryotic translation initiation factor 4 gamma 2	6,7	102343	1	11,2	1	10,0	0	0,0	0	0,0	0	0,0	1	9,7	0	0,0
1783	28958118	SMC3	Structural maintenance of chromosomes 3	6,8	141489	1	11,7	0	0,0	1	8,7	0	0,0	0	0,0	1	8,0	1	7,9
1784	2896146	ALYREF	transcriptional coactivator ALY, partial	12,0	24467	0	0,0	0	0,0	1	9,8	0	0,0	0	0,0	1	9,3	0	0,0
1785	29028316	PPIA	AF022115_1 cyclophilin	8,0	17972	38	61,4	16	49,5	14	36,7	6	28,1	25	72,4	16	51,0	10	34,6
1786	290543591	YTHDF2	YTH domain family protein 2 isoform 2	9,3	56859	0	0,0	1	10,0	1	8,7	1	9,5	0	0,0	1	8,0	1	9,7
1787	2909856	NDUFA6	NADH-ubiquinone oxidoreductase subunit CI-B14	10,4	15118	0	0,0	1	10,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1788	291045307	AAAS	aladin isoform 2	7,0	55815	1	10,5	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1789	29126903	EED	EED protein, partial	7,0	48766	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1790	29171702	PPA2	inorganic pyrophosphatase 2, mitochondrial isoform	7,1	37902	1	11,0	2	10,0	0	0,0	2	18,8	0	0,0	3	17,5	3	21,8
1791	293336691	HDAC2	histone deacetylase 2	5,5	55365	1	11,1	0	0,0	0	0,0	2	18,8	0	0,0	1	8,7	2	19,3
1792	29373940	CDC42BPA	CDC42 binding protein kinase alpha (DMPK-like)	6,0	195931	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	1	9,7
1793	29383	RPL13	BBC1	12,2	24292	2	20,9	2	14,7	2	17,2	2	18,7	2	12,2	2	15,9	3	16,6
1794	29421172	CROCC	KIAA0445 protein	5,5	217830	1	20,0	0	16,4	1	9,8	0	0,0	0	0,0	1	14,3	0	0,0
1795	294357246	HLA	MHC class I antigen	6,2	20921	0	0,0	2	10,4	0	0,0	0	0,0	0	0,0	2	8,1	0	0,0
1796	29436380	MYH9	MYH9 protein	5,7	158752	35	195,5	61	206,9	76	261,3	58	251,8	83	324,8	61	246,2	52	214,6
1797	29476889	JPH1	JPH1 protein, partial	9,8	60098	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
1798	2959876	SYNGR2	synaptogyrin 2	6,8	18009	1	11,3	0	0,0	1	9,9	0	0,0	0	0,0	1	9,7	0	0,0
1799	296040438	UGDH	UDP-glucose 6-dehydrogenase isoform 3	7,6	44396	1	14,4	0	0,0	0	0,0	0	0,0	0	0,0	1	9,4	0	0,0
1800	296080770	PAFAH1B2	platelet-activating factor acetylhydrolase IB s	4,8	14870	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	1	8,0	1	8,8
1801	296179429	HADH	hydroxyacyl-coenzyme A dehydrogenase, mitochondria	9,3	34259	3	16,0	9	29,8	4	22,7	8	46,8	11	60,4	5	35,4	6	28,3
1802	296317244	ESYT1	extended synaptotagmin-1 isoform 1	5,4	123984	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1803	296317337	VDAC2	voltage-dependent anion-selective channel prote	7,5	33353	7	32,8	4	18,9	5	18,4	1	9,5	0	0,0	5	21,5	4	19,3
1804	296434312	FLAD1	FAD synthase isoform 4	5,4	32370	1	12,5	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1805	29653	NUP214	putative oncogene	7,0	213766	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,8
1806	296736	PSMA6	macropain subunit iota	5,5	24581	3	11,2	0	0,0	0	0,0	1	9,5	0	0,0	1	9,5	0	0,0
1807	2969905	DSCR3	hypothetical protein	9,5	28388	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
1808	29708	CTSH	cathepsin H	6,9	27350	1	11,6	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,8
1809	29725611	PPP2R4	serine/threonine-protein phosphatase 2A activator i	5,9	36757	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,8	0	0,0
1810	29788768	TUBB2B	tubulin beta-2B chain	4,6	49954	1	11,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1811	29788785	TUBB	tubulin beta chain	4,6	49672	4	11,5	5	10,0	8	9,3	6	9,5	9	12,2	7	9,1	8	9,7
1812	29789409	NDUFAF2	mimitin, mitochondrial	9,4	19857	1	11,1	2	10,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1813	297906	RBBP4	IEF SSP 9306	4,8	46159	2	10,6	1	9,8	2	9,3	0	0,0	2	12,2	1	8,7	1	8,9
1814	29791717	PDCD6	PDCD6 protein	4,6	5737	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
1815	29826282	PPM1G	protein phosphatase 1G	4,1	59272	2	13,6	1	9,8	1	9,3	0	0,0	0	0,0	2	12,2	2	12,3

1816	29826287	MRPL47	39S ribosomal protein L47, mitochondrial isoform a	10,8	29432	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	2	8,0	1	7,9
1817	29826319	ADD1	alpha-adducin isoform a	5,5	80956	0	0,0	0	0,0	0	0,0	1	9,5	0	0,0	0	0,0	0	0,0
1818	29836823	ENSG00000228325	immunoglobulin kappa light chain variable region	8,8	9007	1	11,4	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1819	29837086	ENSG00000223931	immunoglobulin heavy chain	9,4	11971	0	0,0	0	0,0	0	0,0	1	9,4	0	0,0	0	0,0	0	0,0
1820	2984585	STOML2	P1.11659_4	6,4	38750	4	37,7	2	14,8	4	29,3	2	18,8	2	12,2	3	18,0	2	12,9
1821	2996631	MX2	MX2	5,2	28686	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1822	2996644	MX2	MX2	9,2	49855	2	13,9	1	10,0	0	0,0	2	9,5	0	0,0	0	0,0	1	7,9
1823	2996650	KIAA0324	KIAA0324	12,4	191307	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	1	9,6
1824	30009	HMGCS1	Hydroxymethylglutaryl CoA Synthase	5,2	57352	1	10,6	0	0,0	1	9,9	0	0,0	2	12,3	0	0,0	0	0,0
1825	30023820	FAM134C	protein FAM134C	4,7	51397	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1826	300360547	SRSF10	serine/arginine-rich splicing factor 10 isoform	11,7	31195	1	10,7	2	19,9	1	9,8	2	18,8	0	0,0	1	12,6	1	12,7
1827	30039710	PTF1A	pancreas transcription factor 1 subunit alpha	5,0	34952	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1828	30059150	ATP2A2	sarco/endoplasmic reticulum calcium ATPase 2c	4,7	5312	1	10,8	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7	0	0,0
1829	30076	COL4A2	unnamed protein product	9,3	100676	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7	0	0,0
1830	30130	SERPINH1	colligin	8,5	46268	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
1831	30153	COX6A1P2	unnamed protein product	6,5	9751	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	2	9,7
1832	301897469	ENO3	beta-enolase isoform 1	7,6	46988	30	20,6	8	18,9	12	16,6	11	9,5	12	21,9	18	16,2	19	12,3
1833	3021396	ATP2A3	sarco/endoplasmic reticulum Ca2+ -ATPase	5,5	112495	1	11,1	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1834	30268331	MYH9	hypothetical protein	5,8	154161	7	66,6	4	39,3	10	51,3	19	65,4	11	60,3	11	70,4	9	70,2
1835	30293	CTPS1	unnamed protein product	5,9	66706	2	10,5	2	14,8	6	18,4	2	9,5	5	24,2	4	20,6	4	19,2
1836	303398863	HLA	MHC class I antigen	5,5	31656	1	13,5	1	9,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1837	30354553	TYMP	TYMP protein	5,2	49982	2	11,7	5	19,6	3	18,4	1	9,5	3	24,3	5	23,4	3	18,1
1838	30377	KRT13	cytokeratin 13	4,7	45866	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1839	30410796	PSME3	proteasome activator complex subunit 3 isoform 2	5,7	30868	1	17,8	1	10,3	0	0,0	1	16,9	0	0,0	0	0,0	1	9,8
1840	3041847	OSBP2	OXYSTEROL-BINDING PROTEIN-like; similar to P22059 (PID	5,8	64307	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
1841	30425510	ZBTB8OS	protein archease	4,3	20676	1	12,5	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1842	3043658	OPA1	KIAA0567 protein	8,1	113518	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	1	9,3	1	8,8
1843	304562926	IGHG3	immunoglobulin gamma 1 heavy chain variable region	9,6	13430	0	0,0	0	0,0	1	8,6	0	0,0	0	0,0	0	0,0	0	0,0
1844	304563956	IGHV5	immunoglobulin gamma 4 heavy chain variable region	9,4	14697	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1845	30506	DSG1	desmoglein type 1	4,8	113716	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
1846	30524	DLAT	dihydrolipoamide S-acetyltransferase	10,3	23398	1	9,7	0	0,0	1	8,7	0	0,0	0	0,0	1	9,0	1	8,8
1847	30578418	SFXN2	sideroflexin-2	9,7	36233	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1848	30582349	SEC23IP	Sec23-interacting protein p125	4,8	53154	1	10,7	1	10,0	0	0,0	0	0,0	0	0,0	1	8,7	1	13,6
1849	30583475	DIAPH1	diaphanous homolog 1 (Drosophila)	5,3	46323	0	0,0	1	10,0	1	9,8	1	9,4	0	0,0	1	8,0	1	7,9
1850	306417189	HLA	MHC class I antigen	5,5	31728	1	10,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1851	306480793	HLA	MHC class I antigen	6,1	10793	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
1852	306517857	HLA	MHC class I antigen	5,7	21003	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	2	9,7
1853	3068550	CAST	testis calpastatin	4,5	47086	1	11,6	2	10,0	1	8,7	1	9,5	0	0,0	1	9,4	2	9,7
1854	306891	HSP90AB1	90kDa heat shock protein	4,8	83295	128	179,0	82	154,7	59	144,7	63	128,8	72	202,2	65	142,1	84	144,7
1855	306896	ICAM1	intercellular adhesion molecule-1 precursor	7,5	57808	1	12,4	0	0,0	0	0,0	0	0,0	0	0,0	2	17,9	1	7,9
1856	307263	HLA	MHC HLA DR5 cell surface glycoprotein beta chain precur	6,8	30142	0	0,0	1	18,5	2	9,3	5	18,8	0	0,0	1	8,9	0	0,0
1857	307548326	HLA	MHC class I antigen	5,4	31531	2	12,6	2	10,4	0	0,0	0	0,0	0	0,0	0	0,0	2	12,0
1858	30794376	DOLPP1	dolichyldiphosphatase 1 isoform a	9,7	27031	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
1859	30802081	APOB	APOB protein	7,1	92334	1	17,9	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1860	308044580	HSDL2	hydroxysteroid dehydrogenase-like protein 2 iso	5,8	37302	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,9	0	0,0
1861	30866	SRPR	unnamed protein product	9,2	69925	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
1862	308827082	HLA	MHC class I antigen	5,5	31732	3	12,0	5	10,1	3	9,3	2	9,5	0	0,0	4	8,7	4	9,7
1863	3088340	RPS20	ribosomal protein S20	11,1	6858	4	11,5	3	10,0	3	9,3	2	9,5	3	12,2	2	9,0	3	9,7
1864	3088341	RPS21	ribosomal protein S21	9,9	5968	1	11,5	2	10,0	2	14,1	2	18,8	3	24,2	2	14,9	2	15,5
1865	3088347	RPL9	ribosomal protein L9	4,3	5152	2	13,8	1	10,3	1	9,8	4	18,8	3	24,2	1	8,9	0	0,0
1866	30885	HLA	unnamed protein product	6,8	30183	1	11,4	2	10,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
1867	30908859	ACTA1	actin alpha 1 skeletal muscle protein	5,7	28152	17	11,6	22	18,2	20	22,7	20	9,5	15	12,3	20	9,0	22	12,0
1868	310118015	HLA	PREDICTED: HLA class II histocompatibility anti	5,1	27919	0	0,0	2	10,0	0	0,0	2	9,5	0	0,0	0	0,0	0	0,0
1869	310923127	NME2	nucleoside diphosphate kinase B isoform b	10,1	9565	1	11,6	2	19,3	2	8,7	2	9,5	0	0,0	1	8,0	2	7,9
1870	311771525	RBM14	RNA-binding protein 14 isoform 2	8,9	17099	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	1	11,4
1871	311771535	CCT2	T-complex protein 1 subunit beta isoform 2	6,0	52699	8	45,2	8	59,1	8	45,8	7	46,8	11	72,3	9	65,0	7	46,7
1872	311771639	CUL2	cullin-2 isoform a	6,7	89492	0	0,0	0	0,0	0	0,0	1	9,4	0	0,0	0	0,0	1	7,9
1873	31179	ENO1	enolase	5,7	49478	10	25,8	13	29,8	12	27,6	12	28,2	18	36,3	12	26,9	12	28,8
1874	31221	MAPK3	protein serine/threonine kinase	6,3	43110	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,0	0	0,0
1875	312395	ADRBK2	beta-adrenergic kinase 2	7,4	79678	0	0,0	0	0,0	0	0,0	1	9,4	0	0,0	1	9,3	1	9,7
1876	312596881	PSMC5	26S protease regulatory subunit 8 isoform 2	8,3	44766	0	0,0	1	9,7	0	0,0	2	18,8	2	12,2	1	9,0	1	7,9
1877	3126984	RPL14	CAG-isl 7	11,4	23291	2	11,4	1	10,3	3	18,4	4	18,8	6	24,2	3	18,0	1	9,7
1878	312812	PCCB	propionyl-CoA carboxylase	7,4	58206	1	12,4	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0

1879	31283	HEL	unnamed protein product	5,9	69399	19	75,9	30	103,5	26	94,2	26	121,3	37	96,4	26	71,0	27	69,3
1880	312922364	UCHL5	ubiquitin carboxyl-terminal hydrolase isozyme L	5,0	36061	0	0,0	1	9,7	1	8,7	0	0,0	0	0,0	1	8,0	1	7,9
1881	313002	HLA	RING7	7,2	28944	1	11,2	1	10,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1882	313014	ATP6V1E1	vacuolar proton ATPase	8,9	26231	1	10,7	0	0,0	1	9,3	1	9,5	0	0,0	1	9,6	1	9,7
1883	31377644	ATAD1	ATPase family AAA domain-containing protein 1	6,5	40726	0	0,0	0	0,0	1	8,6	1	9,5	0	0,0	0	0,0	0	0,0
1884	31415882	EXOSC8	exosome complex component RRP43	5,0	30040	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
1885	31418053	CCT8	CCT8 protein	5,0	54107	4	48,1	8	44,4	6	32,4	13	84,0	8	48,3	9	55,9	5	39,7
1886	31418096	MTHFD2	Methylenetetrahydrofolate dehydrogenase (NADP+ depend	6,8	26831	1	11,3	2	14,9	1	8,7	1	9,5	0	0,0	0	0,0	2	15,8
1887	31422	ITGAL	unnamed protein product	5,3	128850	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
1888	31455238	HNRNPA2B1	HNRNPA2B1 protein	4,6	28413	1	17,7	3	15,1	6	9,3	13	9,5	6	12,3	5	11,7	8	12,3
1889	31455559	IST1	putative MAPK activating protein	5,1	39751	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,8	0	0,0
1890	3152938	SNX2	sorting nexin 2	4,9	58536	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1891	31542980	IFIT3	interferon-induced protein with tetratricopeptide r	5,0	55966	0	0,0	0	0,0	0	0,0	2	18,8	2	12,2	0	0,0	1	9,7
1892	31543380	HEL	protein DJ-1	6,4	19892	2	17,1	2	10,0	8	27,6	1	9,4	3	12,2	2	14,8	2	16,0
1893	31543385	PCYT1A	choline-phosphate cytidylyltransferase A	6,9	41713	0	0,0	1	10,3	1	8,7	0	0,0	0	0,0	1	8,0	0	0,0
1894	315434216	DAP3	28S ribosomal protein S29, mitochondrial isofor	9,3	41026	0	0,0	0	0,0	1	9,3	0	0,0	0	0,0	0	0,0	0	0,0
1895	315434223	AK3	GTP:AMP phosphotransferase, mitochondrial isofo	9,2	18174	1	11,1	0	0,0	2	17,3	0	0,0	0	0,0	5	18,6	2	9,8
1896	315488014	ENSG00000228325	immunoglobulin variable region	8,8	11724	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,8	0	0,0
1897	3157976	ACTN4	alpha actinin	5,4	105225	0	0,0	1	10,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1898	31621305	LRPPRC	leucine-rich PPR motif-containing protein, mitochon	5,7	157886	4	37,9	4	39,6	10	72,0	6	37,5	9	60,3	6	52,1	9	71,6
1899	31645	HEL	glyceraldehyde-3-phosphate dehydrogenase	8,4	36036	10	30,8	6	19,9	10	27,6	10	28,1	15	36,3	9	23,8	6	19,2
1900	3165457	LY75	DEC-205	6,2	198271	1	16,6	1	10,0	0	0,0	0	0,0	0	0,0	2	18,5	2	15,5
1901	31657179	EDC4	EDC4 protein	5,5	129725	1	9,7	0	0,0	1	8,7	0	0,0	0	0,0	1	8,1	1	9,7
1902	3169010	EIF5B	putative GTP-binding protein	6,2	43810	1	11,2	1	9,7	1	12,7	0	0,0	2	12,2	2	14,8	2	13,6
1903	3169770	IGKV1	immunoglobulin kappa light chain	8,1	23052	0	0,0	0	0,0	3	9,9	0	0,0	0	0,0	1	9,8	0	0,0
1904	31711992	DLAT	dihydrolipoyllysine-residue acetyltransferase compo	7,8	68978	0	0,0	0	0,0	1	8,7	0	0,0	2	12,2	1	8,1	1	7,9
1905	31747519	EIF2AK2	interferon-inducible double-stranded RNA-dependent pr	8,2	57460	1	10,4	1	9,7	1	8,7	0	0,0	0	0,0	0	0,0	1	9,7
1906	31815	GLUD2	glutamate dehydrogenase (NAD(P)+)	8,7	61434	4	38,1	1	10,0	3	22,7	0	0,0	0	0,0	4	32,9	1	12,8
1907	31853	GM2A	G(M2) activator protein	5,0	19355	2	10,5	1	9,7	0	0,0	1	9,5	0	0,0	0	0,0	0	0,0
1908	31873228	NUDT21	hypothetical protein	8,9	26213	0	0,0	0	0,0	0	0,0	1	9,5	0	0,0	1	8,0	0	0,0
1909	31873262	ACOX1	hypothetical protein	7,3	75286	0	0,0	1	10,1	1	8,7	1	9,5	0	0,0	1	8,9	0	0,0
1910	31873364	HEL	hypothetical protein	8,0	33110	0	0,0	1	10,3	1	15,5	0	0,0	0	0,0	1	8,0	0	0,0
1911	31873441	PFKM	hypothetical protein	8,8	12456	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
1912	31873449	CDK5RAP2	hypothetical protein	5,3	183124	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
1913	31874034	CISD2	hypothetical protein	9,8	16794	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
1914	31874548	FKBP8	hypothetical protein	4,8	48637	0	0,0	0	0,0	0	0,0	1	9,4	0	0,0	0	0,0	0	0,0
1915	31874767	ZNF829	hypothetical protein	6,7	60886	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7	0	0,0
1916	31958	EPRS	glutaminyl-tRNA synthetase	7,5	163026	4	33,1	4	29,8	3	27,0	4	28,1	3	24,2	5	34,2	4	35,7
1917	31979	HIST1H2BO	histone H2A.2	10,6	13908	3	11,5	4	10,0	2	9,3	2	9,5	5	12,2	2	9,0	2	9,7
1918	32015	TUBA4A	alpha-tubulin	4,8	49794	2	19,2	0	0,0	2	14,1	4	18,8	3	24,2	2	14,9	1	10,5
1919	320461539	ADK	adenosine kinase isoform d	6,3	34085	0	0,0	2	10,0	2	8,7	0	0,0	0	0,0	1	9,3	1	7,9
1920	3205175	DRB1	HLA-D class II antigen DR1 beta chain	6,5	10919	7	26,1	5	15,1	5	18,4	7	9,5	3	24,2	4	17,9	6	15,4
1921	32055	HCLS1	unnamed protein product	4,6	53999	7	51,7	10	54,4	8	50,1	4	28,1	8	48,3	5	38,9	7	39,5
1922	32080	RAP1GDS1	smg GDS	5,2	61124	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	1	8,1	1	7,9
1923	321117084	RPS10	RPS10-NUDT3 protein	9,6	33142	0	0,0	3	10,0	5	9,3	4	9,5	2	12,2	3	9,1	4	9,7
1924	32129209	RAP2C	ras-related protein Rap-2c isoform 1 precursor	4,7	20727	0	0,0	0	0,0	0	0,0	0	0,0	2	12,2	1	9,8	0	0,0
1925	32132	CD74	unnamed protein product	8,5	24376	8	19,8	4	10,1	3	17,6	1	9,5	3	12,2	2	9,0	2	9,7
1926	32139	HLA	unnamed protein product	5,7	40938	0	0,0	0	0,0	4	8,7	0	0,0	0	0,0	2	9,3	0	0,0
1927	3217034	SCO2	unnamed protein product	8,8	29752	1	9,6	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1928	32171238	BAIAP2L1	brain-specific angiogenesis inhibitor 1-associated	8,9	56864	1	11,2	2	10,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1929	32189371	TMEM165	transmembrane protein 165 precursor	6,6	34907	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,1	0	0,0
1930	32189392	HEL	peroxiredoxin-2 isoform a	5,6	21893	1	14,1	2	10,0	4	18,5	2	9,5	9	36,3	4	18,0	3	16,1
1931	3219284	PSME1	PA28 alpha subunit	5,4	8678	4	17,6	5	15,1	5	23,3	2	18,8	6	24,2	4	18,5	3	25,8
1932	32235	HLA	HLA class I heavy chain	6,0	40996	0	0,0	0	0,0	2	13,5	0	0,0	0	0,0	3	14,7	0	0,0
1933	3228279	ABCB7	ABC transporter 7 protein	9,6	82481	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	1	8,7	0	0,0
1934	32306873	IRF2BP2	interferon regulatory factor-2 binding protein 2A	8,8	61080	1	12,4	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1935	32307117	PPP2R2B	serine/threonine-protein phosphatase 2A 55 kDa regu	6,6	51998	2	16,5	1	10,3	2	9,3	2	9,4	3	12,2	1	9,0	1	9,7
1936	32307161	CUL1	cullin-1	7,9	89679	0	0,0	0	0,0	1	9,9	1	9,5	0	0,0	0	0,0	1	7,9
1937	32335	HMGB2	HMG2B	5,9	21404	2	21,7	4	29,7	5	30,2	4	28,1	6	48,3	4	34,2	4	37,1
1938	323432701	IGKV3	immunoglobulin variable region	8,4	18043	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	1	9,7
1939	323433041	ENSG00000228325	immunoglobulin variable region	9,5	17296	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	0	0,0
1940	32356	HNRNPL	unnamed protein product	6,7	60188	3	19,5	5	29,8	7	32,4	6	37,5	6	24,2	4	21,3	5	21,9
1941	32358	HNRNPU	hnRNP U protein	5,5	88946	18	91,5	11	49,3	13	54,4	12	56,2	20	72,5	10	45,5	15	65,6

1942	32425777	COPG1	COPG protein, partial	5,0	78156	1	13,1	1	10,0	2	17,3	1	9,4	3	24,2	2	18,1	1	12,3
1943	32450330	EPS15	EPS15 protein	4,4	83673	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,8
1944	32455248	PIK3R1	phosphatidylinositol 3-kinase regulatory subunit al	5,8	83580	1	11,7	2	10,0	1	8,7	0	0,0	0	0,0	0	0,0	1	7,9
1945	324711029	ALOX5AP	arachidonate 5-lipoxygenase-activating protein	8,2	24190	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1946	32479521	DVL1	segment polarity protein dishevelled homolog DVL-1	7,1	72863	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
1947	32483374	NOP56	nucleolar protein 56	9,6	66050	1	16,4	3	20,2	5	28,1	4	28,1	2	12,2	3	23,9	3	30,8
1948	32483377	PRDX3	thioredoxin-dependent peroxide reductase, mitochond	7,2	25820	1	11,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1949	32484979	AP3B1	AP-3 complex subunit beta-1 isoform 1	5,7	121301	1	12,5	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1950	32486	HSP90AA1	unnamed protein product	4,4	35761	45	107,7	68	67,0	21	66,6	35	54,3	43	118,1	29	78,5	47	84,6
1951	32488	HSP90AA1	unnamed protein product	4,8	84674	27	76,7	23	74,0	26	86,6	26	65,4	26	108,4	25	65,3	24	70,1
1952	32528301	EPHB4	ephrin type-B receptor 4 precursor	6,5	108270	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	17,4
1953	325301072	SSR4	translocon-associated protein subunit delta iso	5,5	20195	7	28,9	5	24,9	3	23,2	2	18,8	3	24,2	3	14,9	3	19,8
1954	32532	RPS3	unnamed protein product	10,0	26721	1	11,8	1	10,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1955	32628	ICAM3	ICAM-3	5,2	59384	0	0,0	1	10,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1956	32698886	ZNF595	zinc finger protein 595	9,3	74303	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1957	3283998	HK1	testis-specific hexokinase 1	6,5	13034	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7	1	9,8
1958	3288815	CS	citrate synthase	8,1	51707	3	30,9	1	9,7	3	22,7	5	28,1	3	24,2	3	25,3	3	27,6
1959	328942890	IGHV	immunoglobulin heavy chain variable region	8,2	12975	0	0,0	0	0,0	0	0,0	2	9,5	0	0,0	0	0,0	0	0,0
1960	329581693	HLA	MHC class II antigen	5,0	10904	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,6	1	8,0
1961	329581711	HLA	MHC class II antigen	6,4	10656	1	11,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1962	329581893	HLA	MHC class I antigen	6,4	38306	1	13,1	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1963	33096717	FECH	hypothetical protein	8,7	47133	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
1964	331284172	SH3GLB1	endophilin-B1 isoform 3	5,4	43197	1	11,4	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
1965	33150544	ACTR3B	AF086920_1 actin related protein ARP4	5,8	45389	1	12,1	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1966	33150556	EVL	AF087843_1 B6	9,2	44820	1	10,4	1	10,0	1	9,8	0	0,0	0	0,0	1	9,4	1	9,7
1967	33150698	SRRT	AF112994_1 arsenite-resistance protein ARS2	8,1	25496	1	10,9	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1968	33150748	DDX24	AF134475_1 ATP-dependent RNA helicase	10,1	55969	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	1	9,3	1	9,7
1969	33150750	NDUFB11	AF134476_1 neuronal protein	5,2	17943	0	0,0	0	0,0	1	10,0	0	0,0	0	0,0	1	9,8	0	0,0
1970	33150758	CAB39	AF134480_1 MO25-like protein	7,3	39775	0	0,0	1	10,0	0	0,0	0	0,0	0	0,0	1	8,7	0	0,0
1971	33150792	DDX24	AF145022_1 ATP-dependent RNA helicase	10,0	52691	1	11,2	4	14,8	0	0,0	0	0,0	0	0,0	2	8,1	0	0,0
1972	33188449	SRPK2	SRSF protein kinase 2 isoform a	5,0	79029	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
1973	33188456	UBE2D2	ubiquitin-conjugating enzyme E2 D2 isoform 2	8,4	13617	1	12,5	0	0,0	0	0,0	1	9,4	0	0,0	0	0,0	1	7,9
1974	3319956	HNRNPUL1	E1B-55kDa-associated protein	6,5	95810	0	0,0	1	9,7	3	17,3	0	0,0	0	0,0	2	18,5	1	7,9
1975	33239443	SYPL1	synaptophysin-like protein 1 isoform b	7,0	26394	1	10,5	1	10,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1976	33239445	EIF3B	eukaryotic translation initiation factor 3 subunit	4,7	92463	2	19,3	3	24,7	2	14,1	6	46,8	2	12,2	3	20,7	2	18,0
1977	33286418	HEL	pyruvate kinase isozymes M1/M2 isoform a	7,7	57919	147	186,7	87	192,8	119	155,4	95	186,6	114	204,6	121	155,4	100	148,4
1978	33286446	OGFR	opioid growth factor receptor	4,6	73325	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
1979	3329388	TECR	synaptic glycoprotein SC2	9,6	18190	1	11,2	0	0,0	1	9,3	0	0,0	0	0,0	1	8,0	1	9,7
1980	333069600	HLA	MHC class I antigen	6,5	21055	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
1981	33317800	FP3420	AF461898_1 Unknown	9,2	15412	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1982	33327376	CMYA5	unknown protein	4,5	103382	1	12,5	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1983	33337544	SRP72	AF038851_1 putative signal recognition particle	9,6	74589	2	15,3	4	29,5	1	10,0	0	0,0	3	24,3	1	11,7	0	0,0
1984	33337571	EIF2B4	AF057699_1 EIF-2B-delta-like protein	9,7	57555	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
1985	33338074	SMC1A	AF176781_1 MSTP142	10,1	23287	0	0,0	1	10,3	1	9,8	0	0,0	0	0,0	1	9,5	1	9,7
1986	33338090	MST133	MSTP133	5,2	16135	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
1987	33340565	SPTBN4	AF324063_1 non-erythrocytic beta-spectrin 4	5,7	289041	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
1988	33356170	MYO9B	unconventional myosin-IXb isoform 1	8,9	243400	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
1989	333796178	HLA	MHC class II antigen, partial	5,6	21521	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
1990	33413400	ESD	S-formylglutathione hydrolase	6,6	31464	1	14,6	1	10,3	1	9,3	0	0,0	3	12,2	2	11,7	1	8,8
1991	33413435	BID	BID S	4,7	14621	1	10,6	1	10,1	1	9,3	1	9,6	2	12,3	1	9,1	1	9,8
1992	3342564	UBA3	UBA3	5,2	49343	0	0,0	1	9,7	1	9,8	0	0,0	0	0,0	1	9,7	0	0,0
1993	334353017	HLA	MHC class I antigen	5,8	37931	0	0,0	2	10,1	0	0,0	0	0,0	2	12,2	2	9,4	0	0,0
1994	33440520	DIS3	DIS3 mitotic control homolog (S. cerevisiae)	6,8	109039	0	0,0	1	10,0	1	8,7	0	0,0	0	0,0	0	0,0	1	9,7
1995	33451	IGHM	unnamed protein product	5,8	68511	1	10,9	10	29,8	12	36,7	10	28,1	15	48,3	13	32,7	8	25,6
1996	33457348	MYDGF	UPF0556 protein C19orf10 precursor	6,2	18796	3	22,2	1	10,0	2	8,7	0	0,0	0	0,0	2	27,7	1	15,3
1997	33469917	MCM4	DNA replication licensing factor MCM4	6,3	96539	1	13,1	2	19,6	1	9,2	5	37,4	2	12,2	2	16,8	3	25,2
1998	33469968	MCM7	DNA replication licensing factor MCM7 isoform 1	6,0	81289	1	11,1	1	9,7	3	8,7	1	9,5	2	12,1	1	9,5	3	21,3
1999	334849548	HLA	MHC class I antigen	5,5	39321	1	15,6	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2000	334849630	HLA	MHC class I antigen	7,2	39123	0	0,0	0	0,0	3	9,3	0	0,0	0	0,0	0	0,0	0	0,0
2001	33504652	AP2B1	beta adaptin subunit	5,0	98118	0	0,0	0	0,0	3	19,6	1	9,4	0	0,0	1	9,8	1	7,9
2002	33519436	CCNB1IP1	E3 ubiquitin-protein ligase CCNB1IP1	8,3	31526	1	10,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2003	3355597	LRRFIP1	TRIP protein	4,4	86438	1	10,8	2	10,0	1	9,3	1	9,5	0	0,0	1	8,0	1	9,7
2004	33609	IGKV2	immunoglobulin kappa light chain, A23 V-segment	8,8	13061	0	0,0	0	0,0	3	17,6	0	0,0	0	0,0	0	0,0	0	0,0

2005	33620730	KLC1	kinesin light chain 1 isoform 1	5,5	63817	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	1	9,7
2006	336391093	RAB2A	ras-related protein Rab-2A isoform b	5,7	20829	1	12,1	0	0,0	3	19,6	0	0,0	0	0,0	2	14,3	1	8,8
2007	336483820	HLA	MHC class II antigen	6,2	21402	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,1	0	0,0
2008	33710	IGLL5	immunoglobulin lambda light chain	7,6	24457	1	13,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2009	337451	HNRNPAB	hnRNP type A/B protein	9,7	31234	0	0,0	0	0,0	2	8,7	2	18,8	2	12,2	1	12,9	4	16,2
2010	3378617	HEL	aflatoxin B1-aldehyde reductase	6,2	36619	1	10,8	1	9,7	0	0,0	0	0,0	0	0,0	2	9,3	1	9,7
2011	338261	SNRPC	ribonucleoprotein, partial	10,4	11455	1	11,7	0	0,0	1	9,3	0	0,0	2	12,2	0	0,0	1	9,7
2012	338654	OAS2	71 kDa 2'5' oligoadenylate synthetase	8,6	83289	1	11,2	2	19,9	4	28,1	5	37,4	2	12,2	1	12,9	3	25,0
2013	33869643	EEF2	EEF2 protein, partial	8,6	64781	4	19,1	7	39,6	11	27,6	20	56,1	12	48,4	9	29,1	6	28,2
2014	33871444	NASP	NASP protein, partial	4,2	53739	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
2015	33872137	NOP58	NOP58 protein	9,2	58679	1	10,7	2	10,0	2	9,3	1	9,5	3	12,2	1	9,1	2	9,7
2016	33873840	SUPT16H	SUPT16H protein, partial	8,4	71998	1	11,1	0	0,0	1	9,9	0	0,0	2	12,3	1	8,7	1	9,8
2017	33874022	HNRNPM	HNRPM protein, partial	8,6	44444	4	34,5	5	44,4	7	49,5	10	65,4	6	48,3	4	29,0	4	32,8
2018	33874637	ACTN4	ACTN4 protein, partial	5,0	73620	5	38,9	12	54,3	9	50,1	10	37,5	11	60,3	10	56,1	8	50,8
2019	33874734	GSPT1	GSPT1 protein	5,1	68448	0	0,0	0	0,0	1	9,9	0	0,0	0	0,0	0	0,0	0	0,0
2020	33875177	YBX1	YBX1 protein, partial	10,6	29375	1	19,7	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	1	15,8
2021	33876034	HEXA	HEXA protein, partial	4,7	47095	1	11,2	0	0,0	1	8,7	0	0,0	0	0,0	1	8,0	0	0,0
2022	33876422	RPRD1B	RPRD1B protein	8,9	25048	1	13,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2023	33876620	PTDSS1	PTDSS1 protein	8,7	38274	1	10,9	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2024	33877724	TRIM56	TRIM56 protein, partial	6,9	41593	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,8	0	0,0
2025	33877895	MARCKS	MARCKS protein, partial	4,6	14860	1	11,6	3	10,2	2	9,4	2	9,6	2	12,3	2	11,8	4	9,8
2026	33878473	DHX9	DHX9 protein, partial	5,8	67447	3	24,6	5	19,9	6	28,2	2	18,8	5	24,2	4	21,2	4	23,9
2027	33879558	SFPQ	SFPQ protein, partial	10,3	55470	1	11,2	1	9,7	4	28,9	1	9,5	2	12,2	2	13,7	3	19,2
2028	33942072	CNPY3	protein canopy homolog 3 precursor	5,2	30749	1	12,4	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2029	33988037	MSN	MSN protein	9,7	38828	9	31,9	8	39,6	7	22,2	10	28,2	14	36,3	10	32,6	9	29,4
2030	33989959	CAD	CAD protein	7,4	93480	0	0,0	1	10,3	0	0,0	1	9,5	0	0,0	0	0,0	2	18,6
2031	340545472	RNF213	mysterin	6,0	591378	1	10,8	3	25,0	4	22,7	4	18,8	3	24,2	3	21,2	5	25,0
2032	34101268	KLHL8	kelch-like protein 8	6,1	68803	0	0,0	0	0,0	0	0,0	1	9,4	0	0,0	0	0,0	0	0,0
2033	341837759	HLA	MHC class I antigen	5,7	20980	1	10,9	0	0,0	0	0,0	1	9,5	0	0,0	0	0,0	0	0,0
2034	341838240	HLA	MHC class I antigen	6,3	20922	2	10,6	0	0,0	1	9,3	0	0,0	0	0,0	0	0,0	0	0,0
2035	341838432	HLA	MHC class I antigen	7,4	21130	0	0,0	1	16,4	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2036	34190544	KATNAL2	Katanin p60 subunit A-like 2	8,5	52809	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
2037	34190832	TTC6	C14orf25 protein, partial	10,3	53634	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
2038	34192669	PDXDC1	PDXDC1 protein	4,8	25410	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	1	9,3	1	11,4
2039	34192875	IBTK	IBTK protein, partial	7,4	52904	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	11,4
2040	34201	RPL35A	unnamed protein product	11,3	12496	1	13,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2041	34209	SSB	La 4.1 protein	8,1	33759	1	11,9	0	0,0	2	18,4	4	28,1	2	12,2	2	8,0	1	9,6
2042	34223761	DIAPH1	diaphanous 1	5,2	141303	0	0,0	1	10,0	3	13,5	2	9,5	0	0,0	1	11,7	1	7,9
2043	34228	LMNA	unnamed protein product	7,6	79398	2	22,2	14	79,0	25	132,0	12	91,5	12	84,3	19	118,0	12	80,8
2044	34272	RPSA	unnamed protein product	4,6	33314	6	42,6	11	44,5	9	55,0	14	74,8	12	72,3	11	57,3	8	41,7
2045	34276	PTPRC	unnamed protein product	5,9	130898	0	0,0	2	20,4	2	13,5	2	18,8	0	0,0	1	12,2	1	9,6
2046	34281	PTPRC	unnamed protein product	5,7	147254	0	0,0	2	19,9	1	8,7	0	0,0	2	12,2	3	17,7	3	17,5
2047	34327980	ZDBF2	KIAA1571 protein	5,9	200910	1	11,3	0	0,0	0	0,0	0	0,0	0	0,0	1	9,5	0	0,0
2048	34364597	ANXA2	hypothetical protein	8,7	40354	6	52,9	8	39,3	5	31,9	10	56,1	9	60,3	7	42,2	6	41,5
2049	34364617	FN1	hypothetical protein	5,6	252761	0	0,0	0	0,0	0	0,0	10	37,5	0	0,0	0	0,0	0	0,0
2050	34364985	DEK	hypothetical protein	9,2	4601	1	14,1	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2051	34365016	FLNB	hypothetical protein	5,4	257390	1	16,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2052	34365437	ANXA4	hypothetical protein	8,7	12749	1	11,8	0	0,0	1	9,8	1	15,0	0	0,0	1	9,3	1	7,9
2053	34365461	MTR	hypothetical protein	5,5	91732	0	0,0	0	0,0	1	8,6	0	0,0	0	0,0	0	0,0	0	0,0
2054	344179040	SEC16A	protein transport protein Sec16A	11,1	14581	0	0,0	0	0,0	1	8,6	0	0,0	0	0,0	0	0,0	0	0,0
2055	344179069	CAD	CAD protein	5,5	21503	1	11,5	1	10,3	0	0,0	1	9,4	0	0,0	2	15,9	0	0,0
2056	34530385	IL16	unnamed protein product	7,1	123297	1	12,8	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
2057	34531374	KDM1B	unnamed protein product	8,5	65706	1	9,6	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2058	34531995	PES1	unnamed protein product	8,4	15468	2	10,4	1	9,7	0	0,0	0	0,0	0	0,0	1	9,0	0	0,0
2059	34532000	LRPPRC	unnamed protein product	5,7	157962	1	11,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2060	34532240	PPP1R2	unnamed protein product	5,7	17885	0	0,0	1	10,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2061	34532659	PFKM	unnamed protein product	7,8	93220	1	15,9	1	14,1	1	9,3	2	18,8	0	0,0	2	19,4	1	20,5
2062	34532967	CYP4V2	unnamed protein product	6,5	58167	1	10,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2063	34533120	KARS	unnamed protein product	5,1	48422	1	13,3	2	20,0	1	9,2	2	9,5	2	12,2	2	12,1	1	8,8
2064	34533996	AAK1	unnamed protein product	8,7	23111	1	11,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2065	34534085	VAPB	unnamed protein product	5,9	16532	1	12,1	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	1	9,7
2066	34534396	ERICH3	unnamed protein product	5,2	131880	1	11,6	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2067	34534918	HDLBP	unnamed protein product	6,8	94847	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	0	0,0

