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Proteomic profiling of the cerebrospinal fluid of African Americans and Caucasians reveals common and unique biomarkers of Alzheimer's disease

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B.S. University of Richmond, 2015

Advisor: Nicholas Seyfried, Ph.D.

An abstract of

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Molecular and Systems Pharmacology

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ABSTRACT

Proteomic profiling of the cerebrospinal fluid of African Americans and Caucasians reveals common and unique biomarkers of Alzheimer's disease

By Erica Modeste

Despite being twice as likely to get Alzheimer's disease (AD), African Americans have been grossly underrepresented in AD research. While emerging evidence indicates that African Americans with AD have lower cerebrospinal fluid (CSF) levels of Tau compared to Caucasians, other differences in AD CSF biomarkers have not been fully elucidated. In this thesis, we performed unbiased proteomic profiling of CSF from African Americans and Caucasians with and without AD to identify both common and divergent AD CSF biomarkers. Multiplex tandem mass tag-based mass spectrometry (TMT-MS) quantified 1,840 proteins from 105 control and 98 AD patients of which 100 identified as Caucasian and 103 identified as African American. Differential protein expression and co-expression approaches were then utilized to assess how changes in the CSF proteome were related to race and AD. Co-expression network analysis organized the CSF proteome into 14 modules associated with brain cell-types and biological pathways. Consistent with previous findings, the increase of Tau levels in AD was greater in Caucasians than in African Americans by both immunoassay and TMT-MS measurements. Similarly, modules enriched with proteins involved with glycolysis and neuronal/cytoskeletal proteins were more increased in Caucasians than in African Americans with AD. In contrast, a module enriched with synaptic proteins including VGF, SCG2, and NPTX2 was significantly lower in African Americans than Caucasians with AD. CSF modules which included 14-3-3 proteins (YWHAZ and YWHAG) demonstrated equivalent disease-related elevations in both African Americans and Caucasians with AD. A targeted mass spectrometry method, selected reaction monitoring (SRM), with heavy labeled internal standards was then used to measure a subset of CSF module proteins and a receiver operating characteristic (ROC) curve analysis assessed the performance of each protein biomarker in differentiating controls and AD by race. Following SRM and ROC analysis, VGF, SCG2, and NPTX2 were significantly better at classifying African Americans than Caucasians with AD. In total, these findings provide insight into additional protein biomarkers and pathways reflecting underlying brain pathology that are shared or differ by race.

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LIST OF ABBREVIATIONS

Aβ: Amyloid beta peptides

$A\beta_{42}$: Amyloid beta peptide$_{1\text{-}42}$

ACh: Acetylcholine

ACN: Acetonitrile

AD: Alzheimer's disease

ADRC: Alzheimer's Disease Research Center

BBB: Blood brain barrier

BICOR: Biweight midcorrelation coefficient

CBF: cerebral blood flow

CDR: Clinical Dementia Rating

CSF: Cerebrospinal fluid

CV: Coefficient of variation

ε: epsilon

EOAD: Early-onset Alzheimer's disease

FAIMS: High-field asymmetric waveform ion mobility spectrometry

FDR: False discovery rate

GIS: Global internal standards

GO: Gene ontology

GWAS: Genome Wide Association Studies

LC: Liquid chromatography

LC-MS/MS: Liquid chromatography tandem mass spectrometry

LOAD: Late-onset Alzheimer's disease

LFQ: Label-free quantification

LysC: Lysyl endopeptidase

MCI: Mild cognitive impairment

MDS: Multidimensional scaling plots

MoCA: Montreal Cognitive Assessment

MMSE: Mini-Mental Status Examination

MS: Mass spectrometry

NFT: Neurofibrillary tangles

NIA-AA: National Institute on Aging and Alzheimer's Association

PC: Principal component

PET: Positron emission tomography

PHF: Paired helical filaments

$pTau_{181}$: Phosphorylated Tau_{181}

QC: Quality controls

ROC: Receiver operating characteristic

SRM: Selected reaction monitoring

TMT: Tandem Mass Tag

tTau: Total Tau

WGCNA: Weighted Gene Co-expression Network Analysis

LIST OF PROTEINS

ADAM10: ADAM Metallopeptidase Domain 10

ADAM17: ADAM Metallopeptidase Domain 17

ADM: Adrenomedullin

AICD: Amyloid Precursor Protein Intracellular Domain

ALB: Albumin

ALDOA: Aldolase

ANG: Angiogenin

ANG1: Angiopoietin-1

ANP: Atrial Natriuretic Peptide

ANXA5: Annexin A5

APLP1: Amyloid Beta Precursor Like Protein 1

APOE: Apolipoprotein E

APP: Amyloid Precursor Protein

BASP1: Brain Abundant Membrane Attached Signal Protein 1

BGN: Biglycan

BIN1: Bridging Integrator 1

BNP: B-Type Natriuretic

CACNA2D: Calcium Voltage-Gated Channel Auxiliary Subunit Alpha 2/Delta

CADM3: Cell Adhesion Molecule 3

CAMK2A: Calcium / Calmodulin Dependent Protein Kinase II alpha

CD33: CD33 Molecule

CTF83: C-terminal Fragment 83

CTF99: C-terminal Fragment 99

CTSB: Cathepsin B

CTSH: Cathepsin H

CTSZ: Cathepsin Z

C1QA: Complement C1q A Chain

C1QB: Complement C1q B Chain

C1QC: Complement C1q C Chain

C1RL: Complement C1r Subcomponent Like

C2: Complement C2

C3: Complement C3

ECM2: Extracellular Matrix Protein 2

ENO2: Enolase 2

F5: Coagulation Factor V

FGB: Fibrinogen

FLNA: Filamin A

GAPDH: Glyceraldehyde-3-Phosphate Dehydrogenase

GAP43: Growth Associated Protein 43

GDA: Guanine Deaminase

GOT1: Glutamic-Oxaloacetic Transaminase 1

HEXA: Hexosaminidase Subunit Alpha

HEXB: Hexosaminidase Subunit Beta

ICAM1: Intracellular adhesion molecule 1

IDUA: Alpha-L-iduronidase

IGFBP7: Insulin Like Growth Factor Binding Protein 7

IGSF8: Immunoglobulin Superfamily Member 8

LAMA5: Laminin Subunit Alpha 5

LAMC1: Laminin Subunit Gamma 1

LCP1: Lymphocyte Cytosolic Protein 1

LDHB: Lactate Dehydrogenase B

LINGO2: Leucine Rich Repeat and Ig Domain Containing 2

LTBP4: Latent Transforming Growth Factor Beta Binding Protein 4

L1CAM: L1 Cell Adhesion Molecule

MAPT: Microtubule Associated Protein Tau

MYL6: Myosin Light Chain 6

NBL1: Neuroblastoma Suppressor Of Tumorigenicity 1

NID2: Nidogen 2

NPTXR: Neuronal Pentraxin Receptor

NPTX1: Neuronal Pentraxin 1

NPTX2: Neuronal Pentraxin 2

NEFL: Neurofilament Light Chain

NEFM: Neurofilament Medium Chain

NEGR: Neuronal Growth Regulator 1

NEO1: Neogenin 1

NRGN: Neurogranin

NRN1: Neuritin 1

OLFM1: Olfactomedin 1

OPN: Osteopontin

PAI1: plasminogen activator inhibitor-1

PAM: Peptidylglycine Alpha-Amidating Monooxygenase

PARK7: Parkinsonism Associated Deglycase

PCSK1: Proprotein Convertase Subtilisin/Kexin Type 1

PICALM: Phosphatidylinositol Binding Clathrin Assembly Protein

PKM: Pyruvate Kinase M1

PLXNA2: Plexin A2

PPIA: Peptidylprolyl Isomerase A

PSEN1: Presenilin 1

PSEN2: Presenilin 2

PTPRN: Protein Tyrosine Phosphatase Receptor Type N

RTN4R1: Reticulon 4 Receptor

S100A11: S100 Calcium Binding Protein A11

SCG2: Secretogranin II

SDCBP: Syndecan Binding Protein

SHARPIN: Shank Associated RH Domain Interactor

SLIT1: Slit Guidance Ligand 1

SMOC1: Secreted Modular Calcium-binding Protein I

SNCB: Synuclein Beta

SNX1: Sorting Nexin 1

SORL1: Sortilin Related Receptor 1

SORT1: Sortilin 1

SPDGFRB: Soluble Platelet-Derived Growth Factor Receptor-Beta

SYN1: Synapsin 1

SYT1: Synaptotagmin 1

TMEM106B: Transmembrane Protein 106B

TPI1: Triosephosphate Isomerase 1

TREM2: Triggering Receptor Expressed on Myeloid Cells 2

TSPAN14: Tetraspanin 14

VCAM1: vascular cell adhesion molecule 1

VCAN: Versican

VEGFA: Vascular Endothelial Growth Factor A

VGEF: Vascular Endothelial Cadherin

VGF: VGF Nerve Growth Factor Inducible

VSTM2A: V-set and Transmembrane Domain Containing 2a

WDR81: WD Repeat Domain 81

YWAHB: Tyrosine 3-Monooxygenase/Tryptophan 5-Monooxygenase Activation Protein Beta

YWHAE: Tyrosine 3-Monooxygenase/Tryptophan 5-Monooxygenase Activation Protein Epsilon

YWHAG: Tyrosine 3-Monooxygenase/Tryptophan 5-Monooxygenase Activation Protein Gamma

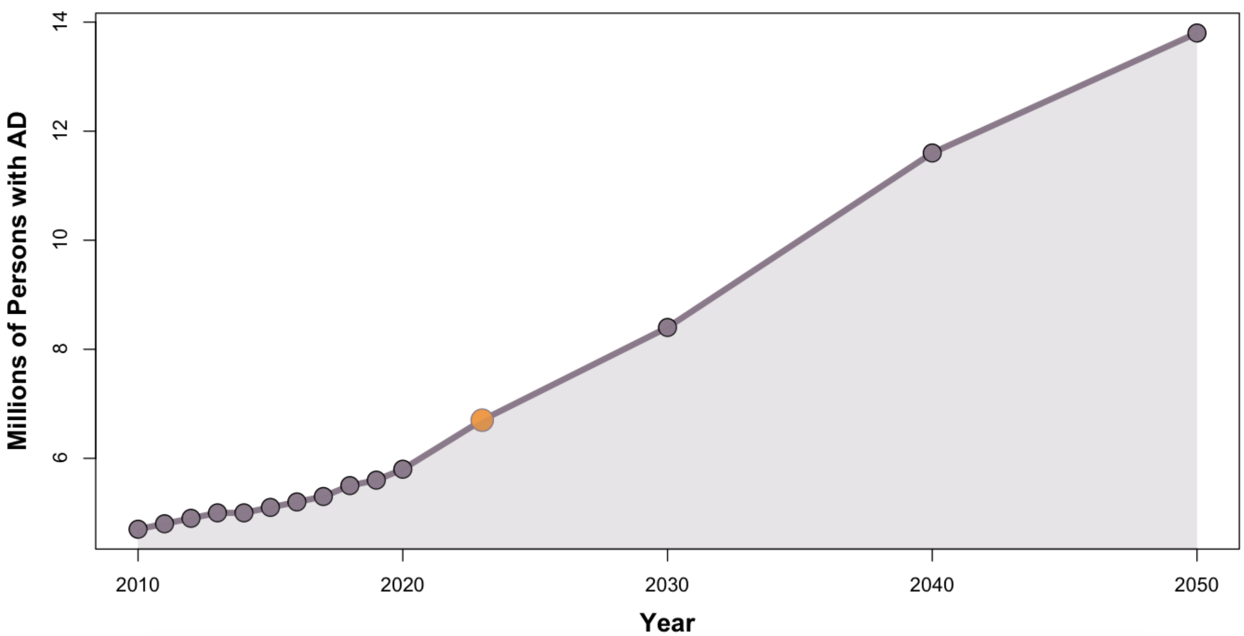
YWHAZ: Tyrosine 3-Monooxygenase/Tryptophan 5-Monooxygenase Activation Protein Zeta

CHAPTER 1:

INTRODUCTION

1.1 The increasing burden of Alzheimer's disease (AD)

Alzheimer's disease (AD) is a progressive and irreversible disorder of the brain that affects memory, thinking, and behavior (1). It is the most common form of dementia, accounting for approximately 60 to 80 % of all dementia cases (2). AD primarily affects older adults, typically starting in individuals over the age of 65 years old (2-6). Notably, the elderly population in the United States has been undergoing rapid expansion since 2011 as the first wave of baby boomers transitioned into the age of 65 (7). The baby boom era, which spanned from 1946 to 1964, marked a distinctive phase in American history characterized by a surge in birth rates following World War II (7). Consequently, with the progression of the baby boomer population from middle to older ages, there has also been a substantial increase in the incidence of AD (7; 8). Up from approximately 4.7 million people in 2010, an estimated 6.7 million people in the United States are currently affected by this disease, and this number is only expected to double by the year 2050 (2; 7; 8) (**Figure 1.1**). Alongside this rise, there also comes the substantial burden the disease places on caregivers and society (2; 8). In 2022 alone, over 11 million Americans selflessly provided 18 billion hours of unpaid care to older adults afflicted with dementia; a collective contribution valued at nearly $340 billion (2). Furthermore, total annual payments for healthcare and long-term care for people with AD and other dementias are expected to increase from $345 billion in 2023 to just under $1 trillion by 2050, exceeding the costs of treatments for cancer and cardiovascular disease (2; 9). This projection includes three-fold increases in government spending in Medicare and Medicaid, as well as out-of-pocket expenditures (2). Taking into account all of these factors, if there is no progress made in preventing or delaying the onset of AD, coupled with the substantial rise in the number of individuals affected by AD, the proportion of the population impacted by the disease will also increase. This, in turn, will escalate the overall societal burden of AD.



Millions of Persons with AD
14
12
10
8
6
2010
2020
2030
2040
2050
Year

Figure 1.1: Projected number of people in the United States with Alzheimer's disease (AD) in millions from 2010 to 2050. The estimated number of people with AD in the United States in 2023 (orange circle) is predicted to nearly double by 2050.

1.2 Monitoring memory loss in those with AD

AD can be most notably recognized by its incapacitating and progressive memory loss. This gradual decline in memory with disease progression is a consequence of spreading neuronal damage across the brain (**Figure 1.2**) (1; 2). Common early signs of memory loss in AD include forgetfulness, difficulty in finding words, misplacing items, and struggling with familiar tasks like tying a shoe (1; 2). As the disease progresses, individuals may begin to experience confusion, mood swings, disorientation, and difficulties in communication and decision-making (1; 2). Ultimately, in the later stages, individuals often require full time care, as they lose the ability to recognize love ones, communicate, and perform basic activities of daily living (1; 2). In the clinic, patients undergo cognitive exams such as the Mini-Mental Status Examination (MMSE) and the Montreal Cognitive Assessment (MoCA). These assessments serve as crucial clinical diagnostic tools for evaluating and monitoring cognitive impairment. (10-12). While the MoCA test is the preferred test for the early detection of dementia such as in cases of mild cognitive impairment (MCI), MMSE is often used for monitoring cognitive decline over time (11; 13).

MCI is an intermediate stage between typical cognitive aging and dementia (11). In the beginning, physicians heavily depended on the MMSE to gauge cognitive impairment in individuals (12). The MMSE was found to be effective in distinguishing cognitively normal individuals from those with cognitive impairment with significant specificity, where a score below 25 on the MMSE was indicative of impairment (12) (**Figure 1.3**). Its efficacy declined, however, when attempting to identify those with MCI, as individuals with MCI could score between 26 and 29, falling within the range for cognitively normal individuals (14-16) (**Figure 1.3**). This highlighted a significant limitation of the test: its difficulty in detecting early dementia-related changes (17). Consequently, the MoCA test was developed with a heightened emphasis on MCI, while maintaining the scoring ranges of the MMSE (11). Aligned with this, the generally accepted optimal threshold for discerning between individuals with typical cognitive function and those with

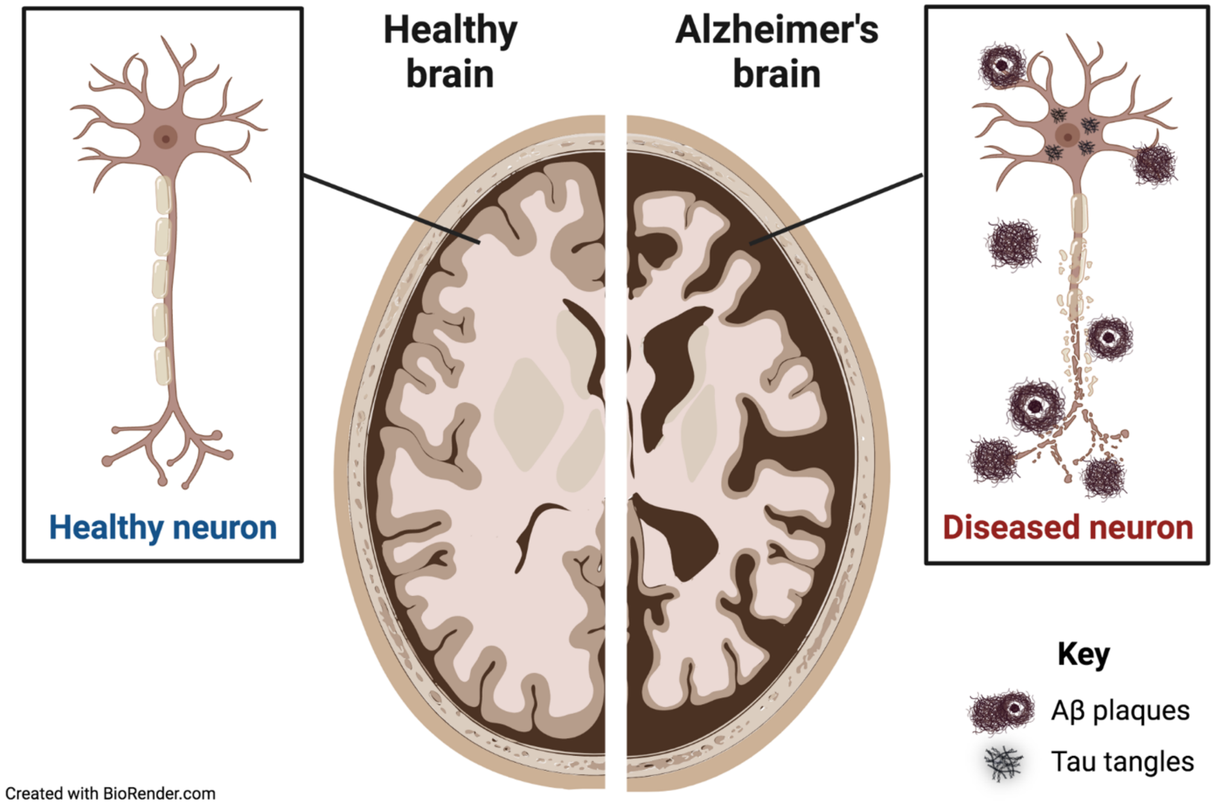

Healthy brain
Alzheimer's brain
Healthy neuron
Diseased neuron
Key
Aβ plaques
Tau tangles
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Figure 1.2: Healthy brain compared to a brain affected by Alzheimer’s disease. In comparison to a healthy brain, brain changes observed in Alzheimer’s disease include injured neuronal cells that are accompanied by abnormal accumulations of amyloid beta (Aβ) plaques and tangles of hyperphosphorylated Tau.

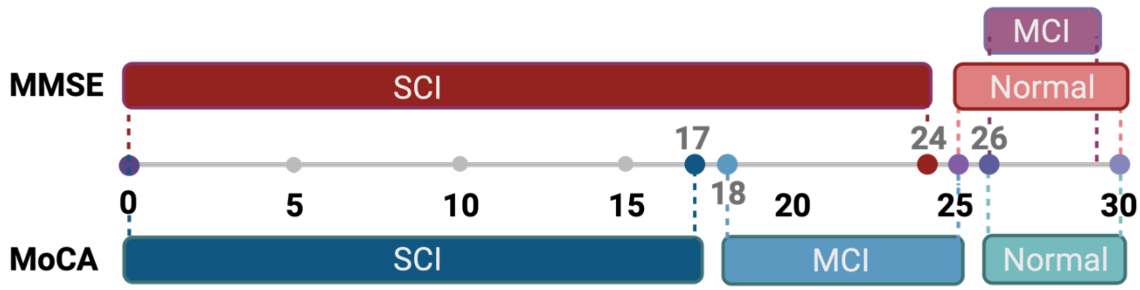

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Figure 1.3: A comparison of the scoring patterns of the Mini-Mental State Examination (MMSE) with the Montreal Cognitive Assessment (MoCA).

MCI in the MoCA test was determined to be 26 (11) (**Figure 1.3**). Though, more recent meta-analysis has suggested that a cutoff score of 23 may be better (18). Moreover, individuals with MCI may score between 18 and 25, while those with dementia typically scored below 18 with significant specificity (**Figure 1.3**). Overall, the MoCA test has demonstrated superior effectiveness compared to the MMSE in monitoring the progression from MCI to severe dementia in clinical settings involving living patients (19-22).

There are various factors to consider when utilizing the specified scores mentioned above. Firstly, studies have indicated that education can significantly impact overall MoCA score (11; 23). It was found that persons with 12 years of education or less tended to have worse performance on the MoCA (11). To mitigate this, it has become common practice to add 1 point to the final score for individuals with 12 years or less of education (11). There is debate, however, as to whether this adjustment adequately addresses education-related disparities (24). In some cases, it has been observed that this adjustment may in fact reduce the test's sensitivity (25). Besides education, age can also impact the score (23; 26; 27). This places older individuals with lower levels of education as the group most vulnerable to obtaining false positive results (24). Finally, studies have revealed that MoCA performance can also be influenced by racial background (26; 28; 29). Including minority participants in a study led to lower cutoffs for distinguishing between normal cognition and MCI (26; 28; 29). In addition, when directly comparing optimal MoCA score cutoffs across multiple races, it was found that the optimal cutoff for both African Americans and Hispanics was lower than that of Caucasians (30). This implies that lower MoCA cutoffs may be more appropriate when assessing the MoCA score of minority individuals (26; 28-30). In conclusion, considering factors such as education, age, and racial background is essential for accurately interpreting and applying MoCA scores in clinical settings.

1.3 The initial discovery of AD

Alois Alzheimer was a German psychiatrist and neuropathologist who discovered AD through his work with a patient named Auguste Deter. In 1901, Deter, who was in her early 50s, was admitted to the mental asylum where Alzheimer worked for exhibiting symptoms of memory loss, confusion, and hallucinations (31). Intrigued by her condition, Alzheimer meticulously documented the continued progression of her disease up until her death on April 6, 1906. Following her death, Alzheimer was able to investigate the brain of Auguste both morphologically and histologically. During the autopsy, Alzheimer noted significant abnormalities in her brain, including unusual protein deposits (now identified as amyloid plaques) and tangled nerve fibers (now known as neurofibrillary tangles) (31; 32). These observations led him to hypothesize that Deter's symptoms stemmed from physical changes in her brain (31). Shortly thereafter, Alzheimer published his findings, presenting the case as a distinct form of dementia that differed from the typical symptoms associated with aging (31). His work laid the groundwork for understanding Alzheimer's disease as a progressive neurodegenerative disorder characterized by cognitive decline and distinct brain pathology. Today, the disease bears Alois Alzheimer's name in recognition of his pioneering research.

1.4 Neuropathological hallmarks of AD

1.4.1 Amyloid Cascade: The amyloid cascade hypothesis is a central theory in AD research that proposes that the deposition of amyloid-beta (Aβ) peptides in the brain occurs prior to and initiates a series of events that culminate in neurodegeneration and the distinctive symptoms of AD (**Figure 1.4**). More specifically, according to this hypothesis, the abnormal accumulation of Aβ peptides leads to the formation of amyloid plaques, which disrupt neuronal function and activate inflammatory responses (33). As a consequence, a cascade of subsequent events is initiated, including the hyperphosphorylation of Tau protein, the formation of neurofibrillary tangles, synaptic dysfunction, and ultimately neuronal death (32). Given its crucial role, the formation and inhibition of Aβ has profoundly shaped investigations into the underlying mechanisms of AD and the creation of potential therapeutic approaches, which primarily focused on Aβ pathways (32; 33). The abnormal accumulation of insoluble Aβ plaques in the extracellular space surrounding neurons has become a hallmark pathology of AD (34; 35) (**Figure 1.2**). Aβ is

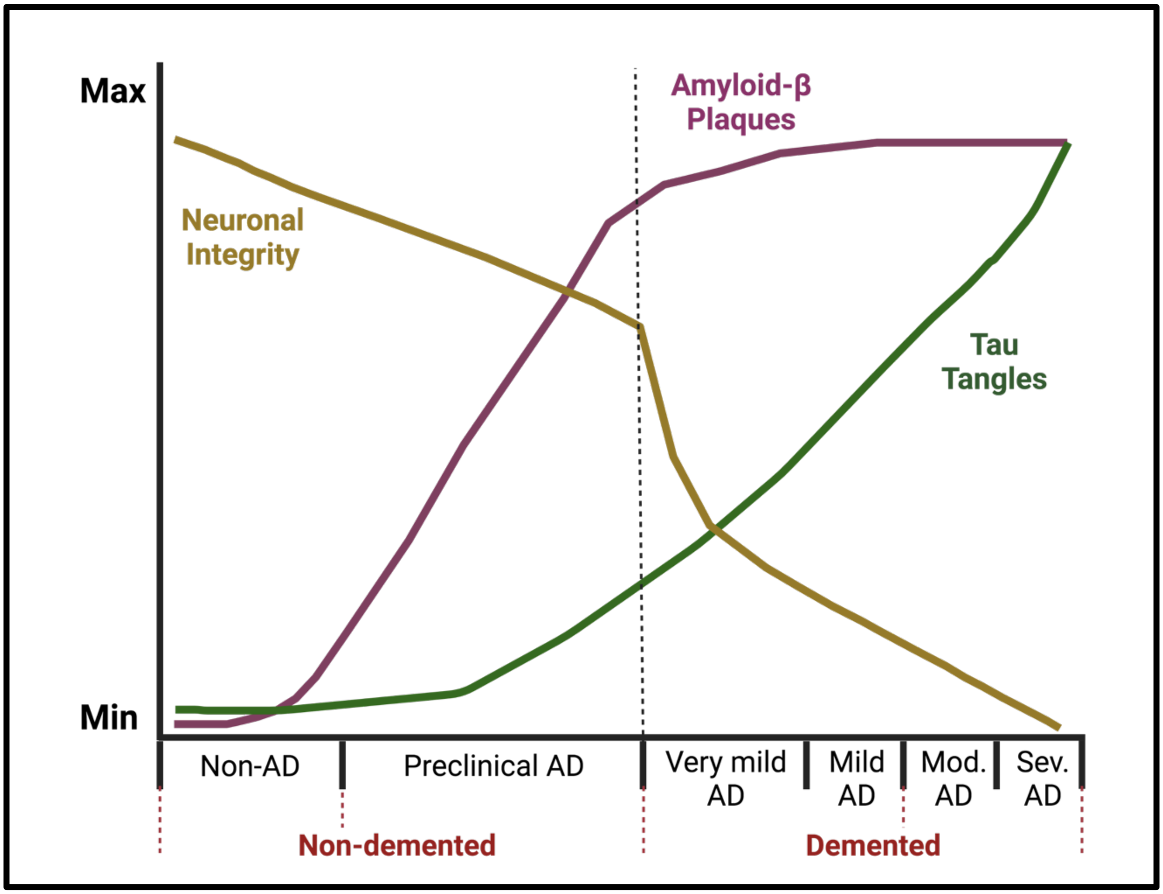

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Figure 1.4: Hypothesized time course of neuropathological and clinical changes in Alzheimer's disease based on biomarker alterations. In Alzheimer's disease (AD), the conversion from a non-demented to demented state is associated with a buildup of amyloid beta (Aβ) plaques (purple line), a more gradual accumulation of neurofibrillary Tau tangles (green line), and neuronal and synaptic loss (yellow line). Modified from Craig-Schapiro, R., Fagan, A. M., and Holtzman, D. M. (2009) Biomarkers of Alzheimer's disease. *Neurobiol Dis* 35, 128-140.

a peptide ranging from 38-43 amino acids long and is the result of sequential cleavages on amyloid precursor protein (APP) by β-secretase and γ-secretase (36) (**Figure 1.5A**). Initially, APP is cleaved by β-secretase producing a long soluble secreted form of APP (sAPPβ) and a C-terminal fragment 99 (CTF99) (37) (**Figure 1.5A**). Subsequently, CTF99 is cleaved by γ-secretase complex to form Aβ and an intracellular amyloid precursor protein intracellular domain (AICD) (38) (**Figure 1.5A**). This cleavage can produce peptides of 43, 45, 46, 48, 49, or 51 amino acids, which are subsequently processed to generate two forms of Aβ, $Aβ_{40}$ or $Aβ_{42}$ (39). While $Aβ_{40}$ is the most prevalent form, $Aβ_{42}$ has been noted to be more prominently present in amyloid plaques (40). Because this pathway leads to the formation of the Aβ peptides that make up the plaques found in AD, its considered amyloidogenic and is associated with the pathological changes observed in AD. The accumulation of Aβ peptides in the brain is central to the amyloid cascade hypothesis, even though Aβ can be extensively present in the human brain without AD symptoms (36; 41-43) (**Figure 1.4, purple line**). The production of Aβ peptides is not the sole outcome of APP processing. Alternatively, APP can also undergo cleavages that diverts the protein toward a non-amyloidogenic pathway (**Figure 1.5B**). Here, α-secretase cleaves APP to release soluble APPα (sAPPα) and CTF83 (**Figure 1.5B**). Importantly, this pathway prevents the generation of Aβ as the cleavage site for α-secretase is within the Aβ domain (37). γ-secretase then cleaves CTF83 to form AICD and p3. This neuroprotective pathway promotes neuronal survival, neurite outgrowth and neural stem cell proliferation, providing an avenue for mitigating AD (44-47). Under typical circumstances, these two pathways operate in equilibrium, permitting neurons to remove unnecessary Aβ as required. Nevertheless, in AD, the balance shifts towards heightened Aβ formation, triggering the cascading events described earlier.

1.4.2 Pathologic Tau: The next hallmark of AD is the formation of neurofibrillary tangles (NFT) that consist of hyperphosphorylated microtubule-associated protein Tau (MAPT). Tau is primarily located intracellularly within neurons, but it can also be found in other cell types of the

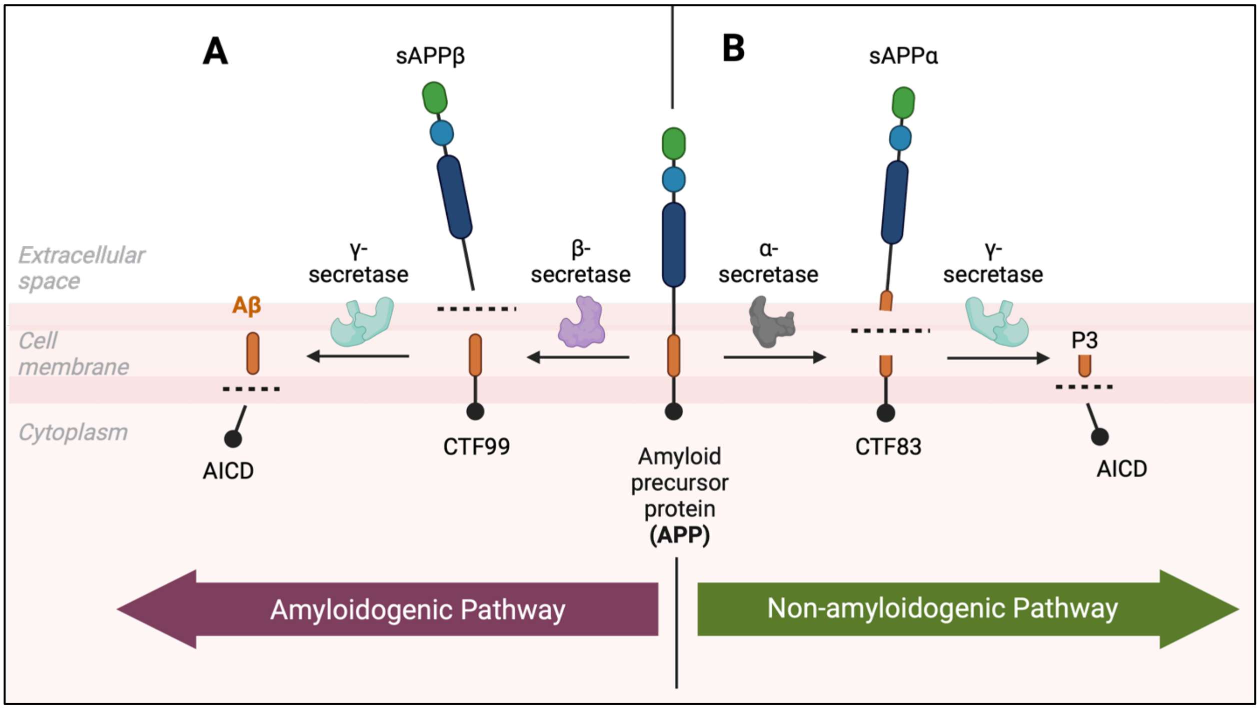

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Figure 1.5: The amyloidogenic and non-amyloidogenic pathways for processing the amyloid precursor protein (APP). (A) The amyloidogenic pathway involves cleavages by β-secretase and γ-secretase resulting in the generation of a long-secreted form of APP (sAPPβ), and C-terminal fragments, CTF99, amyloid precursor protein intracellular domain (AICD), and Aβ. **(B)** The nonamyloidogenic pathway involves cleavages by α-secretase and γ-secretase resulting the generation of a long-secreted form of APP, sAPPα, and C-terminal fragments, CTF83, AICD, and P3.

brain, such as microglia (34; 35). In the brain, normal Tau protein plays a crucial role in promoting tubulin assembly and microtubule stabilization. Microtubules are essential structures for maintaining the structural integrity of neurons and facilitating intracellular transport, acting like highways within neurons, allowing molecules and organelles to move to different parts of the cell. Tau protein binds to and stabilizes these microtubules, helping to maintain their structure and function. In addition to this, Tau is also involved in regulating synaptic function, which is essential for communication between neurons. It interacts with various proteins involved in synaptic transmission, contributing to the proper functioning of synapses. Overall, normal Tau protein in the brain is involved in maintaining the structural integrity of neurons by stabilizing microtubules and regulating synaptic function; both of which are critical for normal brain function.

The distinction between normal Tau and pathologic Tau primarily lies in several structural and functional characteristics: conformation, phosphorylation, and aggregation (1). Normal Tau protein is typically structured in a way that allows it to bind and stabilize microtubules within neurons. In contrast, pathological Tau undergoes conformational changes, leading to the formation of abnormal Tau aggregates, such as NFTs (48). In addition to conformational changes, phosphorylation, which is the addition of phosphate groups to proteins, plays a crucial role in deciphering Tau's normal function from that of pathologic Tau. Under normal conditions, Tau is moderately phosphorylated, allowing it to bind and unbind to microtubules effectively. However, in AD, Tau becomes hyperphosphorylated, leading to its detachment from microtubules and the formation of insoluble aggregates (3). Under normal conditions, Tau remains soluble and distributed throughout the neuron, and primarily associated with microtubules. Pathological tau, on the other hand, aggregates into insoluble structures, such as paired helical filaments (PHFs) and NFTs which disrupt neuronal function. These insoluble structures then obstruct transport of essential nutrients and molecules vital for the regular function and survival of neurons (1), making it a more immediate precursor to neurodegeneration (**Figure 1.4, green and yellow lines**) (49-51).

1.5 The ATN framework for staging AD progression

As defining features of AD, Aβ deposition (A), Tau tangle formation (T), and neurodegeneration (N) make up the basis of the ATN framework (52). Essentially, this framework proposes different sets of biomarkers to represent hallmark pathological features (Aβ and Tau) and cognitive aspects (neurodegeneration) of AD, utilizing them to categorize patients along the AD continuum (52). In this framework, amyloid biomarkers represent the earliest indicators of AD neuropathological changes in living persons (53-57). Given this, Aβ biomarkers help determine whether an individual falls within the AD continuum (52). Examples of biomarkers indicative of Aβ plaques include amyloid positron emission tomography (PET) imaging of radiolabeled ligands binding to Aβ plaques in the brain and reduced levels of $A\beta_{42}$ in cerebrospinal fluid (CSF) (58-62). The quantification of both Aβ and Tau are required for the diagnosis of AD. Therefore, the presence of pathologic Tau biomarkers is what ultimately determines whether an individual within the AD continuum truly has AD (52). Examples of Tau biomarkers include monitoring elevations in the phosphorylation of Tau at residues Thr181, Thr217, and among other sites (59) within the CSF and PET scans of cortical Tau using radiolabeled ligands that bind to Tau tangles (59; 63-65). Finally, biomarkers of neurodegeneration gauge the severity of neuronal injury. However, these markers do not strictly contribute to the understanding of where a person lies along the AD continuum (52). This is because these markers are not specific to neurodegeneration induced by AD, making it difficult to determine whether neuronal injury is directly attributed to disease or some other comorbid condition (52). Despite this, indicators of neurodegeneration still provide vital staging information when combined with measures of pathologic biomarkers for Aβ and Tau (52). Biomarkers of neurodegeneration include total Tau levels in the CSF, cortical PET scans measuring diminished glucose metabolism, and indicators of brain atrophy detected through magnetic resonance imaging (66-73).

1.6 Early-onset AD versus late-onset AD

The majority of people who develop AD are 65 and older. The presentation of AD at older ages is referred to as late-onset AD (LOAD). It is believed that LOAD, like other chronic diseases, is brought on as result of multiple factors, i.e. environmental and genetics, rather than a single genetic cause. The exception to these would-be cases of AD related to uncommon genetic changes that greatly affect risk. In those cases, the person typically develops AD before the age of 65. This presentation of AD at younger ages is referred to as early-onset AD (EOAD). While the greatest risk factors for LOAD are older age, environmental exposures (i.e lifestyle, education, financial attainment), and genetics, EOAD is primarily caused by genetics alone (74-80).

1.6.1 Early-onset AD: EOAD accounts for only ~2 percent of all cases. Individuals who experience familial AD experience rapid decline and die within several years of symptom onset (81). EOAD has been most notably tied to gene mutations that affect the processing or production of Aβ, whose abnormal accumulation contributes to disease. For this reason, despite being on different chromosomes, mutations in *APP*, *PSEN1*, or *PSEN2* are known to cause AD (5; 82-85). Remarkably, both PSEN1 and PSEN2 make up the catalytic components of γ-secretase which assists in the cleavage of APP into Aβ. In addition to these three genetic variants that are known to cause AD, individuals with Down syndrome are often at high risk for developing EOAD (2). This is because they possess an extra chromosome 21, which carries the *APP* gene. Estimates suggests that nearly 50% or more of individuals living with Down syndrome will develop symptoms of AD by their 50s or 60s (86; 87).

1.6.2. Late-onset AD: Contrary to EOAD, LOAD is the most common form of AD, mainly occurring in individuals over 65 (3-6). Also known as sporadic AD, LOAD accounts for the remaining 98% of cases (2; 81). Multiple gene loci have been implicated in LOAD. As a result, LOAD is often considered a polygenic disorder (2). One of the most impactful genetic susceptibilities to LOAD involves the Apolipoprotein E gene (5; 88; 89). Apolipoprotein E (APOE) epsilon (ε) protein has three different variants that differ at residues 112 and 158: APOE ε2 contains a cysteine at both resides 112 and 158 while APOE ε3 contains a cysteine at residue 112 but an arginine at residue 158. Lastly, APOE ε4 has two arginine residues that occupy position 112 and 158 in the full-length protein. Those who inherit a copy of the *APOE ε4* allele have three times the risk of developing AD while those who inherit two copies have an eight- to 12-fold risk (90-92). Contrastingly, the inheritance of the *APOE ε3* allele has no risk of developing AD while the *APOE ε2* offers some protection. Although genetic studies support that *APOE* is the largest modifier of an individual's risk of developing LOAD, half of the individuals with LOAD do not possess an *APOE ε4* allele indicating that other loci influence LOAD development. Innovations in genomic sequencing technology have allowed for the identification of other genetic polymorphisms linked to AD through genome wide association studies (GWAS). Such genes include genes that encode for proteins involved in the dysregulation of microglia (CD33, SHARPIN, TREM2), α-secretase (ADAM10, ADAM17, TSPAN14), endocytosis (BIN1, PICALM, WDR81), the lysosome (CTSB, CTSH, IDUA, TMEM106B), and sorting receptors (SORL1, SORT1, SNX1) (93; 94). More genes are expected to be revealed as genomic studies continue to expand and grow in sample size and ethnic background.

1.7 Risk factors for AD

1.7.1 Age: The most significant contributor to AD risk is age (2; 74). This is evident by the steep increases in the percentage of people with AD with advancing age. For example, five percent of individuals between 65 and 74 years old have AD which then increases to 13.1 % for those aged from 75 to 84 (95). By the time one reaches 85, this number doubles, affecting 33.3% of this population range (95). It is worth highlighting again that these prevalence statistics are projected to steadily increase as the baby-boom generation continues to move throughout these age ranges (8; 95). Although age plays a major role in risk, AD is not a natural outcome of the aging process; in other words, simply reaching an older age is not adequate enough to trigger the onset of AD (96).

1.7.2 Sex: Approximately two-thirds of AD patients are women (97). While men have only a 1 in 10 chance of developing AD, women's likelihood is twice as high, 1 in 5 (95). Although it has been speculated that women's heightened risk of developing AD could be due to their longer lifespan, studies indicate that differences in several biological factors such as sex hormones, immune response, and metabolic regulation can modulate risk (98). One significant factor affecting risk is the sex hormone, estrogen. Estrogen receptors are distributed throughout the brain, regulating various physiological processes, some of which exert protection against AD pathology. Studies show that estrogen achieves this protective effect by stimulating the generation of vesicles containing APP from the Golgi network (99; 100). This mechanism then facilitates the transport of APP to the cell surface where, it either undergoes cleavage by α-secretase, yielding the soluble and neuroprotective molecule, sAPPα, or is re-internalized through an endosomal/lysosomal degradation pathway (101-103). Both of which precludes the production of insoluble Aβ peptide (99-104). Additionally, estrogen has been shown to decrease the presence of hyperphosphorylated Tau and increase the presence of dephosphorylated of Tau (105). In the perimenopausal phase, however, which occurs 1-4 years prior to menopause, estrogen levels fluctuate significantly. This variability contributes to dysfunction in metabolic, inflammatory, and sensory-processing pathways associated with estrogen (106; 107). Consequently, the eventual loss of estrogen during menopause contributes to females' susceptibility to AD (108; 109). In contrast, men do not undergo an equivalent of perimenopause. Instead, they experience a gradual decline in testosterone (110). This gradual transition elucidates the age-related dysfunction in male hormonal pathways compared to those in females (110).

1.8 Modifiable risk factors for AD

1.8.1 Role of modifiable risk factors in AD: Although age and sex cannot be changed, some risk factors can be modified to reduce the risk of cognitive decline and dementia without relying on a cure or medicine (111). In fact, studies suggest that addressing modifiable risk factors may prevent or delay up to 40% of all dementia cases (112). Notably, nearly a third of cases of

AD and other dementias in the United States are associated with at least one of eight modifiable risk factors: physical activity, smoking, depression, low education, diabetes, midlife obesity, midlife hypertension, and hearing loss (113). Of these, the greatest factors to AD risk have been shown to be midlife obesity, physical inactivity, and low educational attainment (113).

Timing also holds significant importance in relation to modifiable risk factors in that the age in which these risk factors develop affects the impact on AD risk. For example, developing obesity, hypertension, and high cholesterol during midlife can elevate one's risk of dementia in later stages of life (114-120). For example, those between 40 and 79 years old lacking a number of modifiable risk factors (low education, hypertension, hearing loss, traumatic brain injury, alcohol or substance abuse, diabetes, smoking and depression) have been shown to exhibit cognitive performance akin to individuals 10-20 years younger with multiple modifiable risk factors (121). Conversely, the onset of obesity and hypertension in late life, after the age of 80, is associated with a reduced risk in dementia (122; 123). Moreover, addressing modifiable risk factors during midlife was connected to decreased dementia risk, even among individuals with a heightened genetic predisposition to dementia (124). In essence, while genetic inheritance is unalterable, exerting an influence on cognitive function becomes feasible by avoiding modifiable risk factors.

1.8.2 Cardiovascular health: The interdependence between brain health and cardiovascular health has been recognized for a considerable time. This connection is likely rooted in the fact that, despite accounting for just 2% of the body's weight, the brain utilizes approximately 20% of the body's oxygen and energy resources. In this context, a healthy heart is crucial for facilitating adequate blood supply to the brain, while healthy blood vessels ensure the delivery of oxygen and nutrient-rich blood to this vital organ. As a result of this intricate relationship between brain and cardiovascular health, many factors that increase the risk of cardiovascular disease are also associated with a higher risk of dementia (125). Notably, these factors encompass conditions such as hypertension and diabetes (114; 116; 118; 119).

1.8.3 Smoking / physical activity / diet: Due to the close relationship between cardiovascular health and brain function, behaviors that impact the heart's well-being can also influence the brain, thereby affecting the risk of developing dementia. Not surprisingly, smoking has been associated with an elevated risk of dementia (126), whereas engaging in physical activity has been shown to decrease risk (127-136). Now despite extensive exploration into various forms of physical activity, determining the specific types, frequencies, and durations that yield the most significant reduction in risk remains an ongoing challenge. In addition to physical activity, emerging evidence suggest that adhering to a heart-healthy diet could decrease one's risk of dementia (137-142). A heart-healthy diet places emphasis on fruits, vegetables, whole grains, fish, poultry, nuts, legumes, and beneficial fats such as olive oil while simultaneously limiting the intake of saturated fats, red meat, and sugar (2).

1.9 Social determinants of health

Historically, the healthcare sector bore the primary responsibility for addressing health and disease concerns, as it was widely recognized for its role in delivering care to those most in need (143). However, it's increasingly evident that medical care alone is not sufficient to improve health outcome or mitigate health disparities (144). In fact, research suggests that differences in life expectancy and disease prevalence among various demographics are largely shaped by the conditions in which individuals are raised, live, work, and age (143). These nonmedical factors, encompassing socioeconomic status, educational attainment, job opportunities, social support networks, healthcare accessibility, and the quality of the physical environment, profoundly influence health outcomes and overall well-being, and are collectively referred to, today, as social determinants of health (143). Some of these factors that most notably affect disease risk include education, employment, income, environment, discrimination and exposure to stress.

1.9.1. Education: Education can improve health by increasing health knowledge and healthy behaviors (144). In support of this, higher educational attainment has been linked to engaging in health-promoting behaviors and adopting health-related recommendations earlier

(145; 146). This could partially be attributed to literacy (147; 148). It is believed that literacy enables individuals with higher education levels to make more informed health-related decisions for themselves and their families (147; 148). Education also holds significance in health by influencing employment opportunities (144). Higher levels of education are associated with reduced unemployment rates, a factor strongly correlated with poorer health and increased mortality (149). Similarly, individuals with higher educational attainment are more inclined to hold positions offering healthier physical working environments, superior health-related benefits, and higher compensation (150; 151). Lastly, education may also affect health by influencing social and psychological factors where higher education levels have been correlated with heightened perceived personal control, a factor frequently associated with improved health outcomes and health-related behaviors (145; 147). In summary, higher levels of education are associated with improved health outcomes because education equips individuals with the knowledge and ability to make healthier choices, to obtain secure employment conducive to better access to healthcare, and to exercise greater personal control over their health.

1.9.2. Employment: The physical aspects of work can have clear impacts on health (144). For instance, occupations involving repetitive movements and/or high physical demands increase the likelihood of workers experiencing muscular or skeletal injuries and disorders (152). Similarly, individuals with sedentary jobs who are physically inactive face elevated risks of obesity and chronic diseases such as diabetes and heart disease (153). Besides physical factors, the psychosocial aspects of work also have an impact on health (144). Psychosocial factors refer to the circumstances wherein a person's social environment, cultural norms, interpersonal relationships, and overall well-being shapes their mindset and behavior. For instance, employees in roles marked by high demands coupled with low control or perceived imbalance of efforts and rewards face an increased risk of experiencing poor health (154; 155). Those who are socially disadvantaged frequently contend with lower wages or income and are typically the ones most likely to confront these health-harming physical and psychosocial conditions in their workplaces

(156). In conclusion, both the physical and psychosocial aspects of work play crucial roles in determining individuals' health outcomes, with socially disadvantaged groups often bearing a disproportionate burden of these adverse conditions, further exacerbating health disparities.

Work can also affect health through the opportunities and resources it provides (144). In general, for most Americans, earnings from employment constitute their primary economic resource. Consequently, health can be influenced by employment-related benefits such as medical insurance, paid leave, flexible scheduling, workplace wellness initiatives, resources for child and elder care, and retirement benefits (144). Positions with higher salaries are likelier to provide benefits, increased financial security, and the means to afford healthier living environments (144). On the flip side, those categorized as the working poor generally earn inadequate income to meet basic needs and are less likely to have access to health-related benefits (157; 158). In summary, the opportunities and resources available through employment significantly impact health outcomes. While higher salaries often come with benefits and financial security conducive to healthier living, those who are poor often face challenges accessing basic necessities and health-related benefits. This underscores how the socioeconomic impacts of employment can contribute to disparities in health.

1.9.3 Environment: There are many characteristics of one's environment and neighborhood that can influence health (144). Regarding physical characteristics, the quality of air and water, along with the accessibility of nutritious foods and safe exercise spaces, can collectively influence an individual's health (159-165). For example, exposure to pollutants, unsafe living conditions, and limited access to green spaces can contribute to respiratory problems, injuries, and chronic diseases such as cardiovascular diseases. In addition to the physical characteristics, the availability and quality of the services a neighborhood offers could also influence health. Services such as schools, transportation, medical care and employment resources can influence health by shaping individuals' opportunities to earn a living (166-168). Interestingly, neighborhood features can be linked to health even when considering individuals within the same neighborhood (169). Remarkably, some researchers have found poorer health among disadvantaged individuals living in relatively advantaged neighborhoods (170-172). This could be largely due to the adverse psychological effects of feeling worse off than one's neighbors, the perception of having weaker social ties to other residents in the neighborhood, or even having increased exposure to discrimination (173). In conclusion, the environment, or neighborhood, in which one lives plays a significant role in shaping an individual's health outcomes. Beyond the physical aspects such as air and water quality and access to nutritious foods and safe exercise spaces, the availability and quality of neighborhood services also exert considerable influence. Surprisingly, even within the same neighborhood, disparities in health outcomes can persist, highlighting the complex interplay of social and psychological factors. As we continue to explore these dynamics, it becomes increasingly clear that addressing health disparities requires a multifaceted approach that considers not only physical environments but also social and economic factors.

1.9.4 Stress: Coping with daily challenges can be particularly taxing, especially when an individual's financial and social resources are restricted (144). Recent evidence suggests that, in fact, chronic stress connects many social determinants of health and likely plays a causal role in their effects on health (174; 175). Stressful experiences, such as those associated with social disadvantage, like economic hardship and racial discrimination, triggers the release of cortisol, cytokines, and other substances that can damage immune defenses, vital organs, and physiologic systems (174; 176-179). Subsequently, this harm contributes to the accelerated onset or advancement of chronic conditions, such as cardiovascular disease, and the physical toll from chronic stress may hasten the aging process (175; 180-182). In fact, evidence suggest that the accumulated strain from repeatedly attempting to cope with daily challenges, especially with limited resources, may actually cause more physiological damage than a single significantly stressful event would (180). In conclusion, the intricate relationship between chronic stress and health emphasizes the urgent need for comprehensive interventions that address the systemic inequities contributing to daily challenges. This highlights the increased significance of allocating resources and establishing support systems to address health disparities.

1.9.5 Discrimination and social exclusion: In the United States and many other societies, race or ethnic group is another important social factor that influences health, primarily because of racism (144). It's important to note that the associations between discrimination and health are not uniquely observed in the United States and has been also observed in other countries (178). Racism encompasses not only explicit, intentional acts and beliefs of discrimination, but also entrenched societal systems that, even without explicit discriminatory intent, systematically limit the opportunities and resources available to certain individuals based on their race or ethnic background (144). Racial segregation in residential areas is a critical mechanism by which racism generates and sustains social disadvantage (168; 183). African American and Hispanic individuals are more prone to living in underprivileged neighborhoods characterized by poorly equipped schools, leading to lower educational achievement and quality, which can result in health consequences through the pathways outlined earlier (184). Racism can also have a more direct impact on health by triggering chronic stress. Persistent stress resulting from encounters with racial or ethnic bias, including subtle instances lacking overt prejudicial intent, can potentially contribute to health inequalities based on race or ethnicity, regardless of one's neighborhood, income, or educational attainment (178; 185). In fact, research suggests that African Americans and Hispanic Americans with more education or income are exposed to more discrimination than those who are disadvantaged (144). Acknowledging the widespread impact of racial or ethnic bias on health outcomes underscores the imperative of addressing systemic inequities to achieve genuine health equity.

1.9.6 Final conclusions: Ultimately, insufficient and unequal living conditions arise from flawed social policies, unfair economic structures, and ineffective governance (143). As a result, tackling the social determinants of health necessitates a holistic approach involving government at various levels, civil society, local communities, businesses, international organizations, and global initiatives (143). Consequently, policies and programs designed to enhance health outcomes must encompass all sectors of society, rather than solely concentrating on healthcare (143). Collaboration among these sectors is crucial for implementing policies and programs that address the root causes of health disparities, especially across racial and ethnic background.

1.10 Therapeutic attempts to slow the progression of AD

Despite decades of research, we still have no disease modifying treatment and no cure. Although the clinical symptoms of AD are frequently diagnosed in older age, the degenerative process of AD can begin many years prior to disease onset where individuals can remain cognitively normal for 10-20 years despite accumulating pathology (**Figure 1.4**) (186-188). Given this, AD has remained an elusive disease to treat and cure. Current treatments available mainly alleviate the cognitive deficits associated with AD. Cholinesterase inhibitors, such as galantamine, rivastigmine, donepezil, and memantine, have remained routine treatment options for the symptomatic relief of mild to moderate AD. Drugs such as these were first implemented to combat the theory that the loss of acetylcholine (ACh) neurons is to blame for the cognitive deficits observed in AD (189). Similarly, declines in nicotinic ACh receptors and M2 muscarinic ACh receptors have been shown to be responsible for AD progression (190; 191). Overall, these treatments have remained ineffective in removing the root of AD pathogenesis, merely targeting symptoms so as to only temporarily improve a patient's cognitive outcome. Consequently, it has become a critical goal of AD research to develop drugs that target the underlying mechanisms and processes involved in the progression of AD. Such therapies would aim to modify the course of the disease by reducing the build-up of Aβ plaques and Tau tangles, which are hallmarks of AD pathology. For this reason, immunotherapeutic strategies such as Aβ-directed immunotherapy dominated the AD research for its potential to directly target the plaques associated with disease. Passive immunotherapies, such as bapineuzumab and ALZ 801, relied on the direct injection of monoclonal antibodies into the patient's body, utilizing the immune system to increase clearance of pathologic Aβ fragments (192). Remarkably, recent amyloid immunotherapy treatments lacanemab and donanemab were found to not only reduce amyloid burden in the brain but also moderately slow cognitive decline (193; 194). Despite this, however, they were unable to reverse the neuronal loss and cognitive impairments observed in advanced stages of AD (193-196). This failure has been attributed to the initial treatment being administered at too advanced stage of AD in which neuronal damage is severe (195; 197; 198). Thus, it has become a prioritization of AD research to shift towards the early detection and or prevention of AD (52).

1.11 Cerebrospinal fluid (CSF) as a gateway to neuropathological changes in AD

CSF has become a promising source of biomarkers for the early detection and monitoring of AD in living patients. CSF is made by highly vascularized tissue within the ventricles of the brain called choroid plexus (199). Once created, CSF flows from the lateral ventricles to the third and fourth ventricles, and then into the subarachnoid space and spinal cord (**Figure 1.6A**). This direct contact with the brain gives CSF, removed via lumbar puncture from the spinal cord, the ability to reflect neuropathological changes in the brain of living patients (200). More specifically, decreases in Aβ and elevations in Tau in the CSF have been shown to distinguish healthy controls from AD (201) (**Figure 1.6B**). Decreases in Aβ in the CSF is thought to be the result of increases in accumulations of Aβ into plaques in the brain which have been largely found to be the result of the impaired clearance of Aβ out of neurons during disease (202). Interestingly, only a fraction of Tau found in the CSF is due to the passive release of Tau from dying cells (203). Markedly, increasing levels of Tau in the CSF are predominantly the result of the enhanced secretion or release of Tau from the intracellular regions of neurons into the extracellular space. In fact, studies have shown that Tau hyperphosphorylation may be critical for its secretion (**Figure 1.7**). For example. studies have shown that Tau can be secreted at the synaptic terminal during normal synaptic activity (204; 205). Tau hyperphosphorylation, however, can enhance its secretion at the synaptic terminal as hyperphosphorylated Tau has been shown to be preferentially secreted during both ectosome shedding and exosome fusion (**Figure 1.7B & C**) (204; 206). Moreover, unlike normal physiological Tau, hyperphosphorylated Tau can also be secreted directly across

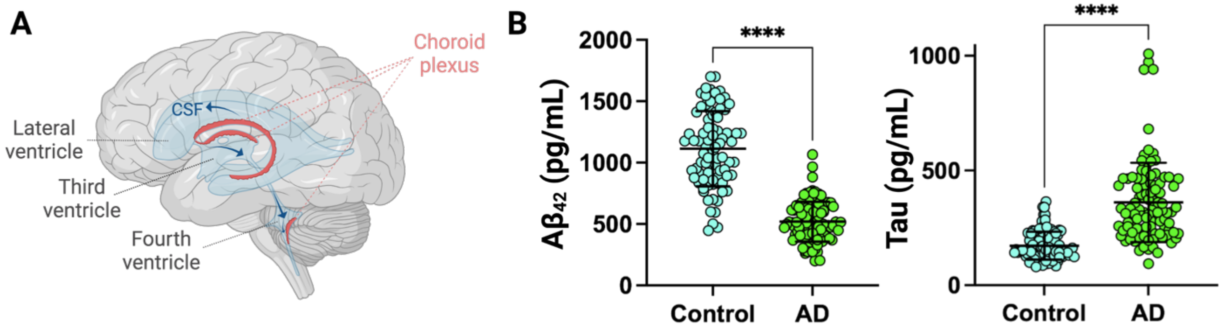

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Figure 1.6. Cerebrospinal fluid (CSF) creation and flow alongside sample immunoassay measurements of Amyloid beta$_{1\text{-}42}$ (Aβ_{42}) and Tau from 105 controls and 98 AD cases. (**A**) CSF is created by and secreted from highly vascularized tissue called the choroid plexus located within each ventricle of the brain. The CSF flows from the lateral ventricles to the the third and fourth ventricles and then into the subarachnoid space and spinal cord. (**B**) Aβ_{42} and total Tau levels as measured by Roche Elecsys Platform between 105 control and 98 AD cases. T-test determined significance and Aβ_{42} values that reached saturation (1700 pg/mL) were excluded.

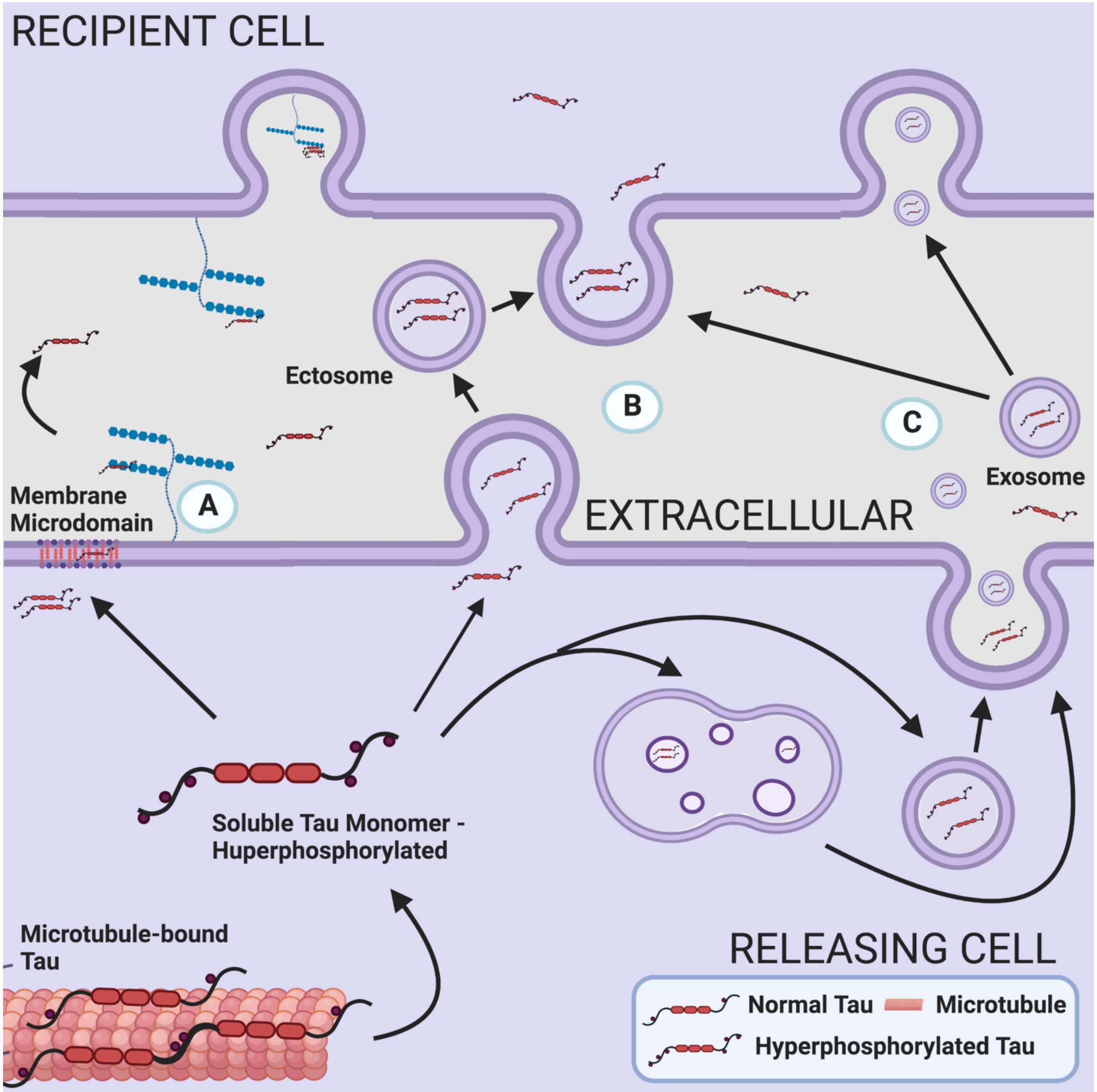

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Figure 1.7. Methods by which pathological Tau can be secreted or released into extracellular space. (**A**) Tau can be actively secreted through the plasma membrane. (**B**) Tau can be released by ectosome shedding from the plasma membrane. (**C**) Tau can be packed into exosomes by inward budding and become secreted by of multivesicular bodies along the plasma membrane. Modified from Brunello, C. A, Merezhko, M., Uronen, R., and Huttunen, H. J. (2019) Mechanisms of secretion and spreading of pathological tau protein. *Cellular and Molecular Life Sciences*. https://doi.org/10.1007/s00018-019-03349-1

the plasma membrane (**Figure 1.7A**) (207; 208). While the exact mechanism by which Tau is secreted into the CSF is unclear, it remains evident that the CSF of AD patients displays changes in Tau composition and that these changes, particularly that of phosphorylated Tau species, significantly correlate with neocortical NFT pathology in the brain (209). Together, these changes observed in CSF biomarkers, Aβ and Tau, give physicians the ability to determine individuals at risk of developing AD and researchers the ability to use CSF as a tool for assessing biological processes reflective of early disease stages (210).

1.12 African Americans: the most at-risk racial group for AD

African Americans are almost twice as likely to have AD compared to Caucasians (211-213). Current evidence suggests that this difference in risk could be explained by a multitude of factors including genetic ancestry and disparities in health, socioeconomic and environmental conditions (214-217). For example, GWAS show that the *ABCA7* gene has stronger associations with AD risk in individuals with African ancestry than in individuals with European ancestry (216; 217). *ABCA7* also has a stronger effect size in African Americans than even the strongest genetic risk factor gene for AD, the *APOE* ε4 allele (216). Yet, despite the *APOE* ε4 allele being more prevalent amongst African Americans, *APOE* ε4 confers a lower risk for AD compared to Caucasians (76). Beyond genetic ancestry, chronic health conditions associated with higher risk for dementia, such as cardiovascular disease and diabetes, also disproportionally affect African Americans (214; 215). Furthermore, societal and environmental disparities that disproportionately affect African Americans, including lower levels and quality of education, higher rates of poverty, and greater exposure to adversity and discrimination, increase risk for both chronic diseases and dementia (214; 215). This highlights how racial differences in AD risk cannot be explained by genetics alone (214). Currently there is a gap in knowledge of the racial differences in underlying pathophysiology related to AD. Therefore, a better understanding of these mechanisms can help move towards a more precise definition of AD across diverse racial, ethnic, and genetic backgrounds. An unbiased analysis into the CSF proteome of African Americans could provide insight into additional biomarkers reflecting underlying brain pathology that differ by race in AD.

1.13 The utility of mass spectrometry (MS)-based proteomics in identifying novel protein signatures in AD

1.13.1 Strategies for MS-based quantification of proteomes: Proteomic analyses of AD brain have predominantly utilized "bottom-up" mass spectrometry (MS) for protein identification and quantification. This workflow generally involved enzymatic digestion of proteins with trypsin, followed by protein separation via liquid chromatography (LC), and subsequent measurement of protein peptides using tandem mass spectrometry (MS/MS) (218). The first stage of measurement (MS1) involves the selection of several precursor peptides for fragmentation. The fragmented peptides are then identified through spectral matching and quantified using well-established statistical and informatic methods during the second stage of tandem MS (219-224). In summary, the “bottom up” approach to MS has become a cornerstone in the comprehensive analysis of proteomic profiles in AD research. Since then, significant advancements have been made to enhance protein identification and quantification, resulting in more detailed proteomic profiles.

Over the years technological strategies have further improved this workflow by enhancing the quantification and depth of proteomic datasets. Initially, label-free quantification (LFQ) was the preferred technique. Using this technique, each sample is individually prepared and analyzed using LC-MS/MS. Since each sample is analyzed individually, a limitation of this technique is that the peptides selected and analyzed can vary significantly between samples. This is due to the inherent nature of MS1 where peptide selection is biased toward the most intense signals (225). When trying to quantify proteins that are lost in a disease, this means that a protein quantified in a healthy state may be completely absent in the disease state and therefore not quantified. This results in a well-documented "missing value" problem, ultimately reducing the number of proteins retained in an LFQ dataset (225-228). Multiplex isobaric peptide labeling with tandem mass tags (TMTs) helps address the issue of missing values by allowing the simultaneous analysis of multiple samples within a single LC-MS/MS run, currently accommodating up to 16 samples per run (229; 230). When combined with off-line fractionation, this strategy can quantify thousands of additional proteins compared to LFQ, which has enabled remarkably deep proteomic analysis of AD brain tissue (227; 228; 231; 232). A study that came out of the Seyfried Lab, Johnson et al., demonstrated this advantage in one of the first TMT-MS network proteome studies of the AD brain. This study quantified 6,533 proteins across 47 brain tissues compared to just 2,736 proteins quantified by LFQ-MS using the same samples (227). Despite these advancements in quantification, TMT-MS may still produce missing values across multiple batches which occurs when analyzing large numbers of samples (233). Targeted approaches such as selected reaction monitoring (SRM) can serve as a mitigate for the limitation of “missing values” by utilizing its ability to identify nearly all detectable peptides within a selected mass range. This allows for comprehensive and accurate quantification of the identified proteins in the sample with minimal to no missing values. This method is often used in research settings for more robust quantification of pre-specified individual peptides (234). Utilizing a targeted approach like this can be useful in validating discovery-driven data that results from tandem MS, as it requires specifying a target beforehand. In conclusion, the evolution of technological strategies, from LFQ to multiplex isobaric peptide labeling and targeted approaches like SRM, has significantly enhanced proteomic workflows, enabling comprehensive and accurate quantification of proteins.

1.13.2 Fundamentals of network construction and module identification: Unbiased proteomics of human brain coupled with network analysis has emerged as a valuable approach for organizing complex proteomic data into groups or “modules” of co-expressed proteins that reflect various biological functions (227; 235-237). Co-expression network analysis operates on the premise that proteins react to biological stimuli as a "system," altering expression collectively within groups or "modules" of a network. Effectively organizing proteomic datasets into the described co-expression protein modules requires a thoroughly validated statistical algorithm. One such extensively validated algorithm, commonly employed in transcriptomic studies, is

Weighted Gene Co-expression Network Analysis (WGCNA) (235; 238-241). This algorithm applies graph theory principles to detect modules of proteins exhibiting highly correlated abundance levels across samples. Through evaluating the connectivity of each protein within a module, researchers can identify module-specific hubs or proteins that play central roles in module function. Typically, the most centrally connected proteins in a module serve as key drivers (238; 240; 242). Module-level abundance profiles can then be correlated with various phenotypic traits of the disease, such as amyloid burden, tangle deposition, and cognitive decline (243). These module-trait correlations reveal protein groups with strong positive or inverse relationships to the disease. In addition to module-trait correlations, module enrichment profiles can also provide important insights into proteomic composition. This analysis seeks to identify the over-representation of module proteins linked to specific cell types, biological functions, or genetic risk factors. It accomplishes this by cross-referencing the proteins within a module with well-validated databases. For instance, cell type enrichment is usually conducted by comparing module proteins with marker lists from established reference proteomes or transcriptomes of purified murine brain cells (218; 227; 228). In addition to cell enrichment lists, numerous resources are available for pathway and ontology analysis. Go Elite is a versatile analytical tool that enables users to incorporate both reference and custom databases to investigate ontological over-representation at biological, molecular, and organellar levels (244). Altogether, network analysis offers the ability to resolve the complex nature of disease by utilizing mathematical and computational tenets of system biology which results in the formation of communities (modules) of proteins, which can be representative of phenotypes that arise out of the molecular pathophysiology of disease.

1.13.3 Why prioritize the study of the proteome over the genome: Proteins are the ideal markers for understanding diseases such as AD because they are most proximal to the phenotypic changes seen in AD. Protein-level analysis offers the advantage of revealing disease-related changes that are not easily detectable in transcriptomic networks. Notably, only 30-40% of the modules in the AD brain network proteome overlap with those in the network transcriptome.

(235; 245). Furthermore, despite the fact that differential protein expression within these overlapping modules has been found to exhibit a reasonable degree of concordance, with a correlation coefficient of approximately 0.5, it has been repeatedly observed that the targets within the most concordant modules across transcriptomics and proteomics exhibit highly discordant changes at the protein and RNA levels (235; 245; 246). These discrepancies highlight the complexity and non-linear relationship between the transcriptome and proteome, stressing the importance of the numerous events that occur from the initial transcription of DNA to the point when a protein performs its function. This also aligns with the observation that only half of the disease-related variance in the AD network proteome is mirrored in transcriptome-level gene expression, while the remaining 50% results from transcriptional and post-translational effects (246). These findings align with previous comparisons of protein and mRNA data (237), and strongly supports the value of protein profiling in AD research, highlighting the unique aspects of proteomic changes that can only be achieved through protein analysis.

1.13.4 Core modules of the AD brain network proteome: Nearly a dozen comprehensive network-based analyses of the AD proteome in the human brain have led to the identification of six highly conserved modules, each with reproducible associations to specific cell types, organelles, and biological functions (217; 221; 225; 226; 235-241). Several modules, such as inflammatory, myelination, and RNA binding/splicing, consistently showed increases in the AD brain network proteome, while others, like synaptic, mitochondrial, and cytoskeleton, displayed consistent decreases. Notably, some of these modules (inflammatory, myelination, synaptic, and mitochondrial) appear to be driven by cell-type-specific perturbations (226), while those lacking such enrichment (RNA binding/splicing and cytoskeleton) represented underlying biochemical changes associated with the disease. The complexity of the modules preserved in AD confirms the multifactorial nature of the condition, which has led to inherent challenges in understanding AD and, consequently, in developing effective interventions.

1.13.5 The CSF proteome as a reflection of AD brain changes: The close proximity of CSF to the brain, along with its ability to reflect changes in amyloid burden and neurodegeneration through markers like Aβ and Tau, provides a compelling rationale for integrating the CSF proteome with the brain proteome. Furthermore, the reflection of other AD pathophysiologies in the CSF would provide additional avenues for detecting and monitoring treatment responses, especially at earlier stages of disease. Our first attempt to validate this interaction via proteomics was based on findings by Johnson et al., which identified that approximately 20 proteins from the highly conserved microglial module showed significant elevations in AD CSF (237). This provided the initial evidence necessary to explore this interaction more deeply. In another large-scale study by the Seyfried lab, Higginbotham et al. used a similar integrative proteomic approach to examine the statistical overlap between the entire AD brain network proteome and differentially expressed proteins in the AD CSF proteome (245). Notably, fifteen of the 44 brain modules identified in this study showed a strong overlap with the markers differentially expressed in AD CSF. Collectively, those 15 modules from the brain were being represent by 300 proteins that were significantly altered in AD CSF compared to controls. Based on their corresponding brain modules, these approximately 300 CSF AD targets were then segregated into five biomarker panels that represented a wide range of brain pathophysiology. These panels included synaptic transmission, vascular biology, myelination, glial-mediated inflammation, and energy metabolism. The panels highlighting brain changes in AD that could potentially be monitored through CSF. This comprehensive approach highlights the potential of CSF proteomics to uncover diverse aspects of AD pathology and to enhance the precision of biomarker-based diagnosis and therapeutic monitoring.

1.14 Summary

Evidence of differences in AD biomarkers between African Americans and Caucasians exists yet the underrepresentation of African Americans in research means data to support such alterations is lacking. This demonstrates a greater need for broad investigations into the underlying biological differences of AD in African Americans as a means to identify AD biomarkers that are representative of and generalizable across diverse racial, ethnic, and genetic backgrounds. Including participants from diverse racial backgrounds ensures that research findings are more representative of the entire population and can be generalized to different racial and ethnic groups. Without this, there lies a risk of bias and limited applicability of research outcomes to specific populations. The following research will demonstrate how an integrated proteomic and network approach can be utilized to comprehensively define the proteomic profiles of AD within individuals of African American or Caucasian background. We hypothesize that the biological pathways most relevant or impacted by changes in Tau burden will demonstrate varying expression levels in the CSF of African Americans and Caucasians with AD. Through a combination of unbiased system level and target approaches, I have been able to (i) directly characterize CSF within a large cohort of individuals (ii) gain insight into race-specific molecular signatures of AD and (iii) validate novel race-dependent signatures for AD pathogenesis using an independent mass spectrometry technique. In total, there is a significant gap in our knowledge of the racial differences underlying molecular mechanisms of AD biology. A better understanding of these mechanisms is critical to move the field towards clearer biological methodologies for the early detection of AD across a diverse population of people.

CHAPTER 2:

MATERIALS AND METHODS

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A full list of tables can be accessed at the following link:

https://molecularneurodegeneration.biomedcentral.com/articles/10.1186/s13024-023-00638-z

2.1 CSF samples

All cerebrospinal fluid (CSF) samples were collected as part of ongoing studies at Emory's Goizueta Alzheimer's Disease Research Center (ADRC) including participants in the ADRC Clinical Core, the Emory Healthy Brain Study, and the ADRC-affiliated Emory Cognitive Neurology Clinic. All participants provided informed consent under protocols approved by Emory University's Institutional Review Board. Clinical diagnosis of AD as well as classification as cognitively normal controls was based on review of clinical history, neurological examination, detailed cognitive testing, and diagnostic studies including Magnetic Resonance Imaging and CSF AD biomarker testing. Diagnosis of AD was made by subspecialty certified Cognitive and Behavioral Neurologists with additional input from Neuropsychologists based on current NIA-AA criteria (247; 248). A consensus clinical diagnosis of controls was made without consideration of CSF biomarkers by a panel of experts at the Emory Goizueta ADRC. Criteria for assigning diagnosis are provided in the National Alzheimer Coordination Center coding guidelines, form D1, based on clinician judgment. The basis for this judgment includes many metrics, with controls considered to have normal cognition and normal behavior after reviewing all testing including Montreal Cognitive Assessment (MoCA), Clinical Dementia Rating (CDR) score, and detailed neuropsychological testing. Hence, control participants may have MoCA scores that are lower than traditional cut points for impairment on this screening test. CSF was collected by lumbar puncture and banked according to best practice guidelines outlined by the National Institute on Aging for Alzheimer's Disease Centers (https://alz.washington.edu/BiospecimenTaskForce.html), and identical pre-analytic steps were followed in all groups. Measurements of Amyloid-beta$_{1\text{-}42}$ (Aβ_{42}), total Tau (tTau), and phosphorylated Tau$_{181}$ (pTau$_{181}$) was performed on the Roche Diagnostics Elecsys platform (249-251) using recommended protocols. In total, the cohort was comprised of 105 healthy controls and 98 AD. The racial background of each case was based upon self-identification. Of the 203 cases, 100 identified as Caucasian or White while 103 identified as African American or Black. Case metadata can be found in **Appendix Table 6.1**.

2.2 Protein digestion of CSF

In order to sample the CSF proteome in an unbiased manner and given that we have previously shown that immunodepletion resulted in only a marginal improvement in proteomic coverage, the CSF samples were not immunodepleted prior to digestion (252; 253). First, 70 μL of CSF was transferred to 1 mL deep well plates for digestion with lysyl endopeptidase (LysC) and trypsin. The samples were then reduced and alkylated with 1.4 μL of 0.5 M tris-2(-carboxyethyl)-phosphine (ThermoFisher) and 7 μL of 0.4 M chloroacetamide in a 90°C water bath for 10 min. The water bath was then turned off and allowed to cool to room temperature along with samples for 5 minutes. Following this, water bath sonication was performed for 5 min. The samples were then allowed to cool again to room temperature for 5 mins prior to adding urea. Then 78 μL of 8M urea buffer (8M urea, 10mM Tris, 100mM NaH_2PO_4, pH 8.5) and 3.5 μg of LysC (Wako), was added to each sample, resulting in a final urea concentration of 4M. The samples were then mixed well, gently spun down, and incubated overnight at 25°C for digestion with LysC. The following day, samples were diluted to 1M urea with a blend of 468 μL of 50 mM ammonium bicarbonate (254) and 7 μg of trypsin (ThermoFisher). The samples were subsequently incubated overnight at 25°C for digestion with trypsin. The next day, the digested peptides were acidified to a final concentration of 1% formic acid and 0.1% trifluoroacetic acid. This was immediately followed by desalting on 30 mg HLB columns (Waters) and then eluted with 1 mL of 50% acetonitrile (ACN) as previously described (228). To normalize protein quantification across batches, 100 μl was taken from all CSF samples and then combined to generate a pooled sample. This pooled sample was then divided into global internal standards (GIS) (255). All individual samples and the pooled standards were then dried using a speed vacuum (Labconco).

2.3 Tandem mass tag labeling of CSF peptides

All CSF samples were balanced for diagnosis, race, age, and sex (in that order) across 16 batches using ARTS (automated randomization of multiple traits for study design) (256). Using a 16-plex Tandem Mass Tag (TMT) pro kit (Thermo Fisher Scientific, A44520, Lot number: VH3111511), 13 channels of each batch were allocated to a CSF sample (127N, 127C, 128N, 128C, 129N, 129C, 130N, 130C, 131N, 131C, 132N, 132C, 133N). The remaining 3 channels were occupied with a GIS pool (126), a standard biomarker negative pool (133C), and a standard biomarker positive pool sample (134N). Information regarding the origination of these pooled samples were reported previously (257). **Appendix Table 6.2** provides the sample to batch arrangement. In preparation for labeling, each CSF peptide digest was resuspended in 75 μl of 100 mM triethylammonium bicarbonate buffer meanwhile 5 mg of TMT reagent was dissolved into 200 μl of ACN. Once both were in suspension, 15 μl of TMT reagent solution was subsequently added to the resuspended CSF peptide digest. After 1 hour, the reaction was quenched with 4 μl of 5% hydroxylamine (Thermo Fisher Scientific, 90115) for 15 min. Then, the peptide solutions were combined according to the batch arrangement. Finally, each TMT batch was desalted with 60 mg HLB columns (Waters) and dried via speed vacuum (Labconco).

2.4 High-pH peptide fractionation

Dried samples were re-suspended in high pH loading buffer (0.07% vol/vol NH_4OH, 0.045% vol/vol FA, 2% vol/vol ACN) and loaded onto a Water's BEH column (2.1 mm x 150 mm with 1.7 µm particles). A Vanquish UPLC system (ThermoFisher Scientific) was used to carry out the fractionation. Solvent A consisted of 0.0175% (vol/vol) NH_4OH, 0.01125% (vol/vol) FA, and 2% (vol/vol) ACN; solvent B consisted of 0.0175% (vol/vol) NH_4OH, 0.01125% (vol/vol) FA, and 90% (vol/vol) ACN. The sample elution was performed over a 25 min gradient with a flow rate of 0.6 mL/min with a gradient from 0 to 50% solvent B. A total of 96 individual equal volume fractions were collected across the gradient. Fractions were concatenated to 48 fractions and dried to completeness using vacuum centrifugation.

2.5 Mass spectrometry analysis and data acquisition

All samples (~1µg for each fraction) were loaded and eluted by an Easy-nLC 1200 (Thermofisher Scientific) with an in-house packed 15 cm, 150 µm i.d. capillary column with 1.7 µm CSH (Water's) over a 35 min gradient. Mass spectrometry (MS) was performed with a high-field asymmetric waveform ion mobility spectrometry (FAIMS) Pro front-end equipped Orbitrap Lumos (Thermo) in positive ion mode using data-dependent acquisition with 1 second top speed cycles for each FAIMS compensative voltage. Each cycle consisted of one full MS scan followed by as many MS/MS events that could fit within the given 1 second cycle time limit. MS scans were collected at a resolution of 120,000 (410-1600 m/z range, 4x10^5 AGC, 50 ms maximum ion injection time, FAIMS compensative voltage of -45 and -65). Only precursors with charge states between 2+ and 5+ were selected for MS/MS. All higher energy collision-induced dissociation MS/MS spectra were acquired at a resolution of 50,000 (0.7 m/z isolation width, 35% collision energy, 1×10^5 AGC target, 86 ms maximum ion time). Dynamic exclusion was set to exclude previously sequenced peaks for 30 seconds within a 10-ppm isolation window.

2.6 Database search and protein quantification

All raw files were analyzed using the Proteome Discoverer Suite (v.2.4.1.15, Thermo Fisher Scientific). MS/MS spectra were searched against the UniProtKB human proteome database (downloaded in 2019 with 20338 total sequences). The Sequest HT search engine was used to search the RAW files, with search parameters specified as follows: fully tryptic specificity, maximum of two missed cleavages, minimum peptide length of six, fixed modifications for TMTPro tags on lysine residues and peptide N-termini (+304. 304.2071 Da) and carbamidomethylation of cysteine residues (+57.02146 Da), variable modifications for oxidation of methionine residues (+15.99492 Da), serine, threonine and tyrosine phosphorylation (+79.966 Da) and deamidation of asparagine and glutamine (+0.984 Da), precursor mass tolerance of 10 ppm and a fragment mass tolerance of 0.05 Da. Percolator was used to filter peptide spectral matches and peptides to a false discovery rate (FDR) <1%. Following spectral assignment, peptides were assembled into proteins and were further filtered based on the combined probabilities of their constituent peptides to a final FDR of 1%. Peptides were grouped into proteins following strict parsimony principles. A complete TMT reporter ion abundance-based table output of assembled protein abundances without adjustments can be found at https://www.synapse.org/EmoryDiversityCSF.

2.7 Adjustment for batch and other sources of variance

Only proteins quantified in ≥ 50% of samples were included in subsequent analysis (n = 1,840 proteins). Of the 1,840 proteins, 1,327 proteins were quantified across all samples. As previously reported (236; 237; 252; 258), batch correction was performed using a Tunable Approach for Median Polish of Ratio, (https://github.com/edammer/TAMPOR), an iterative median polish algorithm for removing technical variance across batch. Multidimensional scaling plots (MDS) were used to visualize batch contributions to variation before and after batch correction. Noticeably, prior to batch correction, cases within the same batch clustered together and batches ran consecutively tended to cluster more closely together (**Figure 2.1A)**. Following batch correction using a median polish algorithm, the cases were no longer clustering by batch (**Figure 2.1B**)**.** The data was then subjected to outlier removal using a robust principal component analysis method, *PcaGrid* (259). A scree plot graphing the eigenvalue against the principal component (PC) number was utilized to determine the number of PCs to include in the parameters (**Figure 2.1C**). Briefly, the parameters used for outlier detection were as follows: the desired number of principal components = 7, method = mean absolute deviation, and criterion for computing cutoff values = 0.99 (**Figure 2.1D**). This resulted in the detection and removal of 15 outliers, resulting in a final n=189 samples. Bootstrap regression was then performed to remove for covariates such as age at collection and sex. Variance partition analysis was performed to confirm appropriate regression of these traits (**Figure 2.1E & F**). Since the *variancePartition* package does not allow missing values, proteins with missing quantifications were temporarily imputed using the *impute.knn* function of the impute R package. The final cleaned dataset after regression and log2 transformation can be found at https://molecularneurodegeneration.biomedcentral.com/articles/10.1186/s13024-023-00638-z.

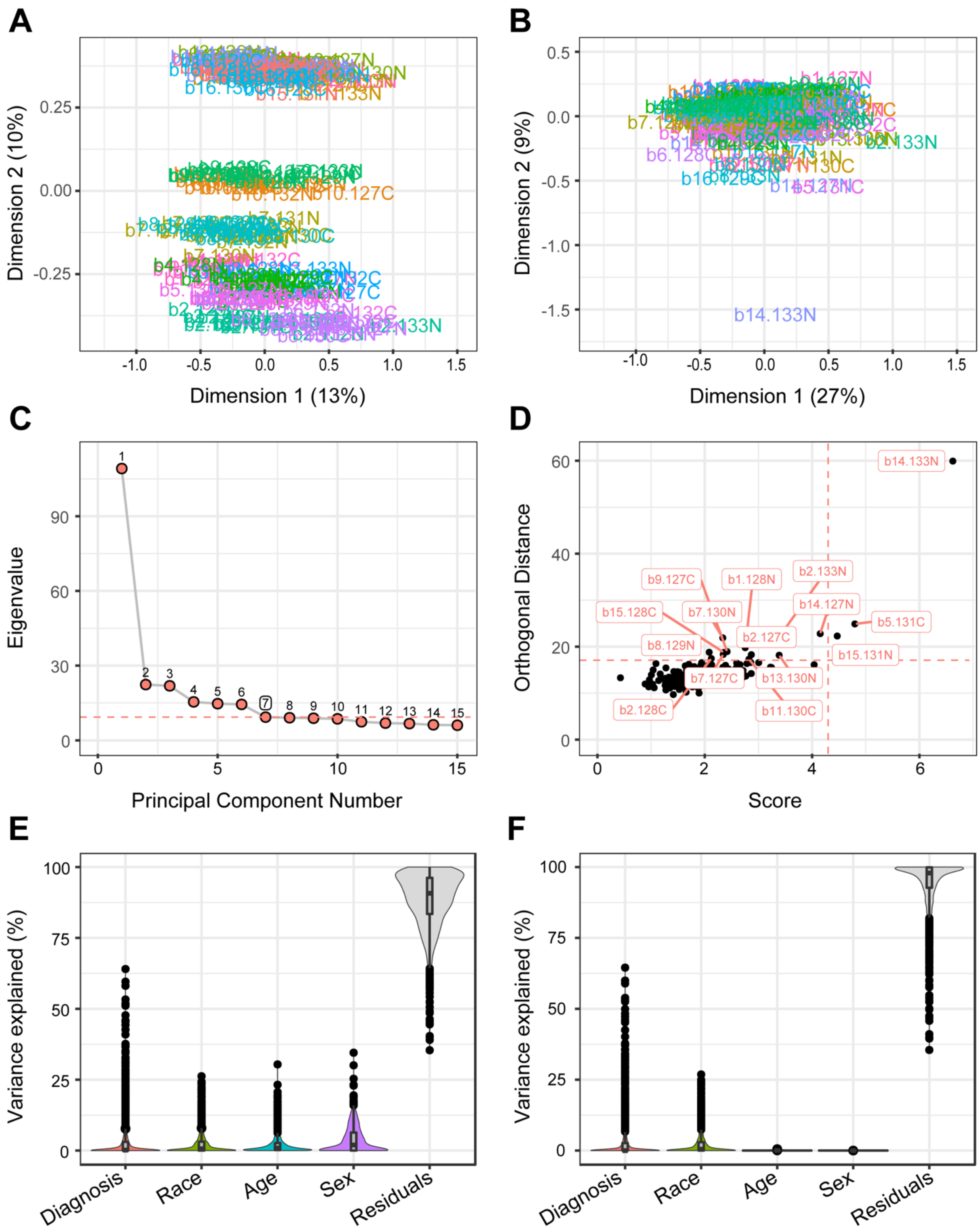

A
Dimension 1 (13%)
Dimension 2 (10%)
B
b14.133N
Dimension 1 (27%)
Dimension 2 (9%)
C
Principal Component Number
Eigenvalue
D
b14.133N
b9.127C
b1.128N
b2.133N
b15.128C
b7.130N
b14.127N
b5.131C
b2.127C
b8.129N
b15.131N
b7.127C
b13.130N
b2.128C
b11.130C
Score
Orthogonal Distance
E
Variance explained (%)
Diagnosis
Race
Age
Sex
Residuals
F
Variance explained (%)
Diagnosis
Race
Age
Sex
Residuals

Figure 2.1: Batch correction, outlier removal and bootstrap regression. Multidimensional scaling plots (MDS) were used to illustrate batch contributions to variance before and after batch correction. In MDS plots, the distance a case is from one another is reflective of how similar or dissimilar a case is from the other. (**A**) Prior to batch correction, the samples clustered by batch (**B**) After batch correction, the samples no longer cluster by batch. (**C**) After batch correction, a principal component (PC)-based outlier removal method was utilized to detect outliers. By graphing the eigenvalue of each component against the PC number, the elbow or bend in the graph, which in this case was 7, was indicative of the ideal number of components to include within the parameters. (**D**) With a criterion for computing cutoff values set to 0.99, the cutoffs for the detection of outliers for the orthogonal distance and score were 16.79257 and 4.654674 respectively. This resulted in the detection of 15 outliers (b1.128N, b11.130C, b13.130N, b14.127N, b14.133N, b15.128C, b15.131N, b2.127C, b2.128C, b2.133N, b5.131C, b7.127C, b7.130N, b8.129N, b9.127C). B14.133N was such an extreme outlier because it was an empty channel. (**E**) After outlier removal, the matrix underwent bootstrap regression to remove variations in the dataset that were due to age and sex. Variance partition plots were employed to illustrate the percent contribution of diagnosis, race, age, and sex to the variance of each protein. (**F**) Following bootstrap regression, variations explained by age and sex were removed.

2.8 Differential expression analysis

One-way ANOVA followed by Tukey's post hoc adjustment for multiple comparisons was performed on four groups (Control-Caucasian, Control-African American, AD-Caucasian, and AD-African American) to identify differentially expressed proteins across diagnosis and within each race. Differentially expressed proteins for comparisons of interest (i.e., Control-Caucasian vs AD-Caucasian and Control-African American vs AD-African American) were then presented as volcano plots using the *ggplot2* package in R v4.1.2. A list of all comparisons computed with corresponding adjusted p-values is provided in **Appendix Table 6.3**.

2.9 Weighted Gene Co-expression Network Analysis

As previously published (235-237; 252), the blockwiseModules function from the WGCNA package in R was utilized to derive the weighted protein co-expression network. Briefly, the following parameters were used: soft threshold power beta = 3, deepSplit = 4, minimum module size = 5, merge cut height = 0.07, and a signed network with partitioning about medoids. Using the *pairwise.wilcox.test* R function with Bonferroni correction, a pairwise Wilcox test was performed to calculate pairwise comparisons between each group with corrections for multiple testing.

2.10 Gene ontology and cell type enrichment analysis

To characterize co-expressed protein module biology, gene ontology (GO) annotations were retrieved from the Bader Lab's monthly updated .GMT formatted ontology lists downloaded July 5, 2022 (260). A Fisher's exact test for enrichment was performed into each module's protein membership using an in-house script (https://github.com/edammer/GOparallel). For cell type enrichment analysis, an in-house marker list was used as previously described (236). A Fisher's exact test was performed for each module member list using the merged human cell type marker list to determine cell type enrichment. For brain-CSF module overlap a one-sided Fisher's exact test to compare significance of module membership.

2.11 Selected reaction monitoring

Selected reaction monitoring (SRM) assays were performed on 195 of the 203 cases to determine whether a separate targeted proteomic approach could replicate proteomic changes seen in TMT discovery proteomics. An attempt was made to include all 203 samples from discovery TMT for SRM analysis however, samples 52524, 51520, 52055, 48617, 48615, 48769, 49537, 45707 had low remaining sample volume and had to be removed. Sample 62762 was later removed due to irregularities in retention time shifts. Peptide selection, sample preparation, peptide quantification, and data acquisition for the SRM assay was performed as previously described (257). Briefly, peptides were selected based on their robust detection and significant differential expression in previous CSF discovery proteomic projects for synthesis as heavy standards (237; 252). More specifically, the peptide had to i) have one or more spectral matches, ii) be significantly differentially abundant when evaluating AD versus Control cases, iii) and map to proteins that appeared in brain-based biological panels outlined in Higginbotham et al 2020 (252) that differed in AD. Ultimately, this led to approximately 200 peptides being nominated for synthesis by Thermo Fisher Scientific (Thermo PEPotec SRM Peptide Libraries; Grade 2; crude as synthesized). In addition to the 195 clinical samples from before, two pools of CSF were utilized as AD biomarker positive and AD-biomarker negative quality controls (QC) standards (257). After the CSF samples were blinded and randomized, each sample (50 µL) was reduced, alkylated, denatured and then subjected to digestion as described (257). After digestion, the heavy labeled standards, 15uL per 50 µL of CSF, were added to each digested sample. Each digested sample then underwent acidified, desalted and dried under vacuum. Following this, the peptide targets were quantified using TSQ Altis Triple Quadrupole mass spectrometer as previously described (257). The resulting raw files were uploaded to Skyline-daily software (version 21.2.1.455) for peak integration and quantification by peptide ratios. Peptides were filtered by first assessing retention time reproducibility, then by matching light and heavy transitions, and finally by determining the peptide ratio precision using the coefficient of variation (CV) as described by

Watson et al 2023 (257). The technical CV of each peptide was calculated based on the peptide area ratio for the AD-positive and AD-negative QC pools (**Appendix Table 6.4**). CSF peptide targets with CVs ≤ 20% in at least one pooled standard were determined as peptides with high precision and were kept for subsequent analysis, leaving a total of 85 peptides that mapped to 58 proteins. The total area ratio for each targeted peptide in each sample made up the final data matrix. Due to the nature of SRM in that each peptide is explicitly targeted, a value for each peptide is always assigned in each sample (down to and including the limit of detection) as previously published by our group (257). As a result, the total area ratio for each targeted peptide in each sample made up the final data matrix, leaving a matrix with no blank cells or missing values. In preparation for analysis, this matrix of peptide ratios was $\log_2$ transformed and true zero values were replaced after $\log_2$-transformation with the minimum value for that peptide minus 1. Bootstrap regression was then used to regress for age and sex (**Appendix Table 6.5**). Bicor was then utilized to calculate the correlation between SRM peptides and TMT-MS protein measurements (**Appendix Table 6.6**). In cases where multiple peptides mapped to one protein, the most correlated peptide was kept for further analysis (**Appendix Table 6.7**). One-way ANOVA analysis with Tukey adjustment was then utilized once again to examine pairwise interactions **(Appendix Table 6.8**) and receiver operating characteristic (ROC) curve analysis was performed as previously described (257) (**Appendix Table 6.9**).