2068	34535034	RNF213	unnamed protein product	8,1	20870	0	0,0	0	0,0	2	9,3	0	0,0	0	0,0	1	8,0	0	0,0
2069	34535074	GSDMD	unnamed protein product	10,2	55072	1	12,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2070	34535789	CIRBP	unnamed protein product	11,2	15343	0	0,0	0	0,0	1	8,6	1	9,4	3	24,2	0	0,0	0	0,0
2071	34536452	AHNAK	unnamed protein product	5,7	180689	1	12,5	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2072	34559851	ASAH1	HSD-33	7,8	46395	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2073	34577083	RSU1	ras suppressor protein 1 isoform 2	9,2	25546	0	0,0	1	10,3	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
2074	34638	TAP2	TAP2	7,9	75664	4	26,3	4	14,8	2	14,2	5	28,1	0	0,0	3	14,3	2	12,7
2075	34707	SOD2	Manganese superoxide dismutase	8,4	24711	1	11,0	2	10,0	1	15,5	0	0,0	0	0,0	2	15,8	2	17,6
2076	34783055	LPCAT3	LPCAT3 protein	9,2	50888	1	10,8	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
2077	34783559	SRA1	SRA1 protein, partial	8,2	23154	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
2078	348239	NONO	unnamed protein product	9,4	54268	7	47,7	11	24,7	9	40,4	10	28,1	8	36,3	6	23,8	7	30,0
2079	34850061	STMN2	stathmin-2 isoform 2	8,6	20829	1	11,6	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,6
2080	349732206	PRPF4	U4/U6 small nuclear ribonucleoprotein Prp4 isof	7,1	58303	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2081	349732256	TXN	thioredoxin isoform 2	5,7	9453	1	11,9	3	10,0	4	9,3	6	9,4	3	12,2	2	8,7	3	12,3
2082	34996489	PHIP	PH-interacting protein	9,0	206647	1	13,1	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2083	35053	HEL	uracil DNA glycosylase	8,2	35493	162	120,5	162	79,2	149	68,5	166	65,6	217	108,6	272	86,7	274	67,1
2084	35121	NUMA1	NuMA protein	5,6	236297	1	10,9	0	0,0	1	9,9	2	18,8	0	0,0	1	9,8	2	16,2
2085	35125	OAS1	unnamed protein product	4,4	12451	0	0,0	2	10,0	0	0,0	1	9,4	0	0,0	0	0,0	0	0,0
2086	35187024	HLA	MHC class II antigen	4,8	10808	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	1	10,5
2087	35222	HSPA6	unnamed protein product	5,6	70854	3	18,0	3	17,9	0	0,0	2	9,5	0	0,0	3	20,0	1	12,8
2088	3522980	HLA	MHC class I antigen	5,9	40894	3	34,9	10	51,4	12	39,3	8	43,1	5	31,5	9	48,0	9	56,3
2089	35309	HMBS	unnamed protein product	7,4	39330	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,8	0	0,0
2090	3540239	NDUFS2	NADH dehydrogenase-ubiquinone Fe-S protein 2 precursor	7,3	52485	1	10,6	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	2	16,2
2091	354459350	RAP1B	ras-related protein Rap-1b isoform 2	9,2	16015	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	2	9,8
2092	354721179	RAB5B	ras-related protein Rab-5B isoform 2	7,1	19072	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7	1	7,9
2093	35493952	UBE3B	ubiquitin-protein ligase E3B isoform 1	8,1	123079	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2094	35514	PLCG2	unnamed protein product	6,2	146120	1	9,7	3	10,1	2	9,3	1	9,5	2	12,2	2	9,1	1	9,8
2095	35518	PLEK	unnamed protein product	8,1	40084	4	21,7	4	9,8	10	31,9	10	46,8	5	24,3	3	14,4	4	18,7
2096	3560128	HLA	HLA-A alpha2 exon3	8,2	10588	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2097	35844	RNH1	unnamed protein product	4,5	49906	2	26,5	0	0,0	1	9,8	1	9,4	2	12,2	4	29,0	0	0,0
2098	35869	GTF2F1	RNA polymerase II associated protein RAP74	7,5	58256	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
2099	36038	HEL	rho GDP dissociation inhibitor (GDI)	4,9	23194	6	40,9	3	29,8	5	32,4	8	28,1	3	24,2	5	26,5	5	35,1
2100	36049	RPN2	unnamed protein product	5,4	69303	11	59,0	11	59,3	11	59,8	16	84,1	5	36,3	12	71,3	5	38,3
2101	36138	RPL6	ribosomal protein L6	10,8	32862	12	52,9	7	39,3	15	49,5	7	28,1	14	60,3	8	41,5	8	36,8
2102	36142	RPS15A	ribosomal protein homologous to yeast S24	10,7	14698	17	20,9	7	10,1	3	9,3	8	9,5	8	12,3	7	11,7	9	9,8
2103	363543330	ABHD14B	abhydrolase domain-containing protein 14B isofo	6,2	18028	1	12,0	0	0,0	1	9,9	0	0,0	0	0,0	1	9,1	1	10,6
2104	3641621	CPD	gp180-carboxypeptidase D-like enzyme	5,7	152915	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2105	3646132	NFS1	putative tRNA splicing protein	7,6	35373	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	1	7,9
2106	36535	SOD	unnamed protein product	8,7	2548	2	11,5	3	10,0	2	9,2	1	9,4	3	12,2	1	9,0	2	9,7
2107	365733590	CD48	CD48 antigen isoform 2 precursor	8,2	28837	2	11,9	0	0,0	0	0,0	0	0,0	0	0,0	2	9,3	0	0,0
2108	365768592	HLA	MHC Class I antigen	8,6	21116	0	0,0	0	0,0	0	0,0	0	0,0	2	12,3	0	0,0	0	0,0
2109	367460087	MYH10	myosin-10 isoform 2	5,3	228998	1	16,4	0	0,0	0	13,8	1	9,4	0	0,0	0	0,0	0	0,0
2110	37046660	RPL7L1	RPL7L1 protein	11,0	28590	1	10,8	1	10,3	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
2111	371447621	ENSG00000223931	immunoglobulin G heavy chain variable region	8,2	13414	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2112	37181863	SIGLEC14	SIGLEC5	7,9	43726	1	13,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2113	37183096	UNQ2523	VGPW2523	5,2	35964	1	11,2	0	0,0	2	8,7	1	9,5	0	0,0	2	8,1	0	0,0
2114	37183270	APMAP	C20orf3	5,7	41606	1	10,8	1	10,3	1	8,8	1	9,5	2	12,2	1	9,1	1	12,0
2115	371872752	TMCO1	transmembrane and coiled-coil domain-containing pr	10,7	27061	2	10,8	2	10,0	1	9,3	1	9,5	0	0,0	2	9,1	2	9,7
2116	371877598	ALOX5	arachidonate 5-lipoxygenase isoform 3	5,5	71545	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	11,4
2117	3721864	ZMPSTE24	Ste24p	8,0	54813	1	11,1	1	9,7	1	9,9	0	0,0	0	0,0	1	9,4	0	0,0
2118	37231	TOP2B	DNA topoisomerase II	8,1	182692	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2119	373251164	GLS	glutaminase kidney isoform, mitochondrial isofo	7,8	65442	1	10,5	0	0,0	3	9,9	2	9,5	2	12,2	2	8,9	2	8,0
2120	37359212	TNFRSF1B	soluble tumor necrosis factor receptor superfamily me	6,8	28463	1	11,6	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
2121	37433	TFRC	unnamed protein product	6,2	84902	6	56,5	10	69,2	7	50,1	13	84,0	9	72,3	9	62,3	11	61,5
2122	37498644	HLA	MHC class II antigen	5,5	25006	0	0,0	1	17,4	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2123	375173849	HLA	MHC class I antigen, partial	6,2	20887	1	10,9	0	0,0	0	0,0	0	0,0	0	0,0	2	9,4	1	9,7
2124	37547	SNRPA1	unnamed protein product	9,0	28444	0	0,0	1	9,7	1	9,8	2	18,8	2	12,2	1	9,3	0	0,0
2125	3757678	ETFA	electron transfer flavoprotein alpha subunit	4,0	3327	1	11,0	0	0,0	1	9,8	0	0,0	0	0,0	1	9,4	1	9,7
2126	37589015	TRAP1	TRAP1 protein, partial	7,7	79358	1	11,8	1	9,7	1	8,7	0	0,0	0	0,0	1	9,6	1	15,4
2127	37589562	IAH1	IAH1 protein	5,6	25846	0	0,0	3	10,0	1	9,9	0	0,0	0	0,0	1	8,9	1	7,9
2128	37594464	NUDT5	ADP-sugar pyrophosphatase	4,7	24328	0	0,0	1	9,7	1	8,7	0	0,0	2	12,2	0	0,0	0	0,0
2129	37620220	TPD52L2	HCCR-binding protein 2	4,7	12587	2	16,5	4	24,8	1	8,7	0	0,0	0	0,0	2	11,7	1	9,7
2130	37622149	DNTTIP2	estrogen receptor binding protein	5,7	84444	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9

2131	37645	VAV1	VAV	6,2	91901	1	11,5	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	2	19,3
2132	37695550	HERC5	HECT E3 ubiquitin ligase	7,4	116760	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	11,5
2133	37724561	GNB2L1	lung cancer oncogene 7	8,2	37890	11	36,9	11	29,8	3	19,0	7	46,8	9	36,3	6	30,5	4	19,9
2134	37748529	RPL12	RPL12 protein	8,9	14200	2	10,6	3	10,0	6	9,3	8	9,5	6	12,3	3	9,1	8	9,7
2135	37782424	NT5DC1	LP2642	7,2	25973	0	0,0	2	10,1	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2136	37787307	NAPRT	nicotinate phosphoribosyltransferase-like protein	5,4	57546	0	0,0	1	10,3	2	8,7	0	0,0	0	0,0	0	0,0	0	0,0
2137	37848	VIM	unnamed protein product	10,4	14856	1	11,1	0	0,0	0	0,0	2	18,8	3	24,2	0	0,0	1	7,9
2138	379317598	COX2	cytochrome c oxidase subunit II, partial (mitochondr	4,4	24838	1	9,6	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
2139	37963813	GYPB	glycophorin B	8,0	8204	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
2140	380039475	HLA	MHC class I antigen, partial	5,9	31412	1	16,8	1	12,9	0	13,8	2	15,0	2	19,4	1	12,2	1	13,0
2141	38014274	GRIPAP1	GRIPAP1 protein	4,9	63762	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2142	38016914	SAMHD1	SAM domain and HD domain-containing protein 1	6,7	72182	1	12,9	2	15,1	1	8,7	1	9,4	2	12,1	1	12,1	1	9,7
2143	38045948	UBA7	ubiquitin-like modifier-activating enzyme 7	5,6	111676	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	1	8,9	0	0,0
2144	380714665	CUL3	cullin-3 isoform 3	7,9	89732	0	0,0	0	0,0	0	0,0	1	9,4	0	0,0	1	9,7	0	0,0
2145	38079	NDUFS1	75 kDa subunit NADH dehydrogenase precursor	5,7	79555	1	11,3	1	10,3	3	19,6	0	0,0	0	0,0	2	18,5	3	38,5
2146	380837121	SEC22B	vesicle-trafficking protein SEC22b precursor	8,7	24722	1	15,4	1	10,3	3	23,3	2	18,8	0	0,0	2	20,0	1	9,7
2147	38157986	UBE2L6	ubiquitin/ISG15-conjugating enzyme E2 L6 isoform 2	6,9	10068	1	11,2	0	0,0	1	9,9	0	0,0	2	12,3	0	0,0	0	0,0
2148	38194550	STAT1	signal transducer and activator of transcription 1 va	4,1	5291	4	11,5	5	10,1	5	9,3	5	9,5	8	12,3	4	9,1	5	9,8
2149	38196957	FASN	FASN protein, partial	6,2	84212	4	23,7	8	49,2	8	50,1	5	44,9	6	48,3	4	31,7	6	41,5
2150	38196980	MIOS	MIOS protein	6,5	60449	0	0,0	0	0,0	0	0,0	1	9,4	0	0,0	0	0,0	0	0,0
2151	38201627	EIF4G1	eukaryotic translation initiation factor 4 gamma 1	5,0	166570	1	11,7	0	0,0	1	9,8	0	0,0	0	0,0	0	0,0	1	7,9
2152	38201710	DDX17	probable ATP-dependent RNA helicase DDX17 isoform 1	8,2	80254	3	35,8	3	29,4	5	40,4	10	65,4	9	60,3	5	44,1	4	35,4
2153	38371739	RAB15	ras-related protein Rab-15	10,3	23519	2	11,3	1	10,2	0	0,0	0	0,0	2	12,2	0	0,0	1	10,5
2154	38372919	BSG	basigin isoform 1 precursor	5,3	42201	3	22,6	1	10,0	1	9,8	1	9,5	2	12,2	3	26,9	2	13,5
2155	38373669	SEC24C	protein transport protein Sec24C	6,7	118325	0	0,0	1	10,3	1	8,7	1	9,4	0	0,0	1	9,1	1	9,7
2156	3851288	IGHV5	immunoglobulin A heavy chain	8,2	10486	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2157	385139457	SEC22B	SEC22 vesicle trafficking protein B, partial	9,5	4115	1	10,8	0	0,0	1	8,6	0	0,0	0	0,0	0	0,0	1	9,6
2158	385139461	SEC22B	SEC22 vesicle trafficking protein B, partial	4,7	6105	2	10,5	2	19,3	5	18,4	0	0,0	2	12,3	3	15,9	3	13,6
2159	38522	EEF1D	human elongation factor-1-delta	4,8	31222	0	0,0	0	0,0	0	0,0	2	9,6	0	0,0	0	0,0	1	7,9
2160	385298680	EFTUD2	116 kDa U5 small nuclear ribonucleoprotein comp	4,7	108265	1	10,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
2161	38541687	TPM3	TPM3 protein	4,5	18494	5	16,5	4	18,9	1	12,7	4	18,8	5	21,9	3	17,4	0	0,0
2162	38566176	PGAM1	Phosphoglycerate mutase 1 (brain)	6,8	28821	29	59,9	23	69,2	25	55,0	14	56,2	15	84,4	25	59,3	20	64,4
2163	38569394	IKBKAP	elongator complex protein 1	5,6	150254	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,4	0	0,0
2164	38569423	ACLY	ATP-citrate synthase isoform 2	6,9	119772	0	0,0	1	10,3	1	8,6	0	0,0	0	0,0	0	0,0	1	11,4
2165	38570156	NT5DC1	5'-nucleotidase domain-containing protein 1	5,9	51827	1	13,5	0	0,0	1	8,7	0	0,0	0	0,0	1	8,0	1	9,7
2166	3859248	BV08S1J2	T cell receptor beta chain CDR3	4,1	2570	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
2167	386776	HLA	MHC HLA-Bw47 precursor, partial	5,7	40572	1	9,6	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	2	9,7
2168	386787	SDC2	heparan sulfate proteoglycan core protein, partial	10,0	43389	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7	0	0,0
2169	38679884	SRI	sorcin isoform B	5,0	20346	0	0,0	0	0,0	0	0,0	2	18,7	2	12,2	2	9,5	2	9,6
2170	38679912	UPF2	uncharacterized protein C9orf114	7,2	42009	0	0,0	0	0,0	0	0,0	1	9,5	0	0,0	0	0,0	1	9,8
2171	38683799	ANKRD13A	ankyrin repeat domain-containing protein 13A	4,8	67601	1	10,7	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	1	9,7
2172	38683836	CD47	leukocyte surface antigen CD47 isoform 2 precursor	7,9	33174	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2173	386873	HLA	hla antigen, partial	5,9	40549	1	12,1	0	0,0	0	0,0	0	0,0	0	0,0	1	9,5	2	9,7
2174	386917	HLA	MHC HLA-DC-beta	8,2	29871	3	23,4	2	10,0	2	14,1	2	18,8	2	12,2	2	11,7	2	12,3
2175	386921	HLA	MHC HLA-DPw4b-beta chain precursor, partial	7,7	26294	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2176	386927	HLA	MHC HLA-DR2(Dw2)a glycoprotein beta-chain, partial	6,1	27047	1	11,9	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2177	387912555	PTER	phosphotriesterase-related protein isoform 2	6,5	33417	1	9,7	1	9,7	1	8,7	0	0,0	0	0,0	0	0,0	1	7,9
2178	3882273	UFL1	KIAA0776 protein	6,3	90052	1	11,0	2	19,9	3	13,6	1	9,5	3	12,3	2	12,7	1	9,7
2179	3882301	SASH1	KIAA0790 protein	6,1	143614	1	12,5	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2180	388240742	HLA	MHC classI antigen, partial	6,1	38221	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	11,4
2181	388240801	LMNB2	lamin-B2	5,4	69949	1	10,9	2	10,0	1	8,7	0	0,0	0	0,0	2	14,7	2	13,6
2182	389565487	PDCD6	programmed cell death protein 6 isoform 4	4,9	14432	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
2183	3901030	KRT75	cytokeratin type II	7,7	59505	1	11,5	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2184	392494079	DBT	lipoamide acyltransferase component of branched-ch	8,6	53469	1	11,5	0	0,0	1	9,3	0	0,0	2	12,2	1	12,1	1	9,7
2185	392494742	HLA	MHC class I antigen, partial	5,9	31772	1	10,9	2	10,2	0	0,0	0	0,0	2	12,3	0	0,0	0	0,0
2186	392513662	ILF2	interleukin enhancer-binding factor 2 isoform 2	4,7	38892	2	19,6	1	9,7	3	23,3	4	28,1	5	24,2	3	23,8	3	15,5
2187	3929617	NAPA	alpha SNAP	5,1	33248	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,8
2188	394025704	ARPC5	actin-related protein 2/3 complex subunit 5 iso	5,6	16613	1	11,5	0	0,0	0	0,0	0	0,0	0	0,0	1	12,4	2	20,2
2189	394025725	ACADVL	very long-chain specific acyl-CoA dehydrogenase	6,9	62564	1	11,3	0	0,0	1	8,6	0	0,0	0	0,0	0	0,0	0	0,0
2190	3947688	SEC24A	Sec24A protein	7,9	118792	2	15,2	0	0,0	1	9,8	1	16,9	2	12,2	1	16,0	2	15,7
2191	395455053	SREK1	splicing regulatory glutamine/lysine-rich prote	4,5	10695	0	0,0	0	0,0	2	8,7	1	9,5	0	0,0	1	8,0	1	7,9
2192	39644486	TFEB	TFEB protein, partial	5,2	37101	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
2193	39644631	XPO5	XPO5 protein, partial	5,5	104708	1	13,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0

2194	39644669	GUK1	GUK1 protein, partial	5,8	20333	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	1	7,9
2195	39645231	LAMP1	LAMP1 protein, partial	8,4	26542	1	11,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2196	39645467	ANXA4	ANXA4 protein	5,5	33553	3	25,9	3	19,9	5	35,5	4	28,1	2	12,2	3	19,6	6	37,2
2197	39645576	NUP205	NUP205 protein, partial	7,6	70000	0	0,0	1	10,3	0	0,0	0	0,0	0	0,0	1	9,4	0	0,0
2198	39645644	MAGEL2	MAGEL2 protein, partial	7,6	74319	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7	0	0,0
2199	397138632	MAP2K3	PREDICTED: dual specificity mitogen-activated p	4,9	16288	1	11,3	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	1	11,4
2200	39753957	TOR1AIP1	torsin-1A-interacting protein 1 isoform 2	8,3	66230	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	1	9,7
2201	3980313	COPE	Epsilon COP	4,8	34495	1	10,8	3	24,9	2	9,3	5	37,4	0	0,0	1	11,7	7	36,5
2202	39930469	RPF2	ribosome production factor 2 homolog	10,4	35565	0	0,0	1	10,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2203	39938007	IGHG3	immunoglobulin heavy chain variable region	9,2	16737	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7	1	11,4
2204	39963074	PRPF8	PRP8 pre-mRNA processing factor 8 homolog (S. cerevis	9,0	273561	0	0,0	1	9,7	1	8,7	1	9,4	0	0,0	0	0,0	1	9,7
2205	39963655	GCN1L1	GCN1L1 protein, partial	5,8	26935	0	0,0	1	9,7	3	9,3	0	0,0	0	0,0	1	8,0	1	12,7
2206	40068518	PGD	6-phosphogluconate dehydrogenase, decarboxylating	6,9	53122	4	41,8	6	39,6	12	78,1	14	65,4	5	36,2	7	53,8	7	41,8
2207	401664560	HYDIN	hydrocephalus-inducing protein homolog isoform	5,7	575870	1	13,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2208	40225995	HDLBP	HDLBP protein	6,1	100591	0	0,0	0	0,0	1	9,9	1	9,5	0	0,0	1	9,0	1	9,7
2209	40254924	LRRC59	leucine-rich repeat-containing protein 59	10,0	34912	2	10,6	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2210	40254982	FAM107B	protein FAM107B	6,6	34760	1	10,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2211	40255009	SLC30A7	zinc transporter 7	6,5	41627	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2212	402694604	HLA	MHC class I antigen, partial	6,0	21036	0	0,0	0	0,0	0	0,0	1	15,1	0	0,0	0	0,0	1	9,9
2213	4028622	EPFP1	chaperonin 10-related protein	9,6	10296	2	15,3	14	24,7	12	27,5	12	28,1	11	24,2	11	18,0	16	28,2
2214	40288274	NUDT1	7,8-dihydro-8-oxoguanine triphosphatase isoform p18	4,8	17933	0	0,0	1	10,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2215	40352901	DYNC1H1	DYNC1H1 protein	9,9	22182	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2216	40362722	IMPDH2	inosine monophosphate dehydrogenase type II	5,0	7242	0	0,0	0	0,0	0	0,0	1	9,5	0	0,0	1	9,0	1	7,9
2217	40362724	IMPDH2	inosine monophosphate dehydrogenase type II	4,4	3072	1	12,4	0	0,0	0	0,0	1	9,4	0	0,0	0	0,0	0	0,0
2218	404435530	HLA	MHC class I antigen, partial	5,9	21097	2	11,8	0	0,0	3	9,9	0	0,0	0	0,0	2	9,0	0	0,0
2219	404722	GNA13	guanine nucleotide regulatory protein	8,0	44064	1	10,8	0	0,0	1	9,8	0	0,0	0	0,0	0	0,0	0	0,0
2220	40548328	NACA2	nascent polypeptide-associated complex subunit alph	4,5	23205	1	11,7	0	0,0	1	9,3	1	9,5	0	0,0	1	9,4	1	8,8
2221	40548422	CHMP4A	charged multivesicular body protein 4a	4,9	29785	1	11,9	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2222	406822414	APOE	apolipoprotein E, partial	8,7	26852	2	14,9	1	10,0	0	0,0	0	0,0	0	0,0	2	8,7	1	9,7
2223	4071058	TSC2	tuberin	7,0	200677	0	0,0	1	10,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2224	40787656	NCKAP1L	NCKAP1L protein, partial	6,1	94704	0	0,0	1	10,0	3	22,7	4	18,8	3	12,2	2	13,7	3	21,3
2225	40788953	TAGLN2	KIAA0120	8,4	24417	3	29,1	10	28,8	11	40,6	10	35,6	14	58,0	12	38,2	7	23,9
2226	40807029	ERAP2	ERAP2 protein	6,4	105526	0	0,0	0	0,0	1	9,3	0	0,0	2	12,2	2	27,8	2	28,9
2227	40807167	KIF5B	KIF5B protein, partial	6,7	38717	0	0,0	1	9,7	1	9,9	0	0,0	2	12,1	0	0,0	0	0,0
2228	40807447	PRCC	proline-rich protein PRCC	4,9	52418	1	12,4	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2229	40807491	ACSL1	long-chain-fatty-acid--CoA ligase 1	6,8	77944	1	10,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2230	40850891	HEATR1	HEATR1 protein, partial	6,1	125361	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
2231	40889023	RPL4	ribosomal protein L4	11,6	47673	2	24,5	7	39,6	6	31,8	4	28,1	5	24,2	4	27,0	4	29,9
2232	4092052	NDUFA7	CI-B14.5a homolog	10,9	13181	2	10,9	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	1	9,7
2233	4096591	POLR1A	DNA-directed RNA polymerase I, largest subunit	6,8	194172	1	12,5	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2234	410169889	NME2	PREDICTED: nucleoside diphosphate kinase B-like	9,1	20820	3	18,2	7	18,0	5	18,5	7	17,0	11	21,9	5	16,8	4	22,3
2235	410171187	HEL	PREDICTED: peptidyl-prolyl cis-trans isomerase	7,8	17780	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	11,4
2236	4107243	HLA	MHC class II HLA-DRB1	4,7	10866	1	12,1	3	10,0	2	8,7	2	9,5	0	0,0	2	8,9	3	20,5
2237	41281709	NFKBID	NF-kappa-B inhibitor delta	7,0	33481	0	0,0	2	10,1	0	0,0	0	0,0	0	0,0	1	14,4	0	0,0
2238	41281885	UQCR10	cytochrome b-c1 complex subunit 9 isoform a	9,9	7290	1	11,5	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2239	41350407	RCN1	proliferation-inducing gene 20 protein	4,3	19543	2	10,8	3	10,0	1	9,3	0	0,0	0	0,0	3	11,7	3	9,7
2240	41351374	PSMD12	Proteasome (prosome, macropain) 26S subunit, non-ATPa	8,4	46394	1	11,1	1	9,7	1	8,7	0	0,0	0	0,0	1	8,0	3	23,5
2241	41393545	RAB5C	ras-related protein Rab-5C isoform a	8,5	23464	3	27,5	1	10,0	0	0,0	1	9,4	0	0,0	1	8,0	2	15,6
2242	41393554	LUC7L	putative RNA-binding protein Luc7-like 1 isoform b	10,4	43710	1	9,6	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
2243	41393599	CPOX	coproporphyrinogen-III oxidase, mitochondrial precu	8,2	50134	1	13,1	4	39,3	3	22,7	0	0,0	2	12,1	2	24,1	3	27,3
2244	41474123	RPS26	unknown	11,4	12986	3	12,1	0	0,0	0	0,0	0	0,0	0	0,0	1	8,9	0	0,0
2245	4165018	ACSL3	Acyl-CoA synthetase 3	8,4	80346	1	12,1	0	0,0	1	9,2	1	9,4	0	0,0	1	9,3	1	10,6
2246	4186034	HLA	HLA-DQB106new2 protein	8,8	10758	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	11,4
2247	4191327	ZRANB2	ZIS1	8,9	38224	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,8
2248	4220894	MED26	transcriptional co-activator CRSP70	9,5	65481	1	10,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2249	42384238	NHS	Nance-Horan syndrome protein isoform 2	6,6	160734	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
2250	4240263	FAF2	KIAA0887 protein	5,3	52422	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	1	7,9
2251	42476013	NHLRC2	NHL repeat-containing protein 2	5,2	79444	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	0	0,0
2252	42476024	THUMPD1	THUMP domain-containing protein 1	7,9	39316	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	2	9,7
2253	42476111	GNA12	guanine nucleotide-binding protein subunit alpha-12	10,3	44261	1	11,5	0	0,0	0	0,0	0	0,0	2	12,2	1	9,0	0	0,0
2254	42476299	GIGYF2	PERQ amino acid-rich with GYF domain-containing pro	5,3	150051	1	13,1	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2255	42490910	RPL13	Ribosomal protein L13	12,2	24266	0	0,0	0	0,0	2	8,7	0	0,0	0	0,0	1	8,7	1	7,9
2256	42490988	ATP5J	ATP synthase, H+ transporting, mitochondrial F0 compl	10,0	12609	2	11,5	1	10,0	1	9,3	1	9,4	2	12,2	1	9,1	1	9,7

2257	42542637	TP53RK	TP53 regulating kinase	9,8	28142	1	12,4	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2258	42544136	RRM2B	ribonucleoside-diphosphate reductase subunit M2 B i	4,7	40718	1	10,8	1	10,0	0	0,0	1	9,4	0	0,0	1	8,9	0	0,0
2259	42544159	HSPH1	heat shock protein 105 kDa	5,1	96865	3	27,5	5	29,5	4	23,3	6	37,5	0	0,0	4	21,3	3	17,4
2260	42544231	LRRN2	leucine-rich repeat neuronal protein 2 precursor	7,1	78840	0	0,0	0	0,0	0	0,0	1	9,4	0	0,0	0	0,0	0	0,0
2261	4261934	PEBP1	S76773_1 neuropolypeptide h3, partial	8,9	15965	5	32,6	5	39,6	6	31,3	6	37,5	5	24,3	4	29,0	4	25,0
2262	4262000	YWHAZ	S79449_1 14-3-3 protein/cytosolic phospholipase A2, pa	8,7	7939	3	11,5	5	10,0	2	9,2	4	9,5	6	12,2	3	9,1	2	9,7
2263	42734438	FAM49B	protein FAM49B	5,7	36749	1	14,9	1	10,3	0	0,0	1	9,4	0	0,0	1	8,0	0	0,0
2264	42741671	NAT1	arylamine N-acetyltransferase 1 isoform a	6,1	33880	1	11,7	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
2265	42789729	LRMP	lymphoid-restricted membrane protein	5,3	56195	1	10,8	2	10,1	1	8,7	1	9,4	2	12,2	1	8,0	0	0,0
2266	42794758	ACSL5	long-chain-fatty-acid--CoA ligase 5 isoform b	6,5	75972	1	12,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2267	42794769	PAK1	serine/threonine-protein kinase PAK 1 isoform 2	5,5	60628	1	13,1	0	0,0	1	8,7	0	0,0	2	12,2	1	9,6	0	0,0
2268	429509595	HLA	MHC class I antigen, partial	7,2	21147	1	12,1	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	11,4
2269	432139059	ENSG00000223931	immunoglobulin heavy chain variable region, partial	9,0	11300	1	13,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2270	4323183	ENSG00000228325	immunoglobulin light chain variable region	9,1	11874	0	0,0	0	0,0	0	0,0	1	9,5	0	0,0	0	0,0	0	0,0
2271	432376	MPST	rhodanese	6,0	32967	1	11,1	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2272	4323910	ENSG00000228325	immunoglobulin kappa light chain variable region	9,7	11106	0	0,0	0	0,0	1	9,8	0	0,0	0	0,0	0	0,0	0	0,0
2273	433413	ECHS1	mitochondrial short-chain enoyl-CoA hydratase	7,8	31262	1	11,4	0	0,0	1	9,2	0	0,0	0	0,0	1	9,7	0	0,0
2274	4337109	BAG6	BAT3	6,2	130201	0	0,0	1	10,0	1	9,9	0	0,0	0	0,0	2	13,7	0	0,0
2275	434755	PMPCA	KIAA0123	6,8	58672	1	12,4	1	10,3	0	0,0	1	9,4	0	0,0	1	8,0	0	0,0
2276	434765	NOLC1	ORF	10,0	74511	1	10,8	0	0,0	1	9,2	2	9,4	0	0,0	1	8,7	3	15,7
2277	434779	RRS1	KIAA0112	11,3	44446	1	10,8	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
2278	435476	KRT9	cytokeratin 9	5,1	62130	5	38,4	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2279	435700	CD44	CD44R5	4,9	43001	2	11,2	3	10,0	2	9,3	2	9,5	2	12,2	2	12,1	2	8,8
2280	436224	TMEM41B	KIAA0033	9,7	36981	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	0	0,0
2281	4379034	ARHGEF2	unnamed protein product	5,4	29080	0	0,0	1	9,7	0	0,0	0	0,0	2	12,3	1	8,9	0	0,0
2282	4379045	SKIV2L	helicase	5,7	137790	1	12,8	1	10,3	1	9,2	0	0,0	2	12,2	1	8,9	1	9,7
2283	4389501	ACO2	aconitase	7,1	85617	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2284	4406703	SELT	Unknown	6,2	15845	1	11,2	1	9,8	1	9,3	0	0,0	0	0,0	1	9,1	1	9,7
2285	441435	N/A	Ig kappa light chain (VJC)	7,2	13910	0	0,0	0	0,0	0	12,1	0	0,0	0	0,0	0	0,0	0	0,0
2286	4432748	RPS27	ribosomal protein S27	9,4	7692	1	12,2	0	0,0	1	8,6	0	0,0	0	0,0	1	9,3	1	10,6
2287	4432754	RPL27A	ribosomal protein L27a	10,3	3709	2	14,4	1	10,0	3	18,4	2	9,5	3	24,2	3	17,9	2	12,3
2288	4432757	RPLP0	ribosomal protein P0	4,5	9519	5	19,3	2	14,8	2	9,3	4	18,8	2	12,2	2	12,1	1	9,7
2289	4467837	GPX1	glutathione peroxidase	6,2	21900	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,7	0	0,0
2290	44890424	MARCKSL1	MARCKS-like 1	4,5	19534	1	11,5	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	11,4
2291	44890577	PPP1R2	PPP1R2 protein	9,1	8593	0	0,0	1	9,8	0	0,0	0	0,0	0	0,0	1	8,0	1	11,4
2292	44979607	IMPDH2	IMP dehydrogenase 2	7,9	18294	0	0,0	0	0,0	1	9,3	0	0,0	2	12,2	1	8,7	1	8,8
2293	4501859	ACADSB	short/branched chain specific acyl-CoA dehydrogenase	6,6	47467	0	0,0	2	10,0	1	9,3	2	9,6	0	0,0	2	9,0	2	9,7
2294	4501867	ACO2	aconitate hydratase, mitochondrial precursor	7,3	85407	5	45,5	10	53,3	10	58,7	7	46,8	0	0,0	9	56,7	10	61,5
2295	4501993	AGPS	alkyldihydroxyacetonephosphate synthase, peroxisomal	7,0	72893	1	12,3	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	1	9,7
2296	4502027	ALB	serum albumin preproprotein	5,9	69367	11	22,8	13	19,9	25	18,5	26	18,8	39	24,3	6	18,0	11	25,1
2297	4502049	AKR1B1	aldose reductase	6,6	35854	2	14,4	3	24,9	2	13,6	4	18,8	0	0,0	3	15,9	2	16,9
2298	4502107	HEL	annexin A5	4,8	35938	6	47,4	17	64,7	22	75,0	19	74,8	17	96,3	20	77,0	16	63,2
2299	4502125	NUDT2	bis(5'-nucleosyl)-tetraphosphatase [asymmetrical]	5,1	16811	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,1	2	8,0
2300	4502171	APRT	adenine phosphoribosyltransferase isoform a	5,7	19590	2	19,8	1	10,0	1	9,2	1	9,4	0	0,0	2	14,7	2	14,8
2301	4502203	ARF3	ADP-ribosylation factor 3	7,4	20602	5	19,3	3	15,1	5	32,4	5	18,8	8	36,3	3	21,2	1	15,3
2302	4502205	ARF4	ADP-ribosylation factor 4	7,0	20512	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
2303	4502209	ARF5	ADP-ribosylation factor 5	6,4	20531	3	21,0	5	19,9	3	13,6	6	28,1	5	36,3	4	23,4	1	7,9
2304	4502211	ARF6	ADP-ribosylation factor 6	9,3	20083	1	11,3	1	10,2	0	0,0	0	0,0	0	0,0	1	8,0	1	7,9
2305	4502227	ARL1	ADP-ribosylation factor-like protein 1	5,5	20399	1	9,7	2	10,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2306	4502271	ATP1A2	sodium/potassium-transporting ATPase subunit alpha-2	5,4	112247	1	12,2	0	0,0	0	0,0	2	18,8	0	0,0	1	9,6	1	8,8
2307	4502281	ATP1B3	sodium/potassium-transporting ATPase subunit beta-3	8,4	31494	2	16,7	1	10,3	1	9,9	1	9,5	0	0,0	2	13,3	2	15,5
2308	4502297	ATP5D	ATP synthase subunit delta, mitochondrial precursor	5,2	17472	1	11,5	2	10,3	1	9,9	1	9,4	2	12,2	1	9,0	2	19,3
2309	4502389	BANF1	barrier-to-autointegration factor	5,8	10060	5	16,0	3	10,0	7	18,5	4	9,5	2	12,3	5	9,1	6	16,1
2310	4502419	HEL	flavin reductase (NADPH)	7,5	22120	1	12,4	0	0,0	1	9,8	1	9,4	0	0,0	1	9,6	1	9,8
2311	4502551	CALU	calumenin isoform a precursor	4,3	37108	1	9,7	1	9,8	1	8,7	0	0,0	0	0,0	0	0,0	2	13,6
2312	4502599	CBR1	carbonyl reductase [NADPH] 1	8,4	30376	1	11,4	0	0,0	2	14,2	0	0,0	0	0,0	2	9,6	1	13,7
2313	4502643	CCT6A	T-complex protein 1 subunit zeta isoform a	6,2	58006	7	53,5	14	53,4	21	83,0	14	65,4	22	108,4	14	62,3	12	53,1
2314	4502679	CD63	CD63 antigen isoform A	7,7	25638	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2315	4502741	CDK6	cyclin-dependent kinase 6	6,0	36939	1	11,2	1	10,0	0	0,0	1	9,5	0	0,0	0	0,0	0	0,0
2316	4502899	CLTA	clathrin light chain A isoform a	4,3	23663	1	11,7	0	0,0	0	0,0	0	0,0	0	0,0	1	9,8	0	0,0
2317	4502997	CPA1	carboxypeptidase A1 precursor	5,4	47141	3	11,6	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2318	4503097	CSNK2A2	casein kinase II subunit alpha'	8,8	41214	0	0,0	1	10,0	1	8,7	1	9,5	0	0,0	1	8,0	0	0,0
2319	4503117	CSTB	cystatin-B	7,5	11141	5	21,4	5	19,9	3	18,4	2	9,5	6	36,3	4	18,0	3	19,3

2320	4503143	HEL	cathepsin D preproprotein	6,1	44553	1	16,3	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
2321	4503243	CYP51A1	lanosterol 14-alpha demethylase isoform 1 precursor	8,6	57260	1	10,6	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7	0	0,0
2322	4503253	DAD1	dolichyl-diphosphooligosaccharide--protein glycosylt	6,9	12479	1	13,5	0	0,0	0	0,0	0	0,0	2	12,2	1	9,5	0	0,0
2323	4503291	DDT	D-dopachrome decarboxylase	7,2	12713	4	11,4	1	10,3	1	9,2	2	9,4	2	12,1	3	9,0	3	9,7
2324	4503327	CYB5R3	NADH-cytochrome b5 reductase 3 isoform 1	7,4	34217	4	30,5	4	24,8	2	18,5	2	18,8	3	24,3	4	35,4	2	21,2
2325	4503351	DNMT1	DNA (cytosine-5)-methyltransferase 1 isoform b	7,6	183146	2	21,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
2326	4503471	EEF1A1	elongation factor 1-alpha 1	9,4	50142	113	104,1	126	84,2	66	68,4	128	84,1	65	108,5	185	71,5	145	72,2
2327	4503477	EEF1B2	elongation factor 1-beta	4,3	24765	1	11,5	1	10,0	2	9,3	1	9,5	5	12,3	2	9,1	1	9,7
2328	4503481	EEF1G	elongation factor 1-gamma	6,2	50119	15	73,3	18	79,1	13	64,7	13	46,8	17	60,3	13	67,7	15	70,1
2329	4503499	EIF1AX	eukaryotic translation initiation factor 1A, X-chrom	4,9	16442	1	11,7	0	0,0	1	8,6	0	0,0	0	0,0	0	0,0	1	9,6
2330	4503509	EIF3A	eukaryotic translation initiation factor 3 subunit A	6,4	166550	3	25,7	5	34,6	3	18,4	10	74,7	3	24,2	4	34,8	4	32,9
2331	4503513	EIF3S2	eukaryotic translation initiation factor 3 subunit I	5,3	36484	2	16,4	2	15,1	1	8,6	1	9,5	0	0,0	2	18,5	2	12,9
2332	4503519	EIF3F	eukaryotic translation initiation factor 3 subunit F	5,1	37546	0	0,0	3	10,0	5	14,2	4	18,8	3	12,2	4	15,5	4	15,4
2333	4503521	EIF3E	eukaryotic translation initiation factor 3 subunit E	5,7	52202	2	18,4	7	19,9	7	18,5	11	46,8	8	24,3	6	20,6	4	21,3
2334	4503529	EIF4A1	eukaryotic initiation factor 4A-I isoform 1	5,2	46136	16	89,1	17	83,8	17	73,2	22	102,7	18	84,4	14	77,1	13	74,8
2335	4503545	EIF5A	eukaryotic translation initiation factor 5A-1 isofor	4,9	16814	4	25,2	12	24,8	8	27,6	12	28,2	18	36,4	10	23,9	5	21,9
2336	4503609	ETFB	electron transfer flavoprotein subunit beta isoform	8,2	27825	2	11,2	0	0,0	1	9,3	0	0,0	0	0,0	2	15,3	2	13,4
2337	4503707	FGF9	fibroblast growth factor 9 precursor	7,4	23441	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
2338	4503727	FKBP3	peptidyl-prolyl cis-trans isomerase FKBP3	9,7	25159	2	18,2	4	25,0	6	27,0	4	18,8	3	24,2	4	23,9	5	24,4
2339	4503729	FKBP4	peptidyl-prolyl cis-trans isomerase FKBP4	5,2	51786	1	9,7	2	10,0	1	9,3	1	9,5	0	0,0	1	8,1	1	7,9
2340	4503771	FNTA	protein farnesyltransferase/geranylgeranyltransferas	4,8	44390	1	11,8	0	0,0	0	0,0	0	0,0	0	0,0	1	8,9	0	0,0
2341	4503841	XRCC6	X-ray repair cross-complementing protein 6	6,2	69825	11	90,2	18	94,2	18	113,4	24	121,3	18	120,4	18	104,0	16	96,9
2342	4503933	GATM	glycine amidinotransferase, mitochondrial precursor	8,0	48437	0	0,0	0	0,0	0	0,0	2	18,8	0	0,0	2	9,3	0	0,0
2343	4503937	GBAS	protein NipSnap homolog 2 isoform 1	9,7	33743	0	0,0	1	10,0	2	17,2	0	0,0	0	0,0	1	8,9	1	11,4
2344	4503971	GDI1	rab GDP dissociation inhibitor alpha	4,9	50583	8	28,8	16	29,9	17	27,7	12	28,2	18	36,4	15	33,2	9	29,4
2345	4504025	GLRX	glutaredoxin-1	8,1	11777	2	13,4	3	20,0	3	23,3	1	9,6	6	24,3	2	12,3	1	8,8
2346	4504031	GMDS	GDP-mannose 4,6 dehydratase isoform 1	7,0	41931	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,1	1	7,9
2347	4504041	GNAI2	guanine nucleotide-binding protein G(i) subunit alph	5,2	40433	1	14,6	1	10,1	2	14,1	2	18,8	2	12,2	2	14,8	2	9,7
2348	4504067	GOT1	aspartate aminotransferase, cytoplasmic	6,6	46229	4	36,7	7	34,6	6	36,7	5	28,1	3	24,3	6	41,1	4	31,4
2349	4504143	GRM5	metabotropic glutamate receptor 5 isoform b precurso	7,3	128855	1	11,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2350	4504165	GSN	gelsolin isoform a precursor	5,9	85698	1	11,5	2	10,0	1	8,7	0	0,0	0	0,0	2	9,3	1	8,8
2351	4504175	GSTM2	glutathione S-transferase Mu 2 isoform 1	6,0	25726	1	10,6	1	10,0	0	0,0	1	9,5	0	0,0	2	18,5	1	12,7
2352	4504183	HEL	glutathione S-transferase P	5,3	23357	33	77,5	17	59,3	19	68,4	19	74,8	18	72,4	17	55,8	13	50,5
2353	4504201	GTF2H4	general transcription factor IIH subunit 4	9,3	52168	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
2354	4504235	GZMK	granzyme K precursor	9,7	28883	1	11,9	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	1	8,8
2355	4504237	SEMA7A	semaphorin-7A isoform 1 preproprotein	7,4	74805	0	0,0	1	10,3	0	0,0	0	0,0	0	0,0	2	15,3	1	11,4
2356	4504251	HIST2H2AA3	histone H2A type 2-A	11,4	14096	0	0,0	0	0,0	5	9,3	0	0,0	0	0,0	0	0,0	0	0,0
2357	4504255	H2AFZ	histone H2A.Z	11,0	13554	8	29,9	11	29,4	14	41,0	8	37,4	11	36,3	10	35,3	10	31,4
2358	4504279	H3F3A	histone H3.3	11,8	15329	6	24,3	4	10,0	1	8,7	0	0,0	5	12,2	2	9,0	2	10,5
2359	4504301	HIST1H4A	histone H4	11,8	11368	88	76,2	51	69,2	47	54,4	63	46,8	59	72,3	63	71,4	62	63,8
2360	4504341	HAT1	histone acetyltransferase type B catalytic subunit	5,4	49494	1	11,7	1	9,7	0	0,0	0	0,0	2	12,2	0	0,0	0	0,0
2361	4504345	HBA1	hemoglobin subunit alpha	9,1	15258	75	31,0	9	19,9	9	18,4	8	18,8	11	24,3	13	20,6	15	21,9
2362	4504351	HBD	hemoglobin subunit delta	8,2	16056	7	14,7	3	19,8	4	18,4	4	18,7	3	24,2	5	17,3	5	16,6
2363	4504511	DNAJA1	dnaJ homolog subfamily A member 1	6,7	44869	2	18,6	6	14,8	3	27,0	5	18,8	5	12,2	3	12,7	2	19,2
2364	4504517	HEL	heat shock protein beta-1	6,0	22783	4	31,8	2	19,6	2	13,6	2	18,8	2	12,2	2	11,7	2	19,8
2365	450469	ITPR2	type 2 inositol 1,4,5-trisphosphate receptor	6,0	308058	1	10,2	1	10,3	1	9,9	0	0,0	0	0,0	1	8,0	0	0,0
2366	4504715	PABPC4	polyadenylate-binding protein 4 isoform 2	9,6	70764	3	26,0	4	20,2	4	13,6	5	18,9	3	24,3	2	14,9	1	10,6
2367	4504813	CD82	CD82 antigen isoform 1	5,0	29626	0	0,0	0	0,0	0	0,0	2	18,8	0	0,0	1	9,8	2	15,7
2368	4504901	KPNA4	importin subunit alpha-4	4,7	57887	1	11,1	1	9,7	1	9,8	0	0,0	0	0,0	4	8,0	1	7,9
2369	4504937	KYNU	kynureninase isoform a	6,6	52352	1	13,7	1	9,8	0	0,0	0	0,0	0	0,0	0	0,0	1	8,8
2370	4504981	LGALS1	galectin-1	5,2	14717	2	14,0	3	10,1	2	13,5	2	18,8	3	12,3	3	9,1	4	9,7
2371	4505029	LTA4H	leukotriene A-4 hydrolase isoform 1	5,8	69286	1	15,1	1	10,0	1	9,3	2	9,5	0	0,0	2	18,6	1	9,8
2372	4505061	M6PR	cation-dependent mannose-6-phosphate receptor isofor	5,5	30975	1	11,6	0	0,0	0	0,0	1	9,5	2	12,1	1	8,9	0	0,0
2373	4505121	MBD4	methyl-CpG-binding domain protein 4	9,0	66051	1	11,1	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2374	4505145	ME2	NAD-dependent malic enzyme, mitochondrial isoform 1	7,4	65425	2	16,2	4	14,8	3	23,3	2	18,8	5	36,2	2	18,1	3	23,1
2375	4505185	MIF	macrophage migration inhibitory factor	8,0	12458	3	11,6	0	0,0	0	0,0	0	0,0	0	0,0	21	9,4	6	9,7
2376	4505241	MPV17	protein Mpv17	9,7	19734	0	0,0	0	0,0	1	9,9	0	0,0	0	0,0	1	8,0	0	0,0
2377	4505317	PPP1R12A	protein phosphatase 1 regulatory subunit 12A isoform	5,2	115262	0	0,0	0	0,0	0	0,0	0	0,0	2	12,2	1	9,3	0	0,0
2378	4505357	NDUFA4	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit	9,7	9352	2	14,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2379	4505365	NDUFB6	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit	10,0	15471	0	0,0	2	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2380	4505409	NME2	nucleoside diphosphate kinase B isoform a	8,7	17280	1	11,5	2	10,0	2	9,3	4	9,5	2	12,2	2	9,1	2	8,8
2381	4505531	OSBP	oxysterol-binding protein 1	6,9	89421	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,8	0	0,0
2382	4505541	USO1	general vesicular transport factor p115	4,7	107889	2	20,0	2	19,3	2	17,8	1	9,5	2	12,2	3	21,9	3	25,1

2383	4505585	HEL	platelet-activating factor acetylhydrolase IB subuni	5,5	25551	1	12,5	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2384	4505591	PRDX1	peroxiredoxin-1	8,2	22111	6	43,0	4	19,9	6	26,9	7	18,8	8	24,2	6	29,5	4	21,2
2385	4505641	PCNA	proliferating cell nuclear antigen	4,4	28770	4	34,4	1	10,0	0	0,0	2	18,7	3	24,2	0	0,0	2	13,5
2386	4505651	PCYT2	ethanolamine-phosphate cytidylyltransferase isoform	6,5	43817	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2387	4505685	PDHA1	pyruvate dehydrogenase E1 component subunit alpha, s	8,0	43277	1	18,0	0	0,0	1	8,6	1	9,5	0	0,0	1	9,0	1	9,6
2388	4505695	PDPK1	3-phosphoinositide-dependent protein kinase 1 isofor	7,0	63133	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,8
2389	4505823	PIR	pirin	6,5	32114	2	11,1	2	14,8	1	9,3	1	9,4	0	0,0	2	11,7	1	9,6
2390	4505939	POLR2A	DNA-directed RNA polymerase II subunit RPB1	7,0	217187	1	9,7	1	10,0	1	8,7	0	0,0	2	12,2	1	8,0	0	0,0
2391	4505941	POLR2B	DNA-directed RNA polymerase II subunit RPB2	6,4	133878	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2392	4506005	HEL	serine/threonine-protein phosphatase PP1-beta cataly	5,8	37169	0	0,0	0	0,0	1	9,8	0	0,0	0	0,0	0	0,0	0	0,0
2393	4506007	PPP1CC	serine/threonine-protein phosphatase PP1-gamma catal	6,1	36966	6	26,7	10	49,5	5	27,6	8	46,8	8	36,3	7	38,4	5	37,2
2394	4506013	PPP1R7	protein phosphatase 1 regulatory subunit 7	4,7	41546	0	0,0	1	9,7	3	19,7	0	0,0	2	12,2	1	9,4	1	9,7
2395	4506019	PPP2R2A	serine/threonine-protein phosphatase 2A 55 kDa regul	5,8	51674	1	11,0	2	14,8	0	0,0	2	18,8	0	0,0	1	8,0	1	8,8
2396	4506029	PPP6C	serine/threonine-protein phosphatase 6 catalytic sub	5,3	35126	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
2397	4506031	PPT1	palmitoyl-protein thioesterase 1 isoform 1 precursor	6,1	34175	1	10,9	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2398	4506057	PRKACB	cAMP-dependent protein kinase catalytic subunit beta	9,1	40604	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
2399	4506061	PRKAG1	5'-AMP-activated protein kinase subunit gamma-1 isof	6,5	37561	0	0,0	0	0,0	0	0,0	1	9,4	0	0,0	1	8,9	0	0,0
2400	4506067	PRKCA	protein kinase C alpha type	6,6	76765	0	0,0	1	9,7	1	9,9	0	0,0	0	0,0	1	9,3	1	8,8
2401	4506133	PRPSAP2	phosphoribosyl pyrophosphate synthase-associated pro	7,2	40907	1	10,6	2	18,9	1	8,7	1	9,5	0	0,0	2	14,9	2	18,0
2402	4506179	PSMA1	proteasome subunit alpha type-1 isoform 2	6,2	29537	2	14,4	3	24,4	2	13,5	4	28,2	2	12,2	2	16,6	2	16,0
2403	4506181	PSMA2	proteasome subunit alpha type-2	7,3	25899	6	23,8	9	20,0	10	32,5	10	28,2	11	48,3	9	30,1	7	18,2
2404	4506183	PSMA3	proteasome subunit alpha type-3 isoform 1	5,1	28415	1	13,5	2	19,8	4	17,9	5	28,1	3	24,2	3	14,9	3	17,5
2405	4506185	PSMA4	proteasome subunit alpha type-4 isoform 1	7,7	29466	2	18,1	1	10,0	2	9,3	4	18,8	2	12,2	1	9,0	1	13,4
2406	4506191	PSMB10	proteasome subunit beta type-10 precursor	7,7	28918	2	16,8	3	14,9	4	18,5	4	9,5	6	12,3	2	11,7	3	13,5
2407	4506193	PSMB1	proteasome subunit beta type-1	8,2	26490	5	33,3	8	49,5	10	59,2	10	46,8	9	36,3	9	47,1	6	39,0
2408	4506195	PSMB2	proteasome subunit beta type-2 isoform 1	6,6	22818	4	25,1	1	10,0	4	23,9	4	28,1	6	36,3	3	18,1	4	24,5
2409	4506205	PSMB9	proteasome subunit beta type-9 proprotein	4,8	23246	1	11,5	0	0,0	1	9,3	1	9,4	0	0,0	1	12,8	1	9,7
2410	4506209	PSMC2	26S protease regulatory subunit 7 isoform 1	5,6	48616	2	18,2	0	0,0	2	14,1	1	9,4	0	0,0	1	9,3	1	9,7
2411	4506217	PSMD10	26S proteasome non-ATPase regulatory subunit 10 isof	5,7	24410	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2412	4506243	PTBP1	polypyrimidine tract-binding protein 1 isoform a	9,5	59615	10	40,6	11	54,3	10	49,6	16	56,1	12	48,3	8	31,6	9	49,9
2413	4506271	PTH1R	parathyroid hormone/parathyroid hormone-related pept	7,9	66342	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2414	4506289	PTPN1	tyrosine-protein phosphatase non-receptor type 1	5,8	49949	2	16,4	1	10,0	1	8,6	1	9,4	2	12,2	1	8,7	2	16,6
2415	4506381	RAC2	ras-related C3 botulinum toxin substrate 2	7,5	21411	2	16,0	1	10,3	1	9,8	0	0,0	0	0,0	1	9,5	2	9,7
2416	4506387	RAD23B	UV excision repair protein RAD23 homolog B isoform 1	4,6	43153	3	16,0	2	14,1	0	0,0	1	9,5	2	12,2	2	13,7	0	0,0
2417	4506399	RAE1	mRNA export factor	7,7	40969	0	0,0	1	9,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2418	4506439	RBBP7	histone-binding protein RBBP7 isoform 2	4,8	47802	2	11,5	2	14,8	1	9,3	2	18,8	2	12,3	2	14,3	3	23,0
2419	4506455	HEL	reticulocalbin-1 precursor	4,7	38891	0	0,0	1	10,4	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2420	4506467	RDX	radixin isoform 2	6,0	68564	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2421	4506473	REL	proto-oncogene c-Rel	5,5	68520	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
2422	4506491	RFC4	replication factor C subunit 4	8,0	39682	1	10,5	3	10,2	1	9,8	2	9,6	0	0,0	0	0,0	1	7,9
2423	4506561	RNF4	E3 ubiquitin-protein ligase RNF4 isoform 1	6,6	21301	1	10,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2424	4506587	RPA3	replication protein A 14 kDa subunit	4,8	13570	0	0,0	0	0,0	2	9,3	0	0,0	2	12,2	2	9,1	2	9,7
2425	4506589	RTCA	RNA 3'-terminal phosphate cyclase isoform b	7,8	39318	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
2426	4506605	RPL23	60S ribosomal protein L23	11,0	14866	2	12,8	2	15,1	3	13,5	2	9,5	2	12,2	1	9,1	3	17,2
2427	4506609	RPL19	60S ribosomal protein L19	12,0	23467	2	19,1	1	10,1	2	13,6	4	18,8	2	12,3	2	17,3	2	18,1
2428	4506617	RPL17	60S ribosomal protein L17 isoform a	10,6	21398	8	32,8	2	14,8	4	22,7	5	28,1	6	48,3	5	30,1	5	25,6
2429	4506619	HEL	60S ribosomal protein L24	11,7	17780	3	19,5	2	10,0	2	18,4	2	18,8	2	12,2	2	18,5	2	13,6
2430	4506621	RPL26	60S ribosomal protein L26	11,0	17259	3	21,0	2	15,1	2	8,7	0	0,0	2	12,2	1	13,2	4	22,7
2431	4506623	RPL27	60S ribosomal protein L27	11,0	15799	6	34,4	6	19,9	2	14,2	7	18,8	5	36,2	3	20,6	3	21,9
2432	4506635	RPL32	60S ribosomal protein L32	11,8	15861	1	11,5	0	0,0	1	9,8	1	9,4	0	0,0	1	8,0	0	0,0
2433	4506645	RPL38	60S ribosomal protein L38	10,6	8219	4	13,1	7	10,1	6	13,6	8	28,2	5	12,2	6	11,7	7	19,3
2434	4506649	RPL3	60S ribosomal protein L3 isoform a	10,6	46110	3	14,4	4	10,0	2	12,7	5	18,8	5	12,2	2	11,8	2	14,7
2435	4506661	RPL7A	60S ribosomal protein L7a	11,1	29996	11	41,7	5	34,6	7	36,1	6	28,2	9	36,3	6	29,4	7	49,6
2436	4506663	RPL8	60S ribosomal protein L8	11,5	28025	3	15,7	4	19,9	4	18,4	5	18,8	5	24,2	3	11,7	4	16,1
2437	4506669	RPLP1	60S acidic ribosomal protein P1 isoform 1	4,0	11496	7	16,1	10	19,9	6	13,6	7	18,8	6	12,3	6	14,9	8	19,2
2438	4506671	RPLP2	60S acidic ribosomal protein P2	4,2	11666	13	58,5	8	39,6	14	45,9	10	28,1	18	48,3	14	44,6	9	37,7
2439	4506675	RPN1	dolichyl-diphosphooligosaccharide--protein glycosylt	5,9	68551	13	89,8	9	44,5	14	82,4	14	93,4	8	48,3	11	70,9	8	58,3
2440	4506681	RPS11	40S ribosomal protein S11	10,7	18432	1	13,9	1	10,0	0	0,0	0	0,0	0	0,0	1	9,3	1	9,7
2441	4506685	RPS13	40S ribosomal protein S13	11,0	17223	8	34,1	3	10,0	5	23,2	6	28,1	9	55,5	6	29,5	4	18,1
2442	4506687	RPS15	40S ribosomal protein S15	10,8	17041	5	26,3	10	19,9	8	18,5	8	28,1	9	24,3	7	17,4	7	21,9
2443	4506695	RPS19	40S ribosomal protein S19	10,7	16061	10	51,3	2	14,8	3	13,6	6	37,4	5	36,3	7	26,3	4	31,4
2444	4506697	RPS20	40S ribosomal protein S20 isoform 2	10,4	13374	4	11,5	4	10,0	5	9,3	1	9,5	6	12,2	3	9,1	5	9,7
2445	4506701	RPS23	40S ribosomal protein S23	11,0	15808	4	24,4	2	15,1	2	18,4	5	28,1	3	12,2	1	9,0	2	15,3

2446	4506715	RPS28	40S ribosomal protein S28	11,2	7842	2	14,4	1	10,2	3	9,3	1	9,4	3	12,2	2	9,0	2	12,3
2447	4506723	RPS3A	40S ribosomal protein S3a isoform 1	10,2	29946	3	23,9	3	22,6	3	22,7	2	18,8	3	24,2	3	21,0	3	22,4
2448	4506741	RPS7	40S ribosomal protein S7	10,6	22128	8	28,1	22	25,1	16	18,5	23	37,5	22	48,4	13	26,6	19	25,1
2449	4506749	RRM1	ribonucleoside-diphosphate reductase large subunit	6,8	90052	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	2	15,7
2450	4506753	RUVBL1	ruvB-like 1	6,0	50229	2	19,3	1	10,3	3	19,6	0	0,0	0	0,0	1	9,5	1	12,9
2451	4506765	S100A4	protein S100-A4	5,8	11729	1	11,6	0	0,0	1	9,8	0	0,0	2	12,1	0	0,0	0	0,0
2452	4506863	SDHC	succinate dehydrogenase cytochrome b560 subunit, mit	10,0	18592	0	0,0	2	10,0	0	0,0	0	0,0	0	0,0	1	8,9	1	8,8
2453	4506889	MAP2K4	dual specificity mitogen-activated protein kinase ki	8,0	44269	0	0,0	1	10,0	1	8,7	0	0,0	0	0,0	1	14,3	0	0,0
2454	4506901	SRSF3	serine/arginine-rich splicing factor 3	12,1	19311	4	37,6	3	19,8	2	14,1	2	9,4	2	12,2	2	9,0	3	15,4
2455	4506903	SRSF9	serine/arginine-rich splicing factor 9	8,9	25524	1	10,8	1	10,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2456	4506921	SGTA	small glutamine-rich tetratricopeptide repeat-contai	4,6	34045	0	0,0	2	19,8	2	9,3	1	9,4	2	12,2	1	8,9	1	7,9
2457	4507129	SNRPE	small nuclear ribonucleoprotein E	9,8	10805	1	11,5	0	0,0	1	9,2	2	9,4	2	12,2	1	9,0	1	10,5
2458	4507135	SNRPN	small nuclear ribonucleoprotein-associated protein N	11,7	24596	1	10,7	1	10,0	1	8,6	1	9,4	0	0,0	0	0,0	1	9,7
2459	4507149	HEL	superoxide dismutase [Cu-Zn]	5,7	15937	1	11,6	0	0,0	1	8,7	1	9,4	0	0,0	0	0,0	1	11,4
2460	4507181	SPN	leukosialin precursor	4,9	40323	2	9,7	2	10,0	0	0,0	0	0,0	0	0,0	1	9,3	1	9,7
2461	4507215	SRP54	signal recognition particle 54 kDa protein isoform 1	9,1	55686	1	10,4	2	15,1	3	8,7	1	9,5	0	0,0	2	12,9	2	13,6
2462	4507231	SSBP1	single-stranded DNA-binding protein, mitochondrial p	9,9	17242	3	21,0	2	10,0	2	14,2	1	9,5	2	21,8	3	18,0	2	16,1
2463	4507241	SSRP1	FACT complex subunit SSRP1	6,4	81075	1	11,7	0	0,0	1	8,7	0	0,0	0	0,0	1	8,0	1	9,6
2464	4507521	HEL107	transketolase isoform 1	7,5	67878	12	61,8	27	39,7	16	49,6	18	56,2	14	48,4	11	44,9	16	61,2
2465	4507525	SEC62	translocation protein SEC62	6,7	45862	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
2466	4507583	FAS	tumor necrosis factor receptor superfamily member 6	7,8	37714	1	11,7	1	9,8	0	0,0	0	0,0	0	0,0	2	18,6	1	9,7
2467	4507605	CD70	CD70 antigen	8,5	21119	2	10,7	2	19,5	1	8,7	1	9,5	0	0,0	3	16,6	3	19,3
2468	4507645	TPI1	triosephosphate isomerase isoform 1	6,5	26670	33	91,9	35	69,2	28	68,4	34	65,4	37	84,4	36	79,7	38	67,0
2469	4507651	HEL	tropomyosin alpha-4 chain isoform 2	4,5	28523	4	38,7	5	28,5	6	36,1	2	17,0	14	81,9	6	34,7	4	38,9
2470	4507669	TPT1	translationally-controlled tumor protein	4,7	19577	2	11,5	1	10,0	1	9,3	0	0,0	3	12,3	1	9,1	1	9,7
2471	4507709	TSTA3	GDP-L-fucose synthase	6,1	35893	0	0,0	1	10,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
2472	4507761	UBA52	ubiquitin-60S ribosomal protein L40 precursor	10,3	14710	19	39,6	12	32,6	11	22,7	11	35,6	15	36,2	8	26,3	10	23,6
2473	4507783	UBE2H	ubiquitin-conjugating enzyme E2 H isoform 1	4,4	20637	1	11,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
2474	4507789	UBE2L3	ubiquitin-conjugating enzyme E2 L3 isoform 1	8,8	17843	5	21,8	5	19,0	5	21,9	6	18,9	9	21,9	4	16,9	5	21,9
2475	4507791	UBE2M	NEDD8-conjugating enzyme Ubc12	7,7	20901	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
2476	4507793	HEL	ubiquitin-conjugating enzyme E2 N	6,2	17139	5	19,4	7	23,8	5	18,5	6	18,9	5	12,3	5	21,2	4	19,9
2477	4507797	UBE2V2	ubiquitin-conjugating enzyme E2 variant 2	8,5	16345	1	12,5	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2478	4507879	VDAC1	voltage-dependent anion-selective channel protein 1	8,9	30754	29	90,7	18	57,4	16	50,1	19	74,7	12	60,3	16	53,2	19	56,9
2479	4507909	WAS	wiskott-Aldrich syndrome protein	6,2	52913	1	11,5	2	10,1	0	0,0	0	0,0	0	0,0	1	9,4	1	9,7
2480	4507913	WASF1	wiskott-Aldrich syndrome protein family member 1	6,0	61634	0	0,0	0	0,0	0	0,0	1	9,5	0	0,0	1	9,3	1	7,9
2481	4507943	XPO1	exportin-1	5,7	123386	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,8	0	0,0
2482	4507949	HEL	14-3-3 protein beta/alpha	4,6	28083	4	34,6	5	29,8	7	31,8	6	28,1	11	48,4	4	29,4	6	25,6
2483	4508047	ZYX	zyxin	6,2	61278	1	9,7	1	9,7	0	0,0	0	0,0	2	12,2	1	9,7	1	7,9
2484	4514554	PTBP3	Rod1	9,5	56502	1	12,8	1	10,3	1	17,7	0	0,0	0	0,0	0	0,0	1	9,7
2485	45181463	TAP1	TAP1	7,2	80919	1	11,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2486	4520225	ROCK2	Rho kinase	5,7	160885	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
2487	4522023	HEL	similar to calgizzarin; similar to PID:g3115349	8,9	11491	0	0,0	0	0,0	1	8,7	1	9,4	2	12,3	2	9,7	1	7,9
2488	452523	WDR43	KIAA0007	5,4	75721	1	11,2	0	0,0	1	9,9	0	0,0	0	0,0	1	9,3	0	0,0
2489	452647	HLA	HLA-C alpha chain (Cw*CL10V)	6,0	40856	0	0,0	1	10,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2490	4529892	HSPA1B	HSP70-2	5,4	70026	1	12,5	5	29,8	3	22,3	1	9,4	0	0,0	2	11,7	4	21,8
2491	4529894	HSPA1L	HSP70-HOM	5,7	70406	1	23,1	2	17,3	4	31,2	2	16,9	2	21,8	3	26,7	3	25,7
2492	45331213	RANBP6	ran-binding protein 6 isoform 1	4,7	124714	2	13,8	0	0,0	0	0,0	0	0,0	2	21,8	2	19,4	1	14,2
2493	45439306	DARS	aspartate--tRNA ligase, cytoplasmic	6,1	57137	4	33,1	3	28,9	4	27,5	4	28,1	5	36,3	4	32,1	4	30,2
2494	45439316	PPIE	peptidyl-prolyl cis-trans isomerase E isoform 2	5,3	33067	0	0,0	1	10,0	0	0,0	0	0,0	0	0,0	0	0,0	2	15,7
2495	45445267	PRPF8	apoptosis-regulated protein 2	9,3	50464	0	0,0	0	0,0	1	8,7	1	9,5	0	0,0	1	9,5	0	0,0
2496	45446743	DDX42	ATP-dependent RNA helicase DDX42	6,6	102975	1	12,0	1	10,0	1	9,9	1	9,5	0	0,0	1	11,7	1	7,9
2497	4557014	CAT	catalase	7,0	59757	1	11,1	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	2	23,3
2498	4557032	HEL	L-lactate dehydrogenase B chain	5,7	36639	20	92,6	20	88,6	25	73,2	19	84,1	31	132,4	19	89,5	15	77,6
2499	4557233	ACADS	short-chain specific acyl-CoA dehydrogenase, mitocho	8,0	44279	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
2500	4557237	ACAT1	acetyl-CoA acetyltransferase, mitochondrial precurso	9,1	45181	8	53,1	5	19,9	6	27,6	6	37,4	5	24,2	6	30,1	6	26,2
2501	4557305	HEL	fructose-bisphosphate aldolase A isoform 1	8,0	39402	27	47,2	20	44,4	16	36,7	17	37,5	22	48,4	31	47,8	21	42,1
2502	4557323	APOC3	apolipoprotein C-III precursor	5,1	10853	2	11,8	0	0,0	0	0,0	0	0,0	0	0,0	1	8,9	0	0,0
2503	4557367	BLMH	bleomycin hydrolase	5,8	52563	0	0,0	2	10,1	0	0,0	1	9,5	0	0,0	1	8,1	1	7,9
2504	4557377	BTK	tyrosine-protein kinase BTK	7,6	76282	2	10,4	1	10,3	1	8,7	0	0,0	0	0,0	2	8,0	1	8,8
2505	4557553	EMD	emerin	5,2	28995	0	0,0	1	9,7	1	8,7	0	0,0	0	0,0	2	17,9	1	11,4
2506	4557587	FAH	fumarylacetoacetase	6,5	46375	0	0,0	1	9,7	1	9,9	0	0,0	0	0,0	1	9,3	2	7,9
2507	4557741	PAFAH1B1	platelet-activating factor acetylhydrolase IB subuni	7,0	46620	2	22,0	1	9,7	1	8,7	0	0,0	0	0,0	1	9,3	2	9,7
2508	4557797	NME1	nucleoside diphosphate kinase A isoform b	5,8	17131	7	29,5	12	29,8	6	34,9	10	37,5	14	36,3	9	28,9	5	30,7

2509	4557831	PCBD1	pterin-4-alpha-carbinolamine dehydratase precursor	6,3	11982	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,8
2510	4557839	PMM2	phosphomannomutase 2	6,4	28083	1	12,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
2511	45595564	NUP210	NUP210 protein	5,8	105810	1	11,1	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2512	45709259	CACYBP	Calcyclin binding protein	8,1	26183	4	32,7	6	39,6	5	27,6	11	37,5	6	24,2	4	31,7	3	21,9
2513	4572588	STAU1	staufen protein	10,0	55289	0	0,0	0	0,0	0	0,0	1	9,4	0	0,0	0	0,0	0	0,0
2514	45751608	MYO1C	Myosin IC	9,7	117949	0	0,0	2	20,4	2	9,3	2	18,8	0	0,0	0	0,0	1	7,9
2515	45786143	LGALS3	Lectin, galactoside-binding, soluble, 3	8,9	26179	0	0,0	1	10,2	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
2516	4581463	PNN	MEMA	6,0	67164	0	0,0	1	10,3	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
2517	45829841	SLC25A5	SLC25A5 protein, partial	10,2	35295	6	38,1	4	24,3	8	36,7	1	9,5	6	36,2	6	27,0	5	22,4
2518	460849	ENSG00000223931	anti-HIV gp120 antibody heavy chain variable region	9,6	15576	0	0,0	0	0,0	1	8,6	0	0,0	0	0,0	0	0,0	0	0,0
2519	46094058	PAPSS1	bifunctional 3'-phosphoadenosine 5'-phosphosulfate	6,4	70815	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
2520	46249393	ARHG	rho-related GTP-binding protein RhoG precursor	8,1	21290	1	11,5	1	10,0	2	18,4	1	9,4	0	0,0	3	26,9	2	21,3
2521	46249756	PDCD6IP	PDCD6IP protein	6,1	96818	1	17,7	1	9,8	1	8,7	0	0,0	0	0,0	2	17,2	1	12,3
2522	46250459	B3GALTL	Beta 1,3-galactosyltransferase-like	7,7	56582	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2523	46253743	IGHG3	immunoglobulin heavy chain	7,1	14215	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
2524	46360168	HEL	prohibitin	5,5	29821	4	31,0	5	25,0	7	37,9	10	65,4	2	12,2	7	39,1	4	36,6
2525	46362557	SF3B3	Splicing factor 3b, subunit 3, 130kDa	5,0	135517	1	10,4	1	10,1	1	9,3	4	28,1	2	12,3	0	0,0	1	7,9
2526	46389558	ENSA	alpha-endosulfine isoform 6	9,1	12819	1	13,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	2	9,7
2527	46593007	UQCRC1	cytochrome b-c1 complex subunit 1, mitochondrial pr	5,9	52627	1	11,5	1	10,3	1	9,3	2	18,8	2	12,1	2	8,9	1	9,7
2528	46812698	SUN2	UNC84B protein, partial	5,4	49424	2	20,8	2	10,0	3	17,2	5	28,1	0	0,0	2	12,9	2	15,7
2529	4688902	ACAP2	centaurin beta2	6,6	87904	0	0,0	2	15,2	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
2530	47076940	HSH2D	unnamed protein product	8,1	32606	0	0,0	1	10,3	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
2531	47078295	ADA	adenosine deaminase	5,6	40765	0	0,0	2	10,0	2	9,3	0	0,0	0	0,0	1	8,9	1	10,6
2532	47115243	TFAM	TFAM	10,1	29083	1	14,9	2	20,4	2	17,2	0	0,0	0	0,0	2	17,5	2	13,5
2533	47123412	RPLP0	RPLP0 protein	8,4	27299	0	0,0	1	10,3	1	9,8	1	9,4	0	0,0	1	8,9	0	0,0
2534	47132589	PKN1	serine/threonine-protein kinase N1 isoform 2	6,0	103913	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2535	47132620	KRT2	keratin, type II cytoskeletal 2 epidermal	8,0	65414	4	44,4	0	0,0	1	9,9	0	0,0	2	12,2	1	9,8	0	0,0
2536	47132622	MTAP	S-methyl-5'-thioadenosine phosphorylase	6,8	31218	1	14,2	0	0,0	0	0,0	1	9,5	0	0,0	1	9,3	1	10,6
2537	47271443	SRSF2	serine/arginine-rich splicing factor 2	12,4	25458	2	12,5	1	10,3	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
2538	473947	DDOST	KIAA0115	5,9	50712	5	33,9	5	29,6	4	18,5	4	18,9	2	12,2	3	20,6	4	23,2
2539	47419914	WARS	tryptophan--tRNA ligase, cytoplasmic isoform a	5,8	53147	44	138,0	39	128,3	39	113,5	18	91,5	28	96,4	38	105,8	37	102,6
2540	47479563	ASB12	Ankyrin repeat and SOCS box-containing 12	5,5	33925	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
2541	47519639	MAP4	microtubule-associated protein 4 isoform 1	5,2	120986	3	12,4	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2542	4757714	ACP1	low molecular weight phosphotyrosine protein phospha	6,3	18024	1	12,1	0	0,0	1	8,6	1	9,4	0	0,0	1	8,9	1	7,9
2543	4757718	ACTL6A	actin-like protein 6A isoform 1	5,3	47462	1	11,4	1	10,1	0	0,0	2	9,5	0	0,0	1	9,0	2	8,0
2544	4757766	ARHGAP1	rho GTPase-activating protein 1	5,8	50436	1	12,5	0	0,0	1	8,7	0	0,0	0	0,0	1	9,7	0	0,0
2545	4757768	HEL	rho GDP-dissociation inhibitor 1 isoform a	4,9	23189	1	10,8	2	9,8	1	8,7	0	0,0	2	12,2	1	9,1	1	9,7
2546	4757798	ATG5	autophagy protein 5	5,4	32448	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
2547	4757812	ATP5J2	ATP synthase subunit f, mitochondrial isoform 2a	10,0	10900	6	22,8	2	10,0	4	18,4	4	18,8	6	24,2	3	17,9	4	19,2
2548	4757876	BST2	bone marrow stromal antigen 2	5,3	19770	1	12,8	3	10,0	2	9,3	0	0,0	3	12,2	2	9,1	3	16,1
2549	4757926	RBM39	RNA-binding protein 39 isoform b	10,6	58657	0	0,0	0	0,0	1	9,8	0	0,0	0	0,0	0	0,0	1	7,9
2550	4757952	CDC42	cell division control protein 42 homolog isoform 1	6,2	21240	4	11,5	3	10,0	6	9,3	2	9,5	3	12,2	5	9,1	3	9,7
2551	4758012	CLTC	clathrin heavy chain 1	5,4	191614	17	132,2	40	177,1	35	170,5	43	195,9	31	192,6	37	209,2	26	165,2
2552	4758018	CNN2	calponin-2 isoform a	7,1	33698	1	10,6	2	10,0	1	9,3	4	18,9	6	24,3	2	12,3	2	12,8
2553	4758040	COX6C	cytochrome c oxidase subunit 6C proprotein	10,8	8763	3	17,6	1	10,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
2554	4758112	DDX39B	spliceosome RNA helicase DDX39B	5,3	48992	3	28,1	5	19,9	2	14,1	7	56,1	3	24,2	2	18,3	3	27,6
2555	4758138	DDX5	probable ATP-dependent RNA helicase DDX5	9,1	69130	2	21,0	2	19,9	3	22,1	4	28,2	11	60,4	2	11,7	2	19,2
2556	4758248	EFNB1	ephrin-B1 precursor	9,2	38007	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2557	4758256	EIF2S1	eukaryotic translation initiation factor 2 subunit 1	4,9	36094	1	12,8	2	19,9	4	23,4	4	28,2	3	24,3	3	26,9	2	18,7
2558	4758304	PDIA4	protein disulfide-isomerase A4 precursor	4,8	72914	20	164,0	11	64,1	13	81,0	11	82,2	8	60,3	11	87,4	10	91,6
2559	4758340	FARSA	phenylalanine--tRNA ligase alpha subunit	7,7	57545	1	11,3	7	29,5	5	33,1	0	0,0	2	12,2	5	35,2	5	27,7
2560	4758442	GMFB	glia maturation factor beta	5,1	16714	1	13,8	1	10,1	0	0,0	1	9,5	0	0,0	1	8,9	1	7,9
2561	4758456	GOSR1	Golgi SNAP receptor complex member 1 isoform 1	9,8	28594	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	0	0,0
2562	4758516	HDGF	hepatoma-derived growth factor isoform a	4,6	26770	2	21,2	4	25,1	1	9,4	1	9,5	0	0,0	2	14,4	2	9,8
2563	4758606	HEL	integrin-linked protein kinase	8,0	51420	2	15,4	1	9,7	1	9,3	0	0,0	0	0,0	1	8,7	1	9,7
2564	4758638	HEL	peroxiredoxin-6	6,0	25036	2	19,7	5	25,0	8	27,6	0	0,0	2	12,2	6	20,5	5	25,6
2565	4758670	LPXN	leupaxin isoform 2	5,6	43333	3	19,2	6	29,8	5	23,3	6	18,8	6	24,2	9	32,6	6	28,2
2566	4758756	NAP1L1	nucleosome assembly protein 1-like 1	4,2	45375	8	53,4	9	49,5	6	36,7	11	56,1	5	36,3	7	44,7	5	35,1
2567	4758774	NDUFB10	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit	8,6	20759	1	11,5	0	0,0	1	9,8	0	0,0	2	12,1	1	8,9	0	0,0
2568	4758790	NDUFS5	NADH dehydrogenase [ubiquinone] iron-sulfur protein	9,5	12499	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2569	4758874	TM9SF2	transmembrane 9 superfamily member 2 precursor	7,1	75757	1	10,5	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	1	7,9
2570	4758906	SERPINB9	serpin B9	5,5	42404	3	34,4	13	74,3	12	73,3	5	28,1	14	84,4	16	77,6	11	67,3
2571	4758940	MP68	6.8 kDa mitochondrial proteolipid isoform 1	10,4	6644	3	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0

2572	4759012	RAB9A	ras-related protein Rab-9A	5,1	22838	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	2	9,8	1	8,8
2573	4759100	SRSF11	serine/arginine-rich splicing factor 11 isoform 1	11,0	53524	1	12,4	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2574	4759112	SLC16A3	monocarboxylate transporter 4	7,9	49470	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
2575	4759156	SNRPA	U1 small nuclear ribonucleoprotein A	10,3	31280	1	11,0	1	10,3	1	8,6	0	0,0	0	0,0	1	9,6	0	0,0
2576	4759158	SNRPD2	small nuclear ribonucleoprotein Sm D2 isoform 1	10,4	13509	1	12,4	0	0,0	3	9,9	0	0,0	0	0,0	1	9,8	2	9,8
2577	4759160	SNRPD3	small nuclear ribonucleoprotein Sm D3	10,7	13898	1	12,2	0	0,0	1	9,2	1	9,4	2	12,2	1	12,8	1	8,8
2578	4759212	TBCA	tubulin-specific chaperone A	5,1	12856	2	10,8	1	10,3	2	13,6	0	0,0	3	24,2	2	14,8	2	17,5
2579	4759224	PDCD5	programmed cell death protein 5	5,7	14286	0	0,0	0	0,0	1	9,8	1	9,4	0	0,0	1	9,7	1	7,9
2580	4759254	TRAF6	TNF receptor-associated factor 6	6,0	59574	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
2581	4759276	RRP9	U3 small nucleolar RNA-interacting protein 2	7,7	51822	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2582	4759302	VAPB	vesicle-associated membrane protein-associated prote	7,1	27210	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
2583	47600819	IGHV	immunoglobulin heavy chain	9,4	12687	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2584	4761483	ENSG00000228325	immunoglobulin lambda light chain variable region	6,4	9368	1	13,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2585	47678375	COMT	COMT	5,2	30070	0	0,0	1	10,0	1	9,3	1	9,5	0	0,0	1	8,0	1	11,4
2586	47681481	USP3	UBP protein	8,2	56649	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2587	47717102	ATP6V1H	V-type proton ATPase subunit H isoform 1	6,0	55865	0	0,0	0	0,0	1	9,9	0	0,0	0	0,0	1	9,4	0	0,0
2588	47938338	HMGA1	HMGA1 protein	11,6	11563	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	1	9,7
2589	47938913	HYOU1	HYOU1 protein	5,5	75344	12	79,7	5	24,7	15	60,4	7	28,1	6	36,2	5	26,0	7	37,2
2590	47939217	INPP4B	INPP4B protein, partial	5,4	92511	1	12,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2591	47939618	HNRPA1	Heterogeneous nuclear ribonucleoprotein A1	9,6	34162	2	10,3	0	0,0	1	9,9	4	9,5	2	12,2	0	0,0	1	11,5
2592	47940482	RPS16	RPS16 protein	11,4	17108	5	32,5	5	29,7	6	27,5	6	28,1	11	36,2	4	23,6	5	28,7
2593	4803698	MYL1	unnamed protein product	4,8	21164	1	11,3	0	0,0	1	13,2	0	0,0	0	0,0	2	9,6	1	9,8
2594	4809279	ANXA7	annexin A7 isoform 2	5,4	52740	1	11,3	2	19,3	3	23,3	1	9,5	0	0,0	1	9,1	2	12,3
2595	48145673	HNRNPH1	HNRPH1	5,8	49131	3	18,5	6	10,0	1	9,9	0	0,0	0	0,0	7	27,8	6	18,4
2596	48145955	NUDT21	CPSF5	9,4	26170	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	11,4
2597	48146215	OXCT	OXCT	7,2	56192	1	11,6	0	0,0	0	0,0	0	0,0	0	0,0	3	26,4	1	12,8
2598	48146259	HEL	CCT2	6,0	57461	0	0,0	3	9,7	0	0,0	0	0,0	0	0,0	2	8,6	0	0,0
2599	48146851	IPO4	IPO4	4,6	82402	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,8	0	0,0
2600	48255933	HMGN1	non-histone chromosomal protein HMG-14	10,1	10641	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,9
2601	48257068	HEL	HSPA8 protein, partial	5,2	64674	68	111,7	31	79,1	34	78,1	34	84,1	49	108,4	34	80,3	35	81,8
2602	48257073	QARS	QARS protein, partial	6,7	81706	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2603	48257074	NMT1	NMT1 protein, partial	7,7	56605	1	11,5	2	15,2	4	22,7	4	28,1	2	12,2	2	21,0	3	24,5
2604	48257075	BCAT2	BCAT2 protein, partial	8,4	42920	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	2	9,7
2605	48257098	HEL	VCP protein, partial	4,8	71066	8	20,8	10	25,0	14	50,1	14	46,8	14	48,3	11	38,3	11	31,4
2606	48257307	TMEM165	TMEM165 protein	6,2	24300	1	12,4	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2607	4826686	DDX1	ATP-dependent RNA helicase DDX1	6,8	82433	2	16,9	4	34,8	4	27,6	8	28,2	9	48,3	4	23,3	3	20,1
2608	4826760	HNRNPF	heterogeneous nuclear ribonucleoprotein F	5,3	45654	9	34,1	9	25,0	9	27,0	10	28,1	11	24,3	6	21,1	10	32,6
2609	4826774	ISG15	ubiquitin-like protein ISG15 precursor	7,4	17869	4	22,6	1	10,0	2	14,2	5	28,2	2	12,3	1	12,6	4	16,1
2610	4826870	HEL	nucleobindin-2 precursor	4,9	50223	1	11,2	1	10,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2611	4826878	OXSR1	serine/threonine-protein kinase OSR1	6,0	58023	1	12,2	0	0,0	1	8,7	1	9,4	0	0,0	1	8,0	0	0,0
2612	4826898	PFN1	profilin-1	8,4	15055	12	24,7	6	10,1	7	9,3	6	9,5	11	12,2	5	9,1	5	12,9
2613	4826908	PIK3R2	phosphatidylinositol 3-kinase regulatory subunit bet	6,1	81606	1	11,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2614	4826932	PPID	peptidyl-prolyl cis-trans isomerase D	6,8	40745	0	0,0	2	15,1	0	0,0	0	0,0	2	12,2	1	8,0	1	7,9
2615	4826964	RAD23A	UV excision repair protein RAD23 homolog A isoform 1	4,4	39591	1	10,7	1	10,1	0	0,0	0	0,0	0	0,0	1	9,4	1	9,8
2616	48376549	RPS4X	RPS4X protein, partial	10,4	27261	5	35,6	3	19,0	8	32,4	8	37,5	6	36,3	2	21,0	3	30,8
2617	4837737	YBX2	germ cell specific Y-box binding protein	11,3	38542	2	14,5	2	10,0	2	14,2	0	0,0	5	24,2	1	9,0	3	22,4
2618	485388	EIF4A2	eukaryotic initiation factor 4AII	5,2	46395	2	11,5	1	9,7	1	8,7	0	0,0	0	0,0	2	12,6	3	21,8
2619	48675813	TNPO2	transportin-2 isoform 2	4,7	100408	0	0,0	1	10,0	1	8,7	0	0,0	0	0,0	1	9,6	1	9,7
2620	4868411	HLA	AF142459_1 MHC class II antigen	5,9	10865	5	21,2	15	19,9	7	18,8	2	9,5	3	24,2	8	9,1	5	22,2
2621	4868427	HLA	AF142467_1 MHC class II antigen	6,1	10835	2	11,4	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2622	48735185	EEF1A1	EEF1A1 protein	9,4	47870	1	12,5	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2623	4877315	HLA	human leucocyte antigen A	6,1	10459	3	11,5	3	10,0	2	9,3	2	9,5	2	12,2	0	0,0	3	9,7
2624	488299	UQCRFS1	Rieske Fe-S protein	8,4	29653	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
2625	4884102	TUBB2B	hypothetical protein	4,7	36816	0	0,0	0	0,0	0	0,0	1	9,4	0	0,0	0	0,0	0	0,0
2626	4884374	AKAP8	hypothetical protein	4,9	39939	0	0,0	0	0,0	1	9,8	0	0,0	0	0,0	0	0,0	0	0,0
2627	4885123	CD80	T-lymphocyte activation antigen CD80 precursor	7,5	33030	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,9	0	0,0
2628	4885153	CRKL	crk-like protein	6,3	33778	1	10,5	1	9,7	1	9,9	0	0,0	2	12,2	2	9,5	1	9,7
2629	4885373	HIST1H1A	histone H1.1	11,5	21843	5	24,1	8	24,7	7	18,4	8	18,8	12	36,3	6	26,2	4	22,4
2630	4885381	HIST1H1B	histone H1.5	11,4	22581	7	57,4	6	24,3	7	54,1	4	18,8	9	36,2	8	47,6	7	43,0
2631	4885417	UBE2K	ubiquitin-conjugating enzyme E2 K isoform 1	5,2	22388	1	12,1	0	0,0	3	19,6	0	0,0	0	0,0	0	0,0	0	0,0
2632	4885545	PDK3	pyruvate dehydrogenase kinase, isozyme 3 isoform 2 p	8,6	46921	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
2633	4885585	SAE1	SUMO-activating enzyme subunit 1 isoform a	5,0	38432	0	0,0	1	10,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2634	48994190	MYOM1	myomesin 1	6,5	187628	1	11,6	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0