CHAPTER 3: RESULTS

These Results were originally published in *Molecular Neurodegeneration*:

Modeste, E.S., Ping, L., Watson, C.M. *et al.* Quantitative proteomics of cerebrospinal fluid from African Americans and Caucasians reveals shared and divergent changes in Alzheimer's disease. *Mol Neurodegeneration* **18**, 48 (2023). https://doi.org/10.1186/s13024-023-00638-z

A full list of tables can be accessed at the following link:

https://molecularneurodegeneration.biomedcentral.com/articles/10.1186/s13024-023-00638-z

3.1 CSF cohort characteristics

This study was comprised of two balanced groups of cerebrospinal fluid (CSF) samples from African American and Caucasian individuals, matched for age and sex with roughly equal numbers of control and Alzheimer disease (AD) cases (**Table 3.1**). This included 53 Caucasian controls, 52 African American controls, 47 AD Caucasians, and 51 AD African Americans. The majority were female and on average the controls (64.5 years) were slightly younger than AD (68 years). Notably, there were no statistical differences between the ages of the African Americans and the Caucasians within diagnosis (control: p=0.8848, AD: p=0.9998). As expected, AD cases had lower Montreal Cognitive Assessment (MoCA) scores than controls, but there were no statistically significant differences between MoCA scores across race within controls and AD (control: p=0.7559, AD:p=0.2055). The AD cases also had lower Amyloid-beta ($A\beta_{42}$) levels and elevated total Tau (tTau) and phosphorylated Tau_{181} ($pTau_{181}$) levels. Notably, $A\beta_{42}$ levels were significantly lower in African American Controls compared to Caucasian controls (p = 0.0021) but not different between African American AD and Caucasian AD. This may indicate potentially early changes in brain amyloid deposition or processing of APP in African American controls versus Caucasian controls. Notably, the distribution of APOE4 carriers did not differ significantly by race in the control population and so does not account for the pattern observed (**Appendix Table 6.1)**. Conversely, tTau and $pTau_{181}$ levels were significantly lower in African Americans with AD (tTau:p<0.0001, $pTau_{181}$:p<0.0001) but not different between African American and Caucasian controls. Data on comorbid conditions, including whether or not the person had hypertension, diabetes, dyslipidemia, or cerebrovascular disease, is presented for all cases in **Appendix Table 6.1**. Notably, none of the comorbid conditions was statistically overrepresented in either racial group.

Sample Size	CT Cau	CT AA	p – value [a]	AD Cau	AD AA	p – value [a]
	53	52		47	51	
Characteristics						
Sex	33 F, 20 M	33 F, 19 M	-	29 F, 18 M	32 F, 19 M	-
Age [b]	65 ± 8	64 ± 8	0.8848	68 ± 9	68 ± 9	0.9998
MoCA [c]	26 ± 2	25 ± 3	0.7559	16 ± 6	14 ± 6	0.2055
*$A\beta_{42}$ [d]	1195.2 ± 262.0	1021.4 ± 301.1	**0.0021**	558.2 ± 169.9	483.4 ± 151.8	0.4026
tTau [d]	186.2 ± 61.6	158.5 ± 56.5	0.6573	423.7 ± 189.2	301.5 ± 134.8	**< 0.0001**
$pTau_{181}$ [d]	16.6 ± 5.6	14.1 ± 4.9	0.7787	43.3 ± 20.8	30.1 ± 14.1	**< 0.0001**
$tTau/A\beta_{42}$ [d]	0.14 ± 0.03	0.14 ± 0.03	0.9994	0.78 ± 0.31	0.66 ± 0.30	0.0850

[a] p-values were calculated using one-way ANOVA with Tukey correction, bold indicates $p < 0.05$.

[b] Age in years. Values given as average ± standard deviation

[c] Most recent Montreal Cognitive Assessment (MoCA) score. Values given as average ± standard deviation

[d] $A\beta_{42}$, tTau, $pTau_{181}$, and $tTau/A\beta_{42}$ in pg/mL. Values given as average ± standard deviation

*$A\beta_{42}$ levels that reached saturation (1700 pg / mL) were excluded from calculations and analysis

Abbreviations: CT, Control; AD, Alzheimer's disease; Cau, Caucasian / White; AA, African American / Black

Table 3.1. Cohort Characteristics

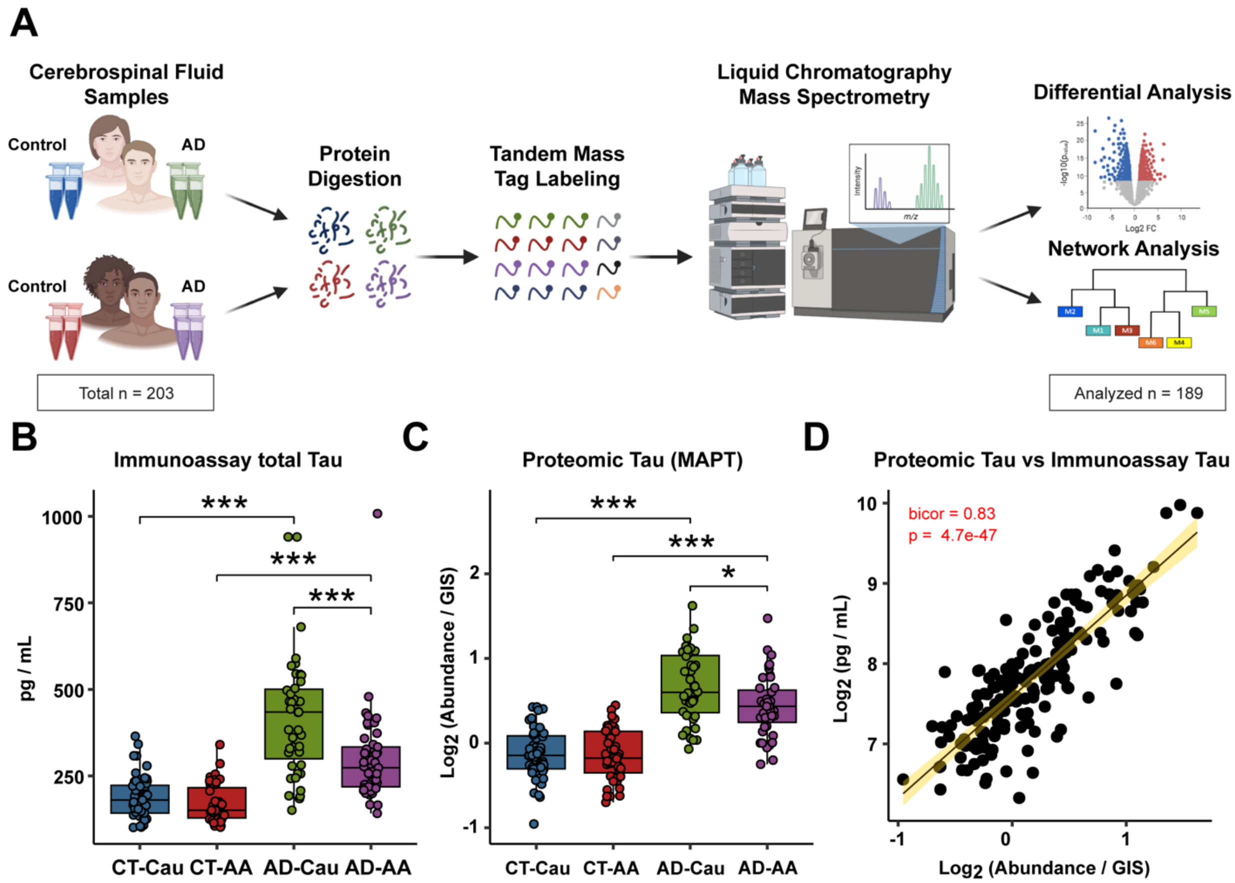
3.2: Discovery tandem mass spectrometry analysis of cerebrospinal fluid from African Americans and Caucasians reveals unique and shared changes in Alzheimer's disease

3.2.1 Correlation analysis uncovers a strong relationship between mass spectrometry and immunoassay measurements of Tau

Following enzymatic digestion, tandem mass tag (TMT) labeling, and off-line fractionation, all samples were subjected to liquid chromatography mass spectrometry (MS) (**Figure 3.1A**). In total, TMT-MS proteomic analysis identified 34,330 peptides mapping to 2,941 protein groups across the 203 samples (16 total batches). To account for missing protein measurements across batches, we included only those proteins quantified in at least 50% of samples following outlier removal as previously described (227; 235-237; 252), resulting in the final quantification of 1,840 proteins. Protein abundance was adjusted for batch and age and sex were regressed. As expected, Tau levels were significantly elevated in both African Americans and Caucasians with AD across both platforms compared to controls (**Figure 3.1B and C**). Consistent with the immunoassay measurements, TMT-MS Tau levels also showed significantly lower levels in African Americans with AD compared to Caucasians with AD (**Figure 3.1C**). Notably, protein levels of Tau (MAPT) by TMT-MS correlated strongly to independently measured tTau levels via immunoassay ($r=0.83$, $p = 4.7e-47$) (**Figure 3.1D**). Thus, in this study, both platform measures of CSF Tau support a reduction of total Tau levels in African Americans with AD, consistent with previous findings (261; 262).

3.2.2 Differential expression analysis of African American and Caucasian CSF proteome reveals unique and shared changes in AD

Differential expression analysis was performed to identify changes in the CSF proteome by race in AD (**Appendix Table 6.3**). Consistent with previous proteomic analyses of AD CSF (237; 252; 263-265), there was a significant increase in Tau (MAPT), 14-3-3 proteins, (YWHAZ, YWHAG, and YWHAE), SMOC1, neurofilaments (NEFM and NEFL) and proteins involved in



Part A of this figure was created with BioRender.com

Figure 3.1: Schematic of experimental workflow and correlation between proteomic Tau and total Tau immunoassay measurements. (**A**) Schematic of experimental workflow for quantification of cerebrospinal fluid proteome. (**B**) Total Tau levels as measured by Roche Elecsys Platform between control (CT) and AD cases and stratified by self-identified race: Caucasian (Cau) or African American (AA) (**C**) Tau levels measured by mass spectrometry. One-way ANOVA with Tukey post-hoc correction determined pairwise relationships (**D**) Correlation of Tau levels by TMT-MS (x-axis) to paired immunoassay total Tau levels (y-axis). Biweight midcorrelation coefficient (bicor) with associated p-value is shown. Only 179 cases were included in the linear regression analysis because of sample outlier removal and missing values in the TMT-MS.

glucose metabolism in both African Americans and Caucasians with AD compared with race matched controls (**Figure 3.2A & B**). However, Caucasians with AD exhibited a bias towards proteins that were increased in AD, where the number of differentially expressed proteins (DEPs) was nearly double (n=183 proteins) the number of decreased DEPs in AD (n=74 proteins) (**Figure 3.2A**). In contrast, in African Americans, the number of increased and decreased DEPs was more balanced (151 increased proteins vs. 162 decreased proteins) (**Figure 3.2B**). A Venn diagram illustrates the overlap of DEPs from African Americans and Caucasians with AD (**Figure 3.2C**), with the majority of proteins (n=168 proteins) differentially expressed in both races. Furthermore, a correlation analysis of both shared and unique DEPs showed overall high agreement in direction of change (bicor=0.887, p=2.47e-136, **Figure 3.2D)**. However, there were some exceptions including SLIT1 and VSTM2A, which were significantly increased in Caucasians, but decreased in African Americans with AD. Both proteins are predominantly enriched in neuronal-cell types (266; 267). Thus, despite the differences in the number of significant DEPs in African Americans compared to Caucasians with AD, the direction of change with disease remains largely similar across both races.

3.2.3 Network analysis of the CSF proteome reveals modules related to pathways and brain cell-types

Co-expression network analysis of the AD brain proteome organizes proteins into modules related to molecular pathways, organelles, and cell types impacted by AD pathology (227; 235-237). Moreover, integration of the human AD brain and CSF proteome revealed that approximately 70% of the CSF proteome overlapped with the brain proteome (252). While proteomic networks in AD brain have been examined, network changes in the AD CSF proteome, including those associated with race and AD biomarkers are less well understood. Thus, we applied Weighted Gene Co-expression Network Analysis (WGCNA) to define trends in protein co-expression across 1840 CSF proteins in all individuals. These parameters identified 14 modules

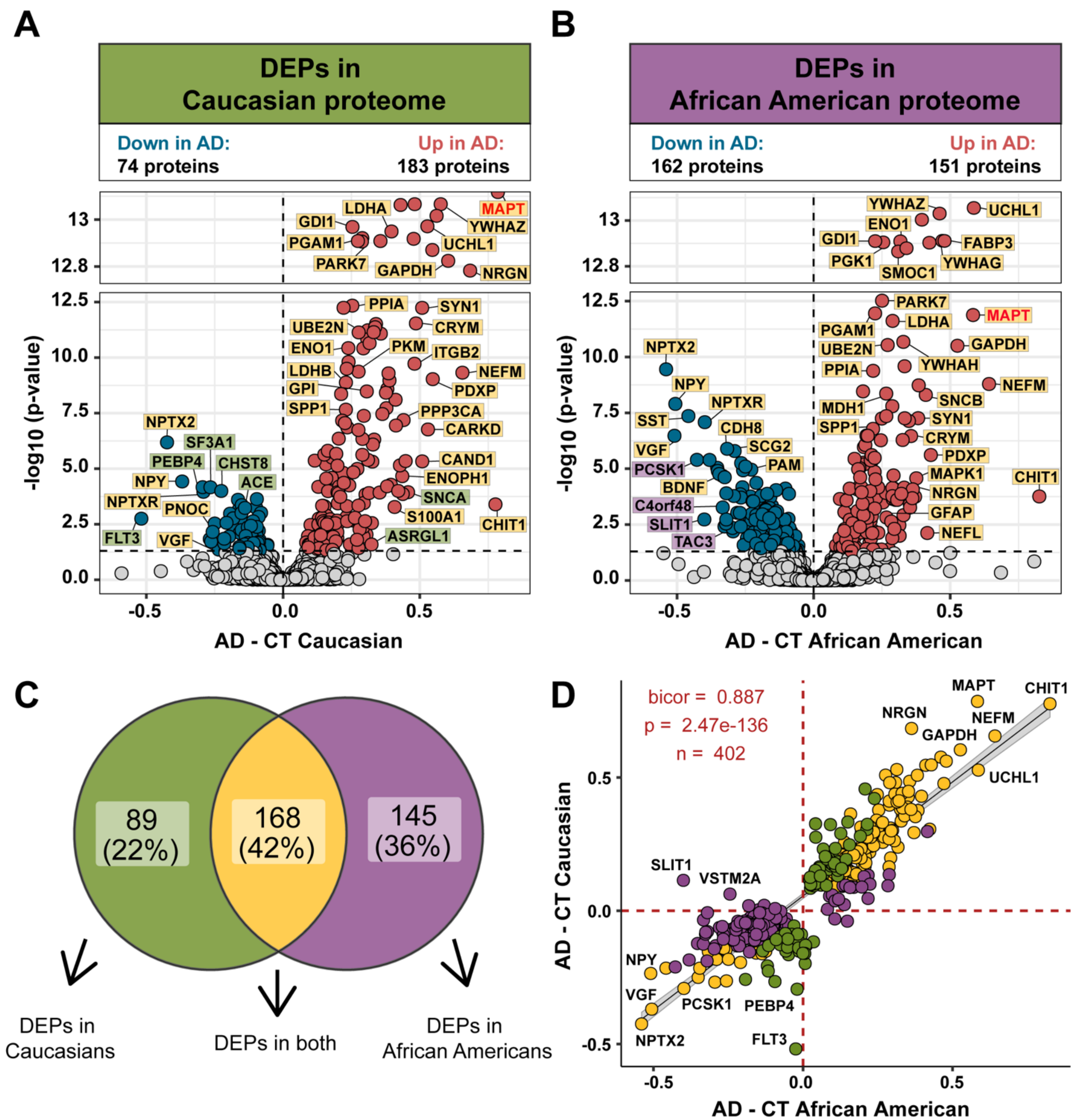
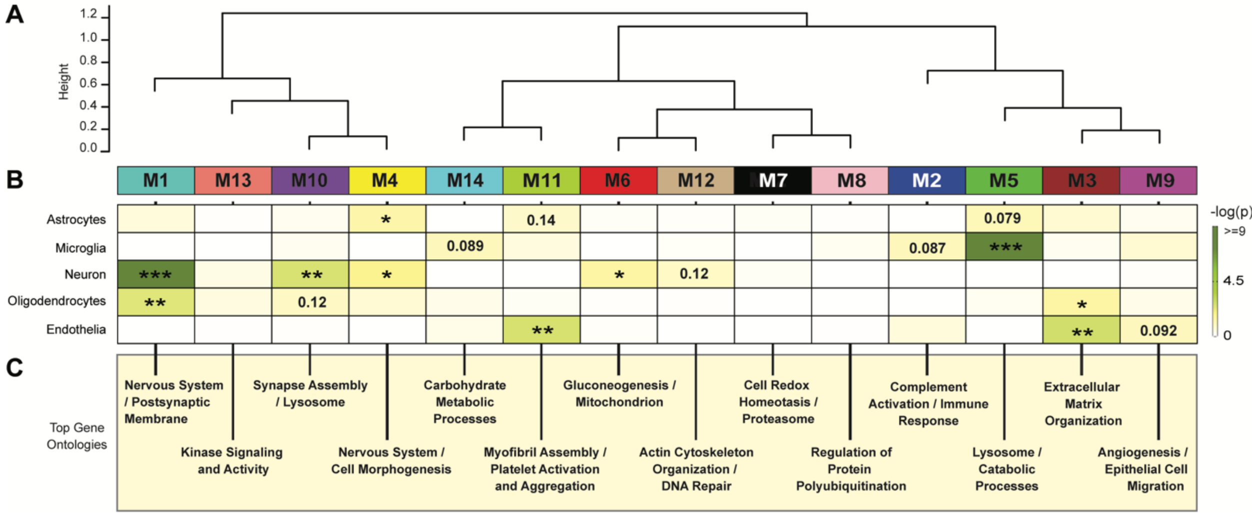

A
DEPs in Caucasian proteome
Down in AD: 74 proteins
Up in AD: 183 proteins
B
DEPs in African American proteome
Down in AD: 162 proteins
Up in AD: 151 proteins
-log10 (p-value)
AD - CT Caucasian
AD - CT African American
C
89 (22%)
168 (42%)
145 (36%)
DEPs in Caucasians
DEPs in both
DEPs in African Americans
D
bicor = 0.887
p = 2.47e-136
n = 402
AD - CT Caucasian
AD - CT African American

Figure 3.2. Differential expression of Caucasian and African American CSF proteomes in AD. Volcano plot displaying the log_2 fold change (FC) (x-axis) against one-way ANOVA with Tukey correction derived -log10 p-value (y-axis) for all proteins (n=1840) comparing AD versus Controls for Caucasians (**A**) and African Americans (**B**). Cutoffs were determined by significant differential expression ($p<0.05$) between control (CT) and AD cases. Proteins with significantly decreased levels in AD are shown in blue while proteins with significantly increased levels in disease were indicated in red. Select proteins were denoted and labeled by whether they were differentially expressed in both proteomes (yellow), in only the Caucasian proteome (green), or in only the African American proteome (purple). (**C**) Venn diagram illustrating the number of differentially expressed proteins (DEPs) that were uniquely changed in one proteome (green or purple) or changed in both proteomes (yellow) (**D**) The correlation between the fold change of all DEPs (n=402) across the African American proteome (x-axis) and the Caucasian proteome (y-axis) were strongly correlated (bicor=0.887, p=2.47e-136), regardless of whether the DEP was significant in one (green or purple) or both proteomes (yellow).

(M), ranked by size, ranging from the largest M1, with 370 proteins to the smallest, M14, with 16 proteins (**Figure 3.3A**). Many of these modules were significantly enriched for brain-specific cell types (**Figure 3.3B**) as well as established brain gene ontologies (GO), cellular functions and/or organelles (**Figure 3.3C**). The three largest modules were associated with categories of “Postsynaptic Membrane” (M1), “Complement Activation” (M2), and “Extracellular Matrix” (M3) whereas M5 represented “Lysosome / Catabolism” and M6 “Gluconeogenesis”. Other modules included those with GO terms linked to “Cell Morphogenesis” (M4), “Cell Redox / Proteasome” (M7), “Protein Polyubiquitination” (M8), “Angiogenesis / Cell Migration” (M9), “Synapse Assembly” (M10), Myofibril Assembly (M11), “Actin Cytoskeleton” (M12), “Kinase Signaling / Activity” (M13), and “Carbohydrate Metabolism” (M14).

Protein-based network analysis in AD brain tissue has shown that the cellular composition represents a major source of biological variance and that many of the network modules are enriched in proteins that are expressed by specific brain cell types (236; 237). To determine if a similar relationship exists with protein-based networks in CSF, we evaluated the overlap of proteins in each module with brain cell-type specific makers (**Figure 3.3B**), generated previously from cultured or acute isolated neurons, oligodendrocytes, astrocytes, endothelial, and microglia from brain (266; 267). The largest module, M1, was enriched with neuron/synaptic proteins (i.e., NPTX1, NPTXR, SCG2, VGF, NRN1, and L1CAM) and to a lesser degree oligodendrocyte proteins (i.e., IGSF8, VCAN, APLP1). Neuronal loss or the active secretion of neuronal proteins into the extracellular space could account for the presence of neuronal proteins in the CSF. The M4 module was also enriched for neuronal protein markers including RTN4R1, LINGO2, OLFM1, and PLXNA2, associated with “Nervous Systems and Cell Morphogenesis”. Modules most enriched with microglia markers were M2 (i.e., C2, C3, C1RL, C1QA, C1QB, C1QC, LCP1, etc.) and M5 (i.e., HEXB, CTSZ, HEXA, CTSA, CTSB) consistent with a role in complement activation and lysosome function, respectively. Finally, endothelial markers were mainly overrepresented in



A
Height
1.2
1.0
0.8
0.6
0.4
0.2
0.0
B
M1
M13
M10
M4
M14
M11
M6
M12
M7
M8
M2
M5
M3
M9
Astrocytes
Microglia
Neuron
Oligodendrocytes
Endothelia
0.14
0.079
0.089
0.087
0.12
0.12
0.092
-log(p)
>=9
4.5
0
C
Top Gene Ontologies
Nervous System / Postsynaptic Membrane
Kinase Signaling and Activity
Synapse Assembly / Lysosome
Nervous System / Cell Morphogenesis
Carbohydrate Metabolic Processes
Myofibril Assembly / Platelet Activation and Aggregation
Gluconeogenesis / Mitochondrion
Actin Cytoskeleton Organization / DNA Repair
Cell Redox Homeotasis / Proteasome
Regulation of Protein Polyubiquitination
Complement Activation / Immune Response
Lysosome / Catabolic Processes
Extracellular Matrix Organization
Angiogenesis / Epithelial Cell Migration

Figure 3.3: Network analysis classifies the CSF proteome into modules associated with specific brain cell-types and gene ontologies. (**A**) Weighted Gene Co-expression Network Analysis cluster dendrogram groups proteins (n=1840) into 14 distinct protein modules (M1-M14). (**B**) Cell-type enrichment was assessed by cross referencing module proteins by matching gene symbols using a one-tailed Fisher's exact test against a list of proteins determined to be enriched in neurons, oligodendrocytes, astrocytes, microglia and endothelia. The degree of cell-type enrichment increases from yellow to dark green with asterisks denoting the following statistical significance (*p≤0.05; **p≤0.01; ***p≤.001). Top gene ontology (GO) terms were selected from significant GO annotations.

modules M3 (i.e., NID2, ECM2, NID1, LTBP4, LAMA5, LAMC1), M9 (IGFBP7, F5, SDCBP, BGN) and M11 (FLNA, ANXA5, S100A11, MYL6) consistent with roles in extracellular matrix, angiogenesis and myofibril assembly, respectively. Thus, as seen in the network analysis of bulk proteome from human brain (236; 237), certain modules of co-expressed proteins in CSF were enriched with markers of specific brain cell-types. To further support this observation, we assessed the protein overlap between modules in CSF and modules from a recent large-scale consensus TMT-MS proteomic network of bulk human AD brain tissue (236). (**Figure 3.4**). Except for M9, M10 and M14, which had minimal overlap with the brain, all other modules (79% total) in the CSF network significantly overlapped with at least one of the 44 brain modules (B-M1 to B-M44). For example, there is overlap with CSF proteins in M1 “Postsynaptic Membrane” with several neuronal modules in the consensus brain network (B-M1, B-M4, B-M5, B-M10, and B-M15). In addition, M2 “Complement Activation” in CSF overlaps with modules in human brain associated with complement and immune response (B-M26 and B-M40), whereas M3 “Extracellular Matrix” strongly overlap with B-M27 in brain enriched with endothelial cell markers (**Figure 3.4**). Collectively, this supports that the co-expression in protein levels is, in part, shared between CSF and brain tissue, which could reflect changes in activation or phenotypes of specific brain cell types.

3.2.4 CSF protein modules correlate to race and clinicopathological phenotypes of AD

We assessed module correlation to race, cognitive scores (MoCA), and the hallmark AD biomarkers $A\beta_{42}$, tTau, and $pTau_{181}$. The protein network resulted in three main groups/clusters based on module relatedness (**Figure 3.5A).** The first cluster (Group 1) was comprised of four modules (M2 “Complement Activation”, M5 “Lysosome / Catabolism”, M3 “Extracellular Matrix”, and M9 “Angiogenesis / Cell Migration”. Of these modules, M3 and M9 exhibited baseline racial differences in abundance levels (**Figure 3.5B**)**.** Notably, the eigenprotein, which corresponds to

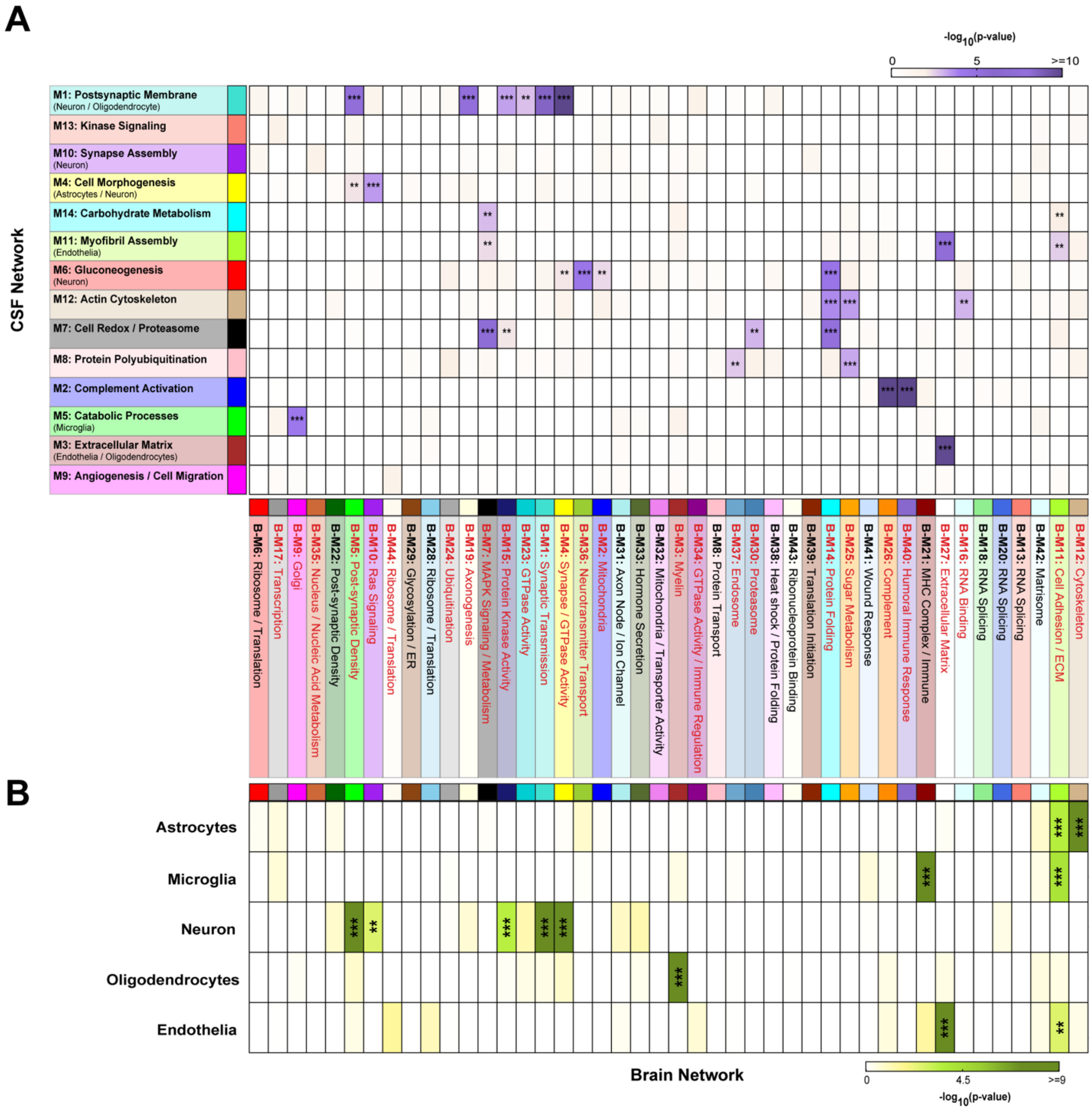

A
-log10(p-value)
0
5
>=10
CSF Network
M1: Postsynaptic Membrane (Neuron / Oligodendrocyte)
M13: Kinase Signaling
M10: Synapse Assembly (Neuron)
M4: Cell Morphogenesis (Astrocytes / Neuron)
M14: Carbohydrate Metabolism
M11: Myofibril Assembly (Endothelia)
M6: Gluconeogenesis (Neuron)
M12: Actin Cytoskeleton
M7: Cell Redox / Proteasome
M8: Protein Polyubiquitination
M2: Complement Activation
M5: Catabolic Processes (Microglia)
M3: Extracellular Matrix (Endothelia / Oligodendrocytes)
M9: Angiogenesis / Cell Migration
B-M6: Ribosome / Translation
B-M17: Transcription
B-M9: Golgi
B-M35: Nucleus / Nucleic Acid Metabolism
B-M22: Post-synaptic Density
B-M5: Post-synaptic Density
B-M10: Ras Signaling
B-M44: Ribosome / Translation
B-M29: Glycosylation / ER
B-M28: Ribosome / Translation
B-M24: Ubiquitination
B-M19: Axonogenesis
B-M7: MAPK Signaling / Metabolism
B-M15: Protein Kinase Activity
B-M23: GTPase Activity
B-M1: Synaptic Transmission
B-M4: Synapse / GTPase Activity
B-M36: Neurotransmitter Transport
B-M2: Mitochondria
B-M31: Axon Node / Ion Channel
B-M33: Hormone Secretion
B-M32: Mitochondria / Transporter Activity
B-M3: Myelin
B-M34: GTPase Activity / Immune Regulation
B-M8: Protein Transport
B-M37: Endosome
B-M30: Proteasome
B-M38: Heat shock / Protein Folding
B-M43: Ribonucleoprotein Binding
B-M39: Translation Initiation
B-M14: Protein Folding
B-M25: Sugar Metabolism
B-M41: Wound Response
B-M26: Complement
B-M40: Humoral Immune Response
B-M21: MHC Complex / Immune
B-M27: Extracellular Matrix
B-M16: RNA Binding
B-M18: RNA Splicing
B-M20: RNA Splicing
B-M13: RNA Splicing
B-M42: Matrisome
B-M11: Cell Adhesion / ECM
B-M12: Cytoskeleton
B
Astrocytes
Microglia
Neuron
Oligodendrocytes
Endothelia
Brain Network
0
4.5
>=9
-log10(p-value)

Figure 3.4: Protein overlap between modules in CSF network and modules in a human AD brain network. (**A**) Protein module enrichment across the CSF and brain was assessed by matching gene symbols of proteins in each module from the CSF network against gene symbols for protein in each module from a human AD consensus brain network using a one-tailed Fisher's exact test The degree of enrichment increases from pink to light purple to dark purple with asterisks denoting the following statistical significance (**$p \leq 0.01$ and ***$p \leq .001$). (**B**) Similar to CSF, cell-type enrichment was assessed by cross referencing brain module proteins against a list of proteins determined to be enriched in neurons, oligodendrocytes, astrocytes, and microglia using a one-tailed Fisher's exact test. The degree of cell-type enrichment increases from yellow to green-yellow to dark green with asterisks denoting the following statistical significance (**$< p \leq 0.01$ and ***$p \leq .001$).

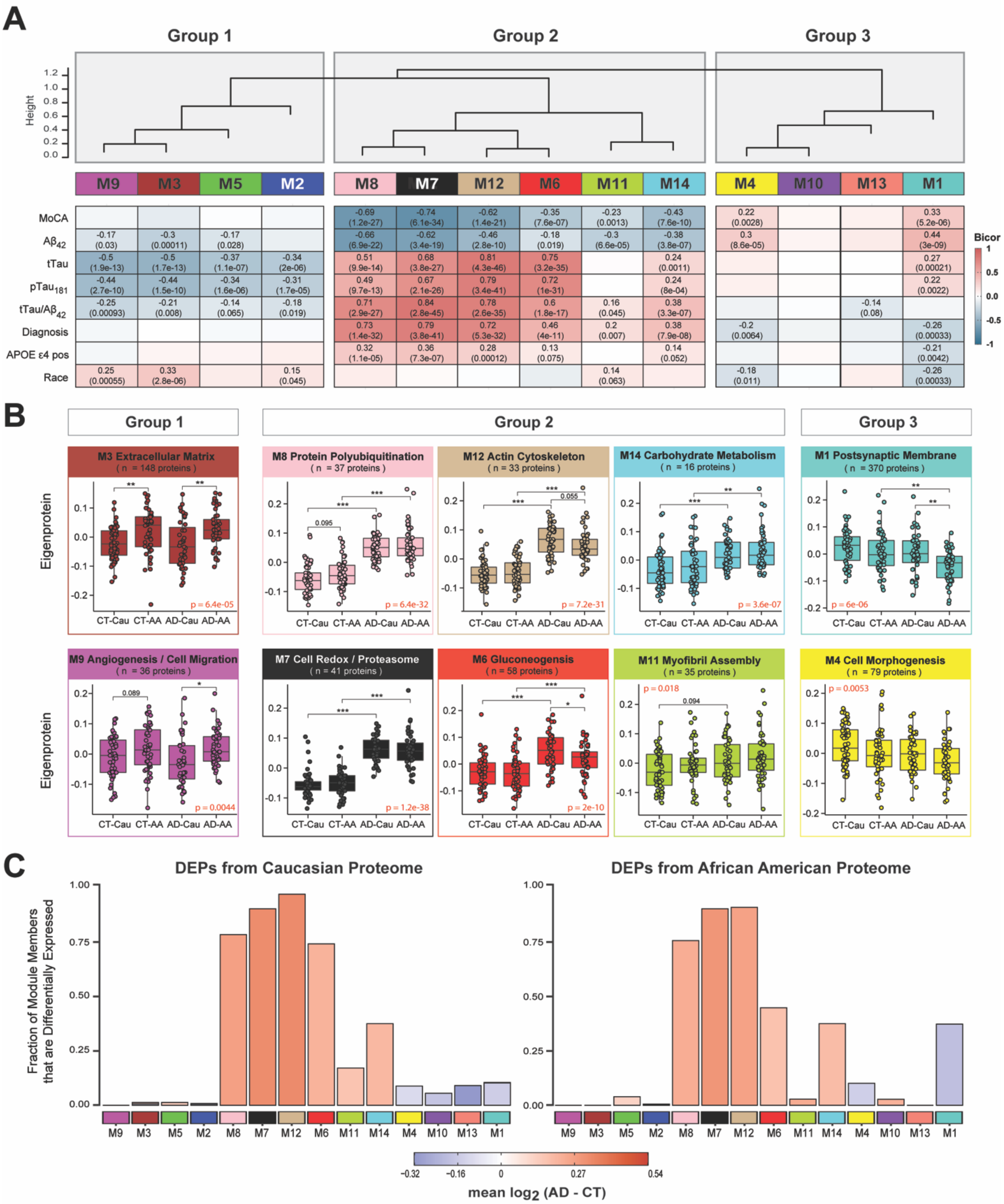

A
Group 1
Group 2
Group 3
Height
M9 M3 M5 M2 M8 M7 M12 M6 M11 M14 M4 M10 M13 M1
MoCA
Aβ42
tTau
pTau181
tTau/Aβ42
Diagnosis
APOE ε4 pos
Race
Bicor
B
M3 Extracellular Matrix
M8 Protein Polyubiquitination
M12 Actin Cytoskeleton
M14 Carbohydrate Metabolism
M1 Postsynaptic Membrane
M9 Angiogenesis / Cell Migration
M7 Cell Redox / Proteasome
M6 Gluconeogenesis
M11 Myofibril Assembly
M4 Cell Morphogenesis
Eigenprotein
CT-Cau CT-AA AD-Cau AD-AA
C
DEPs from Caucasian Proteome
DEPs from African American Proteome
Fraction of Module Members that are Differentially Expressed
mean log2 (AD - CT)

Figure 3.5: CSF protein modules correlate to race and clinicopathological phenotypes of AD. (**A**) Modules were clustered based on relatedness defined by correlation of protein co-expression eigenproteins (indicated by position in color bar). There were three main clusters in the network: Groups 1, 2 and 3. Biweight midcorrelation (bicor) analysis of module eigenprotein levels with diagnostic measures of AD, including MoCA score, immunoassay Amyloid-beta$_{1\text{-}42}$ (Aβ_{42}), total Tau (tTau), phosphorylated Tau$_{181}$ (pTau$_{181}$), ratio measures of tTau/Aβ_{42}, diagnosis, whether the sample has *APOE* ε4 allele or not, and race. The strength of positive (red) and negative correlations are shown by a heatmap with annotated bicor correlations and associated p-values. (**B**) Eigenprotein values distributed by race and diagnosis of representative modules for each cluster. (**C**) Differential protein abundance AD samples compared to controls, by module with Caucasian proteome on the left and African Americans on the right. The height of the bars represents the fraction of module member proteins that DEPs compared to controls. The bars are color coded by heatmap for average $\log_2$ difference in abundance, where red represents an increase in abundance in AD, and blue represents a decrease in abundance in AD.

the first principal component of a given module and serves as a summary expression profile for all proteins within a module, were increased for these two modules in African Americans compared to Caucasians. Of note, these modules were enriched with endothelial cell markers (**Figure 3.3B**) which suggests that genetic ancestry and/or environmental differences influence expression or secretion of these cell-type markers. Similarly, M2 and M5, both of demonstrated enrichment for microglial markers, trended towards higher levels in both African American controls and AD (**Figure 3.3B and 3.6**), suggesting an accompanying immune response to the vascular alterations seen in modules M3 and M9.

The second cluster of modules (Group 2) was comprised of six modules (M8, M7, M12, M6, M11, and M14) that were all increased in AD (**Figure 3.5A**). These AD modules also demonstrated significant negative correlations to MoCA scores and, conversely, significant positive correlations to tTau/Aβ_{42} ratio. With the exception of M11, these modules also exhibited positive correlations to APOE ε4 risk (**Figure 3.5A**). Interestingly, a hub protein of the M12 “Actin Cytoskeleton” module was Tau (MAPT). Consistent with CSF levels observed for Tau by immunoassay and TMT-MS (**Figure 3.1B and C**), the M12 eigenprotein had lower levels in African Americans, compared to Caucasians with AD, albeit not significant (p=0.055) (**Figure 3.5B**). Notably, M6 “Gluconeogenesis” was significantly lower in African Americans compared to Caucasians with AD, highlighting another module of CSF proteins that differed by race in AD (**Figure 3.5A and B**). This also indicated that the increased glycolytic signature of AD previously reported in CSF (237; 252) is higher in Caucasians with AD. Consistently, a greater proportion of increased DEPs in Caucasians with AD mapped to M6 compared to African Americans with AD (**Figure 3.5C)**. In contrast, M7 “Cell Redox / Proteasome” and M8 “Protein Polyubiquitination”, had the strongest correlations to tTau/Aβ_{42} ratio and cognition (**Figure 3.5B**), and both demonstrated strong, equivalent elevations in African Americans and Caucasians with AD (**Figure 3.5B**). This is consistent with an equivalent fraction of increased DEPs mapping to these modules in African American and Caucasians with AD (**Figure 3.5C)**. Therefore, proteins in these

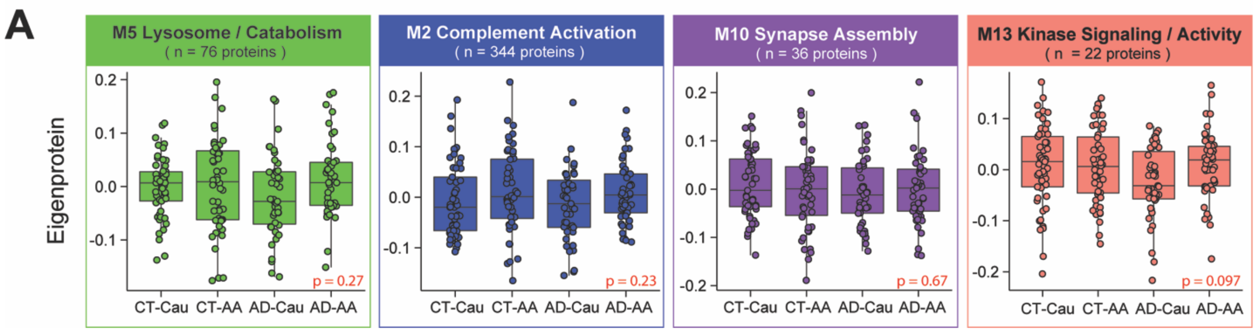

A
M5 Lysosome / Catabolism
(n = 76 proteins)
M2 Complement Activation
(n = 344 proteins)
M10 Synapse Assembly
(n = 36 proteins)
M13 Kinase Signaling / Activity
(n = 22 proteins)
Eigenprotein
p = 0.27
p = 0.23
p = 0.67
p = 0.097
CT-Cau CT-AA AD-Cau AD-AA

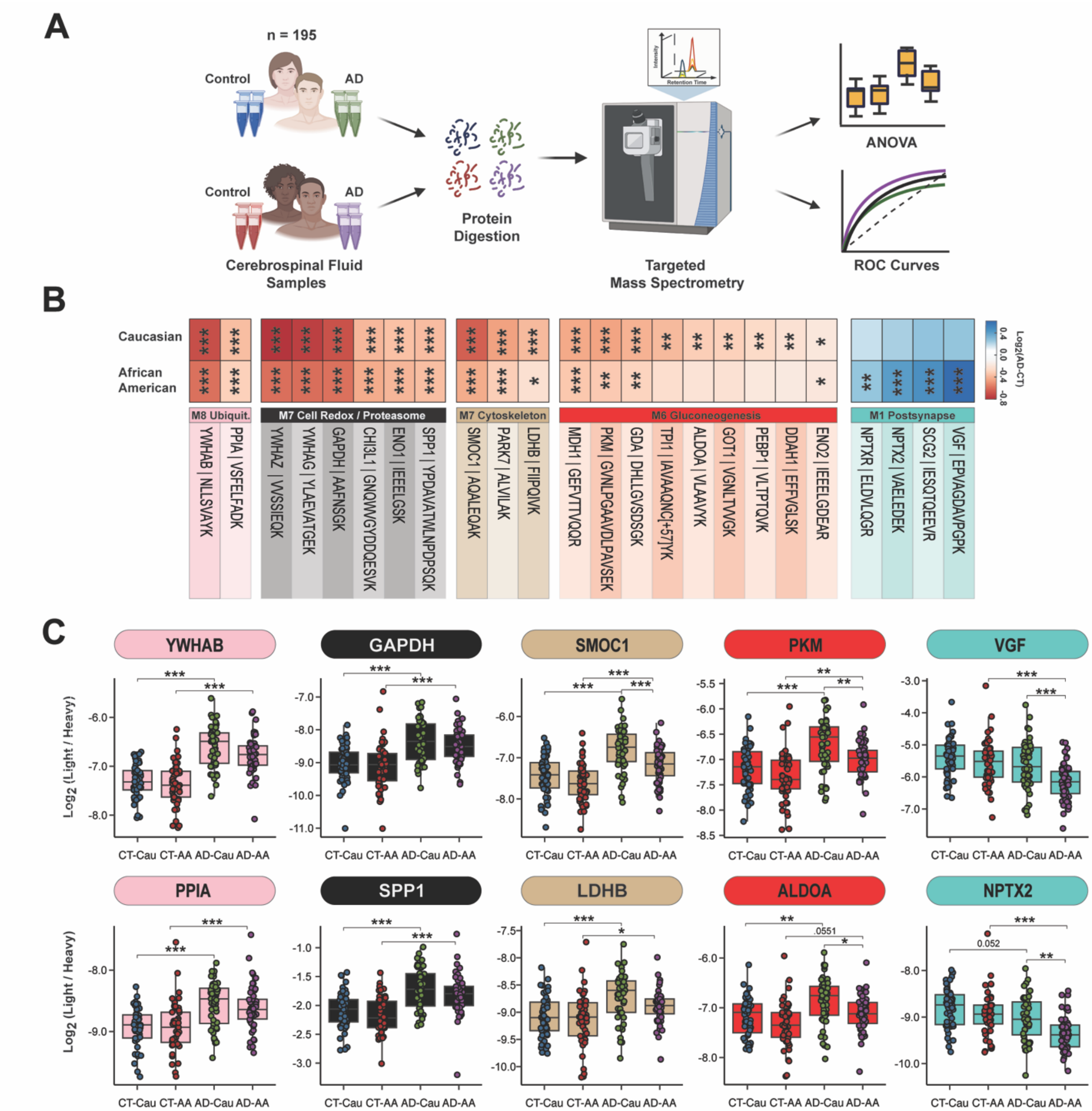
Figure 3.6: Additional CSF network protein modules. (**A**) Eigenprotein levels were distributed by race and diagnosis for remaining modules not shown in main Figure 4. This includes M5, M2, M10, and M13.

modules including 14-3-3 family members (YWHAZ, YWAHB, YWHAG, YWHAE) likely represent the best class of CSF AD biomarkers that are not influenced by race. M14 “Carbohydrate Metabolism” and M11 “Myofibril Assembly” were both elevated in both African Americans and Caucasians with AD (**Figure 3.5A and B**), yet to a lesser degree than M7 and M8.

The final group of modules (Group 3) contained two modules, M1 “Postsynaptic Membrane” and M4 “Cell Morphogenesis”, that showed strong correlations to both race and AD diagnosis (**Figure 3.5A**). Both modules were i) decreased in AD compared to controls and ii) and were lower in African Americans compared to Caucasians. In addition, both M1 and M4 were enriched with neuronal markers and positively associated with cognitive MoCA scores (**Figure 3.5A**). Markedly, pairwise statistical analysis of eigenprotein levels for M1 across diagnosis and race revealed significantly lower levels in African Americans with AD (**Figure 3.5B**). To this end, most of the decreased DEPs in African Americans with AD mapped to M1 and to a lesser degree M4, whereas decreased DEPs in Caucasians with AD were equally distributed to M1, M4, M13 and M10 (**Figure 3.5C**). Notably, M10 and M13 within Group 3 did not show any differences with AD or race and did not significantly correlate with traits explored in this study (**Figure 3.5 and Figure 3.6**). Overall, network analysis effectively organizes the CSF proteome into protein modules that are strongly linked to hallmark AD biomarkers ($A\beta_{42}$, tTau and $pTau_{181}$) and cognition, which in some cases were also influenced by race.

3.3 Selected reaction monitoring validates protein alterations across Alzheimer's disease and race

To further validate these network findings, we used a targeted mass spectrometry method, selected reaction monitoring (SRM), with heavy labeled internal standards to measure CSF proteins across 195 of the 203 cases included in the discovery TMT-MS assays (**Figure 3.7A**). The proteins and corresponding targeted peptides were previously selected based on their robust detection and significant differential expression in previous CSF discovery proteomic datasets



Part A of this figure was created with BioRender.com

Figure 3.7 Validation of shared and divergent CSF protein levels across AD and race. (**A**) Schematic of experimental workflow for SRM analysis of cerebrospinal fluid proteome (**B**) Heatmap of peptides that were significantly differentially expressed between Control and AD Caucasians or African Americans. Stars are indicative of the level of significant difference (*$p \leq 0.05$; **$p \leq 0.01$; ***$p \leq 0.001$) seen for each peptide between AD and Control within each race. Meanwhile the colors are indicative of the $\log_2$ fold change (FC) of each peptide from Control and AD for each race where blue is indicative of the degree of decrease and shade of red is indicative of the degree of increase. (**C**) Log_2 abundance of peptides that mapped to modules of interest distributed by race and diagnosis. Pairwise significance was calculated using one-way ANOVA with Tukey adjustment.

(252; 268). We used pooled CSF samples of control, and AD cases as quality controls replicates (n=29 samples total) to assess technical reproducibility. Of the peptides targeted, 85 (mapping to 58 proteins) had a coefficient of variation of <20% in both the control and AD pools with no missing values (**Appendix Tables 6.4**). Following adjustments of co-variates (i.e., age and sex), peptide levels were highly correlated with protein levels measured by TMT-MS from the same samples (**Appendix Table 6.6**). If a protein was measured by more than one peptide the most correlated peptide to the TMT-MS protein level was selected for further analysis. The final peptide list can be found in **Appendix Table 6.7**. ANOVA analyses determined pairwise significance between the four groups (i.e., Control-Caucasians vs Control-African Americans vs AD-Caucasians vs AD-African Americans, **Appendix Table 6.8**). **Figure 3.7B** highlights peptides (n=24) that reached significance and that mapped to proteins in CSF modules associated with race and/or AD. Consistent with the TMT-MS protein measurements, proteins measured by SRM within M7 (GAPDH and YWHAG) and M8 (YWAHB and PPIA) had strong elevations ($p < 0.001$) in abundance in AD in both races, whereas proteins in M12 (SMOC1, PARK7, and LDHB) had a greater magnitude of change in Caucasians than African Americans with AD (for a list of all M12 members, see Supplemental Table 6) . Similarly, a majority of the proteins measured by SRM in M6 (PKM, GDA, TPI1, GOT1, ALDOA and ENO2) were more increased in Caucasians than African Americans with AD (**Figure 3.7B and C**). Proteins in the synaptic M1 module (VGF, SCG2, NPTX2, and NPTXR) were significantly decreased in African Americans with AD compared to Caucasians (**Figure 3.7B and C**), again consistent with TMT-MS protein level abundance. Notably, African Americans with or without APOE ε4 allele in the AD group had reduced levels of these CSF peptide biomarkers compared to Caucasians indicating that race and not APOE status was driving the difference in abundance (**Figure 3.8A**). Furthermore, these differences across race remained consistent even after removing patients with one or more comorbid condition (i.e., hypertension, diabetes, dyslipidemia, or cerebrovascular disease; **Figure 3.8B**).

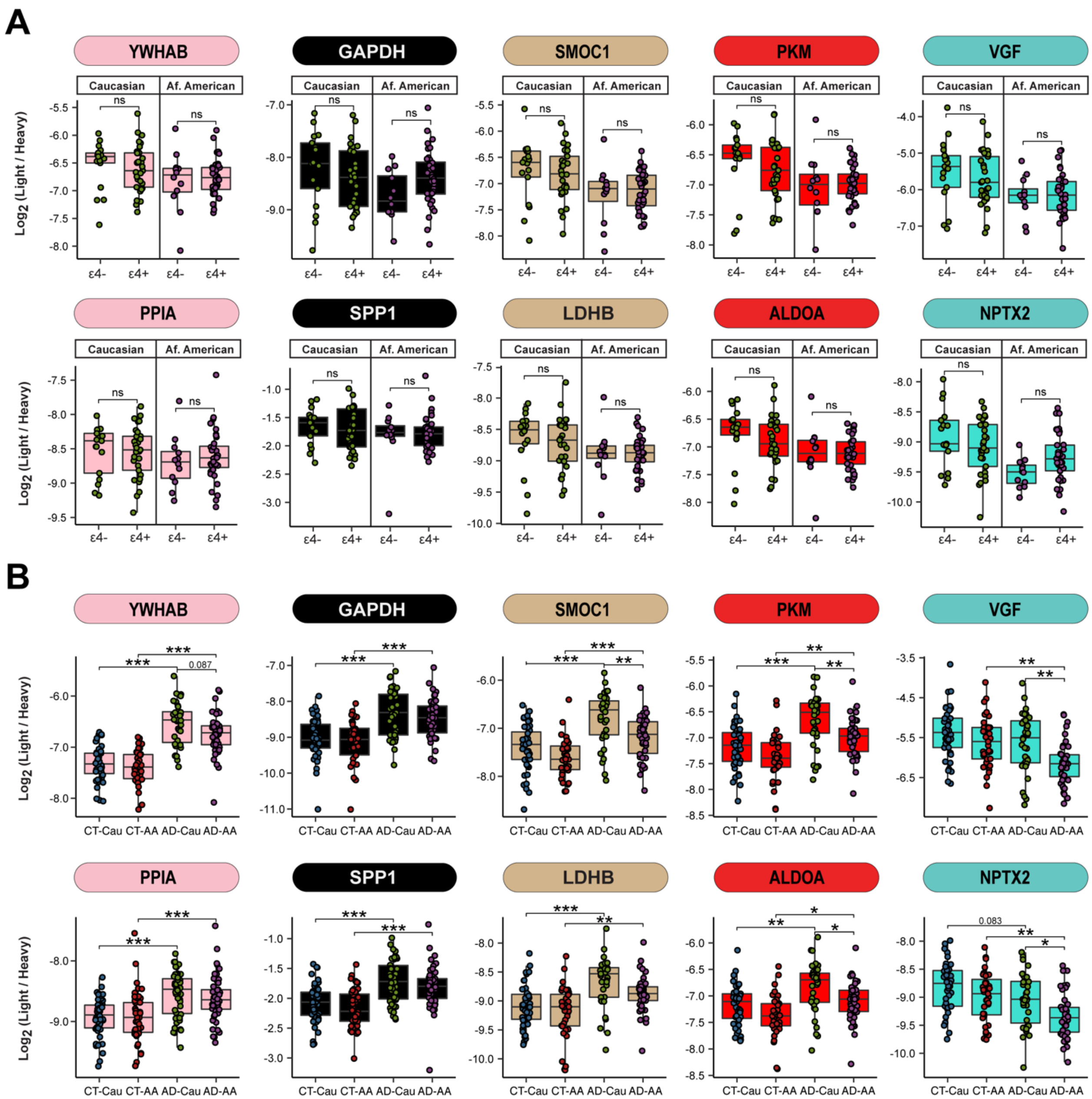

A
YWHAB
GAPDH
SMOC1
PKM
VGF
PPIA
SPP1
LDHB
ALDOA
NPTX2
Caucasian
Af. American
Log2 (Light / Heavy)
ε4-
ε4+
ns
B
YWHAB
GAPDH
SMOC1
PKM
VGF
PPIA
SPP1
LDHB
ALDOA
NPTX2
CT-Cau CT-AA AD-Cau AD-AA
0.087
0.083

Figure 3.8. Stratification of SRM CSF protein measurements by APOE genotype and comorbidity. (**A**) Within each race, protein levels for were not affected by APOE ε4 genotype for YWHAB, GAPDH, SMOC1, PKM, VGF, PPIA, SPP1, LDHB, ALDOA, and NPTX2. (B) Within each race, protein levels were not affected by patient co-morbidities (hypertension, diabetes, dyslipidemia, or cerebrovascular disease) for YWHAB, GAPDH, SMOC1, PKM, VGF, PPIA, SPP1, LDHB, ALDOA, and NPTX2.

Finally, a receiver operating characteristic (ROC) curve analysis was performed to assess the performance of each peptide biomarker in differentiating controls and AD by race (**Figure 3.9 and Appendix Table 6.9**). We generated an area under the curve (AUC) for AD in African American and Caucasian individuals for each protein biomarker (considered separately in each race). As expected, proteins mapping to M8 and M7 including 14-3-3 proteins (YWHAB, YWHAG and YWHAZ) were equally able to discriminate AD from control irrespective of racial background. Notably, despite having lower levels in African Americans with AD compared to Caucasians with AD, only a modest improvement in the AUC for SMOC1 was observed for classifying AD in Caucasians AUC=0.8255 (p=1.71e-08, CI=0.7421-0.9090) compared to African Americans AUC=0.7618 (p=4.12e-06, CI=0.6660-0.8576). Similar findings were observed for another M12 protein, LDHB, as well as M6 proteins PKM and ALDOA. However, the M1 protein VGF was only nominally significant at classifying AD in Caucasian AUC=0.6030 (p=0.0406, CI=0.4887-0.7173), yet highly significant in African Americans AUC=0.7593 (p=5.03e-06, CI=0.6634-0.8552). Similar results were observed for other synaptic M1 proteins, NPTX2 and SCG2, whereas NPTXR showed only a modest improvement in the AUC between African Americans compared to Caucasians with AD (**Figure 4.9 and Appendix Table 7.15**). Collectively this supports a hypothesis that African Americans with AD have lower levels of a subset of neuronal biomarkers compared to Caucasians with AD.

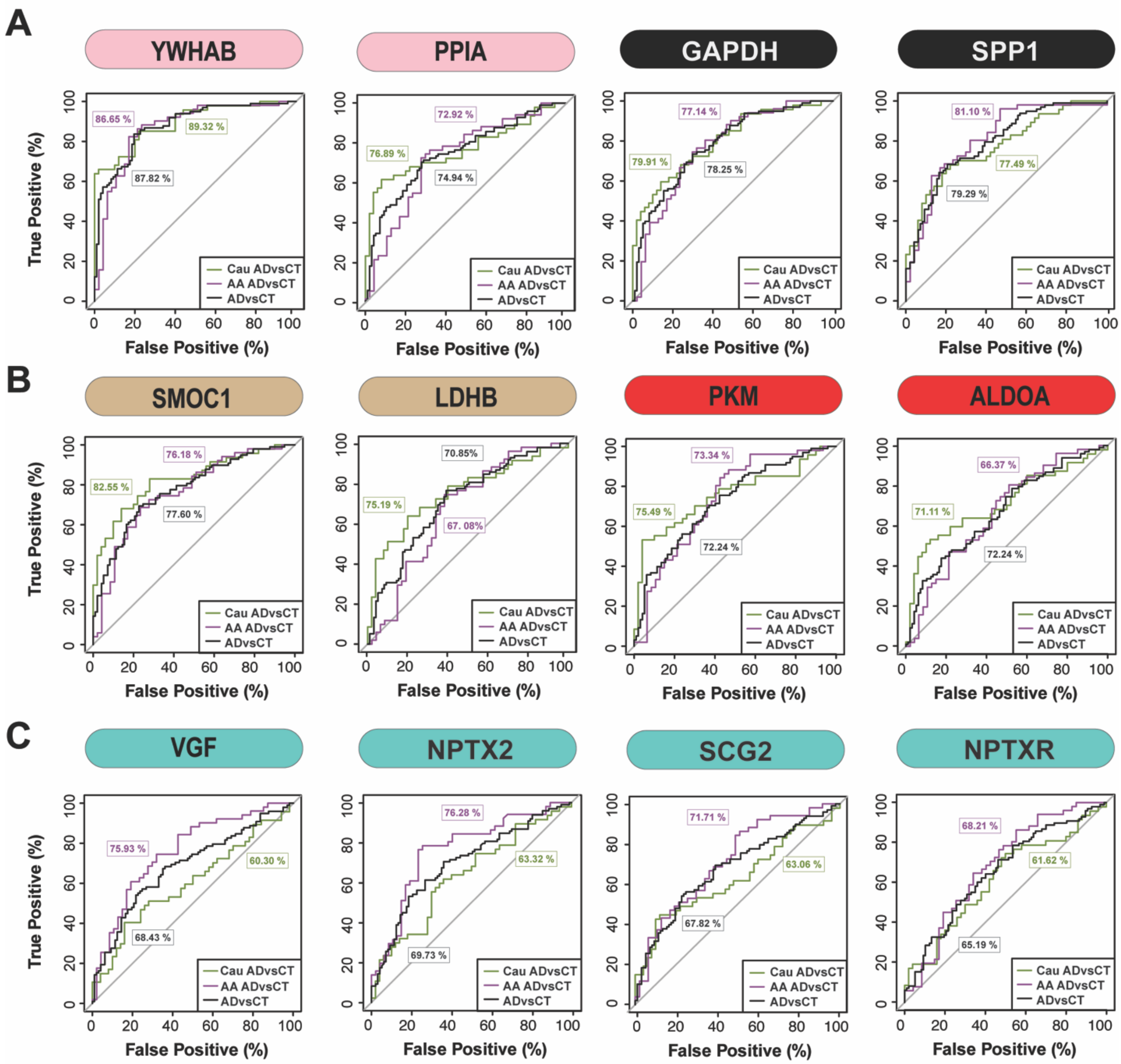

A
YWHAB
86.65 %
89.32 %
87.82 %
PPIA
72.92 %
76.89 %
74.94 %
GAPDH
77.14 %
79.91 %
78.25 %
SPP1
81.10 %
77.49 %
79.29 %
B
SMOC1
76.18 %
82.55 %
77.60 %
LDHB
70.85%
75.19 %
67. 08%
PKM
73.34 %
75.49 %
72.24 %
ALDOA
66.37 %
71.11 %
72.24 %
C
VGF
75.93 %
60.30 %
68.43 %
NPTX2
76.28 %
63.32 %
69.73 %
SCG2
71.71 %
63.06 %
67.82 %
NPTXR
68.21 %
61.62 %
65.19 %
Cau ADvsCT
AA ADvsCT
ADvsCT
True Positive (%)
False Positive (%)

Figure 3.9: ROC analysis evaluated CSF protein classification of AD by race. (**A**) YWHAB, PPIA, GAPDH, and SPP1 had similar performance in classifying Caucasians and African Americans with AD (**B**) SMOC1, PKM, LDHB and ALDOA showed modest improvement in the AUC for Caucasians with AD compared to African Americans with AD (**C**) VGF, SCG2, and NPTX2 were better classifiers for AD in African Americans compared to Caucasians, whereas NPTXR showed modest improvement in classification of AD in African Americans. All protein AUCs with p-values and confidence internals (CI) are provided in **Supplemental Table 15**.

CHAPTER 4: DISCUSSION

Segments of this discussion were originally published in *Molecular Neurodegeneration*:

Modeste, E.S., Ping, L., Watson, C.M. *et al.* Quantitative proteomics of cerebrospinal fluid from African Americans and Caucasians reveals shared and divergent changes in Alzheimer's disease. *Mol Neurodegeneration* **18**, 48 (2023). https://doi.org/10.1186/s13024-023-00638-z

Here we performed an unbiased quantitative analysis of the CSF proteome to identify protein biomarkers reflective of underlying AD brain physiology that are shared or unique across race. Using network analysis, we organized the CSF proteome into 14 modules of proteins with highly correlated levels in CSF. Notably, these modules were associated with cell-types and biological pathways in brain and largely overlapped with modules from a consensus human AD brain proteomic network (236). Consistent with previous findings (261; 262), we also show that Tau levels were lower in African Americans with AD compared to Caucasians in CSF. Notably, Tau mapped to a CSF module enriched with other related neuronal/cytoskeletal proteins with a magnitude of increase greater in Caucasians than in African Americans with AD. This indicated that an entire network of proteins, rather than a single protein, is changing differently with disease between these two racial groups. In contrast, CSF modules which included 14-3-3 proteins, were elevated equivalently in both African Americans and Caucasians with AD, suggesting similar changes in pathophysiology. Lastly, a module enriched with neuronal/synaptic proteins including VGF, SCG2, and NPTX2 was significantly lower in African Americans than Caucasians with AD. These findings were consistent when VGF, SCG2, and NPTX2 levels in CSF were measured using SRM analysis, which also showed significantly better classification of African Americans with AD compared to Caucasians. Together, our findings suggest that there are likely distinct mechanisms underlying the abundance and/or secretion of neuronal markers including Tau and VGF that differ by race. Collectively, these data underscore the need for further investigations into how AD biomarkers and underlying physiology vary across different racial backgrounds.

4.1 Protein co-expression between the brain and CSF reflects the intricate role of CSF in brain function and health.

In a previous study we performed unbiased TMT-MS on a small discovery cohort of control and AD CSF samples (n=40) and mapped these proteins onto a human AD brain co-expression network, revealing that approximately 70% (n=1936) of the CSF proteome (N=2,875) overlapped with the brain network (N=8817) (252). Additionally, it was found that 271 of the proteins that were significantly altered in the CSF were also differentially expressed in the brain (245). The increased sample size in this study afforded the opportunity to extend beyond this analysis by constructing an independent co-expression network on the CSF proteome and assessing its overlap with modules in a consensus brain network. This analysis revealed a strong overlap between CSF and brain modules, with 11 of the 14 CSF modules significantly overlapping with one or more brain modules, further supporting that protein co-expression in the brain is conserved in the CSF. These findings are not surprising considering the close relationship between CSF and brain. It is already known that substrates needed by the brain can be transported from the blood through the choroid plexus into the CSF, and then from the CSF into the extracellular space within the brain (269). Inversely, CSF aids in the removal of brain metabolism waste products, such as glycosylated proteins, excess neurotransmitters, and other unnecessary molecules, from the cerebral region (269). As a result of these exchanges, changes in brain chemistry can ultimately influence CSF composition, allowing the CSF to mirror neuropathological changes in the brain. Our studies suggests that the observed changes in CSF are mainly driven by cell-type alterations, as most CSF modules were enriched with either neuronal (M1, M4, M6, M10 and M12), glial (M2, M5, and M14), astrocyte (M4 and M5), oligodendrocyte (M1and M3), and endothelial-specific markers (M3, M9, and M11). The remaining modules that did not exhibit enrichment with cell type markers represented processes related to cellular signaling (M13) and degradation pathways (M7 and M8), including kinase signaling and activity, protein polyubiquitination, and cell redox/proteasome processes. This reflects another crucial function of the CSF, which is aiding in the clearance of waste products from the brain (269). In conclusion, network analysis of the CSF underscores the intricate relationship between CSF and brain biology in AD, revealing shared protein alterations and cell-type enrichments across both compartments. These findings support our understanding of CSF as a conduit for biomarkers of neuropathological changes in AD and provide insights into the underlying mechanisms driving early disease progression.

4.2 CSF network analysis indicated differences in endothelial markers across race, irrespective of disease, yet there is insufficient evidence to indicate that these differences stem from variations in endothelial damage.

In regards to the CSF network biology that differed by race, it's noteworthy that modules significantly enriched in endothelial proteins (M3 and M9) were elevated in African Americans across both control and AD individuals. M3 is primarily comprised of extracellular matrix (ECM) proteins, and ECM proteins make up the dynamic network of macromolecules providing structural support for cells and tissues. In the brain, ECM proteins are vital for maintaining the integrity of the blood-brain barrier (BBB) and neurovascular units (262-265). ECM proteins in the BBB are crucial for preserving brain tissue homeostasis by preventing the entry of unwanted cells and molecules and by removing metabolic waste. Additionally, ECM proteins within the neurovascular unit play a crucial role in regulating cerebral blood flow (CBF), ensuring sufficient blood supply to meet the demands of neurons (266; 267). Consequently, malfunctioning ECM proteins in the brain can result in compromised function of both the BBB and neurovascular units. Notably, two critical vascular changes associated with AD are the breakdown of the BBB (270; 271) and compromised CBF (272). Moreover, these dysfunctions can subsequently trigger increases in proteins associated with angiogenesis, the process of forming new blood vessels. Pathological angiogenesis has been significantly implicated in perpetuating AD by fostering further Aβ generation, which, in turn, can exacerbate BBB dysfunction and impaired CBF (273). It is noteworthy that the M9 module is enriched with proteins involved in angiogenesis and is also elevated in African Americans compared to Caucasians, irrespective of disease status. In conclusion, the increased presence of endothelial proteins among African Americans implies that vascular differences may play a role in the heightened susceptibility to AD within this demographic. This highlights the necessity for additional investigation into how differences in vascular health between racial groups may impact the susceptibility and advancement of AD.

Currently, growing evidence suggests that endothelial dysfunction plays a significant role in the cognitive decline associated with AD (268), raising the question of whether the elevated levels observed in African Americans could indicate such injury. Furthermore, endothelial impairment is common among individuals with atherosclerosis, hypertension, diabetes, and chronic kidney disease (266), conditions that are more prevalent in the African American population. Several studies have already highlighted plausible biomarkers for endothelial dysfunction (268). Osteopontin (OPN) (269; 270) and cell adhesion molecules like VCAM1 and ICAM1 (271-273) are indicators of vascular inflammation, while albumin (ALB) (274-277), soluble platelet-derived growth factor receptor-beta (sPDGFRβ) (278), vasoactive molecules such as atrial natriuretic peptide (ANP), adrenomedullin (ADM), and B-type natriuretic (BNP) (279; 280), metalloproteinases (MMPs) (281-286), and blood coagulation proteins like fibrinogen (FGB) (287) and plasminogen activator inhibitor-1 (PAI1) (288) reflect vascular damage. Additionally, growth factors such as vascular endothelial cadherin (VGEF) (289-297), angiogenin (ANG) (292; 298), and angiopoietin-1 (ANG1) (299) have been shown to be altered during endothelial injury. When overlaying these indicators over proteins assigned to module memberships in the CSF proteome, it was found that only one of these markers, ANG, mapped to M9 or M3. Most of the other proteins identified within this CSF proteome (ICAM1, CDH5, ALB, MMP2, FGB) mapped to the blue module, which remained largely unchanged across both control and AD groups as well as between races. One exception was sPDGFRβ, which mapped to the M1 module. Increased CSF levels of sPDGFRβ have been linked to BBB breakdown in individuals with mild cognitive impairment (274). It has also been demonstrated that heightened levels of sPDGFRβ correlate with cognitive decline in the early stages of AD (275). Nevertheless, the module members of M1 decrease with disease progression, and even exhibit even greater declines in African Americans. Remarkably, alongside being identified as elevated in AD, sPDGFRβ levels have been noted to be lower in African Americans compared to Caucasians (276). Together, the data is insufficient to support that the elevated levels of endothelial markers observed in African Americans in this study are indicative of endothelial impairment or injury. However, this study still indicates fundamental differences in the levels and/or activation states of cells residing in the vasculature between African Americans and Caucasians. Whether this biological difference is observed in brain tissues or relates to a higher incidence of vascular health disparities between African Americans and Caucasians (300) requires further investigation. Genomic analysis could prove invaluable in this endeavor, shedding light on whether these elevations are attributable to genetic variations. Furthermore, it is crucial to consider the influence of social determinants of health, such as education, socioeconomic status, and exposure to adversity and discrimination, on overall health, and thus AD risk and progression. Future studies should aim to integrate CSF protein levels with vascular risk factors, environmental metrics, and sociodemographic data to better elucidate the underlying racial differences in the CSF proteome. This holistic approach will help uncover the complex interplay between genetic, environmental, and social factors that contribute to AD pathogenesis and inform on the development of targeted interventions for diverse populations.

4.3 Unveiling the interplay between neuronal alterations in AD and the role of the CSF in mirroring cognitive decline

The current biological framework for the pre-symptomatic stages of AD is based on the presence of Aβ deposition (A), tauopathy (T), and neurodegeneration (N) also termed the A/T/N framework (277). CSF remains the gold standard for A/T/N biomarkers of neurodegenerative disease as it maintains direct contact with the brain and reflects biochemical changes in amyloid (**Figure 4.1, purple line**), Tau (**green line**) and neurodegeneration (**yellow line**). A strength of our study was the balanced nature of African American samples, which offered the ability to examine racial differences in both cognitively normal controls with individuals diagnosed with AD. Our mass spectrometry measurements of Tau strongly correlated with immunoassay levels

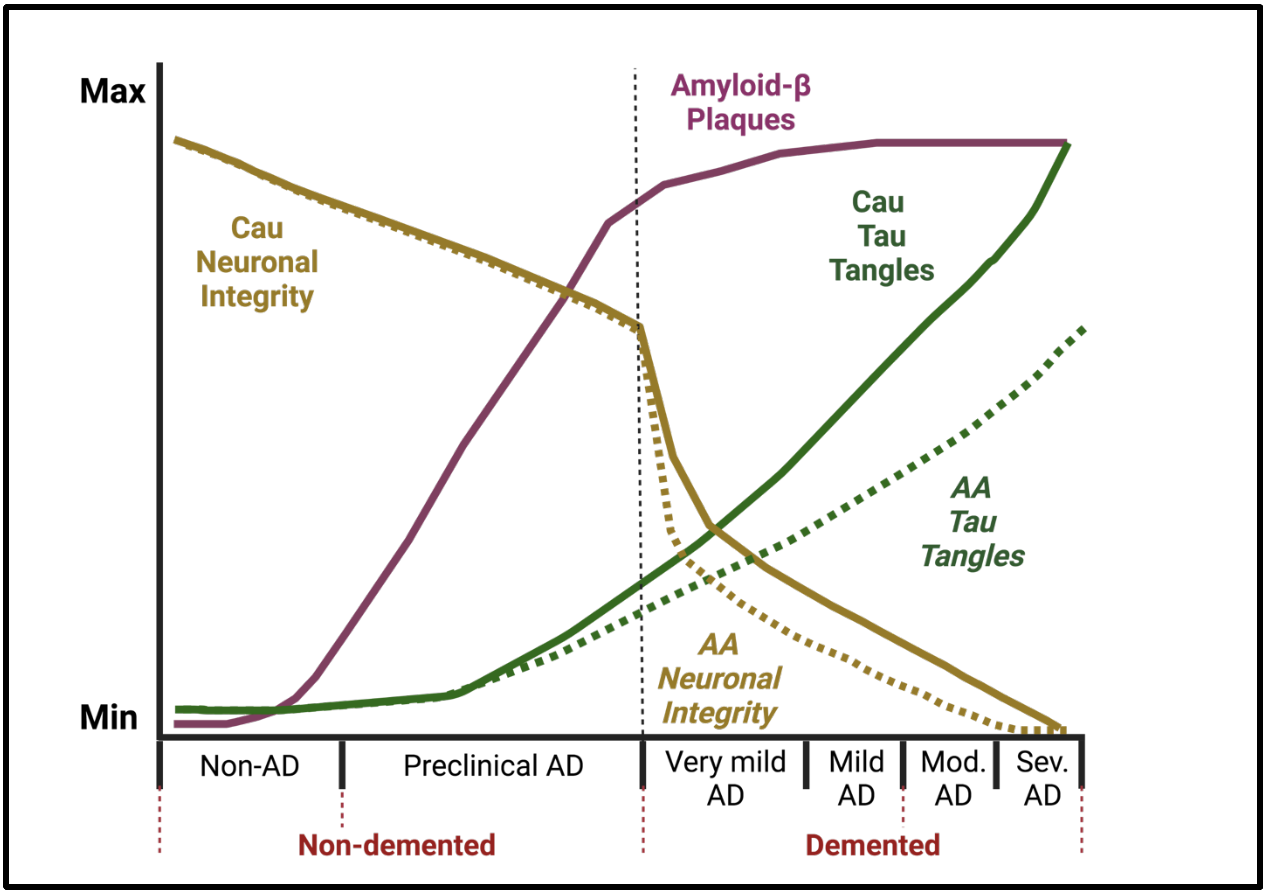


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Figure 4.1: Hypothesized time course differences in neuropathological and clinical changes based on biomarker alterations between Caucasians and African Americans with Alzheimer's disease. In Alzheimer's disease (AD), the conversion from a non-demented to demented state is associated with a buildup of amyloid-beta (Aβ) plaques (purple line), the accumulation of neurofibrillary Tau tangles (green line), and neuronal and synaptic loss (yellow line). Based on biomarker studies, the trajectory of change for the accumulation of Tau and the subsequent neuronal loss differs in African Americans with AD (dashed lines).

measured on the Roche Elecsys platform reinforcing measurements made by TMT-MS. Increased Tau in CSF is considered to result from neurodegeneration, however, it has also been shown to be increased in early pre-symptomatic disease stages when neurodegeneration is limited (277; 278) (**Figure 4.1, preclinical AD**). Recently, Tau CSF levels have been linked to enhanced synaptic plasticity where high levels of CSF Tau levels can be reflective of increased neuronal plasticity (279). Network analysis revealed a cluster of proteins, M12, along with another module, M6, exhibiting similar fluctuations in levels as Tau across racial groups, suggesting the involvement of other proteins that may function similarly to Tau in early disease synaptic plasticity. Other proteins that have been associated with synaptic plasticity include Calcium/calmodulin-dependent protein kinase II (CaMKII), cAMP-response element binding protein (CREB), Protein Kinases A and B (PRKAC1A and PRKAC1B), and growth-associated protein (GAP43) (269-273). Interestingly, all these proteins, including CAMK2A, CAMK2B, PRKAC1A, PRKAC1B, and GAP43, were categorized within the M6 module, indicating the potential association of other proteins within this module in synaptic plasticity. Further exploration of these proteins and their implications in racial disparities could provide valuable insights into AD pathogenesis and aid in developing targeted interventions.

Significantly, a considerable portion of synaptic proteins identified in this study aligned with M1 and M4. These modules demonstrated an overall decrease in levels with cognitive decline. We, also, observed that African Americans in this study had on average lower levels of neuronal markers mapping to M1 and M4 in the network, which are reduced in AD. Paradoxically, African Americans also have lower levels of neuronal proteins in M6 and M12, which all increase in AD. Consistent with this observation, in a recent CSF proteomic study in an asymptomatic Caucasian European population stratified by Tau CSF levels, individuals deemed to have high Tau levels maintained levels of M1 post-synaptic proteins (CADM3, NEO1, NPTX1, CHGB, PCSK1, NEGR, L1CAM, PTPRN, CACNA2D, PAM, VEGFA, NBL1 etc.) compared to individuals with lower Tau levels (279). This observation is analogous to differences we see between African

Americans and Caucasians with AD. M1 members VGF and NPTX2, strongly correlate to antemortem cognitive measures (280-282) and VGF and NPTX2 have been nominated as biomarkers of neurodegeneration (N) as their CSF levels enhance prediction of MCI to AD (282-284). Collectively, this would suggest that a specific sub-group of individuals with AD, including African Americans, have a higher burden of neurodegeneration (N) despite low CSF Tau levels (**Figure 4.1**, **dashed lines)**. Longitudinal studies examining changes in CSF levels of neuronal proteins and other module constituents over time, with a specific focus on diverse racial populations, will be essential. By tracking the temporal patterns of protein biomarkers, researchers can gain a better understanding of critical timeframes for potentially delaying cognitive decline associated with the disease and addressing racial disparities in disease progression. Moreover, longitudinal studies can offer insights into the efficacy of therapeutic interventions and assist in devising personalized treatment approaches.

Collectively, these data suggest that there are likely distinct mechanisms responsible for the dysregulation of neuronal proteins, resulting in two separate pools of neuronal proteins that either go up or down with disease in CSF. Further investigations should be conducted to explore the distinct mechanisms that contribute to the differences in abundance and/or secretion of neuronal markers such as Tau and other proteins increased in AD CSF like CAMK2A, SNCB, and SYN1, In conjunction, the interplay between the neuronal markers that increase and neuronal markers that decrease with disease like VGF, NPTX2, and SCG2, which have also been found to differ by race, should be further explored.

4.4 Future directions

Although a strength of our study was the large number of African Americans included, there are several limitations that should be noted. First, we acknowledge that many of the protein changes we observe in the CSF across race could be due to ancestral or genetic differences (285; 286). There were no genetics *a priori* performed on these study participants to confirm enrichment of African *vis a vis* European ancestry (287) as we stratified race solely by self-identification. Future studies, which include the integration of genetics and protein abundance to define protein quantitative trait loci (pQTL) will be necessary to resolve which proteins are under genetic control across race (288-290). It is noteworthy that the expression level of most modules which differed between racial groups were decreased in African Americans relative to Caucasians. Upon integration with whole genome profiling of larger cohorts, these patterns may help in the future to identify pQTLs or other mechanisms influencing synthesis and turnover of proteins that differ by race. Additionally, only a few studies to date have investigated proteomic difference by race in AD (291; 292), which have predominately focused on brain tissues and not on the scale of this current study. However, a major initiative of the Accelerating Medicine Partnership (AMP)-AD partnership (293) is to increase the number of diverse tissues included in multi-omic analyses, which will complement data generated from these previous studies. To support this effort, 81 brain tissue samples, obtained from Emory's Alzheimer's Disease Research Center, were prepared for future analysis. These samples have since been integrated with brain tissues from other AMP-AD partners, broadening the scope of the large-scale brain analyses (294; 295). Furthermore, despite the well documented differences in the quality of education, higher rates of poverty, and greater exposure to adversity and discrimination that increase risk for dementia (214; 215), these metrics were not captured on the participants in this study. Integrating CSF protein levels with vascular risk factors, and other environmental metrics in larger cohorts may help better resolve some of the underlying racial differences in the CSF proteome. Finally, in this study we adjusted for co-factors such as age and sex to pinpoint changes that are most likely to be associated with race and AD. Sex and age have an impact on the abundance of CSF Tau and other protein levels (296). Therefore, future studies that assess the interactions between, age, sex and race will be informative. Nevertheless, this study reveals an impressive view of protein co-expression in AD CSF across race, which provides new insights into the pathways underlying cell-type changes and further evidence that race may mediate these in AD. Future directions in AD research should aim to unravel the distinct mechanisms underlying racial differences in AD biomarkers and underlying physiology. Integrating genetic, proteomic, and sociodemographic data, along with longitudinal investigations, will contribute to a more comprehensive understanding of AD pathogenesis and facilitate the development of targeted interventions for diverse populations affected by AD.