2635	4914604	PRPF31	hypothetical protein	5,5	55425	1	13,1	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2636	49168554	G3BP	G3BP	5,3	52165	1	14,4	1	14,0	4	27,6	0	0,0	6	48,3	1	12,3	4	27,0
2637	4929136	TUBA1A	AF141348_1 alpha-tubulin	4,7	36435	0	0,0	0	0,0	1	9,8	1	9,5	2	12,2	2	9,8	0	0,0
2638	4929703	NOP16	AF151875_1 CGI-117 protein	10,3	21149	0	0,0	1	10,0	0	0,0	1	9,4	0	0,0	0	0,0	1	7,9
2639	49355721	FAM162A	protein FAM162A	10,2	17343	1	12,4	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
2640	49456879	BCL2A1	BCL2A1	5,2	20265	1	11,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
2641	49472822	EIF3G	eukaryotic translation initiation factor 3 subunit	5,8	35593	1	12,1	0	0,0	0	0,0	1	9,4	0	0,0	0	0,0	1	8,8
2642	495126	RPL11	ribosomal protein L11	9,9	20116	2	13,1	3	15,1	2	9,3	7	28,1	5	24,2	2	9,1	2	9,7
2643	49522841	LGALS9C	Lectin, galactoside-binding, soluble, 9C	9,4	39615	1	11,9	0	0,0	1	9,3	1	9,4	0	0,0	1	8,0	1	7,9
2644	49659929	HIST2H2BD	histone H2B/s	11,0	18019	1	13,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2645	498156	POP1	KIAA0061	9,0	101433	1	9,6	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	1	9,7
2646	49900979	CAPN1	CAPN1 protein	5,3	81831	4	32,3	4	29,5	2	17,2	4	18,8	5	36,3	4	29,8	2	15,5
2647	5002645	EIF5B	IF2 protein	5,3	138811	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,8
2648	5020074	HEL	AF146651_1 glyoxalase-I	5,1	20721	2	12,5	3	14,9	3	18,5	2	9,5	2	12,3	2	15,5	0	0,0
2649	50250919	MMA	malignant melanoma associated protein	10,7	5456	1	10,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2650	50262342	SUB1	activated RNA polymerase II transcription cofactor 4	9,1	8637	1	11,5	0	0,0	1	9,8	2	18,8	5	24,2	2	9,3	1	8,8
2651	50301240	EXOSC10	exosome component 10 isoform 1	8,5	100832	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	1	8,0
2652	5031571	ACTR2	actin-related protein 2 isoform b	6,3	44761	7	39,3	6	28,5	8	41,5	11	56,1	8	48,3	10	48,3	10	47,3
2653	5031595	ARPC4	actin-related protein 2/3 complex subunit 4 isoform	8,7	19649	4	15,9	1	10,1	8	31,9	5	28,2	5	24,2	3	23,8	2	18,1
2654	5031599	ARPC2	actin-related protein 2/3 complex subunit 2	7,0	34315	3	25,6	7	34,6	3	18,4	6	37,5	6	36,3	5	24,0	2	12,3
2655	5031601	ARPC1B	actin-related protein 2/3 complex subunit 1B	8,3	40932	6	43,6	5	29,7	3	22,7	2	26,2	5	36,3	4	30,1	2	21,3
2656	5031635	HEL	cofilin-1	8,2	18503	28	46,8	14	39,6	12	36,7	19	46,8	23	60,4	15	39,0	12	35,2
2657	5031707	LRRC32	leucine-rich repeat-containing protein 32 precursor	5,7	71961	1	11,6	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
2658	5031741	DNAJA2	dnaJ homolog subfamily A member 2	6,0	45746	2	10,5	4	14,9	3	17,3	4	18,8	0	0,0	2	8,9	2	15,3
2659	5031767	HSF1	heat shock factor protein 1	4,9	57261	0	0,0	1	9,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2660	5031789	IMPA1	inositol monophosphatase 1 isoform 1	5,0	30190	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2661	5031851	STMN1	stathmin isoform a	5,7	17303	0	0,0	1	9,7	1	9,8	0	0,0	0	0,0	2	9,6	0	0,0
2662	5031897	MAB21L1	protein mab-21-like 1	8,7	40957	1	11,6	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2663	5031947	NIT1	nitrilase homolog 1 isoform 1	7,6	35897	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	1	9,7
2664	5031973	PDIA6	protein disulfide-isomerase A6 precursor	4,8	48103	34	93,9	17	64,2	19	83,0	19	65,5	18	96,4	21	75,1	19	86,0
2665	5031977	NAMPT	nicotinamide phosphoribosyltransferase precursor	6,7	55503	3	24,2	21	83,9	19	73,9	12	65,5	5	24,3	21	76,6	18	71,1
2666	5031981	PSMD14	26S proteasome non-ATPase regulatory subunit 14	6,1	34559	1	16,3	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
2667	5031985	NUTF2	nuclear transport factor 2	5,0	14479	1	10,5	1	9,7	1	8,7	0	0,0	0	0,0	1	8,0	0	0,0
2668	5032007	PURA	transcriptional activator protein Pur-alpha	6,0	34892	1	11,3	0	0,0	0	0,0	0	0,0	0	0,0	1	9,4	1	9,8
2669	5032051	RPS14	40S ribosomal protein S14	10,5	16274	6	38,6	4	25,0	4	22,7	4	18,8	9	36,3	4	23,7	4	23,0
2670	5032131	STX6	syntaxin-6	4,7	29177	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	1	8,0
2671	5032161	TCEB1	transcription elongation factor B polypeptide 1 isof	4,6	12455	0	0,0	0	0,0	0	0,0	1	9,4	0	0,0	0	0,0	0	0,0
2672	5032181	TIMM17B	mitochondrial import inner membrane translocase subu	9,3	18255	1	12,5	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2673	5032193	TRAF1	TNF receptor-associated factor 1 isoform a	5,7	46145	1	11,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2674	50345294	HN1	hematological and neurological expressed 1 prote	8,3	19898	1	11,9	0	0,0	1	8,8	0	0,0	3	24,2	2	18,6	1	9,8
2675	50345988	ATP5C1	ATP synthase subunit gamma, mitochondrial isofor	9,6	32978	5	24,1	4	19,8	3	23,3	6	28,1	2	12,2	3	20,6	3	25,0
2676	50415798	LMNB1	LMNB1 protein, partial	5,2	38142	3	27,3	7	39,6	5	37,3	5	37,5	9	72,3	6	38,8	4	31,4
2677	50428938	ASNA1	ATPase ASNA1	4,7	38794	1	10,9	1	9,7	1	8,7	0	0,0	2	12,2	1	9,1	1	9,7
2678	50592988	UQCRC2	cytochrome b-c1 complex subunit 2, mitochondrial pr	8,9	48425	5	49,5	3	19,9	7	50,1	8	37,5	5	36,2	6	40,8	6	42,4
2679	50592994	TXN	thioredoxin isoform 1	4,7	11738	4	10,9	3	10,3	2	9,3	0	0,0	0	0,0	4	8,7	2	9,7
2680	50592996	TUBB3	tubulin beta-3 chain isoform 1	4,7	50433	0	0,0	0	0,0	1	9,9	0	0,0	0	0,0	1	15,9	0	0,0
2681	50658063	SMC4	structural maintenance of chromosomes protein 4	6,4	147163	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	0	0,0
2682	50845388	ANXA2	annexin A2 isoform 1	8,5	40412	1	11,5	0	0,0	0	0,0	0	0,0	2	12,3	1	9,8	0	0,0
2683	509243	PPP2R4	phosphotyrosyl phosphatase activator	5,9	36790	2	9,7	1	10,0	0	0,0	0	0,0	0	0,0	1	8,1	1	9,7
2684	509291	ATP5F1	H+-ATP synthase subunit b	9,7	28895	4	33,6	8	39,6	6	22,7	7	37,5	3	12,2	4	17,5	5	25,6
2685	510307	EIF4G3	translation initiationfactor eIF-4gamma	5,3	79402	0	0,0	0	0,0	2	8,6	1	9,4	2	12,2	1	8,0	1	12,7
2686	5107134	HLA	AF148862_1 MHC class I antigen heavy chain	5,8	40885	4	10,5	3	10,1	2	13,6	2	9,5	3	12,3	0	0,0	1	9,7
2687	51094479	RPL35	similar to 60S ribosomal protein L35	11,5	11492	1	10,4	0	0,0	0	0,0	1	9,4	0	0,0	0	0,0	0	0,0
2688	51094492	MYO1G	myosin IG	8,9	116440	4	31,9	11	59,1	9	67,5	8	46,8	8	60,3	10	72,5	6	39,7
2689	51094513	PGAM2	phosphoglycerate mutase 2 (muscle)	9,8	28220	6	24,6	4	10,0	7	27,5	5	18,8	8	24,2	7	20,6	8	22,4
2690	51094727	SEPT7	similar to cell division cycle 10 homolog	8,7	44830	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
2691	51094799	RPL17	similar to 60S ribosomal protein L17 (L23) (Amino aci	9,6	11885	1	10,4	2	10,3	1	8,7	1	9,5	0	0,0	1	8,0	3	9,8
2692	51094802	RPS17L	similar to dJ753D5.2 (novel protein similar to RPS17	9,6	13741	1	11,8	1	10,0	1	9,2	1	9,4	3	12,2	1	9,0	1	9,7
2693	51094813	RPL15	similar to 60S ribosomal protein L15	9,8	23771	1	10,7	0	0,0	10	8,7	0	0,0	0	0,0	0	0,0	5	10,6
2694	51094832	RPS14	similar to ribosomal protein S14	9,4	38560	1	10,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
2695	51094833	EEF1B2	similar to eukaryotic translation elongation factor 1	4,5	24873	2	15,4	2	10,0	4	18,4	6	28,1	2	12,2	2	12,1	2	12,3
2696	51094858	TPI1	similar to Triosephosphate isomerase (TIM)	9,6	24344	1	11,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2697	51094896	RPS27	similar to ribosomal protein S27	9,9	16879	1	11,4	0	0,0	0	0,0	2	9,4	0	0,0	1	9,7	2	9,6

2698	51094971	EIF4H	similar to mKIAA0038 protein	9,2	32605	1	10,8	0	0,0	1	9,8	1	9,4	0	0,0	1	9,3	1	9,7
2699	51094986	TPM3	similar to tropomyosin 3	4,3	24802	1	11,7	3	10,0	2	9,3	2	9,5	2	12,2	1	9,1	1	9,7
2700	51095055	HSPA8	similar to Chain , Heat-Shock Cognate 70kd Protein (4	7,8	25580	5	27,8	4	14,8	7	27,5	7	18,8	14	36,3	5	24,2	5	22,4
2701	51095083	RPS2	similar to 40S ribosomal protein S2	10,3	21070	6	25,9	5	19,9	5	18,4	2	9,5	5	12,2	2	14,7	3	15,5
2702	51095143	NRCAM	neuronal cell adhesion molecule	5,5	131020	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
2703	51103375	ENSG00000223931	immunoglobulin variable region VH gamma domain	7,2	12898	0	0,0	0	0,0	0	0,0	0	0,0	2	12,1	0	0,0	0	0,0
2704	51105870	PSMC5	hypothetical protein DKFZp586I1420	9,9	14972	0	0,0	0	0,0	1	9,3	1	9,4	0	0,0	1	8,9	2	9,7
2705	51173724	BYSL	bystin	8,2	49602	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
2706	51243055	MTFP1	mitochondrial fission process protein 1 isoform a	9,6	17992	1	11,1	1	10,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
2707	512470	HLA	HLA-DMA	4,5	28832	1	11,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2708	5138928	SCFD1	vesicle transport-related protein	6,0	72481	1	11,3	1	9,7	0	0,0	0	0,0	0	0,0	1	9,0	1	8,8
2709	51476877	HYOU1	hypothetical protein	9,5	13820	6	22,8	3	14,8	4	18,4	1	9,4	2	12,2	4	14,8	4	19,3
2710	51477078	CNNM3	hypothetical protein	9,5	15389	1	11,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2711	51477111	DHTKD1	hypothetical protein	6,4	60910	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,1	0	0,0
2712	51477708	HNRNPD	heterogeneous nuclear ribonucleoprotein D0 isofo	8,7	30654	1	11,1	2	10,0	2	9,3	2	9,5	2	12,2	2	12,1	2	9,7
2713	51479156	ATP5L	ATP synthase subunit g, mitochondrial	10,0	11410	2	14,6	0	0,0	1	9,3	0	0,0	0	0,0	1	9,1	1	10,6
2714	516516	KIF5A	neuronal kinesin heavy chain	5,6	117392	0	0,0	1	9,7	1	8,7	0	0,0	0	0,0	0	0,0	0	0,0
2715	5174391	HEL	alcohol dehydrogenase [NADP(+)]	6,3	36574	5	43,1	4	32,9	4	31,0	6	54,3	5	36,3	5	29,0	3	30,0
2716	5174419	CLPP	putative ATP-dependent Clp protease proteolytic subu	8,1	30162	0	0,0	0	0,0	2	17,2	0	0,0	0	0,0	1	9,0	1	10,6
2717	5174613	NAP1L4	nucleosome assembly protein 1-like 4	4,4	42824	2	10,4	3	10,0	2	8,7	0	0,0	3	24,3	1	15,2	1	9,7
2718	5174731	TSNAX	translin-associated protein X	6,1	33113	1	10,4	1	10,0	0	0,0	1	9,4	0	0,0	2	12,8	0	0,0
2719	5174735	TUBB4B	tubulin beta-4B chain	4,6	49832	1	11,4	2	14,8	2	18,4	0	0,0	2	21,9	2	16,8	3	19,3
2720	5174741	UCHL3	ubiquitin carboxyl-terminal hydrolase isozyme L3 iso	4,7	26164	2	22,3	0	0,0	1	8,7	2	18,9	0	0,0	1	8,9	1	9,7
2721	51873036	OGDH	2-oxoglutarate dehydrogenase, mitochondrial isoform	6,4	115916	2	13,2	2	10,0	4	27,6	0	0,0	2	12,2	2	17,4	3	20,7
2722	51944953	NOMO1	nodal modulator 1 precursor	5,5	134324	1	10,9	1	10,0	0	0,0	0	0,0	2	12,2	1	8,0	0	0,0
2723	520587	PRKCD	protein kinase C delta-type	7,5	71935	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2724	5231228	RNASET2	ribonuclease T2 precursor	6,7	29482	0	0,0	1	10,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2725	52487191	ERP44	endoplasmic reticulum resident protein 44 precursor	5,0	46953	0	0,0	1	10,3	1	8,7	0	0,0	0	0,0	2	16,8	1	9,7
2726	52545516	SUCLG2	hypothetical protein	5,2	20484	1	11,7	0	0,0	1	9,9	0	0,0	0	0,0	0	0,0	0	0,0
2727	52545709	PTCD3	hypothetical protein	5,8	41920	0	0,0	0	0,0	0	0,0	1	9,5	0	0,0	0	0,0	0	0,0
2728	52545797	SMARCC2	hypothetical protein	9,9	11528	1	10,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2729	5262459	NDUFB8	hypothetical protein	6,3	21730	1	10,8	0	0,0	0	0,0	0	0,0	0	0,0	2	18,5	1	10,5
2730	5262545	ORC3	hypothetical protein	7,5	82410	0	0,0	0	0,0	1	8,6	1	9,4	0	0,0	0	0,0	0	0,0
2731	5262636	ATG4B	hypothetical protein	4,8	44310	1	12,2	1	9,7	0	0,0	0	0,0	0	0,0	1	8,1	0	0,0
2732	52627149	TERF2IP	telomeric repeat-binding factor 2-interacting prote	4,5	44242	1	11,1	1	10,1	0	0,0	0	0,0	0	0,0	1	9,4	1	9,8
2733	52630342	HLA	HLA class I histocompatibility antigen, Cw-1 alpha	5,6	40630	8	21,8	10	18,0	7	14,7	5	15,1	3	21,9	4	15,7	19	16,8
2734	5281124	ALG6	AF102851_1 dolichyl-P-Glc:Man9GlcNAc2-PP-dolichyl gluc	8,4	58162	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
2735	5292161	PSMD4	26S proteasome non-ATPase regulatory subunit 4	4,5	40718	1	14,1	1	10,3	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
2736	5305706	PACSIN2	AF128536_1 cytoplasmic phosphoprotein PACSIN2	5,0	55887	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	13,1
2737	531167	PSME3	Ki nuclear autoantigen	6,1	30886	1	11,6	1	9,7	2	9,3	0	0,0	0	0,0	0	0,0	1	9,7
2738	535895	N/A	TCR delta chain (VJ)	10,2	2935	0	0,0	0	0,0	1	9,8	0	0,0	0	0,0	0	0,0	0	0,0
2739	53831995	SF3A1	splicing factor 3A subunit 1 isoform 2	5,1	81659	2	25,7	1	10,3	3	17,8	0	0,0	2	12,2	2	13,3	2	19,2
2740	5410451	MX1	AF135187_1 interferon-induced protein p78	5,5	75516	28	118,7	30	143,5	20	101,2	39	177,3	35	144,5	18	89,1	28	114,9
2741	54112117	SF3B1	splicing factor 3B subunit 1 isoform 1	6,7	145811	2	15,9	2	19,6	3	22,7	5	28,1	3	24,3	5	41,5	3	21,8
2742	54311161	RAB33B	RAB33B, member RAS oncogene family	6,5	25699	1	12,8	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2743	5453539	PAICS	multifunctional protein ADE2 isoform 2	7,0	47061	2	21,9	1	9,8	2	17,8	1	9,4	3	24,2	2	17,5	1	12,3
2744	5453549	HEL	peroxiredoxin-4 precursor	5,8	30541	2	15,5	1	9,7	2	13,5	1	9,4	3	24,2	2	14,7	3	19,8
2745	5453559	ATP5H	ATP synthase subunit d, mitochondrial isoform a	5,1	18473	5	27,4	5	29,5	4	22,7	1	9,5	2	12,1	6	26,9	5	28,8
2746	5453597	CAPZA1	F-actin-capping protein subunit alpha-1	5,4	32905	8	37,5	8	29,8	7	27,6	8	37,5	12	60,4	7	27,5	8	33,5
2747	5453599	CAPZA2	F-actin-capping protein subunit alpha-2	5,5	32931	4	26,5	3	14,8	5	27,6	5	18,8	3	12,2	3	14,9	4	19,8
2748	5453607	CCT7	T-complex protein 1 subunit eta isoform a	7,5	59348	3	28,7	7	39,3	10	59,3	10	65,5	11	60,3	8	43,9	9	61,1
2749	5453668	ATG7	ubiquitin-like modifier-activating enzyme ATG7 isofo	5,8	77941	0	0,0	0	0,0	1	8,7	1	9,4	2	12,2	0	0,0	0	0,0
2750	5453690	DNAJB1	dnaJ homolog subfamily B member 1	8,9	38045	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	2	9,3	1	9,7
2751	5453760	NEDD8	NEDD8 precursor	9,1	9072	1	11,5	2	19,3	2	14,1	0	0,0	0	0,0	2	12,2	0	0,0
2752	5453958	PPP5C	serine/threonine-protein phosphatase 5 isoform 1	5,9	56860	1	11,3	0	0,0	0	0,0	1	9,4	0	0,0	0	0,0	0	0,0
2753	5453980	DNAJC3	dnaJ homolog subfamily C member 3 precursor	5,8	57562	2	19,8	0	0,0	0	0,0	0	0,0	2	12,4	0	0,0	0	0,0
2754	5453990	PSME1	proteasome activator complex subunit 1 isoform 1	5,7	28705	12	38,4	16	69,3	26	86,7	17	74,8	15	72,5	13	52,9	12	72,2
2755	5453994	RAD21	double-strand-break repair protein rad21 homolog	4,4	71671	1	12,4	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2756	5454002	DNPH1	deoxyribonucleoside 5'-monophosphate N-glycosidase i	4,8	19090	1	11,5	1	9,8	1	9,9	0	0,0	0	0,0	1	8,1	0	0,0
2757	5454004	DPF2	zinc finger protein ubi-d4	5,9	44156	1	11,6	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2758	5454084	SPTLC1	serine palmitoyltransferase 1 isoform a	5,7	52726	0	0,0	0	0,0	1	9,9	0	0,0	0	0,0	0	0,0	0	0,0
2759	5454096	STK4	serine/threonine-protein kinase 4	4,8	55631	0	0,0	2	10,0	2	13,5	2	18,8	0	0,0	2	9,6	3	17,5
2760	5454132	TNFAIP3	tumor necrosis factor alpha-induced protein 3	8,1	89596	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	1	8,8

2761	5454154	PPIH	peptidyl-prolyl cis-trans isomerase H	8,1	19190	1	10,9	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	1	9,8
2762	5454158	VARS	valine--tRNA ligase	7,3	140476	1	11,8	3	24,7	2	9,3	1	9,5	5	12,2	3	20,4	3	18,1
2763	5457339	ENSG00000228325	immunoglobulin light chain variable region	4,8	8931	0	0,0	0	0,0	1	9,8	0	0,0	0	0,0	0	0,0	0	0,0
2764	54607053	PRIC295	translational activator GCN1	7,1	292709	6	40,9	2	20,5	7	41,0	2	9,5	3	24,3	5	41,6	3	26,4
2765	54648253	KHSRP	KHSRP protein	7,8	72897	1	17,0	1	9,8	1	9,9	4	18,8	3	24,2	3	24,3	3	28,0
2766	54673639	BID	BH3 interacting domain death agonist	6,6	26828	1	9,7	0	0,0	2	18,4	1	9,5	0	0,0	2	14,4	2	13,6
2767	546901	ACAT2	cytosolic acetoacetyl-coenzyme A thiolase	6,3	41277	4	24,1	1	10,0	1	9,3	2	18,8	3	12,2	3	23,8	1	10,6
2768	54695940	RAB11B	RAB11B, member RAS oncogene family	5,4	24490	2	21,4	1	10,0	3	19,6	4	18,8	2	12,2	2	13,7	1	7,9
2769	54696300	PSMA5	proteasome (prosome, macropain) subunit, alpha type,	4,6	26407	2	19,9	2	19,6	3	27,0	2	18,8	6	36,2	4	27,3	4	26,2
2770	54696428	HMGB2	high-mobility group box 2	8,3	23905	0	0,0	1	10,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
2771	54792069	SUMO2	small ubiquitin-related modifier 2 isoform a precur	5,2	10853	1	11,5	1	10,0	1	9,2	1	9,4	2	12,2	2	8,9	2	10,5
2772	54792138	HELZ	probable helicase with zinc finger domain	7,0	218979	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
2773	54859722	NUP160	nuclear pore complex protein Nup160	5,2	162121	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
2774	550021	RPS5	ribosomal protein S5	9,9	22778	1	12,3	0	0,0	3	9,3	1	9,5	0	0,0	0	0,0	1	7,9
2775	550023	RPS9	ribosomal protein S9	11,2	22572	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2776	550343	BCAP31	BAP31	8,4	28007	1	11,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,8	1	8,8
2777	551622	IARS	isoleucyl-tRNA synthetase	5,8	144959	1	12,1	2	15,1	5	17,8	5	28,1	0	0,0	4	21,0	7	44,1
2778	551638	SSR1	SSR alpha subunit	4,3	32184	1	11,7	0	0,0	0	0,0	1	9,4	2	12,2	2	14,3	0	0,0
2779	5524927	TREX1	deoxyribonuclease III (DNase III)	8,1	32376	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,7	1	9,8
2780	55249572	CSNK2A1	CSNK2A1 protein	7,9	45909	0	0,0	0	0,0	1	9,3	0	0,0	0	0,0	0	0,0	1	11,4
2781	5531827	NSFL1C	p47	4,9	40573	2	13,4	2	10,1	0	0,0	0	0,0	0	0,0	1	9,4	1	9,8
2782	5542014	DKC1	dyskerin	9,8	58736	2	13,5	2	15,1	2	17,8	2	18,8	0	0,0	1	8,7	3	23,3
2783	55613379	C14orf166	CLE	6,0	27970	2	10,4	3	10,0	3	9,3	4	18,8	2	12,2	4	17,6	3	9,7
2784	55663118	MGST3	microsomal glutathione S-transferase 3	10,2	18399	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
2785	55663902	LYPLAL1	lysophospholipase-like 1	7,8	26317	0	0,0	2	19,9	0	0,0	0	0,0	0	0,0	1	9,3	1	12,7
2786	55664827	SNX27	sorting nexin family member 27	6,0	61266	1	10,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2787	55665464	MACF1	microtubule-actin crosslinking factor 1	5,1	670114	0	0,0	1	10,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2788	55665638	ASCC3	novel RNA helicase family (RNAH) protein	6,7	250484	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2789	55665781	TPM3	tropomyosin 3	4,6	28923	3	19,9	3	9,8	2	9,3	0	0,0	6	12,3	3	9,1	1	9,7
2790	55741709	RBM25	RNA-binding protein 25	6,0	100186	0	0,0	1	10,1	1	9,3	0	0,0	2	12,3	0	0,0	1	9,7
2791	557468	MYO1E	myosin-IC	9,2	127041	0	0,0	1	10,3	1	9,8	0	0,0	0	0,0	1	9,7	1	16,0
2792	55749769	CWC22	pre-mRNA-splicing factor CWC22 homolog	6,6	105448	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
2793	55770850	CYP24A1	1,25-dihydroxyvitamin D(3) 24-hydroxylase, mitochon	8,9	58857	3	11,2	1	10,0	2	9,2	0	0,0	0	0,0	2	8,9	0	0,0
2794	558526	PSMB5	proteasome subunit X	8,7	22898	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2795	558596	PREP	prolyl oligopeptidase	5,4	80764	1	11,9	0	0,0	0	0,0	0	0,0	0	0,0	1	8,9	1	11,5
2796	55859735	CAP1	CAP, adenylate cyclase-associated protein 1 (yeast)	7,3	28674	1	10,9	0	0,0	1	9,9	0	0,0	0	0,0	0	0,0	0	0,0
2797	55859738	CAP1	CAP, adenylate cyclase-associated protein 1 (yeast)	8,0	51883	6	11,6	9	10,1	9	9,4	6	9,5	11	12,3	7	9,1	6	9,8
2798	55953123	RWDD1	RWD domain-containing protein 1 isoform a	3,9	27921	0	0,0	1	10,0	0	0,0	1	9,5	0	0,0	0	0,0	0	0,0
2799	55956788	NCL	nucleolin	4,4	76615	18	112,8	21	94,0	20	104,4	24	84,1	32	144,5	20	109,2	12	79,1
2800	55956916	MYO1E	unconventional myosin-Ie	9,2	127062	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
2801	55956919	HNRNPAB	heterogeneous nuclear ribonucleoprotein A/B isoform	6,6	35949	1	11,5	1	10,0	2	9,3	1	9,4	3	12,2	1	9,0	1	9,7
2802	55957227	PEA15	phosphoprotein enriched in astrocytes 15	4,7	17288	4	15,3	3	10,1	1	9,3	1	9,5	2	12,2	2	14,2	3	9,7
2803	55957228	PEA15	phosphoprotein enriched in astrocytes 15	4,9	12512	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
2804	55957503	LMNA	lamin A/C	6,6	55763	1	9,7	3	10,0	4	9,4	1	9,5	2	12,3	4	9,1	4	9,8
2805	55958559	MRPL2	novel protein	11,8	32971	1	11,6	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
2806	55959242	SPATA6	spermatogenesis associated 6	8,9	28924	0	0,0	0	0,0	0	0,0	1	9,4	0	0,0	0	0,0	0	0,0
2807	55960095	DST	dystonin	5,0	857309	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
2808	55960587	SF3B4	splicing factor 3b, subunit 4, 49kDa	5,8	20690	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	1	8,0	1	7,9
2809	55961074	KIF2C	kinesin family member 2C	9,4	37922	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	0	0,0
2810	55961080	RPS8	ribosomal protein S8	10,8	21880	1	14,7	2	19,9	1	9,3	1	9,5	2	12,2	1	9,0	1	8,8
2811	55962163	RHOC	ras homolog gene family, member C	7,9	21995	0	0,0	0	0,0	0	0,0	1	9,5	0	0,0	0	0,0	0	0,0
2812	559703	CYFIP1	KIAA0068	6,7	147136	1	19,4	5	29,4	3	18,4	4	9,5	2	12,2	2	14,7	3	24,8
2813	56159917	MYO18A	SP-A receptor subunit SP-R210 alphaS	5,6	180550	1	11,2	1	10,0	0	0,0	1	9,5	0	0,0	0	0,0	0	0,0
2814	56203414	SNX3	sorting nexin 3	6,4	16316	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	1	9,7
2815	56203428	CPNE1	copine I	5,6	42733	1	13,4	0	0,0	0	0,0	0	0,0	0	0,0	1	9,5	1	9,7
2816	56203793	MICAL1	microtubule associated monoxygenase, calponin and LI	10,0	26793	0	0,0	1	10,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2817	56203953	PYCR2	pyrroline-5-carboxylate reductase family, member 2	6,1	19599	1	13,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2818	56204043	PSMA7	proteasome (prosome, macropain) subunit, alpha type,	9,3	21085	2	14,0	3	14,8	2	13,6	2	18,8	2	12,2	2	11,7	2	9,7
2819	56204205	CCBL2	cysteine conjugate-beta lyase 2	8,2	29888	1	10,5	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2820	56204396	ATP1A1	ATPase, Na+/K+ transporting, alpha 1 polypeptide	5,3	16057	1	13,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2821	56205083	CD58	CD58 molecule	5,8	27019	0	0,0	0	0,0	0	0,0	1	9,4	0	0,0	0	0,0	0	0,0
2822	56205490	ACADM	acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight	7,7	50252	10	61,1	4	24,9	10	45,9	2	18,8	8	36,2	6	23,8	6	34,6
2823	56208229	SRPK1	SFRS protein kinase 1	5,8	74226	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0

2824	56243533	SDF2L1	stromal cell-derived factor 2-like protein 1 precur	6,6	23580	1	11,6	0	0,0	1	9,3	0	0,0	2	12,2	1	9,1	1	9,7
2825	563646	IGHM	Ig rearranged alpha-chain gene VH1-DN1-JH4 region, mono	9,9	13408	1	14,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2826	56407627	RPL34	leukemia-associated protein	11,6	7038	1	12,4	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
2827	56549135	TAGLN3	transgelin-3	7,2	22474	0	0,0	0	0,0	1	9,8	0	0,0	0	0,0	1	9,5	1	11,4
2828	56550081	BUB3	mitotic checkpoint protein BUB3 isoform b	6,4	36936	1	10,8	0	0,0	1	9,3	0	0,0	2	12,2	1	8,7	2	9,7
2829	565651	PSMB4	proteasome subunit HsN3	5,6	29193	3	24,1	2	19,9	1	9,3	5	28,2	5	36,3	2	11,7	1	8,8
2830	56676330	HP1BP3	heterochromatin protein 1-binding protein 3	10,1	61189	1	11,3	2	9,7	1	8,7	0	0,0	0	0,0	2	11,7	1	10,6
2831	56682959	FTH1	ferritin heavy chain	5,2	21227	0	0,0	0	0,0	1	8,6	0	0,0	0	0,0	1	9,3	0	0,0
2832	56699409	RBMX	RNA-binding motif protein, X chromosome isoform 1	10,3	42314	1	14,1	2	14,8	2	9,3	0	0,0	3	24,2	1	9,0	2	10,6
2833	56789234	TARS	TARS protein, partial	6,5	78606	4	42,2	2	19,9	1	8,7	1	9,5	0	0,0	1	8,7	2	17,5
2834	56790945	PPP1CA	serine/threonine-protein phosphatase PP1-alpha c	6,2	38613	1	10,4	1	10,0	0	0,0	0	0,0	2	12,2	1	8,0	0	0,0
2835	5679490	IGHV1	immunoglobulin heavy chain variable region	8,1	13998	1	12,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2836	56847620	BTF3L4	transcription factor BTF3 homolog 4 isoform 1	5,9	17252	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,8	0	0,0
2837	5689403	KIAA1033	KIAA1033 protein	7,2	138430	1	9,7	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	0	0,0
2838	5689551	KIAA1107	KIAA1107 protein	5,9	140800	0	0,0	0	0,0	0	0,0	1	9,4	0	0,0	0	0,0	0	0,0
2839	56972026	EIF2S3L	Unknown (protein for IMAGE:30389268), partial	7,7	50404	0	0,0	1	10,0	0	0,0	0	0,0	0	0,0	1	9,4	0	0,0
2840	57013276	TUBA1B	tubulin alpha-1B chain	4,8	50152	1	10,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,8
2841	57014043	LMNA	lamin A/C transcript variant 1	6,8	74082	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	2	19,4	0	0,0
2842	57160757	HUWE1	HECT, UBA and WWE domain containing 1	5,6	186204	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	0	0,0
2843	57208257	RPN2	ribophorin II	5,2	18259	1	10,5	1	10,3	1	9,3	1	9,5	0	0,0	1	12,9	2	9,7
2844	57209007	AARS2	alanyl-tRNA synthetase 2, mitochondrial (putative)	5,8	107322	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
2845	57209094	VBP1	von Hippel-Lindau binding protein 1	7,0	22659	2	16,0	2	10,1	3	9,3	2	9,5	2	12,2	1	8,9	2	13,6
2846	57210030	HSD17B10	hydroxysteroid (17-beta) dehydrogenase 10	7,7	17206	3	17,3	0	0,0	3	19,6	2	18,8	0	0,0	3	22,5	0	0,0
2847	57222570	CDAN1	codanin-1	6,3	134120	0	0,0	0	0,0	0	0,0	0	0,0	2	12,2	1	8,1	0	0,0
2848	5726629	SNX12	AF171229_1 sorting nexin 12	9,1	18885	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
2849	5729718	TPBG	trophoblast glycoprotein precursor	6,4	46033	1	12,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2850	5729730	API5	apoptosis inhibitor 5 isoform b	5,6	56771	1	10,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
2851	5729810	EBP	3-beta-hydroxysteroid-Delta(8),Delta(7)-isomerase	7,8	26335	0	0,0	1	10,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2852	5729840	TUBGCP2	gamma-tubulin complex component 2 isoform 2	6,4	102515	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
2853	5729856	GRAP	GRB2-related adapter protein	6,6	25337	1	11,1	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2854	5729864	HBS1L	HBS1-like protein isoform 1	6,2	75473	1	11,4	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2855	5729875	PGRMC1	membrane-associated progesterone receptor component	4,4	21653	1	10,7	0	0,0	0	0,0	0	0,0	0	0,0	1	8,7	2	9,7
2856	5729937	MTX2	metaxin-2	5,9	29764	0	0,0	2	10,0	2	9,3	1	9,5	0	0,0	2	9,1	1	9,7
2857	5729953	NUDC	nuclear migration protein nudC	5,1	38244	1	11,7	0	0,0	2	18,4	0	0,0	0	0,0	0	0,0	1	12,3
2858	5729980	PMVK	phosphomevalonate kinase	5,5	21996	0	0,0	2	19,9	0	0,0	0	0,0	0	0,0	2	9,3	1	8,8
2859	5729991	PSMC4	26S protease regulatory subunit 6B isoform 1	5,0	47348	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
2860	5730023	RUVBL2	ruvB-like 2	5,4	51157	2	25,6	1	10,0	1	8,7	2	26,2	2	12,2	0	0,0	1	11,4
2861	5730041	SUGT1	suppressor of G2 allele of SKP1 homolog isoform SGT1	5,0	37786	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
2862	5730120	YKT6	synaptobrevin homolog YKT6	6,5	22418	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
2863	5731237	ENSG00000228325	AF165103_1 immunoglobulin kappa light chain variable r	9,3	12421	0	0,0	0	0,0	1	13,9	0	0,0	0	0,0	0	0,0	0	0,0
2864	5759125	PTMA	prothymosin a14	3,5	11059	1	12,4	0	0,0	1	8,6	0	0,0	0	0,0	0	0,0	1	11,4
2865	576556	RAB21	KIAA0118	5,8	17833	0	0,0	1	10,0	3	18,5	0	0,0	0	0,0	2	19,0	1	12,9
2866	577299	RFTN1	KIAA0084	5,9	70464	3	25,4	4	19,9	4	23,3	2	18,8	0	0,0	5	20,5	4	24,5
2867	57863253	ZNF500	zinc finger protein 500	6,8	53675	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2868	57863257	TCP1	T-complex protein 1 subunit alpha isoform a	5,7	60325	6	43,2	5	34,8	7	44,6	10	65,4	6	48,3	6	47,0	6	46,1
2869	57997035	SEPT11	hypothetical protein	6,7	38848	1	18,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
2870	57997043	ATL3	hypothetical protein	5,5	60560	1	11,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
2871	57997098	PSMD2	hypothetical protein	4,6	70190	1	11,5	3	19,9	2	17,3	1	9,5	0	0,0	1	8,7	2	16,3
2872	57997122	DOCK8	hypothetical protein	6,4	230919	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2873	57997481	IPCEF1	hypothetical protein	7,3	49092	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
2874	57997484	NOP9	hypothetical protein	6,9	69415	1	10,5	1	10,1	0	0,0	0	0,0	2	12,3	0	0,0	1	8,0
2875	57997485	PSMD13	hypothetical protein	7,4	8050	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,7	0	0,0
2876	57997547	G3BP1	hypothetical protein	10,1	13875	0	0,0	0	0,0	0	0,0	1	9,5	0	0,0	0	0,0	0	0,0
2877	57999430	FSCB	hypothetical protein	4,1	89207	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2878	57999509	NDUFA5	hypothetical protein	5,3	13564	1	14,3	4	18,0	5	27,1	4	9,5	6	12,3	4	23,2	4	22,4
2879	5802966	HEL32	destrin isoform a	7,8	18507	1	12,5	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2880	5803013	HEL	endoplasmic reticulum resident protein 29 isoform 1	7,3	28975	2	13,1	0	0,0	1	9,8	1	9,5	3	12,2	1	12,1	1	12,8
2881	5803036	HNRNPA0	heterogeneous nuclear ribonucleoprotein A0	9,6	30822	2	11,2	2	15,1	2	9,3	6	28,1	2	12,2	2	9,6	2	9,7
2882	5803056	LAPTM5	lysosomal-associated transmembrane protein 5	8,7	29919	0	0,0	0	0,0	1	9,8	0	0,0	0	0,0	0	0,0	0	0,0
2883	5803135	RAB35	ras-related protein Rab-35 isoform 1	8,4	23026	1	11,4	0	0,0	1	9,8	0	0,0	2	12,2	1	9,3	0	0,0
2884	5803137	RBM3	putative RNA-binding protein 3	9,2	17171	0	0,0	0	0,0	1	8,7	4	9,5	5	12,2	0	0,0	0	0,0
2885	5803149	RNP24	transmembrane emp24 domain-containing protein 2 prec	4,9	22743	1	11,6	1	10,3	0	0,0	1	9,5	0	0,0	0	0,0	0	0,0
2886	5803157	MSMO1	methylsterol monooxygenase 1 isoform 1	6,8	35197	1	11,1	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0

2887	5803165	SEC61B	protein transport protein Sec61 subunit beta	12,1	9956	1	11,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2888	5803167	SF3A3	splicing factor 3A subunit 3	5,1	58849	0	0,0	0	0,0	2	17,3	0	0,0	0	0,0	1	9,7	2	15,7
2889	5803187	TALDO1	transaldolase	6,4	37541	3	25,6	3	15,1	3	23,8	1	9,4	3	24,2	3	26,8	2	17,5
2890	5803191	TCEA1	transcription elongation factor A protein 1 isoform	8,4	33951	1	12,8	0	0,0	0	0,0	0	0,0	2	12,1	0	0,0	0	0,0
2891	5803207	U2AF1	splicing factor U2AF 35 kDa subunit isoform a	8,9	27854	2	11,2	2	10,1	2	9,3	2	9,5	2	12,2	2	9,1	3	9,7
2892	5803217	UQCR11	cytochrome b-c1 complex subunit 10	10,2	6571	1	10,8	0	0,0	0	0,0	1	9,5	0	0,0	0	0,0	0	0,0
2893	5803227	YWHAQ	14-3-3 protein theta	4,5	27765	1	13,0	4	28,5	5	23,3	2	18,8	6	24,3	2	18,1	4	25,0
2894	58036935	AP3B2	hypothetical protein	6,9	127014	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2895	5817200	AHI1	hypothetical protein	7,0	96708	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
2896	5817221	TKFC	hypothetical protein	9,0	17072	1	12,0	0	0,0	1	9,3	0	0,0	0	0,0	2	13,7	0	0,0
2897	5821140	RTN4	ASY	4,6	40334	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
2898	5821147	SRRM2	RNA binding protein	10,8	29353	0	0,0	1	10,0	0	0,0	0	0,0	0	0,0	0	0,0	1	11,4
2899	58222968	ENSG00000228325	anti-tetanus toxoid immunoglobulin light chain variab	8,2	11923	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7	0	0,0
2900	58331173	CCT6B	T-complex protein 1 subunit zeta-2 isoform 1	6,9	57803	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2901	58331246	GAD1	glutamate decarboxylase 1 isoform GAD67	7,4	66878	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2902	58372399	LTF	lactoferrin	8,0	78323	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
2903	587202	HK2	Human hexokinase II cDNA	5,7	102368	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
2904	587334	ENSG00000228325	immunoglobulin kappa light chain variable region	9,5	12457	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2905	587442	ATP6V1B2	V-ATPase B2 subunit	11,9	4658	1	12,1	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2906	5901922	CDC37	hsp90 co-chaperone Cdc37	5,0	44469	2	19,3	1	10,4	2	13,6	1	9,5	2	12,2	2	15,5	2	19,2
2907	5901998	LSM6	U6 snRNA-associated Sm-like protein LSm6	9,9	9110	1	10,8	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2908	5902076	SRSF1	serine/arginine-rich splicing factor 1 isoform 1	10,7	27726	2	26,4	2	19,5	3	22,7	6	28,1	6	48,3	3	26,6	3	19,8
2909	5902090	SLC2A3	solute carrier family 2, facilitated glucose transpo	7,0	53906	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,1	0	0,0
2910	5902102	SNRPD1	small nuclear ribonucleoprotein Sm D1	12,1	13263	4	13,1	6	14,8	4	9,3	7	18,8	9	12,3	6	18,0	3	15,5
2911	5902181	DNPEP	aspartyl aminopeptidase	7,1	52429	1	9,7	3	9,8	1	9,3	1	9,4	0	0,0	2	11,7	1	9,7
2912	5911903	MTHFD1L	hypothetical protein	6,5	99439	2	23,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2913	5911913	HNRNPH3	hypothetical protein	5,3	22323	1	11,5	4	25,0	2	17,9	0	0,0	3	12,2	2	14,8	2	18,6
2914	5919228	ATP1A1	Na,K-ATPase catalytic subunit alpha-A protein	3,9	3548	1	11,7	1	10,2	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
2915	59710104	PLXNA3	plexin-A3 precursor	6,9	207702	1	12,5	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2916	59803473	EIF3C	cell migration-inducing protein 17	5,4	105404	0	0,0	2	10,0	1	8,7	0	0,0	0	0,0	1	12,6	2	13,6
2917	59850762	UACA	uveal autoantigen with coiled-coil domains and anky	6,6	162486	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2918	59896138	RPL11	cell growth-inhibiting protein 34	10,0	20095	0	0,0	2	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2919	599830	ALAS1	unnamed protein product	8,5	71098	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	11,4
2920	6002803	RAB14	AF152463_1 RAB14 protein	5,8	23928	1	11,0	2	14,8	2	14,1	0	0,0	0	0,0	1	9,1	1	9,7
2921	6005717	ATP5I	ATP synthase subunit e, mitochondrial	9,7	7915	1	11,7	1	10,0	0	0,0	0	0,0	0	0,0	0	0,0	1	11,4
2922	6005743	DDX19B	ATP-dependent RNA helicase DDX19B isoform 1	5,9	53908	0	0,0	1	10,3	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
2923	6005757	SUPT16H	FACT complex subunit SPT16	5,4	119914	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
2924	6005842	PROSC	proline synthase co-transcribed bacterial homolog pr	7,3	30326	1	10,8	0	0,0	1	8,7	0	0,0	0	0,0	1	8,0	2	13,6
2925	6005846	TWF2	twinfilin-2	6,4	39549	1	11,5	3	29,8	3	18,5	4	18,8	3	24,2	3	16,0	2	16,1
2926	600727	GARS	glycyl-tRNA synthetase	5,8	77531	4	41,2	8	54,8	7	53,2	7	56,1	2	21,9	7	53,4	6	40,4
2927	602021	SNRNP70	unnamed protein product	10,9	35775	1	10,4	1	10,0	1	8,7	1	9,4	0	0,0	2	17,7	1	13,4
2928	60257354	COII	cytochrome c oxidase subunit II	4,6	25565	1	11,6	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2929	603074	ACLY	ATP:citrate lyase	6,9	120825	6	41,1	12	89,5	9	67,2	7	56,1	3	24,2	11	69,7	12	82,9
2930	6031192	SLC25A3	phosphate carrier protein, mitochondrial isoform a p	9,7	40077	5	34,8	7	44,4	3	18,4	5	37,4	3	12,2	5	32,3	7	43,6
2931	603764	DAP3	ionizing radiation resistance conferring protein	10,1	43593	0	0,0	1	10,3	2	14,1	0	0,0	0	0,0	1	8,0	1	12,3
2932	6048403	PSME2	AF079558_1 proteasome activator PA28 beta	5,3	27343	20	47,4	42	83,9	29	64,1	37	65,5	43	72,4	31	68,8	25	56,8
2933	60688486	FKBP2	FK506 binding protein 2, 13kDa	9,2	15622	1	11,2	0	0,0	1	8,6	1	9,4	0	0,0	0	0,0	1	11,4
2934	608723	ABCE1	2'-5' oligoadenylate binding protein	6,4	45564	1	16,4	0	0,0	0	0,0	1	9,5	2	12,2	1	12,6	1	8,8
2935	61104905	HSP90AA4P	heat shock protein 90Ad	4,9	47713	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	1	9,7
2936	61104911	HSP90AB2P	heat shock protein 90Bb	4,9	49123	11	14,9	6	9,8	6	10,0	0	0,0	5	12,3	0	0,0	0	0,0
2937	61104923	GRP94c	heat shock protein 94c	6,1	51726	1	13,1	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,8
2938	6165618	IFI30	AF097362_1 gamma-interferon inducible lysosomal thiol	4,7	29131	1	9,6	2	10,0	1	8,7	1	9,5	2	12,2	1	9,3	1	11,4
2939	61656607	TRA1	tumor rejection antigen (gp96) 1	4,6	92340	172	258,0	57	167,5	65	172,6	54	149,4	39	144,5	70	176,3	75	199,3
2940	61656609	TRAP1	TNF receptor-associated protein 1	7,4	57234	0	0,0	1	10,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2941	61743946	ABI1	abl interactor 1 isoform c	6,9	49377	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	1	8,0	1	9,8
2942	61744477	SLC3A2	4F2 cell-surface antigen heavy chain isoform b	4,8	68082	2	18,2	2	15,1	3	19,6	2	18,8	3	24,2	2	21,0	2	15,5
2943	61966781	PTRHD1	putative peptidyl-tRNA hydrolase PTRHD1	9,5	15787	1	10,5	1	9,7	0	0,0	0	0,0	0	0,0	1	8,0	1	8,8
2944	620110	COPB1	beta-Coat protein	5,0	33445	2	11,4	2	10,0	0	0,0	2	9,5	2	12,2	1	9,0	1	9,7
2945	62087150	GART	phosphoribosylglycinamide formyltransferase, phospho	7,0	112120	2	25,3	4	24,4	4	27,5	2	18,8	3	24,2	3	20,6	4	32,5
2946	62087156	RB1	Retinoblastoma-associated protein variant	8,1	109756	0	0,0	0	0,0	1	8,7	1	9,4	2	12,2	0	0,0	0	0,0
2947	62087162	LIG1	DNA ligase I variant	5,5	91953	1	12,5	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2948	62087174	KIF4A	Chromosome-associated kinesin KIF4A variant	5,9	140320	1	10,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2949	62087250	PIK3CD	phosphoinositide-3-kinase, catalytic, delta polypept	7,3	96667	1	11,2	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0

2950	62087300	PRKDC	protein kinase, DNA-activated, catalytic polypeptide	8,1	82507	1	11,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2951	62087308	FLII	flightless I homolog variant	5,0	125277	0	0,0	1	17,4	1	8,7	2	9,5	0	0,0	0	0,0	0	0,0
2952	62087360	KCNQ3	potassium voltage-gated channel KQT-like protein 3 v	10,1	50002	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
2953	62087404	GBP1	guanylate binding protein 1, interferon-inducible, 6	8,1	32687	0	0,0	0	0,0	0	0,0	1	9,5	0	0,0	2	9,3	2	8,8
2954	62087410	LY75-CD302	lymphocyte antigen 75 variant	6,6	154596	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
2955	62087444	HSD17B4	hydroxysteroid (17-beta) dehydrogenase 4 variant	8,1	51089	2	13,2	2	19,9	3	19,6	1	9,5	0	0,0	1	11,7	1	9,7
2956	62087534	RPL4	ribosomal protein L4 variant	11,5	48997	5	33,6	8	29,5	12	36,1	7	37,5	8	24,3	7	21,8	10	27,0
2957	62087554	SLC2A1	solute carrier family 2 (facilitated glucose transpo	9,8	57000	0	0,0	0	0,0	1	8,7	0	0,0	2	12,2	1	12,8	1	7,9
2958	62087556	UBE2I	ubiquitin-conjugating enzyme E2I variant	9,2	19350	1	11,4	3	10,0	1	8,7	2	9,4	2	12,2	2	12,3	2	9,7
2959	62087562	SDHA	succinate dehydrogenase complex, subunit A, flavopro	6,9	73158	1	13,5	1	10,3	0	0,0	0	0,0	0	0,0	1	8,7	1	7,9
2960	62087566	ACAT2	Acetyl-CoA acetyltransferase, cytosolic variant	7,1	42117	1	10,5	1	9,8	1	8,7	0	0,0	2	12,3	1	9,1	1	9,8
2961	62087568	TRIM25	tripartite motif-containing 25 variant	7,9	72231	2	15,6	1	10,3	1	9,9	2	18,8	2	12,2	1	8,0	1	8,8
2962	62087594	RBM14	RNA binding motif protein 14 variant	9,7	55631	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
2963	62087660	PDCD5	programmed cell death 5 variant	7,3	10861	0	0,0	0	0,0	1	8,6	0	0,0	2	12,2	1	9,0	0	0,0
2964	62087780	RPL21	ribosomal protein L21 variant	11,0	18892	3	11,5	3	10,0	3	9,3	4	9,5	3	12,2	2	14,2	4	12,9
2965	62087882	HSPA4	heat shock 70kDa protein 4 isoform a variant	5,3	87986	2	20,1	2	19,9	1	9,3	2	18,8	2	12,2	2	18,0	3	26,3
2966	62087910	RPS10	ribosomal protein S10 variant	10,3	19861	6	17,5	6	19,9	10	18,4	8	18,8	14	24,3	7	18,0	6	16,0
2967	62087970	DPYSL2	dihydropyrimidinase-like 2 variant	5,8	68184	1	12,4	1	10,4	0	0,0	2	9,5	0	0,0	1	8,9	0	0,0
2968	62088006	DNM2	dynamin 2 isoform 4 variant	8,9	55111	1	12,1	1	10,3	0	0,0	0	0,0	2	12,2	2	15,9	1	11,4
2969	62088022	CORO1A	hypothetical protein FLJ41407 variant	8,0	59596	21	48,9	9	25,0	13	36,2	13	37,5	15	36,4	8	21,1	12	26,3
2970	62088042	LDHB	lactate dehydrogenase B variant	10,4	15006	0	0,0	2	10,0	4	13,6	1	9,5	0	0,0	2	8,0	1	9,7
2971	62088106	TXNL1	thioredoxin-like 1 variant	4,6	31356	2	10,7	2	10,0	0	0,0	1	9,5	2	12,2	1	8,7	1	8,8
2972	62088150	SUB1	activated RNA polymerase II transcription cofactor 4	9,9	15117	4	26,9	4	25,0	4	18,4	6	18,8	6	24,2	3	21,0	4	18,7
2973	62088156	CAMK2D	calcium/calmodulin-dependent protein kinase II delta	7,9	58814	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	1	11,4
2974	62088286	ACTR3	ARP3 actin-related protein 3 homolog variant	5,5	42240	8	41,5	14	44,7	13	45,9	11	37,5	17	72,4	14	50,0	13	46,7
2975	62088344	DDX24	DEAD (Asp-Glu-Ala-Asp) box polypeptide 24 variant	8,6	75030	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,8	0	0,0
2976	62088386	IREB2	iron-responsive element binding protein 2 variant	6,5	87704	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2977	62088392	GLUD1	glutamate dehydrogenase 1 variant	6,1	32324	1	11,3	1	9,7	0	0,0	0	0,0	0	0,0	1	9,7	0	0,0
2978	62088592	HTT	huntingtin variant	6,8	127093	1	11,0	1	10,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
2979	62088608	LBR	lamin B receptor variant	9,7	70859	2	16,6	1	10,1	2	13,6	6	28,2	2	12,3	2	15,0	2	13,6
2980	62088624	EPB41L2	EPB41L2 protein variant	6,5	76295	0	0,0	1	10,0	0	0,0	1	9,5	2	12,2	0	0,0	1	7,9
2981	62088650	CLK3	dual specificity protein kinase CLK3 variant	9,6	66582	0	0,0	0	0,0	1	9,3	0	0,0	2	12,2	0	0,0	0	0,0
2982	62088688	SEC13	SEC13-like 1 isoform b variant	5,7	33554	1	12,1	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2983	62088700	POLD1	polymerase (DNA directed), delta 1, catalytic subuni	7,4	111840	1	11,6	1	10,0	1	8,7	0	0,0	2	12,2	1	8,9	0	0,0
2984	62088708	ABCF1	ATP-binding cassette, sub-family F, member 1 variant	7,6	67405	1	11,4	1	10,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
2985	62088756	ADRBK1	beta adrenergic receptor kinase 1 variant	7,9	41557	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,5	0	0,0
2986	62088814	CYB5A	cytochrome b-5 isoform 1 variant	5,4	14573	0	0,0	1	9,7	1	9,3	0	0,0	0	0,0	1	9,5	2	19,2
2987	62088910	VAPB	VAMP-associated protein B/C variant	10,0	9432	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,8	0	0,0
2988	62089042	GBE1	Glucan , branching enzyme 1 variant	6,5	86114	1	11,6	1	10,0	4	27,0	0	0,0	0	0,0	2	11,7	3	19,8
2989	62089044	RPA1	replication protein A1, 70kDa variant	7,4	69411	1	11,2	1	9,7	0	0,0	0	0,0	2	12,3	0	0,0	2	15,7
2990	62089056	SLC1A5	solute carrier family 1 (neutral amino acid transpor	5,1	57372	0	0,0	0	0,0	2	14,1	0	0,0	0	0,0	0	0,0	1	9,7
2991	62089082	SPTBN1	spectrin, beta, non-erythrocytic 1 isoform 1 variant	5,3	276150	1	12,1	0	0,0	1	9,8	0	0,0	0	0,0	1	9,5	1	9,7
2992	62089126	ANXA11	annexin A11 variant	7,0	54894	2	14,4	4	19,9	3	26,9	6	46,7	3	24,2	2	17,4	2	20,7
2993	62089194	SRSF5	CS0DF038YO05 variant	11,4	37255	1	12,4	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
2994	62089202	AP1M1	adaptor-related protein complex 1, mu 1 subunit vari	9,2	53245	2	18,9	2	14,8	1	9,9	1	9,5	0	0,0	2	21,9	2	15,7
2995	62089218	GSTM3	glutathione S-transferase M3 variant	5,7	27203	0	0,0	1	10,0	0	0,0	0	0,0	0	0,0	1	9,7	0	0,0
2996	62089230	SLC25A6	ADP,ATP carrier protein, liver isoform T2 variant	10,2	35365	3	18,0	2	10,0	3	16,6	2	9,5	3	12,2	2	9,1	2	9,7
2997	62089240	CPNE1	copine I variant	5,4	56761	1	9,7	2	10,0	2	9,3	0	0,0	2	12,3	2	9,1	1	9,7
2998	62089296	CAPN2	Calpain 2, large [catalytic] subunit precursor variant	4,8	83090	1	10,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
2999	62089342	ICAM2	intercellular adhesion molecule 2 precursor variant	7,6	38359	0	0,0	0	0,0	0	0,0	0	0,0	2	12,1	0	0,0	0	0,0
3000	62089404	CORO1C	coronin, actin binding protein, 1C variant	8,1	56351	2	14,6	2	14,9	5	22,7	4	18,8	2	12,3	5	23,9	5	21,9
3001	62089428	MAN2B1	mannosidase, alpha, class 2B, member 1 precursor var	6,7	113287	0	0,0	0	0,0	0	0,0	0	0,0	2	12,2	0	0,0	0	0,0
3002	62122550	CUL4A	cullin-4A	8,1	87723	1	11,0	0	0,0	0	0,0	1	9,4	2	12,2	0	0,0	1	9,7
3003	62131678	YWHAE	14-3-3 protein epsilon isoform transcript variant 1	4,6	26486	9	60,3	8	34,9	8	23,3	6	28,1	12	60,3	7	36,7	7	33,4
3004	62198241	CUTA	protein CutA isoform 1	5,2	20926	3	11,2	3	10,1	2	9,3	4	9,6	2	12,3	4	12,3	2	8,0
3005	62203284	PARP10	Hypothetical protein LOC90835	5,6	33882	1	10,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3006	62203298	HEL	Isocitrate dehydrogenase 1 (NADP+), soluble	6,6	46657	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3007	62205265	MAT2B	Methionine adenosyltransferase II, beta	7,3	37461	1	9,7	1	9,8	1	8,7	0	0,0	0	0,0	1	8,0	0	0,0
3008	62420916	ACT	actin-like protein	7,7	11556	117	11,7	41	10,2	41	9,4	14	9,6	48	12,4	58	9,2	53	10,7
3009	62420995	ACT	actin-like protein	5,9	11432	83	11,6	25	10,1	18	9,4	6	9,5	23	12,3	18	9,1	8	9,8
3010	62421069	ACT	actin-like protein	6,6	11537	33	10,9	2	16,0	2	10,4	0	0,0	0	0,0	5	12,6	1	16,2
3011	62421077	ACT	actin-like protein	6,2	11611	13	11,3	0	0,0	0	0,0	0	0,0	0	0,0	6	9,4	0	0,0
3012	62421103	ACT	actin-like protein	6,2	11514	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9

3013	62421144	ACT	actin-like protein	5,9	11600	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
3014	62421162	ACT	actin-like protein	6,2	11537	10	11,8	0	0,0	6	12,7	0	0,0	0	0,0	12	14,3	20	14,1
3015	62421170	ACT	actin-like protein	6,1	11557	0	0,0	1	10,0	1	8,6	1	9,4	0	0,0	1	8,0	1	9,6
3016	624704	STT3A	putative transmembrane protein precursor	8,2	80453	1	15,7	1	9,7	1	8,6	0	0,0	0	0,0	1	8,0	1	9,6
3017	62530384	ECI1	enoyl-CoA delta isomerase 1, mitochondrial isoform	8,6	32798	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7	0	0,0
3018	62896523	VIM	vimentin variant	4,9	53684	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	1	9,7
3019	62896529	PSMC3	proteasome 26S ATPase subunit 3 variant	5,0	47432	3	26,1	1	10,1	4	29,4	4	28,1	5	36,3	4	27,5	3	21,4
3020	62896531	ALDH4A1	aldehyde dehydrogenase 4A1 precursor variant	8,0	61711	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3021	62896539	CCT8	chaperonin containing TCP1, subunit 8 (theta) varian	5,3	59632	2	16,4	2	15,1	2	13,5	1	9,4	2	12,2	1	13,3	1	9,7
3022	62896547	BCAP31	B-cell receptor-associated protein 31 variant	8,9	27943	0	0,0	0	0,0	0	0,0	0	0,0	2	12,2	0	0,0	0	0,0
3023	62896557	TPP1	tripeptidyl-peptidase I precursor variant	6,0	61230	1	9,7	4	20,0	2	9,3	1	9,5	3	12,3	3	14,4	2	13,6
3024	62896579	QARS	glutaminyl-tRNA synthetase variant	6,8	87711	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3025	62896595	ACADVL	acyl-Coenzyme A dehydrogenase, very long chain precu	9,0	70400	5	48,5	2	9,8	5	36,7	2	18,8	6	45,9	4	32,6	3	19,2
3026	62896671	RHOA	ras homolog gene family, member A variant	5,8	21738	1	12,5	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3027	62896687	EIF3M	dendritic cell protein variant	5,3	42472	1	11,3	8	29,8	4	17,8	8	37,5	2	12,3	2	11,7	5	18,7
3028	62896697	MYL12A	myosin regulatory light chain MRCL3 variant	4,5	19775	0	0,0	2	17,4	0	0,0	1	9,5	0	0,0	1	9,8	3	8,9
3029	62896705	DYNC1LI1	dynein light chain-A variant	6,0	56405	0	0,0	1	10,3	1	9,8	0	0,0	2	12,2	0	0,0	0	0,0
3030	62896713	EIF2S3	eukaryotic translation initiation factor 2, subunit	8,4	51064	2	11,1	0	0,0	1	8,7	0	0,0	0	0,0	2	9,3	1	9,7
3031	62896731	MCM3	minichromosome maintenance protein 3 variant	5,4	90962	0	0,0	0	0,0	0	0,0	1	9,4	2	12,1	0	0,0	0	0,0
3032	62896775	ATP5O	mitochondrial ATP synthase, O subunit precursor vari	10,4	23243	5	29,1	5	19,9	9	37,3	6	9,5	11	36,3	7	32,6	5	15,5
3033	62896777	LMAN2	lectin, mannose-binding 2 variant	6,6	40248	2	15,6	1	9,7	2	17,8	0	0,0	0	0,0	1	8,7	1	11,4
3034	62896789	EMC2	KIAA0103 variant	6,4	34762	1	11,5	0	0,0	0	0,0	0	0,0	0	0,0	1	8,7	1	9,7
3035	62896799	EIF3H	eukaryotic translation initiation factor 3, subunit	6,1	39852	2	17,0	4	19,9	2	19,0	1	9,5	2	12,2	2	11,7	2	18,1
3036	62896813	GLA	galactosidase, alpha variant	5,2	48753	1	11,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3037	62896815	HSPA8	heat shock 70kDa protein 8 isoform 2 variant	5,5	53481	4	14,7	2	10,0	3	9,3	4	9,5	3	12,3	4	9,1	3	9,7
3038	62896841	TTC1	tetratricopeptide repeat domain 1 variant	4,7	33436	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	1	8,8
3039	62896877	PRDX3	peroxiredoxin 3 isoform a precursor variant	7,7	27606	3	21,0	4	19,9	6	23,9	6	28,1	5	24,2	8	29,9	7	27,1
3040	62896903	TYK2	tyrosine kinase 2 variant	7,0	91713	0	0,0	1	9,8	1	9,9	0	0,0	0	0,0	0	0,0	0	0,0
3041	62896917	PSMD12	proteasome 26S non-ATPase subunit 12 isoform 1 varia	7,1	52892	1	10,4	2	10,0	2	9,3	0	0,0	3	12,2	2	9,1	2	9,7
3042	62896945	DCTN2	dynactin 2 variant	4,9	44821	2	11,8	1	10,3	3	19,6	1	9,5	0	0,0	1	8,9	3	23,5
3043	62896951	WDR54	hypothetical protein FLJ12953 similar to Mus musculu	5,6	35874	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3044	62896957	LACTB2	lactamase, beta 2 variant	6,3	32790	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	1	9,7
3045	62897063	NUP54	nucleoporin 54kDa variant	6,6	55564	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
3046	62897071	HYOU1	oxygen regulated protein precursor variant	5,0	111260	4	25,9	0	0,0	3	26,1	1	9,5	0	0,0	2	18,6	2	15,5
3047	62897075	HSPA9	heat shock 70kDa protein 9B precursor variant	5,8	73616	0	0,0	1	10,0	1	9,3	0	0,0	0	0,0	2	11,7	2	13,4
3048	62897077	PPAT	phosphoribosyl pyrophosphate amidotransferase propro	6,3	57367	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,0	1	8,8
3049	62897173	FKBP5	FK506 binding protein 5 variant	5,6	51199	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3050	62897195	GLUD1	glutamate dehydrogenase 1 variant	8,0	61340	2	17,4	0	0,0	1	9,9	0	0,0	0	0,0	1	9,5	1	9,7
3051	62897207	AARS	alanyl-tRNA synthetase variant	5,2	106825	3	29,6	4	34,6	8	54,9	4	28,2	5	36,2	7	51,4	5	34,3
3052	62897211	MTHFD2	methylene tetrahydrofolate dehydrogenase 2 precursor	9,1	37274	1	11,2	1	9,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3053	62897219	RBM14	RNA binding motif protein 14 variant	9,9	69520	1	11,4	1	10,0	1	8,6	0	0,0	0	0,0	1	8,6	1	9,7
3054	62897229	NARS	asparaginyl-tRNA synthetase variant	5,9	62911	1	11,2	1	10,0	0	0,0	1	9,5	2	12,2	1	13,3	2	21,0
3055	62897295	TSN	translin variant	6,0	26272	3	10,5	4	10,1	1	9,3	5	9,5	0	0,0	2	9,1	2	9,7
3056	62897321	HSD17B12	steroid dehydrogenase homolog	9,7	34351	0	0,0	1	10,3	2	9,3	0	0,0	0	0,0	1	9,3	1	8,8
3057	62897359	RNMTL1	RNA methyltransferase like 1 variant	9,0	47049	1	11,6	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3058	62897391	IDH2	isocitrate dehydrogenase 2 (NADP+), mitochondrial pr	8,5	50892	6	42,1	11	64,1	17	64,1	5	37,5	8	36,3	15	70,8	13	50,5
3059	62897461	GMPPA	GDP-mannose pyrophosphorylase A variant	6,8	46319	2	14,1	4	19,9	0	0,0	1	9,5	0	0,0	1	12,3	1	9,7
3060	62897507	IDH3A	isocitrate dehydrogenase 3 (NAD+) alpha precursor va	6,5	39602	5	34,0	5	34,2	6	36,1	4	18,8	6	36,3	9	47,3	7	30,8
3061	62897599	SEC13	SEC13-like 1 isoform b variant	5,1	35511	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,8
3062	62897603	TOMM22	mitochondrial import receptor Tom22 variant	4,1	15487	1	10,9	1	10,4	2	14,2	2	18,8	2	12,2	0	0,0	0	0,0
3063	62897643	MTHFD2	methylene tetrahydrofolate dehydrogenase 2 precursor	9,1	37274	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
3064	62897665	CPT2	Carnitine O-palmitoyltransferase II, mitochondrial p	7,1	64706	1	10,8	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
3065	62897681	CALR	calreticulin precursor variant	4,1	46920	73	104,7	45	94,0	39	81,8	41	93,4	28	84,4	34	76,6	43	79,1
3066	62897685	TIMM44	translocase of inner mitochondrial membrane 44 homol	8,4	51305	1	10,6	0	0,0	1	9,3	0	0,0	0	0,0	1	9,5	2	15,5
3067	62897735	IFI44L	histocompatibility 28 variant	6,3	46907	1	10,9	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3068	62897739	DCPS	mRNA decapping enzyme variant	5,9	38610	2	19,2	1	9,7	2	14,1	1	9,5	0	0,0	1	13,4	1	15,1
3069	62897753	PGAM1	phosphoglycerate mutase 1 (brain) variant	6,8	28814	0	0,0	1	10,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3070	62897755	MTCH2	mitochondrial carrier homolog 2 variant	7,9	33291	2	15,0	2	14,8	3	9,4	2	18,8	2	12,2	2	12,7	4	15,5
3071	62897789	NDUFS8	NADH dehydrogenase (ubiquinone) Fe-S protein 8, 23kD	5,4	23718	0	0,0	2	10,0	1	9,2	1	9,4	3	24,2	2	11,6	2	9,6
3072	62897823	MAGT1	implantation-associated protein variant	9,9	38046	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3073	62897977	LMAN1	lectin, mannose-binding, 1 precursor variant	6,3	57540	4	22,1	6	49,5	6	22,8	1	9,5	5	24,3	6	32,6	7	34,6
3074	62898009	SEC11A	signal peptidase complex (18kD) variant	9,9	20595	0	0,0	0	0,0	1	9,8	1	9,5	0	0,0	0	0,0	0	0,0
3075	62898071	NDUFS3	NADH dehydrogenase (ubiquinone) Fe-S protein 3, 30kD	6,3	30142	1	15,1	2	19,3	1	8,7	0	0,0	0	0,0	1	9,6	2	16,2

3076	62898077	TPM2	tropomyosin 2 (beta) isoform 2 variant	4,5	32945	0	0,0	0	0,0	0	0,0	0	0,0	2	12,2	0	0,0	0	0,0
3077	62898103	GOT2	aspartate aminotransferase 2 precursor variant	9,3	47529	3	37,1	3	24,6	5	40,9	4	28,1	5	36,3	6	50,0	4	35,1
3078	62898183	LAMTOR3	mitogen-activated protein kinase kinase 1 interactin	7,3	13545	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	1	8,8
3079	62898205	SF3B4	splicing factor 3b, subunit 4 variant	8,5	44368	1	9,7	0	0,0	1	9,9	2	18,8	3	24,2	2	13,7	2	13,5
3080	62898249	NECAP2	hypothetical protein FLJ10420 variant	8,7	28325	1	11,6	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3081	62898293	PDCD6	programmed cell death 6 variant	5,0	21897	1	11,4	1	10,0	1	9,2	1	9,4	2	12,2	2	12,1	2	12,2
3082	62898307	ALDH2	mitochondrial aldehyde dehydrogenase 2 precursor var	6,7	56349	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
3083	62898359	GMPS	guanine monophosphate synthetase variant	6,2	76678	0	0,0	0	0,0	0	0,0	1	9,4	0	0,0	1	11,7	2	16,6
3084	62898395	ME1	cytosolic malic enzyme 1 variant	5,7	64090	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3085	62898429	DTYMK	deoxythymidylate kinase (thymidylate kinase) variant	8,8	23743	0	0,0	0	0,0	1	9,8	0	0,0	0	0,0	0	0,0	1	7,9
3086	62898443	HNRNPH3	heterogeneous nuclear ribonucleoprotein H3 isoform a	6,9	36907	0	0,0	0	0,0	0	0,0	0	0,0	2	12,1	0	0,0	0	0,0
3087	62898712	MAP2K3	mitogen-activated protein kinase kinase 3 isoform B	7,2	39330	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
3088	62898744	RANBP1	RAN binding protein 1 variant	5,1	23210	1	12,9	0	0,0	2	9,2	1	9,4	2	12,2	1	12,1	1	9,7
3089	62898864	ARL6IP5	ADP-ribosylation-like factor 6 interacting protein 5	10,2	21539	6	22,9	2	14,8	4	14,2	4	18,8	5	24,3	5	20,7	3	17,6
3090	62898870	ATP1A3	Na+/K+ -ATPase alpha 3 subunit variant	5,1	111760	1	11,0	0	0,0	1	9,8	0	0,0	0	0,0	1	9,7	1	9,7
3091	62898892	DAK	DKFZP586B1621 protein variant	7,3	58994	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
3092	62898948	YARS	tyrosyl-tRNA synthetase variant	6,9	59163	4	35,8	6	19,9	4	26,4	4	18,8	3	24,2	6	47,0	4	33,4
3093	62898984	CSK	c-src tyrosine kinase variant	6,6	50618	1	13,3	1	9,7	3	18,4	5	28,1	2	12,2	1	8,6	1	11,4
3094	62898994	TPD52	N8 protein long isoform (Fragment) variant	5,7	23764	1	17,3	2	14,8	2	14,1	1	9,4	0	0,0	1	11,1	2	16,6
3095	62912479	HLA	HLA class I histocompatibility antigen, alpha chain	5,5	40039	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	1	8,8
3096	63055057	ACTBL2	beta-actin-like protein 2	5,3	42004	2	18,2	3	23,8	4	25,4	2	24,4	0	0,0	3	22,1	3	18,8
3097	63101262	PKM2	PKM2 protein	8,0	40164	0	0,0	0	0,0	1	8,6	0	0,0	0	0,0	0	0,0	0	0,0
3098	63102287	RAB13	RAB13 protein, partial	9,2	27200	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	1	9,7
3099	63102435	SEC23B	Sec23 homolog B (S. cerevisiae)	6,4	86496	2	10,5	1	10,0	0	0,0	0	0,0	0	0,0	1	8,0	1	11,4
3100	63252888	P4HA1	prolyl 4-hydroxylase subunit alpha-1 isoform 2 p	5,6	61031	0	0,0	0	0,0	2	17,2	1	9,4	0	0,0	1	8,0	1	7,9
3101	63252902	TPM1	tropomyosin alpha-1 chain isoform 2	4,5	32659	2	19,5	1	10,0	2	9,3	2	9,5	5	12,2	2	9,0	2	9,7
3102	6330243	ERGIC1	KIAA1181 protein	6,9	36880	1	12,4	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
3103	6330302	LRRC47	KIAA1185 protein	8,7	44500	0	0,0	0	0,0	1	9,9	0	0,0	0	0,0	0	0,0	1	9,7
3104	6331199	MTA3	KIAA1266 protein	8,7	68377	1	11,1	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3105	6331213	PARP14	KIAA1268 protein	8,2	114078	1	11,3	0	0,0	1	9,9	0	0,0	2	12,3	0	0,0	1	7,9
3106	633226	TPR	Tpr	4,9	265600	1	19,5	2	15,2	0	0,0	1	9,4	0	0,0	1	15,5	1	12,8
3107	643589	DLST	dihydrolipoamide succinyltransferase	8,9	48586	2	15,4	0	0,0	1	9,9	1	9,5	0	0,0	1	8,7	1	8,8
3108	6453494	ALDH1L1	hypothetical protein	7,9	26213	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3109	6453523	GOLPH3	hypothetical protein	8,2	23930	1	12,4	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
3110	64653183	SERPINB10	Serpin peptidase inhibitor, clade B (ovalbumin), memb	5,5	45397	0	0,0	1	10,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3111	6467479	EIF2AK2	double stranded RNA activated protein kinase	7,5	61998	1	10,7	3	10,0	4	16,5	6	28,1	6	24,2	3	18,0	3	22,4
3112	6468766	LNPEP	oxytocinase/insulin-responsive aminopeptidase, varian	5,4	117300	1	12,4	2	20,4	3	9,9	1	9,5	2	12,2	1	9,3	3	23,4
3113	6491737	NAGK	N-Acetylglucosamine kinase	5,8	37417	1	11,2	1	10,0	0	0,0	0	0,0	2	12,2	1	8,0	1	7,9
3114	6526992	BIN2	breast cancer associated protein BRAP1	4,9	61884	1	12,5	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3115	6537162	VAMP2	AF135372_1 synaptobrevin 2	8,6	12650	1	11,4	0	0,0	0	0,0	0	0,0	0	0,0	1	9,4	0	0,0
3116	6560618	ELOVL5	AF111849_1 PRO0530	10,7	7004	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3117	6563220	CMPK1	AF112216_1 UMP-CMP kinase	5,3	22223	4	37,5	7	39,3	8	41,0	8	46,8	8	60,3	8	45,1	8	42,4
3118	6563288	UBQLN2	AF189009_1 ubiquitin-like product Chap1/Dsk2	5,1	65747	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
3119	6598323	GDI2	rab GDP dissociation inhibitor beta isoform 1	6,1	50645	13	55,1	12	44,4	13	58,7	11	37,5	23	84,4	11	42,7	13	62,6
3120	6599138	EIF5B	hypothetical protein	5,3	129043	1	11,3	1	10,1	1	9,3	2	18,8	2	12,3	1	9,1	2	12,4
3121	6599266	MBNL3	hypothetical protein	9,2	31885	0	0,0	0	0,0	1	8,6	0	0,0	0	0,0	0	0,0	0	0,0
3122	6624942	NDUFS3	hypothetical protein	5,2	22219	1	10,8	1	9,7	0	0,0	1	9,4	0	0,0	1	9,3	1	7,9
3123	663142	CAST	calpastatin	4,8	20019	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
3124	6634031	TTI1	KIAA0406 protein	5,5	122620	1	11,2	1	9,7	0	0,0	0	0,0	2	12,2	0	0,0	0	0,0
3125	66347210	PABPC1L	chromosome 20 open reading frame 119	9,5	37738	1	12,5	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3126	66347229	RPS18	ribosomal protein S18	11,9	9768	4	16,2	4	10,0	3	14,1	4	18,8	5	12,2	3	9,0	4	12,9
3127	6635197	RASA4	KIAA0538 protein	7,5	91907	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
3128	66365795	HIST1H1E	Histone cluster 1, H1e	11,5	21894	4	27,3	2	18,9	7	26,6	8	18,7	8	36,2	6	29,5	3	24,3
3129	6677723	RFC5	replication factor C subunit 5 isoform 1	6,8	38478	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
3130	6678271	TARDBP	TAR DNA-binding protein 43	5,8	44741	2	14,5	3	19,9	1	9,9	5	37,5	2	12,2	3	15,3	2	12,7
3131	6679074	NUPL2	nucleoporin-like protein 2	9,6	44872	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
3132	6683496	BAZ1B	bromodomain adjacent to zinc finger domain 1B	8,1	176014	1	11,1	0	0,0	0	0,0	1	9,5	0	0,0	0	0,0	1	7,9
3133	6683815	SEPT9	MLL septin-like fusion protein MSF-B	6,1	47470	3	19,0	3	30,0	5	23,3	4	18,8	3	24,3	4	21,2	4	19,8
3134	6688174	N/A	putative truncated metabotropic glutamate receptor 6	12,3	2729	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7	0	0,0
3135	6688179	PGRMC1	progesterone membrane binding protein	4,7	11941	2	12,5	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3136	6688197	HEL20	PAP-inositol-1,4-phosphatase	5,4	33423	1	13,8	1	10,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
3137	6688230	CAMK2D	calcium/calmodulin dependent protein kinase II delta	5,7	27534	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	1	9,7
3138	6688311	C1	C1	6,0	105051	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9

3139	66932947	A2M	alpha-2-macroglobulin precursor	6,0	163292	0	0,0	0	0,0	1	9,2	0	0,0	0	0,0	0	0,0	0	0,0
3140	66932975	GPHN	gephyrin isoform 2	5,1	79749	1	20,5	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3141	67089147	FDFT1	squalene synthase	6,1	48116	1	11,0	0	0,0	0	0,0	1	9,5	0	0,0	0	0,0	0	0,0
3142	6715419	HLA	MHC class I antigen	6,0	21050	1	13,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3143	67511376	CRELD2	Cysteine-rich with EGF-like Domains 2 (CRELD2) beta	4,9	30694	1	11,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3144	6807649	CYFIP2	hypothetical protein	6,5	145674	1	11,8	0	0,0	0	0,0	1	9,5	0	0,0	1	8,0	2	19,3
3145	6807655	IDH1	hypothetical protein	6,2	46627	6	41,9	3	24,7	3	22,7	1	9,4	3	24,2	3	30,4	3	22,4
3146	6807907	HEL	hypothetical protein	4,6	47557	8	56,1	5	29,8	8	50,1	11	56,1	6	36,3	7	47,2	5	40,9
3147	6807962	SF3B1	hypothetical protein	6,0	16489	1	10,4	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3148	6808223	TMOD3	hypothetical protein	7,6	10056	1	11,3	1	10,3	0	0,0	0	0,0	0	0,0	2	9,3	1	7,9
3149	6808229	FRYL	hypothetical protein	4,5	17952	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
3150	68303549	ASL	argininosuccinate lyase isoform 3	5,7	48714	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7	0	0,0
3151	6841250	BRK1	AF161418_1 HSPC300	6,3	12377	0	0,0	0	0,0	0	0,0	1	9,5	0	0,0	0	0,0	0	0,0
3152	6841292	SWAP70	AF161439_1 HSPC321	4,8	16271	1	11,6	0	0,0	1	8,6	1	9,4	0	0,0	1	9,5	0	0,0
3153	6841318	SEC31A	AF161452_1 HSPC334	9,6	34948	0	0,0	1	10,0	0	0,0	0	0,0	2	12,1	1	8,0	0	0,0
3154	6841462	NOP58	AF161469_1 HSPC120	9,7	52496	1	13,3	0	0,0	1	8,7	1	9,4	0	0,0	2	16,8	2	12,9
3155	6841464	HACD3	AF161470_1 HSPC121	9,4	44424	2	11,1	1	9,7	1	9,3	1	9,5	0	0,0	1	9,1	2	9,7
3156	6841532	UFC1	AF161504_1 HSPC155	7,3	19468	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3157	68448544	CD74	HLA class II histocompatibility antigen gamma ch	8,4	33497	5	32,5	3	20,2	9	27,6	4	18,8	3	24,3	3	20,6	3	21,8
3158	68509926	DHX15	putative pre-mRNA-splicing factor ATP-dependent RNA	7,1	90914	3	18,2	4	24,7	5	36,7	7	46,8	5	36,3	5	22,5	3	16,0
3159	685120	N/A	insulin activator factor	5,5	83959	0	0,0	0	0,0	2	9,2	0	0,0	5	12,2	0	0,0	0	0,0
3160	6855637	ILF2	AF113702_1 PRO3063	4,7	26234	1	13,0	0	0,0	1	9,9	0	0,0	0	0,0	1	12,6	1	12,7
3161	6857800	ISG20	interferon-stimulated gene 20 kDa protein	9,2	20345	0	0,0	2	10,0	0	0,0	0	0,0	0	0,0	0	0,0	2	9,7
3162	6857818	NPM3	nucleoplasmin-3	4,4	19345	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
3163	6912238	PRDX5	peroxiredoxin-5, mitochondrial isoform a precursor	8,7	22008	5	40,6	4	24,7	7	41,5	5	28,1	5	36,3	7	44,2	6	30,2
3164	6912292	HEL25	chromobox protein homolog 5	5,6	22226	1	9,7	1	9,7	0	0,0	1	9,4	0	0,0	0	0,0	1	11,4
3165	6912396	GRHPR	glyoxylate reductase/hydroxypyruvate reductase	7,1	35650	2	11,0	2	14,8	3	18,4	1	9,5	0	0,0	3	16,9	1	12,3
3166	6912420	HS2ST1	heparan sulfate 2-O-sulfotransferase 1 isoform 1	8,9	41863	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3167	6912482	LETM1	LETM1 and EF-hand domain-containing protein 1, mitoc	6,3	83336	2	34,8	1	10,1	0	0,0	0	0,0	0	0,0	2	18,6	2	19,4
3168	6912486	LSM4	U6 snRNA-associated Sm-like protein LSm4 isoform 1	10,4	15332	0	0,0	1	10,0	0	0,0	0	0,0	0	0,0	1	8,0	1	9,7
3169	6912586	PGLS	6-phosphogluconolactonase	5,7	27548	1	10,4	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3170	6912604	ANP32C	acidic leucine-rich nuclear phosphoprotein 32 family	4,0	26744	1	10,8	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	1	11,4
3171	6912634	RPL13A	60S ribosomal protein L13a isoform 1	11,4	23578	1	17,2	2	10,0	1	9,8	0	0,0	2	12,2	1	9,5	1	9,7
3172	6912674	SNAPIN	SNARE-associated protein Snapin	9,7	14875	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3173	6912676	SNW1	SNW domain-containing protein 1	9,9	61495	1	11,1	0	0,0	0	0,0	0	0,0	0	0,0	1	9,4	0	0,0
3174	6912708	TIMM10	mitochondrial import inner membrane translocase subu	5,9	10315	1	11,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3175	6912714	TIMM9	mitochondrial import inner membrane translocase subu	7,0	10360	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,8
3176	6912734	TNPO3	transportin-3 isoform 1	5,3	104204	1	11,0	2	19,3	1	9,8	0	0,0	2	12,1	0	0,0	0	0,0
3177	693933	ENO1	2-phosphopyruvate-hydratase alpha-enolase	7,2	47091	92	95,5	44	58,5	37	55,1	37	46,9	43	72,5	71	56,3	85	47,4
3178	6983723	UGD	UDPglucose dehydrogenase	5,5	5928	1	11,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3179	6984209	LCK	AF228313_1 tyrosine kinase LCK, partial	5,2	56577	1	13,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	1	9,7
3180	6996014	HARS	histidine--tRNA ligase, cytoplasmic isoform 1	5,6	57392	1	10,5	1	10,0	2	14,2	1	9,5	0	0,0	1	9,0	1	9,7
3181	7018426	OLA1	hypothetical protein	7,7	44684	1	11,5	0	0,0	1	9,2	0	0,0	0	0,0	1	8,9	0	0,0
3182	7018436	UBA2	hypothetical protein	5,0	71152	0	0,0	0	0,0	1	9,3	1	9,5	2	12,2	1	8,9	1	9,7
3183	7019415	SEC61A1	protein transport protein Sec61 subunit alpha isofor	8,0	52246	0	0,0	1	10,3	1	9,3	2	9,5	3	24,2	1	8,9	1	7,9
3184	7019569	VPS4A	vacuolar protein sorting-associated protein 4A	7,7	48880	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	2	7,9
3185	7019858	HUWE1	unnamed protein product	6,4	46832	0	0,0	0	0,0	1	9,8	0	0,0	2	12,2	1	9,7	1	9,7
3186	7019942	XRN2	unnamed protein product	9,2	63785	0	0,0	1	10,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
3187	7020129	VPS4A	unnamed protein product	6,0	26831	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	2	8,1	0	0,0
3188	7020479	GSDML	unnamed protein product	5,0	45894	1	12,5	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3189	7020529	TRMT10C	unnamed protein product	9,6	29592	0	0,0	0	0,0	0	0,0	1	9,5	0	0,0	0	0,0	0	0,0
3190	7020584	NPM1	unnamed protein product	4,4	19373	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	11,4
3191	7020656	COL5A2	unnamed protein product	9,9	13597	1	12,4	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3192	7020961	TTC38	unnamed protein product	5,2	37664	1	10,4	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3193	7021042	TM9SF3	unnamed protein product	8,0	52620	1	10,4	1	10,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
3194	7021059	PTCD3	unnamed protein product	5,0	31864	0	0,0	0	0,0	0	0,0	1	9,5	0	0,0	0	0,0	0	0,0
3195	7021321	GEMIN4	AF173856_1 Gemin4	5,7	119991	1	11,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3196	7021971	FNBP1	unnamed protein product	5,3	61561	1	15,7	2	19,9	3	23,9	2	18,8	0	0,0	2	18,1	1	12,7
3197	7022134	SAMM50	unnamed protein product	6,7	51905	2	15,4	0	0,0	0	0,0	0	0,0	0	0,0	2	13,3	2	19,3
3198	7022185	SLFN12	unnamed protein product	8,6	66943	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,8	0	0,0
3199	7022287	IARS2	unnamed protein product	6,7	86393	0	0,0	0	0,0	1	9,3	0	0,0	0	0,0	1	9,6	1	9,7
3200	7022293	PRPF38B	unnamed protein product	11,0	64441	0	0,0	0	0,0	0	0,0	1	9,5	0	0,0	0	0,0	0	0,0
3201	7022321	COPS4	unnamed protein product	5,5	44987	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9