CHAPTER 5: REFERENCES

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CHAPTER 6: Appendix

Table 6.1: Cohort characteristics

Number Cases	GUID	TMT ID	SRM ID	Study	Diagnosis	Age	Sex	Race	Educ	MoCA	APOE	Aβ42	tTau	pTau	tTau/Aβ42	pTau/Aβ42	Cerebrovascular	Diabetes	Dyslipidemia	Hypertension	Outlier
1	37512	b1.131N	S011_P1C02_37512	CRIN	AD	81.1	Female	Black or African American	18	19	e3/e4	498.5	277.1	31.12	0.5558676	0.0624273					
2	39138	b6.128C	S075_P1C10_39138	CRIN	AD	81	Female	Caucasian or White	16	23	e3/e4	644	680.5	76.64	1.056677	0.1190062					
3	42719	b12.130N	S147_P2E9_42719	CRIN	AD	73.9	Male	Black or African American	12	8	e4/e4	274.4	247.5	25.44	0.9019679	0.0927114					
4	44707	b15.129N	S192_P3D5_44707	CRIN	AD	68.9	Male	Caucasian or White	22	17	e3/e4	570.4	540.9	56.91	0.9482819	0.0997721					
5	44820	b15.132N	S187_P3G4_44820	CRIN	AD	50.9	Male	Black or African American	15	6	e3/e3	372.2	317.1	31.98	0.8519613	0.0859215					
6	45034	b1.129N	S005_P1E01_45034	CRIN	AD	76.6	Male	Caucasian or White		21	e3/e3	1066	464.8	44.54	0.4360225	0.0417824				YES	
7	45101	b11.131C	S137_P2C8_45101	CRIN	AD	74.9	Male	Caucasian or White		22	e3/e3	759.6	435.2	51.52	0.5729331	0.0678252	YES				
8	45128	b13.128C	S160_P3D1_45128	CRIN	AD	74.8	Male	Black or African American	18	19	e4/e4	414.6	308.6	31.34	0.7443319	0.0755909				YES	
9	45130	b2.128C	S021_P1E03_45130	CRIN	AD	50	Female	Caucasian or White			e3/e4	487.9	972.8	109.5	1.9938512	0.2244312					YES
10	45573	b3.128C	S037_P1E05_45573	CRIN	AD	72.6	Female	Caucasian or White	12	12	e3/e4	520.8	434.3	42.33	0.8339094	0.0812788					
11	45739	b13.131C	S161_P3E1_45739	CRIN	AD	75.5	Male	Caucasian or White	16	21	e3/e4	485.9	184.4	17.96	0.379502	0.0369623	YES	YES	YES	YES	
12	45831	b12.132N	S149_P2G9_45831	CRIN	AD	75.8	Female	Caucasian or White		17		685.4	319.1	29.71	0.4655676	0.043347					
13	45918	b12.131C	S155_P2E10_45918	CRIN	AD	72.1	Female	Black or African American	18	18		475.2	195.3	18.51	0.4109848	0.038952					
14	46008	b11.132C	S140_P2F8_46008	CRIN	AD	68.7	Female	Caucasian or White	20		e3/e4	696.4	940.7	86.69	1.3508041	0.1244831					
15	46040	b3.131N	S038_P1F05_46040	CRIN	AD	84.1	Male	Caucasian or White	20	19	e3/e3	628.8	462.5	52.83	0.735528	0.0840172					
16	46076	b4.128C	S047_P1G06_46076	CRIN	AD	60.1	Female	Black or African American	12	20		677.4	199.5	22.21	0.2945084	0.0327871			YES	YES	
17	46246	b13.132C	S168_P3D2_46246	CRIN	AD	75.2	Female	Black or African American	18	22	e3/e3	674.3	230.3	24.35	0.3415394	0.0361115				YES	
18	46306	b14.130C	S173_P3A3_46306	CRIN	AD	61	Female	Caucasian or White	18	12	e3/e3	414	150.8	15.27	0.3642512	0.0368841				YES	
19	46640	b6.127C	S076_P1D10_46640	CRIN	AD	76.1	Male	Black or African American	14	9		368.2	273.3	27.83	0.7422596	0.0755839					
20	46642	b1.132C	S012_P1D02_46642	CRIN	AD	68.3	Female	Caucasian or White		14	e4/e4	433.6	433.5	40.91	0.9997694	0.0943496			YES		
21	47135	b14.128N	S177_P3E3_47135	CRIN	AD	74.5	Male	Caucasian or White	16	21	e3/e4	965.3	543.5	65.97	0.5630374	0.0683414					
22	47232	b6.133N	S077_P1E10_47232	CRIN	AD	49.8	Female	Black or African American	12	15	e3/e3	405.8	403.9	40.19	0.9953179	0.0990389					
23	47248	b10.129N	S128_P2B7_47248	CRIN	AD	59.4	Female	Caucasian or White	14	20	e4/e4	280.7	333.5	30.38	1.1881012	0.1082294		YES		YES	
24	47251	b16.130C	S204_P3H6_47251	CRIN	AD	65.5	Female	Caucasian or White		17	e2/e3	294.7	256.2	27.05	0.8693587	0.0917883					
25	43738	b14.127N	S174_P3B3_43738	EHBS	Control	69.9	Female	Black or African American	14	27	e3/e4	1039	147.1	13.06	0.1415784	0.0125698	YES	YES			YES
26	44869	b5.128N	S053_P1E07_44869	EHBS	Control	66.1	Male	Black or African American	18	23	e3/e3	1124	136.3	11.51	0.1212633	0.0102402					
27	45707	b16.128N		EHBS	Control	72.7	Female	Black or African American	18	24	e2/e3	1700	254.8	23.86	0.1498824	0.0140353	YES				
28	46085	b1.128N	S009_P1A02_46085	EHBS	Control	51.3	Male	Black or African American	16	25	e2/e4	768.5	83.66	8	0.1088614	0.0104099		YES			YES
29	48153	b8.127N	S093_P2G2_48153	EHBS	Control	72.4	Female	Caucasian or White	16	30	e2/e3	1387	174.4	15.06	0.125739	0.010858					
30	48358	b14.129N	S176_P3D3_48358	EHBS	Control	66.1	Female	Caucasian or White	16	24	e3/e3	1700	197.4	17.56	0.1161176	0.0103294					
31	48617	b12.127C		EHBS	Control	57.7	Female	Black or African American	13	28	e3/e3	1285	153.2	13.09	0.1192218	0.0101868					
32	48769	b15.133N		EHBS	Control	75	Female	Caucasian or White	14	26	e3/e3	1700	227.9	19.72	0.1340588	0.0116			YES	YES	
33	49324	b5.128C	S060_P1D08_49324	EHBS	Control	60.2	Female	Caucasian or White	20	27	e2/e3	1431	164.1	15	0.1146751	0.0104822					
34	49417	b2.128N	S016_P1H02_49417	EHBS	Control	71.6	Female	Caucasian or White	16	26	e3/e3	1411	177.8	15.41	0.1260099	0.0109213					
35	49537	b15.128N		EHBS	Control	51	Female	Black or African American	18	25	e2/e4	862.4	105.4	9.97	0.1222171	0.0115608					
36	49903	b10.131C	S126_P2H6_49903	EHBS	Control	64.9	Male	Caucasian or White	18	27	e3/e3	1084	180.2	15.51	0.1662362	0.0143081			YES	YES	
37	49941	b6.132C	S074_P1B10_49941	EHBS	Control	69.7	Male	Caucasian or White	16	26	e3/e3	1165	156	13.65	0.1339056	0.0117167					
38	50259	b14.131N	S182_P3B4_50259	EHBS	Control	50.1	Female	Black or African American	20	28	e3/e4	447.4	80.22	8	0.1793026	0.0178811	YES				
39	50273	b8.133N	S094_P2H2_50273	EHBS	Control	69	Female	Caucasian or White	20	28	e3/e4	1700	220.9	19.62	0.1299412	0.0115412					
40	50409	b16.130N	S199_P3C6_50409	EHBS	Control	64.8	Female	Caucasian or White	18	23	e3/e4	823.1	166.1	14.15	0.2017981	0.0171911					
41	50452	b4.130N	S052_P1D07_50452	EHBS	Control	59.5	Female	Caucasian or White	18	29	e3/e4	920.5	123.8	10.98	0.1344921	0.0119283				YES	
42	50502	b13.130C	S165_P3A2_50502	EHBS	Control	55.5	Female	Black or African American	13	28	e3/e3	892	105.2	9.58	0.1179372	0.0107399		YES			
43	50534	b4.128N	S041_P1A06_50534	EHBS	Control	71.5	Female	Caucasian or White	14	25	e3/e4	1595	364.5	35.32	0.2285266	0.0221442					
44	50619	b5.127C	S056_P1H07_50619	EHBS	Control	64.7	Female	Caucasian or White	12	23	e3/e3	1700	191.3	17.42	0.1125294	0.0102471					
45	50650	b3.129C	S033_P1A05_50650	EHBS	Control	59.4	Female	Caucasian or White	18	28	e3/e3	1541	308.1	27.24	0.1999351	0.0176768					
46	51023	b9.129C	S107_P2E4_51023	EHBS	Control	68.4	Female	Black or African American	16	28	e3/e3	1239	236.4	21.54	0.190799	0.017385					
47	51123	b9.132C	S114_P2D5_51123	EHBS	Control	50	Female	Caucasian or White	14	26	e3/e3	1410	154	14.36	0.1092199	0.0101844					
48	51135	b6.129C	S067_P1C09_51135	EHBS	Control	61.9	Female	Caucasian or White	16	24	e3/e4	594.6	104.6	8.34	0.1759166	0.0140262				YES	
49	51175	b12.128C	S153_P2C10_51175	EHBS	Control	65.5	Female	Caucasian or White	20	24	e3/e3	1442	233.3	21.18	0.1617892	0.0146879					
50	51224	b16.127C	S200_P3D6_51224	EHBS	Control	66.2	Male	Caucasian or White	18	28	e3/e3	1235	142.2	14.92	0.1151417	0.012081					
51	51264	b8.128N	S095_P2A3_51264	EHBS	Control	61.2	Female	Caucasian or White	12	31	e3/e3	1700	241.6	21.36	0.1421176	0.0125647				YES	
52	51319	b8.132C	S096_P2B3_51319	EHBS	Control	68.7	Female	Black or African American	18	20	e3/e3	762.1	116.5	10.26	0.1528671	0.0134628					
53	51370	b1.130C	S010_P1B02_51370	EHBS	Control	70.4	Female	Caucasian or White	16	26	e2/e3	1353	136.8	13.55	0.1011086	0.0100148					
54	51431	b7.128C	S082_P2D1_51431	EHBS	Control	69.8	Female	Caucasian or White	14	29	e3/e4	1700	208.2	18.12	0.1224706	0.0106588					
55	51499	b4.132N	S042_P1B06_51499	EHBS	Control	74.5	Male	Caucasian or White	20	28	e2/e3	832.6	125.4	10.12	0.1506125	0.0121547					
56	51520	b9.133N		EHBS	Control	53.5	Female	Black or African American	15	23	e3/e3	699.8	113.7	9.14	0.162475	0.0130609	YES				
57	51551	b2.130N	S023_P1G03_51551	EHBS	Control	66.4	Female	Caucasian or White	13	24	e2/e3	1423	147.8	13.02	0.1038651	0.0091497					
58	51559	b4.132C	S045_P1E06_51559	EHBS	Control	64.5	Female	Caucasian or White	18	25	e3/e3	1176	122.4	11.5	0.1040816	0.0097789					
59	51760	b13.131N	S159_P3C1_51760	EHBS	Control	57.1	Male	Black or African American	13	26	e3/e3	856.5	128.3	11.73	0.1497957	0.0136953					
60	52055	b10.127C		EHBS	Control	66.8	Female	Black or African American	16	28	e2/e3	997	149.1	15.38	0.1495486	0.0154263		YES	YES	YES	
61	52131	b3.130N	S034_P1B05_52131	EHBS	Control	75.7	Female	Caucasian or White	13	27	e2/e3	1242	170.1	14.81	0.1369565	0.0119243					
62	52154	b7.132N	S083_P2E1_52154	EHBS	Control	74.1	Female	Caucasian or White	18	28	e3/e3	1258	180.4	15.42	0.1434022	0.0122576					
63	52475	b12.128N	S145_P2C9_52475	EHBS	Control	69.5	Male	Caucasian or White	16	27	e3/e3	1700	234.6	19.29	0.138	0.0113471				YES	
64	52524	b2.130C		EHBS	Control	62.1	Female	Caucasian or White	20	27	e3/e3	1171	139.8	11.55	0.1193851	0.0098634					

65	52538	b14.132N	S171_P3G2_52538	EHBS	Control	58.7	Female	Caucasian or White	18	25	e2/e4	1700	194.6	17.49	0.1144706	0.0102882					
66	52626	b9.131C	S108_P2F4_52626	EHBS	Control	66.6	Female	Caucasian or White	18	26	e3/e3	1700	219.5	23.23	0.1291176	0.0136647					
67	52791	b11.129C	S132_P2F7_52791	EHBS	Control	64	Female	Black or African American	13	28	e3/e3	501.8	86.27	8	0.1719211	0.0159426					
68	53030	b15.127N	S184_P3D4_53030	EHBS	Control	56.5	Female	Black or African American	16	29	e3/e3	1518	171.5	16.19	0.1129776	0.0106653					
69	53612	b1.132N	S002_P1B01_53612	EHBS	Control	52.7	Female	Black or African American	18	28	e3/e4	1240	174.9	16.67	0.1410484	0.0134435					
70	53618	b4.129N	S043_P1C06_53618	EHBS	Control	70.5	Female	Black or African American	18	26	e3/e3	1004	124	11.5	0.123506	0.0114542					
71	53705	b12.129N	S146_P2D9_53705	EHBS	Control	54.5	Female	Caucasian or White	16	23	e2/e3	1459	162.6	13.71	0.1114462	0.0093968					
72	53729	b5.130C	S054_P1F07_53729	EHBS	Control	72.7	Female	Caucasian or White	18	28	e3/e3	986.2	144.7	14.81	0.1467248	0.0150172					
73	53731	b11.128N	S139_P2E8_53731	EHBS	Control	70.9	Female	Black or African American	18	27		1479	136.5	12.51	0.0922921	0.0084584					
74	53741	b6.129N	S068_P1D09_53741	EHBS	Control	53.6	Female	Caucasian or White	18	26	e3/e3	1532	213.8	18.31	0.1395561	0.0119517					
75	55244	b3.127N	S035_P1C05_55244	EHBS	Control	64.6	Female	Black or African American	14	24	e3/e4	1158	161.4	14.97	0.1393782	0.0129275					
76	55286	b7.128N	S084_P2F1_55286	EHBS	Control	56.6	Female	Black or African American	16	26	e3/e3	789.4	94.69	8.38	0.1199519	0.0106157					
77	55838	b13.132N	S166_P3B2_55838	EHBS	Control	66.7	Female	Caucasian or White	16	23	e3/e4	1177	258.1	24.54	0.2192863	0.0208496					
78	56007	b11.127N	S133_P2G7_56007	EHBS	Control	64.8	Male	Caucasian or White	16	25	e3/e4	1700	208.8	19.3	0.1228235	0.0113529					
79	56326	b10.127N	S121_P2C6_56326	EHBS	Control	70.9	Female	Caucasian or White	16	25	e3/e3	1700	307.8	30.74	0.1810588	0.0180824					
80	56580	b12.127N	S154_P2D10_56580	EHBS	Control	57.3	Male	Caucasian or White	16	26	e3/e3	835	100.9	9.51	0.1208383	0.0113892					
81	57907	b4.127C	S044_P1D06_57907	EHBS	Control	64.4	Male	Caucasian or White	20	28	e3/e4	1005	133.1	10.98	0.1324378	0.0109254				YES	
82	58595	b6.130N	S069_P1E09_58595	EHBS	Control	64.9	Male	Black or African American	18	22	e2/e3	600.4	91.22	8	0.151932	0.0133245		YES	YES	YES	
83	58815	b11.128C	S135_P2A8_58815	EHBS	Control	61.6	Male	Black or African American	14	25	e3/e3	943.3	145.6	13.16	0.1543517	0.013951					
84	59913	b2.129C	S017_P1A03_59913	EHBS	Control	75.4	Male	Black or African American	12	22	e3/e3	1570	238.8	23.37	0.1521019	0.0148854					
85	62211	b2.131N	S018_P1B03_62211	EHBS	Control	57.1	Male	Caucasian or White	16	30	e2/e3	1583	189.3	16.31	0.1195831	0.0103032					
86	62762	b11.127C		EHBS	Control	57.2	Male	Caucasian or White	18	29	e3/e4	1473	196.5	17.48	0.1334012	0.0118669					
87	63141	b10.131N	S119_P2A6_63141	EHBS	Control	51.1	Male	Caucasian or White	16	25	e2/e3	1004	111	9.17	0.1105578	0.0091335					
88	63456	b1.127N	S003_P1C01_63456	EHBS	Control	69.5	Male	Black or African American	18	27	e2/e3	835.3	129.7	12.11	0.1552736	0.0144978					
89	66352	b5.133N	S061_P1E08_66352	EHBS	Control	77.8	Male	Black or African American	20	28	e3/e3	1498	176.6	15.66	0.1178905	0.0104539					
90	66827	b8.130C	S101_P2G3_66827	EHBS	Control	72.5	Male	Caucasian or White	16	24	e2/e4	1125	147.8	12.48	0.1313778	0.0110933					
91	66984	b2.133N	S019_P1C03_66984	EHBS	Control	51.7	Male	Black or African American	13	23	e3/e4	764.7	125.6	10.6	0.1642474	0.0138616					YES
92	68545	b9.130C	S110_P2H4_68545	EHBS	Control	57.3	Male	Black or African American	18	27	e3/e3	1368	167.5	17.34	0.1224415	0.0126754			YES		
93	68620	b3.131C	S030_P1F04_68620	EHBS	Control	51.5	Male	Black or African American	13	20	e3/e3	935.7	120.5	10.99	0.1287806	0.0117452			YES	YES	
94	70714	b14.129C	S172_P3H2_70714	EHBS	Control	57.4	Male	Black or African American	12	21	e2/e4	1221	142	12.96	0.1162981	0.0106143					
95	72374	b6.131N	S070_P1F09_72374	EHBS	Control	52.1	Male	Black or African American	13		e2/e3	686.6	101.8	10.21	0.1482668	0.0148704					
96	73786	b8.129C	S097_P2C3_73786	EHBS	Control	61.6	Male	Caucasian or White	18	29	e2/e3	1700	244.2	20.31	0.1436471	0.0119471				YES	
97	74682	b15.132C	S185_P3E4_74682	EHBS	Control	64.5	Male	Black or African American	18	26	e3/e3	1180	143.7	12.27	0.1217797	0.0103983					
98	75351	b1.129C	S004_P1D01_75351	EHBS	Control	72.1	Male	Caucasian or White	14	29	e2/e3	1700	185.6	17.01	0.1091765	0.0100059					
99	76023	b3.127C	S031_P1G04_76023	EHBS	Control	51.9	Male	Caucasian or White	18	26	e2/e3	869.6	107.5	9.97	0.1236201	0.011465					
100	76348	b6.127N	S071_P1G09_76348	EHBS	Control	52.1	Male	Caucasian or White	14	28	e3/e3	916.9	102	9.78	0.1112444	0.0106664					
101	76615	b15.130N	S186_P3F4_76615	EHBS	Control	64.6	Male	Black or African American	16	23	e3/e3	876.8	154	13	0.1756387	0.0148266					
102	76950	b8.127C	S098_P2D3_76950	EHBS	Control	69.4	Male	Caucasian or White	16	25	e2/e3	954.9	142.6	14.71	0.149335	0.0154048					
103	78086	b10.132N	S120_P2B6_78086	EHBS	Control	72.6	Male	Black or African American	18	29	e2/e3	471.7	99.68	8.9	0.2113208	0.0188679					
104	86092	b13.129C	S167_P3C2_86092	EHBS	Control	51.5	Male	Caucasian or White	16	24	e3/e4	1176	131.1	11.57	0.1114796	0.0098384					
105	41324	b1.127C	S001_P1A01_41324	MEmory	AD	66.8	Female	Black or African American	13	26	e4/e4	666.9	358.2	33.78	0.537112	0.0506523					
106	41483	b7.127N	S081_P2C1_41483	MEmory	Control	77.3	Female	Black or African American	18	28	e3/e3	1700	234.1	18.9	0.1377059	0.0111176		YES			
107	42541	b2.132N	S014_P1F02_42541	MEmory	AD	58.2	Male	Black or African American	22	19	e3/e4	390.8	207.6	18.01	0.531218	0.046085	YES				
108	42570	b8.130N	S103_P2A4_42570	MEmory	Control	78.1	Female	Black or African American	18	22	e2/e3	1700	240.4	19.18	0.1414118	0.0112824					
109	42947	b15.129C	S183_P3C4_42947	MEmory	Control	82	Female	Caucasian or White	18	24	e3/e3	1700	341.5	25.9	0.2008824	0.0152353					
110	43820	b16.128C	S197_P3A6_43820	MEmory	Control	60.7	Female	Caucasian or White	18	29	e3/e3	878.4	94.12	8	0.1071494	0.0091075					
111	44067	b1.130N	S013_P1E02_44067	MEmory	Control	61.1	Female	Black or African American	18	26	e2/e3	983.5	128.3	10.76	0.1304525	0.0109405	YES				
112	44291	b2.132C	S015_P1G02_44291	MEmory	Control	71.5	Female	Black or African American	16	19	e3/e3	1196	163.8	14.46	0.1369565	0.0120903					
113	44511	b9.132N	S105_P2C4_44511	MEmory	AD	77	Female	Black or African American	20	26	e3/e3	739	213.9	21.26	0.2894452	0.0287686					
114	44893	b16.131N	S198_P3B6_44893	MEmory	Control	60.7	Female	Black or African American	14	26	e2/e3	691.8	121.5	10.25	0.1756288	0.0148164					
115	45238	b14.132C	S175_P3C3_45238	MEmory	Control	62.2	Female	Black or African American	16	21	e3/e3	1700	246.8	25.07	0.1451765	0.0147471					
116	45487	b14.131C	S170_P3F2_45487	MEmory	AD	75.6	Female	Black or African American	16	8	e4/e4	327.9	478.9	42.26	1.4605063	0.1288808					
117	45861	b4.127N	S040_P1H05_45861	MEmory	Control	66.4	Female	Black or African American	16	26	e2/e3	898.3	125.8	11.27	0.1400423	0.0125459					
118	46043	b13.127N	S157_P3A1_46043	MEmory	Control	70.3	Female	Caucasian or White	16	23	e3/e3	1700	238.1	18.9	0.1400588	0.0111176					
119	46103	b12.131N	S144_P2B9_46103	MEmory	Control	70.3	Female	Black or African American	13	28	e3/e3	1045	141.9	12.36	0.1357895	0.0118278					
120	46233	b13.129N	S158_P3B1_46233	MEmory	Control	61.3	Female	Black or African American	16	28		1608	340.3	29.25	0.2116294	0.0181903					
121	46390	b4.129C	S051_P1C07_46390	MEmory	Control	55.3	Female	Black or African American	18	28	e2/e4	1075	150.3	13.18	0.139814	0.0122605					
122	46931	b3.133N	S029_P1E04_46931	MEmory	Control	71.6	Female	Black or African American	16	25	e3/e3	1239	157.3	14.01	0.1269572	0.0113075					
123	47147	b10.130N	S118_P2H5_47147	MEmory	Control	60.2	Female	Caucasian or White	16	25	e3/e4	1185	188.1	15.74	0.1587342	0.0132827					
124	47480	b11.132N	S131_P2E7_47480	MEmory	Control	72.1	Male	Black or African American	16	29	e3/e3	1547	226	19.56	0.1460892	0.0126438					
125	48786	b9.130N	S113_P2C5_48786	MEmory	Control	72.4	Female	Black or African American	18	27	e3/e4	1700	231.6	19.17	0.1362353	0.0112765	YES				
126	48937	b12.129C	S152_P2B10_48937	MEmory	Control	65.5	Female	Black or African American	18	25	e3/e3	1700	225.2	19.33	0.1324706	0.0113706				YES	
127	50313	b6.132N	S066_P1B09_50313	MEmory	Control	66.1	Female	Black or African American	16	26	e3/e3	1277	206.7	18.93	0.1618637	0.0148238				YES	
128	56968	b5.131N	S055_P1G07_56968	MEmory	Control	78.3	Male	Caucasian or White	18	27	e3/e3	1700	279	24.04	0.1641176	0.0141412					
129	57339	b2.129N	S020_P1D03_57339	MEmory	Control	63.9	Female	Black or African American	20	27	e3/e3	816.1	125	10.81	0.1531675	0.0132459					
130	57450	b11.130C	S134_P2H7_57450	MEmory	Control	69.4	Male	Black or African American	14	26	e2/e3	1034	146.2	12.62	0.1413927	0.012205					YES
131	57502	b7.131N	S085_P2G1_57502	MEmory	Control	64.6	Female	Black or African American	14	20	e3/e3	937.7	150.6	12.35	0.1606057	0.0131705					
132	63982	b9.128C	S109_P2G4_63982	MEmory	Control	75.2	Male	Caucasian or White	15	25	e3/e3	1566	234.8	19.28	0.1499361	0.0123116					
133	69030	b3.132N	S036_P1D05_69030	MEmory	Control	69.7	Male	Black or African American	15	24	e3/e3	1700	285.2	21.76	0.1677647	0.0128					
134	46282	b8.131C	S102_P2H3_46282	NeuCog	AD	73.4	Female	Caucasian or White	16	22	e4/e4	490.6	383.2	40.13	0.7810844	0.0817978				YES	
135	46442	b1.133N	S006_P1F01_46442	NeuCog	AD	59.5	Female	Caucasian or White	12	11	e3/e4	652.7	465.3	51.58	0.7128849	0.0790256	YES				
136	46743	b12.132C	S148_P2F9_46743	NeuCog	AD	76	Male	Caucasian or White	13	19		882.4	278.7	25.14	0.3158432	0.0284905					
137	47238	b3.128N	S027_P1C04_47238	NeuCog	AD	80.2	Female	Caucasian or White	18	16	e3/e4	750.3	940.5	94.51	1.2534986	0.1259629					
138	47351	b14.128C	S178_P3F3_47351	NeuCog	AD	69.2	Female	Black or African American	12	13		407.1	340.6	34.48	0.8366495	0.0846966					
139	47368	b11.130N	S141_P2G8_47368	NeuCog	AD	69	Female	Black or African American	12	8	e4/e4	588	225.8	21.27	0.3840136	0.0361735					
140	47498	b9.127N	S116_P2F5_47498	NeuCog	AD	73	Female	Caucasian or White	15	13	e3/e4	718.2	503.2	52.3	0.7006405	0.0728209					
141	48024	b3.132C	S039_P1G05_48024	NeuCog	AD	82.7	Male	Black or African American	20	23	e4/e4	630.3	200	19.29	0.3173092	0.0306045					
142	48222	b12.133N	S156_P2F10_48222	NeuCog	AD	62.5	Male	Black or African American	15	16	e4/e4	303.8	141.6	13.91	0.4660961	0.0457867					
143	48615	b7.132C	S090_P2D2_48615	NeuCog	AD	69.4	Female	Caucasian or White	14	24	e3/e4	516.1	443.2	43.95	0.8587483	0.0851579					
144	48746	b8.132N	S092_P2F2_48746	NeuCog	AD	78	Female	Black or African American	12	14		382.9	238.7	25.79	0.6234004	0.0673544					
145	49087	b7.131C	S091_P2E2_49087	NeuCog	AD	69	Male	Black or African American	12	4		469.2	218.5	19.15	0.4656863	0.0408142					
146	49419	b1.131C	S007_P1G01_49419	NeuCog	AD	72.4	Female	Black or African American	20	20	e3/e4	764.5	396.9	43.64	0.5191629	0.0570831					
147	49450	b16.129C	S201_P3E6_49450	NeuCog	AD	75.2	Female	Black or African American	16	13		642.4	1008	102.5	1.5691158	0.1595579					
148	49545	b13.128N	S162_P3F1_49545	NeuCog	AD	66.6	Male	Caucasian or White	16	10	e3/e3	474.5	368	32.28	0.7755532	0.0680295					
149	51464	b10.132C	S122_P2D6_51464	NeuCog	AD	60.5	Female	Black or African American	18	4	e4/e4	598	327.2	26.04	0.5471572	0.0435452					
150	52945	b9.127C	S117_P2G5_52945	NeuCog	AD	74.5	Male	Black or African American	14	22	e3/e3	275.8	302.6	28.65	1.0971719	0.1038796		YES	YES	YES	YES
151	53398	b9.129N	S111_P2A5_53398	NeuCog	AD	66.3	Male	Black or African American	19	9	e2/e3	651.2	256.3	25.52	0.3935811	0.0391892					
152	53819	b4.131N	S046_P1F06_53819	NeuCog	AD	70.6	Female	Caucasian or White	16	21	e3/e4	655.5	256.6	24.38	0.3914569	0.037193					
153	54179	b7.130C	S079_P2A1_54179	NeuCog	AD	56	Male	Black or African American	11	4	e3/e4	273.1	205.5	17.8	0.7524716	0.0651776			YES		
154	54601	b16.129N	S196_P3H5_54601	NeuCog	AD	71.2	Male	Black or African American	12	12	e3/e4	635	313.1	34.38	0.4930709	0.0541417					
155	54755	b3.129N	S032_P1H04_54755	NeuCog	AD	67.8	Female	Black or African American	18	8	e3/e4	428.8	224.5	21.89	0.5235541	0.0510494					
156	56582	b13.127C	S163_P3G1_56582	NeuCog	AD	75.1	Female	Caucasian or White	20	20	e3/e3	624.2	544.9	54.51	0.8729574	0.0873278					
157	57056	b8.131N	S099_P2E3_57056	NeuCog	AD	62.4	Male	Caucasian or White	16	15	e3/e3	413	487	58.31	1.1791768	0.1411864					
158	57251	b11.131N	S138_P2D8_57251	NeuCog	AD	73.5	Female	Black or African American	17	14	e3/e4	752.5	309.7	33.41	0.4115615	0.0443987					
159	57326	b9.131N	S106_P2D4_57326	NeuCog	AD	49.5	Female	Caucasian or White	13	5	e3/e4	745.6	589.8	61.31	0.7910408	0.0822291					
160	57498	b11.133N	S142_P2H8_57498	NeuCog	AD	52.3	Male	Black or African American	12	4	e3/e3	448.2	165.5	14.24	0.3692548	0.0317715					
161	58885	b4.133N	S048_P1H06_58885	NeuCog	AD	70.6	Female	Black or African American	12	18		559.1	288.5	28.94	0.5160079	0.0517618					
162	59128	b5.130N	S062_P1F08_59128	NeuCog	AD	60.1	Female	Caucasian or White	16	25	e3/e3	772.2	574.5	54.28	0.7439782	0.0702927			YES	YES	
163	64149	b15.131C	S193_P3E5_64149	NeuCog	AD	73.4	Female	Caucasian or White	14	10	e3/e4	613.9	360.6	37.24	0.5873921	0.0606613					
164	64402	b2.127C	S025_P1A04_64402	NeuCog	AD	63.3	Female	Caucasian or White	16	12	e3/e3	492.1	299.7	31.81	0.6090226	0.0646413					YES
165	66276	b8.128C	S100_P2F3_66276	NeuCog	AD	65.2	Female	Black or African American	18	14		350	257.5	24.03	0.7357143	0.0686571			YES		
166	66735	b6.130C	S072_P1H09_66735	NeuCog	AD	71.7	Female	Caucasian or White	16	13	e3/e4	262.1	281.5	15.19	1.0740176	0.057955					
167	67579	b6.128N	S078_P1F10_67579	NeuCog	AD	55.5	Male	Caucasian or White	14	1	e3/e3	513.9	568.3	48.72	1.1058572	0.0948044					
168	67976	b2.127N	S022_P1F03_67976	NeuCog	AD	72.7	Female	Black or African American	12	9	e3/e4	279.3	402.6	46.03	1.4414608	0.1648049					
169	68342	b4.130C	S049_P1A07_68342	NeuCog	AD	80.1	Female	Black or African American	10	14	e3/e4	622.4	373.2	36.56	0.5996144	0.0587404					
170	69732	b1.128C	S008_P1H01_69732	NeuCog	AD	70.3	Female	Caucasian or White	20	15	e4/e4	470.7	317.6	34.32	0.6747397	0.0729127				YES	
171	70529	b7.129N	S086_P2H1_70529	NeuCog	AD	60.6	Female	Caucasian or White	16	1	e3/e4	355.2	207.1	20.19	0.5830518	0.0568412					
172	71200	b3.130C	S028_P1D04_71200	NeuCog	AD	72.7	Male	Caucasian or White	18	18	e3/e4	394.3	191	20.63	0.4844027	0.0523206					
173	72191	b14.130N	S180_P3H3_72191	NeuCog	AD	54	Male	Caucasian or White	21	18	e3/e3	498.2	329.3	37.77	0.6609795	0.0758129					
174	72848	b5.131C	S063_P1G08_72848	NeuCog	AD	82.8	Male	Black or African American	17	14	e3/e4	514.6	271.1	28.09	0.5268169	0.0545861					YES
175	73152	b13.130N	S169_P3E2_73152	NeuCog	AD	49.5	Male	Black or African American	12	18		202.6	93.76	9.1	0.4627838	0.0449161					YES
176	73518	b7.129C	S080_P2B1_73518	NeuCog	AD	80.2	Female	Black or African American	12	21	e3/e3	608.6	416.9	39.79	0.6850148	0.0653796					
177	73621	b10.128C	S129_P2C7_73621	NeuCog	AD	82.6	Male	Caucasian or White	18	24	e3/e3	623.7	466.1	48.17	0.7473144	0.0772326					
178	73808	b5.127N	S064_P1H08_73808	NeuCog	AD	69.3	Female	Black or African American	12	15		734.1	423.4	41.06	0.5767607	0.0559324					
179	74051	b2.131C	S026_P1B04_74051	NeuCog	AD	57.3	Female	Black or African American	15	7	e3/e4	674.4	431.7	43.01	0.6401246	0.0637752					
180	74112	b10.129C	S130_P2D7_74112	NeuCog	AD	76.2	Male	Black or African American	18	13	e3/e4	479	166.8	15.19	0.3482255	0.0317119					
181	76896	b13.133N	S164_P3H1_76896	NeuCog	AD	62.8	Male	Caucasian or White	16	21		534.1	242.3	21.49	0.4536604	0.0402359					
182	77355	b8.129N	S104_P2B4_77355	NeuCog	AD	70.4	Female	Black or African American	14	15	e4/e4	369.8	471.3	45.9	1.2744727	0.1241211					YES
183	77501	b15.131N	S194_P3F5_77501	NeuCog	AD	57.4	Female	Caucasian or White	16	7	e3/e4	482.1	395.6	36.17	0.8205766	0.0750259					YES
184	77792	b7.127C	S087_P2A2_77792	NeuCog	AD	73.8	Female	Black or African American	19	23	e3/e4	579.3	471.9	52.72	0.8146038	0.0910064			YES	YES	YES
185	78317	b5.132C	S057_P1A08_78317	NeuCog	AD	71.5	Male	Caucasian or White	14	19	e3/e4	478.8	244.1	25.41	0.5098162	0.0530702					
186	79243	b10.128N	S123_P2E6_79243	NeuCog	AD	68.3	Female	Black or African American	12	14		439	224.9	23.7	0.5123007	0.0539863					
187	80265	b5.129C	S058_P1B08_80265	NeuCog	AD	75.4	Female	Caucasian or White	16	18		471.7	335.1	37.8	0.7104092	0.0801357					
188	80287	b10.133N	S124_P2F6_80287	NeuCog	AD	56	Male	Caucasian or White	18	22		612	497.5	53.22	0.8129085	0.0869608					
189	82876	b11.129N	S143_P2A9_82876	NeuCog	AD	80.5	Female	Black or African American	16	20	e3/e3	358.9	254	23.54	0.707718	0.0655893					
190	83314	b16.127N	S202_P3F6_83314	NeuCog	AD	77	Female	Caucasian or White	20	22	e3/e3	508.4	465	33.94	0.9146341	0.0667585			YES		
191	83366	b4.131C	S050_P1B07_83366	NeuCog	AD	79.4	Female	Caucasian or White	12	20	e3/e3	447.2	192.5	19.6	0.4304562	0.0438283					
192	83459	b6.131C	S073_P1A10_83459	NeuCog	AD	59.5	Female	Black or African American	14	10	e3/e4	498	333.7	32.5	0.6700803	0.065261		YES	YES	YES	
193	83798	b14.127C	S181_P3A4_83798	NeuCog	AD	58.8	Female	Black or African American	16	16	e3/e4	424.6	230.6	21.15	0.5430994	0.0498116					
194	84217	b12.130C	S150_P2H9_84217	NeuCog	AD	52.6	Male	Black or African American	20	22	e3/e3	454.4	289.5	26.69	0.6371039	0.0587368					

195	84355	b5.129N	S065_P1A09_84355	NeuCog	AD	76	Male	Black or African American	20	20		564.5	315.6	30.98	0.5590788	0.0548804					
196	84561	b5.132N	S059_P1C08_84561	NeuCog	AD	50.1	Female	Black or African American	14	7	e3/e4	308	215.2	20.51	0.6987013	0.0665909					
197	85026	b9.128N	S112_P2B5_85026	NeuCog	AD	63.1	Female	Black or African American	12	16	e4/e4	200	209	20.3	1.045	0.1015					
198	85961	b15.127C	S195_P3G5_85961	NeuCog	AD	67	Female	Caucasian or White	14	17	e3/e4	540.8	382.5	39.76	0.7072855	0.0735207		YES	YES	YES	
199	86582	b10.130C	S125_P2G6_86582	NeuCog	AD	58.2	Male	Caucasian or White	18	9	e3/e3	598.3	471.6	51.68	0.7882333	0.0863781					
200	86780	b15.128C	S188_P3H4_86780	NeuCog	AD	63.6	Male	Black or African American	16	20		515.3	356.3	40.27	0.6914419	0.0781487					YES
201	86840	b7.133N	S088_P2B2_86840	NeuCog	AD	52.1	Male	Caucasian or White	14	12	e3/e3	436.5	522.8	66.65	1.197709	0.1526919					
202	87070	b7.130N	S089_P2C2_87070	NeuCog	AD	77	Female	Caucasian or White	22	13	e3/e3	273.5	155.9	14.33	0.5700183	0.0523949					YES
203	87124	b15.130C	S189_P3A5_87124	NeuCog	AD	64	Female	Black or African American	20	7	e3/e4	383.6	294.7	33.76	0.7682482	0.0880083					
Empty Channel		b14.133N																			YES

Table 6.2: TMT Batch Arrangement.

	Batch 1	Batch 2	Batch 3	Batch 4	Batch 5	Batch 6	Batch 7	Batch 8	Batch 9	Batch 10	Batch 11	Batch 12	Batch 13	Batch 14	Batch 15	Batch 16
Plex																
126	GIS	GIS	GIS	GIS	GIS	GIS	GIS	GIS	GIS	GIS	GIS	GIS	GIS	GIS	GIS	GIS
127N	63456	67976	55244	45861	73808	76348	41483	48153	47498	56326	56007	56580	46043	43738	53030	83314
127C	41324	64402	76023	57907	50619	46640	77792	76950	52945	52055	62762	48617	56582	83798	85961	51224
128N	46085	49417	47238	50534	44869	67579	55286	51264	85026	79243	53731	52475	49545	47135	49537	45707
128C	69732	45130	45573	46076	49324	39138	51431	66276	63982	73621	58815	51175	45128	47351	86780	43820
129N	45034	57339	54755	53618	84355	53741	70529	77355	53398	47248	82876	53705	46233	48358	44707	54601
129C	75351	59913	50650	46390	80265	51135	73518	73786	51023	74112	52791	48937	86092	70714	42947	49450
130N	44067	51551	52131	50452	59128	58595	87070	42570	48786	47147	47368	42719	73152	72191	76615	50409
130C	51370	52524	71200	68342	53729	66735	54179	66827	68545	86582	57450	84217	50502	46306	87124	47251
131N	37512	62211	46040	53819	56968	72374	57502	57056	57326	63141	57251	46103	51760	50259	77501	44893
131C	49419	74051	68620	83366	72848	83459	49087	46282	52626	49903	45101	45918	45739	45487	64149	GIS
132N	53612	42541	69030	51499	84561	50313	52154	48746	44511	78086	47480	45831	55838	52538	44820	GIS
132C	46642	44291	48024	51559	78317	49941	48615	51319	51123	51464	46008	46743	46246	45238	74682	GIS
133N	46442	66984	46931	58885	66352	47232	86840	50273	51520	80287	57498	48222	76896	48615	48769	GIS
133C	Low	Low	Low	Low	Low	Low	Low	Low	Low	Low	Low	Low	Low	Low	Low	Low
134N	High	High	High	High	High	High	High	High	High	High	High	High	High	High	High	High

Table 6.3: TMT-MS ANOVA Table

			ANOVA p -values with Tukey Adjustment						Difference (AD - CT)					
Gene ID | Unirprot ID	F-Value	Pr(>F)	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA
ALB|P02768	0.48887791	0.690420873	0.89793558	0.999594943	0.96432078	0.84908803	0.630942157	0.981868149	-0.063263322	0.009186191	0.041026296	0.072449512	0.104289618	0.031840106
C3|P01024	1.59429782	0.192277241	0.634546933	0.807016256	0.940960859	0.159239454	0.907279632	0.432062001	-0.085730587	0.062847139	-0.039047686	0.148577726	0.046682901	-0.101894825
FN1|P02751	0.89731104	0.443682271	0.841309859	0.997246177	0.869269618	0.917184738	0.371383771	0.757451727	0.030512959	0.007099267	-0.026874708	-0.023413692	-0.057387667	-0.033973975
C4B|P0C0L5	1.06359786	0.365843082	0.835839078	0.596880843	0.310256501	0.981018761	0.835972555	0.967275064	-0.068420331	-0.099073606	-0.134247664	-0.030653274	-0.065827333	-0.035174058
C4A|P0C0L4	2.71074086	0.046428111	0.398912175	0.78434816	0.614746632	0.060039083	0.974151362	0.122031645	0.294618495	-0.171412736	0.217819145	-0.466031231	-0.076799351	0.389231881
A2M|P01023	3.2996656	0.021598496	0.192819955	0.112638003	0.014319858	0.997161397	0.790622714	0.879207825	0.061388526	0.067439797	0.088802174	0.006051271	0.027413648	0.021362377
SPARCL1|Q14515	9.9696779	4.00E-06	0.000138923	0.040264067	6.83E-06	0.295835705	0.966927351	0.094459222	0.229652554	0.137853957	0.25326742	-0.091798597	0.023614866	0.115413463
TF|P02787	2.31737052	0.077073361	0.999830766	0.382995823	0.185451461	0.349592677	0.165862967	0.979933826	-0.003892071	0.077753477	0.095949363	0.081645548	0.099841434	0.018195886
FCGBP|Q9Y6R7	21.2062133	7.49E-12	1.71E-09	0.43212066	1.54E-07	2.14E-06	0.63735382	0.000134496	-0.774670703	-0.170901712	-0.642273401	0.603768991	0.132397302	-0.471371689
CP|P00450	0.59075926	0.62179271	0.999164214	0.706542368	0.995454492	0.630880645	0.982755539	0.815866421	-0.011092584	0.087298993	0.018630138	0.098391577	0.029722722	-0.068668855
CHGB|P05060	8.62230513	2.19E-05	0.826535362	0.011881298	5.45E-05	0.129020885	0.002189735	0.494227249	0.037083155	0.130430914	0.187419324	0.093347759	0.150336168	0.056988409
HSPG2|P98160	0.64697481	0.585792512	0.898350192	0.748923842	0.534701269	0.992152884	0.93004395	0.987878692	-0.023741793	-0.033207564	-0.043626958	-0.00946577	-0.019885165	-0.010419394
CFH|P08603	0.04505591	0.987263171	0.998531838	0.985233634	0.993217131	0.997810016	0.99965546	0.999724569	0.00856181	0.018203534	0.013634117	0.009641724	0.005072307	-0.004569417
APOB|P04114	0.22299306	0.880336326	0.990848178	0.968499184	0.989870702	0.875769919	0.927969592	0.998501123	0.041307891	-0.061598734	-0.040647904	-0.102906625	-0.081955795	0.02095083
SERPINA1|P01009	0.06625047	0.97772151	0.999970634	0.994971873	0.997789507	0.992016892	0.999089691	0.971539134	0.00401129	-0.021829819	0.016164317	-0.025841108	0.012153027	0.037994136
FAT2|Q9NYQ8	1.99508723	0.116257838	0.098658	0.835618451	0.956322691	0.427520601	0.232093475	0.984749168	-0.147864412	-0.052199085	-0.031061614	0.095665327	0.116802798	0.021137471
SPP1|P10451	27.3800163	1.06E-14	0.284177182	1.64E-07	4.43E-13	0.000700377	2.19E-08	0.114750947	-0.068686076	-0.217467218	-0.298265735	-0.148781142	-0.229579659	-0.080798517
LRP1|Q07954	3.26392688	0.022628525	0.236068108	0.714158369	0.016037389	0.819605032	0.749008922	0.211250852	-0.040919615	-0.022338094	-0.061781715	0.018581522	-0.020862099	-0.039443621
GSN|P06396	0.57733044	0.630598786	0.985725084	0.997300461	0.627485447	0.998613636	0.842146933	0.74010989	-0.011867187	-0.006560321	-0.039128958	0.005306866	-0.027261772	-0.032568638
RELN|P78509	2.3270414	0.076123433	0.091867239	0.999208665	0.785528387	0.113248587	0.432678594	0.846564221	-0.142246895	-0.007688231	-0.053982905	0.134558664	0.08826399	-0.046294673
CHGA|P10645	7.0446014	0.000164569	0.006139845	0.000538149	0.000753636	0.936016513	0.975123335	0.997698928	0.283267252	0.332712677	0.317812476	0.049445426	0.034545224	-0.014900201
ENPP2|Q13822	3.45917866	0.017540785	0.046203699	0.974222074	0.108479798	0.115259762	0.963040544	0.245071076	-0.153103854	-0.024112119	-0.126035811	0.128991736	0.027068043	-0.101923693
NRCAM|Q92823	10.0375246	3.68E-06	0.001747814	0.000473932	2.67E-06	0.99474813	0.533211369	0.671552488	0.178391434	0.190148014	0.241371936	0.01175658	0.062980502	0.051223922
CNTN1|Q12860	6.47487162	0.000343476	0.398553953	0.770267791	0.000286836	0.918263034	0.067404523	0.008057763	0.045580359	0.027227447	0.114723622	-0.018352912	0.069143263	0.087496175
COL6A3|P12111	0.85081179	0.467781397	0.983792323	0.876298973	0.428847344	0.982012524	0.6754379	0.871162799	-0.011975801	-0.024198968	-0.047804757	-0.012223167	-0.035828956	-0.023605789
GC|P02774	2.01298092	0.113649126	0.468900491	0.763891357	0.999965885	0.073608388	0.407923922	0.767284694	-0.133615833	0.087309529	0.003987359	0.220925362	0.137603191	-0.08332217
CHL1|O00533	8.12372984	4.13E-05	0.005163857	0.00092268	4.71E-05	0.979511756	0.723394298	0.91081621	0.180892771	0.201658453	0.234992006	0.020765682	0.054099235	0.033333553
C7|P10643	9.45982795	7.59E-06	0.00132803	0.067936818	4.69E-06	0.519916973	0.659018726	0.045591194	-0.219572722	-0.140661051	-0.284332992	0.078911671	-0.064760269	-0.14367194
NRXN3|Q9Y4C0	8.14066387	4.04E-05	0.021920932	0.02337146	1.13E-05	0.999624804	0.252990293	0.186670378	0.135964156	0.131271747	0.219643908	-0.004692409	0.083679752	0.088372161
MEGF8|Q7Z7M0	0.92144694	0.431582775	0.830418934	0.867854298	0.992374023	0.367552625	0.653451148	0.954731665	-0.039919656	0.035193424	0.01246828	0.075113081	0.052387936	-0.022725144
PLG|P00747	0.7134568	0.545101777	0.630234118	0.999771702	0.934167784	0.564422713	0.912933126	0.899844632	-0.119552584	0.008360151	-0.056328593	0.127912735	0.06322399	-0.064688745
TNXB|P22105	10.075929	3.51E-06	0.000357284	0.999999324	0.002282835	0.000291313	0.895527298	0.001915854	-0.163278112	-0.000477856	-0.136309729	0.162800256	0.026968383	-0.135831874
CFB|P00751	4.68480899	0.003532272	0.269195156	0.305183142	0.804901153	0.002588087	0.750773842	0.034812845	-0.182909575	0.170712831	-0.086163384	0.353622406	0.096746191	-0.256876215
NELL2|Q99435	11.0341787	1.07E-06	0.001161206	0.000556563	5.19E-07	0.999737348	0.399462279	0.427488663	0.206828172	0.211668234	0.289192633	0.004840062	0.082364461	0.077524399
C5|P01031	0.14250909	0.934360444	0.999996951	0.999317014	0.967628907	0.99962091	0.964438735	0.93290494	0.002333974	0.013818511	-0.050073453	0.011484537	-0.052407426	-0.063891964
NRXN1|Q9ULB1	4.76724206	0.003171407	0.059704228	0.163327556	0.001538093	0.957508647	0.72319132	0.375530594	0.112490208	0.090262534	0.157335525	-0.022227675	0.044845316	0.067072991
LAMA2|P24043	1.71536943	0.165360266	0.964062062	0.356177868	0.870174603	0.153732476	0.595210783	0.786171241	-0.013385687	0.044903078	0.020396939	0.058288765	0.033782626	-0.024506139
IGHG1|P01857	11.1589549	9.13E-07	0.000259436	0.986017899	0.000184202	0.000749529	0.999203417	0.0005622	-0.484287002	-0.038714487	-0.469739003	0.445572515	0.014547999	-0.431024516
F5|P12259	8.2290272	3.61E-05	0.000614342	0.928431764	0.002548009	0.004285637	0.935374893	0.016333292	-0.282982358	-0.042496555	-0.242488091	0.240485803	0.040494267	-0.199991537
HPX|P02790	0.2227478	0.880508008	0.906573168	0.993988385	0.905146076	0.973150013	0.999989391	0.974661998	0.062279486	0.023138381	0.059536532	-0.039141104	-0.002742954	0.03639815
SERPINA3|P01011	2.34591466	0.074302454	0.553364656	0.511827871	0.042778559	0.999991337	0.595100265	0.590521042	-0.095722608	-0.097787911	-0.183256767	-0.002065303	-0.087534159	-0.085468856
SERPINC1|P01008	0.94458189	0.420244997	0.502880161	0.999975997	0.796616309	0.514304178	0.947185917	0.810503678	-0.125946107	-0.003555971	-0.078457917	0.122390136	0.04748819	-0.074901946
FBLN1|P23142	14.0262572	2.81E-08	2.59E-05	0.951570569	1.40E-05	0.000172942	0.999579044	0.000104985	-0.143622976	-0.015664277	-0.140543491	0.127958699	0.003079485	-0.124879214
NRXN2|Q9P2S2	3.72698127	0.012362972	0.616774463	0.254150328	0.006693593	0.934835279	0.200315979	0.491971097	0.048176252	0.071192181	0.123500203	0.023015929	0.075323951	0.052308022
APP|P05067	1.07318853	0.361737864	0.975058303	0.682707401	0.348460828	0.907377011	0.626085638	0.951724662	0.022688016	0.05848197	0.085246306	0.035793954	0.06255829	0.026764337
FGB|P02675	1.47707641	0.22224208	0.864121122	0.944126759	0.186030016	0.995197479	0.639213498	0.458494298	-0.099914891	-0.06974466	-0.24586849	0.030170231	-0.145953598	-0.176123829
ITIH4|Q14624	0.38730788	0.762273426	0.801634356	0.908780026	0.769133778	0.993860696	0.999999335	0.991817867	0.100425724	0.072111072	0.101733802	-0.028314652	0.001308078	0.02962273

			ANOVA p -values with Tukey Adjustment						Difference (AD - CT)					
Gene ID | Unirprot ID	F-Value	Pr(>F)	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA
SCG2|P13521	16.0362186	2.62E-09	0.02851025	1.61E-06	7.62E-09	0.074793016	0.004468312	0.780263086	0.155945237	0.289181153	0.338355559	0.133235916	0.182410322	0.049174406
PTPRS|Q13332	8.85546959	1.63E-05	0.004487514	0.006682571	6.34E-06	0.996577086	0.471324262	0.318449331	0.087522861	0.082131885	0.123348261	-0.005390976	0.0358254	0.041216376
F2|P00734	1.43362931	0.234419914	0.483593425	0.998394185	0.565279325	0.373626076	0.997092777	0.44404567	-0.127628467	0.014357508	-0.110290795	0.141985975	0.017337672	-0.124648302
TTR|P02766	6.00858668	0.000628767	0.009179375	0.569264102	0.001333151	0.208373224	0.978667319	0.067830437	-0.193875995	-0.076550178	-0.217172717	0.117325817	-0.023296722	-0.140622539
APOE|P02649	8.31106478	3.25E-05	0.051445202	0.073289831	8.34E-06	0.996672113	0.115569228	0.058205072	0.117574777	0.108115321	0.215903497	-0.009459456	0.09832872	0.107788175
CNDP1|Q96KN2	4.64921345	0.003700556	0.037587728	0.36153785	0.002890852	0.673166621	0.90330226	0.2350461	0.132740453	0.07818978	0.165067104	-0.054550674	0.032326651	0.086877325
FBN1|P35555	5.67183542	0.000974238	0.051616102	0.872875507	0.097489516	0.005023269	0.979672103	0.010231567	-0.097618249	0.027926142	-0.083385263	0.125544391	0.014232986	-0.111311405
PAM|P19021	12.6933678	1.40E-07	0.031214326	1.11E-05	3.43E-07	0.172213402	0.036576931	0.923058525	0.131965986	0.228357484	0.256305323	0.096391498	0.124339337	0.027947839
CLU|P10909	2.5283622	0.058760291	0.991989366	0.808002671	0.06434247	0.93349179	0.136399648	0.378284659	0.007711408	0.023618754	0.064340449	0.015907346	0.056629041	0.040721695
C1S|P09871	2.39738977	0.06954983	0.273353389	0.999315561	0.172362949	0.32007269	0.998768934	0.206949294	-0.050078375	-0.003345291	-0.054106225	0.046733084	-0.00402785	-0.050760934
APLP1|P51693	14.1000763	2.57E-08	4.53E-05	0.000579321	1.27E-08	0.877734685	0.476688269	0.108919427	0.199812943	0.167878593	0.259924682	-0.03193435	0.060111739	0.092046089
CNTN2|Q02246	2.11182096	0.100229791	0.878337732	0.641728601	0.072368143	0.977286739	0.358989355	0.588976415	0.039173475	0.060181547	0.122057242	0.021008072	0.082883768	0.061875696
CACNA2D1|P54289	10.2669909	2.76E-06	0.008346358	6.74E-05	4.35E-06	0.631918291	0.31304216	0.954027648	0.190802907	0.260555972	0.28944172	0.069753065	0.098638813	0.028885748
KNG1|P01042	0.73185589	0.534212836	0.865547867	0.896050849	0.999998104	0.450744995	0.843647596	0.891555278	-0.076150591	0.06712313	0.001623423	0.143273721	0.077774014	-0.065499707
ITIH1|P19827	0.11773896	0.94960564	0.981779298	0.999490792	0.998663908	0.960508715	0.947966584	0.999975373	-0.050609001	0.014702176	0.019838748	0.065311177	0.070447749	0.005136572
C6|P13671	1.32500349	0.267630687	0.385250162	0.999999923	0.671144063	0.367910017	0.949539873	0.655049564	-0.176408664	0.000644834	-0.119021604	0.177053498	0.05738706	-0.119666438
AGT|P01019	1.3732034	0.252391119	0.845080045	0.983596806	0.237441824	0.964740931	0.743012872	0.415138817	0.024634956	0.010612946	0.053885022	-0.01402201	0.029250066	0.043272076
CRTAC1|Q9NQ79	3.41631667	0.018549979	0.074430871	0.050886349	0.026534789	0.999787242	0.993515506	0.997789669	0.097399388	0.100707894	0.107581704	0.003308506	0.010182316	0.00687381
FGG|P02679	1.65971296	0.177256526	0.873690531	0.900395274	0.140357455	0.999774548	0.538318242	0.457052795	-0.108750322	-0.096639775	-0.294173113	0.012110547	-0.185422791	-0.197533338
IGHG2|P01859	4.84978502	0.002847073	0.002579419	0.551526017	0.042756814	0.097686109	0.698659079	0.548782999	-0.440453098	-0.15859896	-0.311393514	0.281854139	0.129059584	-0.152794555
NEO1|Q92859	10.0466381	3.64E-06	0.003741427	0.120140747	1.69E-06	0.556003757	0.341679544	0.011713324	0.112769486	0.070619244	0.165231712	-0.042150242	0.052462226	0.094612469
SERPIND1|P05546	0.72718607	0.536961064	0.80971264	0.959062496	0.966938963	0.501995224	0.965983723	0.754411077	-0.056409372	0.030788686	-0.027887982	0.087198057	0.02852139	-0.058676668
APOA4|P06727	3.07884616	0.02879557	0.286907566	0.631501457	0.017504102	0.923399214	0.697863015	0.286175028	0.18311037	0.119589828	0.290820799	-0.063520541	0.107710429	0.17123097
ITIH2|P19823	0.15242326	0.928030393	0.993575764	0.999999228	0.943137937	0.992289154	0.992206274	0.936440816	0.032328996	-0.001538763	0.065553857	-0.033867759	0.033224862	0.067092621
EFEMP1|Q12805	2.23277131	0.085892185	0.093273699	0.970935727	0.432198815	0.216302939	0.785800152	0.703708358	0.061752988	0.01137918	0.037970869	-0.050373807	-0.023782119	0.026591688
CLSTN1|O94985	3.89603878	0.009911264	0.092966765	0.104916853	0.00610904	0.999434778	0.835731784	0.757048589	0.099749266	0.094863937	0.134185941	-0.004885329	0.034436676	0.039322005
DKK3|Q9UBP4	4.10886082	0.007502965	0.253154691	0.193334833	0.00316732	0.999715544	0.415439877	0.445939012	0.052833712	0.055433622	0.09516103	0.00259991	0.042327318	0.039727408
SEMA7A|O75326	2.18079448	0.091790628	0.541030073	0.968819191	0.09300922	0.80019865	0.79329226	0.22862421	0.078882774	0.026064578	0.131244172	-0.052818196	0.052361398	0.105179594
AFM|P43652	0.57927611	0.629318117	0.993170316	0.772349868	0.968294917	0.613836247	0.88481307	0.950361493	-0.030233401	0.104967532	0.048765135	0.135200933	0.078998535	-0.056202398
HP|P00738	0.67356848	0.56926534	0.782667077	0.99827572	0.6417515	0.859450274	0.997743866	0.736820151	-0.209802284	-0.036670662	-0.249502974	0.173131622	-0.03970069	-0.212832312
A1BG|P04217	0.95082246	0.417229947	0.707818585	0.972160497	0.886078411	0.428581121	0.979172648	0.631376999	-0.094202349	0.037336007	-0.060823169	0.131538357	0.03337918	-0.098159177
KRT1|P04264	0.47160769	0.702434452	0.968601121	0.999996837	0.895646216	0.962916958	0.648163044	0.899246224	-0.103671327	0.004573007	0.152365628	0.108244334	0.256036955	0.147792621
C1R|P00736	2.81704257	0.040456677	0.110232812	0.901878327	0.081148129	0.369495879	0.99999885	0.314634565	-0.074336674	-0.02195045	-0.074801771	0.052386224	-0.000465097	-0.052851321
APOA1|P02647	0.52510261	0.665557867	0.982132381	0.940072979	0.615049837	0.9976943	0.846680791	0.917369896	0.043148986	0.064335823	0.133838327	0.021186837	0.090689342	0.069502504
VGF|O15240	15.6055007	4.33E-09	0.005536477	3.35E-07	2.26E-08	0.126135166	0.043869653	0.978226381	0.308808433	0.50934507	0.543919768	0.200536637	0.235111335	0.034574698
SERPING1|P05155	3.06183164	0.029439987	0.210670604	0.938897589	0.040562236	0.493918098	0.928054397	0.151205142	-0.088495586	-0.025462572	-0.115229019	0.063033014	-0.026733434	-0.089766448
IGHA1|P01876	3.14181479	0.02652999	0.08971556	0.969154054	0.086867085	0.213167439	0.999555187	0.215579422	-0.360440873	-0.067337208	-0.344617786	0.293103665	0.015823087	-0.277280577
CST3|P01034	11.3897536	6.87E-07	0.000366018	0.819347394	1.73E-05	0.00639774	0.956253934	0.000525447	0.167243768	0.034657641	0.187355565	-0.132586127	0.020111797	0.152697924
PTPRZ1|P23471	6.95648461	0.000184362	0.026323025	0.999862498	0.002757956	0.028428985	0.943052996	0.0028954	0.092462044	0.002306461	0.110142731	-0.090155583	0.017680687	0.10783627
C2|P06681	1.57988008	0.195746045	0.731914806	0.829716073	0.804699341	0.236872328	0.997874804	0.275469511	-0.074403164	0.059821124	-0.061796786	0.134224288	0.012606378	-0.121617909
PTPRF|P10586	12.1926209	2.57E-07	5.13E-05	0.021001263	3.05E-07	0.290530517	0.826281863	0.032850867	0.137613606	0.085155516	0.162459131	-0.05245809	0.024845525	0.077303615
NCAM2|O15394	12.3573261	2.10E-07	8.48E-05	0.770634278	1.09E-05	0.002514598	0.995221561	0.000504451	0.17813095	0.037458867	0.187301689	-0.140672083	0.009170739	0.149842822
NCAM1|P13591	12.6543682	1.46E-07	8.69E-05	0.175336543	4.16E-07	0.063495501	0.790912042	0.002403615	0.145409854	0.065031863	0.17453543	-0.080377991	0.029125577	0.109503567
SORL1|Q92673	0.38560606	0.7634974	0.999838704	0.846792751	0.860026396	0.885456243	0.897610243	0.999958466	0.003882871	0.040288821	0.037981776	0.036405951	0.034098905	-0.002307045
SCG3|Q8WXD2	8.58715257	2.29E-05	0.01169402	0.000175104	5.19E-05	0.70538667	0.571299644	0.997369287	0.172350683	0.231072597	0.24117711	0.058721914	0.068826427	0.010104513
FGA|P02671	1.08128213	0.358304927	0.922642231	0.933732314	0.302370362	0.999950611	0.706862253	0.653532279	-0.092235423	-0.084789746	-0.243578086	0.007445678	-0.151342662	-0.15878834
PTPRD|P23468	16.2000164	2.16E-09	2.26E-06	0.330275652	1.00E-07	0.00173593	0.984618783	0.000203565	0.175110248	0.054745134	0.186464438	-0.120365113	0.01135419	0.131719303

			ANOVA p -values with Tukey Adjustment						Difference (AD - CT)					
Gene ID | Unirprot ID	F-Value	Pr(>F)	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA
VWF|P04275	1.3751776	0.251784344	0.916302355	0.702061436	0.749992542	0.313617948	0.3480429	0.999544119	-0.0254996	0.04138857	0.037404301	0.066888169	0.062903901	-0.003984269
COL6A1|P12109	1.51937355	0.210956964	0.329685867	0.691410913	0.999948142	0.920296749	0.270927074	0.629886901	-0.068285094	-0.043048513	0.002007924	0.025236581	0.070293018	0.045056437
KLK6|Q92876	0.7735167	0.510163107	0.589296694	0.704674188	0.528980511	0.996385369	0.999991166	0.993927565	0.03947025	0.032782348	0.040345645	-0.006687902	0.000875395	0.007563297
NFASC|O94856	8.14935332	3.99E-05	0.02947684	0.041370857	1.05E-05	0.997161965	0.200854791	0.114862111	0.104975817	0.097569088	0.176530425	-0.00740673	0.071554607	0.078961337
ECM1|Q16610	5.59851432	0.001071829	0.438329846	0.000458421	0.11319566	0.069225096	0.910457037	0.226697965	0.058404966	0.152703117	0.083253902	0.094298151	0.024848936	-0.069449215
MAN2A2|P49641	1.31766584	0.270023556	0.999909929	0.454490266	0.491564289	0.504745333	0.543702388	0.999674232	0.002765641	0.063008651	0.059039448	0.06024301	0.056273807	-0.003969203
COL1A1|P02452	1.39775873	0.244939355	0.861661329	0.971815904	0.628400656	0.609204787	0.192257191	0.870782392	-0.035553368	0.019327274	0.05167502	0.054880643	0.087228388	0.032347746
PROS1|P07225	2.20543017	0.08894731	0.117210337	0.991896564	0.438053698	0.195456941	0.835207488	0.607544709	-0.088716307	-0.01100245	-0.056644945	0.077713858	0.032071362	-0.045642496
LTBP4|Q8N2S1	18.2967197	1.94E-10	3.75E-05	0.999999367	4.37E-07	2.60E-05	0.89263995	2.53E-07	-0.152719483	0.000385659	-0.175205046	0.153105142	-0.022485563	-0.175590705
NID1|P14543	6.6861259	0.000261357	0.002908391	0.806239016	0.002779503	0.037664508	0.998291052	0.040628343	-0.110250732	-0.027256019	-0.105186028	0.082994713	0.005064704	-0.077930008
APLP2|Q06481	0.5439244	0.652833056	0.82534297	0.984116189	0.999988369	0.609712851	0.791429988	0.986268227	-0.049427572	0.02007083	0.001738963	0.069498402	0.051166535	-0.018331867
LAMB2|P55268	4.11947765	0.007399478	0.865837823	0.077773049	0.992617597	0.009480349	0.951163227	0.02898218	-0.017893361	0.054277324	-0.006064538	0.072170685	0.011828824	-0.060341861
IGHG3|P01860	10.3819681	2.39E-06	0.000308442	0.872720092	0.056444562	9.76E-06	0.283504001	0.004868378	-0.622247242	0.111054205	-0.363807431	0.733301447	0.258439812	-0.474861635
AGRN|O00468	1.07929407	0.359145513	0.572806672	0.773331479	0.307593581	0.98403412	0.981412718	0.86820926	0.036602033	0.026527332	0.046980122	-0.010074701	0.010378089	0.02045279
PKM|P14618	26.1545069	3.77E-14	0.103546667	2.82E-06	4.68E-05	1.67E-11	4.27E-10	0.871315639	0.094973813	-0.21052424	-0.181018146	-0.305498053	-0.27599196	0.029506093
PLXNB2|O15031	2.52157054	0.059276974	0.071508784	0.099553547	0.387419336	0.996908165	0.763235198	0.859573492	-0.081737308	-0.074977359	-0.050393829	0.00675995	0.03134348	0.02458353
C9|P02748	0.27962137	0.840063947	0.992947005	0.956370495	0.99334826	0.862881599	0.999997421	0.852738721	-0.027673526	0.050601098	-0.025786651	0.078274624	0.001886875	-0.076387749
FSTL4|Q6MZW2	2.69103299	0.047627048	0.819230175	0.249709083	0.040013284	0.777459599	0.306949742	0.859561048	0.052173786	0.108167664	0.152244004	0.055993878	0.100070217	0.04407634
IGFBP6|P24592	1.6744892	0.174021184	0.524077565	0.984816345	0.516766357	0.30922747	0.999927547	0.292759877	-0.075185787	0.018966932	-0.072075437	0.094152719	0.00311035	-0.091042369
CFI|P05156	1.57135216	0.197825511	0.999990571	0.237109826	0.845016055	0.260411504	0.863933945	0.67077794	0.002517638	0.155737791	0.066098882	0.153220153	0.063581244	-0.089638909
NCAN|O14594	1.28485107	0.280966615	0.693626264	0.542146543	0.220052065	0.996821516	0.869166168	0.9405175	0.067859482	0.080543939	0.113652492	0.012684457	0.04579301	0.033108553
NID2|Q14112	3.77511247	0.011609095	0.069367106	0.986661163	0.271126791	0.025996525	0.868283538	0.128402862	-0.105024023	0.014029135	-0.073451128	0.119053158	0.031572895	-0.087480263
SERPINF1|P36955	9.27647657	9.56E-06	0.004329836	0.631985074	0.068723453	3.76E-05	0.682319959	0.001334997	-0.136932096	0.046551681	-0.093998079	0.183483777	0.042934017	-0.14054976
B4GAT1|O43505	5.77612962	0.000850595	0.2977124	0.131141434	0.000308358	0.981908006	0.110967216	0.217541009	0.054519793	0.06599274	0.122070206	0.011472947	0.067550413	0.056077466
PTGDS|P41222	1.64117666	0.181395942	0.164466998	0.98281514	0.828295646	0.303505434	0.554869089	0.962368363	0.059258954	0.010238632	0.023165059	-0.049020323	-0.036093895	0.012926428
FBLN2|P98095	1.10048893	0.350272694	0.490966695	0.995509561	0.531984052	0.622869092	0.999072158	0.670865692	-0.056508384	-0.009062208	-0.051233008	0.047446176	0.005275376	-0.042170801
ATRN|O75882	4.80834079	0.003005536	0.066053799	0.684175222	0.654374064	0.002156805	0.478631478	0.094342641	-0.097344132	0.042335366	-0.043147679	0.139679499	0.054196454	-0.085483045
LAMB1|P07942	2.94880834	0.034098598	0.457852216	0.446454266	0.995263955	0.017925576	0.29511429	0.558729844	-0.038704188	0.038140615	0.005947906	0.076844803	0.044652094	-0.032192709
CNTNAP4|Q9C0A0	2.38261077	0.070883023	0.862627465	0.973368286	0.070215337	0.982696866	0.372942772	0.172758192	0.043294802	0.02313713	0.129343484	-0.020157672	0.086048682	0.106206354
ECM2|O94769	1.3118074	0.271948126	0.781774032	0.962660589	0.239078374	0.963500141	0.815403828	0.493690681	-0.040963984	-0.02044291	-0.077746147	0.020521074	-0.036782163	-0.057303237
LTBP2|Q14767	12.2150738	2.50E-07	0.032594378	0.727025889	4.90E-07	0.291056864	0.042361694	4.58E-05	-0.138899498	-0.050977117	-0.267850796	0.087922381	-0.128951298	-0.216873679
AZGP1|P25311	0.75065888	0.523253963	0.470435637	0.976247707	0.953870907	0.711758375	0.754796176	0.999633189	-0.114402198	-0.031692097	-0.039119217	0.082710101	0.075282981	-0.00742712
FLNA|P21333	0.81042156	0.489564697	0.900285948	0.672634767	0.445825184	0.976240763	0.875360776	0.986363249	-0.044989456	-0.071427714	-0.092135735	-0.026438259	-0.047146279	-0.02070802
KRT10|P13645	1.00282781	0.392810795	0.999933949	0.570330853	0.606733772	0.616681028	0.65360381	0.999744369	0.011450799	0.253019319	0.236211522	0.24156852	0.224760723	-0.016807796
MMP2|P08253	0.82319209	0.482591463	0.994177838	0.621846371	0.970303068	0.467700671	0.894865439	0.851868318	-0.010316374	0.047628232	0.01716653	0.057944607	0.027482905	-0.030461702
KRT9|P35527	0.39875404	0.754053858	0.850588155	0.996882056	0.996435025	0.926629252	0.718519771	0.972450014	-0.205518928	-0.051065885	0.05219182	0.154453043	0.257710748	0.103257705
SERPINF2|P08697	0.84666736	0.469980062	0.86111382	0.872145591	0.989322245	0.410640642	0.674455119	0.964907544	-0.069905602	0.065861417	0.026507621	0.135767019	0.096413223	-0.039353796
HBB|P68871	2.17938887	0.091955499	0.381331987	0.988199661	0.132647843	0.561312451	0.961040177	0.240097179	-0.549828111	-0.108398335	-0.712220673	0.441429775	-0.162392562	-0.603822337
LGALS3BP|Q08380	3.67292397	0.013268008	0.279616273	0.895880727	0.187555377	0.060689261	0.999338869	0.0304619	-0.070661199	0.026937605	-0.075310167	0.097598804	-0.004648969	-0.102247773
DAG1|Q14118	7.5784509	8.29E-05	0.011764463	0.716505809	0.000183371	0.154198747	0.755122102	0.00762311	0.048669423	0.016115177	0.063615101	-0.032554246	0.014945678	0.047499924
CTSD|P07339	3.31758683	0.021099662	0.039504559	0.726614252	0.053867147	0.328062211	0.994151343	0.424247425	-0.165997973	-0.062578921	-0.150796977	0.103419052	0.015200995	-0.088218057
COL12A1|Q99715	2.88952395	0.036826698	0.069596788	0.838914045	0.089491052	0.338999193	0.995676765	0.422006405	-0.097115002	-0.031969733	-0.088363905	0.065145269	0.008751097	-0.056394172
PSAP|P07602	0.63148847	0.595567693	0.681184428	0.990899608	0.704751241	0.835975892	0.99968826	0.860960947	0.04008888	0.010382391	0.036786777	-0.029706489	-0.003302102	0.026404387
CNTNAP2|Q9UHC6	2.27186581	0.08170083	0.169920386	0.529706822	0.076748622	0.874481884	0.994548016	0.718900879	0.119389618	0.07633245	0.133284248	-0.043057168	0.01389463	0.056951799
ITIH5|Q86UX2	21.2820258	6.89E-12	3.98E-09	0.574398073	1.40E-07	1.54E-06	0.745916323	4.59E-05	-0.245173681	-0.046999513	-0.208733297	0.198174168	0.036440385	-0.161733784
IGHG4|P01861	0.8348921	0.476272482	0.607847828	0.989399487	0.58647001	0.782424108	0.999990199	0.771510796	-0.260547772	-0.064336505	-0.254423722	0.196211267	0.00612405	-0.190087217
TGFBI|Q15582	0.61358246	0.607006136	0.945972038	0.995266216	0.590286677	0.988041079	0.908298526	0.730170787	0.02097417	0.008787402	0.045483998	-0.012186769	0.024509828	0.036696597

			ANOVA p -values with Tukey Adjustment						Difference (AD - CT)					
Gene ID | Unirprot ID	F-Value	Pr(>F)	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA
CD163|Q86VB7	0.84172692	0.472611914	0.870028151	0.898688063	0.959896352	0.461103497	0.990107408	0.609290893	0.03243335	-0.028687555	0.019984072	-0.061120905	-0.012449278	0.048671627
AHSG|P02765	1.22391131	0.302368309	0.973271839	0.654713444	0.714051074	0.392571977	0.443201625	0.999281044	-0.042338213	0.110849522	0.099246477	0.153187736	0.14158469	-0.011603045
C8A|P07357	0.57154518	0.634416198	0.999557172	0.720862683	0.801433274	0.79007441	0.861731795	0.998241917	0.01092377	0.103961406	0.087764315	0.093037636	0.076840545	-0.016197091
ALDOA|P04075	29.792571	9.22E-16	0.016341149	4.31E-06	5.35E-05	5.29E-13	7.75E-12	0.897265701	0.128252923	-0.213776253	-0.185800453	-0.342029176	-0.314053376	0.0279758
MRC1|P22897	4.37422239	0.005302329	0.017104745	0.670325567	0.015585574	0.228347651	0.999344964	0.238271165	0.13714657	0.050690833	0.131731484	-0.086455738	-0.005415087	0.081040651
MCAM|P43121	5.07959176	0.00210875	0.927692754	0.427025016	0.002120466	0.815234669	0.019219681	0.156599011	0.025426557	0.06133821	0.14270004	0.035911652	0.117273482	0.08136183
KRT2|P35908	0.7388347	0.530125406	0.852473886	0.473288182	0.709602073	0.928498721	0.996275417	0.975321081	0.175502245	0.306809185	0.221530361	0.13130694	0.046028116	-0.085278824
IGKC|P01834	7.00377011	0.000173459	0.004429987	0.986480962	0.005339008	0.010999367	0.995663665	0.013602737	-0.381506611	-0.036990336	-0.356656564	0.344516275	0.024850048	-0.319666228
NUCB1|Q02818	1.28458352	0.281057481	0.799793331	0.969999368	0.766828972	0.522182954	0.230419678	0.954125371	-0.027832647	0.013330245	0.028206893	0.041162891	0.05603954	0.014876649
NPTXR|O95502	23.9961958	3.66E-13	0.003304634	8.24E-08	4.99E-13	0.09676144	0.000109889	0.164001839	0.240834581	0.39839547	0.532231909	0.15756089	0.291397328	0.133836439
KRT16|P08779	0.40054793	0.752767789	0.998828223	0.825962639	0.998393065	0.749807808	0.988899379	0.886422763	-0.045534161	0.256192802	0.048118236	0.301726963	0.093652397	-0.208074565
BTD|P43251	1.77657473	0.153157499	0.985549126	0.173848432	0.485346377	0.34117992	0.722341269	0.902863379	0.010036246	0.057602475	0.039126441	0.047566229	0.029090195	-0.018476034
PLTP|P55058	0.75325208	0.521756038	0.998778955	0.980185443	0.624150378	0.950205155	0.534228896	0.843568026	-0.004540837	0.011366964	0.034550787	0.015907801	0.039091624	0.023183823
CALR|P27797	2.15985193	0.094277128	0.282287134	0.674543345	0.074444933	0.895281529	0.947758791	0.561719739	0.054054415	0.033091382	0.069913764	-0.020963033	0.015859348	0.036822381
HRG|P04196	0.55389124	0.646151479	0.898896372	0.974556695	0.975772452	0.67550675	0.669942431	0.999998087	-0.077648551	0.04594109	0.044120643	0.123589641	0.121769194	-0.001820447
LAMC1|P11047	5.91705862	0.00070817	0.154244547	0.207530773	0.834109163	0.000391309	0.52691483	0.021777766	-0.054598505	0.049355654	-0.02073693	0.103954159	0.033861574	-0.070092585
SERPINI1|Q99574	1.53613859	0.206634557	0.728530055	0.19248326	0.330292159	0.793021777	0.933295877	0.984201035	0.055078841	0.103351485	0.085554265	0.048272643	0.030475424	-0.017797219
L1CAM|P32004	0.33627775	0.799121568	0.999606144	0.816796535	0.935715622	0.871452531	0.964875977	0.989102925	0.004240742	0.03509028	0.022970939	0.030849537	0.018730196	-0.012119341
CPE|P16870	1.56015301	0.20058799	0.180974657	0.353247109	0.66912209	0.97319827	0.756000165	0.942308454	-0.093927044	-0.074314662	-0.04988139	0.019612382	0.044045654	0.024433272
BCAN|Q96GW7	0.37853695	0.768586333	0.998109408	0.989177906	0.75824991	0.99914118	0.858241813	0.906724816	0.007547127	0.013250434	0.040514058	0.005703307	0.032966931	0.027263624
VCAM1|P19320	1.23849177	0.297117178	0.301661378	0.996789677	0.831095385	0.398242016	0.761630197	0.916746758	0.068259682	0.007914912	0.031484423	-0.06034477	-0.036775259	0.023569511
QSOX1|O00391	2.20555329	0.088933318	0.999350585	0.140462869	0.801316673	0.11345742	0.736714058	0.55148349	-0.00284196	0.048845552	0.020093459	0.051687512	0.022935419	-0.028752093
CGREF1|Q99674	5.41645413	0.001358779	0.745164549	0.004129006	0.010742933	0.08754311	0.174551709	0.980796533	0.05418452	0.179408218	0.160151991	0.125223698	0.105967472	-0.019256227
ALCAM|Q13740	9.63300833	6.11E-06	0.006484003	0.005376387	1.80E-06	0.999986245	0.262460115	0.222896933	0.096495119	0.095523574	0.148122979	-0.000971545	0.05162786	0.052599405
PON1|P27169	0.22309376	0.880265827	0.935167459	0.999732865	0.997828165	0.956825727	0.857588188	0.992299418	-0.09057606	-0.013541862	0.026686055	0.077034199	0.117262115	0.040227916
CHI3L1|P36222	11.4119828	6.69E-07	0.822299736	7.61E-05	0.129148746	1.87E-06	0.0132317	0.073849889	0.058213377	-0.293064683	-0.140061996	-0.35127806	-0.198275373	0.153002687
SERPINA7|P05543	1.88235211	0.134073353	0.737044989	0.981512102	0.323276627	0.49389089	0.924310942	0.147493267	-0.091843605	0.0330895	-0.145826265	0.124933105	-0.05398266	-0.178915765
KRT6C|P48668	0.57516272	0.632410199	0.624764219	0.704129793	0.858551599	0.999186503	0.972466528	0.9904014	0.490200558	0.438105238	0.31929448	-0.052095319	-0.170906077	-0.118810758
MEGF10|Q96KG7	9.70993615	5.55E-06	0.000369654	0.993713291	0.01225236	0.000100852	0.628236788	0.004304384	0.128911036	-0.008017911	0.092554173	-0.136928947	-0.036356863	0.100572084
KRT6A|P02538	0.03300622	0.991926185	0.998883863	0.997214954	0.98958643	0.999960398	0.998672037	0.9995342	0.038801341	0.051324951	0.078384529	0.01252361	0.039583187	0.027059578
APOH|P02749	1.25084614	0.29273264	0.430744217	0.993169839	0.994719901	0.274606397	0.544779398	0.951455913	-0.150474112	0.026001913	-0.023278818	0.176476025	0.127195294	-0.049280731
COL1A2|P08123	0.04336137	0.987956416	0.993690709	0.999954426	0.999828668	0.996412358	0.985335266	0.999181249	-0.011631643	-0.002169544	0.003297058	0.009462099	0.014928701	0.005466602
OGN|P20774	8.97799965	1.39E-05	0.000391357	0.56847401	0.000166313	0.024009809	0.999999991	0.015173563	-0.158278844	-0.048846593	-0.158388515	0.109432251	-0.00010967	-0.109541922
WFIKKN2|Q8TEU8	5.93596672	0.00069098	0.014687776	0.775164438	0.001994324	0.146058718	0.970426609	0.036847236	-0.218556373	-0.066995785	-0.249471763	0.151560587	-0.030915391	-0.182475978
LTBP1|Q14766	3.99167414	0.008745955	0.479382011	0.59067695	0.004581377	0.996538967	0.246709703	0.142445658	-0.055604872	-0.047448191	-0.125176359	0.008156681	-0.069571487	-0.077728168
AMBP|P02760	0.34171422	0.795186468	0.970305578	0.954567554	0.997194612	0.769222981	0.993331905	0.879721541	-0.041475488	0.0469078	-0.017599466	0.088383289	0.023876022	-0.064507266
IGF2R|P11717	0.71584848	0.543677115	0.723433712	0.609679916	0.991502481	0.998722391	0.854698021	0.758529598	-0.022357083	-0.0255791	-0.005894612	-0.003222017	0.016462472	0.019684488
CSPG4|Q6UVK1	1.60090174	0.190707853	0.325359631	0.707155629	0.178058958	0.908332845	0.994907543	0.774078887	-0.049388441	-0.030253695	-0.056187991	0.019134746	-0.00679955	-0.025934296
VTN|P04004	0.36728117	0.776703249	0.999986532	0.814394874	0.974294056	0.802094171	0.968852137	0.961993567	-0.003365752	0.08636435	0.040588952	0.089730101	0.043954703	-0.045775398
SOD3|P08294	8.08843388	4.32E-05	0.001297388	0.966431983	0.002323999	0.005235725	0.984716659	0.009474927	-0.214599101	-0.025870043	-0.195137717	0.188729059	0.019461384	-0.169267675
HPR|P00739	9.01716245	1.33E-05	0.004650144	0.988358756	0.002789038	0.001268845	0.99999376	0.000659425	-0.506849173	0.046887443	-0.503130832	0.553736616	0.003718341	-0.550018275
EPHA4|P54764	9.05486248	1.27E-05	0.001522631	0.001561235	9.94E-06	0.999538532	0.733710926	0.644834525	0.192859746	0.187302014	0.244183324	-0.005557732	0.051323579	0.05688131
KRT14|P02533	0.55553634	0.645052498	0.99988978	0.809785204	0.81777755	0.778675602	0.786476094	0.999981482	-0.01556108	0.200055773	0.192036277	0.215616852	0.207597356	-0.008019496
CEMIP|Q8WUJ3	0.76924093	0.512592541	0.999940262	0.995576404	0.593130387	0.991882992	0.566662002	0.729547137	0.001743992	-0.007171894	-0.037847458	-0.008915885	-0.03959145	-0.030675565
KLKB1|P03952	0.20478406	0.892992842	0.994200555	0.961924952	0.876089741	0.996089873	0.963989015	0.994025701	0.029633319	0.055169034	0.083136559	0.025535716	0.05350324	0.027967524
THBS4|P35443	1.52571868	0.20931115	0.986131947	0.978933667	0.218601266	0.999971038	0.409098932	0.408424906	-0.013614921	-0.015303598	-0.07295472	-0.001688677	-0.0593398	-0.057651123
ROBO1|Q9Y6N7	3.30336139	0.021494675	0.972058106	0.096880551	0.423836661	0.034038296	0.206557734	0.823060941	-0.013868251	0.071733175	0.046076999	0.085601427	0.05994525	-0.025656176

			ANOVA p -values with Tukey Adjustment						Difference (AD - CT)					
Gene ID | Unirprot ID	F-Value	Pr(>F)	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA
HBA2|P69905	2.19820358	0.08977235	0.371124592	0.981522081	0.122549157	0.583576052	0.957059579	0.248493051	-0.617670194	-0.140490354	-0.804399653	0.47717984	-0.186729459	-0.663909299
RBP4|P02753	1.28620825	0.280506096	0.715052017	0.807280528	0.999882548	0.207068849	0.647789222	0.824215085	-0.074381687	0.061208584	0.004597749	0.135590271	0.078979436	-0.056610835
VCAN|P13611	9.48284222	7.38E-06	0.039149317	0.924475575	0.000871962	0.005481851	0.732907278	4.95E-05	0.083483291	-0.018854321	0.114254954	-0.102337611	0.030771663	0.133109275
APOD|P05090	1.21626838	0.305154323	0.614525716	0.935528222	0.939229025	0.266712225	0.897083368	0.628658568	0.073720207	-0.034568017	0.033051478	-0.108288224	-0.040668729	0.067619495
TMEM132C|Q8N3T6	6.63637328	0.000278716	0.001509559	0.179942831	0.000672038	0.292512043	0.999994309	0.236698699	0.115797838	0.061596962	0.116549874	-0.054200876	0.000752036	0.054952912
SEZ6|Q53EL9	2.25208151	0.08379635	0.965127301	0.996007314	0.274840123	0.993977853	0.108388925	0.167299502	-0.016375275	-0.007571079	0.059477744	0.008804196	0.075853019	0.067048823
AEBP1|Q8IUX7	7.95316106	5.13E-05	0.003687884	0.775208663	0.000291507	0.052583075	0.958217729	0.00792865	-0.142138943	-0.038137057	-0.162023121	0.104001886	-0.019884179	-0.123886065
POMGNT1|Q8WZA1	13.2529454	7.10E-08	7.50E-05	0.836368296	5.32E-06	0.001458092	0.983656276	0.000160473	0.249610797	0.045371885	0.269027995	-0.204238912	0.019417198	0.22365611
SERPINA6|P08185	0.92538066	0.429637079	0.97292474	0.805517807	0.778136822	0.547109649	0.5093982	0.999990232	-0.039641045	0.08025851	0.082834233	0.119899555	0.122475278	0.002575723
ENO2|P09104	14.2160222	2.24E-08	0.302643471	1.08E-06	1.93E-06	0.002405202	0.004232567	0.994169033	-0.060916404	-0.184060549	-0.175753006	-0.123144145	-0.114836603	0.008307543
GAPDH|P04406	42.7673764	4.83E-21	0.986654469	3.13E-11	2.44E-13	7.08E-12	1.50E-13	0.867298107	0.024774285	-0.526172023	-0.578982656	-0.550946307	-0.603756941	-0.052810633
CADM1|Q9BY67	3.79327745	0.01133665	0.409848878	0.274119083	0.005105091	0.996732239	0.319813416	0.413660276	0.058216461	0.065968667	0.120133829	0.007752207	0.061917369	0.054165162
PCOLCE|Q15113	2.36530212	0.072476248	0.320420592	0.998019324	0.265004512	0.225838407	0.999995322	0.176886155	-0.054045129	0.005441365	-0.054759096	0.059486494	-0.000713967	-0.060200461
IL6ST|P40189	15.2925071	6.25E-09	0.001102805	0.908054304	1.41E-07	0.008708615	0.271167406	2.61E-06	0.152416121	0.026148455	0.222281174	-0.126267666	0.069865053	0.196132719
C8B|P07358	0.39157618	0.759205682	0.999478363	0.8468469	0.839117669	0.900302043	0.895329145	0.999999988	0.012089426	0.08473774	0.084419158	0.072648314	0.072329732	-0.000318583
PZP|P20742	0.79222605	0.49963751	0.783781105	0.436116587	0.914243639	0.950641734	0.987506066	0.80307233	0.154538435	0.241072728	0.10219609	0.086534293	-0.052342345	-0.138876638
LDHB|P07195	25.1738043	1.05E-13	0.984166337	8.67E-07	6.48E-09	1.98E-07	1.31E-09	0.834343797	0.012738548	-0.189052477	-0.217000783	-0.201791025	-0.22973933	-0.027948306
GAS6|Q14393	2.16725777	0.093390435	0.81507406	0.08302863	0.273258194	0.460575385	0.820285028	0.916173456	0.02138862	0.05644328	0.041735049	0.035054659	0.020346429	-0.01470823
ENO1|P06733	52.1065461	1.85E-24	0.017798336	1.23E-13	1.18E-13	3.35E-09	3.73E-11	0.908292888	-0.100045444	-0.317505054	-0.338618621	-0.217459609	-0.238573177	-0.021113567
HSPA5|P11021	3.56218625	0.015333353	0.973215246	0.163029577	0.026572514	0.369998237	0.091736785	0.893635848	0.007251864	0.03413282	0.045289797	0.026880956	0.038037932	0.011156977
COL14A1|Q05707	2.85087584	0.038720255	0.224505693	0.850300024	0.989204319	0.033260876	0.101211983	0.953634648	-0.075846014	0.031133552	0.011824878	0.106979566	0.087670891	-0.019308675
HBD|P02042	2.47789505	0.062707871	0.3390059	0.997678439	0.118313191	0.428737075	0.966992571	0.164581885	-0.508824465	-0.055177053	-0.644055661	0.453647412	-0.135231195	-0.588878607
NEGR1|Q7Z3B1	6.05652384	0.000590817	0.16205766	0.015440757	0.000315988	0.824559715	0.225339731	0.711587311	0.090131695	0.126819272	0.169825195	0.036687577	0.0796935	0.043005923
ALDOC|P09972	9.00720054	1.34E-05	0.284943252	0.015960052	0.195020784	2.12E-05	0.001041983	0.689025313	0.073300935	-0.120145532	-0.07782537	-0.193446467	-0.151126305	0.042320162
LPHN1|O94910	10.0271119	3.73E-06	0.989137284	0.001742724	0.000126114	0.00604183	0.000571839	0.930101327	0.008113195	0.09213633	0.106713771	0.084023135	0.098600576	0.014577441
DCC|P43146	11.5740199	5.48E-07	0.044596029	0.014014236	1.15E-07	0.987264516	0.013322978	0.028300178	0.120324567	0.135275	0.254861421	0.014950433	0.134536854	0.119586421
GANAB|Q14697	5.43644825	0.001323822	0.264056278	0.301243816	0.433303977	0.002422206	0.004703204	0.991879582	-0.065636809	0.061163584	0.051585732	0.126800393	0.117222541	-0.009577851
LCP1|P13796	1.76299551	0.155788223	0.687071734	0.935890529	0.517612701	0.325488659	0.996781304	0.188528116	-0.060941722	0.031510151	-0.072015222	0.092451874	-0.011073499	-0.103525373
CDH2|P19022	4.23729249	0.006342545	0.127665384	0.023908735	0.006120908	0.932424963	0.75783275	0.980606069	0.062892027	0.079754092	0.090036514	0.016862065	0.027144488	0.010282423
DPP6|P42658	0.98125699	0.402787132	0.862360838	0.921358316	0.882247581	0.488523517	0.415541534	0.999734692	0.031557446	-0.024832003	-0.028237471	-0.056389448	-0.059794917	-0.003405468
MFGE8|Q08431	4.02930411	0.008325887	0.998092992	0.848979939	0.022763079	0.761268005	0.014825009	0.161369029	0.00879281	-0.039695979	-0.137699422	-0.048488788	-0.146492232	-0.098003443
SPARC|P09486	1.38940519	0.247451213	0.451269352	0.965403001	0.982058201	0.20355763	0.647335117	0.819808234	-0.062164054	0.019229859	-0.014939999	0.081393913	0.047224054	-0.034169859
IGFBP7|Q16270	1.98230906	0.118156104	0.199269964	0.998130845	0.775218801	0.131888074	0.681119348	0.657676121	-0.121705122	0.010389825	-0.055780352	0.132094947	0.06592477	-0.066170177
PAPLN|O95428	0.58776711	0.623748131	0.911861274	0.725949803	0.600831654	0.984280158	0.948848915	0.997910274	-0.037094321	-0.056883667	-0.066353055	-0.019789346	-0.029258734	-0.009469388
LRG1|P02750	2.03624237	0.11034242	0.17168696	0.559826061	0.121034651	0.855900644	0.999927081	0.804844619	0.20725944	0.128182426	0.212956898	-0.079077014	0.005697458	0.084774472
PCDH17|O14917	8.04726562	4.55E-05	0.038561365	0.105320291	1.30E-05	0.964374938	0.179856646	0.049708223	0.102663608	0.084800065	0.177281072	-0.017863544	0.074617463	0.092481007
THBS2|P35442	3.8933942	0.009945601	0.070127171	0.988059155	0.044625476	0.134189264	0.999955108	0.092154732	-0.097125021	-0.01251344	-0.099024609	0.084611581	-0.001899588	-0.086511169
SERPINA4|P29622	1.11813606	0.343033217	0.348621035	0.922177151	0.519183229	0.713198571	0.982728479	0.881514824	-0.154773133	-0.057226937	-0.121593692	0.097546197	0.033179441	-0.064366756
HYOU1|Q9Y4L1	8.62633709	2.18E-05	0.213391973	0.450427709	1.19E-05	0.956647401	0.026522708	0.003844811	0.040713421	0.030198829	0.097705493	-0.010514592	0.056992072	0.067506664
GALNT7|Q86SF2	7.85617243	5.81E-05	0.029697293	0.577201193	5.40E-05	0.400374685	0.37531386	0.006132237	0.106842707	0.047719908	0.166253189	-0.059122799	0.059410481	0.11853328
CHRD|Q9H2X0	3.63218384	0.01399346	0.583966122	0.128009612	0.00933912	0.814199889	0.266981309	0.780178859	0.037164446	0.06260252	0.088486321	0.025438074	0.051321875	0.025883801
MANBA|O00462	3.25007073	0.023040872	0.050774222	0.998310973	0.664689597	0.029226463	0.403678826	0.541499491	-0.08405915	0.0053095	-0.035244648	0.089368649	0.048814501	-0.040554148
TPI1|P60174	2.34230672	0.074647239	0.947847164	0.3266126	0.489553874	0.11813442	0.204368664	0.987839753	0.021403471	-0.064984597	-0.052963829	-0.086388069	-0.0743673	0.012020768
PTPRN2|Q92932	11.9787452	3.34E-07	0.106190807	1.18E-05	2.20E-06	0.057876127	0.02564599	0.994278122	0.123210911	0.258038765	0.270823718	0.134827855	0.147612807	0.012784953
HSP90B1|P14625	6.17570738	0.000506141	0.016357386	0.857633953	0.00183205	0.111820209	0.957467789	0.021507554	-0.144048512	-0.037106435	-0.167493979	0.106942077	-0.023445467	-0.130387544
GOT1|P17174	11.4352386	6.50E-07	0.128939155	0.017630652	0.062130774	3.73E-06	2.35E-05	0.948596095	0.100113969	-0.131889628	-0.108774055	-0.232003597	-0.208888023	0.023115573
GOLM1|Q8NBJ4	0.81967015	0.484506651	0.810354448	0.916993572	0.998727259	0.415044232	0.705208036	0.954960021	-0.026820472	0.018940503	0.004376885	0.045760975	0.031197357	-0.014563618

			ANOVA p -values with Tukey Adjustment						Difference (AD - CT)					
Gene ID | Unirprot ID	F-Value	Pr(>F)	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA
TMEM132A|Q24JP5	6.30583914	0.000427547	0.006246156	0.829189438	0.00282332	0.061173107	0.999906881	0.036286196	0.136297345	0.034216186	0.138826946	-0.102081159	0.002529601	0.10461076
SELENBP1|Q13228	4.45242787	0.004786718	0.920552459	0.109386131	0.006918407	0.383370419	0.052718397	0.768215732	0.030770913	0.106906382	0.150689841	0.07613547	0.119918928	0.043783458
SEZ6L2|Q6UXD5	5.12101056	0.001997744	0.093444849	0.03176996	0.001053399	0.984419179	0.538376591	0.74665485	0.088589654	0.101898225	0.13749432	0.013308571	0.048904666	0.035596095
LAMA5|O15230	3.57831227	0.015013762	0.999459706	0.02799968	0.340825222	0.042051971	0.419670262	0.613451611	0.002341286	0.055816987	0.032487198	0.053475702	0.030145912	-0.023329789
NRP2|O60462	4.16751362	0.006948792	0.999830328	0.043129358	0.107515901	0.037977802	0.095339963	0.970733741	-0.001725634	0.057147271	0.04795389	0.058872905	0.049679524	-0.00919338
NA|P0DMV9	0.80152109	0.494471717	0.833782864	0.934675735	0.954949285	0.475860914	0.983265828	0.664358665	0.038574587	-0.026313968	0.022482194	-0.064888555	-0.016092393	0.048796162
FAM3C|Q92520	4.06896136	0.007904984	0.043090598	0.036251595	0.009990084	0.999999766	0.983387715	0.980597801	0.121863416	0.121471093	0.137999861	-0.000392322	0.016136445	0.016528767
IGFBP2|P18065	2.405347	0.068842223	0.747069805	0.471074365	0.043450993	0.976499713	0.398203874	0.637608597	-0.034282869	-0.04809912	-0.085866353	-0.013816251	-0.051583485	-0.037767233
ADAM22|Q9P0K1	2.68135952	0.048226652	0.437378353	0.717442678	0.03010954	0.962365095	0.636787759	0.310027575	0.072074669	0.049187889	0.126762281	-0.02288678	0.054687611	0.077574392
SEZ6L|Q9BYH1	3.73209103	0.012280675	0.120541143	0.025035902	0.017867272	0.94491137	0.926447778	0.999954052	0.133013815	0.165733933	0.168546623	0.032720118	0.035532808	0.002812691
GOLIM4|O00461	0.64424378	0.587508375	0.898483923	0.508801139	0.852969536	0.910420659	0.999877693	0.922952568	0.029315965	0.056855583	0.032144344	0.027539618	0.002828379	-0.024711239
TNR|Q92752	0.47940675	0.69699714	0.999971378	0.999999616	0.783701773	0.999986366	0.765313847	0.768772104	-0.001637625	-0.000378482	0.034016494	0.001259143	0.035654119	0.034394976
GAP43|P17677	19.210517	6.89E-11	0.032505637	0.000588608	0.00739031	1.29E-09	4.16E-08	0.841468797	0.139109649	-0.195143895	-0.156105434	-0.334253544	-0.295215082	0.039038462
GRIA4|P48058	3.21270585	0.024190382	0.637077977	0.637042537	0.013909896	0.999987697	0.286294596	0.245650624	0.067834664	0.066006398	0.165892601	-0.001828266	0.098057937	0.099886203
CDH13|P55290	5.33495802	0.001511117	0.011795535	0.026243116	0.001642043	0.98482288	0.974265096	0.849946532	0.199031485	0.176713947	0.225224849	-0.022317538	0.026193363	0.048510901
IGHA2|P01877	18.4007325	1.72E-10	3.92E-07	0.762824713	2.79E-07	2.37E-05	0.996160075	2.09E-05	-0.945944946	-0.159663688	-0.910154979	0.786281258	0.035789967	-0.75049129
OPCML|Q14982	8.19208309	3.78E-05	0.01217784	0.001456823	2.62E-05	0.948480452	0.46467097	0.788326469	0.1553935	0.182229325	0.225932185	0.026835825	0.070538685	0.04370286
HSPA8|P11142	10.5553641	1.93E-06	0.044343307	0.081347141	0.201324906	6.32E-06	3.10E-05	0.962042947	0.093357227	-0.08248861	-0.066409566	-0.175845837	-0.159766793	0.016079044
CNTN6|Q9UQ52	1.57502924	0.196926341	0.911226912	0.993418185	0.203542271	0.976723162	0.591494837	0.31291611	0.02476028	0.009669295	0.070012997	-0.015090985	0.045252717	0.060343702
PI16|Q6UXB8	1.58002354	0.19571124	0.168167028	0.739149936	0.379355193	0.694615202	0.942765721	0.940633491	0.102046916	0.048920881	0.075266489	-0.053126035	-0.026780427	0.026345608
MAN2A1|Q16706	1.19452991	0.31320562	0.376353978	0.842767432	0.364257656	0.845544006	0.999917141	0.854475546	0.041159291	0.020530482	0.039650215	-0.020628809	-0.001509077	0.019119733
HMCN1|Q96RW7	0.48071708	0.696085542	0.808287992	0.998968942	0.792162686	0.869326046	0.999998546	0.858194572	-0.04567235	-0.007078002	-0.044889198	0.038594348	0.000783152	-0.037811195
CNTN4|Q8IWV2	7.07457484	0.000158335	0.047606666	0.077206075	4.67E-05	0.993626763	0.264304799	0.138993422	0.084535462	0.07616053	0.141431458	-0.008374932	0.056895996	0.065270928
VCL|P18206	0.55858936	0.643015902	0.759653921	0.999422256	0.999790662	0.681632825	0.688001127	0.999981556	0.055145235	-0.006401997	-0.004454864	-0.061547232	-0.059600099	0.001947133
SIRPA|P78324	0.98479591	0.401135692	0.501952309	0.895538203	0.428953124	0.887053427	0.999964886	0.849077811	0.097047477	0.047515229	0.100121033	-0.049532249	0.003073556	0.052605804
IGHM|P01871	1.16794107	0.323312913	0.619593856	0.927254886	0.988601594	0.258362759	0.781317321	0.768840124	0.271963947	-0.134165266	0.068280329	-0.406129214	-0.203683619	0.202445595
SEMA3G|Q9NS98	1.70628059	0.167249602	0.996368861	0.524091811	0.382370893	0.399642523	0.27480797	0.996897719	-0.007228093	0.044131554	0.050535927	0.051359647	0.05776402	0.006404373
GALNT2|Q10471	2.35640253	0.073309027	0.193706183	0.99912187	0.988856605	0.138686445	0.083234451	0.997820712	-0.037272692	0.002451687	0.005645274	0.03972438	0.042917967	0.003193587
CNTN3|Q9P232	11.6370019	5.07E-07	0.000799966	0.00522191	1.57E-07	0.921641681	0.326192734	0.077243869	0.14208864	0.119361892	0.20187907	-0.022726748	0.05979043	0.082517178
SPON1|Q9HCB6	8.59940555	2.25E-05	0.322410383	0.118062958	0.03048449	0.000657553	6.52E-05	0.958997763	0.051304904	-0.065277726	-0.079307314	-0.11658263	-0.130612217	-0.014029587
SDF4|Q9BRK5	2.56712446	0.055895023	0.039001878	0.719741938	0.299121392	0.331509231	0.714306972	0.900847922	-0.069858431	-0.026580956	-0.043339459	0.043277475	0.026518972	-0.016758503
CACHD1|Q5VU97	1.16439085	0.324684373	0.962080155	0.927930412	0.284330846	0.999500079	0.59164627	0.642263243	0.023328022	0.028603555	0.081354246	0.005275532	0.058026224	0.052750692
TGOLN2|O43493	1.81937426	0.145141211	0.321130414	0.791869986	0.134742656	0.843129577	0.982856521	0.597325083	0.058295751	0.030651014	0.070383138	-0.027644737	0.012087387	0.039732124
ITIH3|Q06033	0.80289442	0.493712055	0.713554587	0.99999793	0.978028506	0.69278203	0.440052862	0.979820999	0.117356441	-0.001926904	-0.042215286	-0.119283345	-0.159571727	-0.040288382
KRT5|P13647	0.33621508	0.799166934	0.998269672	0.99999932	0.831019426	0.998544905	0.911061436	0.830101366	0.042655228	0.00302878	0.203282562	-0.039626449	0.160627333	0.200253782
HEXA|P06865	4.00676181	0.008575045	0.678960827	0.992671938	0.030514341	0.496164171	0.39168902	0.011454147	0.059401261	-0.014244544	0.14027657	-0.073645805	0.080875309	0.154521114
PGK1|P00558	62.9951061	4.13E-28	0.971662027	1.25E-13	1.24E-13	1.24E-13	1.20E-13	0.851747231	0.012748528	-0.254772095	-0.276638092	-0.267520623	-0.289386619	-0.021865997
ORM1|P02763	0.12818878	0.943281967	0.986390341	0.996289047	0.995200573	0.943168048	0.999411866	0.965402811	-0.037174901	0.023255201	-0.024780386	0.060430102	0.012394515	-0.048035587
CADM4|Q8NFZ8	6.97380073	0.000180291	0.022782311	0.055517785	6.25E-05	0.977531756	0.45249523	0.211205881	0.079755167	0.06872479	0.119146127	-0.011030377	0.03939096	0.050421337
CLSTN3|Q9BQT9	2.55394246	0.056853666	0.843238672	0.21749598	0.055926963	0.705415317	0.347104911	0.938293834	0.027228692	0.062210171	0.080093804	0.034981479	0.052865112	0.017883634
FSTL5|Q8N475	2.58454605	0.054652409	0.135539478	0.987652093	0.703773947	0.058762501	0.633565056	0.476812093	-0.106308322	0.015692895	-0.050171236	0.122001217	0.056137086	-0.065864131
NPTX1|Q15818	10.10431	3.38E-06	0.18847089	0.009836946	1.27E-06	0.699705984	0.007764822	0.129483701	0.102426312	0.156852028	0.261244407	0.054425717	0.158818095	0.104392378
LRRC4B|Q9NT99	5.22029172	0.001754944	0.051816956	0.957135368	0.005803262	0.151484018	0.930096367	0.024540873	0.097477754	0.018679948	0.119521551	-0.078797806	0.022043797	0.100841602
NOTCH3|Q9UM47	7.11282758	0.000150724	0.186137109	0.004451212	0.00011732	0.551575187	0.119094396	0.801723726	0.05380472	0.088499432	0.111098853	0.034694711	0.057294133	0.022599421
DSP|P15924	0.24368562	0.865732097	0.979531416	0.974300627	0.991817866	0.999994603	0.90028927	0.884341193	-0.111997214	-0.11895602	0.078076493	-0.006958806	0.190073707	0.197032513
IGSF8|Q969P0	4.15714836	0.007043661	0.363596488	0.922343123	0.007057861	0.729451288	0.421272183	0.041165682	0.044179015	0.01659574	0.084074322	-0.027583274	0.039895307	0.067478582
MSN|P26038	0.84496406	0.470886098	0.993265014	0.945213562	0.450693731	0.992626423	0.637028514	0.788929305	-0.013466044	-0.027139184	-0.070831838	-0.01367314	-0.057365794	-0.043692654

Gene ID | Unirprot ID	F-Value	Pr(>F)	ANOVA p -values with Tukey Adjustment						Difference (AD - CT)					
			AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA
F10|P00742	1.68125552	0.172558465	0.333285099	0.991560301	0.310382879	0.483512823	0.999971042	0.463570145	-0.097224804	-0.016207216	-0.09483178	0.081017588	0.002393024	-0.078624564
LMAN2|Q12907	3.96523613	0.009053683	0.016108063	0.621822563	0.031472162	0.252634646	0.98053708	0.407054548	0.069956265	0.027435819	0.061314715	-0.042520446	-0.00864155	0.033878896
CLEC3B|P05452	1.15128467	0.329792487	0.886011218	0.942539866	0.689539815	0.566426214	0.987421979	0.322782116	-0.01941274	0.014649707	-0.027921531	0.034062447	-0.00850879	-0.042571238
GDA|Q9Y2T3	21.6828795	4.44E-12	0.006042692	0.000324597	0.027283496	2.18E-11	1.87E-08	0.482885249	0.208950137	-0.25305006	-0.168864266	-0.462000198	-0.377814404	0.084185794
F12|P00748	5.87709942	0.000745926	0.298041125	0.986778693	0.006458268	0.151681807	0.483323208	0.001597684	0.228861888	-0.042737468	0.408024192	-0.271599356	0.179162304	0.45076166
CADM3|Q8N126	3.41216121	0.018650839	0.171198959	0.098438615	0.012672497	0.997250732	0.802763127	0.887959763	0.077920886	0.085297333	0.110871856	0.007376447	0.03295097	0.025574524
TMEM132D|Q14C87	12.4166553	1.95E-07	0.000186797	0.00013892	1.50E-07	0.999967376	0.550246649	0.495428344	0.271394949	0.2685806	0.352373623	-0.002814349	0.080978674	0.083793023
PRNP|P04156	6.31597272	0.000421969	0.002157468	0.036487812	0.000683953	0.753108643	0.999307926	0.643006514	0.129329511	0.094342483	0.133614017	-0.034987028	0.004284506	0.039271534
CACNA2D3|Q8IZS8	4.61106625	0.00388983	0.010198316	0.043219341	0.007684953	0.937411376	0.999857858	0.949717438	0.180523026	0.147684339	0.176476209	-0.032838687	-0.004046817	0.02879187
COMP|P49747	0.18967443	0.903336606	0.886371667	0.949244047	0.969207497	0.996953035	0.989768857	0.999616681	-0.064983387	-0.046951297	-0.038411506	0.01803209	0.026571881	0.008539791
PLOD1|Q02809	11.4585482	6.31E-07	3.20E-05	0.181760453	5.18E-06	0.032533953	0.998499851	0.013104089	-0.196142065	-0.082593692	-0.202644793	0.113548373	-0.006502728	-0.120051101
SNED1|Q8TER0	0.37757026	0.769282805	0.961606432	0.979960948	0.968601514	0.815039521	0.774091604	0.999930619	-0.019976535	0.015480178	0.017687395	0.035456713	0.03766393	0.002207217
GPLD1|P80108	1.7718254	0.154072727	0.993881273	0.816414965	0.273579011	0.671144222	0.172510366	0.792185367	-0.020670226	0.068115004	0.136953697	0.08878523	0.157623923	0.068838693
PRG4|Q92954	6.98654508	0.000177353	0.196395802	0.917203259	0.005330266	0.042368132	0.598673536	0.000383811	-0.234196634	0.073941933	-0.375455077	0.308138567	-0.141258443	-0.44939701
PCDH9|Q9HC56	4.0663459	0.007932077	0.051715201	0.31593792	0.005938024	0.794492838	0.932505076	0.389630152	0.108277242	0.070275235	0.13244385	-0.038002007	0.024166608	0.062168615
RTN4R|Q9BZR6	3.77412916	0.011624028	0.902174001	0.34114557	0.009862128	0.774683648	0.079007971	0.455478852	0.033171435	0.078643838	0.145182619	0.045472403	0.112011184	0.066538781
SUSD5|O60279	1.222172	0.303000297	0.63548837	0.239831764	0.806945756	0.914536936	0.985361735	0.721898076	0.054459941	0.083926527	0.039056382	0.029466586	-0.015403559	-0.044870145
LUM|P51884	1.12559578	0.340013031	0.814192494	0.786560886	0.994840397	0.267729181	0.654007351	0.887446637	-0.055843674	0.057544898	0.014721121	0.113388572	0.070564795	-0.042823777
PEBP1|P30086	13.7223946	4.04E-08	0.451805166	0.001033386	0.002710159	2.15E-06	6.38E-06	0.983240855	0.047839392	-0.120201341	-0.109156315	-0.168040734	-0.156995708	0.011045026
CFD|P00746	3.21818316	0.024018381	0.999976947	0.958233363	0.114767838	0.96826036	0.11129185	0.027920784	0.002429994	0.029749415	-0.129739112	0.027319421	-0.132169106	-0.159488527
LDHA|P00338	59.6974558	4.86E-27	0.159858602	2.42E-12	1.31E-13	1.24E-13	1.12E-13	0.857451166	0.079368356	-0.288917152	-0.317049208	-0.368285508	-0.396417564	-0.028132055
LSAMP|Q13449	6.31558216	0.000422182	0.027189347	0.014923619	0.000219329	0.999267312	0.600686205	0.661492115	0.102965224	0.107529767	0.146644437	0.004564543	0.043679213	0.03911467
DCN|P07585	6.8213654	0.00021947	0.002558186	0.999646255	0.059872076	0.001480548	0.616568041	0.040928152	-0.219207043	0.005945946	-0.147234467	0.225152989	0.071972576	-0.153180413
MDH1|P40925	34.3796476	1.04E-17	0.279548183	4.34E-09	1.14E-07	3.06E-13	5.86E-12	0.859037816	0.075330271	-0.265587575	-0.234600944	-0.340917846	-0.309931215	0.030986631
KRT17|Q04695	0.39706778	0.755264946	0.794595837	0.999993838	0.99768549	0.769821504	0.867522262	0.996336656	-0.313067794	0.008538355	-0.060723463	0.321606149	0.252344331	-0.069261818
CACNA2D2|Q9NY47	3.13545887	0.026750409	0.50101116	0.673015295	0.553053857	0.057752619	0.032391558	0.998367154	-0.050958009	0.039935684	0.045581999	0.090893694	0.096540008	0.005646314
CD14|P08571	0.38915973	0.76094208	0.788171657	0.977146712	0.999995874	0.948219373	0.780454157	0.978114437	0.035517985	0.015109483	0.000817041	-0.020408502	-0.034700944	-0.014292442
PEBP4|Q96S96	10.9110282	1.24E-06	3.89E-05	0.990601263	0.989186946	7.59E-06	6.77E-05	0.921502951	-0.314593152	0.019787186	-0.02027802	0.334380338	0.294315132	-0.040065206
C4BPA|P04003	1.14243032	0.33328394	0.506774196	0.999632344	0.561508958	0.55593781	0.998616723	0.613856488	-0.237288253	-0.016730748	-0.211502156	0.220557505	0.025786097	-0.194771407
FBLN5|Q9UBX5	0.66144013	0.576761802	0.943181168	0.774805736	0.528922353	0.982174239	0.874473256	0.980693166	-0.016722524	-0.027667694	-0.038344576	-0.01094517	-0.021622052	-0.010676882
LAMA4|Q16363	17.1890587	6.87E-10	6.08E-07	0.990332617	2.00E-05	1.70E-06	0.734476736	5.48E-05	-0.221941382	-0.011798219	-0.182399122	0.210143164	0.03954226	-0.170600903
CAT|P04040	1.42106262	0.238056498	0.5708746	0.980727869	0.654347844	0.332559138	0.997305187	0.394156184	-0.2286456	0.066212242	-0.195115022	0.294857842	0.033530578	-0.261327264
TNC|P24821	1.08644952	0.356128156	0.997987848	0.606141252	0.666264299	0.500819834	0.558121982	0.999269239	0.008655353	-0.058352624	-0.052594291	-0.067007977	-0.061249643	0.005758333
PENK|P01210	10.1091266	3.36E-06	0.287626283	0.006192971	0.151363029	5.65E-06	0.000667813	0.571026169	-0.075637916	0.13692769	0.0856646	0.212565606	0.161302516	-0.05126309
PTPRG|P23470	6.73120423	0.000246569	0.10185052	0.062087864	7.33E-05	0.998972543	0.175184893	0.208064691	0.088429733	0.093811299	0.164143041	0.005381566	0.075713307	0.070331741
ERAP1|Q9NZ08	1.54656593	0.203988295	0.73115223	0.906059691	0.670975798	0.318410224	0.999967147	0.251473296	-0.06529193	0.041634379	-0.068033531	0.106926309	-0.002741601	-0.10966791
COL3A1|P02461	1.69819128	0.168948442	0.992084221	0.443273473	0.499164284	0.294316178	0.337480503	0.999239736	-0.011838513	0.060837908	0.05581293	0.072676421	0.067651443	-0.005024979
NRXN3|Q9HDB5	1.27895249	0.284009885	0.464031984	0.594631773	0.250072925	0.995273569	0.985616112	0.931819658	-0.102223802	-0.0858341	-0.125872211	0.016389702	-0.023648408	-0.040038111
GDI1|P31150	71.8158828	7.63E-31	0.955747631	1.23E-13	1.18E-13	1.22E-13	1.07E-13	0.889574121	0.012290686	-0.225283786	-0.241350327	-0.237574471	-0.253641013	-0.016066542
PCDHAC2|Q9Y5I4	3.77702328	0.011580131	0.596530844	0.997475247	0.179495966	0.464766705	0.006197789	0.24518331	-0.034997296	0.005240061	0.054160585	0.040237357	0.089157881	0.048920524
ENDOD1|O94919	0.73780505	0.530726981	0.924538601	0.472793742	0.752660676	0.856453427	0.987026172	0.960499023	0.015208318	0.034320945	0.0230724	0.019112627	0.007864082	-0.011248545
NRXN1|P58400	1.58278706	0.195041925	0.93933711	0.941416001	0.171734335	0.999995658	0.480787984	0.43978957	0.035484481	0.034092669	0.120503696	-0.001391812	0.085019215	0.086411026
OMD|Q99983	7.82928865	6.01E-05	0.00219038	0.592547425	0.000257333	0.07520806	0.981578463	0.018731727	-0.154985428	-0.052393941	-0.170582323	0.102591487	-0.015596895	-0.118188382
C8G|P07360	1.02924084	0.380885029	0.9474565	0.452495152	0.468508374	0.801471818	0.821949773	0.999913151	0.057484451	0.151395049	0.145274871	0.093910598	0.08779042	-0.006120178
TPP1|O14773	1.26425448	0.288040657	0.361583176	0.99996218	0.857339969	0.32287497	0.796791778	0.827215209	-0.100020094	0.002807774	-0.046139867	0.102827868	0.053880227	-0.04894764
SCG5|P05408	7.42074347	0.000101445	0.001355223	0.027608453	0.000113489	0.734711739	0.971841133	0.420658141	0.139084094	0.10160496	0.154725687	-0.037479134	0.015641593	0.053120727
SPOCK2|Q92563	1.92207257	0.12751514	0.291701275	0.308089057	0.113865857	0.999809077	0.980653199	0.963196712	-0.078802477	-0.075250918	-0.095277708	0.003551558	-0.016475232	-0.02002679

Gene ID | Unirprot ID	F-Value	Pr(>F)	ANOVA p -values with Tukey Adjustment						Difference (AD - CT)					
			AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA
CELSR2|Q9HCU4	7.49296142	9.25E-05	0.000213643	0.03526473	0.000507892	0.379010762	0.972341422	0.601063226	0.207326611	0.129930444	0.186801393	-0.077396167	-0.020525218	0.056870949
PCSK1N|Q9UHG2	2.02030447	0.112597843	0.998593053	0.168030956	0.443547463	0.239454448	0.557186884	0.921372207	0.00595879	0.075867433	0.053561512	0.069908643	0.047602722	-0.022305921
EPHA5|P54756	12.1872243	2.59E-07	0.138666394	0.000183168	3.05E-07	0.182539887	0.005060451	0.541767469	0.08233958	0.158374416	0.205946887	0.076034836	0.123607307	0.047572471
CD109|Q6YHK3	3.18676213	0.025021837	0.074175814	0.974664166	0.944246238	0.022231655	0.199831168	0.745404732	0.124125833	-0.020933534	0.027044426	-0.145059367	-0.097081408	0.04797796
CPQ|Q9Y646	0.23234446	0.873768526	0.896899781	0.999974504	0.995635726	0.87572365	0.959155186	0.992457918	-0.03166889	0.001820149	-0.009937727	0.033489038	0.021731163	-0.011757875
POSTN|Q15063	0.06750194	0.977113161	0.998906983	0.992784114	0.999907515	0.975308728	0.999755048	0.985228579	0.014753905	-0.02711513	0.006143552	-0.041869035	-0.008610353	0.033258682
PCDH1|Q08174	10.3291902	2.56E-06	0.093242223	0.00056795	1.87E-06	0.404688461	0.027578381	0.592446386	0.097550975	0.161597422	0.210539595	0.064046448	0.11298862	0.048942172
THBS1|P07996	4.69396044	0.00349026	0.731181881	0.610784538	0.002348193	0.998412122	0.066901949	0.084896959	-0.057331952	-0.066332282	-0.189828225	-0.00900033	-0.132496272	-0.123495943
AGA|P20933	1.58448343	0.194632141	0.32664442	0.99691976	0.765133744	0.219263873	0.851740692	0.625332134	0.09409729	-0.011068574	0.051180507	-0.105165865	-0.042916783	0.062249081
IGFALS|P35858	0.24428918	0.865323235	0.999556024	0.999937352	0.883165966	0.99994375	0.927608161	0.901223331	0.01190231	0.006022794	0.077402648	-0.005879515	0.065500338	0.071379853
LRP1B|Q9NZR2	1.72449826	0.1634831	0.919084102	0.637248002	0.585301641	0.267109191	0.225099166	0.999940547	-0.02869469	0.051727487	0.054027281	0.080422177	0.082721971	0.002299794
FUCA2|Q9BTY2	9.43336925	7.85E-06	3.34E-05	0.930631375	0.01575575	0.000293508	0.237306709	0.074971536	-0.479155741	-0.060264328	-0.293024925	0.418891413	0.186130816	-0.232760597
BASP1|P80723	14.9057805	9.87E-09	0.002589919	0.065242034	0.229033011	4.05E-08	4.88E-07	0.91509887	0.220780732	-0.149868011	-0.112201288	-0.370648743	-0.332982021	0.037666723
PLOD3|O60568	3.64098342	0.013833493	0.023934598	0.917597563	0.106547577	0.108265417	0.887282798	0.354064063	-0.145681138	-0.031864207	-0.110221597	0.113816931	0.035459541	-0.07835739
HEXB|P07686	2.73489148	0.044999411	0.032247344	0.885168611	0.721777679	0.163646883	0.262348474	0.990039358	-0.131968499	-0.03397152	-0.047649971	0.097996979	0.084318528	-0.013678451
CTSF|Q9UBX1	4.25984455	0.00615815	0.032808922	0.368790742	0.006099204	0.633223873	0.976379868	0.337488437	-0.111697792	-0.06407932	-0.127789807	0.047618471	-0.016092016	-0.063710487
MST1|P26927	0.60678729	0.611384546	0.660972007	0.999989733	0.914040766	0.668598437	0.94758407	0.921099011	-0.127089187	-0.003292568	-0.068883675	0.123796619	0.058205512	-0.065591107
TIMP2|P16035	1.98558455	0.117666676	0.273550073	0.97770413	0.202212821	0.478665994	0.999871148	0.388959011	-0.07467409	-0.016234013	-0.077498869	0.058440077	-0.002824778	-0.061264856
SPOCK1|Q08629	1.19461142	0.313175073	0.307962158	0.425555595	0.693176599	0.993972866	0.887921412	0.964976395	-0.072015638	-0.061485572	-0.043163639	0.010530066	0.028851999	0.018321933
ACTB|P60709	4.33781419	0.005560982	0.792096773	0.302802173	0.1220484	0.041455744	0.01016369	0.971785536	0.047265812	-0.086934058	-0.107878292	-0.13419987	-0.155144103	-0.020944234
CNTNAP5|Q8WYK1	4.69364458	0.003491702	0.042559326	0.108519839	0.002012294	0.969348338	0.838157257	0.542139217	0.095043084	0.079139323	0.1237895	-0.015903761	0.028746415	0.044650177
XYLT1|Q86Y38	0.71738914	0.542760837	0.58896041	0.993267726	0.999996478	0.740242586	0.571062606	0.994028321	-0.058552331	-0.012095239	-0.000943569	0.046457092	0.057608762	0.01115167
SLC38A10|Q9HBR0	10.0219334	3.75E-06	0.004974329	0.380797209	3.90E-06	0.256156696	0.390219228	0.002502199	0.088774221	0.040988228	0.128897129	-0.047785993	0.040122908	0.087908901
HTRA1|Q92743	1.95485543	0.122336314	0.95942788	0.460114378	0.121825839	0.781710718	0.340175741	0.884550599	-0.015580306	-0.044625952	-0.065992079	-0.029045646	-0.050411773	-0.021366127
DNAJC3|Q13217	0.45130101	0.716680205	0.827745769	0.817062191	0.703817697	0.999999994	0.998080522	0.997808771	-0.023861015	-0.023790444	-0.028567161	7.06E-05	-0.004706145	-0.004776717
PGLYRP2|Q96PD5	0.52234605	0.66743295	0.890312421	0.598214339	0.916040839	0.958131875	0.999589675	0.919441338	0.065248123	0.110384815	0.056090016	0.045136692	-0.009158108	-0.0542948
GPC1|P35052	1.42384798	0.237245964	0.926086209	0.562920079	0.930121522	0.912483733	0.601647985	0.202340528	-0.029904223	-0.061248987	0.027845088	-0.031344764	0.057749311	0.089094075
CD55|P08174	4.48600527	0.004581037	0.05661294	0.320099606	0.002847606	0.809358239	0.82996405	0.269207634	0.094407254	0.061837302	0.124796277	-0.032569951	0.030389023	0.062958974
MASP1|P48740	0.66638631	0.57369627	0.992893133	0.999991162	0.624468624	0.994612483	0.801243401	0.630382981	0.013737725	0.001424127	0.057707877	-0.012313598	0.043970152	0.05628375
NPC2|P61916	0.6829672	0.563503661	0.95169917	0.974571978	0.841640478	0.774604451	0.52138706	0.978078145	0.015506699	-0.012028669	-0.022997851	-0.027535367	-0.03850455	-0.010969183
NPEPPS|P55786	14.7423324	1.20E-08	0.983402663	0.000225329	1.84E-05	6.02E-05	4.32E-06	0.958279352	0.008544079	-0.096193945	-0.107212497	-0.104738024	-0.115756576	-0.011018552
SORCS1|Q8WY21	6.84885336	0.00021182	0.069148615	0.001038817	0.000382529	0.58148629	0.456082961	0.998063122	0.135060938	0.203759798	0.212765633	0.06869886	0.077704695	0.009005835
QPCT|Q16769	3.87308473	0.010213287	0.374052382	0.245023987	0.004517635	0.996754912	0.33479426	0.430774519	0.075838751	0.085523676	0.15208073	0.009684926	0.076241979	0.066557054
PLXDC2|Q6UX71	3.19533989	0.024743842	0.38787441	0.841876595	0.018677139	0.85605242	0.587512491	0.144311212	-0.05899052	-0.029868524	-0.104146634	0.029121995	-0.045156114	-0.07427811
CHRDL1|Q9BU40	0.51872426	0.669900938	0.998934929	0.962257756	0.889952769	0.923677467	0.943878162	0.604998018	-0.006182547	0.02029974	-0.029321119	0.026482287	-0.023138572	-0.04962086
MRC2|Q9UBG0	12.8876213	1.10E-07	0.054784323	0.002196193	0.911354841	2.57E-08	0.006120091	0.012320761	-0.078136084	0.10740668	0.019216059	0.185542764	0.097352143	-0.088190621
NTM|Q9P121	7.71980349	6.91E-05	0.013322537	0.096101608	2.58E-05	0.848072427	0.44417794	0.08168894	0.11672271	0.086202709	0.171453724	-0.03052	0.054731015	0.085251015
HABP2|Q14520	1.08759569	0.355646909	0.771106239	0.855636275	0.986873873	0.293608344	0.909144103	0.645145956	-0.098029788	0.079034242	-0.032558841	0.17706403	0.065470947	-0.111593084
ANPEP|P15144	1.68986907	0.170713328	0.855504761	0.999886481	0.246312905	0.816667889	0.741219356	0.203412223	0.040812746	-0.003389339	0.090776018	-0.044202085	0.049963272	0.094165357
MAN1A1|P33908	17.7535386	3.60E-10	0.037903652	7.73E-05	1.56E-10	0.334418644	0.000232339	0.054382144	0.063996186	0.103356871	0.16009164	0.039360684	0.096095453	0.056734769
VIM|P08670	3.58249486	0.01493196	0.325565179	0.199404822	0.007111081	0.995823697	0.466897257	0.590349912	-0.2292408	-0.259442339	-0.417846101	-0.030201539	-0.188605301	-0.158403762
CDH15|P55291	4.29990658	0.00584371	0.004056059	0.102307558	0.045967598	0.616618198	0.763430913	0.992490691	-0.202442914	-0.131783135	-0.147084864	0.070659779	0.05535805	-0.015301729
STAB1|Q9NY15	2.05642804	0.107548627	0.801230565	0.21184145	0.117772839	0.747274984	0.586461009	0.994825279	-0.040490133	-0.0846287	-0.094843705	-0.044138567	-0.054353572	-0.010215005
SERPINA5|P05154	5.50677757	0.00120788	0.005511521	0.891167049	0.016628869	0.038906879	0.95413406	0.102492438	-0.261982357	-0.054512499	-0.222730879	0.207469858	0.039251478	-0.16821838
EFEMP2|O95967	0.74816523	0.524697468	0.608345912	0.920008823	0.550188775	0.925450805	0.999992824	0.90395298	-0.029637758	-0.01492369	-0.03026602	0.014714069	-0.000628261	-0.01534233
IDS|P22304	0.87707315	0.454042777	0.63524424	0.707021327	0.411255449	0.998860636	0.991103994	0.967949786	0.048902458	0.042938484	0.060562803	-0.005963973	0.011660345	0.017624319
NA|P0DOY2	8.06127165	4.47E-05	0.00043995	0.852887438	0.002656047	0.005994531	0.900457509	0.030027474	-0.490693138	-0.094753969	-0.410062673	0.395939169	0.080630465	-0.315308704

			ANOVA p -values with Tukey Adjustment						Difference (AD - CT)					
Gene ID | Unirprot ID	F-Value	Pr(>F)	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA
PCDHGC5|Q9Y5F6	13.3685254	6.18E-08	0.022181954	5.59E-06	1.65E-07	0.163849207	0.034756896	0.925215432	0.155294962	0.265266811	0.296445761	0.109971849	0.141150799	0.03117895
GOT2|P00505	14.4124342	1.77E-08	0.213353376	5.34E-06	2.00E-07	0.013855661	0.001756574	0.940491049	-0.071791603	-0.182688602	-0.202402512	-0.110896998	-0.130610908	-0.01971391
RGMB|Q6NW40	8.27957115	3.38E-05	0.078909804	0.014577098	9.94E-06	0.94620165	0.083677675	0.242234185	0.1059851	0.129851103	0.206941776	0.023866003	0.100956676	0.077090672
PRKCSH|P14314	1.40869038	0.241687985	0.93914634	0.891959418	0.200742577	0.999391428	0.530313716	0.584287385	0.017342933	0.020878596	0.056554885	0.003535664	0.039211953	0.035676289
CA1|P00915	2.53674356	0.058128766	0.162696793	0.982047109	0.146367653	0.303578042	0.999935108	0.285937501	-0.652165712	-0.114101767	-0.635142245	0.538063944	0.017023467	-0.521040478
LCAT|P04180	0.32472136	0.807487889	0.872701922	0.989909102	0.999101346	0.966122061	0.792657366	0.967951693	-0.041245177	-0.016244977	0.00701928	0.0250002	0.048264458	0.023264257
ORM2|P19652	1.160822	0.326068271	0.808529666	0.811596897	0.967371862	0.284552256	0.511452868	0.968652683	-0.095722669	0.092523303	0.046985081	0.188245972	0.142707751	-0.045538221
CDH11|P55287	11.2784427	7.88E-07	0.375056657	0.010387867	5.02E-07	0.457138699	0.000969531	0.079912905	0.035225489	0.066897849	0.116009582	0.03167236	0.080784093	0.049111733
C16orf89|Q6UX73	6.92321849	0.000192442	0.008406922	0.808849122	0.000810182	0.084572586	0.958555954	0.014957189	0.115263846	0.031163164	0.132598205	-0.084100683	0.017334359	0.101435041
F13B|P05160	1.12518146	0.340180157	0.857394273	0.764213107	0.965989165	0.291785816	0.572701605	0.949460962	-0.075900611	0.090699888	0.042549059	0.1666005	0.118449671	-0.048150829
COL18A1|P39060	0.83672865	0.475286637	0.699232381	0.968958707	0.995699505	0.410194814	0.80480785	0.894685428	-0.037037984	0.01505152	-0.007464166	0.052089505	0.029573818	-0.022515686
SEMA3B|Q13214	1.96839653	0.120256943	0.186140345	0.990351906	0.356491243	0.302225885	0.965587005	0.527534816	-0.100637599	-0.014702873	-0.078054895	0.085934726	0.022582703	-0.063352022
HGFAC|Q04756	0.20192273	0.894963621	0.992792623	0.87056184	0.973346233	0.964151482	0.999026908	0.984166207	0.029661826	0.080475213	0.044204104	0.050813387	0.014542278	-0.036271109
OLFML3|Q9NRN5	3.14152367	0.026540046	0.807251818	0.879629747	0.021819436	0.99807833	0.219038264	0.134661184	-0.030233857	-0.024404112	-0.09295829	0.005829745	-0.062724432	-0.068554177
SEMA6A|Q9H2E6	3.30379939	0.021482403	0.992807528	0.769531424	0.026675142	0.906270798	0.062224007	0.244680403	0.01095709	0.037575308	0.10749332	0.026618218	0.09653623	0.069918012
F11|P03951	0.1751859	0.913092701	0.995495087	0.965435897	0.998333619	0.896067138	0.977026014	0.988634137	-0.025555525	0.05008094	0.017378699	0.075636465	0.042934224	-0.032702241
DPP7|Q9UHL4	0.5477494	0.650264134	0.999982308	0.686633826	0.996564017	0.717093798	0.998168274	0.786463591	0.003433282	0.100860224	0.01900492	0.097426942	0.015571638	-0.081855304
TCN2|P20062	6.69369363	0.000258813	0.043424977	0.711880199	0.089535052	0.001393995	0.974384764	0.003196055	-0.146155835	0.057167477	-0.123641707	0.203323312	0.022514128	-0.180809184
PREP|P48147	1.80362909	0.148042367	0.991351368	0.591613036	0.162539818	0.780114716	0.298896549	0.849586096	-0.010591098	-0.044429203	-0.071933859	-0.033838105	-0.061342761	-0.027504656
DDR1|Q08345	4.04494848	0.008157235	0.147937114	0.630607147	0.005556129	0.760709524	0.698039297	0.140562281	0.123978548	0.067742544	0.184903386	-0.056236003	0.060924839	0.117160842
PARK7|Q99497	56.0032655	8.35E-26	0.777101688	3.01E-13	1.14E-13	9.48E-11	1.24E-13	0.098803842	-0.029669333	-0.250360922	-0.317755047	-0.220691589	-0.288085715	-0.067394125
BCAM|P50895	4.35760806	0.005418833	0.096932943	0.938427623	0.162716665	0.019839341	0.984592986	0.035614425	-0.058666465	0.014226621	-0.050026297	0.072893086	0.008640167	-0.064252918
CTSH|P09668	1.98786909	0.117326478	0.294117178	0.95117502	0.999870695	0.097809221	0.294771935	0.923482173	-0.135380622	0.039732828	-0.005186195	0.17511345	0.130194426	-0.044919023
CHIT1|Q13231	11.7232506	4.56E-07	0.985746652	0.000173904	7.51E-05	0.000832197	0.000401949	0.99959265	-0.068557788	-0.825804551	-0.845121777	-0.757246763	-0.776563989	-0.019317226
F9|P00740	1.41382918	0.240173447	0.523633912	0.995343788	0.589407993	0.37065966	0.998170832	0.422808184	-0.12652598	0.021326566	-0.111127535	0.147852546	0.015398445	-0.132454101
CFHR1|Q03591	0.44129976	0.723740462	0.998031727	0.737543165	0.999056166	0.840582424	0.999962038	0.792902988	0.0229722	0.129067608	0.017064933	0.106095408	-0.005907267	-0.112002675
C1QC|P02747	0.55749568	0.643745031	0.986026343	0.595590541	0.947000011	0.811668223	0.997770821	0.878791573	-0.013791091	-0.048854072	-0.020913649	-0.035062981	-0.007122558	0.027940423
HSP90AA1|P07900	27.5760962	8.69E-15	0.929183768	3.29E-07	3.36E-09	1.95E-08	1.56E-10	0.872407146	0.021329534	-0.193177456	-0.218045336	-0.21450699	-0.239374871	-0.024867881
NDRG2|Q9UN36	4.03912374	0.008219626	0.93572786	0.353063645	0.343369471	0.119552398	0.727785578	0.004308703	0.017840097	-0.048758161	0.048148888	-0.066598259	0.030308791	0.096907049
NUCB2|P80303	0.89309886	0.445822422	0.467667631	0.6160643	0.95258901	0.992900698	0.755018367	0.883691422	-0.080612426	-0.065730698	-0.027750228	0.014881728	0.052862198	0.03798047
RNASE1|P07998	15.6948404	3.90E-09	5.18E-07	0.062251749	8.11E-08	0.009128853	0.999826248	0.0040104	0.23932398	0.104682524	0.242565557	-0.134641456	0.003241577	0.137883033
PDIA3|P30101	0.29030035	0.83237185	0.999992284	0.909020603	0.997725424	0.921641376	0.996616015	0.812952309	-0.000524498	-0.012278198	0.003332197	-0.0117537	0.003856695	0.015610395
CPVL|Q9H3G5	5.26989653	0.001644958	0.015202848	0.538175768	0.002737958	0.305323448	0.982910612	0.123145921	-0.234632499	-0.101385698	-0.262164414	0.133246802	-0.027531915	-0.160778717
LPHN3|Q9HAR2	3.31809793	0.021085604	0.842752431	0.813953126	0.016733697	0.999985105	0.159077763	0.150609921	0.030294586	0.031545145	0.104309828	0.00125056	0.074015242	0.072764683
GLG1|Q92896	6.28798216	0.000437559	0.031799404	0.245373569	0.000210259	0.772610708	0.556790128	0.088185506	0.073617535	0.048442921	0.107254973	-0.025174614	0.033637438	0.058812052
SLC3A2|P08195	0.85335786	0.466434808	0.445936933	0.989518301	0.83385212	0.624376017	0.891032887	0.950815489	-0.035604973	-0.007239635	-0.019154429	0.028365338	0.016450545	-0.011914794
CTSB|P07858	1.1416812	0.33358084	0.42444082	0.973866877	0.477501176	0.672954179	0.998399088	0.738862891	-0.06733728	-0.018323296	-0.060330528	0.049013984	0.007006752	-0.042007232
GFAP|P14136	8.96855591	1.41E-05	0.999999649	0.001517286	0.001899663	0.001712915	0.002148764	0.998715017	0.000730418	-0.266369656	-0.25582475	-0.267100074	-0.256555168	0.010544905
QSOX2|Q6ZRP7	1.45882671	0.227283565	0.323699445	0.998618805	0.993407762	0.237026712	0.433774437	0.972573606	-0.080648718	0.007220971	-0.011946402	0.087869689	0.068702316	-0.019167373
GALNT13|Q8IUC8	0.66057549	0.577298863	0.52997953	0.933723088	0.983057664	0.859955774	0.723689473	0.994789291	-0.067102455	-0.028658061	-0.017291955	0.038444394	0.0498105	0.011366105
PRCP|P42785	1.38279977	0.249454294	0.294064714	0.300860745	0.517485986	0.999914618	0.9642446	0.974088101	-0.094341284	-0.091082057	-0.069829168	0.003259227	0.024512116	0.021252889
GDI2|P50395	11.7101521	4.63E-07	0.183985278	0.000869974	3.45E-07	0.291454763	0.003391794	0.312559959	-0.060443615	-0.112544946	-0.160808143	-0.052101331	-0.100364528	-0.048263197
EPHA7|Q15375	10.6020385	1.82E-06	0.376502369	0.044054376	9.00E-07	0.762919688	0.001480414	0.028224992	0.040260478	0.064333643	0.129953257	0.024073165	0.089692779	0.065619615
SEMA3F|Q13275	0.95687482	0.414323304	0.999738789	0.645410828	0.662940475	0.596374898	0.613024903	0.99993442	-0.002741359	0.034766828	0.033152002	0.037508187	0.035893361	-0.001614826
SCRG1|O75711	0.76754405	0.513559153	0.973133636	0.546768292	0.999834881	0.818221131	0.982469993	0.561714948	-0.015546082	-0.046611626	-0.002646228	-0.031065544	0.012899854	0.043965398
C1QB|P02746	0.89150133	0.446636332	0.679485418	0.462592381	0.522127488	0.989616645	0.997610015	0.999165004	-0.040116042	-0.051086283	-0.046637419	-0.010970241	-0.006521377	0.004448864
SLITRK1|Q96PX8	7.67460902	7.33E-05	0.005481294	0.003326538	5.61E-05	0.999938742	0.736013564	0.752058845	0.239486504	0.243393576	0.310023947	0.003907071	0.070537442	0.066630371

			ANOVA p -values with Tukey Adjustment						Difference (AD - CT)					
Gene ID | Unirprot ID	F-Value	Pr(>F)	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA
ICAM5|Q9UMF0	7.84938447	5.86E-05	0.002589772	0.052830219	3.82E-05	0.702134484	0.814145731	0.174806327	0.225367548	0.158142657	0.279034041	-0.06722489	0.053666493	0.120891383
MDGA1|Q8NFP4	6.40575625	0.000375631	0.00014488	0.060821069	0.027293517	0.228280191	0.32022145	0.994703067	-0.220080178	-0.124513223	-0.13624423	0.095566954	0.083835948	-0.011731007
SOD1|P00441	4.02985631	0.008319875	0.270329515	0.686239396	0.588749617	0.019517377	0.010855284	0.999190171	0.078083208	-0.046343239	-0.051623321	-0.124426447	-0.129706529	-0.005280082
EXTL2|Q9UBQ6	5.65296847	0.000998463	0.953143061	0.010004251	0.284335445	0.001912265	0.100208885	0.45659979	-0.016602687	0.0972493	0.053699365	0.113851986	0.070302051	-0.043549935
FAM20C|Q8IXL6	0.25878955	0.85499996	0.872587637	0.994163439	0.999999869	0.954423964	0.862608653	0.993938241	-0.017213347	-0.005625936	-0.000153816	0.01158741	0.01705953	0.00547212
IGLL5|B9A064	4.87475997	0.002755654	0.005872833	0.739135126	0.024154097	0.086809674	0.923265311	0.253379145	-0.461327235	-0.13752131	-0.377539536	0.323805924	0.083787699	-0.240018225
NRP1|O14786	14.6308584	1.37E-08	0.000441213	0.052704229	6.13E-09	0.399671686	0.140654345	0.000864654	0.102106026	0.063154489	0.154383406	-0.038951537	0.052277379	0.091228916
ATP6AP2|O75787	9.8538971	4.63E-06	0.999851422	0.280262697	2.97E-05	0.328906352	5.33E-05	0.020596093	-0.003469463	-0.081258825	-0.208213243	-0.077789362	-0.20474378	-0.126954418
GAA|P10253	1.86285162	0.137410693	0.967691416	0.848327424	0.314892174	0.583183974	0.132982498	0.801686397	-0.024257883	0.041754305	0.086439847	0.066012189	0.110697731	0.044685542
APOA2|P02652	0.74677236	0.525505074	0.998926258	0.902491286	0.651537912	0.843047643	0.565661574	0.965928905	-0.018006294	0.083273947	0.137881406	0.101280241	0.1558877	0.054607459
MINPP1|Q9UNW1	1.338762	0.263196367	0.982738558	0.430594259	0.955408092	0.243564842	0.808742774	0.718012677	-0.008404231	0.03353786	0.011138928	0.041942091	0.019543159	-0.022398932
ISLR|O14498	11.4521688	6.36E-07	0.000359498	0.789397334	0.020245454	5.43E-06	0.518054977	0.00066205	-0.120253275	0.026517147	-0.081492605	0.146770422	0.03876067	-0.108009752
TIMP1|P01033	4.73701538	0.003299227	0.051291576	0.273935938	0.001893069	0.835989325	0.791192229	0.259319526	-0.123095609	-0.083740387	-0.165553179	0.039355221	-0.04245757	-0.081812791
ROBO2|Q9HCK4	2.09314577	0.102641539	0.776613451	0.099608547	0.229797428	0.55458681	0.809349499	0.966057715	0.035969771	0.08487811	0.068375718	0.048908339	0.032405947	-0.016502393
MDH2|P40926	3.40385249	0.018854145	0.899462809	0.064810605	0.043567046	0.297968606	0.234975291	0.99965818	-0.023329682	-0.081493834	-0.084584961	-0.058164152	-0.061255279	-0.003091127
IMPAD1|Q9NX62	3.53265462	0.015936284	0.368538168	0.273174181	0.007376299	0.99905559	0.423823369	0.484355824	0.058958166	0.063901914	0.112340856	0.004943748	0.05338269	0.048438942
VSTM2B|A6NLU5	6.58671118	0.000297201	0.289186315	0.002302277	0.000581056	0.29868439	0.16275637	0.990982689	0.105705495	0.208654206	0.225115707	0.102948711	0.119410211	0.0164615
MFI2|P08582	7.79133097	6.31E-05	0.115025498	0.037131997	1.78E-05	0.979340814	0.075746413	0.161937506	0.097110017	0.113849131	0.198089534	0.016739114	0.100979517	0.084240404
SERPINE2|P07093	3.7718761	0.011658316	0.964225578	0.084111351	0.028976493	0.244483263	0.10970891	0.983478529	-0.036197177	-0.176134331	-0.201969004	-0.139937154	-0.165771828	-0.025834673
B4GALT1|P15291	1.73999056	0.160343836	0.984060845	0.94780955	0.383503459	0.802979428	0.62589038	0.129534736	-0.014378477	0.021213965	-0.060690199	0.035592442	-0.046311722	-0.081904164
PCSK2|P16519	11.9332891	3.53E-07	0.444609961	0.000401102	1.03E-06	0.061998789	0.001055243	0.572048396	0.078752631	0.209113693	0.272624827	0.130361062	0.193872196	0.063511134
FSTL1|Q12841	13.4396882	5.67E-08	0.000526337	0.999252805	3.08E-05	0.000251648	0.963659784	1.19E-05	-0.171664983	0.005334058	-0.191446279	0.17699904	-0.019781296	-0.196780336
RNASET2|O00584	1.0845905	0.35690993	0.894631477	0.989355312	0.34074081	0.977035269	0.79466743	0.515682304	0.029918582	0.012902419	0.06740645	-0.017016163	0.037487867	0.05450403
PGM1|P36871	1.73217462	0.161920352	0.955628582	0.782968978	0.407145267	0.468862029	0.166902002	0.931287829	0.021661991	-0.038561707	-0.062263392	-0.060223698	-0.083925383	-0.023701685
SSC5D|A1L4H1	1.34537599	0.261088853	0.664986509	0.982958785	0.601075164	0.426597795	0.999974191	0.355325703	0.045557852	-0.014294159	0.047154375	-0.05985201	0.001596524	0.061448534
GNPTG|Q9UJJ9	1.46086586	0.226714994	0.220978619	0.897998512	0.991907432	0.585476004	0.316671062	0.972130476	-0.054542014	-0.019220533	-0.007673282	0.035321481	0.046868733	0.011547251
QDPR|P09417	4.93364483	0.002551588	0.013527001	0.389566874	0.003791521	0.416197053	0.99547264	0.247576523	-0.15945962	-0.080428233	-0.17120448	0.079031387	-0.011744861	-0.090776248
FUCA1|P04066	8.07334962	4.40E-05	7.36E-05	0.776718765	0.021111185	0.002145161	0.279955292	0.204429923	-0.297942597	-0.061474325	-0.183421793	0.236468273	0.114520804	-0.121947468
IGFBP5|P24593	3.66809344	0.013352027	0.101271595	0.263905496	0.007914532	0.951086099	0.85501463	0.511221006	-0.08453642	-0.065286192	-0.112758919	0.019250228	-0.028222499	-0.047472727
SEMA4B|Q9NPR2	1.14438417	0.332510676	0.83163784	0.999437283	0.376236307	0.878318656	0.893717926	0.430232386	0.023904773	0.003188833	0.043132816	-0.02071594	0.019228043	0.039943983
SORCS3|Q9UPU3	4.06575192	0.007938242	0.999996597	0.048032283	0.09608719	0.049201878	0.097587509	0.98515319	-0.000743203	0.089242021	0.077718625	0.089985224	0.078461828	-0.011523396
HK1|P19367	10.1643208	3.14E-06	0.118694532	8.42E-05	9.59E-06	0.14474132	0.052054764	0.978221948	-0.082341161	-0.160063451	-0.173868216	-0.07772229	-0.091527055	-0.013804765
PSAT1|Q9Y617	1.08726164	0.355787108	0.893624202	0.74813245	0.944108699	0.321259799	0.571812328	0.964349893	0.028977379	-0.039893351	-0.021714365	-0.06887073	-0.050691744	0.018178987
NOV|P48745	8.98417227	1.38E-05	0.003188404	0.810693525	9.11E-05	0.039597661	0.879983495	0.002374505	-0.145747099	-0.035960635	-0.175440083	0.109786464	-0.029692984	-0.139479448
MSTN|O14793	8.54614625	2.41E-05	0.622328126	0.417839662	0.007692129	0.033292877	0.21353039	1.26E-05	0.042907175	-0.053086478	0.109331896	-0.095993653	0.066424721	0.162418374
TGFBR3|Q03167	3.10660641	0.027774049	0.121226717	0.916088703	0.813482402	0.021789145	0.478723523	0.396176198	0.051131831	-0.014515507	0.019327163	-0.065647338	-0.031804668	0.03384267
CUTA|O60888	1.83811826	0.141758561	0.940497542	0.940126837	0.351214464	0.661417937	0.119728411	0.698379302	-0.024727662	0.024114313	0.068037831	0.048841975	0.092765492	0.043923517
PRELP|P51888	9.34962843	8.72E-06	0.020984508	0.437795578	6.38E-06	0.457715145	0.207082448	0.002564333	-0.140755741	-0.070740414	-0.232000861	0.070015327	-0.09124512	-0.161260447
CNTFR|P26992	4.77348239	0.003145643	0.999287457	0.583899454	0.006146663	0.673839503	0.010608306	0.175531335	0.004075764	0.040020609	0.101949354	0.035944845	0.097873591	0.061928745
TUBA1B|P68363	1.35211391	0.258957845	0.371125133	0.867730558	0.289190346	0.814299937	0.999870958	0.748163204	-0.132331173	-0.061312255	-0.137923556	0.071018918	-0.005592383	-0.076611302
SOD2|P04179	5.69310417	0.000947637	0.972171805	0.03471765	0.040494049	0.010487105	0.012155209	0.999318258	0.023258572	-0.141695791	-0.135521714	-0.164954362	-0.158780286	0.006174077
IGFBP4|P22692	7.46348489	9.60E-05	0.098904286	0.303860415	0.171929966	0.000398568	0.982250697	0.000749623	-0.067736534	0.04971722	-0.057221897	0.117453754	0.010514637	-0.106939117
YWHAE|P62258	95.0765132	2.85E-37	0.588993569	9.93E-14	1.01E-13	8.64E-14	8.66E-14	0.986168079	0.045128613	-0.396058612	-0.384612528	-0.441187225	-0.429741141	0.011446084
NAGLU|P54802	12.9403933	1.04E-07	2.02E-05	0.999956734	0.000675022	1.80E-05	0.696328982	0.000633221	-0.28540065	-0.002860779	-0.222906502	0.282539871	0.062494148	-0.220045722
B2M|P61769	1.43596272	0.233750384	0.431384651	0.999035808	0.974159649	0.501048139	0.194548621	0.938816689	0.069254538	0.006193906	-0.018479025	-0.063060633	-0.087733563	-0.024672931
ACTC1|P68032	4.41890615	0.00500128	0.963644113	0.305781048	0.037933612	0.125255764	0.009823574	0.787878775	0.026482783	-0.093623358	-0.141747557	-0.120106141	-0.16823034	-0.048124199
TFRC|P02786	2.20452264	0.089050513	0.835111819	0.380028519	0.996023847	0.073826196	0.91474355	0.233240735	-0.041489889	0.076953467	-0.010511258	0.118443356	0.03097863	-0.087464726

			ANOVA p -values with Tukey Adjustment						Difference (AD - CT)					
Gene ID | Unirprot ID	F-Value	Pr(>F)	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA
GFRA2|O00451	7.29312494	0.00011952	0.009217759	0.000941225	0.000210973	0.941154518	0.818079634	0.990494552	0.237674777	0.279523778	0.300531195	0.041849001	0.062856419	0.021007417
CALB1|P05937	2.0268388	0.111667803	0.165667927	0.131059134	0.538390829	0.999943478	0.839926235	0.79831852	-0.102131625	-0.104747442	-0.062761945	-0.002615818	0.03936968	0.041985497
PAPPA2|Q9BXP8	6.12658287	0.000539455	0.968644233	0.037380858	0.022193279	0.01075368	0.005788488	0.999288619	-0.021551223	0.124651513	0.130216556	0.146202736	0.151767779	0.005565043
LMAN1|P49257	3.54319153	0.015718496	0.579257588	0.999975298	0.035496857	0.540892169	0.524499026	0.027719849	0.036465345	-0.001137818	0.073934059	-0.037603163	0.037468715	0.075071877
PROC|P04070	0.65837322	0.578668352	0.531140258	0.957580077	0.982543735	0.818779788	0.727052461	0.9988012	0.071201753	0.025928469	0.018563731	-0.045273283	-0.052638021	-0.007364738
PIGR|P01833	6.04449446	0.000600118	0.923504111	0.126448133	0.000825542	0.415741388	0.009199404	0.350323871	-0.062333122	-0.213246581	-0.367190744	-0.150913459	-0.304857621	-0.153944162
CANT1|Q8WVQ1	10.895756	1.26E-06	0.074439808	0.001901496	4.60E-07	0.666135655	0.016040897	0.23518192	0.072787612	0.106324558	0.159195245	0.033536946	0.086407633	0.052870687
ST8SIA3|O43173	1.80027375	0.148667756	0.965847085	0.310267626	0.949552368	0.130617445	0.738791036	0.592295063	-0.02033344	0.073114123	0.02220438	0.093447563	0.04253782	-0.050909743
CDH6|P55285	19.0813431	7.97E-11	0.001586409	9.05E-05	1.26E-11	0.923527257	0.002330005	0.014135531	0.117696373	0.137291962	0.227659751	0.019595589	0.109963378	0.090367788
COL4A2|P08572	0.1381497	0.937105465	0.943014197	0.994304237	0.952425306	0.988494811	0.999906318	0.99287797	-0.02028974	-0.008877471	-0.018073532	0.011412269	0.002216208	-0.009196061
CPN2|P22792	2.26368279	0.082561285	0.218989518	0.967328419	0.787243627	0.077527503	0.699557274	0.482632081	-0.22288876	0.051830756	-0.102389222	0.274719516	0.120499538	-0.154219978
MGAT5|Q09328	0.34357384	0.793840649	0.92653406	0.933351997	0.99833414	0.999979749	0.851442791	0.858878713	-0.015000865	-0.014084101	0.003862015	0.000916763	0.01886288	0.017946117
HSPA13|P48723	3.09783834	0.028092753	0.01863068	0.70548823	0.252328651	0.217096909	0.604685497	0.869788867	-0.099449075	-0.035238213	-0.059350539	0.064210863	0.040098537	-0.024112326
HSPA2|P54652	0.40577143	0.749037411	0.846846216	0.91183528	0.717278586	0.998168507	0.997730757	0.982172615	-0.044406919	-0.035069717	-0.054107958	0.009337201	-0.009701039	-0.019038241
NDST1|P52848	6.36772453	0.0003946	0.460690351	0.614107458	0.037476868	0.038188841	0.000249771	0.453497514	-0.05987207	0.048561959	0.10495338	0.108434029	0.16482545	0.056391421
TAGLN|Q01995	0.84696587	0.469821421	0.962042598	0.961890124	0.73727136	0.76364965	0.431216569	0.951286015	0.040942349	-0.039893599	-0.081703123	-0.080835947	-0.122645472	-0.041809525
SEMA6D|Q8NFY4	6.61894169	0.000285069	0.074306562	0.162966936	9.21E-05	0.975855832	0.252554701	0.091734577	0.089533963	0.074504082	0.155102412	-0.015029881	0.065568449	0.08059833
GGH|Q92820	1.44118016	0.232259767	0.452670655	0.983245579	0.792869179	0.247796388	0.923955187	0.551888717	-0.07622433	0.018342722	-0.045211321	0.094567052	0.031013009	-0.063554043
IGSF21|Q96ID5	3.85215005	0.01049674	0.9479933	0.027887797	0.063472441	0.120601586	0.230785719	0.980625086	0.019627487	0.098593504	0.085639741	0.078966017	0.066012254	-0.012953763
GPX3|P22352	3.92841158	0.009500406	0.138543127	0.188890225	0.004587489	0.996742829	0.682880909	0.522499845	-0.08474757	-0.076656118	-0.126728223	0.008091452	-0.041980654	-0.050072106
FAT1|Q14517	5.97482187	0.00065696	0.003039808	0.999618131	0.104223123	0.00355645	0.503974531	0.1208886	-0.154900839	-0.004371466	-0.095793739	0.150529373	0.0591071	-0.091422273
RGMA|Q96B86	11.5404088	5.71E-07	2.54E-05	0.034464012	1.68E-06	0.153536176	0.986009316	0.05188962	0.223977947	0.12572542	0.239613423	-0.098252526	0.015635477	0.113888003
EPHB6|O15197	4.97489496	0.002417729	0.002514519	0.069825586	0.012809285	0.628318656	0.906394252	0.941468697	0.233249	0.1562011	0.190838162	-0.077047901	-0.042410839	0.034637062
LTF|P02788	11.4937882	6.05E-07	0.001747097	0.998585644	0.000148529	0.000798401	0.970261171	5.47E-05	0.356539129	-0.014927196	0.398193849	-0.371466325	0.04165472	0.413121044
CTBS|Q01459	1.11090151	0.345984917	0.576584586	0.972527354	0.999988237	0.311443526	0.524852384	0.975081214	-0.058577648	0.019324308	0.001389659	0.077901956	0.059967307	-0.017934649
VSTM2A|Q8TAG5	5.00179014	0.002334268	0.003454331	0.01302718	0.024325224	0.958577139	0.856857463	0.991507222	0.284728996	0.244328314	0.222191979	-0.040400682	-0.062537017	-0.022136335
LAMC3|Q9Y6N6	0.90361169	0.440496867	0.998839142	0.533649901	0.682531858	0.639151258	0.780841333	0.992915757	0.006386089	0.056570267	0.045594231	0.050184178	0.039208142	-0.010976036
APOL1|O14791	0.93025706	0.427235314	0.90950766	0.916986384	0.849026763	0.554547998	0.999538897	0.440921687	-0.096420125	0.090849897	-0.111551014	0.187270022	-0.015130888	-0.202400911
LINGO1|Q96FE5	6.48146144	0.000340558	0.103595507	0.012893797	0.00015971	0.893154597	0.245706467	0.642961902	0.168507164	0.21988117	0.300638628	0.051374006	0.132131464	0.080757458
FMOD|Q06828	0.57729809	0.630620094	0.727515451	0.954958775	0.641218014	0.948291092	0.999774162	0.911702313	-0.065323273	-0.031660513	-0.070511237	0.03366276	-0.005187964	-0.038850724
B3GNT2|Q9NY97	10.5490773	1.94E-06	0.122509145	0.000133265	3.76E-06	0.175847126	0.029176946	0.887542825	0.047358993	0.090352931	0.104798825	0.042993937	0.057439832	0.014445895
SHBG|P04278	0.61354583	0.607029686	0.996540949	0.797640775	0.994687073	0.677776427	0.999996187	0.625904101	0.026465044	-0.110081273	0.029081037	-0.136546317	0.002615993	0.13916231
OMG|P23515	4.53463115	0.004298757	0.069258489	0.510774584	0.003151344	0.669385354	0.801669265	0.148200739	0.13048157	0.071359368	0.176676223	-0.059122201	0.046194653	0.105316855
SGCE|O43556	6.12947183	0.000537436	0.020053744	0.07308968	0.000247623	0.943944678	0.688932565	0.314144786	0.081525013	0.066182334	0.111073271	-0.015342679	0.029548258	0.044890937
MDGA2|Q7Z553	6.90424881	0.000197209	0.016275957	0.032252777	7.90E-05	0.988786737	0.561555116	0.33779022	0.125884638	0.11270919	0.178608633	-0.013175449	0.052723994	0.065899443
PLXNB1|O43157	1.04946813	0.371965421	0.999926517	0.749339326	0.890802561	0.789437587	0.868799485	0.291200155	-0.001616518	-0.026728166	0.018677746	-0.025111648	0.020294263	0.045405911
CPB2|Q96IY4	0.3293075	0.804167709	0.959586665	0.991951206	0.975694143	0.860650707	0.79011804	0.999267146	-0.047196004	0.026264535	0.037518174	0.073460539	0.084714178	0.011253639
NDRG4|Q9ULP0	1.71204631	0.166048685	0.523578406	0.401147416	0.123046519	0.998499548	0.867832076	0.924522885	0.054165738	0.060475531	0.083600564	0.006309793	0.029434827	0.023125033
SORT1|Q99523	2.04708392	0.10883327	0.668787402	0.995287794	0.237579847	0.509393353	0.903048126	0.136731284	0.040827282	-0.008307447	0.064524274	-0.049134729	0.023696992	0.072831721
AP2B1|P63010	3.223655	0.023847763	0.796319765	0.153768017	0.970035205	0.015382789	0.504824314	0.305079568	0.029182198	-0.065399004	-0.0135511	-0.094581202	-0.042733298	0.051847903
ENPP5|Q9UJA9	2.03332704	0.110751683	0.989100268	0.998944684	0.238584452	0.967173698	0.130314659	0.292565106	0.016877953	-0.007466041	-0.09580494	-0.024343994	-0.112682893	-0.088338899
CDH5|P33151	2.98265809	0.032631634	0.999732987	0.258150511	0.10907293	0.227395539	0.093833818	0.979399566	-0.004284194	0.084680628	0.102037968	0.088964822	0.106322162	0.01735734
PGAM1|P18669	53.1958375	7.69E-25	0.477453721	1.12E-12	1.88E-13	1.22E-13	1.23E-13	0.993451741	0.041706981	-0.22473565	-0.231922862	-0.266442631	-0.273629843	-0.007187212
YWHAZ|P63104	117.713115	1.13E-42	0.474553456	9.33E-14	8.59E-14	8.59E-14	8.59E-14	0.442452746	0.058660986	-0.460868679	-0.517679092	-0.519529665	-0.576340078	-0.056810413
BGN|P21810	4.04800741	0.00812466	0.012027793	0.857094119	0.083945963	0.088527195	0.823381853	0.382658253	-0.186457018	-0.046520538	-0.136387067	0.13993648	0.05006995	-0.08986653
MAN1B1|Q9UKM7	2.18936695	0.090791341	0.626055278	0.891410292	0.452541852	0.220353305	0.996676761	0.114397083	0.044582972	-0.025760952	0.052106211	-0.070343924	0.007523239	0.077867164
ADAM23|O75077	3.35266157	0.020156257	0.155808454	0.056744463	0.020040262	0.981737658	0.895438151	0.987766917	0.082057732	0.096525144	0.108485792	0.014467412	0.02642806	0.011960648

			ANOVA p -values with Tukey Adjustment						Difference (AD - CT)					
Gene ID | Unirprot ID	F-Value	Pr(>F)	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA
FSCN1|Q16658	11.2819515	7.85E-07	0.992850063	6.10E-05	0.007215537	2.32E-05	0.003211209	0.497326627	0.010444422	-0.168635683	-0.118425748	-0.179080106	-0.12887017	0.050209936
IGLON5|A6NGN9	5.47233038	0.001263335	0.999979659	0.069558453	0.00810366	0.081934851	0.010411303	0.890709135	0.001234586	0.077075378	0.098602688	0.075840792	0.097368101	0.02152731
NOTCH2|Q04721	3.4517337	0.017712072	0.95355959	0.06857587	0.752765733	0.017672893	0.424540443	0.405651995	-0.012957917	0.059516537	0.023437956	0.072474454	0.036395873	-0.036078581
CLIC4|Q9Y696	1.9101188	0.129455601	0.999886547	0.347483953	0.340472702	0.32123198	0.314249622	0.999993152	0.003294029	-0.078219539	-0.077012837	-0.081513568	-0.080306866	0.001206702
CPXM2|Q8N436	3.35088936	0.020202902	0.021976579	0.231546554	0.049275331	0.713490334	0.971327211	0.910298808	-0.147568024	-0.094282161	-0.125941592	0.053285864	0.021626432	-0.031659431
SLITRK4|Q8IW52	6.85605353	0.000209861	0.148586305	0.172891819	6.56E-05	0.999185705	0.113426478	0.070110267	0.118140098	0.110947492	0.238539179	-0.007192606	0.120399081	0.127591687
MFAP4|P55083	2.35514075	0.073427854	0.077658321	0.990866375	0.915995288	0.138456959	0.244782688	0.985190072	-0.082943984	-0.009921553	-0.021163153	0.07302243	0.061780831	-0.011241599
CHST15|Q7LFX5	2.14116175	0.096551455	0.331602809	0.914357561	0.993442453	0.088109149	0.184875875	0.976643676	-0.03825934	0.014381593	0.005707609	0.052640934	0.043966949	-0.008673984
MYOC|Q99972	3.89010776	0.009988438	0.101930732	0.953273262	0.02244448	0.268369411	0.967224966	0.08234086	-0.313837962	-0.069561724	-0.374509237	0.244276238	-0.060671275	-0.304947513
ASAH1|Q13510	1.33787264	0.26348095	0.32452048	0.999822374	0.728970497	0.351968143	0.877399623	0.766157411	-0.109518496	-0.004942626	-0.063246839	0.10457587	0.046271657	-0.058304213
HLA-A|P05534	1.01415353	0.388014793	0.968898243	0.381945923	0.63908998	0.67000014	0.898740693	0.959288639	-0.143288677	-0.499037893	-0.351715653	-0.355749216	-0.208426976	0.14732224
RNH1|P13489	5.937665	0.000689457	0.991219928	0.054279553	0.002817107	0.118276247	0.008917259	0.785626625	-0.015500652	-0.131802165	-0.1780595	-0.116301513	-0.162558847	-0.046257335
GM2A|P17900	0.8784681	0.45332233	0.541984605	0.458964269	0.739551668	0.999692178	0.980942693	0.960388708	0.04678288	0.050060097	0.033889438	0.003277217	-0.012893442	-0.016170659
GALNT18|Q6P9A2	3.36673937	0.019789508	0.997955212	0.184873522	0.103654806	0.133607506	0.071551775	0.995732454	-0.006581751	0.072200023	0.080079245	0.078781774	0.086660995	0.007879222
CD99L2|Q8TCZ2	2.62384648	0.0519482	0.119561072	0.062350973	0.153714065	0.996561591	0.995653417	0.96708639	0.115981062	0.126913335	0.104415503	0.010932274	-0.011565558	-0.022497832
CANX|P27824	4.37517333	0.005295737	0.046929793	0.650926395	0.006593662	0.434402621	0.952363581	0.146527937	0.073949572	0.031975648	0.088291744	-0.041973924	0.014342172	0.056316096
MIA3|Q5JRA6	1.97645244	0.119036116	0.085227561	0.471869681	0.772438593	0.758866003	0.426777136	0.95159238	-0.067633036	-0.040065912	-0.025961873	0.027567124	0.041671163	0.014104039
SIAE|Q9HAT2	2.67356371	0.048715278	0.052405001	0.919826555	0.27208957	0.197480735	0.811343446	0.641927171	-0.172449681	-0.041539374	-0.115228459	0.130910307	0.057221223	-0.073689084
RTN4RL2|Q86UN3	8.44857468	2.73E-05	0.02199399	0.001457403	1.60E-05	0.878932481	0.288068786	0.723129013	0.18734887	0.234808678	0.298035065	0.047459808	0.110686195	0.063226387
GSR|P00390	10.4160148	2.29E-06	0.944396726	0.001918026	3.35E-05	0.014232946	0.000456791	0.775832896	-0.020775891	-0.132361006	-0.165563474	-0.111585115	-0.144787584	-0.033202469
LGALS1|P09382	5.98880436	0.000645134	0.86213715	0.379305682	0.000582087	0.859292563	0.011488994	0.085864281	-0.030030637	-0.059836537	-0.144892527	-0.029805901	-0.11486189	-0.085055989
ATP1A3|P13637	0.31452587	0.814842817	0.999980239	0.863112294	0.999990985	0.873304408	0.999878638	0.832552987	-0.003738194	-0.077594645	0.002807473	-0.073856451	0.006545667	0.080402119
ATP6AP1|Q15904	4.44937677	0.00480586	0.876328695	0.036191922	0.872699637	0.003907611	0.421969533	0.171922119	-0.027075259	0.095290873	0.026025298	0.122366132	0.053100557	-0.069265575
CLSTN2|Q9H4D0	0.45613138	0.713280398	0.790750326	0.821172786	0.717730818	0.999796253	0.999825379	0.998304006	0.04230007	0.038580162	0.045753588	-0.003719908	0.003453518	0.007173426
GALNT1|Q10472	3.67278764	0.013270372	0.373815019	0.345267706	0.970657623	0.006672098	0.152218467	0.575625611	-0.039406729	0.039576078	0.010315864	0.078982807	0.049722594	-0.029260214
DSC2|Q02487	13.4149881	5.84E-08	0.00023559	0.638066662	6.69E-07	0.011833204	0.699601224	0.000113428	0.138064638	0.037801822	0.172320641	-0.100262815	0.034256004	0.134518819
NPTX2|P47972	31.3585678	1.95E-16	0.008398755	3.55E-10	1.25E-13	0.00221082	6.51E-07	0.236184354	0.256281672	0.539940954	0.680800463	0.283659281	0.424518791	0.14085951
PLS3|P13797	0.70756785	0.548621399	0.814593559	0.866501766	0.471484969	0.999194894	0.955669934	0.909209819	-0.053434795	-0.045614848	-0.083429528	0.007819947	-0.029994734	-0.03781468
EZR|P15311	3.50170138	0.016593587	0.63903422	0.743201123	0.243042301	0.127191545	0.012713403	0.828824435	0.065677298	-0.054663525	-0.098958329	-0.120340823	-0.164635627	-0.044294804
GALNT10|Q86SR1	1.41829944	0.238863117	0.841298472	0.968146425	0.211287188	0.979990779	0.711060651	0.435385037	0.022315007	0.011994789	0.049957735	-0.010320218	0.027642728	0.037962946
RNASE4|P34096	2.42501459	0.067123384	0.830214275	0.219691903	0.066085932	0.724877093	0.399586513	0.955025384	-0.035900103	-0.079222298	-0.09960188	-0.043322195	-0.063701776	-0.020379581
ASPH|Q12797	2.07549233	0.104973071	0.88011051	0.693925742	0.634625111	0.260800547	0.977705499	0.091032748	0.018899629	-0.02711491	0.028798575	-0.046014539	0.009898946	0.055913485
HLA-A|P10316	3.63467996	0.013947897	0.337045264	0.494202182	0.006787409	0.989412435	0.444468817	0.246413926	-0.2466805	-0.201533116	-0.457473114	0.045147385	-0.210792614	-0.255939998
DSG2|Q14126	2.68881596	0.047763817	0.029825549	0.773456122	0.472868726	0.239092145	0.459567328	0.964970157	-0.099598532	-0.033324322	-0.049118792	0.066274211	0.05047974	-0.015794471
PRDX1|Q06830	5.44352125	0.001311673	0.861014207	0.045427657	0.002196223	0.276264105	0.032761889	0.785224704	-0.03561156	-0.116004713	-0.155681225	-0.080393152	-0.120069665	-0.039676513
AMY2B|P19961	2.5343737	0.058306653	0.035980883	0.759307615	0.671347513	0.282307987	0.323002691	0.999280696	-0.112029782	-0.039436862	-0.044296007	0.07259292	0.067733775	-0.004859145
NTRK2|Q16620	3.195821	0.024728341	0.198116728	0.106354363	0.017760035	0.9951541	0.820437494	0.917665605	0.071356025	0.079840472	0.101478356	0.008484448	0.030122331	0.021637883
ANGPTL2|Q9UKU9	0.89081131	0.44698826	0.835052805	0.991258407	0.884570645	0.66355574	0.38383984	0.97164292	-0.02664698	0.009024619	0.022026597	0.035671599	0.048673577	0.013001978
CLTC|Q00610	2.55264433	0.059424625	0.070388598	0.923638225	0.23083036	0.265988905	0.912020458	0.599619777	-0.289025432	-0.075211933	-0.216498882	0.213813499	0.07252655	-0.141286949
MAN1C1|Q9NR34	0.18940873	0.90351703	0.997064605	0.999999706	0.917373939	0.997318828	0.973900779	0.916874229	-0.00622321	-0.000279844	-0.018853015	0.005943366	-0.012629805	-0.018573172
SEMA4D|Q92854	1.78351492	0.151829427	0.801938761	0.144551911	0.296558707	0.631001363	0.855998853	0.971707914	0.021874578	0.050290686	0.040391016	0.028416109	0.018516438	-0.00989967
BAI1|O14514	8.84060848	1.66E-05	0.011021247	0.001962563	7.67E-06	0.973743219	0.328337418	0.56572934	0.20036154	0.227336395	0.305061002	0.026974855	0.104699461	0.077724606
BCHE|P06276	0.39837938	0.754322535	0.716606773	0.990454109	0.981134209	0.865841475	0.888598609	0.999856694	-0.052376205	-0.014548218	-0.017957405	0.037827987	0.0344188	-0.003409187
PDIA4|P13667	1.67983491	0.172864595	0.291251754	0.818461078	0.188918674	0.786629243	0.998933443	0.669944338	-0.046496802	-0.022335379	-0.050135925	0.024161423	-0.003639124	-0.027800546
FLNC|Q14315	2.38031617	0.071092248	0.07451735	0.990275723	0.649794231	0.135225758	0.515128852	0.820829948	-0.08666919	-0.01051641	-0.039443668	0.07615278	0.047225521	-0.028927259
CFHR2|P36980	2.99186897	0.032243387	0.776705676	0.945272026	0.133946876	0.430757539	0.653196817	0.029429084	-0.141857754	0.080368825	-0.308113036	0.222226579	-0.166255282	-0.388481861
CSF1R|P07333	0.57678227	0.630959891	0.851174557	0.571886144	0.810652524	0.968949348	0.999977677	0.972042324	0.037822568	0.058738266	0.039607654	0.020915697	0.001785085	-0.019130612

Gene ID | Unirprot ID	F-Value	Pr(>F)	ANOVA p -values with Tukey Adjustment						Difference (AD - CT)					
			AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA
PCSK1|P29120	12.4598532	1.85E-07	0.044991375	4.00E-06	1.39E-06	0.078304692	0.053179162	0.999598693	0.224606163	0.427195894	0.435466092	0.202589731	0.210859929	0.008270199
ART3|Q13508	9.98383191	3.93E-06	0.00084074	0.976143533	0.000260625	0.002936307	0.999634104	0.001028497	0.26931428	0.027932775	0.276041271	-0.241381505	0.006726991	0.248108496
EGFR|P00533	4.3606258	0.005397483	0.176655481	0.722833124	0.313335062	0.011657562	0.975529405	0.025293743	-0.064459399	0.032122998	-0.051790559	0.096582397	0.012668839	-0.083913558
IMPA1|P29218	13.0138744	9.47E-08	0.728159678	0.000260591	0.00343893	3.37E-06	6.55E-05	0.849642691	0.030714609	-0.120514454	-0.098088543	-0.151229062	-0.128803152	0.022425911
SERPINB6|P35237	3.01919346	0.031118345	0.09736517	0.898286504	0.064309618	0.34408517	0.999948104	0.271522202	-0.075415532	-0.02204005	-0.077056088	0.053375482	-0.001640557	-0.055016039
MATN2|O00339	1.7360362	0.161139611	0.162182053	0.994236567	0.798471057	0.246546059	0.58664214	0.910696609	-0.081305853	-0.009640691	-0.033822615	0.071665162	0.047483238	-0.024181924
MARCKS|P29966	4.22996299	0.006403655	0.74157601	0.252199744	0.203286134	0.024159952	0.016165676	0.999852674	0.033785605	-0.060080831	-0.062392862	-0.093866436	-0.096178467	-0.002312031
DPP10|Q8N608	2.15477415	0.094889814	0.703642464	0.525475414	0.90533278	0.073348945	0.281746812	0.885984891	0.055282229	-0.067934509	-0.03306304	-0.123216738	-0.088345269	0.03487147
CTSL|P07711	0.30173691	0.824115444	0.941208841	0.992248122	0.988788458	0.990567335	0.801842214	0.926725596	-0.022563574	-0.010838089	0.012007759	0.011725485	0.034571333	0.022845848
TRHDE|Q9UKU6	1.90729967	0.129917361	0.496513313	0.890568145	0.930918941	0.145361413	0.170961714	0.999174552	-0.063625991	0.031510372	0.02593019	0.095136362	0.08955618	-0.005580182
PCDH10|Q9P2E7	13.3081853	6.64E-08	5.36E-06	0.008039615	1.79E-07	0.200860461	0.972392618	0.058613721	0.265676635	0.164006928	0.287547188	-0.101669707	0.021870552	0.123540259
GPI|P06744	43.6257454	2.28E-21	0.83316542	1.25E-13	2.24E-07	1.22E-13	3.31E-09	0.003256276	0.040982836	-0.423647743	-0.264978359	-0.464630579	-0.305961195	0.158669383
SLITRK5|O94991	7.7922553	6.30E-05	0.016807538	0.062371688	2.01E-05	0.944685328	0.36475382	0.110182127	0.144477761	0.117963226	0.220357264	-0.026514535	0.075879504	0.102394039
CLEC11A|Q9Y240	4.62933688	0.003797996	0.006493323	0.997873066	0.454580417	0.009758997	0.205691028	0.556589693	-0.133673798	-0.007168513	-0.056939313	0.126505286	0.076734485	-0.049770801
CSF1|P09603	0.11507907	0.951187649	0.937445461	0.995171191	0.988287471	0.984673426	0.991884239	0.999817073	0.012352589	0.004940961	0.006524205	-0.007411627	-0.005828383	0.001583244
NEFM|P07197	30.7712494	3.48E-16	0.997373022	1.61E-09	9.20E-10	8.36E-10	4.75E-10	0.999932895	0.019228954	-0.641800702	-0.636532687	-0.661029656	-0.655761641	0.005268015
HS6ST3|Q8IZP7	9.97210025	3.99E-06	0.000668829	0.00105404	3.11E-06	0.995797865	0.722938506	0.553064815	0.240469793	0.226746914	0.301917491	-0.013722879	0.061447699	0.075170577
OLFM1|Q99784	10.7998622	1.42E-06	0.000261705	0.020979039	1.02E-06	0.520391454	0.734103359	0.063186814	0.136084907	0.09219322	0.168255618	-0.043891687	0.032170711	0.076062398
0|P01782	3.69270839	0.012929356	0.157300293	0.960235534	0.189206096	0.046525069	0.99720771	0.054831552	-0.238849454	0.054753948	-0.217073195	0.293603402	0.021776259	-0.271827143
PPIB|P23284	5.27621088	0.001631463	0.00142374	0.594044833	0.045341023	0.055218272	0.575773223	0.519125235	-0.141427165	-0.046179433	-0.094703239	0.095247732	0.046723926	-0.048523806
ADAMTS1|Q9UHI8	1.78689784	0.151186074	0.945013472	0.122221858	0.682276229	0.365643548	0.953747538	0.641667939	0.0280745	0.109100559	0.05346649	0.081026059	0.025391991	-0.055634068
FGFR1|P11362	3.12291953	0.027190606	0.879525114	0.221779062	0.434454922	0.042426454	0.110846834	0.96588771	-0.023983111	0.060408115	0.046282691	0.084391226	0.070265801	-0.014125425
CLIC1|O00299	4.53611837	0.004290404	0.030971321	0.958922026	0.023931454	0.096976164	0.999950481	0.082017889	-0.149076253	-0.026176019	-0.146405106	0.122900234	0.002671147	-0.120229087
PCDH7|O60245	11.9511149	3.45E-07	0.000538469	4.30E-05	4.14E-07	0.957912518	0.500637203	0.799079826	0.186617211	0.209827906	0.249588998	0.023210694	0.062971787	0.039761093
CPM|P14384	0.45184835	0.716294629	0.935222085	0.942161369	0.999716396	0.654449923	0.953947052	0.903490942	-0.02902969	0.027107107	-0.004326872	0.056136797	0.024702818	-0.031433979
IGFBP3|P17936	8.52700066	2.47E-05	0.036924353	0.123285666	7.16E-06	0.943122076	0.142772915	0.028479369	-0.183841356	-0.146260968	-0.324040114	0.037580388	-0.140198757	-0.177779145
FETUB|Q9UGM5	1.28927412	0.279468326	0.903585514	0.8770345	0.731734702	0.480161898	0.989785496	0.2633389	-0.072111911	0.076972119	-0.103475879	0.14908403	-0.031363968	-0.180447998
LRP8|Q14114	7.90091092	5.48E-05	0.30670949	0.022904009	2.48E-05	0.702448415	0.023002052	0.264101226	0.065542485	0.105611418	0.169950666	0.040068934	0.104408181	0.064339248
HEG1|Q9ULI3	5.65875639	0.000990968	0.137669368	0.011166675	0.000702989	0.81135434	0.365001218	0.879749881	0.094543974	0.132747165	0.16307636	0.038203191	0.068532386	0.030329195
P4HB|P07237	3.76069429	0.011829985	0.04647625	0.997603479	0.304199049	0.025020779	0.749039679	0.202919624	-0.057868773	0.004057672	-0.036597765	0.061926445	0.021271008	-0.040655437
PCSK9|Q8NBP7	2.96361227	0.03344917	0.881932769	0.246860918	0.03127525	0.69363789	0.203853088	0.818083132	0.039398001	0.096958293	0.140616309	0.057560292	0.101218308	0.043658016
SPOCK3|Q9BQ16	1.38435628	0.248980938	0.379528137	0.999985157	0.592258791	0.384671082	0.974102692	0.601278176	0.050981069	0.001068679	0.037964297	-0.04991239	-0.013016773	0.036895618
ISLR2|Q6UXK2	5.02192239	0.00227369	0.005428983	0.489375777	0.009353797	0.192801127	0.986548634	0.298340729	0.163754021	0.067537958	0.147789481	-0.096216063	-0.015964541	0.080251523
DDAH1|O94760	24.3590051	2.49E-13	0.016307467	6.41E-06	0.021549353	7.95E-13	6.84E-08	0.101107606	0.112555975	-0.184424858	-0.103588773	-0.296980833	-0.216144747	0.080836086
F13A1|P00488	0.4524215	0.715890962	0.837637853	0.999717263	0.812495141	0.873546128	0.999999899	0.852239671	0.073457147	0.007899354	0.074010956	-0.065557793	0.000553809	0.066111602
C1RL|Q9NZP8	1.17470547	0.320714166	0.991043854	0.688421929	0.333763803	0.858954839	0.52663809	0.941604688	0.020633742	0.075038497	0.112126582	0.054404755	0.09149284	0.037088085
ATP1A2|P50993	0.76618564	0.514333972	0.874535512	0.959886569	0.932302113	0.591621446	0.516187808	0.999713901	0.040054498	-0.025613213	-0.030208422	-0.065667711	-0.07026292	-0.004595209
RBP3|P10745	1.92683223	0.126750331	0.193985846	0.448392374	0.133944319	0.944471922	0.999837187	0.909627177	0.230045681	0.166743614	0.23857011	-0.063302067	0.008524429	0.071826496
MGAT1|P26572	1.03539012	0.37815394	0.73821925	0.549634424	0.333138023	0.992967928	0.929625115	0.986507973	0.030506908	0.038511227	0.047998788	0.008004319	0.01749188	0.009487561
PTPRK|Q15262	2.37580391	0.071505447	0.980491566	0.320196899	0.096479065	0.563613583	0.234110557	0.937898637	0.012903633	0.055789259	0.073944699	0.042885627	0.061041066	0.018155439
CPD|O75976	0.85065676	0.467863493	0.382911902	0.845932232	0.856630862	0.848018376	0.81828848	0.999971372	0.059869194	0.029837978	0.028332152	-0.030031216	-0.031537042	-0.001505826
XXYLT1|Q8NBI6	3.58022909	0.014976218	0.400259925	0.044318077	0.015589386	0.739900867	0.534968226	0.989146143	0.059287197	0.097169888	0.108307453	0.03788269	0.049020256	0.011137566
LRP11|Q86VZ4	7.46589436	9.57E-05	0.003996954	0.111055581	6.72E-05	0.590947087	0.813944508	0.117812978	0.170627859	0.109173526	0.212773978	-0.061454333	0.042146119	0.103600452
CPB1|P15086	20.8218924	1.14E-11	4.14E-07	0.767384969	1.17E-08	2.40E-05	0.9787072	1.12E-06	0.340940746	0.057180183	0.364132072	-0.283760563	0.023191326	0.306951889
PTPRT|O14522	6.47395972	0.000343882	0.28146169	0.000659591	0.002417066	0.164550119	0.336717383	0.968152896	0.082552544	0.176864302	0.157162646	0.094311758	0.074610102	-0.019701656
RDX|P35241	2.44413691	0.06549256	0.567063523	0.623330521	0.844757123	0.061936417	0.139544555	0.974650295	0.087227731	-0.079070799	-0.052514618	-0.16629853	-0.139742349	0.026556181
NOTCH1|P46531	1.80250212	0.148252137	0.999471539	0.643573437	0.190270873	0.723026953	0.248588175	0.847176592	0.003185215	0.031999646	0.053327082	0.02881443	0.050141867	0.021327436

Gene ID | Unirprot ID	F-Value	Pr(>F)	ANOVA p -values with Tukey Adjustment						Difference (AD - CT)					
			AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA
PCDHGC3|Q9UN70	1.62688937	0.184648879	0.775665171	0.699330455	0.933745758	0.17694478	0.977587819	0.309069707	-0.029423059	0.032553027	-0.017419674	0.061976086	0.012003386	-0.049972701
AKR1B1|P15121	12.8535339	1.15E-07	0.049284409	7.74E-05	9.98E-08	0.28330229	0.010808217	0.53670168	-0.078704545	-0.131977076	-0.16999362	-0.053272531	-0.091289075	-0.038016543
MAN2B1|O00754	1.38113849	0.249960431	0.722810213	0.836665983	0.916331865	0.236160194	0.97012591	0.421365258	0.047049912	-0.036653968	0.027691349	-0.083703879	-0.019358563	0.064345316
SIGLEC14|Q08ET2	9.10400514	1.19E-05	0.000731124	0.204095791	2.11E-05	0.180496463	0.914226392	0.027628375	0.249678472	0.239631568	0.568626794	-0.250274905	0.078720322	0.328995226
TKT|P29401	15.8120689	3.40E-09	0.980236212	1.39E-05	6.91E-05	2.98E-06	1.54E-05	0.960484757	0.018200236	-0.22299446	-0.20131983	-0.241194697	-0.219520066	0.021674631
ERBB3|P21860	4.68097419	0.003550027	0.020419226	0.99972271	0.083188457	0.023244038	0.906101516	0.094410018	0.142426071	0.004353723	0.110686946	-0.138072347	-0.031739125	0.106333222
ADAMTS8|Q9UP79	2.82221683	0.040186221	0.942893734	0.173236519	0.997595999	0.049191172	0.978558721	0.095298755	-0.028408851	0.10072798	-0.00906913	0.12913683	0.01933972	-0.10979711
PRRT2|Q7Z6L0	2.42081418	0.067486909	0.048737442	0.896077641	0.663228903	0.211374813	0.395488156	0.9729474	0.174551297	0.045832007	0.072890042	-0.12871929	-0.101661255	0.027058035
VASN|Q6EMK4	23.1721868	8.83E-13	6.76E-09	0.829315047	0.001103721	3.51E-11	0.020845254	2.33E-05	0.193131714	-0.024951653	0.108791673	-0.218083367	-0.084340042	0.133743326
DLD|P09622	30.5790707	4.21E-16	0.716661561	5.32E-07	1.00E-09	2.88E-09	3.06E-12	0.698650731	0.047019145	-0.245876362	-0.291910011	-0.293791509	-0.339825158	-0.046033648
CADM2|Q8N3J6	9.12694108	1.16E-05	0.000140913	0.01646097	2.50E-05	0.474148842	0.997895072	0.322916695	0.203748854	0.136927633	0.211931295	-0.066821221	0.008182441	0.075003662
CAMK2A|Q9UQM7	6.7713942	0.000234097	0.319309878	0.108689653	0.231816343	0.000558604	0.001873919	0.972855376	0.120498345	-0.155325663	-0.12693148	-0.275824008	-0.247429825	0.028394183
CA2|P00918	2.64837695	0.050327508	0.169117709	0.950589777	0.092441086	0.399748481	0.998279663	0.264487905	-0.535987207	-0.135057082	-0.578226369	0.400930125	-0.042239163	-0.443169287
PLXNA1|Q9UIW2	5.88754806	0.000735863	0.37646152	0.020918123	0.000518129	0.60028486	0.10552394	0.724673073	0.077878963	0.137147631	0.184314693	0.059268669	0.10643573	0.047167061
NLGN2|Q8NFZ4	3.69505728	0.012889727	0.999590598	0.314048926	0.026989416	0.382378111	0.039953903	0.705352649	0.003492211	0.056085606	0.089654993	0.052593396	0.086162782	0.033569386
FRRS1L|Q9P0K9	5.88527322	0.000738042	0.085504242	0.006382595	0.000630519	0.832324938	0.478351663	0.935626011	0.132163157	0.178518621	0.209086487	0.046355464	0.07692333	0.030567866
LY6H|O94772	12.8621301	1.14E-07	0.001069676	9.07E-06	1.85E-07	0.726993545	0.301258117	0.893986371	0.278233205	0.352877622	0.401136014	0.074644417	0.122902808	0.048258391
PPIA|P62937	40.6359628	3.20E-20	0.730836628	4.15E-10	1.25E-13	1.72E-07	4.57E-13	0.106256334	-0.033332561	-0.217651754	-0.286474735	-0.184319193	-0.253142174	-0.068822981
KIAA1549L|Q6ZVL6	6.24735663	0.000461223	0.006974305	0.010645903	0.000490685	0.996140765	0.940458041	0.843834129	0.233412298	0.21782665	0.272675581	-0.015585648	0.039263283	0.054848931
ACAN|P16112	2.54945259	0.057183862	0.346684776	0.130966122	0.050135397	0.965159028	0.839048977	0.983975683	-0.148555403	-0.19007902	-0.220142509	-0.041523617	-0.071587106	-0.030063489
GNS|P15586	2.29858865	0.078951437	0.121551081	0.995271158	0.382657363	0.184251978	0.885213907	0.514917246	-0.131417807	-0.013678181	-0.089869075	0.117739626	0.041548732	-0.076190894
NEFL|P07196	5.53943597	0.001209143	0.944632671	0.007517785	0.01589814	0.036947301	0.073185319	0.979825312	-0.071595457	-0.415905987	-0.36881337	-0.34431053	-0.297217912	0.047092617
MET|P08581	4.81139043	0.00299358	0.323648961	0.00709713	0.006360573	0.443461852	0.448476837	0.999969229	0.063829673	0.118860573	0.117320895	0.0550309	0.053491222	-0.001539678
NUTF2|P61970	3.37810848	0.019498172	0.988835576	0.71002765	0.056876433	0.515088536	0.025532327	0.454686261	0.010905294	-0.035598858	-0.082853734	-0.046504153	-0.093759028	-0.047254876
NA|P0DP03	2.05438918	0.107827673	0.324569189	0.94066523	0.779543945	0.10299623	0.837631764	0.405416241	-0.201824545	0.065782531	-0.106611371	0.267607075	0.095213174	-0.172393901
PLXDC1|Q8IUK5	3.6750864	0.013230567	0.518734816	0.008957347	0.099461892	0.295742047	0.827294517	0.764749558	0.056772275	0.128522881	0.090878918	0.071750606	0.034106643	-0.037663963
IGHD|P01880	1.40875886	0.241667742	0.478254245	0.999454755	0.40878997	0.53530955	0.999976658	0.46435809	-0.355772575	-0.027704143	-0.365344624	0.328068432	-0.009572049	-0.337640481
FBLN7|Q53RD9	3.32299724	0.020951326	0.318869573	0.018026517	0.065015348	0.636921813	0.906076794	0.945714867	0.084512222	0.142024748	0.116574652	0.057512526	0.032062429	-0.025450097
CRELD1|Q96HD1	10.6090812	1.80E-06	0.00043931	0.943845492	0.009432227	3.51E-05	0.708479003	0.001066421	-0.213059562	0.028659554	-0.158869779	0.241719116	0.054189782	-0.187529334
LYZ|P61626	1.41679234	0.239304136	0.999966396	0.975340495	0.290321063	0.98305452	0.325235104	0.521645735	-0.003217195	-0.028856437	-0.119470076	-0.025639242	-0.116252882	-0.09061364
BLVRB|P30043	2.24914648	0.08469025	0.279076026	0.975492559	0.525033851	0.125177864	0.944162085	0.273833037	-0.296471672	0.066106599	-0.207965016	0.362578271	0.088506656	-0.274071616
0|P01772	1.43703146	0.233444321	0.410935932	0.997166741	0.702061435	0.291154331	0.948617392	0.559650876	-0.176900996	0.02221281	-0.117313193	0.199113805	0.059587802	-0.139526003
NTNG1|Q9Y2I2	11.3071918	7.61E-07	0.024148001	0.010119719	1.52E-07	0.996729221	0.0306322	0.044373156	0.128360736	0.137625328	0.248233298	0.009264593	0.119872562	0.110607969
CDH10|Q9Y6N8	3.48293305	0.017005209	0.795036146	0.203603316	0.013294941	0.742148249	0.166294971	0.710293759	0.044530659	0.092881491	0.141198283	0.048350832	0.096667624	0.048316791
MST1L|Q2TV78	1.15626459	0.328013779	0.352934305	0.99254227	0.688260555	0.500549772	0.930586426	0.837642405	-0.181067715	-0.030058614	-0.117231524	0.151009101	0.063836191	-0.08717291
ATP1A1|P05023	1.93621459	0.125255652	0.284498077	0.92624557	0.161590218	0.627119083	0.9968653	0.45264589	-0.083477579	-0.028141705	-0.092789435	0.055335875	-0.009311856	-0.064647731
CDH8|P55286	19.3999842	5.57E-11	6.30E-05	1.28E-06	2.40E-11	0.886037033	0.045270718	0.213686468	0.273404938	0.316665652	0.426344692	0.043260714	0.152939754	0.10967904
CECR1|Q9NZK5	1.96797746	0.120320781	0.854283778	0.498645661	0.749163141	0.127107768	0.267344727	0.970753738	0.045238148	-0.077220106	-0.053780289	-0.122458255	-0.099018437	0.023439817
TYRO3|Q06418	11.0550789	1.04E-06	0.000105013	0.020668336	1.15E-06	0.385440221	0.86917428	0.068347707	0.179434735	0.11555513	0.209512444	-0.063879605	0.030077709	0.093957314
TALDO1|P37837	3.19173655	0.024860247	0.259291499	0.879237093	0.795640346	0.048937189	0.027487471	0.998571926	0.065830772	-0.025929753	-0.03124343	-0.091760526	-0.097074202	-0.005313677
CTSC|P53634	2.7434057	0.044506138	0.112998886	0.999995666	0.306520456	0.109870676	0.924353515	0.303345647	-0.141229491	-0.001396959	-0.103604795	0.139832532	0.037624695	-0.102207837
PLD4|Q96BZ4	6.15703465	0.000518553	0.015232104	0.023863979	0.000304057	0.995439186	0.775773425	0.60884536	0.20214436	0.186674937	0.263610641	-0.015469423	0.061466281	0.076935704
ENPP6|Q6UWR7	2.13189689	0.097698545	0.659271134	0.99998822	0.54282737	0.667757896	0.061406744	0.50725739	-0.056561163	-0.001530459	0.062361547	0.055030704	0.118922709	0.063892006
APOM|O95445	0.47663915	0.698924403	0.987631953	0.920195636	0.660179995	0.991116886	0.858128184	0.957679826	0.04314735	0.081088093	0.142964414	0.037940743	0.099817064	0.061876322
UNC5C|O95185	2.79242792	0.041768089	0.823550552	0.068930188	0.092928056	0.404916218	0.49273029	0.997679836	0.025178003	0.069915608	0.064827163	0.044737605	0.03964916	-0.005088445
MMRN2|Q9H8L6	5.42618211	0.001341656	0.513849308	0.059786555	0.722087959	0.000789454	0.068526086	0.403158016	-0.045443528	0.080850446	0.032782408	0.126293974	0.078225936	-0.048068038
0|P01780	6.41098167	0.000373098	0.001970723	0.989157104	0.039253236	0.004724434	0.669282979	0.079968721	-0.415917516	-0.034980094	-0.291359653	0.380937422	0.124557863	-0.256379559