3202	7022475	GSPT2	unnamed protein product	5,2	68852	2	15,4	3	23,7	2	20,9	5	28,2	5	33,9	3	17,4	3	18,1
3203	7022616	SHINC3	unnamed protein product	9,9	27952	1	11,5	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3204	7022824	RPRD1A	unnamed protein product	7,3	35692	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
3205	7022826	LUC7L2	unnamed protein product	10,4	46487	0	0,0	1	10,0	0	0,0	1	9,4	0	0,0	1	8,9	1	9,8
3206	7022952	DNAJC11	unnamed protein product	8,5	63337	1	11,2	1	10,1	1	8,7	0	0,0	0	0,0	1	8,1	0	0,0
3207	7022992	CLIC4	unnamed protein product	5,2	23395	0	0,0	0	0,0	2	8,7	0	0,0	0	0,0	0	0,0	2	9,7
3208	7023033	DDX60	unnamed protein product	7,2	136378	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
3209	7023062	COA1	unnamed protein product	9,2	16723	1	10,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3210	7023065	SMU1	unnamed protein product	6,8	57528	1	11,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3211	7023082	NUP133	unnamed protein product	4,8	128897	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	13,3	1	9,7
3212	7023145	OGDHL	unnamed protein product	6,2	114480	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	0	0,0
3213	7023252	TNRC6A	unnamed protein product	7,0	47302	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
3214	7023323	PSPC1	unnamed protein product	5,9	41740	1	15,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	1	9,6
3215	7023366	PGM2	unnamed protein product	6,3	68270	1	14,9	2	19,9	1	9,8	0	0,0	0	0,0	1	12,6	1	9,7
3216	7023454	ZC3H15	unnamed protein product	5,1	48631	1	12,5	0	0,0	0	0,0	1	9,4	0	0,0	1	8,0	1	7,9
3217	7023491	LUC7L3	unnamed protein product	10,2	51493	1	12,1	0	0,0	0	0,0	1	9,5	0	0,0	0	0,0	1	9,8
3218	7023514	ACOT2	unnamed protein product	9,0	53227	1	11,3	2	10,1	2	17,3	0	0,0	2	12,2	2	9,1	1	9,7
3219	7023552	BXDC2	unnamed protein product	10,3	15297	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	11,4
3220	7023739	DHX30	unnamed protein product	9,4	39072	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3221	70608174	TPD52	tumor protein D52 isoform 2	5,2	22478	1	10,4	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
3222	71044477	DIDO1	death-inducer obliterator 1 isoform b	8,5	129162	1	12,5	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3223	7106760	NOP16	AF151019_1 HSPC185	10,7	26783	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	0	0,0
3224	7106880	CXorf26	AF151079_1 HSPC245	4,5	14125	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
3225	71296893	SNRPG	SNRPG protein	7,1	7102	0	0,0	0	0,0	0	0,0	1	9,4	0	0,0	1	9,5	1	9,7
3226	71535046	LTA	lymphotoxin alpha transcript variant 4	10,7	6720	0	0,0	1	10,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3227	71565154	ADH5	alcohol dehydrogenase class-3	7,3	39725	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
3228	7158824	RBM8A	AF198620_1 RNA binding motif protein 8	5,6	19761	0	0,0	0	0,0	1	9,3	2	18,8	2	12,2	1	12,8	2	17,4
3229	7159730	RPL3	ribosomal protein L3	10,5	39384	3	24,4	8	25,0	5	28,2	11	37,5	11	36,3	8	35,4	4	33,5
3230	71773010	AP1G1	AP-1 complex subunit gamma-1 isoform a	6,4	91704	1	12,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3231	71773329	ANXA6	annexin A6 isoform 1	5,3	75874	93	247,3	56	177,9	59	168,8	59	186,6	54	192,6	59	181,2	55	168,4
3232	71979932	SLC7A5	large neutral amino acids transporter small subunit	7,6	54992	1	10,8	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	1	10,6
3233	7212790	LATS2	large tumor suppressor 2	7,6	115322	1	10,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3234	72198189	BCL2	apoptosis regulator Bcl-2 alpha isoform	6,9	26248	1	9,7	1	10,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3235	7239696	MYLK	myosin light chain kinase	5,8	210774	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3236	7243055	PTCHD2	KIAA1337 protein	7,6	157894	1	11,6	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3237	7243183	TSR1	KIAA1401 protein	8,0	97049	1	11,0	1	10,0	0	0,0	1	9,4	0	0,0	1	9,3	1	8,8
3238	7243189	ZNFX1	KIAA1404 protein	6,9	220979	1	13,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3239	7243209	HEATR5B	KIAA1414 protein	6,3	171963	0	0,0	1	10,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3240	72534670	PLAA	phospholipase A-2-activating protein	5,9	87139	1	10,8	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
3241	7259371	HLA	MHC class I antigen	5,7	20908	2	14,5	6	31,9	2	18,4	7	46,8	5	41,1	5	27,7	3	29,5
3242	7259795	PPP2R4	phosphotyrosyl phosphatase activator	6,2	31730	1	10,4	1	10,3	1	8,7	1	9,5	0	0,0	0	0,0	0	0,0
3243	726098	HEL	glutathione S-transferase-P1c	5,3	23371	0	0,0	0	0,0	2	9,3	4	18,8	3	12,2	0	0,0	0	0,0
3244	727225	PPA2	pyrophosphatase	4,7	13046	2	16,7	2	19,9	3	18,4	2	18,8	3	24,2	1	9,3	3	24,8
3245	7328175	EZR	hypothetical protein	6,4	73936	0	0,0	1	10,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3246	73486658	GOT2	aspartate aminotransferase, mitochondrial precursor	9,3	47499	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3247	73622130	BOLA2B	BolA-like protein 2	8,2	16933	1	11,1	1	10,0	0	0,0	1	9,4	0	0,0	0	0,0	0	0,0
3248	736704	TBCB	cytoskeleton associated protein	4,7	21802	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
3249	73747875	PSM8	proteasome subunit beta type-8 isoform E2 proprotei	7,2	30336	8	30,7	8	34,8	8	36,7	6	37,4	5	24,2	5	30,0	8	41,5
3250	73747885	ADAM12	disintegrin and metalloproteinase domain-containing	8,2	99524	1	11,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3251	73760405	TMPO	thymopoietin isoform beta	9,8	50671	2	20,9	6	24,8	6	36,7	10	46,8	2	12,3	3	21,2	4	30,8
3252	7381095	COX7A2	AF134406_1 cytochrome-c oxidase subunit VIIaL precurso	10,1	9378	1	18,0	0	0,0	1	9,8	0	0,0	2	12,2	2	18,0	1	7,9
3253	74147337	ENSG00000223931	immunoglobulin epsilon heavy chain variable region	8,7	13606	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,8	0	0,0
3254	7427519	MCM6	DNA replication licensing factor MCM6	5,2	92871	1	12,0	0	0,0	1	8,7	2	18,8	2	12,2	0	0,0	1	7,9
3255	75677353	ATAD3B	ATPase family AAA domain-containing protein 3B	9,5	72554	1	17,8	0	0,0	1	8,7	0	0,0	0	0,0	1	8,6	1	11,4
3256	75709192	BABAM1	BRISC and BRCA1-A complex member 1	4,5	36561	1	11,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3257	758100	HLA	SB classII histocompatibility antigen alpha-chain	4,6	26188	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	1	8,0	1	9,7
3258	76150623	NOP2	putative ribosomal RNA methyltransferase NOP2 isofo	9,6	88955	0	0,0	0	0,0	3	19,6	0	0,0	0	0,0	0	0,0	0	0,0
3259	762939	ITGB2	unnamed protein product	6,5	83882	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	13,3	1	9,7
3260	763118	PRKCB	unnamed protein product	4,7	6074	0	0,0	1	10,0	1	9,9	0	0,0	0	0,0	1	9,0	1	9,7
3261	7657013	AATF	protein AATF	4,7	63133	1	10,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3262	7657015	RTCB	tRNA-splicing ligase RtcB homolog	6,8	55211	3	23,3	4	25,0	3	23,3	1	9,5	2	12,2	4	27,2	1	12,3
3263	7657033	HEL74	5'(3')-deoxyribonucleotidase, cytosolic type isoform	6,2	23365	1	10,4	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3264	7657056	EHD3	EH domain-containing protein 3	6,1	60888	3	25,4	8	34,5	3	27,5	4	18,8	2	12,2	4	22,7	3	23,3

3265	7657058	EIF2B2	translation initiation factor eIF-2B subunit beta	5,7	38971	1	11,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,8
3266	7657134	GNPAT	dihydroxyacetone phosphate acyltransferase	6,1	77169	0	0,0	1	9,7	1	8,6	0	0,0	0	0,0	0	0,0	0	0,0
3267	7657162	PFDN6	prefoldin subunit 6	9,4	14584	1	10,9	0	0,0	0	0,0	2	18,8	0	0,0	2	15,9	0	0,0
3268	7657176	CNPY2	protein canopy homolog 2 isoform 1 precursor	4,7	20634	1	14,6	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	1	9,7
3269	7657234	SMAP	small acidic protein	4,4	20333	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
3270	7657257	TOMM20	mitochondrial import receptor subunit TOM20 homolog	8,8	16280	0	0,0	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	0	0,0
3271	7657269	PDS5B	sister chromatid cohesion protein PDS5 homolog B	8,5	164648	1	12,4	0	0,0	1	8,6	0	0,0	0	0,0	1	11,7	1	7,9
3272	7657347	MTCH2	mitochondrial carrier homolog 2	7,9	33332	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
3273	7657369	NDUFA8	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex s	7,5	20087	0	0,0	2	19,3	1	9,3	0	0,0	0	0,0	1	8,7	2	15,5
3274	7657381	PRPF19	pre-mRNA-processing factor 19	6,1	55181	2	12,4	0	0,0	1	8,7	2	9,4	0	0,0	1	8,9	2	7,9
3275	7657407	OBP2B	odorant-binding protein 2b precursor	9,1	19457	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
3276	7657498	MOK	MAPK/MAK/MRK overlapping kinase isoform 1	9,9	47995	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
3277	7657581	SLC25A13	calcium-binding mitochondrial carrier protein Aralar	8,8	74157	1	11,1	1	10,0	0	0,0	0	0,0	0	0,0	1	8,6	1	11,4
3278	7661672	POLDIP2	polymerase delta-interacting protein 2	8,8	42015	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
3279	7661714	FAM3C	protein FAM3C precursor	8,4	24681	2	10,4	2	10,0	1	8,6	1	9,4	0	0,0	0	0,0	0	0,0
3280	7661728	LAMTOR2	ragulator complex protein LAMTOR2 isoform 1	5,2	13489	1	12,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3281	7661804	THYN1	thymocyte nuclear protein 1 isoform 1	9,7	25679	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
3282	7661880	ACAP1	arf-GAP with coiled-coil, ANK repeat and PH domain-c	7,4	81517	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,6	0	0,0
3283	7661914	PSMD6	26S proteasome non-ATPase regulatory subunit 6 isofo	5,3	45513	1	18,3	2	14,8	3	19,6	1	9,5	2	12,2	2	17,2	2	17,2
3284	7661920	EIF4A3	eukaryotic initiation factor 4A-III	6,3	46872	1	11,7	0	0,0	1	9,9	1	9,5	0	0,0	2	20,2	3	25,3
3285	7661964	RASSF2	ras association domain-containing protein 2	9,1	37772	1	10,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3286	7661998	TBC1D5	TBC1 domain family member 5 isoform b	6,1	88986	0	0,0	1	10,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
3287	7662078	TTC37	tetratricopeptide repeat protein 37	7,3	175486	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	11,4
3288	7662502	MCTS1	malignant T-cell-amplified sequence 1 isoform 1	9,1	20537	1	9,7	1	10,0	3	22,7	1	9,5	0	0,0	2	16,0	2	15,7
3289	7669999	MORC1	hypothetical protein	8,4	91854	1	11,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3290	76781674	ENSG00000228325	anti-SARS-CoV immunoglobulin light chain variable reg	6,5	12503	1	10,8	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
3291	7688703	CAND1	AF157326_1 TIP120 protein	5,4	136362	2	20,9	4	20,2	7	45,2	7	37,4	11	60,3	9	50,8	5	39,8
3292	7688965	HSPA8	AF217511_1 uncharacterized bone marrow protein BM034	4,6	14190	4	11,9	0	0,0	4	13,6	4	9,4	6	12,2	3	9,0	5	9,7
3293	7705369	COPB1	coatomer subunit beta	5,7	107143	3	28,6	7	34,9	6	31,9	5	28,1	6	24,3	5	31,9	4	23,0
3294	7705433	EIF3L	eukaryotic translation initiation factor 3 subunit L	5,9	66708	2	20,7	9	39,4	4	18,5	8	28,2	3	24,3	3	17,0	4	27,0
3295	7705437	NIP7	60S ribosome subunit biogenesis protein NIP7 homolog	8,7	20444	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	1	8,0	1	8,8
3296	7705477	TRMT112	tRNA methyltransferase 112 homolog	5,1	14200	1	10,4	1	10,0	1	8,7	0	0,0	0	0,0	1	8,0	1	7,9
3297	7705696	TXNDC12	thioredoxin domain-containing protein 12 precursor	5,1	19188	0	0,0	0	0,0	1	8,6	0	0,0	0	0,0	2	15,9	1	7,9
3298	7705704	GSTK1	glutathione S-transferase kappa 1 isoform a	8,7	25479	1	11,2	1	10,3	1	9,9	2	18,8	0	0,0	1	12,6	1	12,3
3299	7705706	RPS27L	40S ribosomal protein S27-like	9,8	9478	1	9,6	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3300	7705720	MEMO1	protein MEMO1 isoform 1	6,7	33734	1	11,3	0	0,0	0	0,0	1	9,6	2	12,2	0	0,0	0	0,0
3301	7705819	IER3IP1	immediate early response 3-interacting protein 1 pre	8,7	8951	1	12,4	0	0,0	0	0,0	0	0,0	0	0,0	1	8,1	0	0,0
3302	7705851	CHCHD2	coiled-coil-helix-coiled-coil-helix domain-containin	9,5	15494	1	12,4	1	10,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3303	7706121	THEG	testicular haploid expressed gene protein isoform 1	9,4	43425	1	10,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3304	7706318	DHRS7	dehydrogenase/reductase SDR family member 7 precurso	8,3	38280	1	10,5	1	10,1	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3305	7706326	SF3B6	pre-mRNA branch site protein p14	9,7	14586	0	0,0	0	0,0	1	8,7	1	9,4	0	0,0	0	0,0	0	0,0
3306	7706337	COPZ1	coatomer subunit zeta-1 isoform 1	4,5	20199	2	17,6	0	0,0	1	9,2	0	0,0	0	0,0	1	8,0	1	9,6
3307	7706339	PPIL1	peptidyl-prolyl cis-trans isomerase-like 1	8,2	18219	1	11,5	0	0,0	0	0,0	0	0,0	0	0,0	2	9,3	0	0,0
3308	7706343	FAM96B	mitotic spindle-associated MMXD complex subunit MIP1	4,9	17645	1	11,1	0	0,0	0	0,0	0	0,0	0	0,0	1	9,4	1	9,8
3309	7706369	MPC1	mitochondrial pyruvate carrier 1 isoform 1	10,0	12329	0	0,0	1	10,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3310	7706423	LSM7	U6 snRNA-associated Sm-like protein LSm7	4,9	11584	0	0,0	0	0,0	2	13,6	1	9,5	0	0,0	1	8,0	0	0,0
3311	7706425	LSM8	N-alpha-acetyltransferase 38, NatC auxiliary subunit	4,2	10385	1	10,4	1	10,0	1	9,3	1	9,5	2	12,2	1	9,4	1	9,7
3312	7706441	VPS29	vacuolar protein sorting-associated protein 29 isofo	6,3	20488	1	10,5	1	10,1	0	0,0	0	0,0	0	0,0	1	8,9	1	7,9
3313	7706563	RAB8B	ras-related protein Rab-8B	9,4	23585	1	12,9	0	0,0	0	0,0	0	0,0	2	21,8	1	9,7	2	9,6
3314	7706751	TUBG2	tubulin gamma-2 chain	5,4	51092	2	15,2	1	10,1	1	8,7	0	0,0	2	12,3	1	8,0	1	7,9
3315	773575	ARCN1	archain	5,4	53010	1	15,5	1	10,3	4	32,4	1	9,4	2	12,2	2	15,3	3	26,2
3316	77378150	ENSG00000228325	immunoglobulin kappa light chain variable region	8,9	12799	0	0,0	0	0,0	1	8,6	0	0,0	0	0,0	0	0,0	0	0,0
3317	77379994	IGL	immunoglobulin lambda chain variable region	5,4	11731	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	2	9,8
3318	77404397	SND1	staphylococcal nuclease domain-containing protein 1	6,8	101978	15	67,7	18	64,2	20	83,6	14	65,4	11	84,4	11	77,4	13	68,9
3319	7768938	FARSB	phenylalanyl tRNA synthetase	6,4	66172	0	0,0	0	0,0	2	9,3	2	9,5	2	12,2	3	14,7	3	14,9
3320	7770151	LRRC59	AF119917_19 PRO1855	10,7	18800	1	11,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3321	7804450	LARS	leucyl tRNA synthetase	6,8	134411	2	19,7	2	15,1	0	0,0	2	18,8	0	0,0	2	9,3	2	12,3
3322	78057661	SEPT7	septin 7	8,9	48659	2	11,5	1	10,1	1	8,7	1	9,5	2	12,3	1	8,9	1	9,7
3323	780808	PAK2	p21-activated protein kinase	5,6	58076	2	10,5	2	14,9	0	0,0	0	0,0	0	0,0	0	0,0	1	11,4
3324	785996	SF1	ZFM1 protein alternatively spliced product	9,9	59652	3	14,1	3	10,1	6	27,6	5	18,8	5	24,3	1	8,7	3	13,5
3325	7920147	NSF	AF135168_1 N-ethylmaleimide-sensitive factor	6,4	82636	2	10,8	0	0,0	1	8,7	0	0,0	0	0,0	2	18,6	2	9,8
3326	793843	RPL29	ribosomal protein L29	12,1	17668	2	11,5	3	10,0	2	9,3	1	9,4	2	12,2	1	9,0	2	12,3
3327	7959825	N/A	AF116721_63 PRO1472	8,9	17154	0	17,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0

3328	8017397	HLA	HLA class I	5,4	21135	1	11,5	0	0,0	1	8,7	1	9,5	2	12,2	1	9,1	1	7,9
3329	804996	MARS	orf	8,8	53938	2	16,7	4	34,6	4	34,3	4	28,1	0	0,0	3	29,0	4	35,1
3330	8051579	AK4	adenylate kinase isoenzyme 4, mitochondrial	8,7	25250	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	2	17,9	1	7,9
3331	8051608	HMOX2	heme oxygenase 2	5,2	36034	1	10,5	1	10,0	2	18,4	2	18,8	2	12,2	2	17,7	2	18,7
3332	8099346	MARK1	AF154845_1 MARK	9,8	88987	1	13,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3333	8100054	DPM3	dolichol-phosphate-mannose synthase	5,6	10081	1	12,5	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3334	82546830	EXOC4	exocyst complex component 4 isoform a	6,1	110479	1	13,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3335	82546879	GTPBP1	GTP-binding protein 1	8,3	72454	1	10,9	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
3336	825635	CALM1	calmodulin	3,9	17164	10	36,6	7	25,0	11	36,7	8	37,5	14	36,3	9	26,9	9	35,2
3337	825676	HLA	HLA-DPB1	4,6	10422	1	12,1	0	0,0	1	8,7	0	0,0	0	0,0	1	8,0	0	0,0
3338	825683	TMSB4X	unnamed protein product	5,2	4249	15	44,2	0	0,0	0	0,0	0	0,0	0	0,0	5	18,5	3	11,4
3339	825711	ABCD3	70kD peroxisomal integral membrane protein	9,6	75486	2	16,0	1	10,3	0	0,0	0	0,0	0	0,0	1	8,0	1	7,9
3340	82659109	UBR4	E3 ubiquitin-protein ligase UBR4	5,6	573838	0	0,0	1	10,1	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3341	82802829	YBX1	rcNSEP1	10,3	35464	1	11,1	0	0,0	2	9,3	1	9,5	3	12,2	1	9,6	1	9,7
3342	82880645	USP14	ubiquitin carboxyl-terminal hydrolase 14 isoform	5,5	52368	1	13,5	3	30,0	2	13,5	2	18,7	0	0,0	2	15,9	0	0,0
3343	829177	GBP2	guanylate binding protein isoform II	5,4	67184	1	11,2	2	10,0	1	8,7	2	18,8	0	0,0	2	13,3	1	9,7
3344	83367083	UQCRQ	cytochrome b-c1 complex subunit 8	10,4	9907	1	10,4	1	10,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
3345	833999	TUFM	P43	7,7	49534	2	19,1	1	10,0	3	22,7	1	9,5	2	12,2	2	21,2	2	17,5
3346	83641874	CPVL	probable serine carboxypeptidase CPVL precursor	5,3	54145	1	10,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3347	83674980	TPI1	rcTPI1	8,1	26944	1	12,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3348	8393516	NSDHL	sterol-4-alpha-carboxylate 3-dehydrogenase, decarbox	8,1	41882	2	15,0	1	9,7	0	0,0	0	0,0	0	0,0	1	8,0	1	9,7
3349	8394376	STX18	syntaxin-18	5,2	38674	0	0,0	0	0,0	1	9,8	0	0,0	0	0,0	0	0,0	1	7,9
3350	84043963	EIF5B	eukaryotic translation initiation factor 5B	5,3	138808	0	0,0	1	10,3	1	9,9	1	9,5	0	0,0	2	8,1	1	8,0
3351	84181676	CRLF3	type I cytokine receptor like factor	4,8	49351	1	9,7	1	10,3	1	9,9	0	0,0	0	0,0	0	0,0	0	0,0
3352	84570013	C2CD3	C2CD3 protein	6,6	138848	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
3353	84708830	TUBB6	TUBB6 protein	4,6	50091	0	0,0	1	10,1	0	0,0	0	0,0	2	12,3	0	0,0	0	0,0
3354	8489831	BIRC6	AF265555_1 ubiquitin-conjugating BIR-domain enzyme APO	5,6	527588	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
3355	854167	PEA15	PEA-15	4,8	15039	1	11,3	2	15,1	1	8,7	1	9,5	0	0,0	1	12,1	2	9,6
3356	85720343	UTY	ubiquitously transcribed tetratricopeptide repeat pro	8,0	121101	1	13,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3357	862457	HADHA	enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase al	9,4	82941	11	70,9	8	39,6	15	77,2	16	74,7	8	48,3	10	68,5	9	47,9
3358	8655683	RCC2	hypothetical protein	8,4	36109	1	11,1	1	9,7	0	0,0	0	0,0	0	0,0	2	9,3	2	9,7
3359	8659555	HEL60	cytoplasmic aconitate hydratase	6,2	98399	1	10,5	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3360	86788140	ELMO1	engulfment and cell motility protein 1 isoform 2	6,0	28724	1	11,6	1	10,4	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
3361	871299	CPSF6	Human pre-mRNA cleavage factor I 68 kDa subunit	7,0	59190	2	11,7	3	15,1	4	13,6	1	9,5	5	12,3	2	9,1	4	13,6
3362	87196351	DDX3X	ATP-dependent RNA helicase DDX3X isoform 1	6,8	73225	6	35,8	4	19,9	6	36,7	7	28,2	15	72,3	6	30,1	7	35,2
3363	886258	ALCAM	alcam	5,9	65133	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
3364	887366	EIF2B2	ORF; putative, partial	5,6	38772	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
3365	88999583	MYL6	myosin light polypeptide 6 isoform 2	4,3	16943	13	54,3	14	34,8	8	34,9	13	28,1	14	60,3	15	46,7	12	40,3
3366	89059026	MAPK1	extracellular signal-regulated kinase-2 splice varian	6,1	36414	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3367	89179321	UNC45A	protein unc-45 homolog A isoform 3	5,7	101657	0	0,0	0	0,0	0	0,0	0	0,0	2	12,2	1	8,0	0	0,0
3368	8922188	FBXO6	F-box only protein 6	5,7	33933	1	9,7	2	10,0	2	8,7	0	0,0	2	12,2	1	8,0	1	7,9
3369	8922256	IFT57	intraflagellar transport protein 57 homolog	4,8	49090	1	12,4	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3370	8922331	MAGOHB	protein mago nashi homolog 2	6,0	17277	1	11,2	2	10,3	1	8,7	0	0,0	2	12,2	0	0,0	2	9,7
3371	8922477	POLR3E	DNA-directed RNA polymerase III subunit RPC5 isoform	6,0	79880	0	0,0	1	10,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3372	8922479	ARMC1	armadillo repeat-containing protein 1	5,4	31262	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,9	1	11,4
3373	8922498	HEL	pyridoxine-5'-phosphate oxidase	6,7	29989	2	15,2	1	9,7	0	0,0	0	0,0	2	12,2	1	13,3	2	18,4
3374	8922563	DNAJC17	dnaJ homolog subfamily C member 17	8,9	34688	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	1	7,9
3375	8922601	ARL8B	ADP-ribosylation factor-like protein 8B	8,6	21521	1	12,3	2	9,8	2	13,6	4	18,9	0	0,0	2	17,6	2	12,4
3376	8922701	AGK	acylglycerol kinase, mitochondrial precursor	8,0	47119	1	11,9	1	10,3	0	0,0	0	0,0	0	0,0	1	8,7	1	7,9
3377	8922720	TMEM30A	cell cycle control protein 50A isoform 1	8,7	40665	1	10,4	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	1	9,7
3378	8922913	AP5S1	AP-5 complex subunit sigma-1	6,4	22523	0	0,0	1	10,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3379	8922950	MNS1	meiosis-specific nuclear structural protein 1	6,8	60553	1	11,2	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3380	8923001	ABHD10	alpha/beta hydrolase domain-containing protein 10, m	8,7	33914	1	11,6	0	0,0	2	17,2	0	0,0	0	0,0	0	0,0	1	11,5
3381	8923390	CHCHD3	coiled-coil-helix-coiled-coil-helix domain-containin	8,3	26134	2	25,4	0	0,0	0	0,0	0	0,0	2	12,2	1	9,7	0	0,0
3382	8923557	GID8	glucose-induced degradation protein 8 homolog	4,8	26730	0	0,0	0	0,0	0	0,0	0	0,0	2	12,2	0	0,0	0	0,0
3383	8923579	LAMTOR1	ragulator complex protein LAMTOR1	4,9	17746	1	12,1	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3384	8923812	ACOT13	acyl-coenzyme A thioesterase 13 isoform 1	9,6	14942	0	0,0	0	0,0	1	9,9	0	0,0	0	0,0	0	0,0	0	0,0
3385	8923942	NOP10	H/ACA ribonucleoprotein complex subunit 3	10,4	7688	1	10,8	1	9,7	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
3386	8924248	SOX18	transcription factor SOX-18	8,0	40892	1	13,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3387	894178	COASY	unknown, partial	9,5	32109	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7	0	0,0
3388	89514797	HLA	MHC class I antigen	5,2	21024	3	10,5	0	0,0	2	9,3	1	9,5	3	12,2	0	0,0	4	9,7
3389	89573879	RPL18	ribosomal protein L18	12,3	18733	4	32,5	2	10,0	5	26,6	6	28,1	6	33,8	3	13,7	3	20,4
3390	895845	CLIC1	p64 CLCP	5,0	23544	4	26,5	3	10,1	3	9,3	6	28,2	5	36,2	4	21,2	2	12,9

3391	897763	TUBB	unnamed protein product	4,6	48881	135	165,9	105	133,6	87	133,0	100	130,8	122	204,8	98	142,4	123	130,1
3392	899300	TRIM22	gpStaf50	7,0	50456	0	0,0	1	10,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3393	903936	CASP5	cysteine protease	9,3	47815	0	0,0	1	10,3	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3394	91199540	DLD	dihydrolipoyl dehydrogenase, mitochondrial precurso	7,7	54159	5	26,2	4	14,9	7	31,9	5	28,1	5	24,3	6	32,6	6	27,7
3395	91208437	GMIP	GEM-interacting protein	5,4	106683	1	11,7	0	0,0	1	9,3	1	9,5	0	0,0	1	9,0	1	9,7
3396	913174	TMPO	TRPP	6,6	57649	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
3397	914833	KRT6C	keratin type II	5,2	42469	3	24,0	0	0,0	1	8,7	0	0,0	0	0,0	0	0,0	0	0,0
3398	915488	N/A	T-cell receptor alpha V-J junction, partial	6,2	1735	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7	0	0,0
3399	9186908	AKR1C4	3alpha-hydroxysteroid dehydrogenase variant	6,8	37079	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3400	9187989	HLA	MHC class I antigen	5,7	21177	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,4	3	9,8
3401	91979090	IGHV5	immunoglobulin heavy chain variable region	6,5	9746	0	0,0	0	0,0	2	8,7	0	0,0	0	0,0	0	0,0	0	0,0
3402	91984773	APOA1BP	NAD(P)H-hydrate epimerase precursor	7,6	31675	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
3403	91992153	HVCN1	voltage-gated hydrogen channel 1 isoform 1	6,4	31665	1	13,1	2	14,8	2	14,2	1	9,5	2	12,1	2	17,4	2	18,1
3404	91992949	GNB1	GNB1 protein	5,5	36299	1	11,2	2	10,0	0	0,0	2	18,8	0	0,0	1	8,9	1	12,7
3405	92373393	ACTR3B	actin-related protein 3B isoform 2	4,9	39679	1	11,0	4	10,0	3	9,2	1	9,5	6	12,2	4	9,0	1	9,7
3406	9257257	HEL	WD repeat-containing protein 1 isoform 1	6,2	66175	5	47,3	9	59,5	12	45,9	13	56,1	8	60,4	9	46,3	10	46,2
3407	927065	PTI	eukaryotic translation elongation factor 1 alpha 1-like	8,4	42806	0	0,0	0	0,0	1	9,9	0	0,0	0	0,0	0	0,0	0	0,0
3408	9280816	MYO6	myosin VI	8,6	146048	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,3	0	0,0
3409	929663	HNRNPD	unnamed protein product	7,8	24199	2	11,5	3	19,9	4	18,5	6	18,8	8	24,3	3	14,9	3	16,1
3410	930063	ENO2	neurone-specific enolase	4,8	47155	0	0,0	2	15,1	1	9,3	2	18,8	2	12,2	5	35,3	2	12,3
3411	93102364	SWAP70	switch-associated protein 70	5,6	68998	0	0,0	0	0,0	1	9,9	0	0,0	0	0,0	0	0,0	1	8,9
3412	93102389	CEP44	centrosomal protein of 44 kDa isoform a	5,0	44121	0	0,0	0	0,0	0	0,0	0	0,0	2	12,1	0	0,0	0	0,0
3413	93141018	H2AFY	core histone macro-H2A.1 isoform 3	10,2	39618	4	12,5	0	0,0	1	9,9	0	0,0	2	12,2	1	9,8	0	0,0
3414	93277076	CDKAL1	threonylcarbamoyladenosine tRNA methylthiotransfera	7,2	65093	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
3415	93277122	RBM4	RNA-binding protein 4 isoform 1	6,6	40315	0	0,0	1	10,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3416	9368440	GDH	uridine diphospho-glucose dehydrogenase	6,1	16581	1	10,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3417	9408096	RTN4	Nogo-A protein	4,3	129942	0	0,0	2	10,0	2	14,1	0	0,0	0	0,0	1	8,1	1	9,7
3418	9437517	MRPL1	AF212225_1 BM022	8,2	34515	1	9,7	1	10,3	1	8,7	0	0,0	0	0,0	0	0,0	1	9,6
3419	94421471	RNF17	RING finger protein 17 isoform 1	5,1	184643	1	11,2	0	0,0	1	8,6	0	0,0	3	12,2	0	0,0	0	0,0
3420	94681049	CFAP43	WD repeat-containing protein 96	5,6	191983	1	9,6	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3421	94681057	YARS2	tyrosine--tRNA ligase, mitochondrial precursor	9,3	53181	1	11,3	0	0,0	0	0,0	0	0,0	0	0,0	2	15,9	0	0,0
3422	94721250	VAPA	vesicle-associated membrane protein-associated prot	9,3	32595	1	11,6	0	0,0	4	17,2	0	0,0	0	0,0	0	0,0	5	24,8
3423	94818891	ERAP1	endoplasmic reticulum aminopeptidase 1 isoform b	6,0	107216	4	40,0	2	15,1	1	9,3	0	0,0	2	12,3	1	9,3	2	9,7
3424	95007797	FKBP12	FK506 binding protein12	5,5	10120	1	11,4	1	10,0	1	9,3	2	9,5	2	12,3	1	8,7	1	9,7
3425	9506363	SASH3	SAM and SH3 domain-containing protein 3	5,0	41577	1	12,1	2	19,3	0	0,0	0	0,0	0	0,0	1	9,6	1	8,8
3426	9506641	FAM105A	protein FAM105A	9,6	42197	1	12,5	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3427	951277	TRAF4	cystein rich domain associated to RING and TRAF protei	7,9	53425	0	0,0	1	10,3	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
3428	9558733	HSU53209	transformer-2 protein homolog alpha	11,7	32689	1	11,4	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3429	9624998	HNRNPH2	heterogeneous nuclear ribonucleoprotein H2	5,9	49245	7	45,4	4	25,0	6	36,7	8	37,5	8	36,3	4	29,5	7	35,2
3430	9663153	PNPLA2	transport-secretion protein 2.2 (TTS-2.2)	7,4	58185	1	10,8	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3431	9665248	TAP1	antigen peptide transporter 1	7,9	87218	3	24,4	4	29,8	4	22,8	4	28,2	2	12,4	4	26,5	4	37,2
3432	968888	HMGB1	HMG-1	5,6	24994	7	21,9	12	49,5	13	45,3	12	56,2	14	60,4	9	35,3	12	43,0
3433	96975097	RAB6B	ras-related protein Rab-6B	5,3	23463	1	20,8	0	0,0	2	9,2	1	9,4	0	19,4	1	11,1	0	0,0
3434	971270	PSMD7	proteasome subunit p40 / Mov34 protein	6,1	37061	1	15,4	4	25,0	3	17,8	0	0,0	0	0,0	5	20,5	2	14,9
3435	9714272	ILF3	double stranded RNA binding nuclear protein, ILF3	9,9	61957	2	15,6	2	14,8	1	9,8	2	18,8	2	12,2	1	12,6	1	15,4
3436	9755861	N/A	human leucocyte antigen	6,8	26367	0	13,0	0	0,0	0	0,0	0	0,0	0	0,0	0	9,3	0	0,0
3437	976227	PSMC5	26S proteasome subunit p45	8,3	45654	1	9,8	1	9,8	2	21,5	1	9,5	2	12,2	3	21,7	2	15,3
3438	9845511	RAC1	ras-related C3 botulinum toxin substrate 1 isoform R	8,5	21432	1	13,1	1	10,1	1	9,9	1	9,5	0	0,0	1	8,1	2	13,6
3439	9857759	N/A	recombinant IgG4 heavy chain	5,7	42935	0	17,9	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3440	986881	UBA7	ubiquitin-activating enzyme E1-related protein	5,5	111701	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
3441	987661	SMARCA2	transcriptional activator hSNF2a	6,9	179334	1	12,8	1	10,0	0	0,0	0	0,0	0	0,0	0	0,0	1	9,7
3442	987870	ABCE1	RNase L inhibitor	8,6	67559	1	11,5	0	0,0	1	9,3	1	9,5	2	12,3	2	12,3	1	9,7
3443	987948	PIK3C3	phosphatidylinositol 3-kinase	6,3	100989	0	0,0	1	9,7	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0
3444	98986464	TMED10	transmembrane emp24 domain-containing protein 10 pr	7,3	24958	3	10,5	2	9,8	2	14,2	1	9,5	3	12,2	3	12,3	1	12,8
3445	9910244	MRPS22	28S ribosomal protein S22, mitochondrial	7,9	41262	0	0,0	2	10,1	0	0,0	1	9,4	0	0,0	1	9,8	1	9,7
3446	9910382	TOMM22	mitochondrial import receptor subunit TOM22 homolog	4,1	15504	2	11,4	1	10,3	1	9,2	0	0,0	0	0,0	2	8,7	2	10,5
3447	9910460	HEL	omega-amidase NIT2	7,0	30609	1	10,5	3	10,1	3	14,2	1	9,5	0	0,0	2	11,7	2	9,7
3448	9910542	SAR1A	GTP-binding protein SAR1a	6,2	22368	0	0,0	0	0,0	0	0,0	0	0,0	0	0,0	1	8,0	0	0,0
3449	992595	CCT8	Cctq	9,6	3721	0	0,0	0	0,0	0	0,0	1	9,4	0	0,0	0	0,0	0	0,0
3450	992944	HLA	MHC class II cell surface glycoprotein	5,3	10609	0	0,0	1	10,0	0	0,0	6	9,5	2	12,2	2	8,9	1	11,5
3451	9951915	AHCY	adenosylhomocysteinase isoform 1	5,9	47717	14	71,5	8	44,7	10	50,1	8	37,4	9	48,3	8	35,3	10	41,5
3452	996057	TMED9	gp25l2	6,4	25123	2	16,6	1	10,3	1	8,6	1	9,4	2	12,2	1	9,3	1	8,8
3453	9966764	LYPLA2	acyl-protein thioesterase 2	6,8	24738	2	13,4	3	19,9	2	18,5	1	9,5	2	12,2	3	18,0	2	18,7

3454	9966779	EIF2B3	translation initiation factor eIF-2B subunit gamma i	6,0	50222	0	0,0	0	0,0	0	0,0	1	9,5	0	0,0	1	9,8	1	7,9
3455	9966827	PCNP	PEST proteolytic signal-containing nuclear protein	7,7	18907	1	12,1	1	10,0	0	0,0	0	0,0	0	0,0	1	9,3	2	10,6
3456	9966849	TIGAR	fructose-2,6-bisphosphatase TIGAR	7,6	30063	1	12,5	2	14,8	1	9,2	0	0,0	2	12,2	1	8,9	1	9,7
3457	9966867	EIF5A2	eukaryotic translation initiation factor 5A-2	5,3	16775	5	14,5	3	10,0	3	14,1	5	9,5	5	12,2	4	9,0	3	9,7
3458	9968322	ENSG00000223931	immunoglobulin heavy chain variable region	8,2	13344	2	11,6	0	0,0	1	9,8	0	0,0	0	0,0	0	0,0	0	0,0

Appendix 2. Complete list of LDA Significant Protein (LDA-SP) and differentially expressed proteins of NHD subject.

For each protein are reported: Gene Name, Uniprot entry, Reference, F-Ratio, Prob>F, Frequency (Freq) of each group, comparison among the 3 groups with DAve and DCI values. N/A: Not available.