			ANOVA p -values with Tukey Adjustment						Difference (AD - CT)					
Gene ID | Unirprot ID	F-Value	Pr(>F)	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA
CKB|P12277	15.5704497	4.51E-09	0.359301209	0.00020364	1.06E-08	0.059045227	5.62E-05	0.181918939	-0.09049197	-0.227865861	-0.332408991	-0.137373891	-0.241917021	-0.10454313
COL5A1|P20908	3.06092207	0.029474836	0.274200957	0.639826043	0.999833912	0.016100511	0.210243477	0.658489113	-0.094059595	0.059859371	0.003827846	0.153918966	0.097887441	-0.056031525
FOLR2|P14207	2.07883296	0.10452796	0.188950977	0.492723648	0.100722018	0.918113593	0.997555757	0.818974078	0.09844246	0.067429731	0.10741509	-0.031012729	0.00897263	0.039985359
ITM2B|Q9Y287	0.70887921	0.547836204	0.605375015	0.999954371	0.978752377	0.561534119	0.809386077	0.968365882	-0.071609076	0.002833014	-0.021875183	0.07444209	0.049733892	-0.024708198
ACHE|P22303	5.37695376	0.001430588	0.622465314	0.005897538	0.005282195	0.171884122	0.170854438	0.999965506	-0.081375796	-0.217676967	-0.21479811	-0.13630117	-0.133422314	0.002878857
TUBB2A|Q13885	2.79434705	0.043926061	0.050439634	0.997788467	0.828229304	0.078201476	0.262715051	0.909692463	-0.333837907	-0.023058429	-0.104543317	0.310779478	0.22929459	-0.081484888
HBG2|P69891	2.25295572	0.083982284	0.233398654	0.996664835	0.204942977	0.326337367	0.999957954	0.296652441	-0.578733517	-0.062464459	-0.564327108	0.516269058	0.014406409	-0.501862649
PTPRN|Q16849	13.0771928	8.78E-08	0.017484038	4.04E-06	3.10E-07	0.168408852	0.060099491	0.975106675	0.226128735	0.380843967	0.410657289	0.154715232	0.184528554	0.029813322
PROZ|P22891	3.12730435	0.027035865	0.177773384	0.984733685	0.249027098	0.076820141	0.992235961	0.111102034	-0.275612762	0.046583736	-0.239048001	0.322196498	0.036564761	-0.285631737
TXNRD1|Q16881	19.7034908	3.96E-11	0.999997784	3.34E-07	2.55E-06	4.24E-07	3.16E-06	0.942802903	0.000658334	-0.198036136	-0.179122837	-0.19869447	-0.179781171	0.018913299
AXL|P30530	0.42396439	0.736040894	0.967226205	0.968405932	0.96405792	0.999997713	0.77723881	0.772190903	-0.016611907	-0.015956293	0.016312578	0.000655614	0.032924484	0.032268871
CAMK2D|Q13557	5.70238058	0.000936264	0.359950396	0.003371395	0.002485157	0.284318136	0.262186952	0.999999924	-0.081709122	-0.169332336	-0.169609172	-0.087623214	-0.087900051	-0.000276836
CDH22|Q9UJ99	3.49020873	0.016844448	0.999081092	0.106996372	0.07122749	0.153144226	0.10672173	0.999350435	0.006752235	0.10930156	0.114918741	0.102549325	0.108166506	0.00561718
ZP2|Q05996	6.72393878	0.000248894	0.99245238	0.006362914	0.005189632	0.017261548	0.014736185	0.999998513	0.025571081	0.2948631	0.293486272	0.269292019	0.267915191	-0.001376828
LYVE1|Q9Y5Y7	4.61616147	0.003863998	0.997289146	0.02496649	0.045316852	0.047106316	0.081889631	0.991395353	0.009448008	0.133047787	0.119998992	0.123599778	0.110550983	-0.013048795
LBP|P18428	1.75809814	0.156747553	0.953431479	0.359482908	0.879524547	0.141160726	0.578465723	0.777445071	-0.052247291	0.159261029	0.070542006	0.211508319	0.122789297	-0.088719022
RARRES2|Q99969	0.85513178	0.465498461	0.636539113	0.999937737	0.755922419	0.589892036	0.994136328	0.711773424	-0.055763692	0.00254873	-0.044203342	0.058312421	0.01156035	-0.046752072
ADAMTS4|O75173	1.71846864	0.164720683	0.676437998	0.853883046	0.120535545	0.985484131	0.731588102	0.483192152	0.040127663	0.0278734	0.07560906	-0.012254263	0.035481397	0.04773566
YWHAB|P31946	16.7177057	1.18E-09	0.999990935	0.000121256	6.81E-07	0.000132597	8.18E-07	0.711702184	0.001823657	-0.264647632	-0.326543876	-0.266471289	-0.328367533	-0.061896244
PDIA6|Q15084	0.50516098	0.679186465	0.747216872	0.997904784	0.813558046	0.834630182	0.998218552	0.892809403	0.027708878	0.004847117	0.023168814	-0.022861761	-0.004540064	0.018321697
VLDLR|P98155	1.45763698	0.227615908	0.95212659	0.999642629	0.475477768	0.920528932	0.202295286	0.52476503	-0.02511433	0.004617229	0.06511371	0.029731558	0.09022804	0.060496481
EPHA10|Q5JZY3	6.77161331	0.00023403	0.009829704	0.007211501	0.000175643	0.999999658	0.782991731	0.773083783	0.218655619	0.219324681	0.281262708	0.000669062	0.062607089	0.061938028
HSP90AB1|P08238	2.55239907	0.057414974	0.840700386	0.132858265	0.080672022	0.558793984	0.432362786	0.997575264	-0.055203353	-0.140863012	-0.152685508	-0.085659659	-0.097482155	-0.011822496
SKP1|P63208	9.99693486	3.87E-06	0.169543955	0.064869533	0.045811821	5.59E-05	2.55E-05	0.999820956	0.080373755	-0.094415314	-0.097301333	-0.174789069	-0.177675088	-0.002886019
HYAL1|Q12794	2.51494568	0.059785267	0.143081059	0.999917794	0.397367251	0.116837007	0.906121891	0.346546805	-0.119264827	0.003307362	-0.083086539	0.122572189	0.036178287	-0.086393901
CPN1|P15169	2.42600729	0.067037752	0.175706032	0.988102633	0.621567228	0.081110726	0.789101571	0.398865951	-0.268054192	0.041470278	-0.150760763	0.30952447	0.117293429	-0.192231041
CDH1|P12830	1.34261732	0.261965991	0.508762628	0.955667183	0.938849123	0.224404154	0.819448849	0.676231912	-0.074410591	0.026821029	-0.029416182	0.10123162	0.04499441	-0.056237211
ADAM11|O75078	1.98322377	0.118019229	0.999897435	0.554095206	0.210765632	0.521624151	0.19361922	0.927438512	-0.002676444	0.052074057	0.075419354	0.054750502	0.078095799	0.023345297
FGFR2|P21802	2.78752193	0.042034442	0.294271542	0.274726995	0.02415419	0.999999785	0.753626641	0.731100562	0.064386485	0.064084079	0.099275541	-0.000302407	0.034889056	0.035191463
ACE|P12821	6.39714495	0.000379844	0.795780836	0.425516154	0.010677362	0.073767929	0.000435755	0.379489049	-0.035566523	0.057493256	0.115578733	0.093059779	0.151145256	0.058085477
DNER|Q8NFT8	0.51269151	0.674022683	0.999986314	0.931128971	0.715228267	0.943325636	0.743572325	0.969722988	0.001101993	0.019225067	0.032984264	0.018123074	0.031882271	0.013759197
MAN1A2|O60476	3.28101007	0.02213022	0.636076174	0.976128726	0.240584761	0.373486415	0.012314515	0.450872884	-0.045353537	0.015371406	0.068269807	0.060724943	0.113623344	0.052898401
RECK|O95980	0.28994336	0.832629287	0.903799949	0.999796962	0.999295371	0.865927089	0.838970916	0.999974478	-0.025063923	0.002954759	0.004375142	0.028018682	0.029439065	0.001420383
GALNT6|Q8NCL4	0.8423295	0.472290276	0.919119683	0.686448829	0.426927318	0.970819795	0.836258706	0.978893282	0.035404633	0.059578138	0.080067467	0.024173505	0.044662833	0.020489328
FGL2|Q14314	0.88687248	0.449001559	0.94358386	0.377747356	0.875690393	0.739197298	0.998525217	0.800929769	0.023701339	0.066084136	0.030231181	0.042382797	0.006529842	-0.035852955
CFP|P27918	0.28396631	0.836936645	0.988074685	0.944149432	0.999786614	0.81409208	0.994165528	0.909374301	-0.034603196	0.057797474	-0.008496261	0.09240067	0.026106934	-0.066293736
PVRL1|Q15223	11.7147889	4.61E-07	5.42E-05	0.004842811	4.78E-07	0.569307685	0.862650873	0.136499703	0.204545662	0.147514413	0.238281932	-0.057031249	0.033736269	0.090767519
CFL1|P23528	40.847678	2.65E-20	0.136828713	2.59E-10	1.26E-13	2.65E-05	8.32E-12	0.024580043	-0.105663804	-0.332814999	-0.462957308	-0.227151195	-0.357293503	-0.130142308
EXT2|Q93063	5.84732836	0.000775366	0.411543432	0.152880756	0.256820141	0.001859729	0.004147626	0.988050321	-0.045068924	0.059877368	0.051017929	0.104946292	0.096086853	-0.008859439
PLD3|Q8IV08	2.75664386	0.043749756	0.619612868	0.412560063	0.868031705	0.03210792	0.184283709	0.841884718	0.052389756	-0.064967141	-0.031607807	-0.117356896	-0.083997563	0.033359334
0|P01699	1.86716431	0.137171146	0.565768221	0.727285104	0.998092409	0.092302612	0.426831417	0.803241919	-0.176527447	0.138657456	0.022743412	0.315184903	0.199270859	-0.115914044
NELL1|Q92832	3.90990792	0.009733116	0.440017941	0.016181225	0.021330212	0.475905905	0.557444575	0.998308444	0.104254243	0.202869977	0.191955164	0.098615734	0.087700922	-0.010914813
SMOC1|Q9H4F8	93.5856011	6.88E-37	1.29E-07	1.37E-13	5.81E-12	8.59E-14	8.59E-14	0.600631754	0.214283012	-0.309445386	-0.266938543	-0.523728398	-0.481221555	0.042506843
GRN|P28799	0.67961767	0.565552227	0.596323739	0.703182448	0.647896139	0.997019467	0.99891534	0.999900668	0.04245764	0.035656827	0.037723895	-0.006800813	-0.004733744	0.002067069
IGLC7|A0M8Q6	0.41523193	0.742264756	0.811003081	0.732428554	0.896745821	0.999451401	0.995646678	0.984071538	0.241779877	0.272657534	0.181273504	0.030877657	-0.060506373	-0.09138403
PRRT3|Q5FWE3	8.08043612	4.36E-05	0.008494941	0.0007171	5.23E-05	0.927330404	0.640011428	0.941415739	0.146720975	0.174397295	0.198675409	0.027676321	0.051954434	0.024278114
SLC39A10|Q9ULF5	12.0371743	3.11E-07	0.000143933	0.001213727	1.80E-07	0.911045617	0.61561825	0.209572223	0.247083498	0.20984636	0.31406366	-0.037237138	0.066980162	0.1042173

			ANOVA p -values with Tukey Adjustment						Difference (AD - CT)					
Gene ID | Unirprot ID	F-Value	Pr(>F)	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA
STC2|O76061	4.19680367	0.006687563	0.999116437	0.610146938	0.011524341	0.704674327	0.019692719	0.237592896	0.004234677	0.037432713	0.092657656	0.033198035	0.088422979	0.055224944
GSS|P48637	13.9815832	2.96E-08	0.002082112	0.029274164	0.994272298	5.89E-09	0.000489384	0.043029865	0.142119307	-0.106450808	-0.009437892	-0.248570115	-0.151557199	0.097012916
GSTP1|P09211	2.44404325	0.065500452	0.366379556	0.374530676	0.038799378	0.999925975	0.768916817	0.715896946	-0.062167539	-0.059946356	-0.097705936	0.002221183	-0.035538397	-0.03775958
CPAMD8|Q8IZJ3	2.19048175	0.090900063	0.212023205	0.883306422	0.118699746	0.603342942	0.998487338	0.45118257	-0.141683362	-0.052109735	-0.152997305	0.089573627	-0.011313943	-0.10088757
TIE1|P35590	8.67313447	2.05E-05	0.229210205	0.000163012	0.000121171	0.099230963	0.093767384	0.999990715	0.087446409	0.191858369	0.190592194	0.10441196	0.103145785	-0.001266175
PCMT1|P22061	3.55806143	0.015416182	0.251051789	0.939530483	0.175087695	0.071061889	0.999712017	0.03975018	-0.096440328	0.029066038	-0.101086475	0.125506366	-0.004646147	-0.130152513
FAM198B|Q6UWH4	4.60722348	0.003909426	0.89351688	0.912278305	0.032166569	0.519100322	0.196348068	0.003329919	0.021584243	-0.019524675	0.079838562	-0.041108918	0.058254319	0.099363236
GALNS|P34059	2.3623844	0.072748248	0.792968652	0.992748403	0.162649517	0.622559749	0.690893159	0.079743261	-0.050072708	0.014502855	-0.107471571	0.064575563	-0.057398863	-0.121974426
ANXA5|P08758	2.26778483	0.082128851	0.717863038	0.876534457	0.060645283	0.987654757	0.506962841	0.286691268	-0.06816709	-0.047204286	-0.154714039	0.020962804	-0.086546949	-0.107509753
DBI|P07108	3.73495702	0.012234756	0.87776968	0.027294116	0.05272146	0.182418986	0.294172079	0.988886381	-0.024189552	-0.088749683	-0.079144546	-0.064560131	-0.054954994	0.009605137
GBA|P04062	1.00439704	0.392093384	0.998622635	0.996900246	0.542847199	0.983620291	0.656497839	0.39769372	0.006065955	-0.007752105	0.049033941	-0.013818059	0.042967987	0.056786046
ARSA|P15289	6.42833394	0.000364807	0.000691944	0.102389412	0.001753801	0.316348287	0.969233672	0.534231221	-0.210678074	-0.11986852	-0.187365842	0.090809554	0.023312232	-0.067497322
ST6GAL2|Q96JF0	5.95902257	0.000670586	0.017811876	0.015494213	0.000473195	0.99998468	0.806666755	0.772154402	0.147214806	0.14550928	0.190040285	-0.001705526	0.042825479	0.044531005
RNF13|O43567	0.06158369	0.979949165	0.991137627	0.999730315	0.997773206	0.980055473	0.999325733	0.992147499	0.014607069	-0.004393586	0.008703545	-0.019000655	-0.005903524	0.013097131
PRDX2|P32119	1.70115696	0.16832372	0.927379648	0.619761843	0.136928929	0.939718984	0.439606749	0.783305469	-0.072604044	-0.139392202	-0.243176901	-0.066788158	-0.170572857	-0.103784699
CHID1|Q9BWS9	0.4948332	0.686301348	0.74363153	0.999550106	0.999994537	0.794458426	0.705711931	0.999070315	-0.04699687	-0.004879854	0.001094213	0.042117016	0.048091082	0.005974066
APOC4-APOC2|P02655	2.06177479	0.106820172	0.738531079	0.199011775	0.112379599	0.792896801	0.647050089	0.995574137	0.126684049	0.23959471	0.266571655	0.112910661	0.139887606	0.026976945
GRIA2|P42262	5.24762742	0.001693451	0.160550492	0.084824922	0.000631189	0.995759402	0.309338508	0.413227399	0.105240808	0.1165964	0.189294352	0.011355593	0.084053545	0.072697952
PBXIP1|Q96AQ6	2.55894679	0.056487845	0.544203004	0.551455018	0.911393688	0.042312636	0.178408757	0.896333812	0.063243113	-0.061007255	-0.029865997	-0.124250368	-0.09310911	0.031141258
ESD|P10768	1.98348554	0.118251529	0.112728174	0.587289595	0.22154936	0.723679545	0.977761263	0.909774574	-0.131456497	-0.071571722	-0.108447802	0.059884775	0.023008696	-0.036876079
DPYSL2|Q16555	9.46974005	7.50E-06	0.70277629	0.000310877	0.000118103	0.016534976	0.008696815	0.998913883	-0.048904712	-0.182387223	-0.188519064	-0.133482511	-0.139614352	-0.006131841
EPHB2|P29323	13.0215447	9.39E-08	3.35E-05	0.082092289	2.36E-07	0.083901648	0.851600771	0.005521796	0.191047839	0.095141584	0.222749437	-0.095906255	0.031701598	0.127607853
SBSN|Q6UWP8	0.59514432	0.618934007	0.989939252	0.820395059	0.996371056	0.645663564	0.999591299	0.673434971	-0.026081606	0.07192592	-0.017543124	0.098007525	0.008538482	-0.089469044
MXRA8|Q9BRK3	1.20343033	0.309886293	0.842194719	0.994194922	0.313349281	0.93587396	0.832216831	0.445328617	0.026098391	0.007828456	0.051839652	-0.018269934	0.025741261	0.044011196
WFDC2|Q14508	4.9529601	0.002488008	0.510490136	0.017714937	0.00329405	0.423816225	0.186741878	0.966495503	0.057740371	0.120407598	0.138540206	0.062667227	0.080799835	0.018132608
AHNAK|Q09666	3.04171077	0.03022052	0.266004773	0.320986095	0.015965757	0.998524383	0.707000048	0.581047642	-0.10807142	-0.098702867	-0.169247821	0.009368554	-0.061176401	-0.070544954
HLA-B|P30466	3.83047045	0.010798556	0.213568067	0.887587881	0.209964302	0.038799685	0.999729142	0.033808153	-0.19057151	0.069030102	-0.181984856	0.259601612	0.008586654	-0.251014958
FREM2|Q5SZK8	0.9206266	0.432152632	0.874098651	0.812803788	0.999638028	0.349298072	0.810650416	0.843833017	-0.096059085	0.109923187	0.012210076	0.205982273	0.108269161	-0.097713112
CHAD|O15335	0.12265675	0.946650637	0.980302222	0.992564292	0.999082557	0.999394553	0.949925996	0.973695606	-0.020455934	-0.014253551	0.006881444	0.006202383	0.027337378	0.021134995
PTN|P21246	1.96129983	0.12134242	0.368938939	0.180979721	0.133672774	0.984192782	0.966694204	0.999632318	-0.090441562	-0.110118785	-0.115369932	-0.019677222	-0.02492837	-0.005251148
ADAM10|O14672	1.47110089	0.223881199	0.417418015	0.97838284	0.99999998	0.208686299	0.380561426	0.976355455	-0.05407061	0.013666286	0.000127704	0.067736896	0.054198315	-0.013538582
SLC4A1|P02730	0.8458265	0.471113894	0.571551352	0.999881645	0.75135794	0.614977576	0.987039186	0.790903396	-0.438241907	-0.023279543	-0.327474759	0.414962364	0.110767147	-0.304195216
RCN2|Q14257	3.24664188	0.023144059	0.517884936	0.353253006	0.887598588	0.014936748	0.144032568	0.759667029	-0.065924996	0.077095157	0.033023012	0.143020153	0.098948007	-0.044072146
TWSG1|Q9GZX9	3.34762993	0.020288972	0.206724929	0.720357754	0.792388639	0.014770958	0.674306772	0.179824654	-0.053728132	0.027987856	-0.024049096	0.081715988	0.029679036	-0.052036952
GLOD4|Q9HC38	36.1994706	1.87E-18	0.52761337	3.45E-09	9.96E-10	2.15E-12	5.71E-13	0.999858572	0.038530787	-0.180676428	-0.18261884	-0.219207215	-0.221149627	-0.001942412
IGHV3-20|A0A0C4DH32	1.88953303	0.132864153	0.362217775	0.999925135	0.357935402	0.317305718	0.999840188	0.310211136	-0.220996124	0.007796282	-0.211064037	0.228792406	0.009932087	-0.218860319
EMILIN2|Q9BXX0	2.33325811	0.075518848	0.827640945	0.985556332	0.322637545	0.619906847	0.052243326	0.516333365	0.042838326	-0.016925777	-0.081276414	-0.059764103	-0.12411474	-0.064350637
MAN2B2|Q9Y2E5	6.73391036	0.000245709	0.001258318	0.999984506	0.12438581	0.001151389	0.309998445	0.123888106	-0.205741884	-0.001861312	-0.114702967	0.203880572	0.091038916	-0.112841656
PODXL2|Q9NZ53	2.73095354	0.045229377	0.974574028	0.953992727	0.125581828	0.781239868	0.046913221	0.326002181	-0.014684347	0.017613103	0.072853607	0.03229745	0.087537954	0.055240504
IGHV3-74|A0A0B4J1X5	0.97311987	0.407708744	0.580524329	0.981765237	0.95818111	0.373137769	0.822678914	0.808997321	-0.25402814	0.072906635	-0.090501182	0.326934774	0.163526957	-0.163407817
WDR1|O75083	4.74746531	0.003254464	0.981106193	0.156007209	0.006102655	0.331343281	0.023251724	0.641196915	-0.025022041	-0.13433759	-0.206630226	-0.109315549	-0.181608185	-0.072292636
SMPDL3B|Q92485	1.0040697	0.392242944	0.861306776	0.987453442	0.639651081	0.675126123	0.985123597	0.412201926	0.056844209	-0.023329283	0.081309506	-0.080173492	0.024465298	0.10463879
ABI3BP|Q7Z7G0	0.64571457	0.586583877	0.926034371	0.779928848	0.531023227	0.989953851	0.899791009	0.979771275	-0.033235651	-0.049463756	-0.069052277	-0.016228105	-0.035816626	-0.019588521
NA|P0DP25	25.7661261	5.65E-14	0.051504759	9.29E-06	0.000133259	1.34E-11	3.16E-10	0.877873466	0.08941079	-0.167296508	-0.143120297	-0.256707298	-0.232531087	0.024176211
PRDX6|P30041	2.64115036	0.050799714	0.825474138	0.72189123	0.034873278	0.998493949	0.275907384	0.334304477	-0.05246273	-0.062169217	-0.158249836	-0.009706488	-0.105787106	-0.096080619
ASTN1|O14525	4.51697763	0.004534291	0.118206567	0.004689056	0.016985117	0.697570212	0.909571729	0.9712313	0.131975626	0.194702929	0.170202666	0.062727302	0.038227039	-0.024500263
CAMK2B|Q13554	8.71003694	1.96E-05	0.482452986	0.000277271	0.000183596	0.041532084	0.034795436	0.999999964	-0.068866519	-0.195185592	-0.195395275	-0.126319073	-0.126528757	-0.000209684

			ANOVA p -values with Tukey Adjustment						Difference (AD - CT)					
Gene ID | Unirprot ID	F-Value	Pr(>F)	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA
CORO1A|P31146	5.39810778	0.00139167	0.821791327	0.67045576	0.001247605	0.995264203	0.026924077	0.042282682	-0.042692786	-0.05421169	-0.176422425	-0.011518905	-0.133729639	-0.122210735
SEMA3C|Q99985	1.44100935	0.232308426	0.203192448	0.649783117	0.39129515	0.830585735	0.962538467	0.978801466	-0.133490246	-0.076802873	-0.101914821	0.056687372	0.031575424	-0.025111948
CHI3L2|Q15782	3.7348953	0.012235743	0.083442704	0.858767587	0.020567727	0.357899441	0.977945678	0.143126015	-0.192837429	-0.062166934	-0.224121322	0.130670495	-0.031283893	-0.161954388
LTBP3|Q9NS15	3.13747773	0.0266802	0.034879037	0.712045358	0.085331242	0.3161854	0.961581147	0.558063418	-0.099274198	-0.037654414	-0.082169256	0.061619784	0.017104941	-0.044514843
AP1B1|Q10567	0.09541592	0.962476933	0.998395885	0.96749868	0.999999221	0.991449644	0.998548269	0.965788092	-0.013901091	-0.038063861	-0.001034922	-0.02416277	0.012866169	0.037028939
PYGB|P11216	0.79082882	0.501361828	0.421419297	0.889220616	0.904398452	0.838603844	0.772314872	0.999805566	-0.171715236	-0.079165852	-0.070780615	0.092549385	0.100934622	0.008385237
TMEM132B|Q14DG7	4.72396974	0.003355977	0.04751865	0.13307021	0.001802222	0.958926826	0.800344057	0.462039661	0.193521788	0.157034396	0.258296679	-0.036487392	0.064774891	0.101262283
MAG|P20916	1.58016894	0.195675969	0.980653114	0.99993056	0.275122962	0.970067519	0.512434557	0.233905934	0.016451083	-0.002406569	0.073381913	-0.018857652	0.05693083	0.075788482
CST6|Q15828	3.84744306	0.010561545	0.12588792	0.951225617	0.212697697	0.031638734	0.982857827	0.058134055	0.137034961	-0.032172417	0.114985854	-0.169207378	-0.022049107	0.147158271
LGI1|O95970	0.9999905	0.3941108	0.643997366	0.995557091	0.759147866	0.487140157	0.994580643	0.600660585	-0.058772888	0.01132735	-0.046789921	0.070100238	0.011982966	-0.058117272
MOG|Q16653	1.32012709	0.269218743	0.489884116	0.304797273	0.335656117	0.992151982	0.997599768	0.999612581	0.064179884	0.0767499	0.072412264	0.012570017	0.00823238	-0.004337637
JAG1|P78504	6.80190962	0.000225052	0.478446832	0.009225576	0.000256475	0.334112575	0.044146792	0.781562316	0.052765515	0.113746042	0.146124424	0.060980526	0.093358909	0.032378383
PNOC|Q13519	13.0567842	8.99E-08	0.320165016	1.26E-05	1.36E-06	0.011928875	0.002926945	0.982671487	0.126033737	0.350632225	0.376068732	0.224598487	0.250034995	0.025436507
EEF1A1|P68104	0.56431422	0.639207312	0.939596829	0.944863461	0.569690956	0.999985594	0.905211358	0.882990246	-0.045429498	-0.042767486	-0.09705511	0.002662012	-0.051625612	-0.054287624
YWHAG|P61981	70.1305197	2.46E-30	0.897161425	1.23E-13	1.25E-13	1.14E-13	1.21E-13	0.928412186	0.033443816	-0.471222261	-0.443917829	-0.504666077	-0.477361645	0.027304431
PLBD2|Q8NHP8	2.18270438	0.09156707	0.166534382	0.922604542	0.171863946	0.450644783	0.999351026	0.478670205	-0.143327431	-0.042360163	-0.135210206	0.100967268	0.008117224	-0.092850044
NOMO2|Q5JPE7	1.57658785	0.196546373	0.246749321	0.999999094	0.862259755	0.228366605	0.649703156	0.849507318	-0.067293135	0.000477333	-0.026841493	0.067770467	0.040451642	-0.027318825
CBR1|P16152	5.81533521	0.000808305	0.425839009	0.011253445	0.000919161	0.41895973	0.120904163	0.907432651	-0.067108653	-0.133688988	-0.161368869	-0.066580335	-0.094260216	-0.027679881
IGJ|P01591	0.3706348	0.774283197	0.994558536	0.998313335	0.771701885	0.999762427	0.900669961	0.852987868	-0.041709051	-0.027347715	-0.15298153	0.014361337	-0.111272478	-0.125633815
GFRA3|O60609	1.22178808	0.303379735	0.305869461	0.946963174	0.996576169	0.609496186	0.384348193	0.984910011	-0.106543055	-0.032575078	-0.01240486	0.073967977	0.094138196	0.020170219
SFRP4|Q6FHJ7	7.96852752	5.03E-05	0.001381524	0.991831439	0.041409662	0.000382513	0.591919215	0.015698954	-0.259868618	0.019318329	-0.175901231	0.279186947	0.083967387	-0.19521956
ATP1B1|P05026	0.2190279	0.883108126	0.972975769	0.982268968	0.999947083	0.851185444	0.958842121	0.987053826	0.011904243	-0.010005466	-0.001383276	-0.021909709	-0.013287519	0.00862219
CDH4|P55283	7.10227343	0.000152787	0.005523739	0.182009486	0.000122404	0.50657225	0.834646979	0.094434863	0.156113978	0.092124296	0.193945496	-0.063989683	0.037831518	0.1018212
LRRN1|Q6UXK5	4.96288326	0.002455964	0.140187874	0.081661103	0.000988585	0.99797003	0.411298516	0.497229843	0.05743617	0.062125361	0.097152487	0.004689191	0.039716317	0.035027126
PCDH8|O95206	1.67811205	0.173236549	0.298897902	0.252885155	0.223350739	0.999960586	0.999858749	0.999994355	0.119528502	0.122737003	0.124329681	0.003208501	0.004801179	0.001592679
CDH9|Q9ULB4	6.18545008	0.000499783	0.10088792	0.010575994	0.00028306	0.87160074	0.319086995	0.77033571	0.162203064	0.214998224	0.278382055	0.05279516	0.116178992	0.063383832
CD59|P13987	4.72711994	0.003342184	0.692085042	0.006653742	0.019692879	0.146870994	0.297983191	0.971859431	0.034264547	0.099856003	0.087075263	0.065591456	0.052810716	-0.01278074
TMEM132E|Q6IEE7	0.85633299	0.464865277	0.945241101	0.934857898	0.792742919	0.661136657	0.447153741	0.988237215	-0.023611685	0.024467411	0.037350002	0.048079096	0.060961687	0.012882591
CD200|P41217	6.21099711	0.000483493	0.882982264	0.001898844	0.012110556	0.023931408	0.103450269	0.913137432	0.043962697	0.212682433	0.175980185	0.168719736	0.132017488	-0.036702248
TXNDC5|Q8NBS9	0.07740383	0.972146799	0.999937077	0.998190546	0.981509351	0.995885723	0.97296132	0.996903084	0.001560263	-0.004666731	-0.01003583	-0.006226994	-0.011596093	-0.005369099
COL28A1|Q2UY09	0.49478234	0.686336478	0.697530369	0.999827352	0.989049258	0.733688619	0.845877289	0.995129048	-0.102588352	-0.007185117	-0.028326527	0.095403235	0.074261825	-0.02114141
CXorf36|Q9H7Y0	3.65306088	0.0136169	0.281296677	0.080140975	0.008684203	0.94484297	0.563167846	0.874536791	0.078684984	0.102742362	0.133737156	0.024057378	0.055052172	0.030994794
SAA4|P35542	1.41000295	0.241300294	0.756717883	0.725602991	0.997158057	0.180154078	0.840852241	0.572031333	-0.136184571	0.139673536	-0.026217478	0.275858107	0.109967093	-0.165891015
PLXNB3|Q9ULL4	2.07191677	0.105451523	0.815538019	0.987306076	0.108035334	0.94238457	0.544015734	0.204400685	0.03176241	0.011679207	0.078050199	-0.020083204	0.046287788	0.066370992
COLEC12|Q5KU26	8.64950055	2.11E-05	0.001048722	0.133513576	2.51E-05	0.31339211	0.890940833	0.055020409	0.105395605	0.058484822	0.124402537	-0.046910783	0.019006933	0.065917716
GLDN|Q6ZMI3	2.01386868	0.113521186	0.454414435	0.990850301	0.152431604	0.624547578	0.94511331	0.257420683	0.104590244	0.0204952	0.14244876	-0.084095044	0.037858516	0.12195356
MAPT|P10636	61.2827354	4.34E-27	0.016223141	1.32E-12	1.73E-12	0	0	0.987438598	0.225459819	-0.583372134	-0.560063011	-0.808831953	-0.78552283	0.023309123
DNM1|Q05193	0.62739246	0.598171463	0.830926828	0.542500335	0.772497987	0.968365979	0.999897854	0.976187351	-0.046647182	-0.071324884	-0.05012219	-0.024677702	-0.003475008	0.021202694
COL6A2|P12110	6.32876215	0.000415032	0.045793238	0.275541378	0.000184837	0.811932069	0.448968421	0.069216052	-0.13663031	-0.091227659	-0.210950549	0.045402651	-0.074320239	-0.119722891
CTSS|P25774	1.1215176	0.341661209	0.982462457	0.684556173	0.337841949	0.889626236	0.581846593	0.94560405	-0.0202871	-0.058929654	-0.087157441	-0.038642553	-0.066870341	-0.028227787
YWHAH|Q04917	38.4637335	2.29E-19	0.999997518	2.10E-11	2.75E-12	3.12E-11	4.27E-12	0.9979795	0.000861521	-0.328237437	-0.33578335	-0.329098958	-0.336644871	-0.007545912
CHST10|O43529	5.40269342	0.001383374	0.123133157	0.164993438	0.000487027	0.997243455	0.342497733	0.21956449	0.094378071	0.086070398	0.16288129	-0.008307673	0.068503219	0.076810892
SELL|P14151	0.27125355	0.846076057	0.986977285	0.981187474	0.979708837	0.999983803	0.883230861	0.857237211	-0.019023817	-0.021010094	0.021069766	-0.001986277	0.040093583	0.04207986
EFNB2|P52799	6.18301279	0.000501366	0.026781087	0.013884458	0.000285943	0.998906713	0.645834263	0.71821128	0.10651104	0.111899725	0.149017352	0.005388684	0.042506311	0.037117627
A4GALT|Q9NPC4	0.56376953	0.6395691	0.973247774	0.842915568	0.999977528	0.595031702	0.977047637	0.805494608	-0.02425566	0.045231922	-0.002125728	0.069487582	0.022129931	-0.04735765
BLMH|Q13867	2.19766196	0.089834486	0.746441442	0.641972658	0.651486932	0.131368932	0.129142959	0.999969874	0.03401292	-0.038750337	-0.037368257	-0.072763258	-0.071381177	0.001382081
EMILIN1|Q9Y6C2	8.05654573	4.49E-05	0.000932815	0.883442896	0.001477793	0.0091682	0.988444766	0.014998464	-0.217236918	-0.040292132	-0.199755917	0.176944786	0.017481	-0.159463786

			ANOVA p -values with Tukey Adjustment						Difference (AD - CT)					
Gene ID | Unirprot ID	F-Value	Pr(>F)	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA
CETP|P11597	5.57827524	0.001100457	0.99998985	0.026005159	0.018674891	0.026190977	0.018939442	0.999957559	-0.002825492	0.256168097	0.260421987	0.258993589	0.26324748	0.004253891
0|P01766	0.1302182	0.942034844	0.968547955	0.932275105	0.982176997	0.999220548	0.99959513	0.994894206	0.074164986	0.094951187	0.057844998	0.020786201	-0.016319988	-0.037106189
ITGBL1|O95965	3.63173197	0.014001724	0.018911179	0.767509887	0.076453933	0.179151372	0.908888855	0.46656738	-0.165249429	-0.052868159	-0.129163199	0.112381271	0.03608623	-0.07629504
LINGO3|P0C6S8	8.75586535	1.85E-05	0.711347857	0.999507707	0.000178845	0.633145273	0.011363544	8.19E-05	0.070248027	-0.007131987	0.268029474	-0.077380014	0.197781447	0.275161461
TENM1|Q9UKZ4	1.23546878	0.298199064	0.739358247	0.971297321	0.275844793	0.932598166	0.888195991	0.517348619	0.04125111	0.017387004	0.069422256	-0.023864105	0.028171147	0.052035252
FRZB|Q92765	5.88390263	0.000739358	0.14645008	0.175771823	0.989845337	0.000254182	0.060020577	0.269360149	0.092880031	-0.086592212	-0.012742421	-0.179472243	-0.105622452	0.073849791
JUP|P14923	0.08230911	0.969516515	0.997933521	0.999999999	0.99222927	0.997779797	0.961964373	0.991201884	-0.052982881	-0.000467199	0.079040843	0.052515682	0.132023724	0.079508042
DGCR2|P98153	0.1631755	0.921039529	0.997444234	0.999964275	0.964882104	0.99501705	0.909052771	0.972686467	-0.015682859	0.003659517	0.036552021	0.019342376	0.05223488	0.032892504
C1QA|P02745	0.9285507	0.428074462	0.837634628	0.474195938	0.463100122	0.938628318	0.939358552	0.999998436	-0.035203381	-0.059182547	-0.058540327	-0.023979166	-0.023336946	0.00064222
NENF|Q9UMX5	1.42919264	0.235697867	0.903492684	0.600620667	0.19241526	0.95059177	0.58708504	0.881314518	0.01630239	0.028860971	0.045338304	0.012558581	0.029035913	0.016477332
CTSZ|Q9UBR2	2.0284754	0.111436029	0.204885155	0.99970115	0.999991454	0.160453313	0.166615517	0.999883274	-0.096250504	0.004480465	0.001337147	0.10073097	0.097587652	-0.003143318
UBB|P0CG47	5.56964492	0.001112897	0.183218427	0.577107335	0.340120294	0.005940164	0.001312478	0.982517785	0.089291327	-0.054947994	-0.070247569	-0.144239322	-0.159538896	-0.015299574
EGFLAM|Q63HQ2	2.45851811	0.064291737	0.197325894	0.925594908	0.096466755	0.498765189	0.995591572	0.317301246	-0.1065129	-0.032366406	-0.118489865	0.074146494	-0.011976965	-0.086123459
VSIG4|Q9Y279	5.05201634	0.002186065	0.879275027	0.084981659	0.002890318	0.384318653	0.035972012	0.678522372	-0.037297875	-0.116037434	-0.168459702	-0.078739558	-0.131161827	-0.052422268
IL1RAP|Q9NPH3	1.62775436	0.184450376	0.991914581	0.873166158	0.525472801	0.727156124	0.721340004	0.134402748	0.021125934	-0.05468693	0.095928388	-0.075812864	0.074802455	0.150615318
MLEC|Q14165	13.379572	6.09E-08	3.81E-05	0.035888843	7.85E-08	0.180437382	0.719293421	0.008093298	0.128871715	0.073385107	0.156954171	-0.055486607	0.028082456	0.083569064
MANSC1|Q9H8J5	3.38077092	0.019430565	0.718795623	0.968484049	0.020681589	0.926007351	0.283658529	0.06463127	0.035095735	0.014780604	0.09239619	-0.020315131	0.057300455	0.077615586
CARTPT|Q16568	4.54660285	0.004231974	0.912723835	0.038077033	0.011762818	0.193104209	0.084102682	0.98524112	0.033136298	0.132165549	0.14864068	0.099029251	0.115504382	0.016475132
VWA1|Q6PCB0	2.35188523	0.073735309	0.685684727	0.429590564	0.999942825	0.046187396	0.69196374	0.361834627	-0.072826985	0.097085128	-0.003385747	0.169912113	0.069441238	-0.100470875
ALDH1A1|P00352	2.44611434	0.06532615	0.097642475	0.781064577	0.123388005	0.487745017	0.996106394	0.584080865	-0.14721114	-0.058342332	-0.133617169	0.088868807	0.013593971	-0.075274836
PLXNA2|O75051	0.45646125	0.713048465	0.888174975	0.972473268	0.671654405	0.990205051	0.983265742	0.898151636	0.039491122	0.023114842	0.058726062	-0.016376279	0.01923494	0.03561122
GDF11|O95390	2.82043548	0.040279129	0.999533943	0.967382809	0.064092709	0.985866284	0.090633708	0.171105886	0.002988537	0.01228959	0.064953493	0.009301053	0.061964956	0.052663904
PEPD|P12955	0.37059737	0.774310201	0.797855472	0.867345239	0.992641852	0.998388428	0.905956396	0.953589169	-0.070810794	-0.058191051	-0.020336364	0.012619743	0.050474429	0.037854686
OAF|Q86UD1	2.50697129	0.060402781	0.999154605	0.114607101	0.604907146	0.089480674	0.526750351	0.700523344	-0.005523156	0.090696357	0.048730872	0.096219513	0.054254028	-0.041965485
ADAMTSL2|Q86TH1	0.50634143	0.678375657	0.911013446	0.798822172	0.637172807	0.995821856	0.96303109	0.994075425	0.021655911	0.028986932	0.036816139	0.007331021	0.015160228	0.007829207
NLGN4X|Q8N0W4	3.94463762	0.009404835	0.006596972	0.798128569	0.759166959	0.068822622	0.072333378	0.999928353	-0.128358766	-0.034166223	-0.036268191	0.094192542	0.092090574	-0.002101968
ADAM15|Q13444	2.28226177	0.0806203	0.141062037	0.999890791	0.607118058	0.113559075	0.739140836	0.549041989	-0.085138543	0.002587587	-0.046362626	0.08772613	0.038775917	-0.048950213
0|P23083	4.79210372	0.003070002	0.044464581	0.999163759	0.057334908	0.027872841	0.995526916	0.035594948	-0.358514573	0.017544234	-0.328024268	0.376058807	0.030490304	-0.345568503
KIT|P10721	1.46583761	0.225334297	0.46184704	0.714959273	0.991237579	0.971485596	0.272102356	0.500637063	-0.075702788	-0.053299568	0.014398957	0.02240322	0.090101745	0.067698525
EDIL3|O43854	2.75510949	0.043836771	0.897782463	0.808120701	0.035153067	0.9981098	0.204358732	0.256993152	-0.042977174	-0.053550256	-0.15954667	-0.010573082	-0.116569497	-0.105996415
CD5L|O43866	0.41533619	0.742190349	0.753280552	0.978161714	0.819616371	0.927820174	0.998195514	0.965713249	0.140279342	0.055051066	0.116950871	-0.085228275	-0.02332847	0.061899805
SH3BGRL|O75368	9.39261039	8.26E-06	0.997602383	0.036152059	0.000183589	0.02318069	0.000101996	0.431186296	0.007318295	-0.102362431	-0.157169142	-0.109680726	-0.164487437	-0.054806711
CA4|P22748	4.69777686	0.003472889	0.841919565	0.398156324	0.002582667	0.892056994	0.04155739	0.194528953	0.04106305	0.075922157	0.16843112	0.034859108	0.127368071	0.092508963
GGCT|O75223	10.4289893	2.26E-06	0.945411561	0.006852606	0.000530653	0.001120851	6.35E-05	0.91306296	0.02608006	-0.1500677	-0.178963319	-0.17614776	-0.205043379	-0.028895619
PITHD1|Q9GZP4	2.65112953	0.050148786	0.815700788	0.80497452	0.287087032	0.285294007	0.040851523	0.819263309	0.034241001	-0.034098618	-0.065837642	-0.068339618	-0.100078642	-0.031739024
ANXA2|P07355	1.7660634	0.155488066	0.848178043	0.702102659	0.797401037	0.231737567	0.999883686	0.174823649	-0.092056635	0.119497613	-0.099580318	0.211554248	-0.007523683	-0.219077931
0|P01701	0.29657028	0.827847396	0.968317721	0.931482153	0.997422684	0.999196248	0.909986634	0.843394967	0.084670131	0.108584353	-0.034131825	0.023914222	-0.118801956	-0.142716178
SCUBE1|Q8IWY4	0.89380855	0.445461242	0.912118527	0.637863407	0.410607041	0.958951894	0.833066273	0.986089672	-0.03152897	-0.05507325	-0.070393882	-0.02354428	-0.038864912	-0.015320632
BSG|P35613	1.83302613	0.142669957	0.262063417	0.146179841	0.320018857	0.994546465	0.996663191	0.963409847	0.070235156	0.079648025	0.062441514	0.009412869	-0.007793642	-0.017206511
CCER2|I3L3R5	4.61122427	0.003889026	0.425248323	0.016694284	0.005269513	0.497929062	0.310730748	0.990372819	0.085081308	0.162303526	0.178074434	0.077222217	0.092993125	0.015770908
SMPD1|P17405	1.62708235	0.184897193	0.483302744	0.856057677	0.156410026	0.905050298	0.938013809	0.547825755	-0.086188516	-0.046105452	-0.119948778	0.040083064	-0.033760262	-0.073843325
GMFB|P60983	11.4264896	6.57E-07	0.993832196	0.005014495	6.94E-05	0.002334193	2.77E-05	0.707401037	0.009036364	-0.114047891	-0.148856934	-0.123084256	-0.157893298	-0.034809042
MYH9|P35579	2.38623427	0.070821691	0.35790835	0.749398428	0.051538148	0.898221443	0.84062406	0.378356906	-0.167599606	-0.097989991	-0.249255476	0.069609615	-0.081655869	-0.151265485
PVALB|P20472	4.84204343	0.002876023	0.004445345	0.012571981	0.032432572	0.975957738	0.845573318	0.977218365	-0.168452655	-0.148280083	-0.129493088	0.020172571	0.038959567	0.018786995
CRB2|Q5IJ48	0.90204906	0.441285111	0.617136712	0.901201749	0.9958081	0.945172418	0.446030262	0.778121107	-0.056938754	-0.031376358	0.010144293	0.025562396	0.067083047	0.041520651
EPDR1|Q9UM22	1.9124633	0.129072789	0.209855545	0.937381354	0.22958145	0.495800014	0.998842566	0.543985731	-0.145030366	-0.042058399	-0.1344584	0.102971967	0.010571965	-0.092400001
CASC4|Q6P4E1	4.91870437	0.002601884	0.06045244	0.362766335	0.001496159	0.781375155	0.71558936	0.162190313	0.075434589	0.047599718	0.105933813	-0.027834871	0.030499224	0.058334095

Gene ID | Unirprot ID	F-Value	Pr(>F)	ANOVA p -values with Tukey Adjustment						Difference (AD - CT)					
			AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA
CA10|Q9NS85	0.72861441	0.536119353	0.518066585	0.842180876	0.987030695	0.938551854	0.692643102	0.954351462	-0.078185501	-0.045766363	-0.018125575	0.032419138	0.060059926	0.027640788
CEL|P19835	2.41078947	0.068362311	0.432689026	0.666531354	0.997065588	0.041953981	0.291017786	0.761361486	-0.173602668	0.127174848	0.022072806	0.300777516	0.195675474	-0.105102041
MGAT2|Q10469	1.05620869	0.369033705	0.988191239	0.796965287	0.352392608	0.939513994	0.567594628	0.885901392	0.00944361	0.025928231	0.045733043	0.016484622	0.036289433	0.019804811
PCDH19|Q8TAB3	5.55337385	0.001136736	0.001536196	0.053081678	0.005342997	0.607604497	0.947158574	0.883290365	0.232237409	0.156380682	0.199282971	-0.075856726	-0.032954438	0.042902288
DTD1|Q8TEA8	7.78521852	6.36E-05	0.114417168	0.186441625	0.284882003	0.000179427	0.000362933	0.991994487	0.114141908	-0.099525347	-0.086054002	-0.213667255	-0.200195911	0.013471345
CLN5|O75503	1.72741304	0.162888025	0.758818558	0.880872441	0.602931454	0.310935521	0.99710097	0.180436782	0.064837482	-0.047438923	0.077608195	-0.112276404	0.012770713	0.125047118
B4GALNT1|Q00973	0.09520088	0.962611546	0.990114771	0.999997879	0.972270338	0.991305976	0.999480244	0.974270299	-0.014200343	-0.000817512	-0.019268587	0.013382831	-0.005068244	-0.018451075
TNFRSF21|O75509	8.09183254	4.30E-05	0.002221547	0.003023275	3.91E-05	0.997694075	0.839756402	0.718861343	0.19300703	0.18319027	0.235770937	-0.00981676	0.042763907	0.052580668
HPRT1|P00492	32.3087217	7.69E-17	0.079513262	5.66E-08	5.80E-06	2.00E-13	1.53E-11	0.684644038	0.102578088	-0.249517062	-0.205347876	-0.35209515	-0.307925964	0.044169186
CAMK2G|Q13555	6.03567318	0.000620559	0.982038795	0.00723359	0.010206645	0.025804703	0.036028026	0.996728937	-0.020402144	-0.172562454	-0.161985853	-0.15216031	-0.141583709	0.010576601
NQO2|P16083	4.89605684	0.002680026	0.149273602	0.908573705	0.003592522	0.441964797	0.614905927	0.02610604	-0.258370428	-0.07920223	-0.401196918	0.179168198	-0.14282649	-0.321994688
IGHV3-43|A0A0B4J1X8	4.99757974	0.00234714	0.427748822	0.590320408	0.127990479	0.029672989	0.934908847	0.002772124	-0.198657013	0.160097918	-0.27292044	0.358754931	-0.074263427	-0.433018358
CD248|Q9HCU0	6.00941604	0.00062809	0.811987595	0.039787558	0.000896398	0.302071726	0.022154782	0.667838228	0.029595608	0.087064554	0.122503963	0.057468946	0.092908355	0.035439409
LAMP1|P11279	3.49185341	0.016808318	0.360782695	0.413533753	0.972523322	0.009061078	0.582169128	0.173906045	0.058992556	-0.054151731	0.014875705	-0.113144287	-0.044116851	0.069027436
PDYN|P01213	16.9405876	9.15E-10	0.019135315	7.98E-06	7.27E-10	0.210879131	0.001694671	0.305714496	0.151041919	0.249648003	0.333158379	0.098606083	0.182116459	0.083510376
HLA-C|P04222	1.29780689	0.277677592	0.51971751	0.953976731	0.999966282	0.231795363	0.505042124	0.933623057	-0.157544651	0.058111257	-0.004884987	0.215655908	0.152659664	-0.062996244
FKRP|Q9H9S5	3.33593702	0.020600749	0.075330589	0.359316565	0.017467558	0.832142237	0.976221092	0.553184339	0.137095269	0.090042241	0.159523519	-0.047053029	0.022428249	0.069481278
PROCR|Q9UNN8	1.89936138	0.131226152	0.991420953	0.269126896	0.686949424	0.160268936	0.505105074	0.869232551	-0.018510633	0.112509947	0.066879204	0.13102058	0.085389836	-0.045630743
NAGA|P17050	1.66688805	0.175678427	0.459954753	0.997204563	0.925668293	0.334084058	0.145713757	0.974430439	-0.083447869	0.011013788	0.033524043	0.094461657	0.116971913	0.022510256
AKR1A1|P14550	4.14786005	0.007714532	0.999993363	0.021166281	0.295002582	0.020999542	0.288984105	0.685257887	0.001885378	-0.204150454	-0.126131939	-0.206035832	-0.128017317	0.078018515
CRISP3|P54108	2.05257468	0.108076602	0.325734327	0.999775544	0.25230522	0.356726483	0.99991578	0.278655983	0.15432203	0.007540914	0.159699453	-0.146781116	0.005377424	0.15215854
CTGF|P29279	1.92443884	0.12713436	0.997574049	0.815862499	0.213788942	0.713630689	0.15178095	0.713259452	0.009806541	-0.044216633	-0.095510962	-0.054023175	-0.105317503	-0.051294329
GPNMB|Q14956	7.08838338	0.000155544	0.002892125	0.868796767	0.631271223	0.000132733	0.064501421	0.186299359	0.257092981	-0.054370052	0.082596792	-0.311463033	-0.174496189	0.136966844
LFNG|Q8NES3	3.23959192	0.02335766	0.976748423	0.027448958	0.925089187	0.08729814	0.997625117	0.101817874	-0.012222911	-0.081754966	-0.017630871	-0.069532055	-0.00540796	0.064124095
PAMR1|Q6UXH9	0.79507406	0.498050229	0.999754316	0.723283928	0.983667221	0.676445056	0.993361641	0.465784807	0.003501684	-0.040418684	0.013695659	-0.043920368	0.010193976	0.054114344
IDH1|O75874	3.95277374	0.009202467	0.978758098	0.177698831	0.015696213	0.374696418	0.054478593	0.784540864	-0.013456021	-0.067248465	-0.096955382	-0.053792444	-0.083499361	-0.029706917
COCH|O43405	3.52406996	0.016115939	0.208964998	0.764538288	0.551383737	0.018774322	0.88585744	0.089214582	0.112255734	-0.054400503	0.072039236	-0.166656237	-0.040216498	0.126439739
0|P01700	1.35096372	0.259320476	0.54050724	0.956322833	0.871599181	0.247535431	0.919845205	0.559523888	-0.160444999	0.059691639	-0.086857453	0.220136638	0.073587545	-0.146549093
CLUL1|Q15846	1.52282838	0.210059341	0.987025919	0.819311811	0.198375601	0.95378647	0.375513803	0.684687977	0.024204253	0.061335223	0.136212503	0.03713097	0.112008249	0.074877279
SPINT1|O43278	10.396915	2.35E-06	0.725170822	0.989293018	5.76E-05	0.521155452	0.004411977	9.73E-06	0.040903137	-0.011978514	0.169735396	-0.05288165	0.12883226	0.18171391
IFI30|P13284	1.84724473	0.140139059	0.163248044	0.873016263	0.274337134	0.523610154	0.981347281	0.722328051	-0.159722283	-0.056636388	-0.131691468	0.103085895	0.028030816	-0.075055079
ST6GALNAC1|Q9NSC7	7.099174	0.000153398	0.152928985	0.006803187	8.82E-05	0.694072647	0.128087401	0.683788037	0.092544495	0.13970305	0.18514027	0.047158555	0.092595775	0.04543722
NEU1|Q99519	2.4566952	0.064442746	0.198855579	0.937579741	0.101341515	0.477624776	0.996487108	0.307972898	-0.10586497	-0.030228681	-0.116912906	0.075636289	-0.011047936	-0.086684225
COL15A1|P39059	0.15316633	0.927551317	0.957716794	0.987397129	0.999897587	0.997720881	0.93497732	0.97632454	-0.028310012	-0.018068393	0.003501653	0.010241619	0.031811664	0.021570045
NTRK3|Q16288	5.39827845	0.00139136	0.342592718	0.023558322	0.000977732	0.665467578	0.172417559	0.797206141	0.062587374	0.104646335	0.136667265	0.042058961	0.074079891	0.032020931
EFCAB14|O75071	0.79857636	0.496103719	0.873005474	0.999996875	0.573710613	0.876634025	0.963199997	0.573143738	0.031431273	0.000828407	0.050623211	-0.030602866	0.019191938	0.049794804
PRKAR1A|P10644	11.7463895	4.43E-07	0.008829572	0.038570853	0.981629473	9.89E-08	0.001645283	0.077090352	0.127868588	-0.104771759	-0.014354047	-0.232640348	-0.142222635	0.090417712
MEGF9|Q9H1U4	9.03231497	1.30E-05	0.000961974	0.042696292	9.34E-06	0.577606829	0.799366865	0.105195015	0.137216491	0.092231056	0.168519033	-0.044985435	0.031302542	0.076287977
ICAM1|P05362	0.48522058	0.692956785	0.722979267	0.999995476	0.995874752	0.726912953	0.824287337	0.996874387	0.046956842	0.001015627	0.009683309	-0.045941215	-0.037273533	0.008667682
NCSTN|Q92542	1.54616797	0.204088703	0.455085987	0.161606538	0.49288518	0.942675365	0.999090819	0.883070631	-0.071950925	-0.099037566	-0.065543361	-0.027086641	0.006407564	0.033494205
SLITRK3|O94933	1.34902469	0.259932876	0.991877957	0.762755231	0.258089354	0.906215001	0.427236045	0.828217379	0.018623087	0.06204238	0.114143676	0.043419293	0.09552059	0.052101297
CYTL1|Q9NRR1	0.4485199	0.718640701	0.752117713	0.860612726	0.996228465	0.995467781	0.846314862	0.933488799	0.076351983	0.058673582	0.01603973	-0.017678401	-0.060312253	-0.042633852
UNC5B|Q8IZJ1	0.80073133	0.494908996	0.637861645	0.717096983	0.999655823	0.998551296	0.669853149	0.750369313	0.090418777	0.078424745	0.007157094	-0.011994033	-0.083261684	-0.071267651
GPR37|O15354	0.56838838	0.636505154	0.734268929	0.79730009	0.626939528	0.999040773	0.999381982	0.993106225	0.044787018	0.038818933	0.049822273	-0.005968085	0.005035255	0.01100334
PODN|Q7Z5L7	11.1307046	9.46E-07	0.000761132	0.52134002	3.91E-06	0.047439685	0.73046757	0.001048498	-0.237335414	-0.080906146	-0.297771027	0.156429269	-0.060435612	-0.216864881
HLA-B|P30479	0.24154385	0.867268682	0.867038709	0.921182172	0.989573527	0.998567676	0.959483292	0.985804945	-0.14373447	-0.114768067	-0.055020931	0.028966403	0.088713539	0.059747136
PGLS|O95336	2.35682974	0.073268838	0.878818007	0.315398916	0.065641434	0.780609485	0.33704657	0.882924162	-0.030194492	-0.067919095	-0.09575957	-0.037724603	-0.065565078	-0.027840475

Gene ID | Unirprot ID	F-Value	Pr(>F)	ANOVA p -values with Tukey Adjustment						Difference (AD - CT)					
			AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA
BRINP1|O60477	1.34008125	0.263036107	0.950759075	0.996297119	0.276556241	0.987925877	0.612701907	0.377565604	0.023529316	0.009362495	0.075569469	-0.014166821	0.052040153	0.066206974
LTA4H|P09960	1.55227033	0.202554155	0.993782694	0.52834128	0.249033218	0.704737496	0.400483909	0.963512522	-0.012975031	-0.065719317	-0.088035575	-0.052744286	-0.075060544	-0.022316258
LRRTM2|O43300	5.10467515	0.002040807	0.045021148	0.090917095	0.000986397	0.984886938	0.719804584	0.467426813	0.118694453	0.103032006	0.164281367	-0.015662447	0.045586914	0.061249361
GSTM2|P28161	0.25704463	0.856245835	0.991266334	0.999208167	0.954958899	0.998298644	0.847600872	0.91135699	-0.015120303	-0.006552199	0.02540201	0.008568104	0.040522314	0.031954209
NPNT|Q6UXI9	1.53891459	0.205926924	0.616544534	0.724364595	0.939417965	0.996907859	0.261188973	0.341829023	0.085833903	0.071549715	-0.038539553	-0.014284188	-0.124373456	-0.110089268
BIN1|O00499	2.73306124	0.04576909	0.883462434	0.377072599	0.03712981	0.825124592	0.209867926	0.685994185	-0.043733423	-0.094065779	-0.156761806	-0.050332356	-0.113028383	-0.062696027
SERPINA10|Q9UK55	1.96166758	0.121285938	0.973276255	0.357580878	0.981127048	0.170396413	0.999874109	0.157638595	-0.039885722	0.1482449	-0.033594943	0.188130622	0.006290779	-0.181839843
B3GALNT1|O75752	1.89806394	0.131441265	0.71611679	0.883245847	0.098206656	0.985495264	0.634722658	0.386200908	0.038007732	0.025688739	0.079151462	-0.012318992	0.041143731	0.053462723
CFL2|Q9Y281	5.19893057	0.002043671	0.789582578	0.454085483	0.001525648	0.955230509	0.03996378	0.125804077	-0.066715064	-0.103467133	-0.2489574	-0.036752069	-0.182242336	-0.145490267
OLFML2A|Q68BL7	1.18677661	0.316123181	0.946095313	0.484536459	0.340586764	0.830572541	0.702112552	0.99636933	0.028386963	0.071459859	0.081910042	0.043072896	0.053523079	0.010450183
FAM49B|Q9NUQ9	9.87965035	4.48E-06	0.606740177	0.0026183	1.01E-05	0.10941938	0.00226477	0.550133608	-0.054185266	-0.152314699	-0.206597385	-0.098129433	-0.152412119	-0.054282686
PCYOX1|Q9UHG3	2.93494885	0.034717896	0.853486126	0.883233162	0.029179481	0.999747663	0.220796672	0.164354112	0.048416284	0.043132963	0.160330856	-0.005283321	0.111914571	0.117197892
ADCYAP1|P18509	2.19272117	0.090664099	0.999995463	0.37761818	0.831269266	0.414469077	0.83047166	0.059469479	0.002302359	0.153380859	-0.078975425	0.151078499	-0.081277784	-0.232356283
FAM20B|O75063	4.89219287	0.002693591	0.434601091	0.074792592	0.001441028	0.819983079	0.151518261	0.58761144	0.049643454	0.077860813	0.116702062	0.028217359	0.067058609	0.038841249
NRN1|Q9NPD7	9.33733642	8.86E-06	0.873583729	0.000799558	0.000159539	0.012830511	0.003682743	0.988013333	0.026757002	0.133793371	0.144555723	0.107036369	0.117798722	0.010762353
SCN3B|Q9NY72	17.2467861	6.43E-10	1.31E-05	2.08E-05	3.07E-10	0.995280428	0.269293964	0.150492774	0.350176658	0.333432062	0.475375265	-0.016744596	0.125198607	0.141943203
CXCL16|Q9H2A7	1.27786874	0.283346784	0.997622806	0.296645729	0.969080464	0.411824298	0.99442052	0.518967607	-0.007642826	-0.069442403	-0.017452246	-0.061799577	-0.009809419	0.051990158
COL4A1|P02462	0.41097303	0.745306398	0.999713682	0.930468907	0.96584223	0.958173806	0.943949324	0.685997907	0.00278998	0.017709492	-0.013406259	0.014919512	-0.016196239	-0.031115751
PRL|P01236	0.89841716	0.443121676	0.834502983	0.96761974	0.809797831	0.558219215	0.999999955	0.510431821	-0.076631068	0.040740365	-0.077069504	0.117371434	-0.000438435	-0.117809869
ADAMTSL3|P82987	1.82091647	0.144859998	0.444400759	0.999988587	0.284853243	0.4492009	0.996687636	0.285835314	-0.078529023	-0.001620122	-0.089197418	0.076908902	-0.010668394	-0.087577296
C2orf40|Q9H1Z8	4.70793739	0.00342706	0.040646943	0.977786146	0.154684754	0.011479948	0.898914785	0.053890411	-0.274891642	0.040357593	-0.206071514	0.315249236	0.068820128	-0.246429108
METRNL|Q641Q3	4.09302925	0.007659976	0.006297713	0.843956619	0.219551611	0.057106952	0.424572304	0.686168631	-0.125723393	-0.030462979	-0.069824662	0.095260414	0.055898731	-0.039361683
FABP3|P05413	75.3479097	6.89E-32	0.279697039	1.23E-13	1.24E-13	9.86E-14	9.64E-14	0.997727459	0.091184267	-0.478964383	-0.470152204	-0.57014865	-0.56133647	0.008812179
ITGB1|P05556	1.94959034	0.123154157	0.916206427	0.688302785	0.671383723	0.302186238	0.970867901	0.102168107	-0.019147744	0.031714296	-0.031752733	0.05086204	-0.012604989	-0.063467029
HS6ST1|O60243	0.58134398	0.627958775	0.999766111	0.647700192	0.992238839	0.710420319	0.997656058	0.78844507	-0.003138619	-0.041172739	-0.00967396	-0.038034121	-0.006535341	0.031498779
C1QL3|Q5VWW1	2.35667059	0.073532164	0.134721958	0.999102138	0.379935913	0.161374431	0.907438453	0.439638024	0.15303939	0.009238998	0.107385201	-0.143800392	-0.045654189	0.098146203
SEMA6B|Q9H3T3	4.17356213	0.006894025	0.999999964	0.093111029	0.041512918	0.098147534	0.044701408	0.992753843	-0.000274785	0.134866863	0.150066323	0.135141648	0.150341108	0.015199461
HIST2H2BF|Q5QNW6	0.45448837	0.714483058	0.931971083	0.990881254	0.960904587	0.989041588	0.682855851	0.849465444	0.090018593	0.043445365	-0.070428831	-0.046573228	-0.160447424	-0.113874197
PIK3IP1|Q96FE7	5.89125971	0.000732321	0.019741312	0.03120225	0.000412395	0.995123014	0.767753803	0.595847648	0.121752758	0.111936302	0.160457395	-0.009816456	0.038704637	0.048521093
HSPB1|P04792	1.66950351	0.175329466	0.999953041	0.934688358	0.218951798	0.948308049	0.235894606	0.530985629	-0.004491034	-0.051776808	-0.165787445	-0.047285773	-0.16129641	-0.114010637
MMP17|Q9ULZ9	8.60996706	2.31E-05	0.005044439	0.010015118	8.58E-06	0.99430822	0.427133822	0.276569134	0.250978576	0.232477593	0.360024194	-0.018500983	0.109045618	0.127546601
B3GNT9|Q6UX72	2.46315337	0.063909317	0.077886142	0.959892724	0.311636834	0.206279749	0.853859955	0.600713674	-0.096439363	-0.019277163	-0.065645467	0.077162201	0.030793897	-0.046368304
ICOSLG|O75144	13.8910613	3.30E-08	0.003016959	0.995455153	1.62E-06	0.005467591	0.372830272	3.31E-06	0.229294779	0.014848412	0.330498749	-0.214446367	0.10120397	0.315650338
CBLN1|P23435	0.29528528	0.828775089	0.889812097	0.999999964	0.999486469	0.883349138	0.82669183	0.999524783	-0.044490994	0.000280084	0.0066365	0.044771078	0.051127494	0.006356416
CTSA|P10619	2.27633321	0.081234778	0.109577036	0.99313734	0.433717239	0.178512434	0.823118996	0.592497503	-0.152149684	-0.017594667	-0.096310905	0.134555017	0.05583878	-0.078716238
PTPRJ|Q12913	1.35516399	0.257998474	0.944273528	0.939514901	0.530378679	0.668582545	0.224783325	0.864308861	-0.024451101	0.02450728	0.056364724	0.048958381	0.080815824	0.031857443
SEPP1|P49908	0.27047408	0.846635301	0.951284888	0.986885576	0.817473299	0.99681582	0.989400733	0.94889507	0.02072876	0.012750149	0.032453467	-0.007978611	0.011724707	0.019703318
ERBB4|Q15303	2.67781425	0.048448261	0.171852154	0.964431226	0.095601046	0.371194881	0.998457641	0.243473839	0.093265663	0.020987961	0.100378501	-0.072277701	0.007112838	0.079390539
EFNB1|P98172	3.71641052	0.012534971	0.048464851	0.028632189	0.027177292	0.999349053	0.999830193	0.999959263	0.07132057	0.074609503	0.073372377	0.003288933	0.002051807	-0.001237126
B4GALNT4|Q76KP1	1.1479414	0.331106953	0.691732894	0.892842195	0.981866077	0.268895722	0.868387647	0.676344916	0.070867864	-0.044654481	0.023069689	-0.115522345	-0.047798175	0.06772417
CFHR5|Q9BXR6	0.35155437	0.788067041	0.944671839	0.969002662	0.99868174	0.742183981	0.974029232	0.92268246	-0.057484423	0.045514115	-0.015170321	0.102998538	0.042314101	-0.060684436
LGMN|Q99538	4.28272022	0.005976587	0.018644156	0.933102251	0.048773702	0.079219822	0.959984892	0.182063145	-0.191760575	-0.037706896	-0.160760081	0.154053679	0.031000493	-0.123053185
SERPINB1|P30740	2.85155754	0.038686036	0.025169094	0.287326775	0.184272089	0.669066402	0.771117347	0.996989715	0.103781179	0.063072049	0.070019483	-0.04070913	-0.033761696	0.006947435
SULF2|Q8IWU5	1.43435042	0.234212815	0.999360966	0.758329946	0.348774611	0.692276708	0.294113171	0.911299966	-0.00322881	0.025517632	0.041982683	0.028746443	0.045211493	0.016465051
FAIM2|Q9BWQ8	3.54096845	0.015764196	0.008167008	0.260552484	0.163252948	0.465047155	0.569669388	0.996878879	0.181157492	0.100404078	0.111253353	-0.080753414	-0.069904139	0.010849275
BACE1|P56817	0.54576318	0.651597378	0.67410507	0.994084896	0.999854323	0.809960514	0.692011266	0.997500699	0.055555328	0.012301706	0.003469923	-0.043253623	-0.052085405	-0.008831782
COL21A1|Q96P44	1.32822206	0.26658724	0.311119911	0.650453755	0.304369322	0.929748584	0.999843592	0.94324844	0.093864778	0.061436372	0.08990925	-0.032428406	-0.003955527	0.028472879

			ANOVA p -values with Tukey Adjustment						Difference (AD - CT)					
Gene ID | Unirprot ID	F-Value	Pr(>F)	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA
AK1|P00568	1.54864607	0.204057025	0.606784367	0.484752464	0.149498796	0.998749538	0.848044487	0.904060585	-0.09133875	-0.102383507	-0.149318452	-0.011044756	-0.057979702	-0.046934946
FOLR1|P15328	6.7629194	0.000236673	0.000769368	0.988817514	0.083881172	0.001943055	0.327211557	0.159146687	-0.277009065	-0.021990065	-0.160888133	0.255019001	0.116120932	-0.138898069
CDH20|Q9HBT6	2.3210295	0.076712601	0.52245062	0.87769076	0.059072906	0.915959604	0.704127969	0.280182235	0.051072772	0.027194065	0.089826129	-0.023878707	0.038753356	0.062632064
OXT|P01178	1.19640038	0.3125054	0.535061164	0.290722795	0.875117467	0.98081529	0.913960228	0.703610679	-0.076793242	-0.09831932	-0.040864795	-0.021526078	0.035928447	0.057454525
CD93|Q9NPY3	1.67980898	0.172870186	0.607127221	0.76310701	0.996371908	0.122588294	0.442607517	0.856283115	-0.05596812	0.043143558	0.009375238	0.099111678	0.065343358	-0.03376832
GPR37L1|O60883	6.05860132	0.000589225	0.015393815	0.020393458	0.000378602	0.998023635	0.803673684	0.680240344	0.179729419	0.169340317	0.231487833	-0.010389102	0.051758413	0.062147515
CNTN5|O94779	5.97199278	0.000695297	0.001782386	0.023779728	0.002348102	0.788200918	0.990548746	0.905422921	0.242277195	0.181700862	0.223130377	-0.060576334	-0.019146818	0.041429516
ANG|P03950	11.8840738	3.74E-07	0.000350239	0.997559415	9.23E-05	0.000565091	0.999457383	0.000151977	-0.268857044	-0.012108238	-0.276091411	0.256748807	-0.007234367	-0.263983174
PLAUR|Q03405	1.32260039	0.268897517	0.307421081	0.325031072	0.741495622	0.999938484	0.863823183	0.884105069	0.122791217	0.118944013	0.069640403	-0.003847204	-0.053150814	-0.04930361
PLA2G15|Q8NCC3	0.12250114	0.946744719	0.998939704	0.982162074	0.98916427	0.955405283	0.967560504	0.999882745	-0.005776141	0.014618649	0.012033429	0.02039479	0.01780957	-0.00258522
GALNT15|Q8N3T1	4.04373294	0.008170216	0.600862651	0.530405047	0.289134693	0.049199656	0.96730403	0.00833832	0.093117988	-0.098695062	0.126408627	-0.191813049	0.03329064	0.225103689
UBE2L3|P68036	19.006671	8.67E-11	0.805909185	3.61E-06	1.45E-08	0.000244852	2.31E-06	0.74941217	-0.026728693	-0.149705776	-0.177525284	-0.122977082	-0.150796591	-0.027819508
NPDC1|Q9NQX5	5.75859752	0.000870219	0.099779683	0.175793937	0.000301275	0.988136441	0.329838053	0.161180546	0.11066593	0.095339082	0.188813898	-0.015326849	0.078147968	0.093474817
UCHL1|P09936	90.433007	4.56E-36	0.708965133	8.82E-14	8.70E-14	1.10E-13	1.07E-13	0.999436016	-0.053010109	-0.586173492	-0.580785114	-0.533163383	-0.527775005	0.005388378
MAMDC2|Q7Z304	11.1512983	9.22E-07	0.000203163	0.113617676	1.45E-06	0.161980426	0.810911788	0.011477874	-0.207567626	-0.107151244	-0.24939716	0.100416382	-0.041829534	-0.142245916
UBE2N|P61088	37.6369246	4.91E-19	0.9647717	2.90E-11	7.53E-11	2.97E-12	7.32E-12	0.985699892	0.017837776	-0.270846647	-0.258666798	-0.288684423	-0.276504574	0.012179849
RAD23A|P54725	5.65814747	0.000991754	0.999999992	0.022761919	0.01739702	0.024875902	0.019214526	0.99999455	0.000128806	-0.130597701	-0.131673764	-0.130726507	-0.131802571	-0.001076063
SNCG|O76070	14.8000332	1.12E-08	0.15865201	0.043342498	0.00056467	2.47E-05	3.46E-08	0.567841356	0.129339733	-0.159051697	-0.233711134	-0.28839143	-0.363050867	-0.074659437
HAVCR2|Q8TDQ0	0.29620731	0.828109459	0.984354081	0.798651761	0.992253467	0.949572162	0.999704031	0.910551114	0.011896529	0.029552637	0.008891235	0.017656109	-0.003005293	-0.020661402
CYCS|P99999	1.11464108	0.344456376	0.965812937	0.730934366	0.940194373	0.442066128	0.999827298	0.349538309	0.020261939	-0.043402099	0.023519208	-0.063664038	0.003257269	0.066921307
GLA|P06280	1.91705847	0.128325645	0.091027209	0.836035048	0.556763734	0.406173378	0.662337571	0.96738032	-0.088215037	-0.030647915	-0.046830198	0.057567122	0.041384839	-0.016182283
APOA1BP|Q8NCW5	2.88426492	0.03707888	0.63046249	0.680995667	0.467454847	0.098164126	0.039927853	0.988784111	0.047820645	-0.043381839	-0.055286915	-0.091202484	-0.10310756	-0.011905077
IGSF1|Q8N6C5	4.64395334	0.003726096	0.999954202	0.640675841	0.007997475	0.681177502	0.010683137	0.17198805	0.002279081	0.052011077	0.139038208	0.049731996	0.136759127	0.087027131
BAI3|O60242	0.80333765	0.493467076	0.926857584	0.840167231	0.952101432	0.472472473	0.651527971	0.987915972	-0.029113965	0.038164571	0.023736137	0.067278536	0.052850102	-0.014428434
GALC|P54803	2.88364826	0.037108561	0.998880427	0.992549282	0.085393095	0.974598895	0.063466687	0.147984329	-0.012805012	0.023600297	0.197675801	0.036405309	0.210480813	0.174075503
SNCB|Q16143	39.2374568	1.13E-19	0.537466085	4.97E-09	2.75E-11	3.43E-12	1.35E-13	0.860054946	0.087423404	-0.410443152	-0.458378207	-0.497866555	-0.545801611	-0.047935055
TMPRSS5|Q9H3S3	2.80850385	0.041074696	0.460370167	0.79311613	0.027485266	0.942698267	0.556133215	0.227353716	-0.115134655	-0.071619953	-0.214440494	0.043514702	-0.099305839	-0.142820541
RMDN3|Q96TC7	0.603606	0.613441414	0.945385906	0.98830563	0.576958933	0.994923917	0.901419297	0.769220364	0.023413017	0.013289041	0.051417183	-0.010123977	0.028004165	0.038128142
IGF2|P01344	1.82487859	0.144139921	0.381357078	0.992047787	0.226923198	0.535738689	0.995948945	0.353765308	-0.070784135	-0.01219693	-0.080383543	0.058587205	-0.009599408	-0.068186613
VNN1|O95497	1.72156324	0.164084402	0.981396165	0.150390529	0.882976663	0.321108805	0.987361487	0.463337327	0.053654496	0.292042395	0.098857533	0.238387899	0.045203037	-0.193184862
APMAP|Q9HDC9	1.71343854	0.165759939	0.959284183	0.90135726	0.14609764	0.998121647	0.386857327	0.467277746	0.044808462	0.060203982	0.182308214	0.015395521	0.137499752	0.122104231
TAGLN2|P37802	5.59211923	0.001134722	0.229729676	0.33114669	0.000443137	0.991181268	0.191484635	0.079238513	-0.106906561	-0.090821175	-0.215569977	0.016085385	-0.108663417	-0.124748802
TAGLN3|Q9UI15	8.86057534	1.70E-05	0.873944089	0.002093864	0.029007097	0.000147835	0.00295823	0.77342425	0.045023354	-0.208563729	-0.156100008	-0.253587083	-0.201123362	0.052463721
MGP|P08493	2.34433888	0.074452848	0.140229333	0.140918112	0.117458304	0.999916854	0.999990515	0.999985816	-0.154322522	-0.149994679	-0.152271614	0.004327843	0.002050908	-0.002276935
LOXL3|P58215	0.16851084	0.917488313	0.982364001	0.999998449	0.986628396	0.979429545	0.892703829	0.987972939	-0.023704499	0.00099275	0.020292696	0.024697249	0.043997195	0.019299946
THSD7A|Q9UPZ6	0.91371136	0.435732909	0.997894991	0.978991272	0.6632242	0.939477155	0.784364303	0.38838917	0.008797776	-0.018538124	0.052523978	-0.027335901	0.043726201	0.071062102
ADAM9|Q13443	4.14688095	0.00713891	0.018860283	0.997287885	0.796510577	0.009077682	0.139266991	0.667392886	-0.0990338	0.006438938	-0.029254708	0.105472738	0.069779092	-0.035693646
LRP4|O75096	0.60810535	0.61059955	0.675206895	0.663301679	0.955961414	0.999999893	0.911817965	0.908339797	0.092673603	0.092136839	0.040511373	-0.000536764	-0.05216223	-0.051625466
SHH|Q15465	2.04886621	0.108587096	0.085137843	0.419952405	0.270836851	0.805246186	0.904643722	0.994670844	-0.298550829	-0.187344654	-0.216367243	0.111206176	0.082183586	-0.029022589
KIAA0319|Q5VV43	2.29694984	0.079117413	0.629108829	0.974811826	0.078882939	0.8542538	0.668434596	0.187170634	0.056580147	0.019358531	0.108182058	-0.037221616	0.05160191	0.088823526
ANGPTL1|O95841	5.35019753	0.001481382	0.010014279	0.643696054	0.004415376	0.175637246	0.99975662	0.115138853	-0.124963768	-0.045252819	-0.128309896	0.079710949	-0.003346128	-0.083057077
EMILIN3|Q9NT22	1.07398476	0.361398861	0.614392871	0.999620606	0.512265718	0.665694448	0.999679052	0.564196315	0.066770105	0.005419206	0.071838911	-0.061350899	0.005068806	0.066419705
GRB2|P62993	0.85573245	0.465181748	0.442490759	0.993146002	0.964072152	0.594401415	0.700724034	0.996949689	0.048384206	0.008480425	0.014673788	-0.039903781	-0.033710418	0.006193363
STX1B|P61266	1.28530444	0.280812699	0.869337644	0.650042822	0.984307734	0.219358769	0.659229877	0.830913906	0.034175379	-0.050499542	-0.015144765	-0.08467492	-0.049320144	0.035354777
FLRT1|Q9NZU1	0.89884903	0.443059617	0.987828108	0.642974724	0.486897129	0.845834527	0.717404908	0.995412706	0.014021039	0.048300554	0.057589322	0.034279516	0.043568283	0.009288767
RPL8|P62917	0.0289155	0.993337518	0.995592976	0.999992884	0.999999756	0.993766607	0.99534053	0.999981018	-0.068443222	0.00782319	-0.00242449	0.076266411	0.066018732	-0.01024768
APCS|P02743	1.83924428	0.14155778	0.633756034	0.931276262	0.528178504	0.274761678	0.999605902	0.189024019	-0.199737055	0.098316777	-0.216394438	0.298053832	-0.016657383	-0.314711216

			ANOVA p -values with Tukey Adjustment						Difference (AD - CT)					
Gene ID | Unirprot ID	F-Value	Pr(>F)	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA
SEMA3A|Q14563	0.78802559	0.501985771	0.999319192	0.890620062	0.523061941	0.937440585	0.615431648	0.917965215	0.005279703	0.029705863	0.055309731	0.02442616	0.050030028	0.025603868
KLK11|Q9UBX7	2.07801352	0.104636973	0.06817663	0.701867567	0.459245457	0.476027148	0.679929107	0.982962747	-0.182667289	-0.077772241	-0.103188796	0.104895049	0.079478493	-0.025416555
CLMP|Q9H6B4	1.38122211	0.249934931	0.743901516	0.999487696	0.389191256	0.667238556	0.954925033	0.310799671	0.041093953	-0.004458405	0.0613448	-0.045552358	0.020250847	0.065803205
SCUBE2|Q9NQ36	2.1322191	0.097658431	0.424304271	0.814322047	0.986470817	0.076697784	0.222948313	0.940115365	-0.072790758	0.040936457	0.015405652	0.113727215	0.088196411	-0.025530805
BMP6|P22004	3.23131515	0.023610932	0.90972504	0.485948552	0.0188121	0.884608714	0.121922646	0.430348004	-0.035376758	-0.073597645	-0.148802164	-0.038220888	-0.113425406	-0.075204518
MBP|P02686	0.47114272	0.702973383	0.720477523	0.999226019	0.910751	0.788335024	0.966998444	0.951222776	-0.111858098	-0.01351818	-0.065597558	0.098339918	0.04626054	-0.052079378
GGT7|Q9UJ14	0.08915282	0.965926542	0.971074773	0.999999455	0.999588245	0.968445315	0.984348975	0.999421331	0.025750621	-0.000652751	0.005746724	-0.026403373	-0.020003897	0.006399475
CHST12|Q9NRB3	0.7686059	0.512954117	0.631565387	0.986025985	0.606967647	0.818826342	0.999995614	0.806787303	0.053352038	0.014936416	0.052362794	-0.038415623	-0.000989245	0.037426378
NLGN1|Q8N2Q7	2.35030835	0.074155887	0.869138631	0.942487507	0.065599095	0.996264557	0.338180259	0.211920416	0.031473472	0.022625879	0.098176993	-0.008847593	0.066703521	0.075551113
HIST2H2BE|Q16778	0.18073738	0.909375053	0.999963754	0.957195187	0.998678789	0.946759128	0.999591393	0.902361696	-0.006505815	0.069092138	-0.020560671	0.075597952	-0.014054857	-0.089652809
FGFR3|P22607	7.68817435	7.20E-05	0.002822129	0.61413291	0.000282916	0.082780655	0.973331671	0.018132337	0.134831804	0.045256274	0.150578368	-0.08957553	0.015746565	0.105322094
COTL1|Q14019	3.30465674	0.021458403	0.66818771	0.93768497	0.221787836	0.312524333	0.012677198	0.53128546	0.044039236	-0.021929659	-0.07092043	-0.065968895	-0.114959667	-0.048990772
SPON2|Q9BUD6	11.8516859	3.90E-07	8.29E-06	0.989369951	0.522909723	1.36E-06	0.000981341	0.319135986	-0.205495755	0.012535691	-0.053448896	0.218031447	0.15204686	-0.065984587
AJAP1|Q9UKB5	8.14517124	4.01E-05	0.014866718	0.00127622	2.97E-05	0.917100551	0.440538605	0.823649532	0.136923354	0.165663406	0.202160084	0.028740051	0.06523673	0.036496678
ATP1B2|P14415	2.70910068	0.046526746	0.079715448	0.513379282	0.061446971	0.703154788	0.999997797	0.67917305	-0.109590546	-0.06120089	-0.108788677	0.048389656	0.000801869	-0.047587787
DSG1|Q02413	0.23928958	0.868804591	0.997045603	0.994876488	0.934699564	0.969724983	0.855261517	0.985306722	0.051491049	-0.060067502	-0.141714711	-0.111558551	-0.19320576	-0.081647209
CALB2|P22676	25.3965826	8.32E-14	5.47E-05	1.59E-08	1.74E-13	0.408265555	0.002157743	0.160336572	-0.215538312	-0.28781599	-0.380107327	-0.072277678	-0.164569015	-0.092291337
NPTN|Q9Y639	1.58166457	0.195313528	0.955280644	0.384854599	0.229858387	0.719609115	0.535613202	0.99249793	0.016739714	0.050338112	0.05876283	0.033598398	0.042023115	0.008424718
FUT11|Q495W5	1.25382038	0.291685906	0.93839249	0.668537915	0.249523114	0.950748621	0.605645611	0.893298137	0.024335978	0.046437734	0.074312763	0.022101756	0.049976785	0.027875029
NSF|P46459	1.79255938	0.150115214	0.930006608	0.599368316	0.123159773	0.927460875	0.405806456	0.774167327	-0.026236154	-0.052409432	-0.091092545	-0.026173278	-0.064856391	-0.038683113
SLITRK6|Q9H5Y7	2.45026861	0.064977899	0.04026267	0.753915526	0.683049368	0.30794388	0.336065549	0.999671682	-0.256276999	-0.092507823	-0.10119321	0.163769176	0.15508379	-0.008685386
ENTPD6|O75354	4.29461674	0.005884291	0.019067206	0.990659311	0.805842761	0.006651579	0.135318469	0.6116083	-0.123534513	0.012223032	-0.035835811	0.135757544	0.087698701	-0.048058843
LPA|P08519	6.27017874	0.000472199	0.093801968	0.414072304	0.334401144	0.000797455	0.875741289	0.006093335	-0.635126503	0.401624406	-0.436380985	1.036750909	0.198745518	-0.838005391
PTK7|Q13308	1.30871233	0.272969968	0.838746372	0.868379404	0.789849206	0.377879464	0.285236595	0.998944264	-0.029090645	0.026129218	0.030809543	0.055219863	0.059900189	0.004680325
PTPRM|P28827	0.37370814	0.772072858	0.868449249	0.998635298	0.999690245	0.783421279	0.809593508	0.999901003	-0.040004044	0.007857531	0.004713304	0.047861574	0.044717347	-0.003144227
EXT1|Q16394	0.15722408	0.924924352	0.987645052	0.991140641	0.996007283	0.923994002	0.942686916	0.999830139	-0.010145706	0.008811385	0.006569659	0.018957091	0.016715365	-0.002241726
APOC1|P02654	3.2880956	0.021926753	0.175955704	0.837358845	0.022941563	0.596203314	0.889072612	0.170819325	0.263112384	0.104706463	0.352319782	-0.158405922	0.089207397	0.247613319
SLPI|P03973	7.48504373	9.34E-05	0.002322635	0.945674254	0.002526344	0.011679163	0.996781398	0.013510339	-0.261406011	-0.039101913	-0.246814841	0.222304098	0.01459117	-0.207712928
ME1|P48163	6.3626412	0.000407043	0.760122185	0.002770842	0.003131972	0.063870278	0.076401663	0.998438521	-0.040386296	-0.14256109	-0.136259146	-0.102174795	-0.095872851	0.006301944
SF3A1|Q15459	8.55394517	2.39E-05	0.03217052	0.394477882	0.347379792	0.000126392	6.85E-05	0.99996042	-0.16893015	0.093957746	0.096698379	0.262887895	0.265628529	0.002740634
DPP3|Q9NY33	0.97649263	0.405019594	0.79358883	0.90455207	0.953468548	0.376851674	0.971337176	0.602077887	0.048847326	-0.035092104	0.026360844	-0.083939431	-0.022486482	0.061452948
ERAP2|Q6P179	0.7688281	0.51284439	0.999917894	0.999449516	0.663656017	0.99994766	0.628100202	0.574392894	0.012104256	0.02235471	-0.215322475	0.010250454	-0.227426732	-0.237677186
FABP5|Q01469	5.69637992	0.000943605	0.765197336	0.042534344	0.190318378	0.002205481	0.016607756	0.886661763	0.04667616	-0.123949932	-0.091404077	-0.170626091	-0.138080237	0.032545855
RTN4RL1|Q86UN2	8.97922331	1.39E-05	0.047256653	0.031983014	3.28E-06	0.999862421	0.078875426	0.079645722	0.174143957	0.178903908	0.328587332	0.00475995	0.154443374	0.149683424
KIAA0319L|Q8IZA0	1.83848874	0.141692471	0.97093829	0.925961715	0.133644527	0.998485187	0.332084285	0.398432061	0.012502492	0.01700371	0.058422238	0.004501218	0.045919746	0.041418528
WBSCR17|Q6IS24	0.55053654	0.648395939	0.987444031	0.977510281	0.612694074	0.999906485	0.823161196	0.843438562	0.014668874	0.017452079	0.05152796	0.002783205	0.036859086	0.034075881
EIF4A2|Q14240	1.01450627	0.388587063	0.890092727	0.313405504	0.894115773	0.796247086	0.999845696	0.698104854	-0.06788114	-0.154017706	-0.060999666	-0.086136566	0.006881474	0.09301804
CRYM|Q14894	31.1257911	2.45E-16	0.254289225	3.44E-07	8.07E-08	1.88E-11	2.88E-12	0.998633183	0.119706937	-0.356556681	-0.366021271	-0.476263617	-0.485728208	-0.00946459
ITM2C|Q9NQX7	0.8121698	0.488605392	0.999682056	0.536727653	0.825019971	0.608744175	0.876413664	0.953448955	0.006813974	0.092759743	0.058072746	0.08594577	0.051258772	-0.034686997
CCDC126|Q96EE4	3.75634064	0.011897504	0.995447903	0.276398928	0.021241588	0.415129494	0.045830936	0.701597531	0.007930158	0.059252708	0.09341216	0.05132255	0.085482001	0.034159451
DCHS1|Q96JQ0	2.48253032	0.062334697	0.981872018	0.482235079	0.06785806	0.731102722	0.173574863	0.735142789	0.020908048	0.077438045	0.130724312	0.056529998	0.109816265	0.053286267
SYN1|P17600	35.3057621	4.33E-18	0.041266229	5.47E-08	1.26E-06	1.40E-13	5.74E-13	0.861153217	0.174010046	-0.382378204	-0.334498297	-0.556388251	-0.508508343	0.047879907
COL16A1|Q07092	5.19418539	0.001815762	0.026601723	0.993522157	0.018080631	0.047831725	0.999999266	0.034083547	-0.135765965	-0.012348227	-0.135180036	0.123417738	0.000585929	-0.122831809
C1QTNF3|Q9BXJ4	6.48059821	0.000340939	0.297965814	0.495185107	0.000169664	0.979662001	0.078790314	0.021962295	0.134438442	0.104969901	0.311967326	-0.029468541	0.177528884	0.206997425
FTH1|P02794	2.05421594	0.107851415	0.723550387	0.951312993	0.528458887	0.389125118	0.075987369	0.841985741	-0.062014304	0.030707591	0.076544591	0.092721895	0.138558895	0.045837
PRDX3|P30048	21.2782026	6.92E-12	0.886251364	4.20E-06	1.66E-09	0.000138176	1.38E-07	0.473846468	-0.030375426	-0.208857341	-0.265227877	-0.178481915	-0.234852451	-0.056370536
SEMA4C|Q9C0C4	1.12244266	0.341286733	0.393928254	0.908159748	0.435278044	0.783445749	0.998777526	0.837644924	-0.057225803	-0.023659678	-0.051966409	0.033566124	0.005259393	-0.028306731

			ANOVA p -values with Tukey Adjustment						Difference (AD - CT)					
Gene ID | Unirprot ID	F-Value	Pr(>F)	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA
ERP44|Q9BS26	2.17224307	0.092798126	0.109738492	0.99697169	0.629537935	0.15694287	0.644772818	0.746726419	-0.084604131	-0.007421702	-0.042470948	0.077182429	0.042133183	-0.035049247
FAH|P16930	0.28793119	0.834080002	0.844868534	0.955295853	0.85669639	0.988260458	0.999891017	0.992959085	-0.062695077	-0.038343287	-0.05775542	0.024351791	0.004939658	-0.019412133
GLO1|Q04760	27.1871732	1.30E-14	0.48729584	2.46E-06	8.29E-08	2.10E-09	3.85E-11	0.939598072	0.059043334	-0.212157618	-0.234445751	-0.271200953	-0.293489086	-0.022288133
IGHV5-51|A0A0C4DH38	1.15532668	0.328209514	0.875940091	0.697850175	0.991630147	0.259140626	0.710914745	0.835871989	-0.095825076	0.134880417	0.034939464	0.230705492	0.13076454	-0.099940953
LDLR|P01130	7.3415995	0.000112301	0.230720153	0.037586984	0.791201669	4.59E-05	0.022183181	0.244110414	-0.088219559	0.121886116	0.040804297	0.210105675	0.129023856	-0.081081819
SIL1|Q9H173	6.94304148	0.000187585	0.003846231	0.99978956	0.02748079	0.002403863	0.852317602	0.018615481	-0.158271234	0.003733524	-0.122756269	0.162004757	0.035514965	-0.126489793
ENPP4|Q9Y6X5	1.95426655	0.122427526	0.826170334	0.511248649	0.808386064	0.116622771	0.289077445	0.951160774	0.052713872	-0.082663854	-0.052135238	-0.135377726	-0.10484911	0.030528616
CD44|P16070	5.15874169	0.001901732	0.098994262	0.715124095	0.235789582	0.004638004	0.950312804	0.014929615	0.080754332	-0.03597457	0.062756391	-0.116728901	-0.01799794	0.098730961
MPI|P34949	0.73280536	0.533655353	0.961244252	0.774384037	0.999938472	0.474503147	0.942608247	0.783697191	0.023282587	-0.044208315	-0.002505948	-0.067490902	-0.025788535	0.041702367
CRIM1|Q9NZV1	1.18636026	0.318274753	0.997709738	0.999610544	0.400461365	0.999752648	0.520799652	0.436563991	-0.021974127	-0.011818655	-0.173178847	0.010155472	-0.15120472	-0.161360192
RCN1|Q15293	1.82562179	0.144005233	0.369424492	0.997716683	0.956494183	0.262673497	0.130262017	0.988008638	-0.066274197	0.007392353	0.01984329	0.073666551	0.086117487	0.012450936
WISP2|O76076	5.81125627	0.000871149	0.005230149	0.920652619	0.01337301	0.030618872	0.967104629	0.071914068	-0.196952605	-0.036373734	-0.17100919	0.160578871	0.025943415	-0.134635456
HNRNPA2B1|P22626	1.62699751	0.185432982	0.165037779	0.970577305	0.680018323	0.35397887	0.703463836	0.913218155	-0.244204532	-0.051548794	-0.123771396	0.192655737	0.120433135	-0.072222602
TRIL|Q7L0X0	0.45216864	0.716069034	0.736403426	0.975615805	0.999941797	0.923234869	0.744487655	0.98151699	-0.05650542	-0.022386645	-0.002860611	0.034118775	0.053644809	0.019526034
SVEP1|Q4LDE5	0.38089514	0.766900249	0.955306741	0.76287326	0.998158475	0.967941602	0.984055874	0.8375501	-0.046994666	-0.088026941	-0.015329076	-0.041032275	0.031665589	0.072697864
JAM2|P57087	1.26150068	0.288998674	0.479091926	0.303708433	0.403181459	0.993358668	0.999951978	0.995799317	0.044314491	0.052415584	0.045832504	0.008101093	0.001518013	-0.00658308
LSR|Q86X29	2.61287468	0.052689617	0.804000961	0.039631759	0.293764539	0.309169271	0.851533767	0.751383727	0.031238559	0.090389254	0.058117472	0.059150694	0.026878913	-0.032271782
DSC1|Q08554	0.52088743	0.668457137	0.994828089	0.689032652	0.999573472	0.825770453	0.998850115	0.728056707	0.019580788	0.087142539	0.008210355	0.067561751	-0.011370433	-0.078932184
SEMA3E|O15041	1.06326614	0.3659858	0.996908904	0.500879964	0.544052416	0.643614164	0.689162356	0.999602933	0.021659662	0.143409405	0.133239233	0.121749743	0.11157957	-0.010170172
LAMP2|P13473	1.56557236	0.199246697	0.914860085	0.625501617	0.920728272	0.253028703	0.9999541	0.232122975	0.029696906	-0.053357377	0.027490034	-0.083054283	-0.002206872	0.080847412
FAM69C|Q0P6D2	18.6324854	1.32E-10	0.00011084	0.997732527	6.52E-08	0.000177077	0.53230365	1.03E-07	0.224519995	0.009222302	0.290956622	-0.215297692	0.066436627	0.28173432
WSCD1|Q658N2	3.25227561	0.022974761	0.03060387	0.996437636	0.914937435	0.0482385	0.116051472	0.971822331	-0.133743054	-0.010116782	-0.029829568	0.123626273	0.103913486	-0.019712786
HRNR|Q86YZ3	0.88591477	0.450991325	0.995328069	0.446279587	0.841699293	0.6178057	0.939546373	0.91992818	-0.114498647	-0.685341703	-0.392770733	-0.570843056	-0.278272086	0.29257097
DYNLL2|Q96FJ2	13.7779098	3.78E-08	0.055979165	0.013225982	0.034389135	4.19E-07	1.55E-06	0.976489104	0.081061318	-0.094877017	-0.082657652	-0.175938335	-0.16371897	0.012219365
ST3GAL6|Q9Y274	0.92964603	0.427535644	0.671206475	0.960217923	0.998493919	0.360553404	0.740858783	0.904810353	-0.070915288	0.030187486	-0.009634352	0.101102774	0.061280936	-0.039821838
FCN3|O75636	1.76137608	0.156104824	0.386969285	0.973880708	0.710178322	0.178584971	0.932485134	0.422036493	-0.199936141	0.052191295	-0.127524393	0.252127436	0.072411748	-0.179715688
AKAP12|Q02952	2.16379069	0.095620113	0.999257722	0.908300759	0.327021586	0.855124278	0.401035668	0.077373534	-0.015571189	0.08120699	-0.196784326	0.096778179	-0.181213137	-0.277991316
MOXD1|Q6UVY6	5.13815249	0.001991174	0.570568302	0.065678045	0.595171357	0.001519167	0.055520037	0.551457193	-0.065577634	0.122559894	0.059829137	0.188137528	0.125406771	-0.062730757
CFHR3|Q02985	0.38552402	0.763556414	0.852432244	0.739356437	0.940249497	0.997601379	0.993068778	0.963960364	0.11552843	0.142252403	0.078145923	0.026723973	-0.037382507	-0.06410648
S100A9|P06702	0.02820674	0.993592476	0.999766132	0.999750448	0.997603194	0.99807351	0.992618638	0.999637062	0.023809326	-0.023644502	-0.049453263	-0.047453829	-0.073262589	-0.02580876
0|P01825	1.80669789	0.150885396	0.113775712	0.715545627	0.416487264	0.579992049	0.795721049	0.971661607	-0.444749976	-0.193919351	-0.270953001	0.250830624	0.173796975	-0.07703365
CD177|Q8N6Q3	8.32882975	3.18E-05	0.127611177	0.35307599	0.041662057	0.00088368	0.985763792	9.54E-05	-0.366336999	0.267666353	-0.421786461	0.634003352	-0.055449462	-0.689452813
AP2A1|O95782	2.14630315	0.095920554	0.432988929	0.567428606	0.05985822	0.994158546	0.793847028	0.616753174	0.063491873	0.052936916	0.100723701	-0.010554957	0.037231828	0.047786785
TINAGL1|Q9GZM7	1.20354254	0.31008064	0.531313954	0.996924973	0.442415509	0.645554199	0.999852806	0.558013615	-0.080419873	-0.011864601	-0.084678638	0.068555272	-0.004258765	-0.072814036
B3GAT3|O94766	1.72518165	0.163343396	0.160935796	0.542703	0.254140371	0.853244907	0.986020953	0.96086429	-0.065514195	-0.04072258	-0.055139429	0.024791615	0.010374766	-0.014416849
THBS3|P49746	0.97811196	0.404580704	0.715243237	0.976299516	0.396628582	0.912315473	0.960998865	0.645406474	-0.077728959	-0.030274654	-0.111952205	0.047454305	-0.034223246	-0.081677551
CRHBP|P24387	2.7329371	0.045306323	0.64920205	0.45249636	0.897271463	0.043762915	0.95177638	0.110673322	-0.088225774	0.108682709	-0.049905693	0.196908484	0.038320082	-0.158588402
JAM3|Q9BX67	1.29134586	0.278769048	0.914482701	0.580383038	0.986220557	0.222262729	0.740388657	0.761368032	-0.026068173	0.049521262	0.012976167	0.075589435	0.03904434	-0.036545095
SRPX|P78539	0.1508842	0.929020665	0.999876328	0.99772657	0.969484238	0.994200883	0.982376923	0.91494807	-0.005034059	0.012975626	-0.030769875	0.018009685	-0.025735816	-0.043745501
SAA2|P0DJI9	2.18143479	0.09171562	0.617237774	0.997989117	0.19786567	0.49386528	0.898781398	0.126077591	-0.317597818	0.045231093	-0.492318517	0.36282891	-0.174720699	-0.537549609
ULBP2|Q9BZM5	16.2245342	2.10E-09	3.84E-05	0.367807442	1.75E-08	0.011543956	0.539175715	3.61E-05	0.375070249	0.127657358	0.479214746	-0.247412892	0.104144496	0.351557388
C14orf37|Q86TY3	4.45129188	0.004793836	0.230131547	0.10166334	0.002102515	0.98643698	0.380015621	0.569251806	0.089459042	0.105191065	0.161919736	0.015732024	0.072460694	0.056728671
ADAM17|P78536	4.07846682	0.007807298	0.021892979	0.992728886	0.129679517	0.040953831	0.83300909	0.214094488	-0.127528547	-0.011777677	-0.091718657	0.11575087	0.03580989	-0.079940979
GNAI2|P04899	0.42932477	0.732368278	0.722259433	0.858363231	0.812610654	0.994102064	0.99704294	0.999909041	-0.081893495	-0.061885844	-0.066641946	0.020007651	0.015251549	-0.004756101
SDCBP|O00560	0.04666524	0.986591432	0.988636574	0.993651513	0.988069593	0.99989548	0.999999068	0.999936126	0.033612463	0.026770732	0.032234305	-0.006841731	-0.001378157	0.005463574
ADIPOQ|Q15848	1.17980946	0.318765725	0.664714937	0.990200809	0.660336033	0.464240492	0.999950219	0.448855103	0.127784117	-0.033148892	0.122211338	-0.16093301	-0.005572779	0.155360231
NXPH1|P58417	2.38943603	0.070264244	0.263655595	0.808877905	0.064302834	0.764135439	0.942816211	0.377157662	0.092368544	0.043876666	0.119762093	-0.048491878	0.027393549	0.075885427

			ANOVA p -values with Tukey Adjustment						Difference (AD - CT)					
Gene ID | Unirprot ID	F-Value	Pr(>F)	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA
CBLN2|Q8IUK8	1.61722014	0.187750626	0.262993665	0.232324661	0.346517271	0.999932328	0.99544517	0.990989449	0.116285644	0.119898444	0.101923294	0.0036128	-0.01436235	-0.01797515
RGN|Q15493	1.99780558	0.116153067	0.65256224	0.204057193	0.113221905	0.878928823	0.746243308	0.993677728	-0.100302949	-0.163286017	-0.184194856	-0.062983068	-0.083891906	-0.020908839
DBH|P09172	0.63634539	0.59255848	0.999999248	0.993945009	0.643420009	0.995106902	0.666789741	0.790843751	0.001602928	0.031256993	0.13813711	0.029654065	0.136534182	0.106880117
ADAMTSL4|Q6UY14	1.78512271	0.151523335	0.69257629	0.784789047	0.103685803	0.997688541	0.674704271	0.52907328	-0.073851336	-0.061469958	-0.146811488	0.012381378	-0.072960153	-0.085341531
C1QTNF4|Q9BXJ3	3.10713373	0.02789651	0.303726796	0.125797893	0.018383421	0.970775175	0.650150573	0.888966025	0.069780473	0.087217343	0.114625683	0.01743687	0.04484521	0.02740834
MIF|P14174	25.3359257	8.87E-14	0.999495373	5.18E-07	8.60E-10	1.24E-06	2.59E-09	0.685140962	-0.006727898	-0.325754087	-0.38791929	-0.319026189	-0.381191392	-0.062165203
S100B|P04271	3.30334734	0.021495068	0.04114118	0.393282482	0.030711518	0.659896659	0.999989834	0.640805279	-0.145722995	-0.083929552	-0.14412241	0.061793443	0.001600585	-0.060192858
EFNA5|P52803	4.61349172	0.003877512	0.054327164	0.079012438	0.002196433	0.9962214	0.800894489	0.648564152	0.134053238	0.122702178	0.179782945	-0.01135106	0.045729707	0.057080767
PDGFRB|P09619	4.81317408	0.002986609	0.01899629	0.128140313	0.002512621	0.845013729	0.965406466	0.533101771	0.140197568	0.1017544	0.161770812	-0.038443168	0.021573244	0.060016411
RAD23B|P54727	22.2444318	2.41E-12	0.875959241	1.04E-05	1.77E-07	3.70E-07	4.35E-09	0.877136177	0.025487389	-0.162958026	-0.186684285	-0.188445415	-0.212171673	-0.023726259
ANTXR1|Q9H6X2	1.29972776	0.275956194	0.790467645	0.419002867	0.255785386	0.939433908	0.825892752	0.992409538	0.031189101	0.050240756	0.059006894	0.019051656	0.027817793	0.008766138
SMPDL3A|Q92484	10.5950449	1.84E-06	3.81E-05	0.228284648	2.33E-05	0.026263179	0.99927201	0.024686367	-0.292399624	-0.116882906	-0.284725539	0.175516719	0.007674085	-0.167842634
LY75|O60449	7.1609429	0.000141672	0.166595464	0.995631208	0.001591812	0.09463418	0.436368819	0.00051177	0.143577001	-0.015599868	0.244029422	-0.159176868	0.100452421	0.25962929
PFN1|P07737	3.41738965	0.018524024	0.844621349	0.244858895	0.015074671	0.741582269	0.146835516	0.672868305	-0.035544695	-0.078775788	-0.124412017	-0.043231092	-0.088867322	-0.04563623
NIF3L1|Q9GZT8	5.95747513	0.000671935	0.678997872	0.158614877	0.059123992	0.008566469	0.001873981	0.979951997	0.05484828	-0.100007071	-0.117840732	-0.154855351	-0.172689012	-0.017833662
NPPC|P23582	4.30298713	0.005820207	0.403588954	0.264657081	0.002475224	0.996294618	0.226507868	0.306511787	0.06321368	0.071935337	0.137740749	0.008721656	0.074527069	0.065805413
0|P01742	1.18870379	0.315395709	0.820942824	0.993785147	0.520128131	0.665365168	0.969603003	0.345490241	-0.153061181	0.044658595	-0.22931862	0.197719776	-0.076257438	-0.273977215
STMN1|P16949	29.6071813	1.11E-15	0.012166732	3.27E-06	0.000176805	2.80E-13	2.24E-11	0.717799237	0.136663818	-0.223160586	-0.179642868	-0.359824403	-0.316306685	0.043517718
TIMP4|Q99727	1.0797693	0.358944418	0.853445138	0.982817616	0.811742446	0.969555888	0.32188393	0.572863012	-0.043265676	-0.019360581	0.045475623	0.023905095	0.088741299	0.064836204
LRIG1|Q96JA1	1.09186173	0.353860733	0.587484421	0.962066947	0.993892345	0.294295859	0.716178093	0.867935375	-0.070582567	0.026437846	-0.013755509	0.097020413	0.056827058	-0.040193355
PRAP1|Q96NZ9	3.13354651	0.026941671	0.037091927	0.952784601	0.214975165	0.118615533	0.810542729	0.482532023	-0.228238871	-0.043068213	-0.155889113	0.185170658	0.072349758	-0.1128209
DDB1|Q16531	0.91764988	0.43346785	0.999774501	0.691318706	0.647089889	0.645392345	0.599972936	0.999964652	0.003186506	-0.039767173	-0.04137141	-0.042953678	-0.044557916	-0.001604237
GPC4|O75487	1.56923165	0.198345807	0.709069303	0.583450526	0.950711987	0.998268772	0.360151847	0.24668198	-0.062731973	-0.072518277	0.02978973	-0.009786304	0.092521702	0.102308007
ST8SIA5|O15466	1.00764286	0.390613058	0.995729059	0.780613857	0.606917529	0.64848115	0.466352151	0.993098235	-0.015855965	0.063533621	0.080963027	0.079389586	0.096818993	0.017429406
DSC3|Q14574	5.73903226	0.000892656	0.175606581	0.98844768	0.009721405	0.081677848	0.748522615	0.002680285	-0.131623486	0.020156342	-0.19369517	0.151779828	-0.062071684	-0.213851512
SST|P61278	17.5388391	4.60E-10	0.004716059	4.38E-08	4.78E-09	0.055721137	0.022819553	0.992330864	0.263273024	0.458325127	0.478633889	0.195052103	0.215360865	0.020308763
SLITRK2|Q9H156	1.91892122	0.128023962	0.421241134	0.736736838	0.093745969	0.947885635	0.890526467	0.556598156	0.071275377	0.046305295	0.103374315	-0.024970082	0.032098938	0.05706902
IGHV3-49|A0A0A0MS15	5.24947881	0.001689366	0.008744948	0.998999397	0.078027608	0.011551741	0.783340933	0.099721654	-0.421195682	-0.018047761	-0.302078803	0.403147921	0.119116879	-0.284031042
IL6R|P08887	9.20617578	1.05E-05	0.092410843	0.989740134	0.000275521	0.039347386	0.336356923	5.45E-05	0.16130791	-0.020708463	0.272779204	-0.182016373	0.111471294	0.293487667
DNASE2|O00115	0.57332584	0.633239724	0.694997216	0.957603423	0.674556155	0.92914195	0.999995457	0.92631907	-0.072271232	-0.032583029	-0.070788819	0.039688203	0.001482412	-0.038205791
WBP2|Q969T9	3.3360887	0.020596674	0.025272841	0.594795793	0.064473845	0.352123751	0.960197823	0.607574751	0.141795741	0.060707825	0.118066483	-0.081087916	-0.023729258	0.057358658
ACYP2|P14621	3.42190011	0.018415313	0.957939232	0.034243313	0.121678881	0.129613242	0.343462525	0.934934722	-0.018585929	-0.098058263	-0.077739924	-0.079472334	-0.059153995	0.020318339
CPPED1|Q9BRF8	19.9061774	5.25E-11	4.04E-06	0.079254692	1.69E-10	0.02149468	0.403834971	2.57E-05	-0.314841833	-0.139962573	-0.406882599	0.17487926	-0.092040767	-0.266920026
PCDHGB7|Q9Y5F8	2.42611305	0.067524455	0.992680725	0.999673374	0.16705319	0.98154556	0.087020045	0.188035499	-0.018286347	0.006355682	0.133706838	0.024642029	0.151993186	0.127351156
CAND1|Q86VP6	11.6323309	1.23E-06	0.63044754	0.040521828	0.001194664	0.000597107	4.67E-06	0.667159733	0.121600229	-0.276041742	-0.387201672	-0.397641971	-0.508801901	-0.11115993
ATF6B|Q99941	2.24067947	0.086291353	0.272549814	0.98943572	0.453818204	0.149363117	0.967597837	0.269502307	0.102540012	-0.017127051	0.077715817	-0.119667063	-0.024824195	0.094842868
RTBDN|Q9BSG5	8.09872276	4.26E-05	0.00056364	0.024353872	6.00E-05	0.614602945	0.985978163	0.35857598	0.164085332	0.114569678	0.177721357	-0.049515654	0.013636026	0.063151679
CHST7|Q9NS84	7.59601258	8.39E-05	0.00594391	0.92182645	0.04195788	0.000626105	0.832024231	0.005686094	0.249295762	-0.046245638	0.1882109	-0.2955414	-0.061084862	0.234456538
ABHD14B|Q96IU4	0.88669449	0.449092711	0.583372523	0.764330489	0.421300157	0.987905355	0.997464355	0.948396796	-0.106980291	-0.07986293	-0.122588401	0.027117361	-0.01560811	-0.04272547
RNASE6|Q93091	4.37647564	0.005286723	0.070434433	0.999985439	0.043434663	0.0696687	0.999914296	0.0422853	0.085248685	0.001158813	0.087318906	-0.084089872	0.002070221	0.086160094
UBE2V2|Q15819	18.8271447	1.06E-10	0.409660499	6.62E-05	0.000120508	5.06E-08	8.81E-08	0.994180741	0.061517239	-0.174291304	-0.164846073	-0.235808543	-0.226363311	0.009445231
MYH11|P35749	0.54046304	0.655388857	0.997026325	0.802811199	0.702196339	0.906764689	0.835405677	0.998600212	-0.027554353	-0.117210252	-0.136689852	-0.089655899	-0.109135499	-0.0194796
ABCA2|Q9BZC7	1.3732941	0.252363212	0.590045512	0.999559127	0.362677629	0.644594331	0.990173145	0.410033839	-0.056438964	-0.004669952	-0.069572735	0.051769012	-0.013133771	-0.064902783
MIA|Q16674	2.39094921	0.070127777	0.203824755	0.992359075	0.173578978	0.314775461	0.999997076	0.27908006	-0.186542272	-0.025771177	-0.18470963	0.160771095	0.001832641	-0.158938454
HEPH|Q9BQS7	0.97110451	0.408379941	0.793963587	0.672517931	0.335174216	0.99721134	0.877639813	0.94554359	0.057943137	0.070085229	0.102763625	0.012142093	0.044820488	0.032678396
ITGB2|P05107	22.6234988	1.60E-12	0.224723548	0.000226655	4.16E-06	3.41E-08	1.88E-10	0.836259559	0.135428272	-0.289849432	-0.345184614	-0.425277704	-0.480612886	-0.055335182
SEL1L|Q9UBV2	3.28207534	0.022099511	0.603139077	0.024543265	0.068454396	0.402088265	0.658919468	0.967024616	0.058913148	0.132132933	0.1115648	0.073219785	0.052651652	-0.020568133

			ANOVA p -values with Tukey Adjustment						Difference (AD - CT)					
Gene ID | Unirprot ID	F-Value	Pr(>F)	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA
DSTN|P60981	4.14214603	0.0077141	0.040725571	0.06162664	0.007777964	0.993599739	0.967236884	0.874736987	-0.279645614	-0.252803094	-0.326755527	0.02684252	-0.047109913	-0.073952433
BPGM|P07738	0.70322942	0.551704536	0.712739289	0.984307178	0.596041993	0.881924548	0.999793688	0.806071573	-0.25080299	-0.079019766	-0.269726471	0.171783224	-0.018923481	-0.190706704
C1QTNF5|Q9BXJ0	1.388251	0.247800144	0.453962991	0.991089686	0.35627512	0.622398476	0.999733407	0.521964369	-0.085347587	-0.016565673	-0.090384092	0.068781914	-0.005036505	-0.073818419
FCGR2A|P12318	5.23947026	0.001711571	0.007568948	0.987671012	0.053538688	0.017607169	0.836868373	0.109426226	-0.295141662	-0.029124302	-0.2218773	0.266017359	0.073264361	-0.192752998
PGD|P52209	5.62434104	0.001060367	0.043989312	0.271034711	0.000532049	0.805727259	0.621050913	0.12879062	-0.197643577	-0.131585937	-0.284931897	0.06605764	-0.087288321	-0.15334596
RELT|Q969Z4	4.83789493	0.002891658	0.336285945	0.066889171	0.001437746	0.880839492	0.216065001	0.617520172	0.070739596	0.101385052	0.149175494	0.030645456	0.078435898	0.047790442
CAPG|P40121	9.75524081	5.24E-06	0.593815809	0.916288525	0.000921337	0.226209129	4.82E-06	0.007563351	0.083193185	-0.041825695	-0.243056301	-0.125018881	-0.326249486	-0.201230605
LNPEP|Q9UIQ6	1.4703547	0.224086673	0.916633875	0.75820158	0.175065242	0.988977425	0.533027217	0.716737009	-0.036120582	-0.053537791	-0.108647461	-0.017417209	-0.072526879	-0.05510967
OLFM2|O95897	0.19419508	0.900258699	0.975915739	0.98342621	0.996142593	0.999917723	0.915522185	0.930422357	-0.016366642	-0.013990533	0.008319075	0.002376109	0.024685717	0.022309608
ADIRF|Q15847	2.69742405	0.048293698	0.876864458	0.245228986	0.050555626	0.655156682	0.234667036	0.887535178	-0.059798876	-0.149354538	-0.204641398	-0.089555662	-0.144842522	-0.05528686
MDK|P21741	9.01031368	1.34E-05	0.25018837	0.032718477	0.449154666	4.49E-05	0.966768887	0.000118132	0.095774961	-0.138077894	0.07274347	-0.233852855	-0.02303149	0.210821365
PPP5C|P53041	9.4304282	7.88E-06	0.994077321	0.000790157	0.004982706	0.000347152	0.002314392	0.924507014	0.010837708	-0.160175291	-0.135551271	-0.171012999	-0.146388979	0.02462402
SLC8A2|Q9UPR5	0.97702268	0.405074802	0.940758331	0.847788209	0.894892222	0.996367667	0.573858626	0.398225621	0.047783674	0.065673281	-0.055453344	0.017889607	-0.103237018	-0.121126625
LHPP|Q9H008	2.67982819	0.048322251	0.941038198	0.043139032	0.413556621	0.177366806	0.787150661	0.635068068	-0.023648126	-0.107037846	-0.060936791	-0.083389721	-0.037288665	0.046101055
SCRN1|Q12765	13.0461802	1.01E-07	0.995786023	0.00132764	2.94E-05	0.000559819	1.02E-05	0.834799093	0.013181501	-0.213138338	-0.258354179	-0.226319838	-0.27153568	-0.045215841
CDH23|Q9H251	2.55149037	0.057203552	0.96296504	0.629651021	0.500240505	0.900041811	0.239178328	0.041058057	-0.036869343	-0.088936133	0.102094102	-0.05206679	0.138963445	0.191030236
FAM19A5|Q7Z5A7	1.1042609	0.348714051	0.321502166	0.625675909	0.509026411	0.947088177	0.977226945	0.998583564	0.066373412	0.045441565	0.051182406	-0.020931848	-0.015191006	0.005740842
PGRMC1|O00264	0.92150925	0.431551898	0.886932287	0.897715442	0.899528322	0.48454762	0.477154646	0.999996382	-0.018575645	0.017398541	0.016882334	0.035974186	0.035457979	-0.000516207
PXDN|Q92626	1.1822624	0.318064529	0.987974591	0.92305522	0.302473937	0.991134018	0.496591741	0.668334363	-0.014442196	-0.027163782	-0.074146405	-0.012721586	-0.059704209	-0.046982623
DLK2|Q6UY11	6.41576761	0.000370792	0.077997514	0.052254542	0.000118484	0.999706246	0.270501712	0.291637004	0.123317003	0.128020042	0.212457922	0.004703039	0.089140919	0.08443788
PPM1L|Q5SGD2	0.44759608	0.719336222	0.995364622	0.999613901	0.735718698	0.999039146	0.876633721	0.78840205	0.017746707	0.007410713	0.072137604	-0.010335993	0.054390898	0.064726891
SYT1|P21579	4.81971748	0.002961176	0.168031532	0.773004006	0.488612011	0.014021257	0.002734722	0.970314389	0.091446009	-0.041279214	-0.059721396	-0.132725223	-0.151167405	-0.018442182
TPBG|Q13641	4.01529273	0.008554178	0.939082146	0.11311484	0.014925895	0.336690639	0.071933192	0.880161243	0.036569532	0.141450121	0.186236447	0.104880589	0.149666916	0.044786327
IGHV3-72|A0A0B4J1Y9	4.11111083	0.007480913	0.069497425	0.999995742	0.06566222	0.066828145	0.999599584	0.062583922	-0.320828371	-0.002888039	-0.307821165	0.317940332	0.013007206	-0.304933126
LPHN2|O95490	3.34477251	0.020827566	0.561612979	0.015513866	0.114944708	0.340311366	0.8222373	0.815038791	0.078311713	0.178896908	0.128567117	0.100585195	0.050255404	-0.050329791
THSD4|Q6ZMP0	1.99277825	0.116598653	0.948164044	0.999970671	0.160533524	0.956800519	0.440589304	0.16347726	-0.031027803	-0.002406744	-0.113333521	0.028621059	-0.082305719	-0.110926778
0|P01721	10.7525921	1.51E-06	0.002828934	0.772606439	0.005922875	5.87E-05	0.978464807	0.000117625	-0.443587067	0.11698643	-0.395489744	0.560573498	0.048097323	-0.512476175
SPINK5|Q9NQ38	0.06590646	0.977887936	0.998892657	0.995792693	0.996167913	0.982158731	0.982667448	0.999999261	0.011713123	-0.017853587	-0.016899808	-0.02956671	-0.028612931	0.000953779
ANGPTL4|Q9BY76	4.23105423	0.006574005	0.873545278	0.518281158	0.06690696	0.142484157	0.007180222	0.681183188	0.04781139	-0.084611286	-0.150437244	-0.132422676	-0.198248634	-0.065825957
0|P01619	4.93774563	0.002537955	0.029785591	0.999825982	0.038666574	0.032713215	0.995254623	0.042449512	-0.417395554	-0.011442375	-0.3831112	0.405953179	0.034284354	-0.371668825
0|P80748	0.91005777	0.437257595	0.981988828	0.998542383	0.556717815	0.949470827	0.801707633	0.439107296	-0.045431283	0.018845393	-0.15109853	0.064276677	-0.105667247	-0.169943924
NA|P0DP58	5.99116128	0.000643162	0.005173597	0.135320783	0.000721304	0.583996613	0.981743952	0.313710639	0.156646163	0.098429324	0.173537907	-0.058216838	0.016891744	0.075108583
GALNT16|Q8N428	1.45869985	0.22731898	0.721383263	0.892259808	0.857313381	0.292097528	0.243378992	0.999897091	-0.047884373	0.031650548	0.034462551	0.079534921	0.082346924	0.002812003
CTSO|P43234	1.0924275	0.353624441	0.959774053	0.506263123	0.995235463	0.81993203	0.876111623	0.331168968	-0.02160692	-0.058918599	0.009849112	-0.037311679	0.031456032	0.068767711
MT3|P25713	1.8924491	0.132376117	0.980182107	0.123003583	0.889477207	0.278906146	0.989889765	0.395337717	0.023034377	0.128117259	0.040624621	0.105082882	0.017590244	-0.087492638
MESDC2|Q14696	0.34441703	0.793230472	0.911472711	0.98922453	0.993736076	0.75986038	0.97343655	0.934106308	-0.030775127	0.014229642	-0.011557093	0.045004769	0.019218034	-0.025786735
CDH7|Q9ULB5	6.27382603	0.000445663	0.02263318	0.541545393	0.998180784	0.000198507	0.026639798	0.40066006	-0.112295447	0.050606388	-0.006372614	0.162901835	0.105922834	-0.056979002
PVR|P15151	12.8719445	1.12E-07	2.18E-06	0.100261205	3.26E-06	0.012647997	0.984471868	0.022926566	0.248691358	0.105763537	0.232536884	-0.142927821	-0.016154474	0.126773347
DCBLD2|Q96PD2	5.45775523	0.001343221	0.407800045	0.983041016	0.081409909	0.213952997	0.000582178	0.169998599	-0.056730166	0.012982986	0.082631401	0.069713151	0.139361566	0.069648415
AVP|P01185	1.14334378	0.332922224	0.360029941	0.998028654	0.773930682	0.44641791	0.873763986	0.859177048	-0.109123494	-0.011465491	-0.060611039	0.097658003	0.048512455	-0.049145548
EDN3|P14138	6.7783331	0.000232008	0.053699506	0.042271519	7.27E-05	0.999996797	0.290041377	0.274902182	0.134473009	0.135542193	0.223900558	0.001069185	0.08942755	0.088358365
RAB14|P61106	0.2379423	0.869809895	0.999523528	0.987469342	0.865236032	0.996514284	0.916699611	0.972175203	-0.003725402	-0.010948605	-0.024793572	-0.007223203	-0.021068169	-0.013844967
GLRX|P35754	4.08458221	0.007745089	0.999495172	0.127561343	0.046454484	0.105020507	0.037177356	0.981654151	0.004083603	-0.077950959	-0.090797515	-0.082034562	-0.094881118	-0.012846556
IGFBPL1|Q8WX77	3.07011937	0.029124327	0.494203694	0.615079769	0.015921102	0.99583988	0.439070932	0.283516721	-0.099710001	-0.083883022	-0.201795805	0.015826979	-0.102085804	-0.117912783
IGHV6-1|A0A0B4J1U7	2.4985469	0.061061946	0.320199886	0.942027087	0.069947643	0.640391603	0.915690739	0.226528996	-0.310822695	-0.09996758	-0.424253173	0.210855115	-0.113430479	-0.324285594
RTN1|Q16799	20.8441737	1.93E-11	0.295503061	7.30E-05	2.87E-05	2.88E-08	7.86E-09	0.999387807	0.115576542	-0.288320049	-0.295737706	-0.403896591	-0.411314248	-0.007417657
SBSPON|Q8IVN8	2.79932255	0.041396585	0.051188916	0.341482841	0.070860525	0.765792843	0.993747057	0.874461387	0.392582117	0.247212589	0.354400217	-0.145369528	-0.0381819	0.107187627

			ANOVA p -values with Tukey Adjustment						Difference (AD - CT)					
Gene ID | Unirprot ID	F-Value	Pr(>F)	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA
IGHV3-73|A0A0B4J1V6	2.87104276	0.037720477	0.030649803	0.940324609	0.63724776	0.112853587	0.319306005	0.928915343	-0.405681209	-0.081336834	-0.164586755	0.324344375	0.241094454	-0.083249921
DPT|Q07507	2.84572687	0.038979684	0.755532817	0.406232225	0.81844	0.056732819	0.998387499	0.061703038	-0.071594737	0.109553533	-0.060084281	0.18114827	0.011510456	-0.169637814
KRT77|Q7Z794	0.91556993	0.434852924	0.956334122	0.999464694	0.73157168	0.976531108	0.409011162	0.640569122	-0.154623654	-0.033264945	0.29251709	0.121358709	0.447140744	0.325782034
IDUA|P35475	1.15134364	0.329769341	0.446041056	0.981089966	0.467424581	0.667884287	0.999505913	0.700748215	-0.115916632	-0.028871353	-0.107583624	0.087045278	0.008333008	-0.07871227
LILRA2|Q8N149	13.6420333	4.45E-08	3.56E-05	0.678995565	0.051646797	1.40E-07	0.103203758	0.001163996	0.424405936	-0.099063986	0.223352123	-0.523469922	-0.201053814	0.322416109
FAM198A|Q9UFP1	6.36072249	0.000398196	0.001075811	0.979010521	0.084001932	0.003481894	0.377849879	0.187157267	-0.24300547	-0.024527389	-0.144439209	0.218478081	0.098566261	-0.11991182
LRIG2|O94898	5.19424537	0.00181562	0.05519512	0.639392133	0.00173269	0.484506341	0.761063303	0.061255096	0.104191276	0.046893542	0.14266631	-0.057297734	0.038475034	0.095772768
HAGH|Q16775	16.5839955	1.38E-09	0.893800572	2.00E-05	8.17E-05	9.28E-07	4.03E-06	0.969838778	0.04438365	-0.292281058	-0.266012142	-0.336664708	-0.310395792	0.026268916
RAP1B|P61224	2.66164041	0.049472058	0.159606192	0.982011013	0.55427558	0.064033532	0.818186909	0.311897605	-0.171106231	0.029822815	-0.102281328	0.200929045	0.068824903	-0.132104142
UBA1|P22314	1.81593383	0.146658845	0.302795639	0.513740448	0.12023001	0.98134394	0.975614957	0.848348965	-0.169021372	-0.132579888	-0.207849025	0.036441485	-0.038827653	-0.075269138
IGHV3-15|A0A0B4J1V0	2.2764389	0.081223783	0.220561577	0.911079971	0.110784303	0.562789233	0.995552408	0.374529304	-0.233011335	-0.077945321	-0.260091621	0.155066014	-0.027080286	-0.1821463
HAPLN2|Q9GZV7	1.79753581	0.150978382	0.268608068	0.68016624	0.145876028	0.876565547	0.989685289	0.707042705	-0.163032027	-0.097849899	-0.190311101	0.065182128	-0.027279075	-0.092461203
SLIT3|O75094	0.20161632	0.895163321	0.98210117	0.997430287	0.965565049	0.940556752	0.999842377	0.90477801	-0.026375413	0.013239674	-0.03154058	0.039615088	-0.005165167	-0.044780254
CNPY3|Q9BT09	0.45933145	0.711048716	0.764122261	0.999598808	0.999995542	0.811121934	0.730640931	0.999189604	0.054688516	0.005658001	-0.00123631	-0.049030515	-0.055924826	-0.006894311
ANGPTL7|O43827	0.33672614	0.798796976	0.872582994	0.999724384	0.998331123	0.904330055	0.775563221	0.993432795	-0.089349556	-0.010479696	0.018706326	0.07886986	0.108055882	0.029186022
LRRC4|Q9HBW1	0.39191623	0.758961405	0.881959291	0.999966327	0.882952851	0.857287327	0.999976501	0.856715672	0.046178205	-0.00276568	0.043751868	-0.048943885	-0.002426338	0.046517548
NXPH3|O95157	0.65803915	0.578957493	0.870463489	0.976304461	0.948916767	0.982670782	0.54779446	0.761564997	-0.036045945	-0.018884615	0.024277743	0.017161329	0.060323688	0.043162358
GALNT11|Q8NCW6	0.06962214	0.976072295	0.983785332	0.999947377	0.999965496	0.975141825	0.987515907	0.999625617	-0.017032656	0.002414361	-0.002048888	0.019447017	0.014983768	-0.004463249
FOLR3|P41439	2.03641089	0.111256646	0.423375871	0.238447389	0.092669	0.992055396	0.903655193	0.97664891	0.080675221	0.095440434	0.115326169	0.014765213	0.034650948	0.019885735
EIF5A|P63241	2.09082828	0.103573691	0.256677928	0.982818146	0.197731385	0.424511926	0.999982323	0.351228556	-0.199288276	-0.038123304	-0.203114319	0.161164972	-0.003826044	-0.164991016
C1QL1|O75973	8.83849258	1.66E-05	0.00661184	0.665899183	0.059732456	8.22E-05	0.792499228	0.001329075	0.142556923	-0.0480751	0.104016276	-0.190632022	-0.038540647	0.152091375
SEP15|O60613	1.43277036	0.236920288	0.305816625	0.62200104	0.267923242	0.92631163	0.999894183	0.931866451	-0.115373402	-0.074824955	-0.111069058	0.040548447	0.004304343	-0.036244104
UBE2V1|Q13404	17.249236	6.41E-10	0.794275985	6.89E-05	2.96E-05	1.29E-06	4.57E-07	0.999716852	0.049532363	-0.236039377	-0.240685894	-0.285571741	-0.290218257	-0.004646516
IGKV3-11|P04433	8.45266627	2.71E-05	0.002268904	0.953581507	0.000678285	0.010423665	0.99898488	0.00374408	-0.476493216	-0.067236837	-0.494510362	0.409256378	-0.018017147	-0.427273525
STX1A|Q16623	0.14460966	0.932916486	0.998367082	0.966523329	0.998852603	0.9213456	0.987989311	0.984949817	0.022340213	-0.061998954	-0.018443608	-0.084339166	-0.04078382	0.043555346
CALU|O43852	0.5718748	0.634790428	0.662975796	0.957022623	0.710710335	0.904587553	0.999014094	0.939745526	-0.069662156	-0.029794732	-0.061576221	0.039867424	0.008085935	-0.031781489
EEF2|P13639	0.1640136	0.920489517	0.997046574	0.978168701	0.985680291	0.931401974	0.945739366	0.999901626	0.012856236	-0.024736972	-0.020890131	-0.037593208	-0.033746367	0.003846841
HEPACAM|Q14CZ8	2.91154165	0.035789188	0.112661476	0.968798781	0.100409826	0.257387124	0.999899142	0.243233101	-0.086841694	-0.017010805	-0.08441625	0.06983089	0.002425444	-0.067405446
ALAD|P13716	0.92009838	0.433309374	0.972624908	0.727083394	0.400967278	0.946492266	0.738688696	0.966003619	-0.088069128	-0.201347654	-0.289055233	-0.113278526	-0.200986105	-0.087707579
ACAT2|Q9BWD1	7.23069712	0.000155823	0.919755013	0.008396807	0.000689485	0.072900919	0.011271532	0.9044378	-0.06159515	-0.295259467	-0.355372631	-0.233664316	-0.29377748	-0.060113164
IGKV3D-20|A0A0C4DH25	15.6809096	3.96E-09	8.84E-07	0.591298919	2.10E-06	0.000156001	0.967765793	0.000407258	-0.853511041	-0.191056059	-0.784497408	0.662454982	0.069013633	-0.593441349
TXN|P10599	11.374104	7.01E-07	0.83267121	0.148799383	8.41E-05	0.018169362	2.13E-06	0.096878486	0.032318697	-0.079071042	-0.161991225	-0.111389738	-0.194309922	-0.082920183
DDAH2|O95865	2.55296057	0.056925717	0.630620439	0.903841635	0.468251851	0.236786051	0.040092372	0.868888699	0.046012749	-0.025545827	-0.053160338	-0.071558576	-0.099173087	-0.027614511
UBE2D2|P62837	0.76727899	0.514230852	0.930615049	0.952337415	0.446687437	0.999771461	0.801479323	0.748000154	-0.038807239	-0.033438329	-0.097029951	0.00536891	-0.058222712	-0.063591622
BAI2|O60241	12.8230277	1.19E-07	0.000187711	0.000195845	6.78E-08	0.999261229	0.453717805	0.350580929	0.274094374	0.26603614	0.365481714	-0.008058234	0.09138734	0.099445574
SLC39A12|Q504Y0	0.5883924	0.623339173	0.85725991	0.957899959	0.569306989	0.989894809	0.969325247	0.859523521	0.08995678	0.055652185	0.139176177	-0.034304595	0.049219397	0.083523992
EXTL3|O43909	1.32494202	0.267888255	0.791013656	0.904097366	0.210858892	0.993862578	0.764757642	0.586700825	0.060002281	0.043381901	0.120538716	-0.01662038	0.060536435	0.077156815
WIF1|Q9Y5W5	5.42490222	0.001372809	0.055997425	0.181535271	0.000583812	0.935133807	0.574642303	0.213221123	0.193950478	0.14984416	0.288115825	-0.044106318	0.094165347	0.138271665
CPXM1|Q96SM3	1.27710059	0.284033994	0.495020937	0.987493557	0.996932476	0.302690151	0.35147892	0.999134517	0.12960646	-0.029255739	-0.017777055	-0.158862199	-0.147383515	0.011478684
FSTL3|O95633	3.67087675	0.013303551	0.362476009	0.935809565	0.013732695	0.703081614	0.552532701	0.064093515	-0.086803689	-0.030370266	-0.154224456	0.056433423	-0.067420767	-0.12385419
TENM3|Q9P273	2.11334942	0.100991821	0.692492062	0.99645362	0.122265663	0.802237502	0.723687179	0.176737381	0.095751459	0.018189619	0.183299562	-0.077561841	0.087548103	0.165109943
DCD|P81605	2.12382778	0.098708373	0.418971102	0.989601032	0.353569195	0.246635941	0.999984938	0.191173059	-0.214043552	0.042126754	-0.218701688	0.256170306	-0.004658136	-0.260828442
MATN3|O15232	0.67089141	0.571149735	0.997337463	0.997760248	0.749424797	0.99999807	0.649738243	0.633231032	-0.015385742	-0.014010306	0.073361034	0.001375435	0.088746775	0.08737134
ATRNL1|Q5VV63	0.53568197	0.658429673	0.999999108	0.884510373	0.743833453	0.882666902	0.743429214	0.992752574	0.000765761	-0.039984201	-0.054424102	-0.040749963	-0.055189863	-0.014439901
CD9|P21926	0.24471526	0.865020935	0.99506548	0.952316125	0.849862725	0.99258481	0.946650362	0.992769776	0.025651389	0.054648039	0.081928762	0.02899665	0.056277374	0.027280724
FTL|P02792	1.87502612	0.135962925	0.568885532	0.95344444	0.757445296	0.858263067	0.104001558	0.419709103	-0.102757054	-0.040214	0.073777981	0.062543055	0.176535035	0.11399198
COL11A1|P12107	0.58207747	0.627802017	0.888629646	0.672508867	0.649499859	0.978381178	0.974941311	0.99999926	0.053266778	0.082760914	0.083672696	0.029494136	0.030405917	0.000911781

			ANOVA p -values with Tukey Adjustment						Difference (AD - CT)					
Gene ID | Unirprot ID	F-Value	Pr(>F)	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA
GPR56|Q9Y653	3.68472922	0.013064887	0.700469855	0.158963975	0.747138352	0.009615251	0.151538834	0.653573326	0.065625408	-0.123468461	-0.057851767	-0.189093868	-0.123477175	0.065616693
LRP2|P98164	0.97346385	0.407547275	0.802719747	0.885011106	0.33143104	0.997308505	0.868008983	0.755001986	0.083566099	0.06597424	0.152077586	-0.01759186	0.068511487	0.086103346
SELM|Q8WWX9	1.50420833	0.214939892	0.873651317	0.898291802	0.169619221	0.999813957	0.595902173	0.518405779	0.035121556	0.031453866	0.09095063	-0.00366769	0.055829073	0.059496764
GSTO1|P78417	2.34181315	0.074694528	0.152324185	0.510881371	0.072344654	0.863605642	0.996339705	0.7226235	-0.150665918	-0.095965781	-0.165603662	0.054700136	-0.014937744	-0.06963788
SLC5A5|Q92911	0.67694791	0.567188849	0.983282057	0.881050549	0.936656064	0.984027451	0.774013595	0.523138779	-0.036258863	-0.071402844	0.055140509	-0.035143982	0.091399372	0.126543353
FAM19A2|Q8N3H0	7.86446355	5.75E-05	0.000207159	0.064092013	0.000264431	0.258459346	0.992464028	0.35254896	0.375413236	0.215005365	0.351698448	-0.160407872	-0.023714788	0.136693084
HIST1H1E|P10412	0.15105903	0.928887171	0.93386873	0.947832773	0.957461927	0.9999079	0.999320082	0.999923562	0.105255879	0.094138271	0.084340433	-0.011117608	-0.020915446	-0.009797839
LAMP5|Q9UJQ1	6.60546301	0.000290081	0.519985805	0.977362961	0.000578409	0.755274525	0.06266006	0.002121152	-0.070058806	-0.020194771	-0.193300289	0.049864035	-0.123241483	-0.173105518
FCGR3A|P08637	4.00323413	0.008614705	0.19510983	0.153904417	0.003908289	0.999912174	0.542561319	0.558901943	-0.118432332	-0.12209172	-0.19479792	-0.003659388	-0.076365589	-0.072706201
C1GALT1|Q9NS00	3.4364128	0.018069815	0.940426285	0.072390621	0.882114817	0.01627432	0.550308764	0.27840326	-0.026178487	0.108939853	0.032077042	0.135118341	0.058255529	-0.076862812
NME2|P22392	32.406712	6.99E-17	0.99999999	4.42E-08	4.19E-12	6.30E-08	7.15E-12	0.411228758	0.000134561	-0.265906062	-0.331099788	-0.266040623	-0.33123435	-0.065193727
FAM171A1|Q5VUB5	1.04104077	0.375659315	0.99923682	0.980693753	0.596098583	0.956602354	0.68962337	0.341865219	0.004936042	-0.014333484	0.045573724	-0.019269525	0.040637683	0.059907208
PSMA4|P25789	12.182303	3.14E-07	0.999973818	0.000247578	0.000216242	0.000168459	0.000145506	0.999999232	0.002985734	-0.299377533	-0.298489807	-0.302363267	-0.301475541	0.000887726
NRG3|P56975	1.36497531	0.255135186	0.720916287	0.289377813	0.301450808	0.889961486	0.907690671	0.999915931	0.084044986	0.140574582	0.135879214	0.056529596	0.051834227	-0.004695368
OLFML2B|Q68BL8	19.8968162	3.19E-11	5.00E-08	0.885765041	8.23E-07	1.13E-06	0.824301014	1.79E-05	-0.301113597	-0.035324564	-0.259735363	0.265789033	0.041378234	-0.224410799
LRTM2|Q8N967	9.53107801	6.94E-06	0.025547965	0.000166012	9.30E-06	0.52820533	0.211053631	0.938309809	0.198577688	0.291943837	0.329751157	0.093366149	0.131173469	0.03780732
TPM3|P06753	9.26780516	1.16E-05	0.045896071	0.000168327	2.22E-05	0.371187787	0.172905755	0.97562034	-0.179360253	-0.288301305	-0.315254513	-0.108941052	-0.13589426	-0.026953208
ARF3|P61204	11.4346943	7.06E-07	0.557420205	9.95E-05	8.76E-06	0.014866195	0.002647857	0.957051326	-0.063522574	-0.207200545	-0.2300884	-0.143677971	-0.166565827	-0.022887856
SEMA4A|Q9H3S1	0.33236011	0.801957746	0.813091789	0.926601619	0.997902227	0.991488896	0.881428948	0.968171654	-0.076976655	-0.052152428	-0.014963464	0.024824227	0.062013191	0.037188964
B3GNT8|Q7Z7M8	4.4136586	0.005035729	0.244608577	0.907522807	0.084533398	0.053890844	0.977065194	0.011151937	-0.118815	0.041551234	-0.143741082	0.160366234	-0.024926082	-0.185292316
PLA2G7|Q13093	0.53621495	0.65807347	0.970957482	0.99991497	0.686689021	0.979564937	0.924074628	0.709453444	-0.029773455	-0.003990039	-0.070317295	0.025783416	-0.04054384	-0.066327256
LGALS3|P17931	3.75187303	0.01196719	0.297315201	0.580168062	0.603732304	0.014087743	0.930802942	0.050765898	-0.078061611	0.05509226	-0.052255855	0.133153871	0.025805756	-0.107348115
PSMA5|P28066	3.15076646	0.028336842	0.999983634	0.434375207	0.057491584	0.456349302	0.063119448	0.738749439	-0.003823261	-0.157456149	-0.256051264	-0.153632889	-0.252228003	-0.098595115
MB|P02144	3.31096237	0.021282704	0.389859658	0.996889483	0.07644145	0.270386012	0.878396929	0.039863845	-0.301369392	0.038153363	-0.43785434	0.339522755	-0.136484948	-0.476007703
HRSP12|P52758	0.80290832	0.493704367	0.924393667	0.543968799	0.548903497	0.903612014	0.912052332	0.99997704	-0.031025284	-0.064462436	-0.062605984	-0.033437152	-0.0315807	0.001856452
HIST1H1D|P16402	0.33578122	0.799481011	0.993148728	0.943018995	0.989449174	0.840480677	0.999991836	0.803186652	-0.04119983	0.083731487	-0.045365565	0.124931317	-0.004165734	-0.129097051
MERTK|Q12866	8.13319633	4.08E-05	0.000184967	0.282734215	0.000475323	0.053473787	0.968520775	0.117567603	0.171866913	0.070062149	0.154211767	-0.101804765	-0.017655147	0.084149618
HSPD1|P10809	2.29109949	0.081836416	0.0724607	0.400509622	0.166424484	0.821665369	0.986766769	0.954561941	-0.373136677	-0.243747021	-0.322880732	0.129389656	0.050255945	-0.079133711
IGHV1-18|A0A0C4DH31	2.50572133	0.062707245	0.21164072	0.894665563	0.983568275	0.042608353	0.373090737	0.701930976	-0.15842969	0.054713571	-0.028364078	0.213143262	0.130065612	-0.08307765
NLGN3|Q9NZ94	1.66352697	0.1773244	0.199920118	0.986551581	0.996229977	0.343377141	0.266561365	0.999269532	-0.11070003	-0.018568367	-0.011839261	0.092131663	0.098860769	0.006729106
NSG1|P42857	0.52211511	0.667590176	0.931286765	0.999519203	0.926171072	0.958373866	0.604679414	0.879243255	-0.024441543	-0.004353775	0.0238528	0.020087767	0.048294343	0.028206576
THY1|P04216	8.56345772	2.36E-05	0.849902566	0.000132326	0.003369923	0.003535735	0.048469125	0.761681789	0.032522788	0.169969519	0.133227579	0.137446731	0.100704791	-0.03674194
S100A7|P31151	0.84448623	0.471269017	0.674142514	0.976881384	0.999915025	0.418145866	0.686894223	0.961965864	-0.234352211	0.082053381	-0.012097987	0.316405592	0.222254224	-0.094151368
LCN2|P80188	0.09709535	0.961542965	0.975607885	0.999709339	0.999658077	0.956580886	0.986945281	0.997332006	0.042001626	-0.009160937	0.009368467	-0.051162563	-0.03263316	0.018529403
CD74|P04233	2.58572323	0.054569432	0.803126682	0.404188094	0.597159303	0.069952156	0.135186362	0.984651287	-0.03746855	0.062959699	0.04921051	0.100428249	0.08667906	-0.013749189
ARHGDIB|P52566	1.93617415	0.125262057	0.909844338	0.999997985	0.178410767	0.899416681	0.551570822	0.160061973	-0.038830881	0.001007198	-0.112915229	0.039838079	-0.074084349	-0.113922428
0|P01824	17.0582843	7.99E-10	4.01E-07	0.515190779	3.85E-07	0.000129508	0.992236367	0.000162223	-0.737862046	-0.175739855	-0.702399042	0.562122191	0.035463004	-0.526659187
EPB41L2|O43491	2.11132738	0.102674316	0.96645488	0.994861303	0.126226678	0.995700274	0.340875015	0.203269799	-0.043693662	-0.022295554	-0.193329892	0.021398108	-0.14963623	-0.171034338
ACP2|P11117	0.36893418	0.775510239	0.803909766	0.800238371	0.952240798	0.999997943	0.975746581	0.976793563	-0.049908195	-0.048934522	-0.027769837	0.000973673	0.022138357	0.021164684
FAM3A|P98173	3.07255576	0.029032171	0.091749206	0.99966101	0.195632881	0.105332614	0.965238679	0.2224107	-0.118838255	-0.004836245	-0.095840959	0.114002011	0.022997296	-0.091004715
LILRB1|Q8NHL6	1.41313352	0.240914312	0.762287069	0.695313753	0.99999782	0.173143974	0.751351068	0.65705511	-0.077129996	0.083879077	-0.00135506	0.161009073	0.075774936	-0.085234137
SNCA|P37840	8.00732812	6.98E-05	0.901639849	0.224893386	0.002621028	0.03940974	0.000114036	0.328756803	0.073686914	-0.207579445	-0.383190305	-0.28126636	-0.456877219	-0.17561086
IGHV1-3|A0A0C4DH29	2.05368861	0.111204921	0.925819947	0.972574512	0.107557629	0.996841033	0.364481422	0.229218534	0.126328349	0.085191473	0.453723902	-0.041136876	0.327395553	0.368532429
PPP2R4|Q15257	31.112672	7.03E-16	0.558110816	1.85E-09	8.45E-13	2.63E-06	3.80E-09	0.605631683	-0.07691271	-0.384445585	-0.453088393	-0.307532875	-0.376175683	-0.068642808
C12orf49|Q9H741	2.26005596	0.08354908	0.337480637	0.864873519	0.998323496	0.063967503	0.224975777	0.919350306	-0.103561729	0.046720453	0.009911277	0.150282182	0.113473005	-0.036809177
DPP4|P27487	1.56679341	0.200683425	0.595110459	0.815736179	0.999991992	0.144897101	0.570744855	0.826554715	-0.138051673	0.098384056	0.003120529	0.23643573	0.141172203	-0.095263527
ARSB|P15848	8.09749306	5.18E-05	0.000168909	0.919002119	0.016453937	0.001692126	0.400725123	0.092988464	-0.270310332	-0.038468774	-0.17512722	0.231841558	0.095183112	-0.136658446

			ANOVA p -values with Tukey Adjustment						Difference (AD - CT)					
Gene ID | Unirprot ID	F-Value	Pr(>F)	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA
H6PD|O95479	0.87246105	0.457327216	0.439258687	0.982410509	0.756789842	0.663607259	0.92605985	0.932485709	0.159138662	0.038034743	0.09643405	-0.121103919	-0.062704612	0.058399307
BST1|Q10588	3.9340476	0.009430635	0.145510846	0.721887049	0.007723783	0.668458248	0.762026715	0.126059368	0.140820874	0.067164561	0.202878404	-0.073656314	0.06205753	0.135713843
FDPS|P14324	5.22119175	0.001752884	0.998024058	0.096568947	0.006552515	0.151934731	0.013261615	0.790328616	-0.009116502	-0.116409832	-0.161029449	-0.10729333	-0.151912946	-0.044619617
TENM2|Q9NT68	2.80559224	0.041521279	0.063226285	0.222639025	0.063242498	0.91131876	0.998733235	0.94774068	0.140873643	0.104063625	0.132564283	-0.036810018	-0.00830936	0.028500659
NCR3LG1|Q68D85	1.63024485	0.183879973	0.618316131	0.153091594	0.910898496	0.828691792	0.929591485	0.424585688	0.06667823	0.112803175	0.034583342	0.046124945	-0.032094887	-0.078219833
ROR1|Q01973	1.21836283	0.305373764	0.228337181	0.823045933	0.801515321	0.695521349	0.6919529	0.99999702	-0.132281235	-0.057201827	-0.058496882	0.075079408	0.073784353	-0.001295055
CTHRC1|Q96CG8	3.84475439	0.010598742	0.009265971	0.874450894	0.241022995	0.065721661	0.470061284	0.674905304	-0.16559347	-0.038244944	-0.092945941	0.127348526	0.072647528	-0.054700997
CA3|P07451	3.18054358	0.026081058	0.514816847	0.990434079	0.091374862	0.335173224	0.848255463	0.038127142	-0.345057319	0.071401013	-0.54035933	0.416458332	-0.195302011	-0.611760343
MARCO|Q9UEW3	7.51247281	9.39E-05	0.021659192	0.731285012	0.000165943	0.210180814	0.622707157	0.00574987	-0.257652835	-0.087903884	-0.361161935	0.16974895	-0.103509101	-0.273258051
RNASE2|P10153	12.8540497	1.15E-07	8.80E-06	0.589459129	1.55E-05	0.001085335	0.981228061	0.002128537	0.264651002	0.065219547	0.245184487	-0.199431455	-0.019466515	0.17996494
FGFBP2|Q9BYJ0	4.79229133	0.003411419	0.006776131	0.941948538	0.08239846	0.029818999	0.700051342	0.254131904	-0.461467917	-0.07587552	-0.315113421	0.385592397	0.146354495	-0.239237901
IGHV2-70|A0A0C4DH43	13.5536125	4.94E-08	3.10E-05	0.673425236	2.77E-06	0.001913492	0.991802268	0.000302731	-1.04626305	-0.244526715	-1.107697837	0.801736335	-0.061434787	-0.863171122
NUDC|Q9Y266	5.36958343	0.001474838	0.274082078	0.208596307	0.62407078	0.00128189	0.013482033	0.851818123	0.102459453	-0.107815352	-0.065109509	-0.210274805	-0.167568962	0.042705843
EPHB3|P54753	3.54661746	0.015885519	0.850355819	0.030430494	0.999987608	0.224723397	0.85272433	0.025259581	-0.03202604	-0.106276167	-0.001228928	-0.074250127	0.030797112	0.10504724
TFPI|P10646	4.45188037	0.004790148	0.254300021	0.035380137	0.003308549	0.847742693	0.421295213	0.889546642	-0.109432303	-0.15689551	-0.196657701	-0.047463207	-0.087225399	-0.039762191
IGHV1-24|A0A0C4DH33	0.67993439	0.565446347	0.89247926	0.919752649	0.982440295	0.530828114	0.982530072	0.725703166	-0.105218351	0.091564161	-0.052306318	0.196782512	0.052912033	-0.143870479
CRP|P02741	2.20576207	0.088909596	0.842039179	0.060335232	0.572125177	0.353406555	0.976164559	0.555735935	0.185304097	0.549696114	0.274486171	0.364392017	0.089182074	-0.275209943
TPPP3|Q9BW30	1.77703505	0.153069068	0.999631128	0.229088618	0.501552606	0.285746595	0.578767153	0.943281168	-0.004814002	-0.088490721	-0.063455297	-0.083676719	-0.058641295	0.025035424
MSLN|Q13421	1.70986043	0.167482501	0.206089528	0.998411419	0.996719152	0.26951868	0.245024113	0.999981503	-0.216045294	-0.01756361	-0.021306505	0.198481684	0.194738789	-0.003742895
PRKAR1B|P31321	4.77197959	0.003250294	0.586991674	0.220346007	0.282058807	0.008127373	0.011717959	0.998131569	0.077235559	-0.116406912	-0.106291412	-0.19364247	-0.183526971	0.0101155
LRFN2|Q9ULH4	5.70765307	0.000929862	0.999999975	0.077513741	0.006039172	0.083780829	0.006992289	0.827783804	0.000335786	0.192486768	0.257905681	0.192150982	0.257569895	0.065418912
PTPRU|Q92729	0.75453152	0.521111604	0.950419819	0.638591455	0.533719794	0.924327241	0.867742893	0.999162703	0.024989108	0.053650732	0.059389228	0.028661624	0.03440012	0.005738496
CRABP1|P29762	0.48310455	0.694426036	0.940981081	0.993505232	0.867220315	0.835348091	0.99824521	0.714056256	-0.051538924	0.023279178	-0.066347649	0.074818101	-0.014808726	-0.089626827
APOC3|P02656	2.18333834	0.09149298	0.756153872	0.384118908	0.064060057	0.940323292	0.47819539	0.816745394	0.114512848	0.179750681	0.274677283	0.065237833	0.160164435	0.094926602
0|P01624	11.5371462	5.73E-07	2.77E-05	0.817038341	0.000141406	0.000700639	0.924479818	0.00330686	-0.590995636	-0.106836587	-0.51583845	0.484159049	0.075157186	-0.409001862
TGFB1|P01137	1.8260779	0.144875929	0.421454936	0.856606088	0.126823199	0.860306304	0.939701493	0.479459725	-0.076010592	-0.037910608	-0.103353744	0.038099984	-0.027343152	-0.065443136
VEGFC|P49767	3.07677513	0.028873256	0.910000339	0.990903974	0.132322055	0.767382414	0.025222537	0.227332544	-0.033918179	0.014710682	0.105698851	0.048628861	0.13961703	0.090988169
PSME1|Q06323	0.53703579	0.657970681	0.999999797	0.768858502	0.833980032	0.78246081	0.844175251	0.998939215	0.00114202	-0.125944733	-0.108083259	-0.127086753	-0.109225279	0.017861474
HAPLN4|Q86UW8	0.24941467	0.861631201	0.996605948	0.841618303	0.965593721	0.934266684	0.995415147	0.979202735	-0.015756247	-0.05940851	-0.032435688	-0.043652263	-0.016679441	0.026972822
ACYP1|P07311	6.39352484	0.000381629	0.026174052	0.170175809	0.000168423	0.834953944	0.568483384	0.122180298	-0.123344849	-0.087296069	-0.177540852	0.03604878	-0.054196003	-0.090244783
IGKV3D-15|A0A087WSY6	9.02137569	1.32E-05	0.000308962	0.840577512	0.000726352	0.004820143	0.97298146	0.011187987	-0.709869926	-0.138422441	-0.63860361	0.571447484	0.071266316	-0.500181169
HLA-DRB1|Q29974	1.38444501	0.248953979	0.935836134	0.697461354	0.695187518	0.341799052	0.332830631	0.999995969	0.080538418	-0.145153728	-0.142288379	-0.225692146	-0.222826797	0.002865349
TOLLIP|Q9H0E2	5.19865594	0.001805199	0.008474883	0.98254374	0.870373538	0.002096096	0.051742961	0.650420597	0.141715442	-0.015935172	0.032087419	-0.157650614	-0.109628022	0.048022591
VWC2|Q2TAL6	1.13422942	0.33654706	0.679031812	0.543348668	0.284268924	0.997864309	0.931764685	0.973763187	0.061966136	0.071882766	0.094008278	0.009916629	0.032042142	0.022125513
CD46|P15529	6.98902941	0.000176786	0.000509748	0.02127517	0.000644895	0.627263206	0.993329435	0.755154268	0.132550006	0.093463313	0.124057687	-0.039086694	-0.00849232	0.030594374
IGKV1-8|A0A0C4DH67	1.2486026	0.293789985	0.654251651	0.999999952	0.437102705	0.644755609	0.990924509	0.423175232	-0.136494087	-0.000591381	-0.169969569	0.135902706	-0.033475482	-0.169378188
TPM2|P07951	3.83529753	0.010730614	0.124719654	0.068366536	0.007306615	0.997321736	0.793991438	0.880197956	-0.146529564	-0.159337381	-0.205299976	-0.012807816	-0.058770412	-0.045962595
ADAMTS2|O95450	4.88331776	0.00272501	0.389511501	0.925271272	0.002926054	0.751618851	0.258410973	0.018970714	0.083541139	0.031839129	0.176815063	-0.05170201	0.093273924	0.144975934
CD99|P14209	0.10810903	0.955276163	0.978758466	0.969357591	0.999895925	0.999972095	0.985593988	0.977892638	0.029803066	0.032954408	0.004719459	0.003151342	-0.025083607	-0.028234949
CHST3|Q7LGC8	2.26442196	0.082693911	0.630629475	0.865475089	0.464995487	0.193377335	0.995889545	0.104061535	-0.053030189	0.034023189	-0.06270909	0.087053378	-0.009678901	-0.096732279
TPM1|P09493	5.89719974	0.000855784	0.805586128	0.042054716	0.001235613	0.301942532	0.025421991	0.704257638	-0.081308402	-0.23602279	-0.325597149	-0.154714389	-0.244288747	-0.089574358
ADAMDEC1|O15204	3.38669017	0.019281093	0.103575583	0.870967968	0.945531286	0.01257803	0.260260968	0.527605323	-0.180312438	0.058401456	-0.041379955	0.238713894	0.138932483	-0.099781411
OSCAR|Q8IYS5	1.90820728	0.129768526	0.700811606	0.563354779	0.99989565	0.083534712	0.634017493	0.571924582	0.06337448	-0.074137088	-0.003683641	-0.137511568	-0.067058121	0.070453447
CD33|P20138	7.53789913	9.42E-05	0.002531107	0.412419285	0.000210045	0.156925589	0.969777405	0.038643699	-0.369656831	-0.156688694	-0.41331139	0.212968136	-0.04365456	-0.256622696
OLFML1|Q6UWY5	2.87692517	0.037433693	0.290564317	0.999867909	0.095378458	0.312107411	0.967762249	0.103133404	-0.099712507	-0.003921938	-0.124590889	0.09579057	-0.024878382	-0.120668951
NBL1|P41271	5.77454423	0.000852351	0.740413724	0.000950142	0.039549374	0.031412702	0.384938871	0.580298999	0.038154829	0.140483315	0.095753547	0.102328486	0.057598718	-0.044729768
SLC9A3R1|O14745	1.23725368	0.297993381	0.740789528	0.282844061	0.41154045	0.8844664	0.969323688	0.988725533	-0.063801972	-0.109482181	-0.090875376	-0.045680209	-0.027073404	0.018606805

			ANOVA p -values with Tukey Adjustment						Difference (AD - CT)					
Gene ID | Unirprot ID	F-Value	Pr(>F)	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA
UNC5D|Q6UXZ4	4.46261564	0.004723354	0.028640884	0.123668883	0.003736518	0.912735019	0.957531919	0.618463096	0.170882118	0.131365394	0.20061129	-0.039516724	0.029729172	0.069245896
HDHD2|Q9H0R4	10.3784168	2.40E-06	0.261564282	0.012320287	0.061725986	1.16E-05	0.000114994	0.910632584	0.086405649	-0.141727441	-0.112490574	-0.22813309	-0.198896223	0.029236867
HEBP2|Q9Y5Z4	7.94595374	5.42E-05	0.038095956	0.37234329	0.173289678	0.000142549	0.866913598	0.00127682	0.156558124	-0.091068103	0.113337134	-0.247626227	-0.04322099	0.204405238
NT5E|P21589	1.65555834	0.181326974	0.225097882	0.99966996	0.990751775	0.258250105	0.287089391	0.997308661	-0.206518724	-0.010215048	-0.029241384	0.196303675	0.177277339	-0.019026336
SLC1A2|P43004	3.38766153	0.019256674	0.10068304	0.957502378	0.992847181	0.025547604	0.041425332	0.994544806	0.112678714	-0.02408711	-0.012699811	-0.136765824	-0.125378525	0.011387299
S100A8|P05109	0.02690248	0.994025736	0.99754881	0.997917148	0.99250193	0.999998724	0.999838798	0.999693079	0.045577878	0.041984447	0.063215607	-0.00359343	0.017637729	0.02123116
SEMA6C|Q9H3T2	4.23542082	0.006358094	0.873547727	0.999760848	0.017646638	0.827827331	0.14263675	0.011487821	0.038753818	-0.004347736	0.144472321	-0.043101554	0.105718503	0.148820057
PLXND1|Q9Y4D7	1.20810116	0.308394015	0.676606231	0.888319132	0.973821485	0.252357905	0.880003556	0.637351084	-0.049167179	0.030719967	-0.017804908	0.079887147	0.031362271	-0.048524876
AOC3|Q16853	0.03022065	0.992904478	0.99998603	0.998039394	0.999538631	0.996843444	0.999867453	0.991316551	0.003719952	-0.01879582	0.011385903	-0.022515772	0.007665952	0.030181724
GPC5|P78333	2.33231246	0.07588335	0.250277189	0.662671403	0.060179806	0.875635104	0.951267919	0.53263558	-0.13475401	-0.080489647	-0.172012312	0.054264363	-0.037258302	-0.091522665
BTN2A1|Q7KYR7	1.42510566	0.236880825	0.91819038	0.997791884	0.531347181	0.838388199	0.190933875	0.637878942	-0.03076577	0.008565959	0.061561567	0.03933173	0.092327337	0.052995607
TBCA|O75347	13.2700604	6.95E-08	0.792811038	2.43E-05	6.13E-06	0.001317176	0.000463095	0.99725104	-0.03398337	-0.170170666	-0.176977683	-0.136187296	-0.142994313	-0.006807017
SNAP25|P60880	2.57461408	0.057182129	0.999090309	0.075976956	0.585659214	0.09914727	0.668545844	0.56091273	-0.010197496	-0.185308082	-0.090794484	-0.175110586	-0.080596988	0.094513598
TMED4|Q7Z7H5	2.15931997	0.094341133	0.328353962	0.899154755	0.997460442	0.078830468	0.209767638	0.952416886	0.063991037	-0.025480492	-0.006903934	-0.089471529	-0.070894971	0.018576558
COL5A2|P05997	1.84215879	0.142382319	0.595558508	0.716405073	0.094695344	0.996153404	0.733709486	0.574696654	0.070946277	0.058655073	0.126600086	-0.012291204	0.055653809	0.067945012
EMC10|Q5UCC4	7.70714103	7.03E-05	0.007003244	0.071836478	3.14E-05	0.804543297	0.60568487	0.121434988	0.155093293	0.11301907	0.211474872	-0.042074223	0.056381579	0.098455802
SLC12A5|Q9H2X9	2.07275	0.105631641	0.626064084	0.236314526	0.08782143	0.924200568	0.707427698	0.967974351	0.069672346	0.105070581	0.129571015	0.035398235	0.059898669	0.024500434
PEA15|Q15121	54.6510504	2.42E-25	0.753523773	1.32E-13	2.09E-13	1.23E-13	1.23E-13	0.923618454	0.039503994	-0.33971316	-0.316448539	-0.379217155	-0.355952533	0.023264622
SFRP1|Q8N474	5.12637608	0.0019838	0.982359598	0.046932495	0.007821166	0.124822414	0.028069479	0.94234788	-0.020784055	-0.142199104	-0.171672543	-0.121415049	-0.150888489	-0.029473439
ADM|P35318	1.73799346	0.160745263	0.360015043	0.464971068	0.127367093	0.99610193	0.96557855	0.889652209	0.060347997	0.052276039	0.077010549	-0.008071958	0.016662553	0.02473451
BDNF|P23560	12.5741297	1.61E-07	0.088937839	1.72E-05	5.51E-07	0.085731302	0.014155029	0.921354974	0.173488138	0.345440758	0.388933094	0.17195262	0.215444956	0.043492336
HLA-DRA|P01903	2.77643365	0.042642632	0.097540596	0.987250005	0.180934538	0.182271716	0.977557131	0.31722922	0.196028459	0.027382246	0.163108709	-0.168646213	-0.032919751	0.135726462
GPC6|Q9Y625	0.75499986	0.520860119	0.632749565	0.999263687	0.999955779	0.540498653	0.636027352	0.99782815	-0.071762859	0.007431805	-0.002847491	0.079194665	0.068915368	-0.010279296
PCSK5|Q92824	0.61342384	0.607675697	0.99762328	0.904741302	0.750806444	0.830967598	0.651596851	0.990830911	-0.014387275	0.050503495	0.071912788	0.06489077	0.086300063	0.021409293
NUDT5|Q9UKK9	0.81306963	0.488112209	0.666837683	0.515023528	0.56683743	0.996896813	0.999664121	0.999434231	-0.077073765	-0.09081873	-0.083449876	-0.013744965	-0.006376111	0.007368854
STX7|O15400	0.16468848	0.92004611	0.919312256	0.996845058	0.959717274	0.970691438	0.998150504	0.991512666	-0.024973567	-0.007880822	-0.018460355	0.017092745	0.006513212	-0.010579534
IGKV4-1|P06312	8.58855131	2.28E-05	0.000807514	0.999997631	0.008733353	0.000688799	0.815530895	0.007789969	-0.52378078	-0.002455256	-0.409744065	0.521325524	0.114036715	-0.407288809
DMKN|Q6E0U4	5.36705051	0.001449181	0.006484369	0.986647985	0.050454012	0.015649423	0.823484089	0.106024068	0.25748181	0.025731642	0.192465387	-0.231750167	-0.065016423	0.166733744
WFDC1|Q9HC57	1.95093935	0.12294411	0.292132122	0.999996383	0.972022568	0.268676262	0.109249176	0.974664344	-0.157894853	0.001874072	0.037087637	0.159768924	0.19498249	0.035213566
HS6ST2|Q96MM7	1.21520103	0.306648042	0.653783477	0.393175513	0.307278861	0.980559941	0.963468812	0.999827682	0.099188935	0.132121948	0.138340611	0.032933013	0.039151676	0.006218663
EFNB3|Q15768	4.21098533	0.006564632	0.009588446	0.429886152	0.022545234	0.315780811	0.970664712	0.528623512	0.198913629	0.092580453	0.172085909	-0.106333175	-0.026827719	0.079505456
IGLV9-49|A0A0B4J1Y8	0.09591869	0.962212264	0.968331309	0.985220157	0.964734895	0.999419684	0.99999992	0.999418344	-0.110600383	-0.082584077	-0.109190235	0.028016306	0.001410148	-0.026606158
CSRP1|P21291	2.93657925	0.034644469	0.70410578	0.636918063	0.381374488	0.110115355	0.037806694	0.979350418	0.054112641	-0.057954858	-0.076408263	-0.112067499	-0.130520904	-0.018453404
BMP7|P18075	2.91514458	0.037315871	0.677927256	0.82693046	0.264932333	0.208593193	0.927507227	0.035688859	-0.101952227	0.075202025	-0.155843096	0.177154251	-0.053890869	-0.23104512
0|P01814	0.43800798	0.726071661	0.919790972	0.999155005	0.85702769	0.861984723	0.999329251	0.776550179	0.125102536	-0.025430075	0.148249436	-0.150532611	0.0231469	0.173679511
CXADR|P78310	0.91971431	0.434112383	0.644545366	0.485118071	0.483749875	0.995134153	0.997506586	0.999925512	0.073168423	0.088099804	0.084604258	0.014931382	0.011435835	-0.003495546
MARCKSL1|P49006	3.22376438	0.024901313	0.703849151	0.405153071	0.381188148	0.055013721	0.045269102	0.999994749	0.074822681	-0.104602618	-0.103020026	-0.179425299	-0.177842707	0.001582592
IGHV2-26|A0A0B4J1V2	0.69522519	0.556052071	0.999608901	0.63322349	0.964579316	0.57581863	0.939248703	0.87333458	-0.026631835	0.300017098	0.116792854	0.326648933	0.143424689	-0.183224244
RAN|P62826	1.92940224	0.127715561	0.534872086	0.797467	0.091758201	0.960252511	0.851657705	0.492939815	-0.239568218	-0.152196778	-0.377473681	0.08737144	-0.137905463	-0.225276903
CBLN3|Q6UW01	1.4638726	0.225879056	0.232925947	0.994704913	0.746695882	0.335744963	0.761925261	0.869905639	-0.144183024	-0.018250409	-0.072609778	0.125932616	0.071573246	-0.054359369
MAT2A|P31153	18.57445	1.41E-10	0.969264006	2.99E-05	1.31E-06	4.90E-06	1.81E-07	0.937277905	0.022338253	-0.226257564	-0.253179007	-0.248595817	-0.275517261	-0.026921444
CARKD|Q8IW45	17.8974039	5.55E-10	0.993383764	0.003371899	1.26E-08	0.011975187	1.71E-07	0.029908005	-0.02486366	-0.313552078	-0.55468307	-0.288688418	-0.529819409	-0.241130991
CHST14|Q8NCH0	0.86314692	0.461420524	0.655516886	0.982374618	0.997883436	0.411276445	0.728682437	0.938820192	-0.06907614	0.02185392	-0.010280882	0.09093006	0.058795258	-0.032134802
C4BPB|P20851	0.15987683	0.923176753	0.956326549	0.99963566	0.999184616	0.975153696	0.911878474	0.995261428	-0.093510786	-0.018268246	0.023654182	0.075242539	0.117164968	0.041922429
SV2A|Q7L0J3	0.58101518	0.628294289	0.831690232	0.900064409	0.561149091	0.998339312	0.973804726	0.929903354	0.052613312	0.04244234	0.077924317	-0.010170971	0.025311006	0.035481977
HSPE1|P61604	5.63762561	0.001018608	0.858164679	0.131437299	0.00103129	0.529575618	0.01856083	0.373640865	-0.05370478	-0.144171582	-0.246427244	-0.090466802	-0.192722464	-0.102255663
TMEM5|Q9Y2B1	1.74489203	0.162619669	0.72547465	0.680812596	0.916748114	0.14024037	0.320064668	0.959195704	-0.06385433	0.066425074	0.037816253	0.130279404	0.101670583	-0.028608821

			ANOVA p -values with Tukey Adjustment						Difference (AD - CT)					
Gene ID | Unirprot ID	F-Value	Pr(>F)	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA
MANEAL|Q5VSG8	2.5148079	0.059795883	0.78576838	0.247774075	0.049470495	0.809740619	0.385403439	0.896254747	0.053552497	0.103747649	0.14128283	0.050195152	0.087730333	0.037535181
GPR158|Q5T848	4.25105961	0.006229333	0.97755137	0.111463381	0.013669417	0.266319277	0.049493403	0.874625733	0.021160941	0.114986813	0.15186015	0.093825873	0.130699209	0.036873337
ESAM|Q96AP7	5.55897592	0.001128471	0.113298291	0.002735435	0.002413134	0.614845226	0.62698676	0.999958287	0.096092101	0.147351866	0.145408931	0.051259765	0.04931683	-0.001942935
CD302|Q8IX05	4.2028287	0.006635057	0.99681636	0.866483073	0.07777767	0.945633372	0.048908033	0.007150241	-0.009677403	-0.035034351	0.106898655	-0.025356948	0.116576058	0.141933007
REG1A|P05451	0.23401285	0.872592514	0.956367919	0.999906773	0.899834728	0.968370059	0.998720468	0.919513254	-0.062330265	-0.00756314	-0.080285277	0.054767126	-0.017955012	-0.072722137
SHISA7|A6NL88	10.9691757	1.15E-06	0.000753457	0.000284678	8.43E-07	0.998974186	0.53314514	0.602490707	0.216131434	0.223870889	0.287961152	0.007739456	0.071829718	0.064090263
PPBP|P02775	1.23253319	0.299495038	0.997248919	0.436990423	0.999953222	0.344942636	0.99422914	0.433803274	-0.021854881	0.161197207	0.00526129	0.183052088	0.027116171	-0.155935917
AP2A2|O94973	3.59267619	0.014836949	0.496395037	0.17566707	0.008187955	0.923740325	0.285725976	0.654854271	-0.088131947	-0.126638932	-0.195576334	-0.038506985	-0.107444387	-0.068937402
GRID2|O43424	1.31457216	0.271038308	0.463893734	0.999894846	0.50649141	0.490263733	0.998954896	0.534805492	-0.090107049	-0.00398459	-0.081616026	0.086122459	0.008491022	-0.077631437
PVRL2|Q92692	1.25754685	0.29037924	0.619140495	0.827456251	0.23041765	0.980313418	0.926061241	0.723502393	0.041502065	0.028483613	0.061862641	-0.013018452	0.020360576	0.033379028
NRN1L|Q496H8	1.76391622	0.156086106	0.99664626	0.34396127	0.989420871	0.254672919	0.999767427	0.175079752	-0.0151194	0.116276991	-0.021081022	0.131396391	-0.005961622	-0.137358013
CDH18|Q13634	3.8572659	0.010528761	0.23288193	0.056834878	0.007347791	0.943215149	0.623550864	0.913204348	0.122744905	0.158695159	0.198145385	0.035950255	0.07540048	0.039450225
VIP|P01282	0.23213225	0.873804282	0.847511884	0.974701697	0.991724636	0.979276617	0.945389321	0.998844759	-0.084830427	-0.044310531	-0.029360764	0.040519896	0.055469663	0.014949767
LOXL1|Q08397	1.26508051	0.288219979	0.840682539	0.999645755	0.401450804	0.785968746	0.913281507	0.33232054	-0.044802288	0.005172511	-0.078834576	0.0499748	-0.034032288	-0.084007088
SCN4B|Q8IWT1	2.66298719	0.049386	0.088597961	0.999318432	0.968720931	0.060237865	0.190445442	0.934645842	-0.127569394	0.006515581	-0.023343215	0.134084975	0.10422618	-0.029858796
NXPH4|O95158	1.29731934	0.276761756	0.589535334	0.392728387	0.998793192	0.992205563	0.652125164	0.444107709	-0.075154365	-0.091678012	-0.008504483	-0.016523647	0.066649883	0.08317353
PRSS1|P07477	4.77906973	0.003122753	0.008100048	0.999970601	0.315088064	0.007908456	0.354460002	0.322994414	-0.192231989	-0.002516892	-0.097637376	0.189715096	0.094594613	-0.095120483
VSNL1|P62760	4.80860676	0.003179329	0.868485662	0.142707824	0.003039434	0.556516084	0.046181769	0.545005655	-0.047897587	-0.1291776	-0.206284127	-0.081280013	-0.15838654	-0.077106527
IGHV3-64|A0A075B6Q5	23.6979484	5.03E-13	2.44E-08	0.985979455	6.36E-08	8.62E-08	0.959185038	2.31E-07	-0.929040451	-0.050333479	-0.856781065	0.878706972	0.072259386	-0.806447586
FLRT2|O43155	0.51493733	0.672611872	0.924379807	0.999155007	0.797593704	0.872080725	0.995317647	0.710998586	-0.033900097	0.006934307	-0.046273106	0.040834404	-0.012373009	-0.053207413
CRELD2|Q6UXH1	0.97301736	0.40683309	0.724788874	0.953248587	0.94689101	0.948428679	0.369101186	0.688322346	-0.080481585	-0.039276101	0.040296895	0.041205484	0.12077848	0.079572996
NGFR|P08138	16.2336323	2.08E-09	1.02E-05	0.999989882	1.83E-05	6.28E-06	0.980894995	1.09E-05	0.370755241	-0.002218282	0.343132886	-0.372973523	-0.027622355	0.345351168
CKMT1A|P12532	10.5715735	3.10E-06	0.623383941	0.000179388	4.65E-05	0.012219699	0.004197634	0.985064641	-0.106630208	-0.371005158	-0.399894656	-0.26437495	-0.293264448	-0.028889498
C1GALT1C1|Q96EU7	4.75184226	0.003235896	0.999966542	0.087409707	0.017599071	0.103642162	0.022451832	0.944293728	0.001763941	0.089667631	0.109973172	0.08790369	0.108209232	0.020305542
CSF2RA|P15509	8.81064966	1.72E-05	0.000696923	0.999957041	0.006489544	0.000664157	0.840877559	0.006367795	0.284348161	0.003468005	0.226604782	-0.280880157	-0.05774338	0.223136777
KCTD12|Q96CX2	1.10762629	0.347328587	0.838152475	0.978539801	0.795087087	0.601746863	0.289286113	0.954331785	-0.038484329	0.017879905	0.040272304	0.056364233	0.078756633	0.0223924
PKDCC|Q504Y2	2.04079549	0.109706171	0.94170383	0.759059377	0.526405224	0.41118166	0.875121495	0.079239158	-0.036738667	0.061986486	-0.083708183	0.098725153	-0.046969516	-0.145694669
PDGFRL|Q15198	5.89619674	0.000746157	0.013602087	0.710007103	0.001785694	0.179109313	0.976347724	0.050378162	-0.231585021	-0.078336074	-0.261715621	0.153248947	-0.0301306	-0.183379547
STX12|Q86Y82	1.79464598	0.149722376	0.147556559	0.937101211	0.986841176	0.388629819	0.239962411	0.99347752	0.098241547	0.026167493	0.014753022	-0.072074054	-0.083488525	-0.011414471
DLST|P36957	1.59271172	0.19294636	0.992415113	0.977542842	0.327361524	0.900901434	0.195810942	0.552381313	0.01263636	-0.017930233	-0.073812022	-0.030566593	-0.086448382	-0.055881789
OSMR|Q99650	4.40847085	0.005070018	0.074291384	0.996915402	0.026548373	0.109144236	0.99358658	0.041672676	0.092946463	0.007639452	0.102623906	-0.085307011	0.009677443	0.094984454
CHST1|O43916	2.59669984	0.053801657	0.413094172	0.398255954	0.029716159	0.999998178	0.660526431	0.627490872	0.073248447	0.072447273	0.125626303	-0.000801175	0.052377856	0.053179031
0|P01704	3.57057414	0.016312536	0.525362609	0.986416635	0.056774614	0.345849311	0.770787499	0.02406265	-0.336856194	0.078201985	-0.570364753	0.415058178	-0.233508559	-0.648566738
GRP|P07492	1.60276556	0.19113329	0.776615437	0.140752367	0.84527174	0.65142231	0.997741424	0.486764095	0.096473853	0.211302107	0.078583192	0.114828253	-0.017890661	-0.132718914
TMED7|Q9Y3B3	1.09457616	0.352728327	0.979256172	0.757656117	0.32762144	0.939595995	0.584389282	0.896652675	0.012611384	0.030733528	0.051711437	0.018122144	0.039100053	0.020977909
PTPRC|P08575	0.3823906	0.765811231	0.998617776	0.988970003	0.896499067	0.965046284	0.951843623	0.724273891	-0.006904658	0.013554187	-0.029314929	0.020458845	-0.02241027	-0.042869115
PHPT1|Q9NRX4	7.58793662	8.53E-05	0.278949493	0.01315656	4.43E-05	0.635192632	0.044617603	0.462392234	-0.126622426	-0.209947918	-0.306357809	-0.083325492	-0.179735382	-0.09640989
CLIC6|Q96NY7	2.1253455	0.099316376	0.167720112	0.890018831	0.167277518	0.513672947	0.999265491	0.540205178	-0.320681111	-0.10815679	-0.30175459	0.212524321	0.018926521	-0.1935978
TPM4|P67936	1.97729465	0.121341237	0.903344311	0.304087007	0.12211586	0.769703374	0.507686898	0.974000666	-0.077281391	-0.186426188	-0.230461592	-0.109144797	-0.153180201	-0.044035404
0|P01714	4.883991	0.002722614	0.003834841	0.92940033	0.130676623	0.021352738	0.485025041	0.385929999	-0.550005173	-0.094309146	-0.33132672	0.455696027	0.218678453	-0.237017574
IL18BP|O95998	1.63511453	0.182769482	0.176529124	0.358553814	0.350579015	0.969043011	0.961914709	0.99999463	0.091174748	0.071273704	0.070247201	-0.019901044	-0.020927547	-0.001026503
PALM|O75781	7.24006004	0.00012796	0.000104627	0.058875765	0.002649795	0.201037757	0.712697112	0.756898556	0.343876052	0.192041772	0.264046992	-0.15183428	-0.07982906	0.07200522
NA|A0A0J9YX35	0.2971801	0.827407068	0.933119461	0.999061554	0.940461092	0.880060611	0.999939941	0.887010222	-0.072710962	0.016361536	-0.06625072	0.089072498	0.006460242	-0.082612256
PCSK6|P29122	2.46830376	0.063487016	0.669109244	0.781867517	0.041531814	0.996230913	0.468422033	0.312145025	0.061546859	0.049789478	0.137428252	-0.011757381	0.075881393	0.087638773
PTPRR|Q15256	1.82408277	0.144284276	0.988103271	0.576088297	0.154809161	0.785570379	0.304598958	0.850171707	0.015054262	0.057735996	0.092743694	0.042681734	0.077689432	0.035007698
CAP2|P40123	7.45745442	0.00011376	0.006298027	0.695286207	0.986072709	0.000131801	0.001538799	0.864783888	0.210636852	-0.067794313	-0.02076151	-0.278431165	-0.231398362	0.047032804
S100A11|P31949	3.01880845	0.031133923	0.468845085	0.678283779	0.018024746	0.982835111	0.490455895	0.254410221	-0.100959597	-0.07571606	-0.195783621	0.025243536	-0.094824024	-0.12006756

			ANOVA p -values with Tukey Adjustment						Difference (AD - CT)					
Gene ID | Unirprot ID	F-Value	Pr(>F)	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA
KLK7|P49862	20.9445422	9.99E-12	8.45E-08	0.973832396	4.70E-05	5.67E-09	0.36459212	4.55E-06	-0.541301947	0.037866326	-0.398291752	0.579168274	0.143010195	-0.436158078
LAP3|P28838	0.57505665	0.632726257	0.68915364	0.83268255	0.99846587	0.994191911	0.767621862	0.894908965	0.097654215	0.075577807	0.014391267	-0.022076408	-0.083262948	-0.06118654
SUGT1|Q9Y2Z0	1.62754643	0.186305912	0.9712426	0.448172964	0.215264094	0.723017679	0.4452173	0.974421503	-0.03666738	-0.120898442	-0.153057246	-0.084231062	-0.116389866	-0.032158803
PSMB1|P20618	6.41832459	0.000378879	0.901087232	0.000601193	0.055502237	0.008259752	0.277860039	0.401645882	-0.040018103	-0.223893004	-0.139805412	-0.183874901	-0.099787309	0.084087592
ENOPH1|Q9UHY7	10.4302104	4.73E-06	0.714476323	0.041119595	0.00131193	0.001758517	2.17E-05	0.746741931	0.099925841	-0.248361349	-0.335904536	-0.348287189	-0.435830377	-0.087543188
FABP4|P15090	3.73074827	0.012424558	0.877068161	0.175027074	0.809379331	0.033202509	0.999714103	0.01528352	-0.108196151	0.286823689	-0.121128828	0.39501984	-0.012932677	-0.407952517
TNFRSF1A|P19438	1.49382828	0.217706593	0.341849454	0.923145406	0.275702454	0.703771235	0.999970972	0.640346404	0.074488877	0.027209036	0.076341422	-0.047279841	0.001852544	0.049132385
SCPEP1|Q9HB40	3.12905307	0.0271439	0.041913195	0.945579163	0.167653189	0.143924788	0.889474587	0.429500463	-0.244298669	-0.049887033	-0.180981038	0.194411636	0.063317631	-0.131094005
DHH|O43323	1.63961389	0.182299849	0.390165383	0.978563132	0.763846524	0.195964642	0.895702335	0.499738495	-0.162866145	0.040390471	-0.094335653	0.203256616	0.068530492	-0.134726124
S100A4|P26447	1.88328621	0.134189142	0.430923508	0.99860361	0.354646806	0.334981299	0.999982415	0.262139386	-0.19007135	0.019061679	-0.194500839	0.209133029	-0.004429489	-0.213562518
0|P01593	3.15932746	0.025931939	0.345097037	0.963700327	0.171913483	0.137146703	0.990633606	0.050409468	-0.17305007	0.048411762	-0.203007147	0.221461832	-0.029957078	-0.25141891
FHL1|Q13642	1.68938084	0.172224298	0.998098051	0.690513946	0.288566113	0.595739806	0.227388746	0.902257167	0.020163129	-0.121413849	-0.195074607	-0.141576978	-0.215237735	-0.073660757
CDH3|P22223	2.46173198	0.064026347	0.144293276	0.999280176	0.292035995	0.17399597	0.963943358	0.343916886	-0.16596441	-0.009518659	-0.130319701	0.156445752	0.035644709	-0.120801043
NME1|P15531	12.4676758	3.74E-07	0.994089959	0.001197995	1.46E-05	0.003261749	5.26E-05	0.720309903	-0.022399438	-0.328914984	-0.416551949	-0.306515545	-0.394152511	-0.087636965
VIT|Q6UXI7	7.12646419	0.000148101	0.019508905	0.999961393	0.002973912	0.019569714	0.97287255	0.002856469	-0.194938733	-0.003069596	-0.222566155	0.191869137	-0.027627422	-0.219496559
RAB4A|P20338	0.38141115	0.766529589	0.795242355	0.78644213	0.92871908	0.999999343	0.984470028	0.984570886	-0.062647795	-0.061828737	-0.039353399	0.000819058	0.023294395	0.022475338
XYLT2|Q9H1B5	2.28522339	0.080315039	0.083468477	0.269173484	0.158177487	0.922885128	0.976970535	0.995030043	-0.145305541	-0.107627013	-0.121374186	0.037678528	0.023931356	-0.013747172
CA11|O75493	3.11078976	0.027623257	0.963950686	0.082208847	0.083306238	0.240874579	0.248818562	0.999909074	0.031932721	0.15559272	0.151644251	0.123659999	0.11971153	-0.003948469
C16orf91|Q4G0I0	3.82921696	0.010816269	0.567905465	0.126644721	0.006812696	0.824762083	0.234999663	0.725394627	0.09467005	0.156710671	0.22789049	0.062040621	0.13322044	0.07117982
TAC1|P20366	5.99857635	0.000636997	0.999713478	0.183462552	0.003274521	0.159270872	0.002726249	0.468942606	-0.005616055	0.119193306	0.20134602	0.12480936	0.206962075	0.082152715
MCFD2|Q8NI22	1.09181128	0.353881809	0.316426294	0.973848368	0.95282129	0.54831157	0.584632103	0.999735115	-0.063113672	-0.01523751	-0.018334735	0.047876162	0.044778937	-0.003097225
NHLRC3|Q5JS37	1.78534684	0.152068638	0.77311296	0.545276322	0.967149144	0.11000584	0.471997662	0.795338636	-0.054626305	0.073847127	0.024839148	0.128473431	0.079465453	-0.049007978
SHISA5|Q8N114	10.5228234	2.01E-06	6.12E-05	0.999048267	0.005791985	8.08E-05	0.485660433	0.007665169	0.160410364	0.004769435	0.111897942	-0.155640928	-0.048512421	0.107128507
TAC3|Q9UHF0	6.21764802	0.00047934	0.022365907	0.003849307	0.000553152	0.96424931	0.784589163	0.966771453	0.280650221	0.326220595	0.368362148	0.045570374	0.087711927	0.042141553
DRAXIN|Q8NBI3	9.67497291	6.12E-06	0.002778167	0.642715421	0.065805547	2.30E-05	0.589253162	0.001289274	0.285868675	-0.092005971	0.188795244	-0.377874646	-0.097073431	0.280801215
VAPA|Q9P0L0	2.99415888	0.032147578	0.322838036	0.109190721	0.024107607	0.957097137	0.718923872	0.946874807	-0.068488607	-0.088555431	-0.109112015	-0.020066824	-0.040623408	-0.020556584
C4orf48|Q5BLP8	12.0676121	2.99E-07	0.000131984	0.000125639	3.30E-07	0.999555422	0.703778123	0.61312122	0.327555942	0.319592245	0.405653423	-0.007963697	0.078097481	0.086061178
CALCA|P06881	2.92237625	0.035289309	0.090542306	0.999714636	0.394615816	0.066589638	0.812393366	0.326525382	-0.219532867	0.008414177	-0.139941609	0.227947044	0.079591259	-0.148355785
ITGB4|P16144	2.50264525	0.061928053	0.963846742	0.167567556	0.837149598	0.059902094	0.557855053	0.591466595	0.037635967	-0.156373791	-0.063512812	-0.194009758	-0.101148779	0.092860979
GAS1|P54826	0.34992014	0.789266281	0.836081283	0.977908065	0.999955242	0.97025588	0.800573818	0.967090865	-0.054714599	-0.026049016	0.003207028	0.028665583	0.057921626	0.029256043
TMEM130|Q8N3G9	3.42266645	0.019127592	0.994880319	0.080523516	0.950153568	0.139370539	0.861243635	0.016844459	0.018906917	0.185290622	-0.04069447	0.166383705	-0.059601387	-0.225985093
PPP1R7|Q15435	10.0093009	8.04E-06	0.843202409	0.009375621	0.001826144	0.000848913	0.000137771	0.955749995	0.081933041	-0.30709319	-0.355644433	-0.389026231	-0.437577474	-0.048551242
TWF2|Q6IBS0	10.3325381	3.24E-06	0.483621593	0.006878064	0.01624924	4.44E-05	0.000128177	0.988120049	0.067975659	-0.148962799	-0.134703332	-0.216938459	-0.202678991	0.014259467
SH3BGRL3|Q9H299	12.9263171	1.05E-07	0.883991216	0.183248921	1.20E-05	0.033536112	4.43E-07	0.022573794	0.027609185	-0.074210078	-0.175811861	-0.101819263	-0.203421046	-0.101601783
GP1BA|P07359	0.40317064	0.750968151	0.991452474	0.881622122	0.999801243	0.730021637	0.996823374	0.844968268	-0.03455412	0.088544394	-0.009840568	0.123098514	0.024713552	-0.098384962
RFNG|Q9Y644	1.46809469	0.225928816	0.34628322	0.679718456	0.213659597	0.938048424	0.997120308	0.847944908	-0.101005145	-0.066320944	-0.112730631	0.034684202	-0.011725486	-0.046409687
HLA-DPA1|P20036	0.79372898	0.498799388	0.977887573	0.737986902	0.92845486	0.490555366	0.736934913	0.971361858	0.04704257	-0.115997175	-0.067894641	-0.163039744	-0.11493721	0.048102534
TM9SF3|Q9HD45	2.31322961	0.077483638	0.153782259	0.713303731	0.09164788	0.693803561	0.999311997	0.576427339	0.11778835	0.057665413	0.124465362	-0.060122936	0.006677012	0.066799948
CBLN4|Q9NTU7	12.4126578	1.96E-07	0.000207785	2.41E-05	3.34E-07	0.979727952	0.633408865	0.847284875	0.298367345	0.325444106	0.379073671	0.027076761	0.080706326	0.053629565
UBL3|O95164	6.81340139	0.000229275	0.065643471	0.000288877	0.001686866	0.392008574	0.711080672	0.942358172	0.135992472	0.221066199	0.19219491	0.085073727	0.056202438	-0.028871289
ITM2A|O43736	2.90699432	0.036001069	0.103092281	0.984698453	0.656218944	0.0397255	0.600033554	0.413691135	-0.118494331	0.017808706	-0.056681423	0.136303037	0.061812908	-0.074490129
IGHV4-28|A0A0C4DH34	13.3737685	6.14E-08	0.000484421	0.994190202	8.52E-06	0.000988594	0.879958012	1.90E-05	-0.561601085	-0.034597383	-0.661317506	0.527003702	-0.099716421	-0.626720123
SERPINB9|P50453	2.19829114	0.090046147	0.35331931	0.065498857	0.278525169	0.857411611	0.999808108	0.879818526	-0.132388846	-0.194967085	-0.138689677	-0.062578239	-0.006300832	0.056277408
METRN|Q9UJH8	1.49365809	0.217752231	0.99504884	0.735632908	0.228005093	0.869262588	0.361955371	0.81765268	0.011773291	0.048626834	0.088541188	0.036853543	0.076767897	0.039914354
IL1RAPL1|Q9NZN1	6.56606492	0.000314883	0.006305918	0.315225485	0.000387201	0.357250465	0.944238334	0.096330884	0.220018165	0.111206425	0.255914826	-0.10881174	0.035896661	0.144708401
SARAF|Q96BY9	3.13064647	0.028448664	0.354847629	0.814082573	0.020649127	0.862207518	0.615504769	0.177407803	0.121190366	0.064220523	0.207314136	-0.056969843	0.08612377	0.143093613
IGLV8-61|A0A075B6I0	9.82468828	4.80E-06	0.002521801	0.999636516	0.000745015	0.00145366	0.998832165	0.000384928	-0.663434114	0.018138702	-0.689948261	0.681572816	-0.026514147	-0.708086962