#	Gene Name	Uniprot	Protein	F Ratio	Prob>F	LDA-SP			DEP					
						Freq_Wt	Freq_He	Freq_Ho	He vs Wt Dave	He vs Wt DCI	He vs Ho Dave	He vs Ho DCI	Wt vs Ho Dave	Wt vs Ho DCI
1	EEF1A1	P68104	Elongation factor 1-alpha 1			113,51	96,18	164,97	-0,17	-1816,85	-0,53	-8982,00	-0,37	-7165,15
2	HSPD1	P10809	60 kDa heat shock protein, mitochondrial	9,1060	0,0023	64,06	126,41	120,91	0,65	5937,78	0,04	680,56	-0,61	-5257,22
3	ENO1	P06733	Alpha-enolase			111,61	77,54	141,86	-0,36	-3221,64	-0,59	-7055,07	-0,24	-3833,43
4	TUBA1C	Q9BQE3	Tubulin alpha-1C chain	5,5568	0,0147	50,02	94,82	78,77	0,62	3244,84	0,18	1393,47	-0,45	-1851,37
5	MYH9	P35579	Myosin-9	18,3909	0,0001	52,66	87,47	74,60	0,50	2438,38	0,16	1042,37	-0,34	-1396,01
6	NPM1	P06748	Nucleophosmin			12,34	15,15	33,87	0,20	38,64	-0,76	-458,76	-0,93	-497,40
7	CLTC	Q00610	Clathrin heavy chain 1	10,3446	0,0013	17,30	37,31	31,35	0,73	546,29	0,17	204,50	-0,58	-341,80
8	ALK	Q9UM73	ALK tyrosine kinase receptor			15,12	25,94	29,87	0,53	222,17	-0,14	-109,63	-0,66	-331,80
9	UBA1	P22314	Ubiquitin-like modifier-activating enzyme 1	7,5243	0,0050	12,80	19,02	24,33	0,39	98,91	-0,25	-115,06	-0,62	-213,98
10	LMNA	P02545	Prelamin-A/C [Cleaved into: Lamin-A/C	27,8733	0,0000	1,51	19,75	19,99	1,72	193,90	-0,01	-4,78	-1,72	-198,68
11	NAMPT	P43490	Nicotinamide phosphoribosyltransferase	28,7546	0,0000	1,14	16,30	19,36	1,74	132,12	-0,17	-54,55	-1,78	-186,67
12	PSME2	Q9UL46	Proteasome activator complex subunit 2	9,7056	0,0017	20,40	36,97	27,74	0,58	475,24	0,29	298,67	-0,30	-176,56
13	LDHA	P00338	L-lactate dehydrogenase A chain	14,7765	0,0002	10,05	29,78	20,63	0,99	392,86	0,36	230,63	-0,69	-162,22
14	GPI	P06744	Glucose-6-phosphate isomerase	5,3686	0,0164	13,60	24,84	22,43	0,58	216,02	0,10	56,88	-0,49	-159,14
15	DBI	P07108	Acyl-CoA-binding protein	4,7898	0,0234	3,51	10,84	16,86	1,02	52,60	-0,43	-83,40	-1,31	-136,00
16	TLN1	Q9Y490	Talin-1			16,56	25,27	22,77	0,42	182,25	0,10	60,21	-0,32	-122,03
17	LCP1	P13796	Plastin-2	11,5590	0,0008	80,81	110,86	82,28	0,31	2879,72	0,30	2759,96	-0,02	-119,77
18	LAP3	P28838	Cytosol aminopeptidase	14,9399	0,0002	9,56	20,34	17,72	0,72	161,02	0,14	49,82	-0,60	-111,20
19	XRCC5	P13010	X-ray repair cross-complementing protein 5	4,4814	0,0285	11,94	21,23	18,44	0,56	154,05	0,14	55,34	-0,43	-98,71
20	FASN	P49327	Fatty acid synthase	3,8976	0,0418	12,84	27,21	18,98	0,72	287,60	0,36	189,92	-0,39	-97,68
21	RPS7	P62081	40S ribosomal protein S7	5,6775	0,0137	8,46	20,29	15,95	0,82	170,11	0,24	78,67	-0,61	-91,45
22	PARP1	P09874	Poly [ADP-ribose] polymerase 1	9,0662	0,0023	5,82	12,12	14,52	0,70	56,49	-0,18	-32,02	-0,86	-88,51
23	SERPINB9	P50453	Serpin B9	22,0055	0,0000	3,14	11,65	13,59	1,15	62,93	-0,15	-24,52	-1,25	-87,45
24	EPFP1	Q9UNM1	Chaperonin 10-related protein	48,3622	0,0000	1,74	12,46	13,21	1,51	76,12	-0,06	-9,61	-1,53	-85,73
25	IDH2	P48735	Isocitrate dehydrogenase [NADP], mitochondrial	9,3619	0,0020	5,92	11,28	14,17	0,62	46,08	-0,23	-36,84	-0,82	-82,92
26	LMNB1	P20700	Lamin-B1	24,1449	0,0000	6,04	19,19	14,01	1,04	166,00	0,31	86,10	-0,80	-79,90
27	LRPPRC	P42704	Leucine-rich PPR motif-containing protein, mitochondrial	10,3500	0,0013	7,63	16,06	14,69	0,71	99,91	0,09	21,07	-0,63	-78,84
28	XRCC6	P12956	X-ray repair cross-complementing protein 6	5,7701	0,0130	11,18	19,17	16,79	0,53	121,31	0,13	42,91	-0,40	-78,40
29	SPTAN1	Q13813	Spectrin alpha chain, non-erythrocytic 1	14,1790	0,0003	3,10	11,09	12,61	1,13	56,67	-0,13	-18,08	-1,21	-74,75
30	ACTR3	P61158	Actin-related protein 3	19,1470	0,0001	7,56	13,67	13,43	0,58	64,84	0,02	3,23	-0,56	-61,61
31	CCT6A	P40227	T-complex protein 1 subunit zeta	6,7526	0,0075	7,55	17,64	13,20	0,80	127,12	0,29	68,48	-0,55	-58,64
32	RPL4	P36578	60S ribosomal protein L4	10,0322	0,0015	6,69	14,78	12,53	0,75	86,94	0,16	30,75	-0,61	-56,19
33	PLCG2	P16885	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-2	18,9860	0,0001	1,98	8,34	10,69	1,23	32,84	-0,25	-22,30	-1,37	-55,14
34	KPNB1	Q14974	Importin subunit beta-1	4,9504	0,0212	8,30	10,50	13,38	0,23	20,65	-0,24	-34,45	-0,47	-55,10
35	MYL12B	O14950	Myosin regulatory light chain 12B	21,8901	0,0000	4,43	11,88	11,33	0,91	60,75	0,05	6,43	-0,87	-54,31
36	ACLY	P53396	ATP-citrate synthase	5,1582	0,0187	6,00	9,02	11,83	0,40	22,68	-0,27	-29,32	-0,65	-52,00
37	IGHM	P01871	Ig mu chain C region	44,3789	0,0000	0,25	11,40	10,10	1,91	64,95	0,12	13,94	-1,90	-51,01

38	NCF1	P14598	Neutrophil cytosol factor 1	9,4194	0,0020	1,15	10,54	9,91	1,61	54,91	0,06	6,44	-1,58	-48,47
39	GDI1	P31150	Rab GDP dissociation inhibitor alpha	9,3783	0,0020	7,67	16,32	12,16	0,72	103,76	0,29	59,26	-0,45	-44,49
40	IQGAP1	P46940	Ras GTPase-activating-like protein IQGAP1	5,2735	0,0174	6,68	14,69	11,41	0,75	85,63	0,25	42,92	-0,52	-42,71
41	HNRNPA1L2	Q32P51	Heterogeneous nuclear ribonucleoprotein A1-like 2			10,90	16,63	14,13	0,42	78,91	0,16	38,41	-0,26	-40,51
42	ACTN4	O43707	Alpha-actinin-4	10,9115	0,0010	6,77	13,98	11,02	0,70	74,86	0,24	37,01	-0,48	-37,85
43	TAGLN2	P37802	Transgelin-2	9,3806	0,0020	3,10	11,53	9,16	1,15	61,67	0,23	24,51	-0,99	-37,16
44	EHD1	Q9H4M9	EH domain-containing protein 1	11,9216	0,0007	2,43	7,21	8,74	0,99	23,08	-0,19	-12,17	-1,13	-35,25
45	RPS10	P46783	40S ribosomal protein S10	8,3548	0,0033	6,04	12,56	10,22	0,70	60,55	0,21	26,60	-0,51	-33,95
46	ACO2	Q99798	Aconitate hydratase, mitochondrial			4,93	7,90	9,56	0,46	19,07	-0,19	-14,46	-0,64	-33,53
47	ALDOC	P09972	Fructose-bisphosphate aldolase C			4,50	6,37	9,23	0,34	10,14	-0,37	-22,30	-0,69	-32,44
48	SPTBN1	Q01082	Spectrin beta chain, non-erythrocytic 1	20,9939	0,0000	1,98	4,42	8,08	0,77	7,83	-0,58	-22,82	-1,21	-30,65
49	CCT7	Q99832	T-complex protein 1 subunit eta	12,6249	0,0005	2,67	8,97	8,23	1,08	36,63	0,09	6,36	-1,02	-30,27
50	AK2	P54819	Adenylate kinase 2, mitochondrial	7,7946	0,0043	4,08	9,91	8,68	0,83	40,72	0,13	11,39	-0,72	-29,33
51	CAND1	Q86VP6	Cullin-associated NEDD8-dissociated protein 1	17,1167	0,0001	1,42	7,21	7,75	1,34	24,94	-0,07	-4,04	-1,38	-28,99
52	RNF213	Q63HN8	E3 ubiquitin-protein ligase RNF213	8,1099	0,0037	1,71	7,89	7,77	1,29	29,65	0,02	0,97	-1,28	-28,68
53	LSP1	P33241	Lymphocyte-specific protein 1	11,0135	0,0010	3,08	8,04	8,15	0,89	27,61	-0,01	-0,87	-0,90	-28,48
54	TFRC	P02786	Transferrin receptor protein 1			6,46	9,37	9,89	0,37	23,03	-0,05	-5,00	-0,42	-28,04
55	TC4	Q0EFC9	TC4 protein	4,1053	0,0364	1,23	4,18	7,58	1,09	7,98	-0,58	-20,02	-1,44	-28,00
56	HMGB1	P09429	High mobility group protein B1	4,4279	0,0295	7,47	12,79	10,56	0,53	53,94	0,19	26,10	-0,34	-27,84
57	MYO1G	B0I1T2	Unconventional myosin-Ig [Cleaved into: Minor histocompatibility antigen HA-2	7,1101	0,0062	2,78	9,40	7,96	1,09	40,28	0,17	12,45	-0,96	-27,83
58	MTHFD1	P11586	C-1-tetrahydrofolate synthase, cytoplasmic			4,35	8,23	8,51	0,62	24,43	-0,03	-2,31	-0,65	-26,74
59	FSCN1	Q16658	Fascin	5,1585	0,0187	3,45	8,62	8,03	0,86	31,25	0,07	4,96	-0,80	-26,29
60	ACTR2	P61160	Actin-related protein 2	4,8801	0,0221	6,81	7,95	9,95	0,15	8,38	-0,22	-17,90	-0,37	-26,29
61	ALDH18A1	P54886	Delta-1-pyrroline-5-carboxylate synthase	6,1814	0,0103	2,99	9,10	7,79	1,01	36,97	0,15	11,06	-0,89	-25,91
62	PSMA2	P25787	Proteasome subunit alpha type-2	11,3286	0,0009	3,26	9,87	7,81	1,01	43,37	0,23	18,15	-0,82	-25,22
63	ECH1	Q13011	Delta	13,7909	0,0003	1,49	9,55	7,20	1,46	44,46	0,28	19,64	-1,31	-24,82
64	RPSA	P08865	40S ribosomal protein SA	6,0891	0,0108	5,91	11,23	9,19	0,62	45,58	0,20	20,82	-0,43	-24,76
65	COPA	P53621	Coatomer subunit alpha	10,3622	0,0013	4,14	5,73	8,05	0,32	7,86	-0,34	-15,98	-0,64	-23,84
66	HNRNPA2B1	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1	9,0609	0,0023	0,39	6,18	6,90	1,76	19,01	-0,11	-4,71	-1,78	-23,72
67	HIST2H2AB	Q8IUE6	Histone H2A type 2-B			5,28	9,75	8,68	0,59	33,57	0,12	9,86	-0,49	-23,72
68	MATR3	P43243	Matrin-3	8,3284	0,0033	3,11	7,63	7,37	0,84	24,24	0,03	1,93	-0,81	-22,31
69	PRDX3	P30048	Thioredoxin-dependent peroxide reductase, mitochondrial	3,7587	0,0459	3,15	4,95	7,37	0,44	7,28	-0,39	-14,87	-0,80	-22,15
70	CMPK1	P30085	UMP-CMP kinase	6,6626	0,0079	4,44	7,71	7,96	0,54	19,88	-0,03	-1,91	-0,57	-21,79
71	LPXN	O60711	Leupaxin	6,8879	0,0070	3,33	5,80	7,38	0,54	11,25	-0,24	-10,46	-0,76	-21,70
72	PFKP	Q01813	ATP-dependent 6-phosphofructokinase, platelet type	7,3272	0,0055	2,21	4,94	6,85	0,76	9,77	-0,32	-11,27	-1,03	-21,04
73	PFKL	P17858	ATP-dependent 6-phosphofructokinase, liver type	5,2924	0,0172	4,67	5,51	7,94	0,16	4,27	-0,36	-16,30	-0,52	-20,57
74	TUFM	P49411	Elongation factor Tu, mitochondrial			3,86	5,11	7,44	0,28	5,62	-0,37	-14,60	-0,63	-20,21
75	SFPQ	P23246	Splicing factor, proline- and glutamine-rich			8,33	12,43	10,41	0,40	42,63	0,18	23,07	-0,22	-19,56
76	BASP1	P80723	Brain acid soluble protein 1			3,21	6,64	6,94	0,70	16,91	-0,04	-2,05	-0,74	-18,95
77	HEL107	V9HWD9	Transketolase			12,48	19,55	13,79	0,44	113,19	0,35	95,96	-0,10	-17,23
78	EIF5A	P63241	Eukaryotic translation initiation factor 5A-1	4,6289	0,0259	4,29	11,79	7,26	0,93	60,32	0,48	43,17	-0,51	-17,15
79	DYNC1H1	Q14204	Cytoplasmic dynein 1 heavy chain 1			1,46	4,33	6,03	0,99	8,32	-0,33	-8,80	-1,22	-17,11
80	PGD	P52209	6-phosphogluconate dehydrogenase, decarboxylating	4,6637	0,0254	4,17	9,28	7,18	0,76	34,40	0,26	17,32	-0,53	-17,07
81	IDH3A	P50213	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial			5,08	5,22	7,71	0,03	0,69	-0,39	-16,08	-0,41	-16,77
82	CCT4	P50991	T-complex protein 1 subunit delta	8,8255	0,0026	3,71	7,31	6,86	0,65	19,80	0,06	3,17	-0,60	-16,63

83	HNRNPK	P61978	Heterogeneous nuclear ribonucleoprotein K	3,7632	0,0458	15,53	23,51	16,56	0,41	155,85	0,35	139,27	-0,06	-16,58
84	HNRNPA3	P51991	Heterogeneous nuclear ribonucleoprotein A3	28,6445	0,0000	1,38	6,67	5,90	1,31	21,30	0,12	4,86	-1,24	-16,43
85	FBL	P22087	rRNA 2'-O-methyltransferase fibrillarin	5,7679	0,0130	1,74	5,27	5,93	1,01	12,38	-0,12	-3,69	-1,09	-16,07
86	SET	Q01105	Protein SET	7,5727	0,0049	5,10	10,17	7,61	0,66	38,74	0,29	22,82	-0,39	-15,92
87	SYNCRIP	O60506	Heterogeneous nuclear ribonucleoprotein Q	8,7817	0,0027	4,76	8,70	7,37	0,59	26,52	0,17	10,67	-0,43	-15,85
88	IARS	P41252	Isoleucine--tRNA ligase, cytoplasmic	7,4715	0,0051	0,59	3,02	5,56	1,34	4,39	-0,59	-10,91	-1,62	-15,30
89	PSMB1	P20618	Proteasome subunit beta type-1	3,6493	0,0495	4,74	9,34	7,26	0,65	32,41	0,25	17,24	-0,42	-15,17
90	IRF4	Q15306	Interferon regulatory factor 4			3,21	6,86	6,35	0,72	18,35	0,08	3,37	-0,66	-14,98
91	KHDRBS1	Q07666	KH domain-containing, RNA-binding, signal transduction-associated protein 1	10,3354	0,0013	1,60	5,10	5,63	1,05	11,74	-0,10	-2,82	-1,11	-14,56
92	RPL3	P39023	60S ribosomal protein L3	4,9355	0,0214	5,67	11,23	7,81	0,66	47,00	0,36	32,58	-0,32	-14,42
93	RPS15	P62841	40S ribosomal protein S15			4,79	8,84	7,12	0,59	27,64	0,22	13,78	-0,39	-13,86
94	YWHAZ	P63104	14-3-3 protein zeta/delta	8,6066	0,0029	8,68	15,24	10,14	0,55	78,53	0,40	64,79	-0,16	-13,74
95	SWAP70	Q9UH65	Switch-associated protein 70	17,4844	0,0001	0,65	5,33	5,28	1,57	13,99	0,01		-1,56	-13,73
96	LMAN1	P49257	Protein ERGIC-53	6,2053	0,0101	3,62	4,90	6,35	0,30	5,45	-0,26	-8,14	-0,55	-13,58
97	OLA1	Q9NTK5	Obg-like ATPase 1	4,4619	0,0288	3,00	5,27	6,01	0,55	9,42	-0,13	-4,12	-0,67	-13,55
98	RPL38	P63173	60S ribosomal protein L38	4,0464	0,0378	3,94	6,39	6,47	0,48	12,68	-0,01	-0,48	-0,49	-13,16
99	RPL12	P30050	60S ribosomal protein L12	4,0637	0,0374	2,59	5,94	5,66	0,78	14,27	0,05	1,62	-0,74	-12,65
100	STAT3	P40763	Signal transducer and activator of transcription 3	5,9864	0,0115	1,53	6,99	5,23	1,28	23,27	0,29	10,75	-1,09	-12,52
101	HADH	P40939, Q16836	Trifunctional enzyme subunit alpha, mitochondrial; Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	5,1358	0,0189	2,70	7,34	5,66	0,92	23,31	0,26	10,95	-0,71	-12,36
102	FARSA	Q9Y285	Phenylalanine--tRNA ligase alpha subunit	7,7212	0,0045	0,72	4,02	5,00	1,40	7,84	-0,22	-4,42	-1,50	-12,27
103	FH	P07954	Fumarate hydratase, mitochondrial	6,1961	0,0102	2,70	7,20	5,56	0,91	22,27	0,26	10,46	-0,69	-11,81
104	MARS	P56192	Methionine--tRNA ligase, cytoplasmic	8,6296	0,0029	1,23	2,99	4,98	0,83	3,71	-0,50	-7,92	-1,21	-11,63
105	EIF3E	P60228	Eukaryotic translation initiation factor 3 subunit E	8,3093	0,0034	1,89	7,64	5,16	1,21	27,42	0,39	15,93	-0,93	-11,50
106	CCT8	P50990	T-complex protein 1 subunit theta			6,49	9,91	7,96	0,42	27,99	0,22	17,41	-0,20	-10,58
107	HNRNPD	Q14103	Heterogeneous nuclear ribonucleoprotein D0	13,8493	0,0003	1,64	6,58	4,83	1,20	20,34	0,31	10,01	-0,99	-10,33
108	SDHA	P31040	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	5,7328	0,0133	1,91	4,03	4,82	0,72	6,30	-0,18	-3,49	-0,87	-9,79
109	IGK	N/A	immunoglobulin kappa light chain VLJ region	18,4389	0,0001	0,12	5,64	4,39	1,92	15,88	0,25	6,23	-1,90	-9,64
110	CORO1C	Q9ULV4	Coronin-1C	8,3387	0,0033	1,73	3,22	4,66	0,60	3,68	-0,37	-5,67	-0,92	-9,35
111	SF3B1	O75533	Splicing factor 3B subunit 1	6,4563	0,0088	1,32	3,13	4,47	0,81	4,02	-0,35	-5,09	-1,09	-9,11
112	NDUFA5	Q16718	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	12,6261	0,0005	0,50	4,40	4,28	1,59	9,57	0,03	0,52	-1,58	-9,05
113	PNP	P0049, P01298	Purine nucleoside phosphorylase; Pancreatic prohormone	12,5857	0,0005	1,48	5,11	4,46	1,10	11,97	0,14	3,15	-1,00	-8,83
114	HNRNPM	P52272	Heterogeneous nuclear ribonucleoprotein M	6,0085	0,0113	4,22	9,22	5,71	0,74	33,62	0,47	26,23	-0,30	-7,39
115	LONP1	P36776	Lon protease homolog, mitochondrial	4,1924	0,0344	1,88	3,36	4,21	0,56	3,87	-0,23	-3,25	-0,77	-7,12
116	CTPS1	P17812	CTP synthase 1	11,0626	0,0010	0,46	3,52	3,75	1,54	6,11	-0,06	-0,82	-1,56	-6,93
117	PRPF8	Q6P2Q9	Pre-mRNA-processing-splicing factor 8	8,2301	0,0035	1,26	6,61	3,89	1,36	21,06	0,52	14,27	-1,02	-6,79
118	YBX1	P67809	Nuclease-sensitive element-binding protein 1	5,2259	0,0179	2,68	6,18	4,52	0,79	15,54	0,31	8,90	-0,51	-6,63
119	HMGB2	P26583	High mobility group protein B2	5,0285	0,0202	2,35	4,96	4,33	0,71	9,51	0,13	2,90	-0,59	-6,61
120	COPB1	P53618	Coatomer subunit beta	3,7485	0,0462	4,14	7,27	5,51	0,55	17,86	0,28	11,26	-0,28	-6,60
121	ENO2	P09104	Gamma-enolase	14,1673	0,0003	0,00	1,55	3,63	2,00	1,20	-0,80	-5,39	-2,00	-6,59
122	HNRNPL	P14866	Heterogeneous nuclear ribonucleoprotein L	4,1186	0,0361	2,73	5,93	4,44	0,74	13,87	0,29	7,76	-0,48	-6,11
123	NME2	P22392	Nucleoside diphosphate kinase B	4,0802	0,0370	5,52	10,25	6,53	0,60	37,33	0,44	31,24	-0,17	-6,10
124	EIF2AK2	P19525	Interferon-induced, double-stranded RNA-activated protein kinase	9,6590	0,0018	1,14	4,51	3,67	1,19	9,54	0,21	3,44	-1,05	-6,10
125	ADA	P00813	Adenosine deaminase	18,3365	0,0001	0,19	3,99	3,49	1,82	7,92	0,13	1,85	-1,80	-6,07
126	NASP	P49321	Nuclear autoantigenic sperm protein	6,1859	0,0102	2,07	6,04	4,05	0,98	16,11	0,40	10,06	-0,65	-6,05
127	VTN	P04004	Vitronectin	5,1892	0,0183	0,86	2,07	3,56	0,82	1,77	-0,53	-4,21	-1,22	-5,98

128	MYH11	P35749	Myosin-11	12,8363	0,0005	2,08	7,10	4,00	1,09	23,03	0,56	17,21	-0,63	-5,83
129	DDT3	A0A0F7RQT4	D-dopachrome tautomerase 3	3,6456	0,0496	0,67	2,32	3,46	1,10	2,46	-0,40	-3,32	-1,35	-5,78
130	SSB	P05455	Lupus La protein	4,7549	0,0239	1,11	3,53	3,56	1,04	5,62	-0,01		-1,05	-5,72
131	EIF3F	O00303	Eukaryotic translation initiation factor 3 subunit F	11,0223	0,0010	0,00	3,65	3,37	2,00	6,66	0,08	0,98	-2,00	-5,68
132	DDX1	Q92499	ATP-dependent RNA helicase DDX1	6,7539	0,0075	0,97	5,60	3,50	1,41	15,22	0,46	9,57	-1,13	-5,65
133	EIF5B	O60841	Eukaryotic translation initiation factor 5B	11,0300	0,0010	0,89	2,77	3,47	1,03	3,43	-0,23	-2,21	-1,19	-5,64
134	CHD4	Q14839	Chromodomain-helicase-DNA-binding protein 4	7,1071	0,0062	0,96	6,13	3,47	1,46	18,31	0,55	12,74	-1,14	-5,57
135	EIF3M	Q7L2H7	Eukaryotic translation initiation factor 3 subunit M	5,9582	0,0116	1,04	5,62	3,47	1,38	15,27	0,47	9,79	-1,08	-5,48
136	SEPT9	Q9UHD8	Septin-9	4,0313	0,0382	1,59	3,82	3,67	0,82	6,02	0,04	0,54	-0,79	-5,48
137	C14orf166	Q9Y224	UPF0568 protein C14orf166	8,1493	0,0036	0,70	2,68	3,29	1,18	3,35	-0,21	-1,83	-1,30	-5,17
138	HSPA1B	P0DMV9	Heat shock 70 kDa protein 1B	11,4427	0,0008	0,11	2,65	3,13	1,84	3,51	-0,17	-1,39	-1,86	-4,90
139	ATP5O	P48047	ATP synthase subunit O, mitochondrial			4,93	7,41	5,83	0,40	15,34	0,24	10,48	-0,17	-4,86
140	EIF3L	Q9Y262	Eukaryotic translation initiation factor 3 subunit L	4,1604	0,0351	2,04	6,06	3,72	0,99	16,30	0,48	11,44	-0,59	-4,86
141	SQRDL	Q9Y6N5	Sulfide:quinone oxidoreductase, mitochondrial	5,8795	0,0122	0,76	2,87	3,20	1,16	3,83	-0,11	-1,01	-1,23	-4,83
142	NOP56	O00567	Nucleolar protein 56	7,7088	0,0045	0,95	3,44	3,25	1,13	5,46	0,06	0,63	-1,09	-4,83
143	HPRT1	P00492	Hypoxanthine-guanine phosphoribosyltransferase	9,7654	0,0017	0,42	2,39	3,11	1,40	2,77	-0,26	-1,98	-1,52	-4,75
144	CD97	P48960	CD97 antigen	5,4129	0,0160	0,28	2,83	3,08	1,64	3,97	-0,08	-0,74	-1,67	-4,70
145	NOP58	Q9Y2X3	Nucleolar protein 58	5,8787	0,0122	1,20	2,35	3,26	0,65	2,03	-0,33	-2,56	-0,92	-4,59
146	STAT5A	P42229	Signal transducer and activator of transcription 5A	8,7593	0,0027	0,19	1,93	3,02	1,65	1,85	-0,44	-2,68	-1,77	-4,53
147	FKBP3	Q00688	Peptidyl-prolyl cis-trans isomerase FKBP3	5,0631	0,0198	0,99	4,15	3,14	1,23	8,12	0,28	3,69	-1,04	-4,43
148	PTPRC	P08575	Receptor-type tyrosine-protein phosphatase C	8,3974	0,0032	0,00	2,55	2,96	2,00	3,26	-0,15	-1,11	-2,00	-4,37
149	FTL	P02792	Ferritin light chain	6,5362	0,0084	0,11	0,54	2,90	1,32		-1,37	-4,06	-1,85	-4,20
150	GSPT2	Q8IYD1	Eukaryotic peptide chain release factor GTP-binding subunit ERF3B	9,8771	0,0016	0,51	2,97	2,92	1,41	4,27	0,02		-1,40	-4,12
151	RSL1D1	O76021	Ribosomal L1 domain-containing protein 1	8,1549	0,0036	0,11	3,57	2,87	1,88	6,37	0,22	2,26	-1,85	-4,11
152	YWHAQ	P27348	14-3-3 protein theta	8,6928	0,0028	1,34	4,35	3,15	1,06	8,55	0,32	4,47	-0,81	-4,08
153	FARSB	Q9NSD9	Phenylalanine--tRNA ligase beta subunit	18,2263	0,0001	0,00	1,25	2,83	2,00	0,78	-0,77	-3,22	-2,00	-4,00
154	AP1B1	Q10567	AP-1 complex subunit beta-1	10,8091	0,0011	0,35	2,69	2,84	1,54	3,54	-0,06	-0,44	-1,56	-3,98
155	CSE1L	P55060	Exportin-2	13,4503	0,0004	0,53	4,92	2,81	1,61	11,94	0,55	8,13	-1,36	-3,81
156	RCN1	Q15293	Reticulocalbin-1	5,3607	0,0165	1,10	1,23	2,97	0,11		-0,83	-3,65	-0,92	-3,80
157	PYCR1	P32322	Pyrroline-5-carboxylate reductase 1, mitochondrial	26,7715	0,0000	0,00	0,84	2,75	2,00	0,35	-1,07	-3,43	-2,00	-3,78
158	ANP32B	Q92688	Acidic leucine-rich nuclear phosphoprotein 32 family member B	8,7143	0,0028	0,50	3,71	2,76	1,52	6,75	0,29	3,06	-1,38	-3,69
159	PSMC5	P62195	26S protease regulatory subunit 8	6,1698	0,0103	0,16	2,62	2,69	1,77	3,43	-0,03		-1,77	-3,61
160	HNRNPAB	Q99729	Heterogeneous nuclear ribonucleoprotein A/B	3,7172	0,0472	1,13	2,63	2,83	0,80	2,83	-0,07	-0,54	-0,86	-3,37
161	NMT1	P30419	Glycylpeptide N-tetradecanoyltransferase 1	11,5466	0,0008	0,69	2,67	2,68	1,18	3,33	0,00		-1,18	-3,35
162	ARPC2	O15144	Actin-related protein 2/3 complex subunit 2	3,8696	0,0426	2,17	5,33	3,36	0,84	11,86	0,45	8,58	-0,43	-3,28
163	VARS	P26640	Valine--tRNA ligase	4,3312	0,0314	1,04	2,53	2,66	0,84	2,67	-0,05		-0,88	-2,99
164	ILF3	Q12906	Interleukin enhancer-binding factor 3	6,0666	0,0109	2,16	4,69	3,26	0,74	8,65	0,36	5,67	-0,41	-2,98
165	PSMC1	P62191	26S protease regulatory subunit 4	5,8471	0,0124	0,74	2,75	2,55	1,15	3,51	0,08	0,55	-1,10	-2,97
166	KIAA1210	Q9ULL0	Uncharacterized protein KIAA1210	9,8605	0,0016	0,72	1,05	2,54	0,37		-0,83	-2,67	-1,11	-2,96
167	DNM1L	O00429	Dynamin-1-like protein	8,8682	0,0026	0,16	0,43	2,43	0,90		-1,40	-2,85	-1,75	-2,93
168	TPP1	O14773, P49638, Q96AP0	Tripeptidyl-peptidase 1; Alpha-tocopherol transfer protein; Adrenocortical dysplasia protein homolog	7,9290	0,0040	0,16	2,62	2,43	1,77	3,41	0,08	0,48	-1,75	-2,93
169	TMPO	P42166, P42167	Lamina-associated polypeptide 2, isoform alpha; Lamina-associated polypeptide 2, isoforms beta/gamma	5,5057	0,0152	2,45	5,84	3,40	0,82	14,05	0,53	11,27	-0,32	-2,77
170	EIF2S1	P05198	Eukaryotic translation initiation factor 2 subunit 1	7,0095	0,0065	1,13	2,98	2,61	0,90	3,80	0,13	1,03	-0,79	-2,76
171	ARHG	P84095	Rho-related GTP-binding protein RhoG	10,0187	0,0015	0,97	1,30	2,52	0,29		-0,64	-2,33	-0,89	-2,71
172	LYPLA2	O95372	Acyl-protein thioesterase 2	3,6343	0,0500	1,12	2,06	2,56	0,59	1,51	-0,22	-1,15	-0,78	-2,66

173	TIPRL	O75663	TIP41-like protein	6,3819	0,0092	0,30	1,21	2,30	1,21	0,69	-0,62	-1,91	-1,54	-2,61
174	PSMA3	P25788	Proteasome subunit alpha type-3	5,4462	0,0157	0,95	3,30	2,39	1,11	4,98	0,32	2,58	-0,86	-2,41
175	PSMD12	O00232	26S proteasome non-ATPase regulatory subunit 12	4,1263	0,0359	0,68	2,28	2,29	1,09	2,38	0,00		-1,09	-2,40
176	BID	P55957	BH3-interacting domain death agonist	4,8227	0,0230	0,46	2,13	2,22	1,29	2,17	-0,04		-1,31	-2,36
177	HIST1H1A	Q02539	Histone H1.1	6,9567	0,0067	4,58	8,49	5,07	0,60	25,60	0,51	23,24	-0,10	-2,35
178	PCMT1	P22061	Protein-L-isoaspartate	11,1736	0,0009	0,30	1,45	2,19	1,32	1,01	-0,40	-1,34	-1,52	-2,35
179	ARL8B	Q9NVJ2	ADP-ribosylation factor-like protein 8B	8,6170	0,0029	0,23	1,70	2,17	1,53	1,41	-0,25	-0,93	-1,62	-2,34
180	RPA3	P35244	Replication protein A 14 kDa subunit	5,6932	0,0136	0,00	1,06	2,14	2,00	0,56	-0,67	-1,73	-2,00	-2,29
181	HNRNPA1	P09651	Heterogeneous nuclear ribonucleoprotein A1	4,5552	0,0272	0,49	2,78	2,16	1,41	3,74	0,25	1,53	-1,27	-2,21
182	PSMD1	Q99460	26S proteasome non-ATPase regulatory subunit 1	3,9705	0,0398	0,85	0,77	2,26	-0,10		-0,99	-2,26	-0,91	-2,19
183	CPNE1	Q99829	Copine-1	4,2008	0,0342	1,05	1,52	2,30	0,36	0,61	-0,40	-1,48	-0,74	-2,08
184	SDHB	P21912	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial	13,6777	0,0003	0,22	0,34	2,03	0,40		-1,43	-2,01	-1,60	-2,04
185	PDCD6	O75340	Programmed cell death protein 6	7,1456	0,0061	0,72	1,18	2,11	0,48	0,43	-0,57	-1,54	-0,98	-1,97
186	SNRP116	Q15029	116 kDa U5 small nuclear ribonucleoprotein component	6,5680	0,0083	0,56	2,69	1,96	1,31	3,46	0,31	1,70	-1,11	-1,76
187	LACTB	P83111	Serine beta-lactamase-like protein LACTB, mitochondrial	4,0762	0,0371	0,00	1,81	1,87	2,00	1,64	-0,03		-2,00	-1,76
188	CYFIP1	Q7L576	Cytoplasmic FMR1-interacting protein 1	12,3078	0,0006	0,14	3,31	1,86	1,84	5,45	0,56	3,73	-1,72	-1,72
189	OXCT	P55809	Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial	7,7345	0,0045	0,44	0,00	1,89	-2,00	-0,10	-2,00	-1,79	-1,25	-1,69
190	TNFAIP8	O95379	Tumor necrosis factor alpha-induced protein 8	4,1421	0,0355	2,07	3,96	2,77	0,63	5,71	0,35	4,02	-0,29	-1,69
191	TROVE2	P10155	60 kDa SS-A/Ro ribonucleoprotein	5,4419	0,0157	0,44	2,35	1,88	1,37	2,67	0,22	0,99	-1,24	-1,67
192	PRPS1L1	P21108	Ribose-phosphate pyrophosphokinase 3	15,0588	0,0002	0,00	0,46	1,83	2,00	0,10	-1,20	-1,57	-2,00	-1,67
193	HMOX2	P30519	Heme oxygenase 2	8,0209	0,0039	0,35	1,75	1,85	1,34	1,48	-0,05		-1,37	-1,65
194	NCKAP1L	P55160	Nck-associated protein 1-like	6,4527	0,0088	0,00	2,54	1,80	2,00	3,23	0,34	1,61	-2,00	-1,63
195	PSMB10	P40306	Proteasome subunit beta type-10	4,3059	0,0319	1,86	3,83	2,59	0,69	5,59	0,39	3,98	-0,33	-1,62
196	HVCN1	Q96D96	Voltage-gated hydrogen channel 1	4,0806	0,0370	0,94	1,56	1,99	0,49	0,77	-0,24	-0,77	-0,71	-1,53
197	ETFB	P38117	Electron transfer flavoprotein subunit beta	4,4777	0,0286	1,14	0,38	2,08	-1,00	-0,58	-1,38	-2,08	-0,58	-1,51
198	CYCS	P99999	Cytochrome c	8,9739	0,0024	0,16	2,64	1,73	1,77	3,48	0,42	1,99	-1,66	-1,48
199	NDUFS8	O00217	NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial	23,8077	0,0000	0,00	1,77	1,71	2,00	1,57	0,04		-2,00	-1,46
200	GFPT1	Q06210	Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1	5,8238	0,0126	0,57	1,55	1,79	0,92	1,03	-0,15	-0,40	-1,03	-1,43
201	PTGES3	Q15185	Prostaglandin E synthase 3	20,4634	0,0000	0,19	1,72	1,69	1,61	1,46	0,01		-1,60	-1,42
202	PRPSAP2	O60256	Phosphoribosyl pyrophosphate synthase-associated protein 2	4,3052	0,0319	0,58	0,88	1,76	0,41		-0,67	-1,16	-1,01	-1,37
203	OAS3	Q9Y6K5	2'-5'-oligoadenylate synthase 3	6,2180	0,0100	0,14	0,58	1,64	1,22		-0,95	-1,17	-1,68	-1,33
204	OAS2	P29728	2'-5'-oligoadenylate synthase 2	3,8734	0,0425	0,94	3,13	1,87	1,08	4,48	0,51	3,17	-0,67	-1,31
205	CD38	P28907	ADP-ribosyl cyclase/cyclic ADP-ribose hydrolase 1	14,2391	0,0003	0,00	1,08	1,61	2,00	0,59	-0,39	-0,71	-2,00	-1,30
206	ARPC5L	Q9BPX5	Actin-related protein 2/3 complex subunit 5-like protein	7,6304	0,0047	0,64	0,26	1,69	-0,85		-1,47	-1,39	-0,91	-1,23
207	STK4	Q13043	Serine/threonine-protein kinase 4	5,3214	0,0169	0,00	1,46	1,55	2,00	1,06	-0,07		-2,00	-1,21
208	ME2	P23368	NAD-dependent malic enzyme, mitochondrial	4,2398	0,0333	1,57	3,33	2,20	0,72	4,32	0,41	3,12	-0,34	-1,20
209	MESDC2	Q14696	LDLR chaperone MESD	15,3229	0,0002	0,14	0,33	1,54	0,81		-1,29	-1,14	-1,66	-1,18
210	USP7	Q93009	Ubiquitin carboxyl-terminal hydrolase 7	7,4069	0,0053	0,16	0,33	1,54	0,69		-1,29	-1,14	-1,62	-1,18
211	GBP1	P32455	Guanylate-binding protein 1	8,7294	0,0027	0,00	0,67	1,53	2,00	0,22	-0,78	-0,95	-2,00	-1,18
212	SF1	Q13285, Q15637	Steroidogenic factor 1; Splicing factor 1	7,0444	0,0064	1,13	4,44	1,87	1,19	9,21	0,81	8,09	-0,50	-1,12
213	PSMB3	P49720	Proteasome subunit beta type-3	5,2260	0,0179	0,83	3,12	1,70	1,16	4,54	0,59	3,44	-0,69	-1,11
214	SOD2	P04179	Superoxide dismutase [Mn], mitochondrial	4,6415	0,0257	0,28	0,67	1,51	0,82		-0,77	-0,91	-1,37	-1,10
215	TRIP10	Q15642	Cdc42-interacting protein 4	7,5541	0,0049	0,00	0,59	1,48	2,00	0,18	-0,86	-0,92	-2,00	-1,10
216	MTX2	O75431	Metaxin-2	11,7661	0,0007	0,00	1,30	1,48	2,00	0,85	-0,13		-2,00	-1,09
217	CECR5	Q9BXW7	Cat eye syndrome critical region protein 5	15,9640	0,0002	0,00	0,17	1,45	2,00	0,01	-1,59	-1,04	-2,00	-1,06

218	ANXA11	P50995	Annexin A11	6,8508	0,0071	1,58	3,80	2,14	0,83	5,96	0,56	4,91	-0,30	-1,05
219	SRI	P30626	Sorcin	4,8786	0,0222	0,00	0,66	1,38	2,00	0,22	-0,71	-0,74	-2,00	-0,95
220	PYGB	P11216	Glycogen phosphorylase, brain form	4,2109	0,0339	0,19	0,72	1,34	1,18		-0,60	-0,64	-1,51	-0,88
221	RBM8A	Q9Y5S9	RNA-binding protein 8A	3,8187	0,0441	0,00	1,04	1,31	2,00	0,54	-0,23		-2,00	-0,86
222	UBA6	A0AVT1	Ubiquitin-like modifier-activating enzyme 6	4,3693	0,0306	0,00	0,84	1,31	2,00	0,35	-0,44	-0,50	-2,00	-0,86
223	CNN2	Q99439	Calponin-2	3,7563	0,0460	0,49	2,52	1,40	1,35	3,05	0,57	2,19	-0,96	-0,85
224	RAB21	Q9UL25	Ras-related protein Rab-21	4,4356	0,0293	0,00	1,31	1,30	2,00	0,86	0,01		-2,00	-0,85
225	LYAR	Q9NX58	Cell growth-regulating nucleolar protein	6,2455	0,0099	0,00	1,96	1,29	2,00	1,93	0,42	1,10	-2,00	-0,83
226	EIF5	P55010	Eukaryotic translation initiation factor 5	5,2409	0,0178	0,27	1,42	1,31	1,36	0,97	0,08		-1,31	-0,83
227	TWF2	Q6IBS0	Twinfilin-2	12,1803	0,0006	0,78	3,10	1,47	1,20	4,51	0,72	3,74	-0,61	-0,77
228	NDUFA8	P51970	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8	6,4269	0,0089	0,00	0,72	1,23	2,00	0,26	-0,53	-0,50	-2,00	-0,75
229	GMPS	P49915	GMP synthase [glutamine-hydrolyzing]	5,6838	0,0136	0,14	0,20	1,22	0,34		-1,43	-0,72	-1,58	-0,73
230	UFL1	O94874	E3 UFM1-protein ligase 1	6,3292	0,0094	0,28	2,43	1,24	1,59	2,92	0,65	2,20	-1,26	-0,73
231	ACADSB	P45954	Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	6,4704	0,0087	0,00	1,29	1,21	2,00	0,83	0,07		-2,00	-0,73
232	MYBBP1A	Q9BQG0	Myb-binding protein 1A	3,9210	0,0411	0,16	1,75	1,21	1,66	1,52	0,37	0,80	-1,53	-0,71
233	CYB5B	O43169	Cytochrome b5 type B	5,0726	0,0197	0,35	2,25	1,24	1,46	2,47	0,58	1,76	-1,13	-0,71
234	SEC24C	P53992	Protein transport protein Sec24C	10,1253	0,0014	0,00	0,54	1,18	2,00	0,14	-0,75	-0,55	-2,00	-0,70
235	ASMTL	O95671	N-acetylserotonin O-methyltransferase-like protein	8,4491	0,0031	0,00	1,18	1,16	2,00	0,69	0,01		-2,00	-0,67
236	FACL4	O60488	Long-chain-fatty-acid--CoA ligase 4	3,8265	0,0438	0,00	0,51	1,14	2,00	0,13	-0,77	-0,52	-2,00	-0,65
237	ASNA1	O43681	ATPase ASNA1	6,6018	0,0081	0,14	0,59	1,13	1,23		-0,63	-0,47	-1,56	-0,63
238	KCMF1	Q9P0J7	E3 ubiquitin-protein ligase KCMF1	6,4167	0,0090	0,16	0,84	1,13	1,35		-0,30		-1,50	-0,63
239	SRP68	Q9UHB9	Signal recognition particle subunit SRP68	4,7467	0,0241	0,16	0,92	1,11	1,40	0,41	-0,19		-1,49	-0,61
240	DIAPH1	O60610	Protein diaphanous homolog 1	9,3432	0,0020	0,00	2,37	1,08	2,00	2,81	0,75	2,22	-2,00	-0,58
241	CYB5A	P00167	Cytochrome b5	4,1369	0,0356	0,00	0,55	1,06	2,00	0,15	-0,64	-0,41	-2,00	-0,56
242	AP2B1	P63010	AP-2 complex subunit beta	6,3079	0,0096	0,00	1,42	1,06	2,00	1,01	0,30	0,46	-2,00	-0,56
243	MYO1E	Q12965	Unconventional myosin-Ie	4,2727	0,0326	0,00	0,38	1,05	2,00	0,07	-0,93	-0,48	-2,00	-0,56
244	INPP5D	Q92835	Phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 1	10,1807	0,0014	0,00	1,17	1,05	2,00	0,69	0,11		-2,00	-0,55
245	NOL6	Q9H6R4	Nucleolar protein 6	4,6231	0,0260	0,11	0,17	1,04	0,40		-1,45	-0,53	-1,62	-0,54
246	VBP1	P61758	Prefoldin subunit 3	6,6820	0,0078	0,53	2,47	1,16	1,29	2,91	0,72	2,39	-0,74	-0,53
247	SEMA7A	O75326	Semaphorin-7A	5,8549	0,0124	0,00	0,17	1,03	2,00	0,01	-1,43	-0,51	-2,00	-0,53
248	CSNK2A3	Q8NEV1	Casein kinase II subunit alpha 3	3,7378	0,0466	0,19	1,46	1,01	1,55	1,06	0,37	0,57	-1,37	-0,49
249	VAMP8	Q9BV40	Vesicle-associated membrane protein 8	4,0926	0,0367	0,65	0,00	1,18	-2,00	-0,21	-2,00	-0,69	-0,58	-0,48
250	PRKCB	P05771	Protein kinase C beta type	7,4171	0,0053	0,12	0,55	0,98	1,31		-0,56		-1,58	-0,48
251	CLPP	Q16740	ATP-dependent Clp protease proteolytic subunit, mitochondrial	5,1077	0,0193	0,00	0,33	0,97	2,00	0,05	-0,99	-0,42	-2,00	-0,47
252	DNAJB11	Q9UBS4	DnaJ homolog subfamily B member 11	4,5823	0,0267	0,00	0,54	0,97	2,00	0,15	-0,57		-2,00	-0,47
253	AP2A1	O95782	AP-2 complex subunit alpha-1	8,6516	0,0028	0,28	1,71	1,01	1,44	1,43	0,52	0,96	-1,13	-0,47
254	RTN4	Q9NQC3	Reticulon-4	4,3800	0,0304	0,00	1,10	0,94	2,00	0,60	0,15		-2,00	-0,44
255	ARPC5	O15511	Actin-related protein 2/3 complex subunit 5	4,1484	0,0354	0,78	0,00	1,19	-2,00	-0,31	-2,00	-0,71	-0,41	-0,40
256	DNAJA1	P31689	DnaJ homolog subfamily A member 1	4,4597	0,0289	1,99	4,70	2,18	0,81	9,06	0,73	8,66	-0,09	
257	RPL3L	Q92901	60S ribosomal protein L3-like	6,0230	0,0112	0,00	0,17	0,86	2,00	0,01	-1,36		-2,00	-0,37
258	DDX47	Q9H0S4	Probable ATP-dependent RNA helicase DDX47	4,7710	0,0237	0,00	0,34	0,86	2,00	0,06	-0,87		-2,00	-0,37
259	ACTR1A	P61163	Alpha-centractin	6,9485	0,0067	0,00	2,20	0,86	2,00	2,43	0,88	2,06	-2,00	-0,37
260	RAVER1	Q8IY67	Ribonucleoprotein PTB-binding 1	10,9830	0,0010	0,00	0,17	0,85	2,00	0,01	-1,35		-2,00	-0,36
261	RPS6KA1	Q15418	Ribosomal protein S6 kinase alpha-1	12,4252	0,0006	0,00	0,98	0,85	2,00	0,48	0,14		-2,00	-0,36
262	ACOT9	Q9Y305	Acyl-coenzyme A thioesterase 9, mitochondrial	4,5502	0,0273	0,00	0,34	0,85	2,00	0,06	-0,85		-2,00	-0,36