			ANOVA p -values with Tukey Adjustment						Difference (AD - CT)					
Gene ID | Unirprot ID	F-Value	Pr(>F)	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA
UNC5A|Q6ZN44	4.09383999	0.007729084	0.038827832	0.474048391	0.008464205	0.571547784	0.985189306	0.312508263	0.237247827	0.124259485	0.266954427	-0.112988342	0.0297066	0.142694942
RAB4B|P61018	0.67186409	0.571192728	0.559483673	0.998005884	0.979044258	0.668837699	0.757716309	0.996780595	-0.105953602	-0.0140689	-0.029804818	0.091884702	0.076148785	-0.015735917
SPINT2|O43291	2.60961867	0.052911638	0.118639332	0.237362821	0.052731737	0.977977933	0.996147848	0.914813736	0.091375633	0.075170755	0.100109644	-0.016204879	0.00873401	0.024938889
RAB1A|P62820	0.94423555	0.42093748	0.559684193	0.992892858	0.982984751	0.384280286	0.74764609	0.911942476	-0.073156969	0.014530689	-0.01915578	0.087687657	0.054001189	-0.033686469
PSMA1|P25786	14.5765119	1.64E-08	0.994389329	0.000395782	1.50E-06	0.001257408	7.11E-06	0.634513045	-0.022349559	-0.351911139	-0.449686829	-0.32956158	-0.42733727	-0.09777569
CCL14|Q16627	0.86757379	0.459085125	0.740715763	0.963484637	0.997290134	0.430405387	0.594587442	0.990763773	0.071749782	-0.033529642	-0.013481628	-0.105279424	-0.08523141	0.020048014
FAM19A1|Q7Z5A9	4.24196588	0.006473818	0.015826176	0.05062026	0.013460612	0.952806649	0.999200209	0.974469234	0.143496016	0.118739898	0.137465702	-0.024756118	-0.006030314	0.018725804
LIPA|P38571	1.29399243	0.277878072	0.23730724	0.914966231	0.611967862	0.581594746	0.876244456	0.941564382	-0.145438365	-0.048855592	-0.089739121	0.096582773	0.055699244	-0.040883528
PVRL3|Q9NQS3	6.55671817	0.000308958	0.028018683	0.001101275	0.000687167	0.801093828	0.770006563	0.999981515	0.142110623	0.187309366	0.189066142	0.045198742	0.046955519	0.001756777
MT1X|P80297	2.89725214	0.036459189	0.999937312	0.816609664	0.230438906	0.792216272	0.266635925	0.024944924	-0.003451444	0.052770704	-0.111807741	0.056222148	-0.108356297	-0.164578444
PPIC|P45877	9.98122492	3.95E-06	0.000434387	0.989185795	0.000677018	0.001106738	0.988360297	0.001758417	-0.206035735	-0.015571683	-0.190240982	0.190464052	0.015794753	-0.174669299
TMEM108|Q6UXF1	0.37744565	0.769395006	0.970209394	0.715521467	0.946268208	0.931947887	0.999781098	0.949024267	0.057525981	0.132858368	0.067987838	0.075332388	0.010461857	-0.064870531
FAM177A1|Q8N128	0.93863508	0.424752596	0.994423964	0.624644302	0.840092483	0.467330993	0.697938691	0.97712689	-0.019355935	0.093009409	0.062412533	0.112365344	0.081768468	-0.030596876
PRRG1|O14668	6.65061031	0.000273633	0.130547164	0.492074645	0.104530239	0.002143093	0.999999206	0.001115069	0.25192265	-0.158479112	0.250480836	-0.410401762	-0.001441814	0.408959948
LILRB4|Q8NHJ6	1.57288545	0.197739005	0.864265016	0.529060529	0.99978636	0.147949723	0.810207315	0.549668927	0.043383937	-0.073386397	-0.004460278	-0.116770334	-0.047844215	0.068926119
ITFG3|Q9H0X4	0.77612429	0.509928745	0.998447807	0.529716073	0.849007134	0.635628433	0.919817481	0.926302886	0.018687446	0.151038818	0.086978464	0.132351372	0.068291019	-0.064060354
ASTN2|O75129	2.75614857	0.044143542	0.094540897	0.999984581	0.999997269	0.079274714	0.078077307	0.999934653	-0.170227759	0.002473052	-0.001353317	0.172700811	0.168874442	-0.003826369
0|P01817	3.93811194	0.01043227	0.421973031	0.278189206	0.989984784	0.005222797	0.596934366	0.144776211	-0.18751526	0.220503206	-0.037467818	0.408018466	0.150047442	-0.257971024
CREG1|O75629	0.35375733	0.786477356	0.955595834	0.999671344	0.802363568	0.97387726	0.982930644	0.844549112	-0.030043354	-0.005541256	-0.050864299	0.024502098	-0.020820945	-0.045323044
HIST1H4A|P62805	0.69587949	0.555656334	0.999996868	0.607929819	0.989827695	0.603888741	0.988038022	0.767462152	-0.003361665	0.195879505	0.047888101	0.19924117	0.051249766	-0.147991404
SCN2B|O60939	1.30447725	0.274608296	0.998944401	0.976610121	0.373352233	0.94599261	0.305481033	0.610753656	0.005593927	-0.015463573	-0.059928839	-0.021057499	-0.065522765	-0.044465266
GINM1|Q9NU53	0.70156298	0.552227418	0.999951086	0.936279812	0.586376413	0.952545056	0.630174187	0.905742336	0.002376092	0.026348689	0.055587233	0.023972597	0.05321114	0.029238544
RBP1|P09455	1.15745685	0.329743854	0.293670018	0.932432665	0.603072692	0.668857697	0.921592094	0.937263332	-0.158098917	-0.055563526	-0.105904916	0.102535391	0.052194002	-0.05034139
CST4|P01036	0.32506746	0.807235179	0.869462059	0.795729855	0.912058294	0.999472918	0.998865324	0.99275307	0.147726728	0.16913824	0.120331141	0.021411512	-0.027395586	-0.048807098
FABP7|O15540	9.10736078	1.24E-05	0.855785616	0.006847053	0.009335135	0.000353011	0.000482356	0.998333782	0.047847861	-0.194672281	-0.185121115	-0.242520141	-0.232968976	0.009551165
CSPG5|O95196	2.29033771	0.080067072	0.986149212	0.894438655	0.169926438	0.724739189	0.085761805	0.515217273	-0.022776909	0.045100477	0.129690957	0.067877386	0.152467866	0.084590479
GLB1|P16278	0.21360334	0.886886438	0.96954476	0.998671335	0.988730701	0.990216839	0.862206513	0.962148412	-0.027595146	-0.009242235	0.018594885	0.018352911	0.046190031	0.02783712
ARHGDIA|P52565	1.67095726	0.17478938	0.999417575	0.923691911	0.202060109	0.959203563	0.264287999	0.52900423	-0.00532761	-0.027599259	-0.085001468	-0.022271649	-0.079673858	-0.057402209
ADPGK|Q9BRR6	1.49850413	0.218824834	0.864980217	0.320271534	0.999727252	0.791125136	0.799088081	0.230377073	-0.102826406	-0.22329907	0.011431005	-0.120472664	0.114257411	0.234730075
MPZ|P25189	3.03382308	0.030532064	0.462061193	0.974591074	0.141232171	0.230253076	0.9307096	0.045633245	-0.155886077	0.043797859	-0.217825702	0.199683936	-0.061939625	-0.261623562
S100A13|Q99584	0.24195506	0.866970923	0.999757281	0.881459101	0.959745372	0.914148067	0.976885724	0.993713789	-0.004977376	-0.041438481	-0.02731489	-0.036461105	-0.022337514	0.01412359
DDT|P30046	9.19848794	1.06E-05	0.992596881	0.007354697	0.000875573	0.003291071	0.0003503	0.947814295	0.020656602	-0.236503629	-0.274543609	-0.257160231	-0.29520021	-0.03803998
APOF|Q13790	0.60793425	0.610644072	0.753799356	0.999972819	0.994341384	0.768690039	0.576382573	0.99052042	-0.115879923	-0.004799085	0.028004901	0.111080838	0.143884824	0.032803986
HLA-E|P13747	1.17874841	0.319381596	0.395624347	0.571095096	0.348957213	0.986972865	0.999998621	0.986347742	0.115899448	0.091488911	0.114787679	-0.024410537	-0.001111769	0.023298767
PCDHB10|Q9UN67	2.55587969	0.057512707	0.811556928	0.277645393	0.914515124	0.041318434	0.404221476	0.622965926	-0.067141588	0.129080883	0.046294928	0.196222471	0.113436516	-0.082785955
TMEM59L|Q9UK28	2.21731039	0.087607007	0.345672468	0.611278497	0.058835956	0.963693636	0.868649133	0.566664181	0.098655478	0.070706996	0.142490065	-0.027948483	0.043834587	0.071783069
SFRP2|Q96HF1	4.85218113	0.002838172	0.040693033	0.849252595	0.006287847	0.226725652	0.962239373	0.060951731	-0.179487886	-0.053017932	-0.21088516	0.126469955	-0.031397273	-0.157867228
EFNA1|P20827	0.84837201	0.469074719	0.386650338	0.844110578	0.886155534	0.852914042	0.786447996	0.999438482	-0.081135858	-0.040794202	-0.035259741	0.040341655	0.045876117	0.005534462
MBL2|P11226	0.56672495	0.637778992	0.75997166	0.997541195	0.952575182	0.637921403	0.95736812	0.883181995	0.150552553	-0.02860884	0.076414612	-0.179161394	-0.074137941	0.105023453
GALNT5|Q7Z7M9	0.3142427	0.815060797	0.876614668	0.979356825	0.812706931	0.981428072	0.999735674	0.959855517	-0.064740576	-0.032962891	-0.072090146	0.031777684	-0.007349571	-0.039127255
LAIR1|Q6GTX8	0.84254309	0.472176311	0.733639344	0.635310939	0.430401074	0.999205496	0.973415024	0.990158503	-0.159400854	-0.179322229	-0.223483206	-0.019921375	-0.064082352	-0.044160977
IGHV4-4|A0A075B6R2	0.42995983	0.731778209	0.968987317	0.999999925	0.776686864	0.966401161	0.965617777	0.763982297	0.092582071	-0.001180847	0.184979046	-0.093762918	0.092396975	0.186159893
AQP4|P55087	8.92924572	1.48E-05	0.779699609	0.003071286	0.041188347	9.21E-05	0.002157063	0.778670932	0.053731495	-0.194175354	-0.143873447	-0.247906848	-0.197604942	0.050301906
PLEKHB1|Q9UF11	0.26246729	0.852371126	0.96496422	0.977882782	0.992520172	0.999798329	0.869957438	0.89641652	0.022511174	0.018645713	-0.012555808	-0.003865461	-0.035066982	-0.031201521
H2AFX|P16104	0.62606769	0.599015232	0.993965282	0.998487364	0.788503171	0.999617972	0.63578095	0.680650864	0.041782937	0.025502804	-0.143276855	-0.016280133	-0.185059792	-0.168779659
IGLV1-36|A0A0B4J1U3	1.36169816	0.256858393	0.660112361	0.963177997	0.707167431	0.344711235	0.999362267	0.375609771	-0.155656044	0.063128879	-0.139854182	0.218784924	0.015801862	-0.202983061
MGAT3|Q09327	1.55535213	0.202377288	0.986072975	0.99983265	0.285507635	0.974599542	0.515155963	0.238204731	-0.022777318	0.004946631	-0.111389877	0.027723949	-0.088612559	-0.116336508

Gene ID | Unirprot ID	F-Value	Pr(>F)	ANOVA p -values with Tukey Adjustment						Difference (AD - CT)					
			AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA
0|P01703	0.37340454	0.772298881	0.866689107	0.999967039	0.913095048	0.840103195	0.99876263	0.890836706	-0.097474432	0.005472944	-0.078912268	0.102947376	0.018562164	-0.084385212
GNAS|O95467	1.65597985	0.178082904	0.518162476	0.893562416	0.877191012	0.158770336	0.902019278	0.439847903	-0.072254959	0.03629985	-0.037456657	0.108554809	0.034798302	-0.073756507
STMN3|Q9NZ72	4.78421767	0.00310181	0.015842037	0.016553081	0.006044085	0.999672113	0.998790099	0.994040027	0.149810563	0.145050284	0.157012713	-0.004760279	0.00720215	0.011962429
CD84|Q9UIB8	0.43646415	0.727216218	0.999370617	0.99034254	0.864851117	0.975403411	0.921165963	0.690561369	0.011083246	-0.02705898	0.06680507	-0.038142226	0.055721824	0.09386405
CEND1|Q8N111	7.4711613	9.86E-05	0.396978998	0.035756345	0.215675532	0.000170492	0.002829425	0.833886454	0.087699011	-0.146602532	-0.102922631	-0.234301543	-0.190621642	0.043679901
PPP3CA|Q08209	19.2227359	1.70E-10	0.642285772	7.00E-05	1.34E-05	4.69E-07	6.47E-08	0.991630776	0.089056734	-0.331416756	-0.351487304	-0.42047349	-0.440544037	-0.020070548
ADD1|P35611	3.00850014	0.033706347	0.994952768	0.332101645	0.124398814	0.216640064	0.07072553	0.948299162	0.040614084	-0.275964462	-0.361834604	-0.316578546	-0.402448688	-0.085870142
PON2|Q15165	0.77770288	0.508005673	0.950686054	0.97157183	0.807623728	0.757877189	0.462416167	0.969689904	-0.063171675	0.051975345	0.103017252	0.11514702	0.166188928	0.051041907
ALDOB|P05062	1.05425624	0.371089618	0.996533298	0.856971261	0.545831742	0.744070214	0.406223669	0.960724039	-0.039348642	0.145021585	0.228982213	0.184370227	0.268330855	0.083960627
B3GNT7|Q8NFL0	1.50985366	0.213981028	0.21374552	0.858724228	0.372214686	0.650207904	0.972394518	0.858471593	-0.151499007	-0.060788291	-0.119029468	0.090710716	0.03246954	-0.058241176
ROBO4|Q8WZ75	1.75511934	0.15733382	0.753132213	0.302838033	0.142697413	0.890472826	0.698205349	0.983432695	0.05417384	0.092626357	0.111175567	0.038452516	0.057001727	0.01854921
GAL3ST4|Q96RP7	0.57176565	0.634270459	0.811371717	0.99885758	0.862407218	0.722081198	0.998805819	0.778251038	-0.053803815	0.008687351	-0.0450824	0.062491166	0.008721415	-0.053769751
ITGAM|P11215	9.58740398	7.29E-06	0.151997983	0.039349782	0.117602771	2.57E-05	0.000124776	0.948277721	0.158093634	-0.19299007	-0.155691271	-0.351083704	-0.313784905	0.037298799
NME3|Q13232	2.41872343	0.067668571	0.793943432	0.972170102	0.194403899	0.522420315	0.742727429	0.066161189	0.033883899	-0.015618953	0.069730478	-0.049502851	0.035846579	0.08534943
MXRA7|P84157	4.21803083	0.006581058	0.04432426	0.999993904	0.104992755	0.035520635	0.963290457	0.086909777	-0.155449315	0.001459492	-0.128157247	0.156908807	0.027292068	-0.129616739
SLC39A14|Q15043	0.85738095	0.464457438	0.546075476	0.949265206	0.539714323	0.840940765	0.999900925	0.849527036	0.093415188	0.036400189	0.089002224	-0.057014998	-0.004412964	0.052602035
SEMA3D|O95025	3.05447777	0.030986135	0.123952176	0.944619117	0.60415426	0.033255712	0.67723375	0.266776265	-0.209008161	0.049268774	-0.106626146	0.258276935	0.102382015	-0.15589492
STIP1|P31948	2.81939876	0.041416403	0.542539615	0.860011663	0.029969833	0.94020679	0.560303688	0.20398277	-0.133619282	-0.076335815	-0.259085785	0.057283467	-0.125466503	-0.18274997
TGFB2|P61812	6.33639343	0.000410948	0.034477396	0.707109107	0.181743088	0.000982721	0.836605562	0.009323296	-0.196543022	0.075005093	-0.13858541	0.271548114	0.057957611	-0.213590503
ACP6|Q9NPH0	0.62608283	0.5998051	0.999977889	0.753622485	0.994420844	0.742494755	0.996888065	0.592919887	-0.007239136	0.177159864	-0.044755139	0.184399	-0.037516003	-0.221915003
PCDHGA3|Q9Y5H0	0.2160857	0.88512546	0.898569591	0.997079043	0.999999962	0.95802561	0.89039138	0.996637397	-0.041602572	-0.011651211	0.000267863	0.029951361	0.041870435	0.011919074
CSMD2|Q7Z408	2.47713152	0.06276955	0.95704292	0.136962384	0.137945718	0.368081073	0.377281539	0.999938483	0.035489257	0.147090803	0.143471172	0.111601545	0.107981915	-0.003619631
FLT3|P36888	4.9867878	0.002669213	0.040797873	0.997904162	0.720478581	0.025589502	0.001772075	0.821311503	-0.377820008	0.024343085	0.140600589	0.402163093	0.518420597	0.116257504
TXNDC17|Q9BRA2	0.82551649	0.48133079	0.999934166	0.814347036	0.554094037	0.847949655	0.601925147	0.974948265	-0.003193905	-0.048282804	-0.070385602	-0.045088899	-0.067191697	-0.022102798
SPINK1|P00995	1.35859031	0.258681073	0.680166224	0.309103645	0.287558239	0.958345293	0.945843823	0.999933294	-0.159642429	-0.230104379	-0.237533303	-0.07046195	-0.077890874	-0.007428924
SORCS2|Q96PQ0	4.45949175	0.004742694	0.108740654	0.818254936	0.00539505	0.474741175	0.77894042	0.063779492	0.103729732	0.038855392	0.145411578	-0.064874341	0.041681845	0.106556186
GXYLT1|Q4G148	1.06468752	0.367081497	0.641518386	0.543151839	0.99999785	0.999353238	0.640897981	0.540526551	-0.098207318	-0.108259179	-0.001458338	-0.010051862	0.096748979	0.106800841
TMEM25|Q86YD3	1.47130617	0.223824701	0.240156415	0.588782434	0.290918797	0.910767253	0.996943343	0.96175362	0.113689966	0.074205417	0.10176074	-0.039484549	-0.011929226	0.027555323
CXCL12|P48061	3.98418554	0.008832043	0.027017764	0.41295815	0.012324889	0.539624775	0.999392153	0.419684809	-0.189706123	-0.101078828	-0.197422126	0.088627295	-0.007716003	-0.096343298
PRSS23|O95084	0.39884403	0.754000957	0.996684273	0.734254009	0.983320173	0.849283691	0.99890453	0.89733862	0.009876564	0.047038	0.016400432	0.037161435	0.006523868	-0.030637567
CA14|Q9ULX7	0.7760016	0.508864058	0.998276021	0.994037144	0.632355458	0.973455031	0.519497812	0.780720426	-0.007421711	0.011083331	0.049723284	0.018505043	0.057144995	0.038639953
IGHV1-45|A0A0A0MS14	2.01078249	0.114213081	0.211605438	0.991622976	0.818588649	0.115893352	0.645908811	0.64067598	-0.361283007	0.052169393	-0.152586591	0.4134524	0.208696415	-0.204755985
CX3CL1|P78423	5.23728237	0.001831727	0.410543893	0.004467958	0.005535327	0.278218223	0.339264328	0.997652789	0.138462578	0.297054308	0.281544365	0.15859173	0.143081787	-0.015509943
RAB6B|Q9NRW1	0.5123428	0.674511526	0.634972407	0.935011265	0.807482126	0.926101604	0.985598309	0.991142396	-0.073818583	-0.036040626	-0.05319966	0.037777956	0.020618923	-0.017159033
SUMF1|Q8NBK3	2.44934465	0.067362895	0.957763734	0.0594011	0.77173655	0.176305414	0.972643511	0.313703924	0.033313711	0.166078193	0.060126723	0.132764482	0.026813012	-0.10595147
VAT1L|Q9HCJ6	1.13321626	0.336952156	0.297541244	0.551847007	0.594370656	0.963282278	0.935414276	0.999643431	-0.110024682	-0.080384461	-0.074548201	0.029640221	0.035476481	0.005836259
0|P06310	7.14451331	0.0001447	0.003769136	0.717739639	0.000743458	0.068368975	0.993068785	0.02289677	-0.565745393	-0.167912131	-0.608340717	0.397833262	-0.042595324	-0.440428586
B3GAT1|Q9P2W7	0.91100409	0.438356963	0.998998308	0.760099984	0.932717744	0.846551991	0.884585431	0.360228272	-0.011528995	-0.076710972	0.045941251	-0.065181977	0.057470245	0.122652222
NA|A0A0J9YXX1	2.73578158	0.045276117	0.729658016	0.99994212	0.073801511	0.746902041	0.510745744	0.072413363	0.464149666	0.024118423	1.0549819	-0.440031242	0.590832234	1.030863476
GPR180|Q86V85	2.79653708	0.041546281	0.794849226	0.100433936	0.059891531	0.535331454	0.418285981	0.998420037	0.050032872	0.122166401	0.130520341	0.072133528	0.080487469	0.00835394
SLC12A2|P55011	0.22041378	0.882054234	0.999317207	0.992516052	0.953689556	0.979618199	0.981287078	0.857773907	0.009799386	-0.021939552	0.038983941	-0.031738938	0.029184554	0.060923493
FZD8|Q9H461	1.48925082	0.22201369	0.969552695	0.517736308	0.226679732	0.813657855	0.495905454	0.946791732	0.045490952	0.132502716	0.183375789	0.087011763	0.137884836	0.050873073
FAP|Q12884	0.76849214	0.513258804	0.999098677	0.972412479	0.608455015	0.941490128	0.530284695	0.848911372	-0.014366711	0.044242723	0.12391296	0.058609435	0.138279671	0.079670237
EFNA3|P52797	6.21741831	0.000517666	0.070426329	0.843535106	0.000718761	0.340533773	0.460732217	0.009822244	0.168234981	0.055931683	0.26592406	-0.112303297	0.097689079	0.209992377
KIAA1467|A2RU67	2.41775571	0.067995819	0.951454749	0.622715992	0.058878422	0.910677479	0.20730118	0.563431815	0.034354284	0.076795162	0.156065936	0.042440878	0.121711652	0.079270773
ST13|P50502	10.9733963	1.15E-06	0.490942094	0.109801198	0.000980633	0.001740908	2.36E-06	0.41471758	0.081122905	-0.126321527	-0.208849443	-0.207444432	-0.289972348	-0.082527916
SYT2|Q8N9I0	1.87671886	0.135561805	0.187111106	0.320939232	0.174575465	0.983953131	0.999920822	0.989071921	-0.106190227	-0.087524469	-0.103111016	0.018665758	0.003079211	-0.015586547

Gene ID | Unirprot ID	F-Value	Pr(>F)	ANOVA p -values with Tukey Adjustment						Difference (AD - CT)					
			AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA
TOR1B|O14657	3.20338001	0.025329633	0.077598798	0.905188997	0.062735494	0.280909007	0.999948475	0.256106601	-0.206244782	-0.055601936	-0.201933226	0.150642846	0.004311557	-0.14633129
CNPY2|Q9Y2B0	0.50886384	0.676644795	0.711818014	0.968384877	0.740797308	0.922275307	0.999607696	0.9443086	0.067978454	0.028347297	0.061646285	-0.039631157	-0.006332169	0.033298988
TNFSF12|O43508	0.41745924	0.740675642	0.91703226	0.984275948	0.706066042	0.990401669	0.979852986	0.889165088	0.035211764	0.018987681	0.055671748	-0.016224083	0.020459983	0.036684066
TIAM1|Q13009	1.62301923	0.186441062	0.725783243	0.835951691	0.822650958	0.238039074	0.219200395	0.99999938	-0.100557667	0.079434117	0.080533053	0.179991785	0.18109072	0.001098936
PODXL|O00592	0.32992975	0.803716003	0.988924083	0.96178603	0.766390332	0.998636882	0.925070803	0.963515614	0.025460462	0.03775403	0.073002583	0.012293568	0.04754212	0.035248552
PTPLAD1|Q9P035	7.11902988	0.000160059	0.059173054	0.001549015	0.000188544	0.633334281	0.313561324	0.953047552	-0.134466769	-0.196617129	-0.223512697	-0.06215036	-0.089045928	-0.026895568
YKT6|O15498	0.6253671	0.599673512	0.926605818	0.999021286	0.891721824	0.867901857	0.524865893	0.937208475	0.035470273	-0.007937308	-0.039582566	-0.043407581	-0.075052839	-0.031645258
PCDHGA9|Q9Y5G4	1.1092446	0.347107334	0.847802051	0.633639556	0.282839645	0.987017827	0.806473686	0.93832708	0.047380118	0.066649849	0.09794726	0.019269731	0.050567142	0.031297411
IGF1|P05019	0.52320196	0.666891843	0.964577024	0.987106159	0.627114126	0.998727344	0.899673718	0.817343989	-0.022808861	-0.01559171	-0.054928995	0.007217151	-0.032120135	-0.039337286
C1QTNF1|Q9BXJ1	1.70638456	0.167227875	0.544304255	0.798515297	0.999963907	0.113048689	0.540428608	0.751348389	-0.054134103	0.036083891	-0.001795211	0.090217994	0.052338892	-0.037879102
EPHA6|Q9UF33	2.40023501	0.069295999	0.066743448	0.775925421	0.979620146	0.395726111	0.130290237	0.933518257	-0.114539349	-0.042881802	-0.01718957	0.071657547	0.097349779	0.025692232
TMEM9B|Q9NQ34	2.0505174	0.108855678	0.251893698	0.995612515	0.996494285	0.155257076	0.144932701	0.999995352	0.155214625	-0.019023963	-0.017172559	-0.174238587	-0.172387184	0.001851404
CNR1|P21554	4.35517834	0.005569672	0.546143783	0.210971224	0.002694881	0.942580304	0.159790448	0.400186878	0.078855303	0.112140507	0.199252222	0.033285204	0.120396918	0.087111715
MAPK1|P28482	14.972268	2.60E-08	0.826476091	2.67E-05	1.13E-06	0.001461502	0.000118188	0.923590487	-0.07010353	-0.375746375	-0.423148369	-0.305642845	-0.353044839	-0.047401994
NA|A2NJV5	19.4312956	6.28E-11	7.43E-05	0.93480603	9.95E-07	4.11E-06	0.886652453	2.84E-08	-0.951615406	0.121549434	-1.099982631	1.07316484	-0.148367225	-1.221532065
FZD1|Q9UP38	0.59702345	0.617711531	0.758217873	0.980117242	0.637197659	0.92656021	0.998868243	0.853686567	-0.066293032	-0.025403767	-0.07580303	0.040889265	-0.009509998	-0.050399263
ERLEC1|Q96DZ1	0.44617499	0.720531007	0.829495455	0.999788623	0.913829174	0.776374182	0.996469996	0.874952083	0.110519058	-0.010758626	0.08339865	-0.121277684	-0.027120408	0.094157276
PDGFB|P01127	9.3498962	8.72E-06	0.075348473	0.00164134	4.38E-06	0.637448217	0.057011428	0.520172645	0.109487637	0.162072177	0.219762345	0.052584539	0.110274708	0.057690169
PDGFD|Q9GZP0	1.39640793	0.247932762	0.467064167	0.969907821	0.893888855	0.230419033	0.846303928	0.641981183	-0.134066473	0.041596919	-0.062565926	0.175663392	0.071500547	-0.104162846
ESM1|Q9NQ30	5.32798966	0.001584647	0.04118052	0.913281156	0.1555823	0.004810567	0.912522341	0.025888425	-0.246658231	0.059174634	-0.187921908	0.305832865	0.058736322	-0.247096543
MILR1|Q7Z6M3	0.86072449	0.462556374	0.965165122	0.976317898	0.712730396	0.811846194	0.415974403	0.914848066	0.034191842	-0.029060991	-0.073182648	-0.063252834	-0.10737449	-0.044121656
PCP4|P48539	4.0581159	0.008017934	0.258293232	0.015195335	0.013154178	0.680326091	0.678810978	0.999995031	-0.074459943	-0.118930023	-0.118023211	-0.044470079	-0.043563268	0.000906812
NRGN|Q92686	33.048369	3.75E-17	0.000365197	8.38E-05	0.000166194	1.49E-13	1.65E-13	0.992614762	0.342601561	-0.362964331	-0.34136871	-0.705565892	-0.683970272	0.021595621
CPLX2|Q6PUV4	2.23700922	0.086008465	0.953742917	0.338121757	0.537924309	0.123984315	0.242526265	0.985713073	0.028029979	-0.088075541	-0.070372385	-0.11610552	-0.098402364	0.017703156
HLA-DPB1|P04440	2.57930391	0.055023425	0.329538159	0.999999805	0.146178813	0.311646277	0.985576963	0.132736716	-0.194508413	0.000910153	-0.232869813	0.195418566	-0.0383614	-0.233779967
PDGFA|P04085	1.40866779	0.242473666	0.730271098	0.266270265	0.302190506	0.853688156	0.900845424	0.999010247	-0.042474985	-0.074972064	-0.069479211	-0.032497078	-0.027004226	0.005492853
SUMF2|Q8NBJ7	0.21872502	0.88328924	0.998380121	0.99922391	0.950530189	0.999977042	0.899335114	0.907437208	-0.014097451	-0.010717989	0.043027464	0.003379462	0.057124914	0.053745452
SPINK6|Q6UWN8	5.26662392	0.001712041	0.000986078	0.648512962	0.137906745	0.035737168	0.228177374	0.776240239	-0.402614639	-0.119079255	-0.211684548	0.283535384	0.190930091	-0.092605293
CALY|Q9NYX4	0.51520786	0.672478533	0.98540268	0.8331613	0.999997423	0.647981563	0.985415532	0.798231074	-0.027311698	0.063603488	-0.001382216	0.090915186	0.025929482	-0.064985704
SYT7|O43581	2.09124568	0.103755835	0.981946181	0.997646626	0.252771776	0.939200957	0.107693599	0.322094347	-0.051298049	0.025343456	0.243478476	0.076641505	0.294776524	0.21813502
TBCB|Q99426	5.28255573	0.001724838	0.969957847	0.002312203	0.324983141	0.009523254	0.599418541	0.16470865	-0.035664559	-0.284003763	-0.129524734	-0.248339203	-0.093860175	0.154479029
DSCAML1|Q8TD84	4.43674328	0.004938573	0.077539055	0.886105623	0.008561647	0.312536044	0.889524766	0.061564934	0.142007786	0.042247111	0.182677975	-0.099760675	0.040670189	0.140430863
HEBP1|Q9NRV9	3.45239555	0.019222101	0.99947368	0.041339672	0.965142234	0.02860566	0.933705815	0.10281212	0.009108822	-0.217501381	-0.036908918	-0.226610204	-0.04601774	0.180592463
SRGN|P10124	1.7266185	0.163251018	0.258867516	0.951696368	0.996716392	0.535578307	0.153283996	0.870513861	-0.092526791	-0.025919945	0.010068753	0.066606846	0.102595544	0.035988698
CD83|Q01151	0.74897481	0.524228494	0.998645396	0.737806949	0.989975102	0.648665989	0.999002009	0.51703249	0.014181221	-0.090283632	0.026500907	-0.104464852	0.012319687	0.116784539
ARSG|Q96EG1	1.06848008	0.36542481	0.763350626	0.928482274	0.857585419	0.398067766	0.996165858	0.492563742	-0.123395503	0.077212747	-0.096289724	0.20060825	0.02710578	-0.173502471
ABHD14A|Q9BUJ0	8.30551213	3.84E-05	0.037189229	0.189254977	0.512412147	2.90E-05	0.461306178	0.003272019	-0.189624792	0.135792942	-0.091315431	0.325417734	0.098309361	-0.227108373
LINGO2|Q7L985	2.1533706	0.096315271	0.401860842	0.090417228	0.180005283	0.865068221	0.969042345	0.987729127	0.142024373	0.21099912	0.182230881	0.068974747	0.040206508	-0.028768239
TIMP3|P35625	1.533817	0.208370449	0.197913167	0.915138224	0.459277368	0.530062201	0.930215513	0.852815711	-0.122600396	-0.039590634	-0.086610314	0.083009762	0.035990082	-0.04701968
HHIP|Q96QV1	5.34619228	0.001870019	0.031474732	0.885728247	0.005756969	0.142372302	0.925198861	0.033520229	0.275237565	0.070523087	0.335808291	-0.204714478	0.060570726	0.265285204
EVI2A|P22794	9.7354862	5.37E-06	9.53E-05	0.296181914	5.78E-05	0.032195294	0.999520169	0.029233857	0.263044384	0.101721285	0.256746002	-0.161323099	-0.006298382	0.155024716
PLXNC1|O60486	0.42179611	0.737618574	0.96397912	0.842802195	0.709676267	0.988478137	0.94751391	0.995932272	0.034834034	0.057881683	0.073009469	0.023047649	0.038175436	0.015127786
PDIA2|Q13087	8.71684952	2.01E-05	0.000873276	0.997538292	0.003562116	0.001381809	0.938206468	0.005593339	-0.558314649	-0.026711781	-0.477668058	0.531602869	0.080646591	-0.450956277
LMNA|P02545	13.4952363	5.30E-08	9.22E-06	0.508043148	3.70E-06	0.001788074	0.999927123	0.001087871	-0.712809899	-0.193988	-0.704697905	0.518821898	0.008111994	-0.510709904
GNB4|Q9HAV0	1.93197333	0.1259292	0.9976539	0.413233901	0.904094846	0.317992349	0.963849962	0.101411636	-0.014689397	0.117714971	-0.050733539	0.132404369	-0.036044142	-0.168448511
C1orf56|Q9BUN1	0.32953639	0.804000514	0.96054485	0.757028703	0.92320483	0.965021701	0.999635529	0.97805595	-0.025691824	-0.049647328	-0.03064254	-0.023955504	-0.004950716	0.019004789
FXYD6|Q9H0Q3	5.87166836	0.000751212	0.001329679	0.565763667	0.011280281	0.058790247	0.844963538	0.267031322	-0.19936253	-0.067068063	-0.157434163	0.132294467	0.041928367	-0.0903661

Gene ID | Unirprot ID	F-Value	Pr(>F)	ANOVA p -values with Tukey Adjustment						Difference (AD - CT)					
			AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA
CD47|Q08722	3.00077679	0.032039113	0.377133199	0.787405143	0.487856452	0.055252756	0.99237052	0.075929857	-0.108361965	0.061053182	-0.090361913	0.169415147	0.018000052	-0.151415095
UBQLN2|Q9UHD9	1.13180066	0.338197082	0.744207033	0.998746792	0.530057195	0.649376838	0.993812229	0.424306255	-0.071545949	0.010537898	-0.088901062	0.082083846	-0.017355113	-0.09943896
OBP2A|Q9NY56	13.4031775	1.76E-07	1.32E-06	0.158194247	1.25E-05	0.003670911	0.830698751	0.026062162	-1.196650555	-0.446028017	-1.021830842	0.750622538	0.174819713	-0.575802825
TNFSF13B|Q9Y275	0.79650278	0.498235699	0.513190032	0.631933829	0.643890205	0.994110652	0.989256511	0.999941817	0.104937344	0.085817689	0.082083414	-0.019119655	-0.02285393	-0.003734275
PSMB7|Q99436	14.5775138	2.35E-08	0.625913993	0.000542209	0.000844162	2.71E-06	4.51E-06	0.998862704	0.10774902	-0.352810237	-0.340329066	-0.460559257	-0.448078086	0.012481171
PMCH|P20382	0.40135561	0.752280287	0.999974895	0.895092043	0.98827118	0.910943825	0.983086156	0.704138354	-0.003330506	-0.055677888	0.024840366	-0.052347383	0.028170871	0.080518254
LRPAP1|P30533	0.7257858	0.538126024	0.982544897	0.999989688	0.749350842	0.97616074	0.51296867	0.746955818	-0.026757918	0.002121124	0.068271732	0.028879042	0.095029651	0.066150609
TMEFF2|Q9UIK5	1.87645804	0.135073764	0.120181867	0.971295541	0.898089158	0.26507521	0.367753267	0.994488841	0.146527806	0.028240667	0.043628332	-0.118287139	-0.102899474	0.015387665
SERPINA2|P20848	0.46582639	0.706477471	0.797349254	0.957005401	0.699258787	0.97397257	0.999355336	0.939694363	-0.067195686	-0.036364141	-0.075797901	0.030831545	-0.008602215	-0.03943376
PDGFRA|P16234	1.1204174	0.342576745	0.996444385	0.525292596	0.990254761	0.664981698	0.952158556	0.310318812	0.014920882	0.091937831	-0.020168809	0.07701695	-0.035089691	-0.11210664
CRYZ|Q08257	2.76096054	0.04538476	0.073363638	0.061213771	0.366131235	0.999848898	0.784749457	0.740510048	-0.285790732	-0.294513476	-0.181427928	-0.008722743	0.104362804	0.113085547
MYL6|P60660	0.58024892	0.628945106	1	0.99935823	0.705788009	0.999360022	0.705859455	0.765769773	-9.85E-06	-0.01052682	-0.089399521	-0.010516972	-0.089389673	-0.078872701
GUSB|P08236	0.36002951	0.781949088	0.901098964	0.987790973	0.99999958	0.741124563	0.89500135	0.985039065	-0.059327198	0.027498853	-0.000854324	0.08682605	0.058472874	-0.028353176
MYDGF|Q969H8	0.54054789	0.65510561	0.772192289	0.999964731	0.998700644	0.737539961	0.659344249	0.999542201	-0.04754976	0.002220669	0.007238252	0.049770428	0.054788012	0.005017583
ASPRV1|Q53RT3	0.14895842	0.930128559	0.989743046	0.990290583	0.995444494	0.999993721	0.946913579	0.943057774	-0.026099257	-0.023948539	0.017790145	0.002150717	0.043889402	0.041738685
LUZP2|Q86TE4	1.1740322	0.321145607	0.918405838	0.445847613	0.354595108	0.832211591	0.753905788	0.999206463	0.032546384	0.074757738	0.08105193	0.042211354	0.048505546	0.006294192
ICAM2|P13598	2.6497783	0.050236442	0.998955803	0.082681235	0.380620901	0.12269429	0.480625989	0.825644103	0.006747547	0.109773961	0.071854518	0.103026413	0.065106971	-0.037919442
NPC1|O15118	0.92202135	0.431620677	0.816935488	0.9964637	0.876948658	0.694424995	0.357572998	0.951631938	-0.073816549	0.017659895	0.059484709	0.091476444	0.133301258	0.041824814
SDC4|P31431	1.82371108	0.146639986	0.997899657	0.587238019	0.75334034	0.48806175	0.861490226	0.09832569	-0.016176162	0.111267897	-0.08306919	0.127444058	-0.066893028	-0.194337086
IGLV3-16|A0A075B6K0	9.25650964	9.81E-06	0.010982877	0.810724603	0.007823446	0.000429319	0.99994299	0.000226425	-0.556907509	0.154051818	-0.547633361	0.710959326	0.009274148	-0.701685178
NEDD8|Q15843	12.0021758	3.99E-07	0.991908524	0.001187947	0.000129575	0.000439558	4.32E-05	0.945399968	0.014201468	-0.182380586	-0.207869216	-0.196582054	-0.222070684	-0.02548863
YIPF3|Q9GZM5	3.51012684	0.016412041	0.329293947	0.18602844	0.008096208	0.993075837	0.487032046	0.64005096	0.058254413	0.067400569	0.105303984	0.009146156	0.047049571	0.037903414
UFM1|P61960	6.71603993	0.000274887	0.977283798	0.031394934	0.008482435	0.012877044	0.003184745	0.985515824	0.019153252	-0.126212806	-0.141498877	-0.145366058	-0.160652128	-0.015286071
VMO1|Q7Z5L0	0.35999008	0.781990014	0.964272734	0.869271663	0.755008508	0.991574128	0.959126532	0.997035295	0.072225083	0.114739863	0.143054658	0.04251478	0.070829575	0.028314795
IGLV3-10|A0A075B6K4	0.66402994	0.57515527	0.708398767	0.601733024	0.660044347	0.99902255	0.99999576	0.999318574	-0.170161947	-0.192053913	-0.173643442	-0.021891967	-0.003481495	0.018410471
CHST8|Q9H2A9	8.22661249	3.62E-05	0.770159435	0.114601096	0.003763946	0.008732454	0.00010042	0.642616548	-0.051293164	0.116357372	0.174845004	0.167650536	0.226138168	0.058487632
PFN2|P35080	27.2759333	1.65E-14	0.958155587	7.27E-08	1.14E-08	7.53E-09	1.07E-09	0.997817034	0.030205682	-0.348580465	-0.358744168	-0.378786148	-0.388949851	-0.010163703
GLIPR2|Q9H4G4	2.79741684	0.043807536	0.3655649	0.754824499	0.587775551	0.055910945	0.97531159	0.11949346	-0.158203043	0.095118343	-0.118016358	0.253321386	0.040186685	-0.2131347
TMEFF1|Q8IYR6	4.23744703	0.006511824	0.003125565	0.541828109	0.254566338	0.119991627	0.279589843	0.961246147	0.179273286	0.067175229	0.090963134	-0.112098057	-0.088310153	0.023787904
ST8SIA4|Q92187	1.78962709	0.152558323	0.466260212	0.812360917	0.990098051	0.104775515	0.608617973	0.60911981	-0.116629021	0.06833658	-0.022282975	0.184965601	0.094346046	-0.090619555
SUCO|Q9UBS9	1.80943655	0.150305917	0.884092149	0.463622284	0.993734357	0.145444944	0.96150626	0.305858856	-0.067523917	0.125855818	-0.022840494	0.193379735	0.044683423	-0.148696312
RNF130|Q86XS8	2.65426381	0.051969414	0.999003924	0.088951021	0.992717362	0.123004722	0.999311893	0.112297381	-0.014739474	-0.240069702	-0.02689605	-0.225330228	-0.012156576	0.213173652
CD97|P48960	2.82241199	0.041915005	0.445548804	0.054919985	0.991354085	0.698444721	0.61331941	0.099659343	0.104394375	0.179766056	0.020215517	0.075371681	-0.084178858	-0.159550539
CAST|P20810	1.94446361	0.126508656	0.578481297	0.329478879	0.093258847	0.980908112	0.740136744	0.91572544	-0.129996287	-0.168217983	-0.230868457	-0.038221696	-0.100872171	-0.062650475
SLC39A6|Q13433	3.09089574	0.02917785	0.088763511	0.11343531	0.033763574	0.997565277	0.989491794	0.954569317	0.179707292	0.16556485	0.203057379	-0.014142442	0.023350087	0.037492528
BMP1|P13497	0.88658793	0.44977772	0.828951578	0.985791301	0.431249623	0.953647834	0.929838014	0.643438753	0.062412842	0.024731224	0.104671044	-0.037681617	0.042258202	0.07993982
PSMA6|P60900	6.36287021	0.000539688	0.517128073	0.111115303	0.146096197	0.002159478	0.002796049	0.996641957	0.128867791	-0.214978858	-0.195695639	-0.343846649	-0.32456343	0.019283219
NAGPA|Q9UK23	1.59168438	0.193893211	0.987229144	0.823394425	0.182484165	0.955132616	0.342517833	0.630442063	0.022442133	0.05636256	0.132296205	0.033920427	0.109854072	0.075933644
LECT2|O14960	4.47223882	0.004664272	0.220448858	0.323922384	0.986878217	0.001977655	0.342541311	0.151293428	-0.253513433	0.218304218	-0.042040467	0.471817651	0.211472966	-0.260344685
PCDHGA4|Q9Y5G9	1.09044637	0.356699307	0.990560284	0.989366482	0.652675704	0.999998599	0.421196369	0.420722266	-0.034728218	-0.036488222	0.131258328	-0.001760004	0.165986546	0.16774655
SHISA6|Q6ZSJ9	2.63668648	0.051525069	0.198865025	0.998004199	0.895720464	0.252477184	0.034533166	0.802274422	-0.09699691	-0.008321097	0.032608845	0.088675813	0.129605755	0.040929942
FIBIN|Q8TAL6	7.86932429	6.28E-05	0.000983853	0.969778753	0.00458841	0.004239711	0.925971323	0.018090616	-0.251136779	-0.028543443	-0.211839698	0.222593337	0.039297082	-0.183296255
MFAP2|P55001	0.60479157	0.613065813	0.76630646	0.999935274	0.991765986	0.788889395	0.565714646	0.985132557	-0.074819977	-0.004208398	0.020686895	0.070611578	0.095506872	0.024895293
GABARAPL2|P60520	8.94078908	1.55E-05	0.995271164	0.000370923	0.003240974	0.001335222	0.009798016	0.887069956	-0.010695639	-0.178974546	-0.148459188	-0.168278907	-0.137763549	0.030515359
IGLV7-46|A0A075B6I9	5.16421206	0.001888202	0.05033558	0.965629837	0.079843183	0.012103287	0.988966934	0.019515838	-0.37467812	0.066105995	-0.330576504	0.440784115	0.044101615	-0.3966825
LARGE|O95461	7.97246433	5.67E-05	0.011013668	0.003871625	2.66E-05	0.993548829	0.478285275	0.634687102	0.246375101	0.266709314	0.353034022	0.020334213	0.106658921	0.086324708
ASRGL1|Q7L266	3.23330726	0.025053022	0.979732544	0.855564969	0.076923014	0.624765183	0.025712228	0.342246356	0.045647786	-0.091720666	-0.277663053	-0.137368451	-0.323310839	-0.185942388

Gene ID | Unirprot ID	F-Value	Pr(>F)	ANOVA p -values with Tukey Adjustment						Difference (AD - CT)					
			AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA
PDCD6IP|Q8WUM4	1.54977518	0.206187056	0.999520931	0.980531126	0.399425027	0.958465606	0.456561538	0.189555442	-0.015305482	0.052596952	-0.214816245	0.067902434	-0.199510763	-0.267413197
CHPF|Q8IZ52	2.12141262	0.099582466	0.676312566	0.065235926	0.386476378	0.545321608	0.97992475	0.735463468	0.091199591	0.197295027	0.121017807	0.106095436	0.029818217	-0.076277219
NPY|P01303	22.9601555	1.11E-12	0.052707419	1.25E-08	2.61E-11	0.002168722	3.76E-05	0.762877191	0.21227863	0.506111561	0.58143095	0.293832932	0.369152321	0.075319389
PCDHA9|Q9Y5H5	4.39720779	0.00521136	0.531429359	0.155500308	0.959479394	0.003858025	0.810535644	0.042156143	-0.100448087	0.152037273	-0.035762981	0.25248536	0.064685106	-0.187800254
ATF6|P18850	0.53694017	0.657569329	0.655483216	0.976799163	0.998981915	0.867697502	0.715740425	0.992261527	-0.070053845	-0.024104598	-0.008182681	0.045949247	0.061871164	0.015921918
ADAM28|Q9UKQ2	2.1625253	0.093956108	0.169343075	0.371917241	0.093549918	0.959546085	0.998409646	0.899367597	0.183626411	0.140016097	0.197725177	-0.043610314	0.014098766	0.057709079
PIP|P12273	0.7535426	0.522782022	0.813400783	0.941169123	0.466785462	0.984499878	0.95072649	0.786561275	-0.183341778	-0.112800474	-0.289154439	0.070541304	-0.105812661	-0.176353966
MT1F|P04733	0.25088299	0.860637645	0.999997803	0.918178397	0.99941406	0.914357714	0.999668621	0.859613633	-0.001249693	0.042748188	-0.007659347	0.043997881	-0.006409654	-0.050407535
SPESP1|Q6UW49	0.07858756	0.971481636	0.982449245	0.999814223	0.981705823	0.990109905	0.999999773	0.989527405	0.064456187	0.014020419	0.065871644	-0.050435769	0.001415456	0.051851225
IFNAR1|P17181	0.24140258	0.867362283	0.998145104	0.931375155	0.882962946	0.973401208	0.943825718	0.999332604	0.01069846	0.036749216	0.04397743	0.026050756	0.03327897	0.007228213
CADPS|Q9ULU8	0.67074117	0.571071108	0.991261651	0.999445005	0.738060468	0.976028213	0.545139925	0.795012107	0.021439334	-0.00838251	-0.072453541	-0.029821844	-0.093892875	-0.064071031
CD320|Q9NPF0	1.36563393	0.255278345	0.266980418	0.670837493	0.339834649	0.881890413	0.997158637	0.94513104	0.106427624	0.064087507	0.09494558	-0.042340116	-0.011482044	0.030858072
0|P01705	0.13499904	0.93906542	0.922874724	0.995795759	0.993761871	0.977055756	0.978631552	0.99999463	0.176297776	0.062524844	0.068991642	-0.113772932	-0.107306134	0.006466798
CRYAB|P02511	4.00904688	0.008549453	0.919943094	0.095400389	0.014003687	0.351310097	0.09128088	0.906458387	-0.056702144	-0.201656068	-0.257797839	-0.144953924	-0.201095695	-0.056141771
PHB2|Q99623	0.95005863	0.418127839	0.646760843	0.989758945	0.872930461	0.435154722	0.973818814	0.69552234	-0.108610652	0.027952622	-0.06950209	0.136563274	0.039108562	-0.097454712
F11R|Q9Y624	1.60527928	0.191563978	0.989764508	0.987043257	0.359277466	0.918211632	0.574654426	0.184286019	-0.038552202	0.040418731	-0.190640331	0.078970933	-0.15208813	-0.231059062
TNFRSF11B|O00300	2.33983243	0.077811575	0.787396083	0.11548158	0.117223731	0.608973238	0.638963097	0.999652514	-0.120454519	-0.276606932	-0.265201801	-0.156152413	-0.144747282	0.011405131
TOM1L2|Q6ZVM7	3.31794439	0.02254662	0.898478262	0.114335006	0.997452429	0.019044269	0.784457036	0.121824008	0.07548498	-0.240536325	-0.019505541	-0.316021305	-0.094990521	0.221030784
BAMBI|Q13145	4.59471351	0.003973908	0.00711946	0.079578788	0.00931773	0.78479224	0.994413606	0.885385383	0.184663159	0.132438014	0.170978322	-0.052225144	-0.013684837	0.038540307
TGFBR2|P37173	3.22286182	0.024199797	0.468758521	0.368698481	0.992507534	0.01312752	0.592218381	0.194759119	-0.071942278	0.079361065	-0.012943209	0.151303344	0.058999069	-0.092304274
CDH19|Q9H159	1.27150154	0.286687212	0.857822356	0.877453127	0.771442115	0.406592525	0.998395812	0.309989865	0.068888808	-0.064571567	0.083027051	-0.133460375	0.014138243	0.147598618
UGGT1|Q9NYU2	0.2795075	0.84007724	0.902204681	0.999985097	0.954587248	0.87450995	0.996616773	0.936657264	-0.111882051	0.005432542	-0.079682669	0.117314593	0.032199382	-0.085115211
SMOC2|Q9H3U7	2.9451444	0.036348835	0.939680065	0.976835987	0.140607012	0.758809015	0.037298301	0.293477283	0.062185554	-0.042544849	-0.213688115	-0.104730403	-0.275873669	-0.171143266
0|P01709	1.97570822	0.119148393	0.959575827	0.285132302	0.966876741	0.592021082	0.764052115	0.095499428	-0.082655129	-0.28817986	0.073222425	-0.205524731	0.155877553	0.361402285
ENTPD4|Q9Y227	3.00511581	0.033379096	0.403396575	0.528746968	0.991186279	0.018492169	0.206138628	0.655354338	-0.134279095	0.112585509	0.023498233	0.246864604	0.157777328	-0.089087276
TMED3|Q9Y3Q3	1.41955619	0.240684897	0.981255808	0.211723432	0.824990707	0.431245631	0.971136739	0.651500141	-0.031451183	-0.156005153	-0.066709206	-0.12455397	-0.035258023	0.089295946
LPL|P06858	0.56570975	0.638445595	0.820557814	0.932466846	0.993692153	0.991748936	0.655360049	0.813797758	0.047329196	0.031918691	-0.0137223	-0.015410505	-0.061051496	-0.045640991
NRSN2|Q9GZP1	0.31464003	0.814773842	0.995556737	0.986268732	0.793147671	0.999566911	0.901792284	0.935667756	0.018150693	0.026280993	0.06968	0.0081303	0.051529307	0.043399007
ATOX1|O00244	14.8551943	1.05E-08	0.997231736	0.000112947	1.40E-05	6.04E-05	7.27E-06	0.980154062	0.00816	-0.175679884	-0.190587827	-0.183839884	-0.198747827	-0.014907943
IGKV6-21|A0A0C4DH24	1.22419987	0.302280862	0.331866502	0.96505599	0.519004021	0.60161703	0.978001741	0.807162259	-0.355590686	-0.097204318	-0.274239195	0.258386368	0.081351491	-0.177034877
PTTG1IP|P53801	2.29754042	0.081896771	0.16518667	0.980131794	0.210815907	0.311265318	0.993436367	0.391845129	0.215761301	0.039738935	0.190289566	-0.176022365	-0.025471735	0.15055063
FURIN|P09958	2.22674816	0.086838002	0.93762164	0.595887018	0.65009628	0.917728142	0.300459745	0.065860408	-0.038786679	-0.081018946	0.073959244	-0.042232266	0.112745923	0.154978189
PILRA|Q9UKJ1	0.02351044	0.995104151	0.999998638	0.9999411	0.995573854	0.999979875	0.996564995	0.997945429	-0.000945113	-0.003228984	-0.013397583	-0.002283871	-0.01245247	-0.010168599
INHBA|P08476	2.24712419	0.086531055	0.97464058	0.999482755	0.274117497	0.989529376	0.104323949	0.213574961	0.046806136	0.012630088	-0.191120953	-0.034176048	-0.237927089	-0.203751041
KLK10|O43240	1.56438319	0.202626217	0.735142709	0.856560849	0.149783698	0.994407297	0.684733888	0.512543797	0.088701324	0.067573761	0.182845365	-0.021127563	0.094144041	0.115271604
SCAMP1|O15126	2.50756946	0.061230699	0.205095157	0.999821317	0.277421379	0.168339488	0.992283843	0.22962399	0.143025714	-0.005516065	0.123228645	-0.148541779	-0.019797069	0.12874471
COL2A1|P02458	2.12580585	0.098459888	0.76222803	0.963893048	0.452984642	0.46053095	0.06713001	0.74624219	-0.054501042	0.025915261	0.078289853	0.080416303	0.132790895	0.052374592
BMPR2|Q13873	2.06349991	0.106878443	0.478013114	0.074046333	0.753028745	0.77216034	0.959870452	0.435234068	0.074853643	0.12403678	0.049826535	0.049183137	-0.025027107	-0.074210244
0|P01706	22.6976006	1.47E-12	4.30E-09	0.299312007	2.42E-09	1.41E-05	0.995686939	1.26E-05	-1.102208295	-0.289211607	-1.064647232	0.812996688	0.037561062	-0.775435626
ST6GALNAC5|Q9BVH7	3.22206525	0.023897209	0.062198499	0.979832555	0.125542861	0.138314205	0.973957731	0.259025925	0.213074069	0.032243868	0.178215197	-0.180830201	-0.034858872	0.145971329
SLC4A10|Q6U841	1.6249131	0.187614841	0.994499358	0.367234357	0.633636808	0.255577151	0.486413639	0.965441422	0.029086119	-0.182904001	-0.131806792	-0.211990119	-0.16089291	0.051097209
PPT1|P50897	0.68808746	0.560671803	0.516986518	0.987703949	0.927728274	0.70918529	0.848512058	0.99209416	-0.114205214	-0.026566834	-0.048706361	0.08763838	0.065498853	-0.022139526
ANTXR2|P58335	1.24852242	0.293990302	0.299884133	0.432557178	0.466199835	0.994875763	0.985280581	0.999654396	-0.13453817	-0.116048563	-0.108775813	0.018489607	0.025762357	0.00727275
GYG1|P46976	0.83726487	0.47525776	0.945778944	0.857721812	0.947661884	0.522714719	0.999998343	0.518021785	-0.035762948	0.051014298	-0.034718682	0.086777246	0.001044266	-0.08573298
SIGLEC9|Q9Y336	2.81847581	0.042248553	0.986103434	0.088782208	0.770125399	0.048380408	0.575599506	0.414294009	0.053802912	-0.364783722	-0.138420637	-0.418586633	-0.192223549	0.226363085
EPHB4|P54760	0.3661675	0.777528563	0.999786495	0.850174931	0.999372411	0.882473577	0.996674546	0.765316708	0.004715283	0.045714672	-0.006522193	0.040999389	-0.011237476	-0.052236865
MMP14|P50281	0.96180192	0.41196974	0.999196536	0.570832352	0.999731025	0.496491459	0.99996414	0.479119969	0.00577532	-0.055356069	0.003807462	-0.061131389	-0.001967857	0.059163532

			ANOVA p -values with Tukey Adjustment						Difference (AD - CT)					
Gene ID | Unirprot ID	F-Value	Pr(>F)	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA
MPST|P25325	1.03211084	0.380811342	0.787277663	0.996785813	0.588042022	0.659102069	0.989371885	0.447519618	-0.089879174	0.020075098	-0.119107089	0.109954272	-0.029227915	-0.139182187
SQSTM1|Q13501	2.66087364	0.049969927	0.364739772	0.999913046	0.108874173	0.382866367	0.932047748	0.113770452	-0.105128913	-0.003968117	-0.142473566	0.101160797	-0.037344653	-0.13850545
DNAJB2|P25686	0.7835243	0.505102934	0.997906956	0.731566122	0.57242448	0.840144239	0.703435842	0.994960444	-0.011003238	-0.060603509	-0.07427682	-0.049600271	-0.063273582	-0.013673311
JAG2|Q9Y219	1.2626082	0.289634227	0.999914348	0.844296456	0.3716599	0.816266861	0.343681925	0.85522716	-0.005395759	0.070069414	0.136330781	0.075465173	0.141726539	0.066261367
CSTB|P04080	10.2730784	2.74E-06	0.31718927	0.04917087	0.011318716	0.000152545	1.46E-05	0.96683317	0.094324872	-0.138831533	-0.162620238	-0.233156405	-0.25694511	-0.023788705
MASP2|O00187	0.59888856	0.616624152	0.990017101	0.89040874	0.950521168	0.980055919	0.834249725	0.564596678	-0.04929482	-0.110415755	0.080683869	-0.061120934	0.129978689	0.191099623
IGKV1-5|P01602	10.7544696	1.51E-06	0.000198553	0.94365807	0.00019441	0.001288139	0.996566178	0.00137125	-0.647494216	-0.083075074	-0.616224289	0.564419142	0.031269927	-0.533149215
MFAP5|Q13361	1.52662666	0.209338156	0.564210816	0.998045326	0.448970393	0.440303438	0.999441626	0.32705058	-0.105651726	0.014085299	-0.114595787	0.119737025	-0.008944061	-0.128681086
IGLV2-18|A0A075B6J9	4.26272033	0.006302096	0.00452583	0.058800835	0.068303319	0.76325645	0.71716688	0.999840191	-0.694217527	-0.500118125	-0.485508864	0.194099403	0.208708663	0.014609261
TMEM59|Q9BXS4	0.66084125	0.578053224	0.991072905	0.742427885	0.611111178	0.900851909	0.813750022	0.998257925	0.014018484	0.046249368	0.053469112	0.032230884	0.039450628	0.007219745
RANBP1|P43487	3.18123227	0.026315883	0.384856373	0.095828422	0.020093826	0.924520141	0.62261204	0.925193804	-0.189249946	-0.261656768	-0.329697374	-0.072406822	-0.140447428	-0.068040606
IGLV4-60|A0A075B6I1	6.62469665	0.00031167	0.408673623	0.186238782	0.265706732	0.002085259	0.996243746	0.000563344	-0.385609524	0.494574536	-0.437476857	0.88018406	-0.051867332	-0.932051393
MGAT4B|Q9UQ53	1.76491841	0.155711008	0.946912532	0.878057301	0.133771151	0.997722915	0.378545237	0.469387743	0.032167345	0.042813362	0.122407577	0.010646018	0.090240232	0.079594215
FAM3B|P58499	1.83355548	0.144916813	0.132918711	0.425179333	0.27279741	0.888514735	0.9532025	0.995604504	-0.334659032	-0.225193887	-0.257831578	0.109465146	0.076827455	-0.032637691
PRND|Q9UKY0	1.52163256	0.210957386	0.999589278	0.433648626	0.981946025	0.372011833	0.993450994	0.201972374	0.010540152	-0.14945684	0.035958077	-0.159996992	0.025417926	0.185414918
COX16|Q9P0S2	1.72299228	0.164015875	0.304177074	0.338058886	0.159336925	0.999775956	0.990972074	0.980166609	-0.101989815	-0.09708067	-0.118649281	0.004909145	-0.016659467	-0.021568611
CCDC80|Q76M96	1.09338265	0.354173008	0.726394142	0.396567648	0.385554499	0.962788743	0.96587225	0.999990281	-0.081118946	-0.118285563	-0.116135029	-0.037166617	-0.035016083	0.002150534
AHCY|P23526	2.32373694	0.077321132	0.628499656	0.449173875	0.046256074	0.994528198	0.530036818	0.669997042	-0.120656956	-0.145446715	-0.252946072	-0.024789759	-0.132289116	-0.107499357
RNF167|Q9H6Y7	1.35838849	0.259755065	0.995839731	0.333353399	0.487269195	0.519777274	0.692361154	0.981692386	-0.012831498	-0.090305817	-0.071418319	-0.077474319	-0.058586821	0.018887498
CXCL10|P02778	2.47270581	0.066240759	0.595161817	0.865746108	0.047796184	0.945682221	0.597328189	0.220440648	-0.19071682	-0.108571457	-0.38260404	0.082145363	-0.19188722	-0.274032583
0|P01718	3.81588074	0.011006528	0.167730248	0.578250867	0.994384422	0.005154688	0.231826922	0.388701473	-0.345979458	0.208061196	-0.040043547	0.554040654	0.305935912	-0.248104743
FZD7|O75084	7.00525565	0.000193551	0.000251148	0.189361912	0.002968192	0.099575061	0.840521515	0.410122695	-0.248714567	-0.114689873	-0.200948019	0.134024694	0.047766548	-0.086258146
PRSS2|P07478	5.63030921	0.001075726	0.003237426	0.980168107	0.07270721	0.009189543	0.593529387	0.161010843	-0.249071406	-0.026648415	-0.163840377	0.222422991	0.085231029	-0.137191963
PRDX5|P30044	2.33575493	0.076435938	0.734783207	0.719006054	0.048200603	0.999995996	0.486834593	0.426819389	-0.093712395	-0.091674594	-0.219501835	0.002037801	-0.12578944	-0.127827241
IFNAR2|P48551	1.48812872	0.219521015	0.828307066	0.418501495	0.193519172	0.916199769	0.699758587	0.971995801	0.037073009	0.064728079	0.082453287	0.027655071	0.045380278	0.017725208
GREM1|O60565	3.33167828	0.022094789	0.025560159	0.552397494	0.064861704	0.380302913	0.96861953	0.630588243	0.272153948	0.123467341	0.230670205	-0.148686608	-0.041483743	0.107202864
ITLN1|Q8WWA0	1.13512684	0.336869196	0.778209945	0.821785158	0.998446419	0.261386146	0.658019281	0.881183273	0.085271462	-0.075378139	-0.013951455	-0.160649601	-0.099222918	0.061426683
IGLV10-54|A0A075B6I4	0.30260906	0.823480278	0.841699082	0.853789385	0.969932424	0.999983925	0.975824399	0.98076873	-0.278827795	-0.266870089	-0.14380194	0.011957706	0.135025855	0.12306815
CRISPLD1|Q9H336	0.90351222	0.44054701	0.775472748	0.99943519	0.630699785	0.699659086	0.997604268	0.54061111	0.040687608	-0.004826152	0.048436622	-0.04551376	0.007749014	0.053262774
IMMT|Q16891	0.23584957	0.871202764	0.895961095	0.888196973	0.9253231	0.999999997	0.999130989	0.999085209	-0.167992765	-0.167503829	-0.137285737	0.000488935	0.030707028	0.030218093
LEAP2|Q969E1	1.84552964	0.14066775	0.10012678	0.465358283	0.403079236	0.814540546	0.842909895	0.999841445	0.248674988	0.155327301	0.163129973	-0.093347687	-0.085545015	0.007802673
SUMO3|P55854	28.771707	9.82E-15	0.89394863	5.51E-08	3.68E-09	7.25E-09	5.09E-10	0.995814102	0.040249323	-0.3332538	-0.345311818	-0.373503124	-0.385561141	-0.012058017
PRRT1|Q99946	1.62204212	0.188696887	0.994066374	0.273880088	0.976982142	0.223048421	0.917996853	0.431224594	-0.021870252	0.142616407	0.030219689	0.164486659	0.052089941	-0.112396717
RARRES1|P49788	4.79951482	0.003654139	0.019721372	0.947779466	0.700821047	0.003298789	0.246677924	0.360443727	-0.449622635	0.079560021	-0.162672538	0.529182656	0.286950097	-0.242232559
MTIF3|Q9H2K0	0.53463737	0.65909449	0.954344657	0.999197692	0.89898431	0.978547825	0.611202273	0.833797704	0.024048422	0.00589364	-0.030576307	-0.018154782	-0.054624729	-0.036469947
HIST1H3A|P68431	0.24369567	0.865744208	0.999873682	0.970223598	0.98167982	0.95593418	0.990670595	0.83107244	-0.01018968	0.062763413	-0.051777096	0.072953093	-0.041587416	-0.114540509
ARL8B|Q9NVJ2	1.22759138	0.301510024	0.708233679	0.276299902	0.433848716	0.910511843	0.983664221	0.987906321	0.085884872	0.13827556	0.114056765	0.052390688	0.028171893	-0.024218796
MANF|P55145	0.89749761	0.444437821	0.541798983	0.848018377	0.440289071	0.951422702	0.999354549	0.90791868	-0.119163269	-0.072556389	-0.129479351	0.04660688	-0.010316082	-0.056922962
ST6GAL1|P15907	0.94722174	0.420050131	0.786803388	0.841495003	0.338460479	0.999261746	0.883619417	0.816099457	-0.093957335	-0.08134856	-0.167725493	0.012608775	-0.073768158	-0.086376933
CNPY4|Q8N129	0.95637923	0.416545004	0.586194312	0.906431622	0.406278804	0.923543989	0.997715711	0.819774031	-0.097220117	-0.049620774	-0.110900519	0.047599344	-0.013680401	-0.061279745
UBR4|Q5T4S7	0.92992726	0.428822392	0.524216411	0.999277715	0.981563662	0.431684801	0.752218129	0.956189285	-0.304642104	0.027945007	-0.084311717	0.332587111	0.220330386	-0.112256725
ARPP21|Q9UBL0	10.0005402	4.83E-06	0.304194875	0.00765231	0.088902642	1.32E-05	0.000454997	0.804065856	0.11992723	-0.21448531	-0.155809519	-0.33441254	-0.275736749	0.058675791
TMX4|Q9H1E5	1.78764484	0.154310326	0.572907406	0.786358283	0.924791327	0.12625147	0.896368218	0.394490686	-0.133173156	0.093824612	-0.061901453	0.226997768	0.071271702	-0.155726066
MYLK|Q15746	1.46501756	0.228543119	0.961653247	0.580997279	0.66447664	0.306739658	0.367826587	0.997986538	0.043657044	-0.109604019	-0.09509499	-0.153261064	-0.138752035	0.014509029
DNAJB11|Q9UBS4	2.42047776	0.069237458	0.046135503	0.587374819	0.287950056	0.461505778	0.71987165	0.961969768	0.152461383	0.069541927	0.094785275	-0.082919456	-0.057676108	0.025243348
VEGFA|P15692	4.76771619	0.003409304	0.150551752	0.489954885	0.001813122	0.866450492	0.513513708	0.10928193	0.095213609	0.061264842	0.153803186	-0.033948767	0.058589577	0.092538343
CD82|P27701	0.32526406	0.807087184	0.999791462	0.981286433	0.862912739	0.965916298	0.817124399	0.978628875	-0.012128149	0.054785783	0.109384417	0.066913932	0.121512566	0.054598634

			ANOVA p -values with Tukey Adjustment						Difference (AD - CT)					
Gene ID | Unirprot ID	F-Value	Pr(>F)	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA
ACVR1B|P36896	3.31997738	0.021033992	0.230342049	0.02259692	0.047976282	0.795627028	0.932252617	0.985277923	0.142333333	0.209889406	0.185452089	0.067556073	0.043118756	-0.024437317
ARG1|P05089	0.32389441	0.808074158	0.856772385	0.999792358	0.911659039	0.888827809	0.998666705	0.937079463	-0.162629081	-0.016525074	-0.131200175	0.146104007	0.031428906	-0.114675101
IGKV2-40|A0A087WW87	1.79736367	0.152206656	0.600486838	0.141331535	0.257121386	0.787130234	0.921372959	0.99174379	-0.468764072	-0.807355826	-0.702365094	-0.338591754	-0.233601022	0.104990732
NA|A0A0G2JS06	4.85975599	0.002813675	0.086043098	0.643803598	0.54325316	0.002548372	0.666458453	0.05257369	-0.533680211	0.25702482	-0.286235517	0.790705031	0.247444694	-0.543260337
TNFRSF14|Q92956	1.50917401	0.214240484	0.759863412	0.276899283	0.24306495	0.85956829	0.829881475	0.999939336	0.047731161	0.085375319	0.087914908	0.037644157	0.040183747	0.002539589
TMEM165|Q9HC07	1.8798414	0.136342079	0.477099595	0.220323776	0.129816957	0.9637189	0.877253865	0.992780859	0.186427617	0.246472166	0.280327215	0.060044549	0.093899598	0.033855049
S1PR1|P21453	3.40727894	0.018924145	0.726658182	0.174428478	0.014264387	0.761506432	0.2109226	0.760659682	0.04781527	0.092119429	0.134764541	0.044304159	0.086949271	0.042645112
S100A6|P06703	2.27203486	0.081683147	0.464819207	0.995836691	0.236652504	0.323486214	0.985293867	0.139058153	-0.163973247	0.024888063	-0.2017986	0.18886131	-0.037825353	-0.226686663
TLL1|O43897	2.54108778	0.058582433	0.484971518	0.999682717	0.582562429	0.527054539	0.032923145	0.501374712	-0.086734398	-0.005678185	0.073191907	0.081056213	0.159926305	0.078870092
FKBP2|P26885	0.87107437	0.458000809	0.389655715	0.721324514	0.86398865	0.939764101	0.83910485	0.99320525	-0.094208188	-0.060887794	-0.045541201	0.033320394	0.048666986	0.015346593
DEFB1|P60022	0.66530712	0.574528717	0.963897107	0.506780194	0.927881081	0.820435137	0.999644517	0.8418425	-0.064644009	-0.180992636	-0.077639269	-0.116348627	-0.01299526	0.103353367
SLC1A3|P43003	0.96892951	0.410363007	0.848591628	0.745169465	0.331859901	0.997547976	0.826803765	0.909119039	-0.087482435	-0.107572067	-0.175132095	-0.020089631	-0.08764966	-0.067560028
LASP1|Q14847	3.97200188	0.010095289	0.907469245	0.072448623	0.424656959	0.013760028	0.138552979	0.787531088	0.073397158	-0.263550629	-0.163675568	-0.336947787	-0.237072726	0.099875061
ITGA1|P56199	2.02549427	0.114503971	0.194909345	0.999988985	0.603194657	0.165189342	0.861940368	0.561897702	-0.16399123	0.002520945	-0.100857483	0.166512175	0.063133747	-0.103378428
TPST1|O60507	0.01217983	0.998153701	0.999999872	0.999964386	0.998298351	0.999981557	0.998716417	0.999373495	-0.000433324	-0.002704014	-0.009503217	-0.00227069	-0.009069893	-0.006799203
VWC2L|B2RUY7	1.41378482	0.242576097	0.491831372	0.999370947	0.403124203	0.543878707	0.999852093	0.451242877	0.181098556	0.014873141	0.190224818	-0.166225416	0.009126261	0.175351677
C11orf87|Q6NUJ2	3.5675245	0.015364595	0.014913105	0.167931603	0.048940018	0.735036492	0.948902921	0.95607272	0.274114012	0.182881969	0.226704282	-0.091232043	-0.047409729	0.043822314
C11orf54|Q9H0W9	4.76939613	0.003502788	0.001627777	0.069693675	0.130177279	0.529605178	0.364243613	0.992003301	-0.282117848	-0.182711312	-0.162394521	0.099406536	0.119723327	0.020316791
CHST11|Q9NPF2	1.52810443	0.210014252	0.953411311	0.960224219	0.444028631	0.730596473	0.176036642	0.740372395	-0.036323448	0.033860637	0.101015952	0.070184084	0.1373394	0.067155316
CACYBP|Q9HB71	1.96037294	0.123921253	0.924734464	0.191959785	0.222893613	0.493291756	0.547037933	0.999657736	-0.045361549	-0.143946613	-0.137260113	-0.098585064	-0.091898564	0.0066865
SHISA4|Q96DD7	1.54666003	0.206482532	0.169631507	0.863765709	0.941069702	0.537147191	0.399696186	0.996113102	0.150849683	0.055359491	0.040124126	-0.095490192	-0.110725557	-0.015235365
IGKV6D-21|A0A0A0MT36	7.32599854	0.000118697	0.001117384	0.987797056	0.015653519	0.00280626	0.733616208	0.035419389	-0.92250811	-0.076684279	-0.68424319	0.845823831	0.23826492	-0.607558911
TMEM178A|Q8NBL3	1.01988909	0.385231351	0.985487071	0.384490197	0.690819488	0.618101777	0.89100338	0.944766247	0.023966606	0.107204727	0.071323607	0.083238121	0.047357001	-0.03588112
AMICA1|Q86YT9	2.22566554	0.087485297	0.127837786	0.99999981	0.691059576	0.115805323	0.617625842	0.677618017	0.264887234	0.000927716	0.124164082	-0.263959518	-0.140723152	0.123236366
PTHLH|P12272	8.62895822	2.29E-05	0.034608455	0.002832637	9.34E-06	0.877607022	0.150169012	0.50493212	0.253199222	0.320886045	0.441578777	0.067686822	0.188379555	0.120692733
SLC24A2|Q9UI40	2.53352872	0.058370209	0.889135455	0.99999319	0.090185262	0.89513702	0.39516665	0.087474103	0.031309514	0.001127225	0.09726617	-0.030182288	0.065956657	0.096138945
SLIT1|O75093	4.92482273	0.002901726	0.097069837	0.001865178	0.485974907	0.610625231	0.715965853	0.07546753	0.263389264	0.400135512	0.14929767	0.136746249	-0.114091594	-0.250837842
SCGB1A1|P11684	0.55897402	0.642759578	0.999996525	0.740213893	0.999809199	0.759578713	0.999618132	0.664943824	0.002678665	0.124443967	-0.009684585	0.121765303	-0.01236325	-0.134128552
COPG2|Q9UBF2	3.93073597	0.009471569	0.034818924	0.987468661	0.083083107	0.072363525	0.963870571	0.162125003	-0.445091561	-0.052503103	-0.370069299	0.392588459	0.075022263	-0.317566196
SLC6A1|P30531	0.08747785	0.966765829	0.980598145	0.969224714	0.998212303	0.999962977	0.995154955	0.990228943	-0.021932335	-0.024533177	-0.009014571	-0.002600842	0.012917764	0.015518606
PGA4|P0DJD7	1.96323849	0.123371548	0.555303977	0.859554857	0.889648928	0.147404664	0.15158414	0.999566585	-0.232442386	0.135845081	0.118764024	0.368287467	0.35120641	-0.017081057
0|A8MTW9	9.9770419	3.97E-06	0.000226942	0.999760652	0.006914405	0.000122398	0.660582301	0.004252108	0.499204053	-0.010061746	0.368403038	-0.509265799	-0.130801015	0.378464784
GABARAP|O95166	8.19856934	4.14E-05	0.262230175	0.006049556	2.57E-05	0.515048486	0.035070739	0.513103773	-0.064091715	-0.111750985	-0.156634777	-0.04765927	-0.092543062	-0.044883792
FAM171B|Q6P995	0.38808802	0.76179486	0.99698232	0.816272223	0.856438522	0.891246803	0.923224853	0.999765222	0.02562133	0.111123007	0.10066267	0.085501678	0.07504134	-0.010460337
S100A1|P23297	9.82836035	9.18E-06	0.994839118	0.009973201	6.37E-05	0.033999997	0.00052834	0.603073561	-0.025200011	-0.31455609	-0.433034059	-0.289356079	-0.407834048	-0.118477969
PSMB4|P28070	12.8702245	1.24E-07	0.982480164	0.000208488	0.000240597	5.50E-05	6.19E-05	0.998400552	0.032534256	-0.361056975	-0.347683455	-0.393591231	-0.38021771	0.013373521
TAX1BP1|Q86VP1	0.2730198	0.84479306	0.999937935	0.994530324	0.852689648	0.997662383	0.885481719	0.94209591	0.002864538	0.012287977	0.039162615	0.009423439	0.036298077	0.026874638
ELFN2|Q5R3F8	6.40324606	0.000388172	0.005894031	0.036207489	0.000301725	0.8975416	0.916063774	0.498497308	0.242711158	0.192566463	0.288341992	-0.050144695	0.045630834	0.095775529
TFF3|Q07654	1.7221458	0.165456734	0.936731093	0.14038221	0.551599454	0.43167042	0.899756354	0.822952066	-0.040626651	-0.14457127	-0.087863658	-0.103944619	-0.047237007	0.056707612
IGLV5-37|A0A075B6J1	3.1999824	0.024607357	0.399559548	0.947639404	0.166448131	0.147019543	0.974358941	0.040577782	-0.476346661	0.161282513	-0.600787288	0.637629174	-0.124440627	-0.762069801
TXNDC12|O95881	0.94061742	0.423188679	0.378508674	0.97295703	0.919502021	0.605867137	0.70894983	0.99696385	-0.138992138	-0.036232458	-0.052260489	0.10275968	0.086731649	-0.01602803
SPATA31C1|P0DKV0	0.78485176	0.503765803	0.685848061	0.994466981	0.98617526	0.817019642	0.446835967	0.929127907	-0.037461114	-0.008249025	0.011010272	0.029212089	0.048471386	0.019259296
DLG4|P78352	0.049935	0.985193375	0.998625246	0.99566278	0.981117349	0.999884096	0.996868727	0.999054475	-0.014658918	-0.021111244	-0.033266996	-0.006452326	-0.018608077	-0.012155751
KITLG|P21583	1.1018132	0.351857622	0.338632686	0.772472267	0.48820657	0.875937187	0.97622492	0.978686715	0.147695821	0.080596317	0.112696989	-0.067099504	-0.034998832	0.032100673
COL23A1|Q86Y22	2.51671895	0.059648794	0.729996811	0.999999975	0.362544773	0.717973318	0.039014086	0.349388434	-0.063734467	0.000247727	0.095735142	0.063982194	0.15946961	0.095487416
ARL8A|Q96BM9	0.59263819	0.620566777	0.999977718	0.828875252	0.755166368	0.813617013	0.738463432	0.999394089	-0.003954894	0.083017012	0.09414677	0.086971906	0.098101664	0.011129757
RNF150|Q9ULK6	0.92647986	0.429774428	0.717809153	0.966766153	0.411562901	0.927789359	0.960210483	0.678744157	0.057831503	0.025124368	0.084384885	-0.032707135	0.026553382	0.059260517

			ANOVA p -values with Tukey Adjustment						Difference (AD - CT)					
Gene ID | Unirprot ID	F-Value	Pr(>F)	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA
MMP16|P51512	3.97882697	0.009084643	0.131672162	0.47996704	0.005211538	0.866187099	0.653525579	0.210067069	0.149363694	0.097451726	0.226235733	-0.051911968	0.076872039	0.128784008
UST|Q9Y2C2	0.33115745	0.802827631	0.999471719	0.917339823	0.826153332	0.957896417	0.894229161	0.997029618	0.010560341	0.057422192	0.075184813	0.046861852	0.064624472	0.01776262
MEPE|Q9NQ76	2.92133445	0.035729415	0.067198117	0.314038455	0.04201736	0.863831024	0.999796275	0.807333563	0.292649525	0.201196669	0.302098849	-0.091452856	0.009449324	0.10090218
PIANP|Q8IYJ0	8.00078278	4.83E-05	0.003600414	0.000945108	6.80E-05	0.992608072	0.831419105	0.937341502	0.250276286	0.269903821	0.309144376	0.019627535	0.05886809	0.039240555
FZD3|Q9NPG1	1.14907748	0.333163262	0.546465447	0.845299914	0.991321448	0.951176991	0.347513761	0.663194697	0.11572357	0.069885492	-0.024234649	-0.045838078	-0.139958219	-0.094120141
HS3ST1|O14792	0.65896858	0.579116593	0.591058998	0.741275997	0.665928354	0.993374319	0.997765093	0.999716739	-0.0997741	-0.078883143	-0.085756183	0.020890957	0.014017917	-0.00687304
ATP6V1E1|P36543	5.58427989	0.00131284	0.756772568	0.12164468	0.098187183	0.008032801	0.00532332	0.999990805	0.085639918	-0.191648312	-0.194054948	-0.27728823	-0.279694865	-0.002406636
ATP1B3|P54709	1.21663644	0.306978126	0.915866989	0.36096338	0.401693383	0.75876937	0.801591174	0.99975736	-0.041948069	-0.103476671	-0.098180318	-0.061528602	-0.056232249	0.005296353
COLEC11|Q9BWP8	3.52269022	0.017055811	0.187145486	0.656720594	0.998851481	0.008792388	0.208996361	0.527154941	-0.228863681	0.127932144	-0.016015044	0.356795825	0.212848637	-0.143947188
SDC2|P34741	1.94775003	0.125771276	0.479943286	0.988258727	0.392737465	0.288542651	0.999662565	0.216736925	-0.082563456	0.018133502	-0.088060179	0.100696958	-0.005496723	-0.10619368
CCL18|P55774	5.28075738	0.001973055	0.166602649	0.930406133	0.037775576	0.03752261	0.936633051	0.005304438	-0.327981922	0.093644059	-0.417718016	0.421625981	-0.089736094	-0.511362075
TSKU|Q8WUA8	1.24330663	0.29749655	0.440335087	0.655339403	0.274623925	0.981150784	0.994253203	0.913693362	-0.163036315	-0.122386352	-0.189909186	0.040649963	-0.026872871	-0.067522834
PLEKHB2|Q96CS7	6.19359178	0.000494533	0.005652829	0.186794814	0.000534762	0.502889858	0.962942029	0.203589437	0.187531624	0.110176182	0.213637379	-0.077355441	0.026105755	0.103461196
TGFBR1|P36897	5.55670769	0.001304531	0.975623401	0.339792443	0.009142879	0.158711961	0.002311785	0.40897278	0.027255558	-0.108207987	-0.206831748	-0.135463544	-0.234087306	-0.098623761
ACVR1|Q04771	1.33114797	0.266129889	0.281925983	0.988961707	0.627565937	0.444607729	0.893776528	0.81737879	-0.099227471	-0.016987158	-0.061719287	0.082240313	0.037508184	-0.044732129
PDXP|Q96GD0	25.2026342	3.25E-13	0.889422056	2.43E-06	4.48E-08	7.13E-08	9.29E-10	0.871751992	0.059684652	-0.428883259	-0.487661805	-0.488567911	-0.547346457	-0.058778545
BGLAP|P02818	7.84904911	6.39E-05	0.018601417	0.637280112	0.090449574	0.000271796	0.861929184	0.00193887	0.289645491	-0.111059597	0.216103153	-0.400705088	-0.073542338	0.327162749
NINL|Q9Y2I6	0.30759835	0.819878383	0.992016681	0.97178741	0.972200273	0.888596646	0.999103483	0.804959124	0.034262491	-0.051495043	0.050047063	-0.085757534	0.015784572	0.101542106
CCK|P06307	1.85360527	0.139294826	0.091907115	0.538475471	0.661143481	0.726213982	0.561127792	0.995248601	0.165804772	0.093116538	0.077284382	-0.072688234	-0.088520389	-0.015832155
IGLV4-69|A0A075B6H9	9.93833911	4.17E-06	0.033822886	0.852177374	0.001073131	0.002477263	0.795797892	2.80E-05	-0.446388795	0.127559653	-0.590177003	0.573948448	-0.143788208	-0.717736656
PSMA3|P25788	10.5799165	2.31E-06	0.996905648	0.000248814	0.002824319	0.000137858	0.001606712	0.838127546	0.015132637	-0.305619515	-0.247508999	-0.320752152	-0.262641635	0.058110516
MAPRE1|Q15691	6.81997356	0.000316814	0.85288332	0.012773286	0.000992901	0.108520979	0.015768808	0.902091849	-0.076456022	-0.287652698	-0.346585948	-0.211196676	-0.270129926	-0.05893325
ITGA7|Q13683	0.7265194	0.537671258	0.999948938	0.604219054	0.990855804	0.576243006	0.985311158	0.751481537	-0.004116431	0.095138402	0.022206223	0.099254833	0.026322655	-0.072932179
MGAT5B|Q3V5L5	2.41736567	0.070018716	0.136601699	0.999999494	0.419030289	0.134514759	0.868740363	0.417264173	0.202221011	0.001011949	0.133915774	-0.201209062	-0.068305237	0.132903825
MMP19|Q99542	1.82028926	0.145452892	0.688901434	0.992270739	0.309536382	0.511600363	0.94496261	0.178875867	0.086055826	-0.021360296	0.127885252	-0.107416122	0.041829426	0.149245548
FCGRT|P55899	1.34666294	0.261547332	0.259256161	0.965340399	0.994287	0.498315411	0.349944944	0.995581121	-0.121508705	-0.029820226	-0.015661631	0.091688479	0.105847074	0.014158594
GPRC5B|Q9NZH0	0.80741029	0.491994523	0.880064444	0.627661832	0.999796112	0.972134213	0.8243188	0.532186209	-0.05367574	-0.084294268	0.005696138	-0.030618528	0.059371878	0.089990406
HINT1|P49773	9.03731166	1.52E-05	0.749970023	0.004911398	5.30E-05	0.077215763	0.002296127	0.68737548	-0.08707706	-0.295247026	-0.386873306	-0.208169965	-0.299796245	-0.09162628
HCRT|O43612	2.53578817	0.058200416	0.88466981	0.27482537	0.683499038	0.059428905	0.25075324	0.877152939	-0.048086465	0.115501768	0.069469754	0.163588232	0.117556219	-0.046032013
PDLIM5|Q96HC4	19.1647287	2.66E-10	0.279311368	0.000132287	0.000527743	2.92E-08	1.14E-07	0.945896819	0.130060251	-0.320915428	-0.282662066	-0.450975679	-0.412722317	0.038253362
LY96|Q9Y6Y9	0.43200244	0.730471497	0.850166343	0.993322719	0.99981264	0.712513189	0.795453306	0.997226507	-0.079895416	0.02512348	0.007249174	0.105018897	0.087144591	-0.017874306
JMJD8|Q96S16	1.24160463	0.297475195	0.244322121	0.619076315	0.521786318	0.904374025	0.930953549	0.999566426	-0.207996127	-0.133696479	-0.144760627	0.074299648	0.0632355	-0.011064148
SHISA9|B4DS77	8.07415979	6.56E-05	0.000805698	0.001867388	0.000227381	0.985858135	0.999788296	0.968953066	0.350490525	0.319611973	0.357768397	-0.030878551	0.007277872	0.038156424
SULF1|Q8IWU6	0.6024758	0.614580214	0.999756625	0.669737155	0.992688626	0.645592099	0.984754758	0.797350566	0.010186704	-0.126877196	-0.029155925	-0.1370639	-0.039342629	0.097721271
LRP3|O75074	0.06933453	0.976155333	0.972315094	0.9904159	0.998077811	0.998795779	0.992027145	0.999082441	0.05231945	0.034961505	0.019992605	-0.017357945	-0.032326845	-0.0149689
INAFM1|C9JVW0	3.55174292	0.015975541	0.023957968	0.234843597	0.028048534	0.755476092	0.997278278	0.835159885	0.25768261	0.168849452	0.240704258	-0.088833158	-0.016978351	0.071854807
ADA|P00813	8.96822809	2.45E-05	0.035332005	0.695428998	0.007682204	0.001483084	0.994420461	0.000152227	0.338886716	-0.131854459	0.368101012	-0.470741175	0.029214296	0.499955471
HCN2|Q9UL51	0.63857982	0.591681813	0.597184491	0.86492955	0.646223421	0.963149929	0.9992636	0.982245346	0.101079059	0.062847182	0.091361833	-0.038231877	-0.009717227	0.028514651
ELF2|Q15723	2.73603408	0.044932903	0.137176315	0.32893387	0.035440389	0.953580769	0.971396123	0.747180644	0.209238454	0.159500057	0.250204001	-0.049738397	0.040965547	0.090703944
SAE1|Q9UBE0	0.88635216	0.449723021	0.673974852	0.977291229	0.998740558	0.429459017	0.551145897	0.992870071	-0.146735548	0.051017079	0.018260158	0.197752627	0.164995706	-0.032756921
FITM1|A5D6W6	2.19493353	0.09014813	0.091483071	0.518414478	0.966483613	0.733900265	0.200016037	0.774855342	-0.08761109	-0.049854768	-0.016522215	0.037756321	0.071088875	0.033332553
FJX1|Q86VR8	1.60533473	0.189661175	0.964037166	0.248139599	0.349379297	0.52901649	0.664658365	0.99430217	0.024797028	0.094140352	0.081858389	0.069343324	0.057061361	-0.012281963
CTTN|Q14247	2.12793734	0.099114862	0.738836659	0.954502954	0.47031132	0.417145037	0.06865073	0.787574574	0.079480873	-0.039096724	-0.106808008	-0.118577597	-0.186288881	-0.067711284
C17orf53|Q8N3J3	1.10483788	0.348476171	0.579162919	0.973967548	0.999949123	0.317653723	0.514992084	0.97970592	-0.125874501	0.040880233	0.004881861	0.166754734	0.130756362	-0.035998371
FRMPD1|Q5SYB0	18.4284804	1.67E-10	1.14E-06	0.93069271	4.73E-07	1.24E-05	0.999649115	5.95E-06	-0.211569862	-0.02297621	-0.207836876	0.188593651	0.003732985	-0.184860666
FAM174A|Q8TBP5	3.93290086	0.009444789	0.581335688	0.025735684	0.016697754	0.432333563	0.365281671	0.999788363	0.072090283	0.156409139	0.160843345	0.084318856	0.088753063	0.004434207
PKIA|P61925	8.98006299	2.00E-05	0.256130575	0.071853226	0.050675197	0.000242106	9.97E-05	0.999999026	0.181064625	-0.23872742	-0.240023983	-0.419792046	-0.421088608	-0.001296562

			ANOVA p -values with Tukey Adjustment						Difference (AD - CT)					
Gene ID | Unirprot ID	F-Value	Pr(>F)	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA
NCL|P19338	1.44458695	0.234311639	0.291999201	0.342871706	0.346641028	0.994336144	0.994812348	0.999999914	-0.307993349	-0.265898417	-0.266843013	0.042094931	0.041150336	-0.000944596
GART|P22102	0.09388525	0.96330565	0.999822908	0.997556067	0.96109976	0.999542429	0.976758365	0.989360105	-0.00476483	-0.011088882	-0.028802053	-0.006324051	-0.024037223	-0.017713171
CST7|O76096	0.64016123	0.590079783	0.868762822	0.999916765	0.934872717	0.834974247	0.512737868	0.949957954	-0.068212093	0.005303398	0.049845747	0.07351549	0.11805784	0.044542349
DEFA1|P59665	0.35097379	0.788492439	0.910729368	0.999984401	0.884167157	0.89267267	0.999954898	0.862234139	-0.104952455	0.005489178	-0.112595438	0.110441633	-0.007642983	-0.118084616
LTBR|P36941	0.93374813	0.425522781	0.90431958	0.897830278	0.350702133	0.999999998	0.790358201	0.774007787	-0.034836825	-0.034745247	-0.080499702	9.16E-05	-0.045662877	-0.045754456
PRG2|P13727	1.58756438	0.194109258	0.819380236	0.80883652	0.759140882	0.28412765	0.999784353	0.219829542	0.109513521	-0.110845533	0.119714363	-0.220359054	0.010200842	0.230559896
TMSB15A|P0CG35	10.1381401	4.09E-06	0.967064607	0.0039781	0.000818301	0.001017227	0.000184237	0.985343577	0.023316418	-0.169282242	-0.185773473	-0.19259866	-0.209089891	-0.016491231

Table 6.4: SRM Peptide Coefficients of Variation

Gene	Protein Accession	Peptide	ATneg CV Total Area Ratio	ATpos CV Total Area Ratio	CV Total Area Ratio
AHSG	P02765	EHAVEGDCDFQLLK	9.40%	6.70%	22%
ALB	P02768	LVNEVTEFAK	3.80%	1.90%	21.50%
ALB	P02768	LVTDLTK	3.60%	2.50%	21.20%
ALDOA	P04075	VLAAVYK	7.30%	5.60%	16.10%
APOA4	P06727	SLAPYAQDTQEK	5%	3%	21.30%
APOC1	P02654	QSELSAK	8.60%	12.70%	28.80%
APOC2	P02655	TAAQNLYEK	3.50%	4.40%	16.10%
APOE	P02649	ELQAAQAR	4.60%	1.90%	13.30%
C9	P02748	TSNFNAAISLK	10.50%	8.50%	18.50%
C9	P02748	LSPIYNLVPVK	9%	6.70%	17.40%
CALM2	P0DP24	EAFSLFDK	9.80%	5.20%	18.30%
CD44	P16070	TEAADLCK	20.10%	14.60%	13.20%
CD44	P16070	ALSIGFETCR	26.80%	13.80%	13.40%
CHI3L1	P36222	IASNTQSR	6.60%	5.40%	20.10%
CHI3L1	P36222	GNQWVGYDDQESVK	8.90%	7.10%	21.20%
CHI3L1	P36222	QLLLSAALSAGK	6.50%	14.80%	23.40%
CP	P00450	EVGPTNADPVCLAK	10.30%	9.60%	12.70%
CP	P00450	GEFYIGSK	4.50%	2.90%	13.10%
CST3	P01034	ASNDMYHSR	15.40%	9.40%	15.70%
DCN	P07585	VDAASLK	7.40%	7.20%	8.70%
DDAH1	O94760	EFFVGLSK	14.10%	9.40%	18%
DKK3	Q9UBP4	DQDGEILLPR	5.50%	2.70%	12.50%
ENO1	P06733	IEEELGSK	11.70%	8.80%	21.20%
ENO1	P06733	LNVTEQEK	9.20%	8.50%	18.20%
ENO2	P09104	IEEELGDEAR	10.80%	9.90%	16.60%
F2	P00734	YTACETAR	16.50%	16%	18%
F2	P00734	TATSEYQTFFNPR	7.10%	6.60%	18.20%
GAPDH	P04406	AAFNSGK	16.90%	14.70%	27.60%
GAPDH	P04406	YDNSLK	11.60%	8.70%	20.40%
GDA	Q9Y2T3	DHLLGVSDSGK	13.70%	12.30%	23.20%
GOT1	P17174	VGNLTVVGK	7.90%	7.90%	18.40%
GOT1	P17174	IGADFLAR	6.80%	8.50%	16.40%
GSN	P06396	AGALNSNDAFVLK	4.70%	3.80%	12.60%
HBA1	P69905	FLASVSTVLTSK	5.50%	2.90%	97.40%
HBA1	P69905	VGAHAGEYGAEALER	11.70%	10.10%	93.90%
HBB	P68871	VNVDEVGGEALGR	4.40%	2.90%	97.20%
KNG1	P01042	EGDCPVQSGK	11.80%	10.80%	17.80%
KNG1	P01042	QVVAGLNFR	10.40%	5.50%	20.60%
KNG1	P01042	VQVVAGK	5%	2.20%	20.90%
L1CAM	P32004	GQLSFNLR	9.10%	16.10%	13.40%
LAMP1	P11279	VWVQAFK	11.80%	12.70%	16.90%
LAMP2	P13473	YLDFVFAVK	13.10%	12.80%	15.10%
LDHB	P07195	FIIPQIVK	7.30%	5.90%	17.50%
LDHC	P07864	VIGSGCNLDSAR	7.30%	8.80%	23.60%
MDH1	P40925	GEFVTTVQQR	7.20%	5.50%	20%
NCAM1	P13591	GLGEISAASEFK	5.90%	7%	15.50%
NPTX2	P47972	VAELEDEK	10.50%	15.30%	19.60%
NPTXR	O95502	ELDVLQGR	4.70%	3.10%	13.80%
NRXN1	P58400	LAIGFSTVQK	11.50%	9%	15.40%
OGN	P20774	LEGNPIVLGK	6.20%	3.10%	8.60%
OMG	P23515	LESLPAHLPR	8.50%	6.10%	14.90%
PARK7	Q99497	ALVILAK	7.70%	4.90%	18%
PEBP1	P30086	GNDISSGTVLSDYVGSGPPK	7.40%	7.40%	17.70%
PEBP1	P30086	LYEQLSGK	11.70%	8.20%	17.70%
PEBP1	P30086	VLTPTQVK	5.60%	3.10%	14.20%
PGLYRP2	Q96PD5	TFTLLDPK	5%	3.10%	20.30%
PKM	P14618	VVEVGSK	3.50%	5.90%	20%
PKM	P14618	GVNLPGAAVDLPAVSEK	5.50%	5.90%	21.40%
PKM	P14618	GDLGIEIPAEK	6.20%	5.80%	17.70%
PKM	P14618	GDYPLEAVR	5.30%	4.40%	18.60%
PKMisoform		LFEELVR	5.30%	4.40%	20.60%
PON1	P27169	LLIGTVFHK	7.70%	10%	22.10%
PPIA	P62937	VSFELFADK	6.60%	9.80%	18.70%
PRDX2	P32119	QITVNDLPVGR	15.10%	14.20%	32.10%
PTPRZ1	P23471	AIIDGVESVSR	6.50%	3.70%	13%
PTPRZ1	P23471	DIEEGAIVNPGR	5%	4.20%	12%
SCG2	P13521	IESQTQEEVR	8.10%	7.40%	19%
SCG2	P13521	SGQLGIQEEDLR	7.10%	6.90%	21.30%
SMOC1	Q9H4F8	AQALEQAK	13.30%	9.20%	27.20%
SOD1	P00441	AVCVLK	13.60%	9.60%	23.30%
SOD1	P00441	GDGPVQGIINFEQK	11.40%	11.10%	18.50%
SOD1	P00441	HVGDLGNVTADK	11.10%	7%	19.90%
SPP1	P10451	GDSVVYGLR	24.30%	13.80%	14.70%
SPP1	P10451	YPDAVATWLNPDPSQK	9.60%	8.30%	15.30%
SPP1	P10451	QETLPSK	6.70%	7.10%	18.80%
THY1	P04216	HVLFGTVGVPEHTYR	11.40%	10%	17.90%
TPI1	P60174	IAVAAQNCYK	20.90%	24.50%	18.60%
VGF	O15240	EPVAGDAVPGPK	3.90%	2%	24.20%
VGF	O15240	GLQEAAEER	5.10%	5.40%	24.50%
VTN	P04004	GQYCYELDEK	10.50%	5.60%	20.50%
VTN	P04004	DVWGIEGPIDAAFTR	8.70%	7%	20.80%
YWHAB	P31946	NLLSVAYK	8.30%	9%	26.70%
YWHAB	P31946	VISSIEQK	11.80%	6.40%	18.60%
YWHAG	P61981	YLAEVATGEK	17.10%	9.30%	29.50%
YWHAZ	P63104	VVSSIEQK	15.10%	14.10%	35.40%