263	GTPBP4	Q9BZE4	Nucleolar GTP-binding protein 1	4,2761	0,0325	0,00	0,37	0,85	2,00	0,07	-0,79		-2,00	-0,36
264	IARS2	Q9NSE4	Isoleucine--tRNA ligase, mitochondrial	6,4487	0,0088	0,00	0,38	0,83	2,00	0,07	-0,75		-2,00	-0,35
265	BCCIP	Q9P287	BRCA2 and CDKN1A-interacting protein	12,5261	0,0005	0,00	1,00	0,83	2,00	0,50	0,19		-2,00	-0,35
266	PDCD5	O14737	Programmed cell death protein 5	3,8281	0,0438	0,00	1,05	0,82	2,00	0,55	0,24		-2,00	-0,34
267	FAHD2B	Q6P2I3	Fumarylacetoacetate hydrolase domain-containing protein 2B	6,0333	0,0112	0,00	0,38	0,79	2,00	0,07	-0,70		-2,00	-0,31
268	FAM129A	Q9BZQ8	Protein Niban	3,6621	0,0490	0,00	0,76	0,79	2,00	0,29	-0,03		-2,00	-0,31
269	PPAT	Q06203	Amidophosphoribosyltransferase	24,4112	0,0000	0,00	0,00	0,77	0,00		-2,00	-0,29	-2,00	-0,29
270	GSTM5	P46439	Glutathione S-transferase Mu 5	5,4409	0,0158	0,00	1,14	0,75	2,00	0,65	0,41		-2,00	-0,28
271	MCM3	P25205	DNA replication licensing factor MCM3	4,6515	0,0256	0,30	1,89	0,78	1,46	1,74	0,83	1,48	-0,90	
272	UBA2	Q9UBT2	SUMO-activating enzyme subunit 2	5,5380	0,0149	0,00	0,84	0,71	2,00	0,35	0,16		-2,00	-0,25
273	TIGAR	Q9NQ88	Fructose-2,6-bisphosphatase TIGAR	6,2334	0,0100	0,11	1,14	0,71	1,64	0,65	0,47	0,40	-1,45	
274	TIAL1	Q01085	Nucleolysin TIAR	5,4406	0,0158	0,00	0,17	0,70	2,00	0,01	-1,22		-2,00	-0,24
275	IPO7	O95373	Importin-7	5,3395	0,0167	0,00	1,41	0,70	2,00	0,99	0,67	0,75	-2,00	-0,24
276	AIMP1	Q12904	Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	4,8648	0,0224	0,00	0,00	0,70	0,00		-2,00	-0,24	-2,00	-0,24
277	LDHB	P07195	L-lactate dehydrogenase B chain	7,2500	0,0057	0,00	2,13	0,67	2,00	2,27	1,05	2,05	-2,00	-0,22
278	RALY	Q9UKM9	RNA-binding protein Raly	6,2401	0,0099	0,39	0,00	0,77	-2,00	-0,08	-2,00	-0,29	-0,64	
279	ERO1A	Q96HE7	ERO1-like protein alpha	5,1585	0,0187	0,00	0,17	0,65	2,00	0,01	-1,19		-2,00	-0,21
280	GLOD4	Q9HC38	Glyoxalase domain-containing protein 4	10,2927	0,0013	0,00	0,00	0,63	0,00		-2,00	-0,20	-2,00	-0,20
281	MCTS1	Q9ULC4	Malignant T-cell-amplified sequence 1	3,8838	0,0422	0,16	1,46	0,60	1,60	1,06	0,84	0,89	-1,15	
282	ALYREF	Q86V81	THO complex subunit 4	5,3576	0,0166	0,30	1,83	0,65	1,44	1,63	0,95	1,46	-0,74	
283	ARMC1	Q9NVT9	Armadillo repeat-containing protein 1	5,2459	0,0177	0,00	0,00	0,56	0,00		-2,00	-0,16	-2,00	-0,16
284	IGKV1	N/A	immunoglobulin kappa chain variable region	5,1501	0,0188	0,00	1,27	0,56	2,00	0,81	0,78	0,65	-2,00	-0,16
285	ITGB2	P05107	Integrin beta-2	4,5579	0,0271	0,00	0,00	0,56	0,00		-2,00	-0,16	-2,00	-0,16
286	NUP133	Q8WUM0	Nuclear pore complex protein Nup133	4,5579	0,0271	0,00	0,00	0,56	0,00		-2,00	-0,16	-2,00	-0,16
287	LSM8	O95777	U6 snRNA-associated Sm-like protein LSm8	4,8052	0,0232	0,35	1,18	0,64	1,09	0,63	0,59	0,49	-0,59	
288	AP5B1	Q2VPB7	AP-5 complex subunit beta-1	9,5185	0,0019	0,34	1,98	0,62	1,41	1,90	1,04	1,77	-0,58	
289	YTHDF2	Q9Y5A9	YTH domain-containing family protein 2	4,3611	0,0308	0,00	0,71	0,52	2,00	0,25	0,31		-2,00	-0,13
290	KIAA0324	Q9UQ35	Serine/arginine repetitive matrix protein 2	5,0175	0,0203	0,00	0,00	0,50	0,00		-2,00	-0,12	-2,00	-0,12
291	LRRFIP1	Q32MZ4	Leucine-rich repeat flightless-interacting protein 1	4,9816	0,0208	0,14	1,09	0,52	1,54	0,58	0,71	0,46	-1,14	
292	JCHAIN	P01591	Immunoglobulin J chain	5,2921	0,0172	0,00	0,00	0,49	0,00		-2,00	-0,12	-2,00	-0,12
293	TRIP11	Q15643	Thyroid receptor-interacting protein 11	5,2921	0,0172	0,00	0,00	0,49	0,00		-2,00	-0,12	-2,00	-0,12
294	SEC61A1	P61619	Protein transport protein Sec61 subunit alpha isoform 1	7,4117	0,0053	0,00	1,46	0,49	2,00	1,07	0,99	0,95	-2,00	-0,12
295	SGTA	O43765	Small glutamine-rich tetratricopeptide repeat-containing protein alpha	24,7135	0,0000	0,00	1,73	0,49	2,00	1,49	1,11	1,37	-2,00	-0,12
296	SLC2A3	P11169	Solute carrier family 2, facilitated glucose transporter member 3	5,2010	0,0182	0,00	0,00	0,48	0,00		-2,00	-0,12	-2,00	-0,12
297	MAP2K1	Q02750	Dual specificity mitogen-activated protein kinase kinase 1	4,0847	0,0369	0,14	1,21	0,50	1,58	0,72	0,83	0,61	-1,12	
298	ADRBK1	P25098	Beta-adrenergic receptor kinase 1	5,1981	0,0182	0,00	0,00	0,48	0,00		-2,00	-0,11	-2,00	-0,11
299	PIWIL2	Q8TC59	Piwi-like protein 2	5,4595	0,0156	0,00	0,00	0,44	0,00		-2,00	-0,10	-2,00	-0,10
300	SCRN1	Q12765	Secernin-1	5,4595	0,0156	0,00	0,00	0,44	0,00		-2,00	-0,10	-2,00	-0,10
301	TREX1	Q9NSU2	Three-prime repair exonuclease 1	5,4497	0,0157	0,00	0,00	0,42	0,00		-2,00	-0,09	-2,00	-0,09
302	ACIN1	Q9UKV3	Apoptotic chromatin condensation inducer in the nucleus	3,8765	0,0424	0,11	1,05	0,44	1,61	0,54	0,82	0,45	-1,17	
303	DHCR24	Q15392	Delta	5,4521	0,0156	0,00	0,00	0,42	0,00		-2,00	-0,09	-2,00	-0,09
304	NDUFV2	P19404	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial	5,4521	0,0156	0,00	0,00	0,42	0,00		-2,00	-0,09	-2,00	-0,09
305	TNFAIP3	P21580	Tumor necrosis factor alpha-induced protein 3	5,4521	0,0156	0,00	0,00	0,42	0,00		-2,00	-0,09	-2,00	-0,09
306	TTC1	Q99614	Tetratricopeptide repeat protein 1	5,4521	0,0156	0,00	0,00	0,42	0,00		-2,00	-0,09	-2,00	-0,09
307	PPP1R14B	Q96C90	Protein phosphatase 1 regulatory subunit 14B	4,2738	0,0326	0,00	0,87	0,37	2,00	0,38	0,82		-2,00	-0,07

308	COMT	P21964	Catechol O-methyltransferase	7,9229	0,0041	0,00	0,92	0,37	2,00	0,42	0,86		-2,00	-0,07
309	CPSF2	Q9P2I0	Cleavage and polyadenylation specificity factor subunit 2	4,3897	0,0302	0,00	0,76	0,34	2,00	0,29	0,75		-2,00	-0,06
310	EIF4A2	Q14240	Eukaryotic initiation factor 4A-II	6,9805	0,0066	1,84	0,33	1,88	-1,39	-1,64	-1,40	-1,70	-0,02	
311	IFI30	P13284	Gamma-interferon-inducible lysosomal thiol reductase	5,3313	0,0168	0,16	1,13	0,35	1,50	0,63	1,05	0,58	-0,74	
312	PRKRA	O75569	Interferon-inducible double-stranded RNA-dependent protein kinase activator A	4,9917	0,0207	0,00	0,72	0,30	2,00	0,26	0,82		-2,00	-0,04
313	PLXNB2	O15031	Plexin-B2	4,9746	0,0209	0,00	0,89	0,30	2,00	0,40	0,99		-2,00	-0,04
314	GAK	O14976	Cyclin-G-associated kinase	5,6691	0,0138	0,00	0,97	0,30	2,00	0,47	1,06	0,42	-2,00	-0,04
315	RRP12	Q5JTH9	RRP12-like protein	5,6691	0,0138	0,00	0,97	0,30	2,00	0,47	1,06	0,42	-2,00	-0,04
316	HEL57	V9HWH1	Epididymis luminal protein 57	3,9461	0,0405	0,00	1,26	0,30	2,00	0,79	1,23	0,75	-2,00	-0,04
317	SF3A2	Q15428	Splicing factor 3A subunit 2	5,0417	0,0200	0,00	0,88	0,28	2,00	0,38	1,02		-2,00	-0,04
318	SLIRP	Q9GZT3	SRA stem-loop-interacting RNA-binding protein, mitochondrial	4,3085	0,0318	0,12	1,05	0,28	1,60	0,54	1,15	0,51	-0,85	
319	FBXO6	Q9NRD1	F-box only protein 6	3,9509	0,0403	0,16	1,10	0,30	1,49	0,59	1,14	0,56	-0,60	
320	TCERG1	O14776	Transcription elongation regulator 1	3,7219	0,0471	0,14	0,97	0,28	1,49	0,46	1,09	0,43	-0,67	
321	BTF3	O00478,P20290, P78410	Butyrophilin subfamily 3 member A3; Transcription factor BTF3;Butyrophilin subfamily 3 member A2	7,1819	0,0059	1,26	4,31	1,28	1,09	8,50	1,09	8,48	-0,01	
322	CSNK2A2	P19784	Casein kinase II subunit alpha'	6,3166	0,0095	0,00	0,71	0,15	2,00	0,25	1,30		-2,00	-0,01
323	PUF60	Q9UHX1	Poly	6,8677	0,0070	0,00	0,84	0,15	2,00	0,35	1,39		-2,00	-0,01
324	NOP16	Q9Y3C1	Nucleolar protein 16	6,3408	0,0094	0,00	0,71	0,15	2,00	0,25	1,30		-2,00	-0,01
325	ACAD9	Q9H845	Acyl-CoA dehydrogenase family member 9, mitochondrial	6,2344	0,0100	0,00	0,76	0,15	2,00	0,29	1,34		-2,00	-0,01
326	EPB41L2	O43491	Band 4.1-like protein 2	6,5272	0,0085	0,00	0,80	0,15	2,00	0,32	1,37		-2,00	-0,01
327	LDHAL6B	Q9BYZ2	L-lactate dehydrogenase A-like 6B	7,5504	0,0049	0,00	1,13	0,15	2,00	0,64	1,53	0,63	-2,00	-0,01
328	MYO1C	O00159, Q12965	Unconventional myosin-Ic	7,0881	0,0062	0,00	1,33	0,15	2,00	0,89	1,60	0,88	-2,00	-0,01
329	RBM25	P49756	RNA-binding protein 25	13,5116	0,0004	0,00	1,14	0,14	2,00	0,65	1,57	0,64	-2,00	-0,01
330	SNRPA1	P09661	U2 small nuclear ribonucleoprotein A'	6,5208	0,0085	0,00	1,04	0,13	2,00	0,54	1,54	0,53	-2,00	-0,01
331	MT	Q8IVS2	Malonyl-CoA-acyl carrier protein transacylase, mitochondrial	5,4028	0,0161	0,00	0,54	0,00	2,00	0,15	2,00	0,15	0,00	
332	RWDD1	Q9H446	RWD domain-containing protein 1	5,4028	0,0161	0,00	0,54	0,00	2,00	0,15	2,00	0,15	0,00	
333	ATG7	O95352	Ubiquitin-like modifier-activating enzyme ATG7	5,1347	0,0189	0,00	0,62	0,00	2,00	0,19	2,00	0,19	0,00	
334	RB1	P06400	Retinoblastoma-associated protein	5,1347	0,0189	0,00	0,62	0,00	2,00	0,19	2,00	0,19	0,00	
335	CLK3	P49761	Dual specificity protein kinase CLK3	5,1519	0,0187	0,00	0,64	0,00	2,00	0,20	2,00	0,20	0,00	
336	DYNC1LI1	Q9Y6G9	Cytoplasmic dynein 1 light intermediate chain 1	5,1939	0,0183	0,00	0,64	0,00	2,00	0,21	2,00	0,21	0,00	
337	OAS1	P00973	2'-5'-oligoadenylate synthase 1	4,6108	0,0262	0,00	0,71	0,00	2,00	0,25	2,00	0,25	0,00	
338	ISOC1	Q96CN7	Isochorismatase domain-containing protein 1	8,7858	0,0027	0,00	0,92	0,00	2,00	0,43	2,00	0,43	0,00	
339	RBM3	P98179	RNA-binding protein 3	3,6608	0,0491	0,00	1,54	0,00	2,00	1,18	2,00	1,18	0,00	
340	SERPINF2	P08697	Alpha-2-antiplasmin	44,9779	0,0000	0,00	1,75	0,00	2,00	1,54	2,00	1,54	0,00	
341	CRLF3	Q8IUI8	Cytokine receptor-like factor 3	3,8487	0,0432	0,16	0,88	0,13	1,38		1,47		0,18	
342	KIF5B	P33176	Kinesin-1 heavy chain	6,0288	0,0112	0,33	1,35	0,30	1,22	0,86	1,27	0,87	0,09	
343	EIF4H	Q15056	Eukaryotic translation initiation factor 4H	3,6855	0,0483	0,92	1,89	0,91	0,69	1,37	0,70	1,38	0,02	
344	CDK1	P06493	Cyclin-dependent kinase 1	3,8799	0,0423	0,35	1,13	0,30	1,06	0,58	1,16	0,60	0,15	
345	RFC4	P35249	Replication factor C subunit 4	4,8989	0,0219	0,35	1,63	0,15	1,30	1,27	1,67	1,32	0,80	
346	IFT57	Q9NWB7	Intraflagellar transport protein 57 homolog	3,7877	0,0450	0,34	0,00	0,00	-2,00	-0,06	0,00		2,00	0,06
347	PPP1R8	Q12972	Nuclear inhibitor of protein phosphatase 1	3,7877	0,0450	0,34	0,00	0,00	-2,00	-0,06	0,00		2,00	0,06
348	SRGAP3	O43295	SLIT-ROBO Rho GTPase-activating protein 3	3,7877	0,0450	0,34	0,00	0,00	-2,00	-0,06	0,00		2,00	0,06
349	WDR82	Q6UXN9	WD repeat-containing protein 82	3,7877	0,0450	0,34	0,00	0,00	-2,00	-0,06	0,00		2,00	0,06
350	GATAD2B	Q8WXI9	Transcriptional repressor p66-beta	3,7300	0,0468	0,39	0,00	0,00	-2,00	-0,08	0,00		2,00	0,08
351	POTEJ	P0CG39	POTE ankyrin domain family member J	3,6417	0,0497	0,41	0,00	0,00	-2,00	-0,08	0,00		2,00	0,08
352	DRG2	P55039	Developmentally-regulated GTP-binding protein 2	3,6617	0,0490	0,42	0,00	0,00	-2,00	-0,09	0,00		2,00	0,09

353	LRMP	Q12912	Lymphoid-restricted membrane protein	4,5608	0,0271	0,49	1,13	0,15	0,80	0,52	1,53	0,63	1,06	
354	ELAC2	Q9BQ52	Zinc phosphodiesterase ELAC protein 2	5,9313	0,0118	0,53	0,00	0,00	-2,00	-0,14	0,00		2,00	0,14
355	ME1	P48163	NADP-dependent malic enzyme	6,3611	0,0093	0,53	0,00	0,00	-2,00	-0,14	0,00		2,00	0,14
356	SNRPF	P62306	Small nuclear ribonucleoprotein F	4,7144	0,0246	0,62	0,00	0,29	-2,00	-0,19	-2,00	-0,04	0,73	
357	CNPY2	Q9Y2B0	Protein canopy homolog 2	4,9928	0,0207	0,62	0,00	0,27	-2,00	-0,19	-2,00	-0,04	0,78	
358	UBE2M	P61081	NEDD8-conjugating enzyme Ubc12	3,9577	0,0401	0,58	0,00	0,13	-2,00	-0,17	-2,00	-0,01	1,24	
359	RRBP1	Q9P2E9	Ribosome-binding protein 1	5,5798	0,0145	0,59	0,00	0,00	-2,00	-0,17	0,00		2,00	0,17
360	PTDSS1	P48651	Phosphatidylserine synthase 1	6,2274	0,0100	0,60	0,00	0,00	-2,00	-0,18	0,00		2,00	0,18
361	KRT75	O95678	Keratin, type II cytoskeletal 75	5,8352	0,0125	0,65	0,00	0,00	-2,00	-0,21	0,00		2,00	0,21
362	HSU53209	Q549U1	Putative MAPK activating protein	6,0199	0,0112	0,68	0,00	0,00	-2,00	-0,23	0,00		2,00	0,23
363	ATP13A1	Q9HD20	Manganese-transporting ATPase 13A1	10,7411	0,0011	0,69	0,00	0,00	-2,00	-0,24	0,00		2,00	0,24
364	UQCR10	Q9UDW1	Cytochrome b-c1 complex subunit 9	6,1100	0,0107	0,69	0,00	0,00	-2,00	-0,24	0,00		2,00	0,24
365	USP14	P54578	Ubiquitin carboxyl-terminal hydrolase 14	4,6228	0,0260	0,77	1,97	0,30	0,88	1,64	1,47	1,89	0,88	
366	GPX3	P22352	Glutathione peroxidase 3	5,5679	0,0146	0,71	0,00	0,00	-2,00	-0,25	0,00		2,00	0,25
367	DST	Q03001	Dystonin	6,3788	0,0092	0,73	0,00	0,14	-2,00	-0,27	-2,00	-0,01	1,36	
368	CHMP4A	Q9BY43	Charged multivesicular body protein 4a	7,7966	0,0043	0,76	0,00	0,00	-2,00	-0,29	0,00		2,00	0,29
369	SUMF2	Q8NBJ7	Sulfatase-modifying factor 2	5,8507	0,0124	0,83	0,00	0,27	-2,00	-0,35	-2,00	-0,04	1,01	
370	ARF6	P62330	ADP-ribosylation factor 6	4,6429	0,0257	0,85	0,17	0,30	-1,33		-0,55		0,96	
371	RNP24	Q15363	Transmembrane emp24 domain-containing protein 2	4,3782	0,0304	0,80	0,37	0,00	-0,73		2,00	0,07	2,00	0,32
372	PSMD4	P55036	26S proteasome non-ATPase regulatory subunit 4	4,0977	0,0366	0,83	0,17	0,15	-1,32		0,13		1,39	
373	MED8	Q96G25	Mediator of RNA polymerase II transcription subunit 8	4,9287	0,0215	0,83	0,46	0,00	-0,58		2,00	0,10	2,00	0,34
374	FLNB	O75369	Filamin-B	5,1905	0,0183	0,83	0,00	0,00	-2,00	-0,35	0,00		2,00	0,35
375	BOLA2B	Q9H3K6	BolA-like protein 2	4,2845	0,0323	0,88	0,54	0,00	-0,48		2,00	0,15	2,00	0,39
376	COII	P00403	Cytochrome c oxidase subunit 2	20,5212	0,0000	0,90	0,00	0,00	-2,00	-0,40	0,00		2,00	0,40
377	PSPC1	Q8WXF1	Paraspeckle component 1	6,1857	0,0102	1,05	0,00	0,52	-2,00	-0,56	-2,00	-0,13	0,69	0,42
378	APOB	P04114	Apolipoprotein B-100	9,3090	0,0021	0,94	0,00	0,00	-2,00	-0,45	0,00		2,00	0,45
379	PGRMC1	O00264	Membrane-associated progesterone receptor component 1	11,4548	0,0008	1,53	0,00	1,20	-2,00	-1,18	-2,00	-0,72	0,24	0,46
380	SHINC3	A6QKW0	SHINC3	141,8373	0,0000	0,97	0,00	0,00	-2,00	-0,47	0,00		2,00	0,47
381	F13A1	P00488	Coagulation factor XIII A chain	19,1342	0,0001	0,97	0,20	0,00	-1,31	-0,45	2,00	0,02	2,00	0,47
382	SH3BGRL	O75368	SH3 domain-binding glutamic acid-rich-like protein	5,3077	0,0171	1,01	0,00	0,00	-2,00	-0,51	0,00		2,00	0,51
383	ALOX5AP	P20292	Arachidonate 5-lipoxygenase-activating protein	9,2688	0,0021	1,02	0,00	0,00	-2,00	-0,52	0,00		2,00	0,52
384	DAD1	P61803	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1	4,6001	0,0264	1,12	0,26	0,33	-1,25	-0,60	-0,25		1,09	0,57
385	TUBB1	Q9H4B7	Tubulin beta-1 chain	4,0707	0,0372	1,12	0,20	0,00	-1,39	-0,60	2,00	0,02	2,00	0,62
386	RAB2B	Q8WUD1	Ras-related protein Rab-2B	15,5436	0,0002	1,13	0,00	0,00	-2,00	-0,64	0,00		2,00	0,64
387	YWHAH	Q04917	14-3-3 protein eta	9,3489	0,0020	1,34	0,21	0,62	-1,45	-0,87	-0,98		0,74	0,70
388	UNC93B1	Q9H1C4	Protein unc-93 homolog B1	5,5727	0,0146	1,27	0,17	0,13	-1,53	-0,79	0,23		1,62	0,80
389	MTDH	Q86UE4	Protein LYRIC	3,7717	0,0455	1,28	0,82	0,15	-0,44	-0,48	1,38		1,58	0,81
390	TFG	Q92734	Protein TFG	11,6346	0,0008	1,29	0,00	0,00	-2,00	-0,83	0,00		2,00	0,83
391	COPZ1	P61923	Coatomer subunit zeta-1	4,2607	0,0329	1,39	0,38	0,52	-1,15	-0,90	-0,31		0,92	0,84
392	CD48	P09326	CD48 antigen	5,3335	0,0168	1,37	0,34	0,42	-1,20	-0,88	-0,21		1,06	0,85
393	PLEK	P08567	Pleckstrin			3,59	6,38	3,34	0,56	13,94	0,63	14,80	0,07	0,87
394	FAM49B	Q9NUQ9	Protein FAM49B	12,7437	0,0005	1,33	0,37	0,15	-1,13	-0,82	0,85		1,59	0,88
395	PGLS	O95336	6-phosphogluconolactonase	7,7299	0,0045	1,36	0,55	0,27	-0,84	-0,77	0,68		1,33	0,89
396	TTLL12	Q14166	Tubulin--tyrosine ligase-like protein 12	4,3348	0,0313	2,18	0,34	1,72	-1,46	-2,31	-1,34	-1,42	0,24	0,90
397	CCAR2	Q8N163	Cell cycle and apoptosis regulator protein 2	4,2191	0,0338	1,38	0,20	0,33	-1,49	-0,94	-0,49		1,23	0,90

398	PSME1	Q06323	Proteasome activator complex subunit 1			15,57	24,11	15,51	0,43	169,38	0,43	170,32	0,00	0,93
399	RPS26	P62854	40S ribosomal protein S26	3,6808	0,0484	1,44	0,00	0,35	-2,00	-1,03	-2,00	-0,06	1,22	0,97
400	RPL32	P62910	60S ribosomal protein L32	10,5992	0,0012	1,45	0,41	0,15	-1,11	-0,97	0,94		1,63	1,04
401	ATP1B3	P54709	Sodium/potassium-transporting ATPase subunit beta-3	4,9126	0,0217	2,20	0,58	1,65	-1,16	-2,24	-0,95	-1,19	0,28	1,05
402	USMG5	Q96IX5	Up-regulated during skeletal muscle growth protein 5	12,0311	0,0006	1,50	0,34	0,30	-1,26	-1,06	0,13		1,33	1,08
403	NSFL1C	Q9UNZ2	NSFL1 cofactor p47	5,7961	0,0128	1,54	0,51	0,27	-1,00	-1,05	0,61		1,40	1,15
404	PGRMC2	O15173	Membrane-associated progesterone receptor component 2	6,3383	0,0094	1,98	0,34	1,19	-1,41	-1,90	-1,11	-0,64	0,50	1,26
405	APOE	P02649	Apolipoprotein E	10,6912	0,0011	1,92	0,34	1,07	-1,40	-1,78	-1,04	-0,52	0,56	1,26
406	RPS16	P62249	40S ribosomal protein S16			5,81	8,36	5,57	0,36	18,10	0,40	19,44	0,04	1,34
407	PABPC4	Q13310	Polyadenylate-binding protein 4	4,3267	0,0315	2,34	4,14	1,51	0,55	5,84	0,93	7,45	0,43	1,61
408	CPA1	P15085	Carboxypeptidase A1	5,1861	0,0184	1,81	0,00	0,00	-2,00	-1,64	0,00		2,00	1,64
409	DEK	P35659	Protein DEK	11,1452	0,0009	2,04	0,00	0,63	-2,00	-2,09	-2,00	-0,20	1,06	1,89
410	RNH1	O60930, P13489	Ribonuclease H1; Ribonuclease inhibitor	5,3996	0,0161	2,09	0,67	0,59	-1,03	-1,96	0,13		1,12	2,01
411	TPT1	P13693	Translationally-controlled tumor protein	5,0411	0,0201	2,41	1,23	1,12	-0,65	-2,14	0,09		0,73	2,26
412	PGM1	P36871	Phosphoglucomutase-1	4,9593	0,0211	2,40	0,84	0,91	-0,96	-2,53	-0,08		0,90	2,47
413	AP1M1	Q9BXS5	AP-1 complex subunit mu-1	6,9312	0,0068	2,46	0,92	1,00	-0,91	-2,61	-0,08		0,84	2,53
414	DDT	P30046	D-dopachrome decarboxylase	17,0035	0,0001	3,73	1,21	2,95	-1,02	-6,24	-0,84	-3,61	0,24	2,63
415	RPL10	P27635	60S ribosomal protein L10	12,5229	0,0005	2,45	0,40	0,49	-1,44	-2,93	-0,21		1,33	2,88
416	PLIN3	O60664	Perilipin-3	4,3300	0,0314	2,76	1,04	1,32	-0,91	-3,28	-0,24		0,71	2,95
417	PCK2	Q16822	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	4,0044	0,0389	4,07	1,80	3,24	-0,77	-6,64	-0,57	-3,61	0,23	3,03
418	IL4I1	Q96RQ9	L-amino-acid oxidase	7,2718	0,0057	3,17	0,87	1,78	-1,14	-4,64	-0,68	-1,20	0,56	3,44
419	EDARADD	Q8WWZ3	Ectodysplasin-A receptor-associated adapter protein	8,3552	0,0033	3,06	0,53	1,48	-1,41	-4,55	-0,94	-0,96	0,70	3,59
420	PSMB4	P28070	Proteasome subunit beta type-4	3,7047	0,0476	3,07	2,63	1,21	-0,15	-1,25	0,74	2,74	0,87	3,99
421	RAB5C	P51148	Ras-related protein Rab-5C	17,7215	0,0001	2,89	0,54	0,45	-1,37	-4,02	0,19		1,46	4,07
422	MZB1	Q8WU39	Marginal zone B- and B1-cell-specific protein	3,7300	0,0468	4,89	2,06	3,96	-0,81	-9,83	-0,63	-5,73	0,21	4,10
423	STOML2	Q9UJZ1	Stomatin-like protein 2, mitochondrial	5,7753	0,0129	3,78	1,98	2,46	-0,63	-5,19	-0,22	-1,07	0,42	4,12
424	MYDGF	Q969H8	Myeloid-derived growth factor	10,1661	0,0014	3,11	0,67	0,90	-1,29	-4,60	-0,29		1,10	4,42
425	KRT6C	P48668	Keratin, type II cytoskeletal 6C	92,5345	0,0000	2,99	0,17	0,00	-1,79	-4,45	2,00	0,01	2,00	4,46
426	MS4A1	P11836	B-lymphocyte antigen CD20	17,7086	0,0001	3,12	0,89	0,28	-1,11	-4,46	1,04		1,67	4,82
427	RPS8	P62241	40S ribosomal protein S8	4,9091	0,0218	3,84	4,10	2,22	0,06	1,02	0,59	5,94	0,54	4,92
428	NDUFA9	Q16795	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	8,4834	0,0031	3,89	1,21	1,97	-1,05	-6,81	-0,47	-1,20	0,66	5,61
429	MTPN	P58546	Myotrophin	14,0666	0,0003	3,59	0,89	1,27	-1,20	-6,03	-0,35	-0,41	0,95	5,62
430	KRT2	P35908	Keratin, type II cytoskeletal 2 epidermal	32,3861	0,0000	3,52	0,47	0,20	-1,53	-6,07	0,82		1,79	6,16
431	SRSF3	P84103	Serine/arginine-rich splicing factor 3	9,4337	0,0020	4,22	2,27	2,33	-0,60	-6,32	-0,03		0,58	6,18
432	ERAP1	Q9NZ08	Endoplasmic reticulum aminopeptidase 1	11,1415	0,0009	3,70	1,15	0,92	-1,05	-6,19	0,22		1,21	6,43
433	VDAC3	Q9Y277	Voltage-dependent anion-selective channel protein 3	5,2305	0,0179	4,37	2,61	2,34	-0,50	-6,13	0,11	0,67	0,60	6,80
434	GLUD2	P49448	Glutamate dehydrogenase 2, mitochondrial	3,9973	0,0391	4,50	1,43	2,57	-1,04	-9,09	-0,57	-2,28	0,55	6,81
435	PCNA	P12004	Proliferating cell nuclear antigen	10,7453	0,0011	3,92	1,26	0,51	-1,03	-6,88	0,84	0,66	1,54	7,54
436	PTBP1	P26599	Polypyrimidine tract-binding protein 1	3,9052	0,0416	9,51	11,71	8,55	0,21	23,27	0,31	31,98	0,11	8,71
437	RPS23	P62266	40S ribosomal protein S23	11,7085	0,0007	4,35	2,58	1,06	-0,51	-6,12	0,84	2,78	1,22	8,90
438	ATP5C1	P36542	ATP synthase subunit gamma, mitochondrial	3,7144	0,0473	5,15	3,59	2,90	-0,36	-6,86	0,21	2,22	0,56	9,08
439	TARS	P26639	Threonine--tRNA ligase, cytoplasmic	22,2421	0,0000	4,39	1,05	0,86	-1,23	-9,08	0,19		1,34	9,26
440	RPS4X	P62701	40S ribosomal protein S4, X isoform	9,8251	0,0016	6,40	9,85	4,54	0,43	28,05	0,74	38,20	0,34	10,15
441	ATP5J2	P56134	ATP synthase subunit f, mitochondrial	7,3812	0,0054	5,85	3,44	3,47	-0,52	-11,21	-0,01		0,51	11,12
442	HIST1H2AH	Q96KK5	Histone H2A type 1-H	32,7459	0,0000	4,87	0,00	0,13	-2,00	-11,87	-2,00	-0,01	1,89	11,86

443	ARL6IP5	O75915	PRA1 family protein 3	6,5127	0,0085	6,15	3,40	3,57	-0,58	-13,16	-0,05	-0,59	0,53	12,57
444	RPS2	P15880	40S ribosomal protein S2	7,7259	0,0045	7,29	8,34	5,17	0,13	8,21	0,47	21,40	0,34	13,19
445	PRMT1	Q99873	Protein arginine N-methyltransferase 1	19,7307	0,0000	5,21	1,63	0,80	-1,05	-12,25	0,68	1,01	1,47	13,26
446	IDH1	O75874	Isocitrate dehydrogenase [NADP] cytoplasmic	3,9387	0,0407	5,85	2,65	2,67	-0,75	-13,61	-0,01		0,75	13,56
447	ARPC1B	O15143	Actin-related protein 2/3 complex subunit 1B	15,7787	0,0002	6,09	3,79	3,13	-0,47	-11,38	0,19	2,26	0,64	13,64
448	HBD	P02042	Hemoglobin subunit delta	8,0056	0,0039	7,08	3,55	4,74	-0,66	-18,73	-0,29	-4,95	0,39	13,79
449	RPL17	P18621	60S ribosomal protein L17			7,97	4,85	5,93	-0,49	-20,01	-0,20	-5,82	0,29	14,20
450	KRT9	P35527	Keratin, type I cytoskeletal 9	24,9559	0,0000	5,42	0,00	0,00	-2,00	-14,70	0,00		2,00	14,70
451	RAP1A	P62834	Ras-related protein Rap-1A			6,87	4,92	3,99	-0,33	-11,46	0,21	4,18	0,53	15,63
452	RPL27	P61353	60S ribosomal protein L27	7,6458	0,0047	6,41	4,60	2,91	-0,33	-9,94	0,45	6,35	0,75	16,29
453	VDAC2	P45880	Voltage-dependent anion-selective channel protein 2	4,7425	0,0241	7,19	2,90	4,35	-0,85	-21,62	-0,40	-5,25	0,49	16,37
454	F5	P12259	Coagulation factor V	51,0161	0,0000	5,78	0,00	0,56	-2,00	-16,68	-2,00	-0,16	1,65	16,52
455	H3F3A	P84243	Histone H3.3	9,1774	0,0022	6,24	2,13	1,64	-0,98	-17,18	0,26	0,92	1,17	18,10
456	KRT10	P13645	Keratin, type I cytoskeletal 10	11,3200	0,0009	6,49	0,42	0,00	-1,76	-20,96	2,00	0,09	2,00	21,05
457	SSR4	P51571	Translocon-associated protein subunit delta	24,0842	0,0000	7,47	3,59	3,01	-0,70	-21,46	0,17	1,90	0,85	23,36
458	FERMT3	Q86UX7	Fermitin family homolog 3	3,9172	0,0412	10,55	7,62	8,01	-0,32	-26,64	-0,05	-3,11	0,27	23,53
459	ALDOA	P04075	Fructose-bisphosphate aldolase A	8,9003	0,0025	8,51	7,84	4,16	-0,08	-5,41	0,61	22,11	0,69	27,52
460	HSP90AB2P	Q58FF8	Putative heat shock protein HSP 90-beta 2	4,4829	0,0285	7,64	2,85	0,00	-0,91	-25,15	2,00	4,05	2,00	29,20
461	ALB	P02768, Q8TES7	Serum albumin; Fas-binding factor 1	8,6783	0,0028	11,42	23,63	8,47	0,70	214,00	0,94	243,35	0,30	29,35
462	YWHAE	P62258	14-3-3 protein epsilon	5,0739	0,0197	10,34	8,67	6,92	-0,18	-15,82	0,22	13,65	0,40	29,47
463	ACADM	P11310	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial	5,8140	0,0127	10,20	6,23	6,14	-0,48	-32,60	0,01	0,57	0,50	33,17
464	RPS19	P39019	40S ribosomal protein S19	6,7487	0,0075	9,92	3,54	5,60	-0,95	-42,90	-0,45	-9,42	0,56	33,48
465	RPL6	Q02878	60S ribosomal protein L6	4,2645	0,0328	11,90	12,03	8,14	0,01	1,54	0,39	39,21	0,38	37,67
466	RAN	P62826	GTP-binding nuclear protein Ran	4,9496	0,0212	14,10	8,97	11,02	-0,44	-59,14	-0,21	-20,53	0,24	38,61
467	RPL7A	P62424	60S ribosomal protein L7a	8,7933	0,0027	11,09	6,73	6,32	-0,49	-38,83	0,06	2,62	0,55	41,45
468	EIF4A1	P60842	Eukaryotic initiation factor 4A-I	6,2376	0,0099	16,44	17,97	13,45	0,09	26,44	0,29	71,12	0,20	44,68
469	GNB2L1	P63244	Receptor of activated protein C kinase 1	8,3319	0,0033	10,80	7,28	5,02	-0,39	-31,82	0,37	13,94	0,73	45,75
470	RPL7	P18124	60S ribosomal protein L7	7,3147	0,0055	12,66	6,54	7,36	-0,64	-58,79	-0,12	-5,68	0,53	53,11
471	AHCY	P23526	Adenosylhomocysteinase	11,5203	0,0008	13,98	8,98	9,00	-0,44	-57,41	0,00		0,43	57,22
472	STAT1	P42224	Signal transducer and activator of transcription 1-alpha/beta	5,7971	0,0128	30,31	36,56	28,30	0,19	209,09	0,25	267,84	0,07	58,76
473	RPS3	P23396	40S ribosomal protein S3	4,2619	0,0328	14,80	11,86	9,24	-0,22	-39,16	0,25	27,59	0,46	66,75
474	CD74	P04233	HLA class II histocompatibility antigen gamma chain	17,9620	0,0001	13,40	8,16	4,31	-0,49	-56,47	0,62	24,01	1,03	80,48
475	HNRNPU	Q00839	Heterogeneous nuclear ribonucleoprotein U	4,7811	0,0236	17,97	13,36	12,34	-0,29	-72,29	0,08	13,08	0,37	85,37
476	TUBAL3	A6NHL2	Tubulin alpha chain-like 3	15,6794	0,0002	14,19	2,06	2,94	-1,49	-98,53	-0,35	-2,21	1,31	96,32
477	RPS15A	P62244	40S ribosomal protein S15a	5,7286	0,0133	16,52	6,16	8,10	-0,91	-117,50	-0,27	-13,83	0,68	103,67
478	KRT1	P04264	Keratin, type II cytoskeletal 1	36,8794	0,0000	14,84	2,75	1,46	-1,37	-106,28	0,61	2,70	1,64	108,98
479	TMSB4X	P62328	Thymosin beta-4	144,4382	0,0000	14,87	0,00	1,24	-2,00	-110,59	-2,00	-0,77	1,69	109,83
480	CANX	P27824	Calnexin	4,1823	0,0346	23,70	22,37	18,23	-0,06	-30,62	0,20	83,94	0,26	114,57
481	UBA52	P62987	Ubiquitin-60S ribosomal protein L40	8,6147	0,0029	18,97	12,03	8,74	-0,45	-107,58	0,32	34,24	0,74	141,82
482	PDIA4	P13667	Protein disulfide-isomerase A4	32,7492	0,0000	19,90	10,87	10,56	-0,59	-138,97	0,03	3,24	0,61	142,21
483	CORO1A	P31146	Coronin-1A	4,1253	0,0359	24,60	23,53	17,30	-0,04	-25,73	0,31	127,25	0,35	152,98
484	FLNA	P21333	Filamin-A	15,8041	0,0002	21,20	6,57	1,73	-1,05	-203,14	1,17	20,06	1,70	223,20
485	ENO3	P13929	Beta-enolase	4,5334	0,0276	29,66	10,45	18,77	-0,96	-385,18	-0,57	-121,55	0,45	263,63
486	VDAC1	P21796	Voltage-dependent anion-selective channel protein 1	7,4944	0,0051	29,26	16,40	17,46	-0,56	-293,68	-0,06	-18,05	0,50	275,63
487	HYOU1	Q9Y4L1	Hypoxia up-regulated protein 1	16,6180	0,0001	30,40	14,18	12,35	-0,73	-361,55	0,14	24,29	0,84	385,83

488	IGHG1	P01857	Ig gamma-1 chain C region	53,5056	0,0000	29,12	9,53	1,15	-1,01	-378,61	1,57	44,76	1,85	423,38
489	PDIA6	Q15084	Protein disulfide-isomerase A6	36,9414	0,0000	36,07	19,56	21,16	-0,59	-459,11	-0,08	-32,59	0,52	426,52
490	PPIA	P62937	Peptidyl-prolyl cis-trans isomerase A	11,9135	0,0007	37,74	15,33	13,00	-0,84	-594,57	0,16	33,07	0,98	627,65
491	EEF2	P13639	Elongation factor 2	4,3109	0,0318	56,88	52,48	44,50	-0,08	-240,73	0,16	387,01	0,24	627,73
492	CALR	P27797	Calreticulin	15,7987	0,0002	72,51	39,42	38,38	-0,59	-1851,54	0,03	40,44	0,62	1891,99
493	HIST1H4A	P62805	Histone H4	4,6571	0,0255	87,92	52,96	62,50	-0,50	-2462,70	-0,17	-550,56	0,34	1912,14
494	PFN1	P07737	Profilin-1	10,5202	0,0012	80,99	34,48	47,03	-0,81	-2684,92	-0,31	-511,61	0,53	2173,31
495	ANXA6	P08133	Annexin A6	17,4355	0,0001	93,65	57,35	57,35	-0,48	-2740,14	0,00	0,43	0,48	2740,57
496	HBA1	P69905	Hemoglobin subunit alpha	19,0770	0,0001	76,86	12,15	15,35	-1,45	-2880,27	-0,23	-43,97	1,33	2836,30
497	HSP90AB1	P08238	Heat shock protein HSP 90-beta	33,7872	0,0000	127,59	69,39	74,55	-0,59	-5731,66	-0,07	-371,27	0,52	5360,39
498	TRA1	P14625	Endoplasmin	29,1025	0,0000	172,04	55,98	72,06	-1,02	-13231,28	-0,25	-1029,73	0,82	12201,55
499	ACT	Q5TD97	Four and a half LIM domains protein 5	15,1831	0,0002	211,89	60,30	80,41	-1,11	-20630,24	-0,29	-1415,30	0,90	19214,94
500	PS1TP5BP1	Q1KLZ0	HCG15971, isoform CRA_a	3,9463	0,0404	403,08	266,57	292,17	-0,41	-45707,30	-0,09	-7152,63	0,32	38554,67
501	HEL	N/A	inorganic pyrophosphatase	8,7721	0,0027	1084,11	827,81	906,40	-0,27	-245017,49	-0,09	-68142,06	0,18	176875,43

9. SCIENTIFIC PRODUCTS

Scientific Papers

- ✓ Proteomic investigation on Nasu-Hakola Disease: shedding light on frontotemporal TREM2-based dementia. *Manuscript in preparation*.
- ✓ Molybdenum and iron mutually impact their homeostasis in cucumber (Cucumis sativus L.), plants. *New Phytologist*, Oct 13, 2016. Vigani G. Et al.
- ✓ Proteomics as an innovative tool to investigate Frontotemporal Disorders. *Proteomics Clinical Application*, 10, 457–469; 2016 Special Issue. Agresta AM et al.
- ✓ Urine Exosome Proteomic Analysis Reveals Renal Tubule-based Host Response to Leptospirosis Infection in Rats*. PLoS Neglected Tropical Diseases*, Mar 20, 9(3); 2015. Ramachandra Rao S. P et al
- ✓ Proteomic analysis of lymphoblastoid cells from Nasu-Hakola patients: a step forward in our understanding of this neurodegenerative disorder*. PLoS ONE*, dec 3, 9(12); 2014. Giuliano S.et al.

Awards

- ✓ Short Term Mobility Program 2016
- ✓ The Best Flash Poster Presentation at “4th Winter Seminar on Dementia” SINDem4juniors 2016, Bressanone, Italy.
- ✓ Frontispiece Picture for Proteomics Clinical Application 2016 Apr;10(4):456, Special Issue.

Congresses

- ✓ June 22, 2017. Training Course “Sperimentazione Clinica in Neurologia”, Milano (MI), Italy
- ✓ May 11, 2017. University of Milan, Master in Medical Biotechnology and Molecular Medicine. Speaker: “Proteomic technologies”;

- ✓ February 16-17, 2017. Training Course “La plasticità neuronale come strumento per la riabilitazione”, Rozzano (MI), Italy
- ✓ September 01-03, 2016. 10th International Conference on Frontotemporal Dementia, Munich, Germany. Poster: “A novel approach to investigate a rare frontotemporal disorder: proteomic studies about Nasu-Hakola Disease”.
- ✓ April 6, 2016. 5th Proteonet Meeting, Fondazione Filarete, Milan, Italy
- ✓ January 20-22, 2016. 4th Winter Seminar on Dementia, Bressanone, Italy. Oral Presentation: “Proteomics to investigate the molecular bases of Nasu-Hakola Disease”.
- ✓ September 07-09, 2015. 4th International Congress on Analytical Proteomics, Caparica (Almada), Portugal. Oral Presentation: “Clinical investigation on Nasu-Hakola disease by means of *gel-free* proteomic approach”.
- ✓ July 4, 2015. Third Proteonet Meeting, IRCSS – Istituto di Ricerche Farmacologiche Mario Negri. Milan, Italy
- ✓ November 27-28, 2014. ProteomiX - XIV Edition, Acqui Terme (AL), Italy. Oral Presentation: “Exosome: Purification methods overview”.

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