Table 6.5: SRM Ratio Abundances Post-Regression

SUPPLEMENTAL TABLE 11: SRM RATIO ABUNDANCES POST-REGRESSION																						
Gene ID | Protein ID| Peptide Sequence	S001_P1A01_41324	S002_P1B01_53612	S003_P1C01_63456	S004_P1D01_75351	S005_P1E01_45034	S006_P1F01_46442	S007_P1G01_49419	S008_P1H01_69732	S009_P1A02_46085	S010_P1B02_51370	S011_P1C02_37512	S012_P1D02_46642	S013_P1E02_44067	S014_P1F02_42541	S015_P1G02_44291	S016_P1H02_49417	S017_P1A03_59913	S018_P1B03_62211	S019_P1C03_66984	S020_P1D03_57339	S021_P1E03_45130	S022_P1F03_67976
AHSG | P02765 | EHAVEGDC[+57]DFQLLK	-4.116683667	-4.872020265	-3.632265225	-4.87855082	-4.69610594	-4.761281168	-5.00690546	-3.993134888	-5.968824966	-4.837157043	-4.749062196	-3.998120275	-4.722610751	-4.31882417	-4.346191351	-5.815560065	-5.830394781	-5.011796028	-3.529269888	-4.572785029	-4.514084872	-5.045307433
ALB | P02768 | LVNEVTEFAK	5.631864868	4.934004527	6.003262267	4.410495216	5.019985872	4.894139208	4.607492225	5.673696422	3.089905326	4.539969287	5.058522956	5.927753381	4.643997732	5.316478306	5.463128535	4.124491461	4.146837186	4.829765819	6.305269472	5.471268327	5.160155429	4.560348832
ALB | P02768 | LVTDLTK	6.34588322	5.615666721	6.736579262	5.148693935	5.750241471	5.565836422	5.324900165	6.356798039	3.769930289	5.287892584	5.773835309	6.693122168	5.353264464	6.066510143	6.201008856	4.841735026	4.870030405	5.552321352	7.06383812	6.165253461	5.888099219	5.267806867
ALDOA | P04075 | VLAAVYK	-6.579975516	-6.979863835	-7.498233025	-7.28066296	-6.221741917	-6.531882181	-6.891328208	-7.037605663	-8.055927076	-7.52088288	-7.329869849	-6.857438398	-7.678044868	-7.599495139	-7.383126914	-7.766405758	-6.779646048	-6.834411642	-6.993388408	-7.559409862	-6.137393012	-7.15386483
APOA4 | P06727 | SLAPYAQDTQEK	-4.968499499	-5.261112573	-4.751201962	-4.965431712	-4.578209078	-5.193544339	-4.476681398	-4.508129192	-6.86997669	-5.419298056	-5.20521979	-4.15813456	-5.121941679	-4.725483648	-4.269818099	-5.526116814	-6.155647956	-5.258123886	-3.887339385	-4.97821008	-4.544687236	-6.25076291
APOC1 | P02654 | QSELSAK	1.941225378	1.502712795	2.555193808	1.523853788	1.404116611	1.49281554	1.199472164	1.71359534	0.863876568	0.933329019	1.478240757	1.832826689	1.674070716	1.556565971	2.104469968	1.092152461	1.204429852	1.774513717	2.461240139	1.749876886	1.835087009	0.94554405
APOC2 | P02655 | TAAQNLYEK	-7.382592086	-7.826297767	-6.605809637	-8.059136506	-7.696521369	-7.304755135	-8.101837623	-7.52246637	-9.550819158	-8.368465774	-8.032419189	-7.806598268	-7.388622595	-7.605028298	-6.215869835	-8.021227255	-8.163582575	-7.659687118	-5.813820781	-6.760578314	-7.791801756	-7.990193296
APOE | P02649 | ELQAAQAR	-1.435037714	-1.67449804	-2.23434355	-1.808742977	-1.557694733	-1.655834088	-1.767458475	-1.938624513	-2.771666265	-2.645671695	-2.37629663	-2.493576398	-2.582429478	-2.746243946	-2.182835772	-2.54102877	-2.033754186	-1.862004164	-1.976429986	-2.32033262	-1.814524297	-2.410229089
C9 | P02748 | TSNFNAAISLK	-7.364744282	-7.627943687	-7.409550233	-8.249955089	-7.382400968	-8.279126364	-8.51696099	-7.532315234	-10.20053123	-8.806931602	-8.44738942	-7.53391031	-8.401989552	-7.877825137	-7.213073506	-9.411068593	-9.06624474	-8.556242334	-5.743125913	-8.118107281	-7.922969821	-9.059411399
C9 | P02748 | LSPIYNLVPVK	-6.761209437	-7.011083001	-6.493263419	-7.557151512	-6.97783031	-7.370250308	-7.898107317	-6.801412335	-9.081171836	-7.781496102	-7.381046549	-6.740321069	-7.667329819	-7.181733723	-6.393137452	-8.394594871	-8.046756038	-7.93007387	-5.146380058	-7.364835795	-6.971732697	-7.858085453
CALM2 | P0DP24 | EAFSLFDK	-6.069575705	-6.025942053	-6.669254027	-6.33483472	-5.737633575	-5.795949892	-6.098786876	-6.45244476	-6.972980748	-6.981198061	-6.512843964	-6.041544112	-7.002575709	-6.842450102	-6.829729455	-7.353382146	-6.119680817	-6.308605123	-6.23357877	-6.776979747	-5.318432481	-6.391810865
CD44 | P16070 | TEAADLC[+57]K	-9.815016875	-9.325260017	-10.07551204	-9.151982575	-9.133823175	-9.173852954	-9.707761485	-9.863247614	-10.18728228	-10.07612974	-9.947943555	-9.047191297	-9.873973196	-9.566158703	-9.48123449	-9.640153788	-9.571852786	-9.682245004	-9.356293098	-9.986558368	-9.136050354	-9.65531202
CD44 | P16070 | ALSIGFETC[+57]R	-8.924259301	-9.063766931	-9.023154786	-8.982554551	-8.471156077	-8.525450974	-9.378906411	-8.97184398	-9.127186825	-9.049152396	-8.977814169	-8.770623335	-9.132166471	-8.991514775	-9.466206024	-9.104995507	-8.920504902	-9.064021431	-8.436017217	-9.362879292	-8.588937637	-9.589435975
CHI3L1 | P36222 | IASNTQSR	-2.412175513	-2.938242037	-2.887513392	-3.539639807	-2.608081165	-2.372115142	-2.773199999	-2.320632361	-3.858623867	-3.378434679	-3.431947712	-2.780537344	-3.253175897	-2.683276854	-3.483184156	-2.890751752	-2.816512976	-3.1220424	-1.549106166	-3.445377336	-1.6143291	-2.572583856
CHI3L1 | P36222 | GNQWVGYDDQESVK	-4.380632056	-5.13306947	-5.037832761	-5.841587736	-4.593969195	-4.33353714	-4.606808211	-4.488042683	-6.214879835	-5.433219054	-5.532610481	-4.764848117	-5.168784642	-4.722032496	-5.566644555	-5.036428022	-4.978440626	-5.64938446	-3.402460067	-5.698346758	-3.652056578	-4.387140062
CHI3L1 | P36222 | QLLLSAALSAGK	-0.215821158	-0.926531848	-0.681069049	-1.73776227	-0.458774923	0.06218996	-0.426812038	-0.304424319	-1.802564805	-1.432020577	-1.180123697	-0.457570069	-0.941199797	-0.147497089	-1.174571415	-0.557596027	-0.751850919	-1.154719028	0.835577474	-1.262077653	0.260646403	-0.416263782
CP | P00450 | EVGPTNADPVC[+57]LAK	-3.113231873	-3.287262482	-2.723527151	-3.815435876	-3.276353635	-3.379181369	-4.164080956	-3.208238658	-3.975862577	-3.735464742	-3.491880255	-2.836561394	-3.655702367	-3.18960802	-2.770854632	-4.358922049	-4.102311678	3.900709799	-1.39106937	-3.089844577	-3.526954205	-4.35519131
CP | P00450 | GEFYIGSK	-4.48063491	-4.685950934	-4.084440791	-5.332786996	-4.627489625	-4.664515123	-5.264311974	-4.521227059	-5.642774859	-5.028643214	-5.088259279	-4.083165722	-5.117388583	-4.698616687	-3.949355404	-5.589485481	-5.332176677	-5.129258707	-2.478844558	-4.369349204	-4.578331436	-5.255710585
CST3 | P01034 | ASNDM[+16]YHSR	-4.404625875	-3.978352774	-5.104684875	-3.870111278	-3.990747565	-4.290265451	-4.296085435	-4.782054162	-5.02578861	-4.769920116	-4.795255673	-4.733526967	-5.286515288	-5.035419843	-4.862159808	-4.770096852	-4.377618036	-4.472196348	-4.948932215	-5.040161796	-4.259679951	-5.293193475
DCN | P07585 | VDAASLK	-7.079978289	-7.157853021	-7.054630847	-7.228550065	-7.101607384	-7.231493259	-7.229937066	-7.481283795	-7.585161623	-7.226864592	-7.160840167	-6.936061904	-7.11021587	-7.110334831	-7.385279956	-7.588250463	-7.622184935	-7.071650763	-7.69471049	-7.216879051	-7.610562857	-7.273466659
DDAH1 | O94760 | EFFVGLSK	-10.75834419	-10.71709714	-11.16878789	-11.03182398	-10.45144212	-10.54026869	-10.70380644	-11.09222152	-11.61613211	-11.67845175	-10.93963023	-10.65182933	-11.56055244	-11.44057138	-11.47000441	-11.27862707	-11.07365922	-10.68966071	-11.13577622	-10.85908341	-10.54536479	-11.12264714
DKK3 | Q9UBP4 | DQDGEILLPR	-3.477409299	-3.461127649	-3.827976914	-3.711039267	-3.092055679	-3.427153024	-3.406111768	-3.950637237	-4.461435333	-4.322839742	-4.096533747	-3.704925403	-4.206569155	-4.408342374	-4.187437707	-4.321654786	-3.438057857	-3.472756828	-3.918140939	-4.245810171	-3.102322942	-4.204377903
ENO1 | P06733 | IEEELGSK	-8.271150937	-8.610594299	-9.007332027	-8.792110462	-8.289330074	-8.083367042	-8.071389116	-8.879817674	-10.27304886	-9.186009052	-8.744083691	-8.314661846	-9.194953582	-8.817799965	-8.733587794	-9.335317131	-8.595216621	-8.658705303	-8.769382392	-8.663018216	-7.871482553	-8.259824075
ENO1 | P06733 | LNVTEQEK	-8.067267898	-8.909295811	-9.021975002	-8.540909875	-8.016632333	-8.054743594	-8.322653664	-8.784552733	-10.05510697	-9.249620202	-8.555055383	-8.276718518	-8.793953476	-8.654365159	-8.797997166	-9.12104563	-8.608908961	-8.56989131	-8.545015271	-8.864852184	-7.812956647	-8.35200998
ENO2 | P09104 | IEEELGDEAR	-5.668599986	-6.110265916	-6.634469087	-6.14572889	-5.732517004	-5.754706763	-5.788023927	-5.977230799	-6.522727259	-6.654089805	-6.277196737	-5.870682564	-6.303808715	-6.317013681	-6.428495918	-6.534661924	-5.684329688	-5.88984452	-6.272970283	-6.294544581	-5.752966642	-6.064967427
F2 | P00734 | YTAC[+57]ETAR	-8.359612901	-8.684377413	-8.017349272	-8.76828727	-8.273096116	-8.841214855	-9.264176425	-8.515925428	-10.39347364	-8.963921806	-8.393392396	-8.24214302	-9.203450212	-8.242927244	-8.071712821	-9.729362507	-9.522987068	-9.272639753	-7.611351931	-8.434226106	-8.558836298	-8.976282008
F2 | P00734 | TATSEYQTFFNPR	-5.867413319	-6.411145681	-5.523131151	-7.0632245	-6.50607865	-6.739136379	-7.142982165	-6.045085459	-7.869539138	-7.12681387	-6.757249481	-5.751383189	-6.609113061	-6.25041513	-6.063556646	-7.377522946	-7.267900489	-6.749317208	-5.197868171	-6.552314207	-6.401809426	-6.73036991
GAPDH | P04406 | AAFNSGK	-8.11886338	-8.764676832	-9.191024162	-9.153255723	-8.118886089	-7.83028404	-7.735232286	-8.51596116	-10.01900188	-9.260517993	-8.97118131	-7.798902468	-9.042103073	-8.312665818	-9.125560329	-9.431005529	-8.835716406	-8.437639393	-9.063739977	-8.560722548	-9.018572385	-8.335752651
GAPDH | P04406 | YDNSLK	-10.76174674	-11.08876749	-11.7057875	-11.52091879	-10.69277888	-10.26936859	-10.37308175	-11.19077105	-11.70615594	-11.92917986	-11.34663877	-10.31390975	-11.20999794	-11.12766619	-11.72266286	-11.531461	-11.37589996	-11.30443585	-11.44889441	-10.96090147	-11.41237064	-10.8468967
GDA | Q9Y2T3 | DHLLGVSDSGK	-8.585384498	-9.386243184	-9.42963006	-8.768634291	-8.406466422	-8.302491475	-8.888984132	-8.868876114	-10.60899753	-9.435430814	-9.274851547	-8.811251473	-9.990237211	-9.597064216	-10.00235693	-9.44692111	-8.652133966	-8.746996117	-10.19779013	-9.8471229	-8.102592261	-8.815907853
GOT1 | P17174 | VGNLTVVGK	-7.156884837	-7.398732203	-8.189281112	-7.684703025	-6.972663052	-7.159252386	-7.329831777	-7.48545225	-8.691062458	-8.071897991	-7.944300478	-7.491411361	-8.204045841	-8.196761707	-8.316482617	-8.493052564	-7.287134212	-7.366458053	-7.49995857	-7.940721977	-6.683925554	-7.722097527
GOT1 | P17174 | IGADFLAR	-9.186308547	-9.507305225	-10.00078679	-9.705534858	-8.986170398	-9.268951361	-9.578183941	-9.495237263	-10.35462202	-9.833298257	-9.869080354	-9.811752124	-9.985807181	-10.18440835	-10.005049	-10.50857535	-9.417464973	-9.625634488	-9.648232658	-10.01453536	-8.742637459	-10.01736108
GSN | P06396 | AGALNSNDAFVLK	-3.438500956	-3.914422599	-3.623379899	-4.211607071	-3.58516002	-3.816443769	-3.925587784	-3.489693149	-5.157072736	-4.634549076	-4.159528403	-3.599192371	-4.320297539	-3.986827433	-3.761150037	-4.800039922	-4.529280457	-4.001150511	-3.301735255	-4.179895606	-3.657716809	-4.316182936
HBA1 | P69905 | FLASVSTVLTSK	-4.616366363	-8.457839087	-8.732284651	-9.137172648	-8.797155061	-8.322872415	-9.382667053	-9.211359434	-4.783610623	-9.384702147	-4.893038286	-2.522907591	-9.121996516	-7.562575053	-8.197330611	-7.407792779	-9.057312055	-4.839413783	-0.729434138	-8.495794297	-7.365560872	-6.568491752
HBA1 | P69905 | VGAHAGEYGAEALER	-4.317549253	-11.64191971	-10.71102085	-11.43400352	-11.730001	-11.31455117	-11.97314707	-13.5716679	-4.527127971	-10.14249664	-4.540333779	-2.082700179	-9.960124013	-7.399656513	-8.18416625	-7.48341028	-12.05651201	-4.510430445	-0.344845807	-9.347373868	-8.135917564	-6.689890761
HBB | P68871 | VNVDEVGGEALGR	-4.094429254	-10.00409476	-8.559091822	-11.64346025	-10.84443841	-9.147294657	-11.41064663	-10.20356689	-4.316890873	-10.44533783	-4.448253488	-1.948732622	-9.417618497	-7.204555589	-7.969563447	-6.992714734	-9.966163257	-4.359603765	-0.246310294	-8.41919643	-7.219268131	-6.055574436
KNG1 | P01042 | EGDC[+57]PVQSGK	-9.006969581	-9.740121309	-8.479243265	-9.891819509	-9.065660302	-10.05413105	-10.06708858	-8.542043616	-10.51651727	-9.630580011	-9.745450243	-8.39858202	-9.530739528	-9.268664373	-8.554926259	-10.18403103	-10.09717178	-10.31574897	-7.594812067	-9.101367409	-8.888013124	-9.847916821
KNG1 | P01042 | QVVAGLNFR	1.627683814	1.11312801	2.239171704	0.708439249	1.437973872	0.760574808	0.651816595	1.967267322	-0.308364627	0.813845788	1.100066626	1.530590761	0.727377385	1.575894035	2.233757102	0.16305191	-0.014717768	0.395552922	2.856036302	1.489880781	1.230780952	0.320332768
KNG1 | P01042 | VQVVAGK	-4.867707831	-5.39906661	-4.316441906	-5.837045022	-4.997741073	-5.55605306	-5.663073478	-4.546193201	-6.996991384	-5.694729335	-5.477788297	-4.420700062	-5.679736076	-4.997579853	-4.364414873	-6.358337084	-6.35327862	-5.800165966	-3.596126259	-4.980216074	-5.228612491	-6.039049685
L1CAM | P32004 | GQLSFNLR	-4.678997517	-4.351882635	-4.642813731	-4.403104396	-4.758070508	-4.508525299	-4.398294213	-5.044167055	-5.003129686	-5.057008731	-4.722807897	-4.544011675	-4.80693385	-4.741542239	-4.857221169	-5.046349046	-4.219510991	-4.683112411	-5.313792543	-4.594402807	-4.839702159	-5.077942689
LAMP1 | P11279 | VWVQAFK	-7.962231449	-8.220682326	-8.406526593	-8.000539779	-7.905852752	-7.786664978	-7.827778317	-8.308149209	-8.831977414	-8.814069936	-8.484054077	-8.025951993	-8.750325968	-8.260361494	-8.86891526	-8.647208258	-8.16066213	-8.124497788	-8.356671793	-8.13875151	-7.984584577	-8.574577519
LAMP2 | P13473 | YLDFVFAVK	-7.290032908	-7.755714955	-7.511742452	-7.698397998	-7.597426674	-7.305557678	-7.826001754	-7.990483092	-8.697357686	-8.43710106	-8.365932152	-7.41175784	-8.387602553	-7.704679415	-8.481402976	-8.514318656	-7.51115415	-7.910717423	-7.934358408	-8.158359108	-7.336107691	-8.319007054
LDHB | P07195 | FIIPQIVK	-8.406043661	-8.954673107	-9.011650302	-8.243421303	-8.173635722	-8.344284396	-8.806342373	-8.74559432	-9.811769423	-9.484064758	-9.159656152	-8.744643802	-9.251004937	-9.163531116	-9.049956624	-9.708573753	-8.807654301	-8.817788795	-9.08368718	-8.106687419	-9.93371365	
LDHC | P07864 | VIGSGC[+57]NLDSAR	-8.344482509	-9.553816812	-9.589028727	-9.642547552	-8.220603115	-8.597573809	-9.035946115	-8.843341748	-10.17375497	-10.13228131	-9.113745002	-8.603627741	-9.375251415	-9.128158691	-8.916137032	-10.71337566	-9.885561998	-9.293143115	-9.029985538	-9.320412344	-8.206473447	-9.538078859
MDH1 | P40925 | GEFVTTVQQR	-7.070520119	-7.513688364	-7.77308893	-7.620248761	-6.921118247	-6.857464361	-7.167819241	-7.547579893	-8.311873939	-8.113265667	-7.62187773	-7.249393197	-8.397699285	-7.788940848	-8.009287386	-8.370370707	-7.182994136	-7.251458749	-8.018942885	-7.996008766	-6.645748583	-7.279095187
NCAM1 | P13591 | GLGEISAASEFK	-5.334057392	-5.606060666	-6.066232619	-5.355187102	-4.895101097	-5.183510895	-5.464146538	-5.701231944	-6.427560412	-6.101057579	-6.118476028	-5.485815688	-6.243804795	-6.332721952	-6.109596596	-6.295001202	-5.210171041	-5.211682153	-5.997794813	-6.271898763	-5.00937383	-6.210538756
NPTX2 | P47972 | VAELEDEK	-8.525564347	-8.802961447	-8.743746547	-8.41352677	-8.585301034	-8.59411721	-8.782452222	-9.190959572	-9.049311588	-8.920558211	-9.288230925	-9.276039851	-9.10809879	-9.641971891	-9.7378204	-9.202668161	-8.294385186	-8.48006153	-9.505426435	-8.903835443	-8.580704231	-9.485593923
NPTXR | O95502 | ELDVLQGR	-1.864830384	-1.829236286	-2.284569191	-1.700575103	-1.546080376	-1.81025834	-1.973481614	-2.26194104	-2.560158463	-2.233955061	-2.395326403	-2.462160755	-2.410178529	-3.050138631	-2.722272494	-2.549466419	-1.487556271	-1.745072268	-2.740941685	-2.49365844	-1.849336956	-2.700594778
NRXN1 | P58400 | LAIGFSTVQK	-6.737715091	-6.548105967	-6.787451483	-6.817238194	-6.467436693	-6.51188803	-6.69889789	-7.010846622	-7.709474695	-7.147225891	-7.108519327	-7.164716902	-7.655082827	-7.324076362	-7.312035854	-7.749584658	-6.560598802	-6.839360301	-7.322955992	-7.740528351	-6.486825391	-7.495442071
OGN | P20774 | LEGNPIVLGK	-6.089471959	-6.540318116	-6.193865937	-6.636408178	-6.195610595	-6.672109582	-6.311021099	-6.188846495	-7.498516925	-7.025390054	-6.681286997	-6.283840611	-6.844684081	-6.157842875	-6.442558174	-7.443221113	-6.929587178	-6.74738715	-6.053022869	-6.675967797	-6.363220176	-7.072001815
OMG | P23515 | LESLPAHLPR	-3.438726348	-3.569537042	-3.999372372	-3.534316215	-3.175363206	-3.222536761	-3.471953343	-3.918409681	-4.529381379	-4.086377868	-4.039954541	-3.441509869	-4.198585958	-3.946449105	-3.64863868	-4.211016601	-3.472760114	-3.23553439	-4.916714829	-4.047364926	-3.705319586	-4.04210987
PARK7 | Q99497 | ALVILAK	-8.014162767	-8.494087848	-8.708875828	-8.585219557	-7.861619743	-8.013328708	-8.173040762	-8.476909515	-9.681517366	-9.161251742	-8.618949997	-8.268474349	-9.096740834	-8.6249817	-8.782179491	-9.727128365	-8.585162762	-8.703282507	-8.436108209	-8.581652647	-7.637137556	-8.513687172
PEBP1 | P30086 | GNDISSGTVLSDYVGSGPPK	-5.522344219	-5.163302632	-6.478478476	-4.886139165	-4.524159728	-4.650039967	-5.032687402	-5.226656062	-5.814484458	-5.650713257	-5.368270606	-4.827398078	-5.707821866	-5.657092283	-5.370089695	-5.870189912	-4.894443055	-4.854934966	-5.145312849	-5.357294968	-4.394638533	-5.200604794
PEBP1 | P30086 | LYEQLSGK	-7.232629601	-7.749981241	-7.849748938	-7.685775469	-7.044802569	-7.493911757	-7.446548535	-7.554179445	-8.079293315	-8.146596168	-7.919165937	-7.579635741	-8.008599718	-7.631383891	-7.633135569	-8.312879344	-7.493019654	-7.687761093	-7.72580423	-8.458767762	-6.680728305	-7.380179511
PEBP1 | P30086 | VLTPTQVK	-6.242750528	-6.480124231	-6.917858795	-6.513279248	-5.863330055	-6.222487665	-6.385903549	-6.651888077	-7.33956017	-7.072864264	-6.689416374	-6.334389645	-7.110305922	-6.92443422	-6.758832495	-7.520969374	-6.341047357	-6.476161457	-6.954619616	-7.07486386	-5.702118203	-6.642771596
PGLYRP2 | Q96PD5 | TFTLLDPK	-4.262977735	-5.626167437	-3.809518775	-5.28507	-4.532091516	-4.786230864	-5.626355027	-4.038454352	-6.097967511	-5.087834489	-4.854544313	-3.838874195	-4.825682649	-4.653492426	-3.928931387	-5.846236423	-5.469376275	-4.800722146	-3.37725454	-4.483791942	-4.573067732	-5.329279921
PKM | P14618 | VVEVGSK	-6.760376569	-7.17152356	-7.949314264	-7.589500431	-6.646112993	-6.739749181	-7.038056706	-7.442088351	-8.647258427	-7.950707987	-7.67577806	-7.110671568	-7.890482951	-7.609771008	-7.430295261	-8.370554363	-7.121234045	-7.246686389	-7.3643904	-7.82772401	-6.099846473	-7.066882391
PKM | P14618 | GVNLPGAAVDLPAVSEK	-6.506990381	-6.950273566	-7.626595208	-7.10469741	-6.221041023	-6.393514789	-6.894994116	-6.986529864	-8.107870521	-7.593453035	-7.106583036	-6.758748749	-7.511898037	-7.297590432	-7.07152588	-7.768225759	-6.85244503	-6.668456037	-7.046974165	-7.492413124	-5.824779786	-6.820090239
PKM | P14618 | GDLGIEIPAEK	-7.409666384	-7.728982955	-8.157737468	-7.960946324	-7.046443501	-7.198808373	-7.553481027	-7.672135706	-8.822091152	-8.333320537	-7.975659471	-7.641636435	-8.277655574	-8.152873336	-8.11876959	-8.529407219	-7.643119008	-7.65067191	-7.683801097	-8.133269	-6.729873	-7.735452169
PKM | P14618 | GDYPLEAVR	-5.747992815	-6.330854984	-6.705596191	-6.420864168	-5.692842339	-5.958747125	-6.103756628	-6.317848076	-7.410012377	-6.885117307	-6.515088632	-6.13306951	-6.97739924	-6.617454899	-6.499391259	-7.132469932	-6.224178781	-6.288023807	-6.422803287	-6.736279628	-5.281094187	-6.377816362
PKMisoform | NA | LFEELVR	-3.103026281	-3.545584769	-4.101990008	-3.756897841	-2.801148449	-3.076654469	-3.275586732	-3.462911009	-4.473231779	-4.035622288	-3.692086818	-3.472030656	-4.14224509	-3.986848747	-3.827844044	-4.399980573	-3.412635874	-3.474514154	-3.699936177	-4.066138962	-2.600713545	-3.617302479
PON1 | P27169 | LLIGTVFHK	-7.283239474	-7.969299945	-6.265224811	-8.372479347	-8.055690314	-8.667559644	-8.272897668	-7.529697608	-9.980579848	-8.498285628	-7.805686157	-6.886330101	-8.293798089	-7.193709599	-6.937650415	-8.565978517	-8.926598881	-8.756790749	-6.498684479	-7.873267411	-7.603732199	-8.569244189
PPIA | P62937 | VSFELFADK	-8.530690181	-8.878312293	-9.100029663	-8.977784606	-8.219541489	-8.407811824	-8.328560027	-8.641134762	-9.151227408	-9.254252739	-8.721644064	-8.103426953	-9.180171239	-8.743810748	-8.687806155	-9.399982803	-9.00230546	-9.11957377	-8.049436012	-9.670909315	-8.058423834	-8.604911844
PRDX2 | P32119 | QITVNDLPVGR	-4.318320136	-4.758811298	-5.392611032	-4.63928877	-4.06722149	-4.105791952	-4.437917966	-4.729010465	-5.293552135	-5.32664034	-5.339768218	-3.57929026	-4.964869175	-4.931772026	-5.128515164	-5.205832134	-4.763287081	-4.119154324	-2.72004336	-4.606253962	-4.187196721	-5.161094889
PTPRZ1 | P23471 | AIIDGVESVSR	-6.128960463	-6.078869819	-6.781881194	-6.005056516	-5.992423485	-5.872667091	-6.060936102	-6.298247138	-7.095681714	-6.676656845	-6.524144849	-5.970819985	-6.753008163	-6.622391997	-6.740199559	-6.724300286	-6.018271349	-6.051312914	-6.894794541	-6.703424727	-5.868828093	-6.576752256
PTPRZ1 | P23471 | DIEEGAIVNPGR	-7.020779082	-7.059812052	-7.679303944	-6.937463373	-6.820501831	-6.849002546	-7.15097701	-7.422690986	-8.1586613	-7.687194382	-7.379708066	-7.014799559	-7.594521642	-7.838883924	-7.823647508	-7.748765612	-7.137943143	-6.869117938	-7.508021499	-7.696407398	-6.812208052	-7.596653022
SCG2 | P13521 | IESQTQEEVR	-6.695433282	-6.650055612	-7.47416149	-6.962423667	-6.505703783	-7.252398742	-7.65565968	-7.81819984	-7.646142961	-7.553897407	-7.712044628	-8.041433683	-7.991284548	-9.375383534	-8.09627242	-7.795800636	-6.616388724	-7.047037471	-7.909320807	-8.157747511	-7.030038951	-8.05097493
SCG2 | P13521 | SGQLGIQEEDLR	-8.392092343	-9.040863063	-9.559517285	-9.017625396	-8.253294532	-8.893776568	-9.172045273	-9.324554321	-10.1732717	-9.454800856	-9.286399495	-9.376017901	-9.551761738	-10.73746728	-9.713572268	-9.716018256	-9.036634167	-9.186504459	-9.990590573	-9.838320786	-8.492073481	-9.909429073
SMOC1 | Q9H4F8 | AQALEQAK	-6.701854502	-7.645379638	-8.169003312	-7.337195511	-6.381626112	-6.362094437	-7.055877796	-6.66211263	-8.740209397	-7.807636613	-6.910123519	-6.944285728	-8.043204636	-7.408584719	-7.820111429	-7.981710175	-7.456303755	-7.32055887	-7.873324851	-6.049425942	-7.814861291	
SOD1 | P00441 | AVC[+57]VLK	-0.937185723	-0.871531495	-1.59947476	-0.95404097	-0.895622044	-0.778600248	-1.088814266	-1.483665371	-1.999083309	-1.71407504	-1.770799856	-1.785699036	-2.074389168	-2.430582699	-2.217515213	-1.813686455	-0.93687988	-1.05631063	-2.159519923	-2.021001709	-0.999157525	-2.123936568
SOD1 | P00441 | GDGPVQGIINFEQK	-1.703920813	-2.279422331	-2.4369289	-1.9861603	-1.691982021	-1.838521186	-2.04998973	-2.275503504	-3.155578888	-2.803847838	-2.602159182	-2.49384141	-3.048041943	-2.888513295	-2.896593935	-2.874850233	-1.903424003	-2.011422256	-2.525987618	-2.738408945	-1.796322371	-2.862915116
SOD1 | P00441 | HVGDLGNVTADK	-4.245333261	-4.3118733	-4.852536774	-4.250101764	-3.992347678	-4.076494887	-4.282345762	-4.806900599	-5.534515617	-5.091726146	-4.841709253	-4.767274495	-5.300178706	-5.362944104	-5.283287145	-5.196513428	-4.231771176	-4.280455994	-5.24672415	-5.144445967	-4.219853315	-5.200430876
SPP1 | P10451 | GDSVVYGLR	-2.808678233	-3.334545643	-3.41446007	-3.571298032	-2.917677192	-2.998967523	-3.725205687	-3.541948833	-3.623848052	-4.139714378	-3.14297622	-2.971656472	-3.67374181	-3.340340482	-3.841820895	-3.549100549	-2.913885238	-3.773077382	-3.463607598	-3.713610054	-2.74712589	-3.629994382
SPP1 | P10451 | YPDAVATWLNPDPSQK	-1.653288189	-2.402710263	-2.356092381	-2.106624459	-1.318451682	-1.100494161	-1.669808124	-2.164893574	-2.345321377	-2.725021437	-1.715034234	-1.291376983	-2.033366273	-1.726312661	-2.356581538	-2.022574601	-1.739317401	-1.961219206	-1.615397145	-2.009872397	-0.987428842	-1.79815383
SPP1 | P10451 | QETLPSK	1.025290791	-0.162434114	0.612527546	0.390662317	1.153895527	1.273994746	0.750053016	0.370524732	-0.091755375	-0.11282985	0.647575154	1.298488248	0.382611005	0.899989294	0.606262393	0.578636777	0.770244958	0.366055212	0.829156948	0.601218715	1.351115491	0.899456061
THY1 | P04216 | HVLFGTVGVPEHTYR	-3.833983041	-3.794395229	-4.219361992	-3.853809763	-3.485754012	-4.105662367	-4.352866124	-4.579067074	-4.886046521	-4.801868846	-4.949899794	-4.645275753	-4.997680624	-5.386432018	-4.991317796	-5.222344027	-3.611483877	-4.16938868	-5.320358476	-4.874249411	-3.959337364	-5.255507399
TPI1 | P60174 | IAVAAQNC[+57]YK	-9.186888536	-10.34669581	-9.916893574	-10.30935827	-9.709022266	-9.48628228	-9.765850122	-9.964096888	-11.07020131	-10.32781676	-10.08827454	-10.20413543	-10.56880931	-10.95689196	-9.977894405	-10.9790442	-10.15465637	-10.77431923	-9.634227893	-10.06043513	-9.900613893	-10.46117721
VGF | O15240 | EPVAGDAVPGPK	-4.919515984	-4.958707272	-5.849163274	-5.009744318	-4.47426685	-5.334340403	-5.596570889	-5.800552356	-5.611271057	-5.375938906	-5.702068678	-6.256740124	-5.811862587	-7.607442155	-6.495219594	-6.288225621	-4.524147316	-5.01873609	-5.697413845	-6.241589062	-4.931760647	-6.231989702
VGF | O15240 | GLQEAAEER	-7.321270594	-7.453198426	-8.071736305	-7.514966083	-6.765424502	-7.571212895	-8.044113263	-8.267672661	-8.242847209	-7.974909564	-8.15994425	-8.54986613	-8.492306958	-9.996933252	-8.8943473	-8.514182994	-7.220041479	-7.645384503	-8.236939615	-8.76220801	-7.322487582	-8.804670217
VTN | P04004 | GQYC[+57]YELDEK	-5.209290617	-5.787574522	-4.87729027	-5.980655291	-5.759762973	-5.817971704	-6.394104035	-5.102316939	-7.408507839	-5.813257339	-6.057485412	-4.931787449	-5.948182378	-5.56488292	-4.899094526	-6.742000266	-6.869875982	-6.133568368	-4.122215584	-5.874399018	-5.859569317	-6.382506031
VTN | P04004 | DVWGIEGPIDAAFTR	-2.618440236	-3.443747972	-2.161121614	-3.77338173	-3.369479035	-3.564930229	-3.717968217	-2.446356217	-4.650666953	-3.493771725	-3.636929036	-2.59728814	-3.678618025	-3.13696288	-2.254953138	-4.280980931	-4.46999447	-3.743203345	-1.49856455	-3.405024242	-3.343281728	-4.09433759
YWHAB | P31946 | NLLSVAYK	-6.696468393	-7.093945591	-7.214140151	-7.126239346	-6.421345175	-6.495887698	-6.53336932	-6.936337693	-8.257454138	-8.038550866	-6.744132418	-6.143073028	-7.695681223	-6.861878881	-6.935694025	-8.055501258	-7.021845136	-7.163531198	-6.828167212	-7.6711018	-5.610304429	-6.639486532
YWHAB | P31946 | VISSIEQK	-7.741465887	-7.929131526	-8.242452479	-7.889635552	-7.256444835	-7.381705919	-7.642928534	-7.602029455	-8.696356216	-8.441953416	-7.913761988	-7.061808474	-8.248980711	-7.760126772	-7.870244461	-8.512995358	-7.803865309	-7.785867358	-7.643842512	-8.33615627	-6.798568011	-7.600249486
YWHAG | P61981 | YLAEVATGEK	-9.366554644	-10.3296615	-9.786663171	-10.03402043	-8.986449477	-8.875943499	-9.172474802	-8.813367883	-11.4101602	-10.36728787	-9.563746996	-8.852902729	-10.44549477	-9.566709506	-9.765785156	-10.04279857	-9.803891915	-9.320215318	-10.09374798	-10.01462058	-8.185514178	-9.261500602
YWHAZ | P63104 | VVSSIEQK	-6.316025673	-6.854249937	-6.811337457	-6.60235253	-5.790183451	-5.680347014	-6.299145148	-6.314685229	-7.239294502	-7.61411928	-6.603411943	-5.498441669	-7.070164356	-6.383282446	-6.462486706	-7.44645752	-6.39632409	-6.857096524	-5.959360185	-6.934178396	-5.042443776	-5.862886018

SUPPLEMENTAL TABLE 11: SRM RATIO ABUNDANCES POST-REGRESSION																						
Gene ID | Protein ID| Peptide Sequence	S023_P1G03_51551	S025_P1A04_64402	S026_P1B04_74051	S027_P1C04_47238	S028_P1D04_71200	S029_P1E04_46931	S030_P1F04_68620	S031_P1G04_76023	S032_P1H04_54755	S033_P1A05_50650	S034_P1B05_52131	S035_P1C05_55244	S036_P1D05_69030	S037_P1E05_45573	S038_P1F05_46040	S039_P1G05_48024	S040_P1H05_45861	S041_P1A06_50534	S042_P1B06_51499	S043_P1C06_53618	S044_P1D06_57907	S045_P1E06_51559
AHSG | P02765 | EHAVEGDC[+57]DFQLLK	-5.422733799	-4.688737318	-4.432938408	-4.051904646	-5.669160401	-3.281982951	-5.940476804	-3.775985046	-4.763207793	-4.33868031	-5.075771229	-3.998609944	-4.177681357	-4.136008688	-4.536530489	-3.879662568	-4.740025484	-5.33186457	-4.257037377	-4.72066543	-4.862423507	-4.639886974
ALB | P02768 | LVNEVTEFAK	4.290629782	5.297391657	5.416755474	5.769948657	4.29319435	5.979865955	3.77095525	5.858253887	4.605765111	5.162059364	5.016581679	5.786852039	5.784425892	5.451308331	5.24155121	5.963744176	4.990679399	5.318071178	5.444019469	4.74302426	4.759770807	5.42565797
ALB | P02768 | LVTDLTK	4.998674318	5.995207954	6.143081176	6.480194136	5.037427716	6.74557508	4.478517714	6.561911985	5.353856039	5.890938808	5.716829243	6.534910964	6.507787962	6.187476432	5.962034284	6.676198225	5.740590308	6.016542559	6.18756621	5.451977463	5.459205521	6.179749813
ALDOA | P04075 | VLAAVYK	-7.554351206	-6.787027969	-6.624532941	-6.424111176	-7.756891173	-7.351368259	-7.180049789	-7.263685136	-7.435359856	-6.530473972	-7.398216495	-7.263764775	-6.60389785	-7.229935374	-6.607829659	-7.302553764	-7.567648029	-6.136966327	-7.829033139	-7.426075773	-7.768333957	-7.527595243
APOA4 | P06727 | SLAPYAQDTQEK	-5.943899072	-4.233649102	-5.04252829	-4.492483003	-5.97094649	-3.357282698	-5.945838579	-4.140982419	-5.754417661	-4.738544392	-5.26149215	-4.452055199	-3.96394859	-3.389116137	-4.512325592	-4.86100626	-4.70814208	-4.412404684	-4.213974972	-6.174849202	-5.2767577	-5.196173496
APOC1 | P02654 | QSELSAK	1.237938869	1.812883089	1.867448515	1.909063191	2.003643724	2.449353475	0.815492705	1.70863856	0.535875019	1.69597765	1.703557866	1.772163738	1.708540798	1.870212697	2.079001995	2.69511358	1.605126644	2.070805988	1.747248659	1.797998646	1.804027232	1.717401342
APOC2 | P02655 | TAAQNLYEK	-7.722617052	-7.449520391	-7.087885631	-6.47175874	-8.066802287	-6.69472643	-8.486260223	-7.195914859	-8.249517519	-7.575849775	-7.543095369	-7.354484225	-7.383804639	-7.140918759	-7.732842609	-6.4434456	-7.505805663	-7.489434908	-7.71598479	-7.297952721	-7.667562618	-7.432062016
APOE | P02649 | ELQAAQAR	-2.275282114	-1.702145663	-1.776381208	-1.814970483	-2.685607689	-2.109173124	-2.379368758	-1.842871878	-2.204537454	-1.391522328	-2.147984995	-2.083059589	-1.245028071	-2.434375114	-1.989714815	-2.32234322	-2.084456471	-1.589148046	-3.009943491	-2.193470741	-2.512544308	-2.070680434
C9 | P02748 | TSNFNAAISLK	-9.105586715	-7.55962679	-7.790255165	-7.190933766	-8.201439379	-7.10121333	-8.438192229	-7.487652448	-7.745487317	-8.30923735	-8.81361642	-7.197679375	-7.531065948	-7.311570117	-7.309596452	-7.389985788	-8.054960642	-7.994433219	-7.55926539	-8.620902473	-8.250654147	-7.692757469
C9 | P02748 | LSPIYNLVPVK	-8.318809101	-6.743114407	-7.235093605	-6.560574859	-7.393059427	-6.19296101	-7.645965561	-6.660408366	-7.089599072	-7.404862144	-8.164842419	-6.565260142	-6.72610435	-6.417206377	-6.553399532	-6.666449115	-7.138236856	-7.458725794	-6.922278162	-7.741133345	-7.406111027	-6.988555377
CALM2 | P0DP24 | EAFSLFDK	-7.026556303	-5.882762357	-6.121801511	-5.689583325	-7.106667096	-6.614248715	-6.913709067	-6.738564503	-6.69321375	-5.94877174	-6.763063694	-6.521863962	-6.152727199	-6.423727568	-6.107426322	-6.358495684	-7.140512492	-5.741822365	-7.026200585	-6.719669954	-6.672806212	-6.553524527
CD44 | P16070 | TEAADLC[+57]K	-9.568496691	-9.226217755	-9.388648987	-9.329820304	-9.589094	-9.386397196	-9.537961627	-9.680977235	-9.644372515	-9.043191915	-9.937660753	-9.60027584	-8.962790866	-9.653933999	-9.539737528	-9.298052811	-9.461581487	-9.584327983	-10.22687526	-10.07750776	-10.08769513	-9.657791508
CD44 | P16070 | ALSIGFETC[+57]R	-8.994769905	-8.279433791	-8.910578104	-8.691403145	-9.106189142	-9.026992995	-9.464324988	-9.135344198	-8.937854924	-8.524091412	-9.16073756	-9.321770155	-8.913391181	-8.896198708	-8.939251145	-8.888508414	-9.03429827	-9.103635945	-9.213123423	-9.452610402	-9.355915554	-9.133997469
CHI3L1 | P36222 | IASNTQSR	-2.556801853	-2.604698712	-2.431844491	-2.722228963	-3.126256796	-3.788945064	-3.570787762	-3.686214841	-3.050792218	-2.493105004	-3.041508184	-3.127555781	-2.768251539	-3.05278828	-2.793835213	-2.713497469	-3.621589676	-2.848222269	-3.140361329	-3.302590366	-3.53839532	-2.834141792
CHI3L1 | P36222 | GNQWVGYDDQESVK	-4.496561294	-4.559674598	-4.662910978	-4.54141304	-5.283532701	-6.025825491	-5.539595137	-6.203622729	-5.241267155	-4.678232186	-5.172592084	-5.165150758	-4.965196561	-5.273930051	-4.944722459	-4.771430245	-5.878050617	-4.768113484	-5.328456009	-5.537295393	-5.802211373	-4.929315844
CHI3L1 | P36222 | QLLLSAALSAGK	-0.1697859	-0.579514892	-0.344373414	-0.282362033	-1.390245527	-1.646612017	-1.202485566	-1.833179559	-0.79052694	-0.180895269	-0.652354489	-1.153631048	-0.4114842	-0.852161534	-0.653403632	-0.472182335	-1.692217154	-0.606448357	-1.103321388	-1.499722535	-1.656650149	-0.760329022
CP | P00450 | EVGPTNADPVC[+57]LAK	-3.957153688	-2.959154388	-3.396993105	-2.975818842	-3.620012838	-2.330177749	-4.261764068	-2.644934736	-3.631837148	-3.654070711	-3.626832731	-2.869134345	-3.226679798	-2.89408192	-3.457113768	-2.600597742	-3.274944552	-3.329304379	-3.378995316	-3.767333263	-3.567073768	-3.280259767
CP | P00450 | GEFYIGSK	-5.140441063	-4.406770626	-4.589390776	-4.078441145	-5.089277559	-3.29690821	-5.62070912	-3.99591043	-4.913825119	-4.777697285	-4.930693424	-4.042802284	-4.123259789	-3.893802573	-4.370691383	-3.716184031	-4.777870984	-4.719400589	-4.493105359	-5.200516081	-5.199091505	-4.176144762
CST3 | P01034 | ASNDM[+16]YHSR	-5.166455064	-4.017150267	-4.589474603	-4.483349648	-5.050404129	-4.874047816	-4.224617478	-4.673066856	-4.469959553	-3.731806909	-4.604674075	-4.742670684	-3.983212661	-4.613787755	-4.198641204	-5.137905623	-4.896451104	-3.755146652	-5.151695951	-5.097912782	-4.673802463	-4.874043467
DCN | P07585 | VDAASLK	-7.330902562	-7.30342015	-7.027416188	-7.007454461	-7.445200498	-7.087352227	-7.366828584	-7.534553065	-7.403442621	-7.049501313	-7.368273179	-6.73556165	-7.487897502	-7.088888464	-7.26716279	-6.71431946	-6.678825865	-7.228554452	-7.424882111	-7.010700309	-7.320556851	-7.282895822
DDAH1 | O94760 | EFFVGLSK	-11.40534995	-11.0034801	-10.77541293	-10.58029731	-11.20935539	-11.10870206	-11.61866757	-11.13831169	-10.77102153	-10.31660853	-11.00867609	-10.73045403	-10.58636086	-10.83187279	-10.44698654	-10.75116635	-11.62774237	-10.47000441	-11.23217461	-11.45732706	-11.2967785	-11.38126299
DKK3 | Q9UBP4 | DQDGEILLPR	-4.146697858	-3.641665584	-3.470495035	-3.19914065	-4.42978633	-3.771595341	-3.883292877	-4.022210137	-4.368025126	-3.179977744	-4.19953889	-3.950129088	-3.292200417	-4.020556923	-3.708670577	-4.022851761	-4.235006276	-2.734496448	-4.446864479	-4.087793056	-4.140543236	-4.123124308
ENO1 | P06733 | IEEELGSK	-9.010546699	-8.450638943	-8.121071732	-8.156550358	-9.050109489	-8.863248687	-9.118181171	-8.772055983	-8.746862108	-8.172228055	-9.643882347	-8.704084646	-8.412104062	-8.60244168	-8.202504199	-8.510599376	-8.696438109	-8.265808833	-9.196162336	-9.026881175	-9.39372131	-8.985147581
ENO1 | P06733 | LNVTEQEK	-8.814858907	-8.050775046	-7.852308347	-8.047472398	-8.932295941	-8.448620288	-8.864702627	-8.869184105	-8.652206838	-8.101717513	-9.845052681	-8.583188153	-8.453900016	-8.640396228	-8.060018054	-8.406902962	-8.814858907	-8.189187923	-9.122387592	-8.786793472	-9.009230281	-8.756097183
ENO2 | P09104 | IEEELGDEAR	-6.463466579	-5.676564272	-5.398801135	-5.407315817	-6.39637846	-6.542481428	-6.30354607	-6.151959226	-6.621584328	-5.437756424	-6.258389989	-6.294085084	-5.736178672	-6.1564086	-5.50158282	-5.891034073	-6.43309293	-5.613909427	-6.324180408	-6.119254147	-6.455759973	-6.173972883
F2 | P00734 | YTAC[+57]ETAR	-9.594502497	-8.577843094	-8.446063413	-8.26656527	-8.977962548	-8.107874131	-9.172156018	-8.01203419	-8.602026099	-8.77927691	-9.203908117	-8.485293622	-8.170427166	-8.149774008	-8.454263661	-8.410214183	-8.543876424	-8.621909903	-8.330523464	-9.175963311	-8.546335215	-8.806684316
F2 | P00734 | TATSEYQTFFNPR	-7.425683188	-6.472175591	-6.03018935	-5.578551399	-7.161184393	-5.41068981	-7.681678168	-5.673856639	-6.821341696	-6.346010541	-6.60957202	-5.728703412	-5.812258479	-5.930155326	-6.153808002	-5.620881032	-6.485061735	-6.344293054	-6.358599916	-6.937291072	-6.774908484	-6.224968265
GAPDH | P04406 | AAFNSGK	-9.878835482	-7.576786015	-8.005506883	-7.744304659	-8.354019147	-8.737666867	-9.215753068	-9.183323306	-9.384016306	-7.852478531	-9.092489742	-8.959237429	-8.885802215	-9.051928627	-7.814659911	-8.593272052	-8.435891986	-8.55727657	-9.325385808	-9.03227343	-9.150448656	-9.285238571
GAPDH | P04406 | YDNSLK	-12.13448548	-10.50478318	-10.51772567	-10.33364979	-11.01500494	-11.2095329	-11.44600798	-11.71481526	-11.15469056	-10.44849761	-11.420708	-11.43043563	-10.97170835	-11.73853827	-10.50146007	-10.78081527	-10.75597386	-11.20808968	-12.04098289	-11.51558558	-11.6321833	-11.42899241
GDA | Q9Y2T3 | DHLLGVSDSGK	-9.456023517	-8.966908634	-9.198963772	-7.94430573	-9.813907803	-9.567215344	-9.025950075	-9.536740163	-9.732463268	-8.688557073	-9.175839501	-9.564318956	-9.200219563	-8.814950328	-8.735438611	-9.172694675	-9.719057923	-8.361899321	-9.753140735	-9.272889607	-9.097003336	-9.774865536
GOT1 | P17174 | VGNLTVVGK	-8.06633965	-7.164268624	-7.427790643	-7.012565084	-8.343659994	-8.143468126	-7.901833823	-7.991424711	-8.068957662	-6.935376725	-8.065118215	-7.835627439	-7.13170605	-7.847371429	-7.043264062	-7.694172837	-8.122192885	-6.651349768	-8.510083076	-8.548290186	-8.360275843	-8.038158091
GOT1 | P17174 | IGADFLAR	-10.13329492	-9.686451225	-9.554501517	-9.094311551	-10.33317927	-9.845610333	-9.816105647	-9.913319076	-10.05454961	-9.213477571	-10.22871351	-9.934254561	-9.4178763	-9.781869815	-9.450143996	-9.888292112	-9.792258003	-8.883058475	-10.24473218	-10.08225178	-9.860997624	-10.1138008
GSN | P06396 | AGALNSNDAFVLK	-4.438677473	-3.759982	-3.867399893	-3.618306718	-4.328092452	-3.382126183	-4.222578726	-3.625280873	-4.251531959	-3.654488014	-4.098984811	-3.857878979	-3.359242584	-3.617702736	-3.858958467	-3.375171426	-4.160710581	-3.640814992	-4.220105485	-4.169590195	-4.348230313	-4.151758717
HBA1 | P69905 | FLASVSTVLTSK	-7.681178527	-8.533235376	-8.799478395	-9.247150119	-8.423660608	-4.049806424	-8.105319383	-5.029459008	-9.33236752	-8.319454703	-9.187329243	-7.241616425	-4.211963575	-5.064143476	-6.603587179	-6.847373389	-6.624477939	-8.26849164	-9.927016977	-2.460045686	-6.210269236	-9.396460797
HBA1 | P69905 | VGAHAGEYGAEALER	-7.112863082	-10.82107082	-9.816174446	-12.56818278	-8.565961469	-3.588317009	-8.638694995	-4.744975262	-16.79889233	-10.89572552	-10.63872429	-7.130777182	-3.921023237	-4.719216055	-6.178922854	-6.846862364	-6.514637099	-12.61712566	-14.52491904	-2.236613893	-5.755735185	-11.97344378
HBB | P68871 | VNVDEVGGEALGR	-7.36229036	-9.95078287	-9.450317888	-10.44078148	-8.191955781	-3.512567138	-8.216743176	-4.568534192	-10.50756582	-9.907243261	-10.22169394	-6.546875839	-3.752490568	-4.531156314	-6.222756128	-6.544554252	-6.116650217	-10.68300041	-10.55179182	-1.894360174	-5.841835878	-10.47328511
KNG1 | P01042 | EGDC[+57]PVQSGK	-10.78028295	-9.03079575	-8.966382536	-9.212226305	-9.424329642	-8.028752809	-10.25562997	-8.71560367	-9.695777022	-8.988927161	-9.365550255	-8.523919784	-8.576547606	-8.444744824	-9.020645938	-8.109451999	-9.128206249	-9.554926259	-9.000046955	-10.04669106	-9.891618043	-8.660349754
KNG1 | P01042 | QVVAGLNFR	0.016633449	1.045502173	1.305242106	1.264664839	0.455153522	2.646741251	0.25741867	2.032308518	0.95105094	1.1483253	0.772463881	1.989895255	1.960095629	2.03924622	1.464398453	1.947236635	1.519095126	0.944451347	1.18076697	0.711672779	0.66432206	1.696687026
KNG1 | P01042 | VQVVAGK	-6.281853942	-5.091334986	-4.958836452	-4.628442961	-5.921682154	-3.70192406	-6.191848002	-4.359769815	-5.58317901	-5.056696423	-5.211625841	-4.266672492	-4.513469623	-4.432873841	-4.911603244	-4.167385191	-5.129850848	-5.314865283	-5.021398595	-5.777223432	-5.751900734	-4.672742104
L1CAM | P32004 | GQLSFNLR	-4.920527038	-4.506115408	-4.592662872	-4.704771391	-5.166562035	-5.468413812	-4.723101093	-5.11272932	-4.877073184	-4.373795205	-4.483773629	-4.732150778	-4.534335935	-4.837097069	-4.552353452	-4.698600108	-5.012602623	-4.404850885	-4.858168384	-4.529929573	-4.773753027	-5.125579907
LAMP1 | P11279 | VWVQAFK	-8.882868491	-7.991681042	-8.393074136	-7.977456315	-8.201049505	-7.91851028	-8.431249809	-8.358042631	-8.502517839	-7.992430437	-8.281031499	-8.236658847	-8.210860584	-8.198382964	-7.886869851	-7.923816571	-8.882868491	-8.047885401	-8.844153238	-8.521024152	-8.519668862	-8.773630214
LAMP2 | P13473 | YLDFVFAVK	-8.35845461	-7.696552325	-7.604777798	-7.570799463	-8.705638918	-7.856424633	-8.661297178	-7.869657853	-8.178952878	-7.399508091	-8.011257254	-7.813169894	-7.719475	-8.185349938	-7.859704524	-7.478397617	-8.328707267	-7.346753449	-8.353903283	-8.18554181	-8.182261426	-8.087597516
LDHB | P07195 | FIIPQIVK	-9.42387103	-8.729522635	-8.493381177	-8.429905529	-9.474842783	-9.199560106	-9.108510312	-9.068725995	-8.994277426	-8.392532588	-9.341429025	-9.174391431	-8.228063626	-8.997797149	-8.363460943	-8.917507854	-9.082834112	-8.178689938	-9.653933054	-9.26317718	-9.671868893	-9.302169605
LDHC | P07864 | VIGSGC[+57]NLDSAR	-10.17023889	-8.629989941	-8.599594364	-8.768408939	-9.292327971	-8.918195449	-9.888365182	-9.548675544	-9.23076558	-8.549711703	-9.797770727	-9.612355234	-8.078572387	-9.206712817	-8.575897035	-8.840275583	-9.693800848	-8.62885508	-10.36180094	-10.0777562	-10.22101509	-9.52540792
MDH1 | P40925 | GEFVTTVQQR	-8.086234716	-7.19002438	-7.1187818	-6.824786816	-7.903007462	-7.867870367	-7.790686735	-7.903960697	-8.003322312	-6.884473876	-7.818149092	-7.836592955	-7.20842309	-7.689222224	-6.762733921	-7.684710108	-7.739784302	-6.883756504	-8.390948036	-7.997413622	-8.245027817	-7.85310758
NCAM1 | P13591 | GLGEISAASEFK	-5.819151713	-5.300581684	-5.59324001	-5.221039283	-6.304402518	-6.016964633	-5.9790312	-5.801146998	-5.965111503	-4.827944051	-5.74346695	-5.698019915	-5.280191801	-5.902094731	-5.65066724	-5.75796294	-6.202646744	-4.569581501	-6.262758514	-6.194563448	-5.963112482	-5.989936223
NPTX2 | P47972 | VAELEDEK	-8.884531784	-8.776440954	-9.346892179	-8.711841219	-9.035602094	-8.56879606	-8.944197705	-9.170192769	-9.38256786	-8.043877958	-8.968293227	-8.997602909	-9.330510369	-9.546093807	-8.723239912	-9.277671255	-9.369958611	-8.2017675	-9.636776487	-8.841288523	-8.780275013	-9.352846058
NPTXR | O95502 | ELDVLQGR	-2.280363938	-2.06717072	-2.276444214	-1.703106404	-2.688293517	-2.157676201	-2.325949524	-2.24989122	-2.656223696	-1.374464831	-2.2015753	-2.092945404	-2.15463732	-2.706097424	-2.018935989	-2.035384904	-2.519236293	-1.409718308	-2.610713792	-2.210800288	-2.134251702	-2.369463571
NRXN1 | P58400 | LAIGFSTVQK	-7.033743225	-6.533501501	-6.865976341	-6.289295397	-7.641196447	-7.345194403	-7.574870513	-6.840428542	-7.666482106	-6.380961817	-6.919204818	-7.072604267	-6.446396459	-7.286759768	-6.745349461	-7.102900757	-7.259163339	-6.116779563	-7.767817723	-7.111442673	-7.326494229	-7.388344754
OGN | P20774 | LEGNPIVLGK	-6.79656433	-6.440664619	-6.670348971	-6.316633904	-6.911687832	-6.171624693	-6.651845896	-6.422324208	-6.377387457	-6.362342589	-6.692794021	-6.142394127	-5.994893164	-6.491670675	-6.569119436	-6.281373847	-6.549346629	-6.372168846	-6.961422762	-6.599427519	-7.042219572	-6.881579291
OMG | P23515 | LESLPAHLPR	-3.824605625	-3.479028737	-3.595759873	-3.323122545	-3.920824243	-3.551799545	-3.625683479	-3.973329086	-4.27174864	-3.213375752	-3.571678855	-3.87509099	-3.839165401	-4.314602441	-3.989150207	-3.960109001	-4.262923948	-3.141487704	-3.93558614	-4.005299456	-4.026878635	-4.057709764
PARK7 | Q99497 | ALVILAK	-9.062480942	-8.171095671	-8.038509545	-8.167037263	-8.816806393	-8.812858239	-8.906974592	-8.623597584	-8.696911452	-7.992687482	-8.966834624	-8.487409904	-7.880063392	-8.635537185	-8.201423331	-8.51061501	-8.888451542	-8.317511224	-9.341889295	-9.018394235	-9.274579498	-8.961215511
PEBP1 | P30086 | GNDISSGTVLSDYVGSGPPK	-5.510083148	-4.905109753	-4.739074591	-4.424846321	-5.503632474	-5.21600504	-5.495502136	-5.44111567	-5.246116376	-4.798901353	-5.462382823	-5.076500002	-4.556091048	-5.337838178	-5.000889108	-5.066997654	-5.55199679	-4.348353765	-5.796298179	-5.638796767	-5.670197241	-5.719932156
PEBP1 | P30086 | LYEQLSGK	-7.825404193	-7.294408398	-7.36010617	-6.871697633	-7.802721891	-7.869272693	-7.756407822	-7.780373292	-7.670812066	-7.157820848	-7.691381453	-7.630251293	-7.018377292	-7.481601134	-7.139165897	-7.88898886	-8.045369877	-7.350201606	-7.889399073	-7.865095986	-8.097609888	-8.137593071
PEBP1 | P30086 | VLTPTQVK	-7.103403932	-6.431028228	-6.321603505	-6.027522173	-7.125977524	-6.725587093	-6.794396252	-6.999785124	-6.819829576	-6.084465649	-6.87279665	-6.718721642	-6.089775739	-6.713565785	-6.239616409	-6.500371552	-6.909580663	-5.776534497	-7.153337813	-7.101184339	-7.137319713	-7.046509251
PGLYRP2 | Q96PD5 | TFTLLDPK	-5.546149433	-4.676502259	-4.366008041	-4.079534873	-5.249708257	-3.310183523	-6.238600708	-4.29558294	-5.040761211	-4.543538766	-4.927866919	-4.096714835	-4.12532083	-4.579513293	-4.51271464	-4.70366569	-4.847103399	-4.609680971	-4.178646085	-4.92255959	-4.79052954	-4.294285685
PKM | P14618 | VVEVGSK	-7.946383057	-7.098947878	-7.103477434	-6.513284044	-7.909313578	-7.940566523	-7.618868862	-7.564106908	-7.790912234	-6.637562657	-7.840340586	-7.64294433	-6.637131733	-7.377166749	-6.700482314	-7.450787459	-7.73993218	-6.516451904	-7.969560881	-8.062791624	-8.052744592	-7.9797009
PKM | P14618 | GVNLPGAAVDLPAVSEK	-7.518996299	-6.731399264	-6.623558853	-6.326136004	-7.636445206	-7.384439194	-7.430047882	-7.23649621	-7.368119355	-6.385936541	-7.490921708	-7.36243181	-6.365546565	-6.974453922	-6.390442234	-7.081397839	-7.494748753	-6.154487329	-7.860822702	-7.865459373	-7.630573243	-7.477286842
PKM | P14618 | GDLGIEIPAEK	-8.171393088	-7.333572584	-7.473890448	-7.083496779	-8.489470264	-8.120294554	-8.05070078	-7.929421327	-8.272912926	-7.155157934	-7.952812452	-8.086610569	-7.121793263	-7.817182709	-7.160815765	-7.754441345	-8.152027763	-6.904030741	-8.590920189	-8.662010244	-8.462433965	-8.162047588
PKM | P14618 | GDYPLEAVR	-6.866868821	-6.052326801	-6.021909734	-5.742586094	-6.868431302	-6.580930433	-6.50437303	-6.616615946	-6.808711206	-5.771005126	-6.984870287	-6.576495291	-5.673980373	-6.442840885	-5.923818253	-6.363050311	-6.756545406	-5.649027338	-7.167516785	-7.141842349	-7.016092185	-6.835196661
PKMisoform | NA | LFEELVR	-4.17742652	-3.342953237	-3.284165236	-3.015663611	-4.212897153	-4.051834957	-3.800486864	-3.81971032	-3.990978284	-2.991562526	-3.96111013	-3.848160595	-3.045323333	-3.733622862	-3.148476528	-3.734910646	-3.921151664	-2.860694193	-4.37759865	-4.203745762	-4.117791402	-3.964363927
PON1 | P27169 | LLIGTVFHK	-8.84004741	-7.541337534	-7.590638971	-8.006547637	-8.748656138	-7.003042322	-8.91704327	-7.015527988	-8.554697103	-7.667262764	-8.393725997	-6.938539393	-8.246709747	-8.028378929	-8.045534785	-6.68774152	-7.518119315	-8.167132261	-7.464493348	-8.562712844	-7.893940156	-7.073594367
PPIA | P62937 | VSFELFADK	-8.833285178	-8.019263695	-8.47574955	-8.09728463	-8.956857301	-8.859414422	-9.025310921	-8.637765043	-8.599053133	-8.715456617	-9.655409799	-8.802986405	-8.788522856	-8.395120384	-8.32829895	-8.509847668	-9.402650824	-8.798837468	-9.371819924	-8.93400791	-9.123807631	-9.370668786
PRDX2 | P32119 | QITVNDLPVGR	-4.897007461	-4.95680683	-3.944375413	-4.347196478	-4.922179638	-4.43515505	-4.513466284	-4.292027167	-5.258971946	-4.185886255	-5.063208313	-4.530590433	-4.289323556	-4.747977551	-4.874481115	-4.244932022	-4.949474881	-4.24545186	-5.147492618	-3.82480711	-4.986126021	-5.005972433
PTPRZ1 | P23471 | AIIDGVESVSR	-6.580777638	-6.09959135	-6.32191869	-5.944657029	-6.610003513	-6.358904163	-6.353287249	-6.413327244	-6.705365804	-5.646138015	-6.433642219	-6.40044272	-6.123164194	-6.552976587	-6.344511014	-6.382292043	-6.572784847	-5.673085364	-6.962848952	-6.789857703	-6.592711929	-6.49573132
PTPRZ1 | P23471 | DIEEGAIVNPGR	-7.558045447	-7.056827267	-7.293122806	-6.875098769	-7.785812642	-7.417941117	-7.474386721	-7.558265194	-7.817123396	-6.58449915	-7.431627129	-7.438494219	-6.95404654	-7.397584072	-7.323460788	-7.293113904	-7.764496324	-6.330401177	-7.709684732	-7.688663373	-7.633829222	-7.516459696
SCG2 | P13521 | IESQTQEEVR	-7.583639746	-7.11060293	-7.587301853	-7.050652525	-8.268700789	-7.729129597	-7.364570452	-7.658688881	-8.603868418	-6.689457711	-7.778101495	-7.546001988	-7.13042016	-8.119273272	-7.304765081	-7.940142658	-8.115162988	-6.078350512	-8.104030372	-8.051515812	-7.546844876	-7.737852884
SCG2 | P13521 | SGQLGIQEEDLR	-9.355161344	-8.540975128	-9.155448502	-8.387715973	-9.70634309	-9.152117371	-9.400646097	-9.451252033	-10.05745983	-8.090189649	-9.641270994	-9.364771348	-8.684080876	-9.679527589	-8.906899692	-9.675333951	-9.58648689	-7.906172346	-9.785946289	-9.752747728	-9.56998043	-9.740791983
SMOC1 | Q9H4F8 | AQALEQAK	-8.337775819	-6.795135773	-6.767449062	-6.259812797	-7.52722178	-7.300988692	-7.462369626	-7.261587015	-7.599813444	-6.645413752	-7.270180005	-7.530356208	-6.405736714	-7.114729473	-7.447052866	-6.968203852	-7.567257665	-6.521144482	-8.178401304	-7.847244835	-7.973662007	-8.260733298
SOD1 | P00441 | AVC[+57]VLK	-1.955318604	-1.288723594	-1.393170756	-1.234784292	-2.390058019	-2.035228046	-1.538260588	-2.287598434	-1.820962969	-0.833835983	-1.638545553	-2.153457017	-1.611846744	-2.130532816	-1.708159035	-2.296860982	-1.903089787	-0.397903465	-2.168203742	-2.248714364	-1.829478195	-2.048363553
SOD1 | P00441 | GDGPVQGIINFEQK	-2.787733642	-1.9255049	-2.380555618	-1.736525592	-3.451344867	-2.532379985	-2.68411884	-2.783291082	-2.501682508	-1.696786232	-2.721947266	-2.809672563	-2.035257563	-2.779976012	-2.375028448	-2.91483961	-2.57218364	-1.231308881	-3.023497652	-3.167379119	-2.897047068	-2.652336816
SOD1 | P00441 | HVGDLGNVTADK	-6.296137007	-4.5239241	-4.549032223	-4.082414749	-5.587348041	-5.067026703	-4.893362797	-5.376311941	-4.918006297	-3.772500064	-4.9423596	-5.054110033	-4.502855223	-5.118764764	-4.679891782	-5.269896519	-4.939239197	-3.459780474	-5.012517316	-5.417884927	-5.01519776	-4.967525299
SPP1 | P10451 | GDSVVYGLR	-3.97786369	-3.255359428	-3.357165945	-3.044472959	-4.042248264	-3.65799884	-4.025040203	-4.000895504	-3.778780296	-3.348987624	-3.719702717	-2.726885695	-3.740285034	-3.958954034	-3.683065972	-3.507761536	-4.204139546	-3.352049809	-4.165051393	-3.77027088	-3.649318945	-3.934736712
SPP1 | P10451 | YPDAVATWLNPDPSQK	-2.360992061	-1.455202371	-1.738429778	-1.346861916	-2.211375058	-1.669934085	-2.389803808	-2.256301246	-2.159652852	-1.59302752	-1.894582567	-2.523988054	-2.026243997	-1.902216049	-1.799957155	-1.770404137	-2.335643912	-1.732794985	-2.141828578	-2.462757102	-1.946709985	-2.058683621
SPP1 | P10451 | QETLPSK	-0.035643259	0.96793663	1.003397632	1.447505858	0.285454118	0.715480818	-0.386977488	0.494855867	0.292447538	0.895795401	0.496938369	2.366387723	0.45301974	0.784477982	0.743343595	0.861837802	0.340279598	0.816077418	0.107039939	-0.365044758	0.139307062	0.619908588
THY1 | P04216 | HVLFGTVGVPEHTYR	-4.816505168	-4.332729412	-4.585415908	-4.023726539	-5.313690701	-4.455383693	-4.830598197	-4.581871995	-4.486915219	-3.645683058	-4.755946005	-4.490101097	-4.336137562	-5.509897755	-4.391083504	-4.796491811	-4.988663287	-3.620916824	-4.921855009	-4.653887551	-4.95625104	-5.087960704
TPI1 | P60174 | IAVAAQNC[+57]YK	-10.62974834	-9.353096655	-9.662620693	-9.547411687	-10.03614911	-10.44852948	-10.87985582	-10.42502337	-10.78334897	-9.76076693	-10.495671	-10.74655559	-9.841190648	-9.912539617	-9.254688366	-9.331700668	-10.00171712	-9.503963217	-10.14430823	-10.43588176	-11.22082421	-10.60790227
VGF | O15240 | EPVAGDAVPGPK	-5.423239845	-5.367186969	-5.964665947	-4.911218513	-6.530138345	-5.852429561	-5.409086178	-5.902395789	-6.764501492	-4.354359443	-5.883650274	-5.518183678	-5.246835111	-6.162994598	-5.425501359	-6.155248893	-6.313718145	-3.663885809	-6.351494309	-5.944768764	-5.558563098	-6.102797778
VGF | O15240 | GLQEAAEER	-8.054401089	-7.666484032	-8.314032209	-7.27748313	-8.76963489	-8.302678888	-7.867142615	-8.310229253	-9.007707915	-6.823092935	-8.394467465	-8.104845954	-7.705153101	-8.551999177	-7.858859049	-8.632003943	-8.715195002	-6.22915074	-8.884447546	-8.539844775	-8.18897701	-8.691777045
VTN | P04004 | GQYC[+57]YELDEK	-6.207502548	-5.570412491	-5.605320438	-5.141238215	-5.824791456	-4.165353034	-6.529241644	-5.166567575	-6.156729846	-5.402487187	-6.203271475	-5.136844258	-5.241731489	-5.096656795	-5.692110443	-4.723705098	-6.207502548	-6.097033903	-5.406421207	-6.273135975	-5.990629072	-5.25233872
VTN | P04004 | DVWGIEGPIDAAFTR	-4.261016371	-3.743811379	-3.116838094	-2.975006974	-3.490200294	-1.864370277	-4.186648882	-2.395231815	-3.478764378	-3.148604538	-3.938522793	-2.700506256	-2.769130267	-2.81516715	-3.347902501	-2.27939261	-3.356985429	-3.878413664	-2.982973344	-3.865794838	-3.576834571	-2.906033494
YWHAB | P31946 | NLLSVAYK	-7.600620453	-6.359640073	-6.307020733	-6.116567552	-7.383886295	-7.535244447	-7.460577854	-7.391460216	-7.059927971	-6.764777572	-7.791487003	-7.262036979	-6.804642102	-6.491005611	-6.325905238	-6.901288048	-7.645014572	-6.980088144	-7.433158625	-7.345376407	-7.429199096	-7.679576996
YWHAB | P31946 | VISSIEQK	-8.286843498	-7.288663192	-7.592238024	-6.956689434	-8.097562109	-8.069388707	-8.416366221	-7.958842478	-8.066672451	-7.518004575	-8.424891416	-8.18986775	-7.668073646	-7.510688743	-7.234917043	-7.776343444	-8.236217425	-7.570684179	-8.11924973	-8.121230189	-8.18100422	-8.188662882
YWHAG | P61981 | YLAEVATGEK	-10.21901977	-9.04698876	-8.96425071	-8.62795757	-10.38333115	-10.29072608	-9.99788064	-10.09650591	-9.483437812	-9.26451105	-10.64682403	-9.240002044	-9.000925211	-8.812662658	-8.923862088	-9.570137504	-10.51858005	-9.244952992	-10.40815257	-10.69059494	-9.927839933	-9.870891292
YWHAZ | P63104 | VVSSIEQK	-7.19185317	-5.947301951	-5.694140277	-5.296149587	-6.806973165	-6.749602139	-6.925495767	-7.070132373	-6.27108242	-5.961427773	-7.088311002	-6.642559157	-5.906471413	-5.739988652	-6.09397708	-6.663605498	-6.878192691	-6.239253308	-6.672068038	-7.285800707	-6.871628374	-6.816348232

SUPPLEMENTAL TABLE 11: SRM RATIO ABUNDANCES POST-REGRESSION

Gene ID	Protein ID	Peptide Sequence	S046_P1F06_53819	S047_P1G06_46076	S048_P1H06_58885	S049_P1A07_68342	S050_P1B07_83366	S051_P1C07_46390	S052_P1D07_50452	S053_P1E07_44869	S054_P1F07_53729	S055_P1G07_56968	S056_P1H07_50619	S057_P1A08_78317	S058_P1B08_80265	S059_P1C08_84561	S060_P1D08_49324	S061_P1E08_66352	S062_P1F08_59128	S063_P1G08_72848	S064_P1H08_73808	S065_P1A09_84355	S066_P1B09_50313	S067_P1C09_51135
AHSG	P02765	EHAVEGDC[+57]DFQLLK	-4.219815454	-4.690165625	-4.551704659	-4.834492614	-4.421497026	-4.063721943	-4.229530474	-4.980928386	-5.092613148	-3.874295585	-4.361727831	-3.033736562	-4.948205365	-5.713811486	-4.733319604	-4.262695777	-5.425859562	-4.892674341	-5.21534353	-4.692819092	-4.474704885	-4.011970172
ALB	P02768	LVNEVTEFAK	5.376470969	5.215575062	5.118730231	4.800611722	4.803622412	6.166443439	5.128742363	4.14804227	4.58907931	5.806531298	5.058499955	6.555349321	4.96923621	3.914667899	4.67606582	5.470924822	4.669103632	5.11549516	5.081114716	5.171363746	5.306754234	5.6536538
ALB	P02768	LVTDLTK	6.148209046	5.955354231	5.875919806	5.545625866	5.482360347	6.903915262	5.861382158	4.811671852	5.27810749	6.574172784	5.801994899	7.303159822	5.714361014	4.589233685	5.42334329	6.236921862	5.414791677	5.847936651	5.786496107	5.877655285	6.023042834	6.397358165
ALDOA	P04075	VLAAVYK	-7.133752779	-7.189424271	-7.006640861	-6.608569512	-7.483234835	-7.143856565	-7.610659294	-7.490617803	-7.710812954	-6.608979992	-6.958745982	-7.165298505	-7.10054615	-7.569435575	-7.105943582	-7.070415707	-6.173122458	-6.914550281	-6.928745353	-6.948559972	-7.099142385	-7.735604189
APOA4	P06727	SLAPYAQDTQEK	-4.933053935	-5.010297605	-5.22451675	-5.357868966	-4.881048486	-4.785159735	-4.968956368	-5.580425464	-5.293992962	-4.090335175	-5.127352074	-3.414114636	-5.060875908	-6.076718786	-5.380650737	-5.464880418	-5.079075883	-5.748763653	-5.59553152	-5.599618558	-5.174810639	-4.017306095
APOC1	P02654	QSELSAK	1.928241434	1.537957036	2.084450717	1.262868861	1.420094436	2.315523722	1.673732758	0.881184425	1.109080957	1.643261548	1.827381083	2.836094411	1.487962686	0.728642514	2.13593294	2.326723283	1.249970066	1.650744525	1.828681939	1.363509399	1.774406723	1.855279727
APOC2	P02655	TAAQNLYEK	-6.898268037	-7.743055269	-7.327519395	-8.52214323	-7.812760101	-6.298400388	-7.866634022	-8.178029514	-8.368704919	-7.299412001	-7.371191896	-6.514717319	-7.539262479	-9.723816724	-7.567455137	-7.423727542	-7.993598731	-6.944710602	-7.200937363	-7.991924656	-7.485294031	-6.979759303
APOE	P02649	ELQAAQAR	-2.192893909	-2.565003507	-2.240965302	-1.525493926	-2.058491353	-1.538755363	-2.402984376	-2.316725335	-2.647886222	-1.786196392	-1.683670341	-2.480755768	-2.13711634	-2.819174736	-2.002039232	-2.193979648	-1.352848194	-2.486200122	-1.891265463	-2.215119772	-2.312936246	-3.087076279
C9	P02748	TSNFNAAISLK	-7.238585365	-8.030915852	-8.892589511	-8.249207348	-7.566076426	-7.487650092	-8.343256702	-8.589019696	-8.587342954	-7.253445627	-8.003134727	-6.648832689	-8.412894122	-8.794507154	-8.17001725	-8.20893038	-8.682992548	-8.184487428	-7.692493447	-8.144544735	-8.264291825	-7.958394251
C9	P02748	LSPIYNLVPVK	-6.577253032	-7.292580068	-8.412442162	-7.471169742	-7.218766909	-6.572073131	-7.779362973	-7.947285359	-7.902479573	-6.770659699	-7.004526367	-6.039747867	-7.693902363	-7.958393114	-7.55037724	-7.399216276	-7.860863828	-7.540258711	-6.922190001	-7.429566269	-7.448737937	-7.335687422
CALM2	P0DP24	EAFSLFDK	-6.548111544	-6.555960136	-6.480712258	-5.940510211	-6.811910359	-6.497801983	-6.791774216	-6.783529903	-7.02435443	-6.252825105	-6.632304632	-6.583356204	-6.443536117	-6.762882276	-6.697787723	-6.589248013	-5.680851384	-5.887469239	-6.307930522	-6.537681594	-6.281424036	-6.922703609
CD44	P16070	TEAADLC[+57]K	-9.282419176	-9.789803657	-10.07888578	-8.872762799	-9.448079152	-9.115976067	-9.588890453	-10.11112148	-9.963434316	-9.611815398	-9.545070333	-9.629141275	-9.585603386	-9.584887352	-9.724067483	-9.715956604	-9.094658239	-9.843751348	-9.608459303	-9.691152225	-9.35791175	-9.747493841
CD44	P16070	ALSIGFETC[+57]R	-8.939396791	-9.211680253	-9.617468696	-8.483592705	-9.171512999	-8.805384346	-9.156217164	-10.01645803	-9.335679383	-9.030321536	-8.754845958	-9.089874395	-9.519228952	-8.853331605	-9.53496791	-9.0600496	-8.692306094	-9.243504931	-8.784218958	-9.414089103	-8.740712966	-9.236152374
CHI3L1	P36222	IASNTQSR	-3.187591321	-2.849435897	-2.84579108	-2.260893776	-3.482240312	-3.388802793	-3.628772614	-3.223937161	-3.576385426	-2.556428538	-2.912089621	-2.894912485	-3.015410475	-2.607584318	-2.96702412	-3.306809622	-2.84990001	-3.479898581	-2.738986988	-2.860740329	-3.655193392	-3.374717004
CHI3L1	P36222	GNQWVGYDDQESVK	-5.467106678	-4.74183682	-4.954828632	-4.097855544	-5.353175643	-5.281482048	-5.412819545	-5.551533682	-5.494713814	-4.510557251	-4.69920385	-5.217297623	-4.95678763	-4.652016082	-5.203386162	-5.510008764	-4.908363244	-5.349964085	-4.769942484	-4.794305321	-5.589754291	-5.455786893
CHI3L1	P36222	QLLLSAALSAGK	-0.961077665	-0.603887958	-0.754102792	0.065733182	-1.231807783	-1.04549438	-1.081148416	-1.130531151	-1.261100086	-0.325362602	-0.681098319	-0.778076256	-0.59132795	-0.07889376	-0.987316359	-0.899269765	-0.715194095	-1.168352848	-0.493409119	-0.589328868	-1.549690134	-0.979996523
CP	P00450	EVGPTNADPVC[+57]LAK	-2.675050606	-3.111066993	-3.884678812	-3.348588605	-3.43263886	-2.788740863	-3.687767927	-4.203231299	-3.987957474	-3.433371503	-3.377841243	-2.086417499	-3.838757183	-3.816540062	-3.58912377	-3.299195053	-3.717358003	-3.535128616	-3.049429457	-3.553798311	-3.32773429	-3.143009257
CP	P00450	GEFYIGSK	-3.858237168	-4.300801201	-4.944370424	-4.543798271	-4.852979129	-3.916257254	-4.781921078	-5.336374416	-5.279557327	-4.367102956	-4.509212441	-3.356041587	-5.003203299	-5.354941175	-4.740229692	-4.338773971	-4.656676628	-4.837833858	-4.451231343	-4.81073754	-4.499738431	-4.461300004
CST3	P01034	ASNDM[+16]YHSR	-4.71080931	-4.930962375	-4.557813308	-4.17058621	-4.920356428	-4.939147415	-4.868299043	-4.871743818	-5.146707386	-4.143126343	-4.392429136	-5.141858593	-4.394107765	-4.719472163	-4.185653266	-4.383511503	-3.402583402	-5.176174395	-4.802343685	-4.755507041	-4.372028559	-5.378285511
DCN	P07585	VDAASLK	-7.431991631	-7.367766855	-7.206110224	-7.179481812	-7.713443722	-6.831698636	-7.65372626	-7.141330131	-7.732898277	-7.218175176	-7.328290959	-6.905700228	-7.415118022	-7.425160827	-7.491302894	-7.032192185	-7.598064474	-7.225088243	-7.531277859	-6.995075454	-6.932682183	-7.394378823
DDAH1	O94760	EFFVGLSK	-11.26594972	-10.8109095	-10.94402163	-10.57902958	-11.79254786	-10.90206133	-11.31787626	-11.31832999	-11.70760965	-10.47299361	-10.86922529	-10.87221448	-10.74183848	-11.68413604	-11.13410533	-10.81457824	-10.32548267	-10.63695686	-11.24946917	-11.25119063	-11.03897666	-11.15565682
DKK3	Q9UBP4	DQDGEILLPR	-4.294064551	-4.279351278	-3.905499263	-3.336913673	-4.400055779	-3.371266629	-4.228589967	-4.227407751	-4.670325722	-3.624428449	-3.312355657	-4.465418161	-3.958892119	-4.556115727	-3.770241656	-3.838726357	-2.950909877	-4.094637869	-3.63870031	-3.982133643	-4.027410215	-4.405183637
ENO1	P06733	IEEELGSK	-8.66143564	-8.61221998	-8.298865561	-8.174322386	-9.145855993	-8.579762646	-9.127761161	-8.813782334	-9.549330692	-8.690567225	-8.673712582	-8.266241383	-8.585424176	-8.609784943	-8.744801308	-8.42084884	-8.463356594	-7.968314466	-8.328029803	-8.2813093	-9.046064676	-9.205647948
ENO1	P06733	LNVTEQEK	-8.58627998	-8.634651143	-8.354954434	-7.98745834	-8.998981079	-8.809142399	-8.941086812	-8.670724557	-9.045906853	-8.306980635	-8.45877764	-8.230795515	-8.671766572	-8.594763988	-8.671395422	-8.352004861	-8.348346958	-7.789113499	-8.141080823	-8.524483289	-8.66710789	-9.105479202
ENO2	P09104	IEEELGDEAR	-6.412958742	-6.18512912	-5.948290475	-5.743605795	-6.423779797	-6.063870565	-6.332327288	-6.064823083	-6.876522337	-6.373675598	-5.83244206	-6.289335258	-6.26822149	-6.367785766	-6.353508711	-6.264219006	-5.740747659	-6.029460442	-5.879911017	-5.885786969	-6.055284963	-6.728599881
F2	P00734	YTAC[+57]ETAR	-8.032110802	-8.413804902	-8.517537629	-8.775041518	-8.664364513	-8.132752641	-8.664337093	-8.688737548	-9.528823031	-8.386568578	-8.534740622	-7.386551246	-8.592242435	-8.992333105	-8.844976656	-8.847828677	-9.046073117	-8.825789082	-8.893880067	-8.651742351	-8.756389029	-8.733818224
F2	P00734	TATSEYQTFFNPR	-6.056280913	-6.081021855	-6.391465105	-6.351080968	-6.652083403	-5.432164464	-6.596178425	-7.001895574	-7.164023087	-5.84388554	-6.842574491	-4.829555321	-6.697749324	-7.341217296	-6.601837328	-6.0218413	-7.02516862	-6.249720669	-6.203651181	-6.394312958	-6.388769567	-6.310077832
GAPDH	P04406	AAFNSGK	-8.795138821	-8.049053252	-7.835780806	-8.104821683	-9.123364915	-8.275906864	-9.451772417	-9.600388103	-11.00817799	-9.573326928	-8.244020692	-8.312703737	-8.121095993	-8.789299894	-8.685456836	-8.393136648	-8.579567969	-7.056905193	-7.495430602	-9.147595022	-9.743393298	-9.53852046
GAPDH	P04406	YDNSLK	-10.9320663	-10.66505103	-10.42956596	-10.48420966	-11.64403213	-10.7112537	-11.77186893	-11.91975244	-12.54733641	-11.61039841	-10.97244723	-10.7346519	-10.67941275	-11.05124378	-11.36693396	-10.82557473	-10.90605913	-9.528501902	-10.03883533	-11.38455928	-11.28215892	-12.0695406
GDA	Q9Y2T3	DHLLGVSDSGK	-9.174311458	-9.521230346	-9.036807934	-8.850238801	-9.995539222	-9.027810186	-9.804991815	-9.397074221	-9.93138507	-9.645136763	-9.117817503	-9.164987587	-8.879235724	-9.299946998	-9.281179771	-9.388810373	-8.049924627	-8.951259778	-8.609322614	-8.927968277	-9.283225942	-9.53846579
GOT1	P17174	VGNLTVVGK	-7.745915948	-7.784823186	-7.803059855	-6.973411426	-8.393016587	-7.79608983	-8.000990302	-8.078309413	-8.215637	-7.319806226	-7.576720995	-7.809070117	-7.683433029	-8.040889449	-7.61994804	-7.700206057	-6.576236564	-7.815395321	-7.336318759	-7.569484673	-7.495305959	-8.21591176
GOT1	P17174	IGADFLAR	-9.913352782	-9.888084276	-9.623846165	-9.180748386	-10.47312662	-9.402736857	-10.06250048	-9.965902573	-10.6453923	-9.567513391	-9.630425986	-9.851381914	-9.547563587	-9.966055887	-9.584255701	-9.838017801	-8.8462641	-9.677814013	-9.369499983	-9.675159778	-9.393251308	-10.67208714
GSN	P06396	AGALNSNDAFVLK	-4.041638567	-4.101089389	-4.203134946	-3.652977691	-4.16990044	-3.467129696	-4.06033726	-4.126811161	-4.852457579	-3.421137037	-3.908880061	-3.527183134	-3.93153181	-4.344814342	-4.083722449	-3.793463096	-3.710599497	-4.381424187	-3.918213057	-4.337267934	-4.194751594	-4.037179794
HBA1	P69905	FLASVSTVLTSK	-5.373615663	-6.217614828	-8.312586229	-3.740945392	-9.844299291	-5.710775516	-6.371203665	-8.94690695	-1.898016995	-8.371323579	-4.854502228	-1.849497515	-5.557843705	-4.997419721	-6.319104663	-8.807140705	-8.256573858	1.960161261	-2.790409684	-6.700297905	-3.636712649	-8.328661909
HBA1	P69905	VGAHAGEYGAEALER	-4.949310526	-5.360000124	-8.904960433	-3.317380046	-11.43096241	-5.268736301	-5.844231233	-13.79167723	-1.560804668	-10.44647618	-4.651482442	-1.608690962	-5.297257821	-4.586325855	-6.405084687	-11.28069406	-13.18527695	2.264905213	-2.608231994	-6.59874766	-3.343787467	-8.487928845
HBB	P68871	VNVDEVGGEALGR	-4.870683705	-5.667042898	-8.328571509	-3.178651355	-12.35530835	-5.131522923	-5.827344212	-9.720519442	-1.364520014	-9.471425994	-4.322777806	-1.377992709	-5.095116376	-4.44307754	-5.78496879	-9.166488845	-11.18886142	2.462739034	-2.29776047	-6.44914181	-3.087367256	-8.469591712
KNG1	P01042	EGDC[+57]PVQSGK	-8.632727118	-8.996442036	-8.632727118	-9.734714708	-9.405271738	-9.298548419	-9.121245248	-9.909868454	-10.19584012	-8.880377319	-9.247459362	-7.516144378	-9.876902767	-10.09072054	-9.351152544	-9.264956069	-9.819564274	-9.369259821	-9.095208965	-9.711295677	-9.414492205	-8.838888238
KNG1	P01042	QVVAGLNFR	1.309997646	1.638178582	1.688035998	0.910665819	0.869994003	1.116214366	0.88135845	0.414364009	0.406428904	1.697774045	1.116695895	3.097014768	0.974653582	0.324510393	0.662726889	1.470467909	0.310271612	0.915226019	1.378017073	1.021256248	1.511638408	1.534883384
KNG1	P01042	VQVVAGK	-4.827460909	-4.907335852	-4.871438606	-5.525825345	-5.379211134	-5.345038954	-5.20084881	-6.058624405	-5.915418336	-4.548050756	-5.123838914	-3.404145647	-5.4638354	-6.44013804	-5.644135558	-5.084606343	-5.708027043	-5.305444467	-5.187604821	-5.565855141	-5.076492856	-4.541114904
L1CAM	P32004	GQLSFNLR	-4.923703537	-4.697567527	-4.593291245	-4.297805332	-5.106466325	-4.472388211	-4.988672894	-4.776606399	-5.290351022	-4.815509018	-4.546939393	-4.745943775	-4.532277434	-5.409959228	-4.845653086	-4.922441109	-4.53622225	-5.008835893	-4.666891841	-4.505381834	-4.417523161	-5.292261467
LAMP1	P11279	VWVQAFK	-8.310205466	-8.375739993	-8.41208508	-7.74728905	-8.700670941	-8.23850322	-8.371627479	-8.57084935	-9.083591166	-8.239432971	-8.144234862	-8.049866523	-8.593083832	-8.459201184	-8.306036084	-7.962987381	-7.942780586	-8.240529483	-7.8299893	-8.285068878	-8.346475806	-9.06614944
LAMP2	P13473	YLDFVFAVK	-7.885579095	-8.252677605	-8.18674863	-7.6824867	-8.545714862	-7.50567934	-8.002165534	-8.561858459	-8.975052653	-7.588796269	-7.713447805	-7.565626196	-8.07475099	-8.498777934	-8.283631769	-7.869066354	-7.638568759	-7.779164719	-7.828667772	-8.322252548	-8.267371309	-8.274400366
LDHB	P07195	FIIPQIVK	-8.934533421	-8.950554286	-8.779255196	-8.308106452	-9.316937875	-8.671870935	-9.419572524	-9.328217418	-9.618211825	-8.53526726	-8.781617335	-8.937410506	-9.006765894	-9.17858159	-9.283265038	-9.100928377	-8.086209385	-8.602985203	-8.67396236	-8.907831248	-8.834394	-9.739481726
LDHC	P07864	VIGSGC[+57]NLDSAR	-9.195291834	-9.040558662	-8.735860215	-8.234336901	-9.603842969	-8.632426619	-9.796882617	-9.741434992	-9.965500083	-8.595671635	-9.449354404	-8.650955614	-9.097698606	-9.404082672	-10.17386161	-8.982269705	-8.434837601	-8.250614132	-8.731127109	-9.392677188	-8.987185881	-10.69428152
MDH1	P40925	GEFVTTVQQR	-7.484027826	-7.454212497	-7.311191229	-6.943560064	-8.012324652	-7.624287341	-8.025064309	-8.095288214	-8.383431847	-7.322610287	-7.453865349	-7.566830851	-7.322381603	-7.75518885	-7.802050398	-7.567634979	-6.697769528	-7.121112866	-6.928023552	-7.421934069	-7.59724576	-8.255195203
NCAM1	P13591	GLGEISAASEFK	-5.803829404	-6.053817882	-5.98874712	-5.037989281	-6.302640913	-5.400917469	-5.867439846	-5.908061076	-6.379293214	-5.320483737	-5.200907866	-5.912033651	-5.795562674	-6.564892814	-5.578963217	-5.927124125	-4.617823663	-6.118969843	-5.635587855	-5.983285702	-5.787859789	-5.984392281
NPTX2	P47972	VAELEDEK	-9.144751953	-9.050182583	-9.244287627	-8.436765595	-9.607338732	-8.743916464	-9.196781712	-8.597646867	-9.748628328	-8.533498069	-8.506650473	-8.931684762	-9.140677951	-9.77954427	-8.67257162	-8.818501383	-7.957073178	-9.126568823	-8.792006447	-9.650286397	-8.923649977	-9.513853452
NPTXR	O95502	ELDVLQGR	-2.370020417	-2.463017506	-2.426253358	-1.829918739	-3.008922494	-1.99026837	-2.432461786	-2.003723685	-2.922386201	-1.820654894	-1.653431243	-2.254893092	-2.310793422	-2.950192154	-1.772924665	-2.069376246	-1.276235255	-2.497088893	-2.218256496	-2.648207233	-2.273333847	-2.57366005
NRXN1	P58400	LAIGFSTVQK	-7.198059746	-7.085370782	-6.93177968	-6.579449266	-7.569301444	-6.802006426	-7.37623293	-7.076031701	-8.393562457	-6.808108896	-6.69262485	-7.236777058	-7.042469948	-7.788398804	-6.952964724	-7.265823177	-6.085370782	-7.348503386	-6.737615465	-7.049625894	-6.958572821	-7.60896484
OGN	P20774	LEGNPIVLGK	-6.75851892	-6.530481892	-6.720384691	-6.227974484	-6.869325847	-6.046592604	-6.968726589	-6.819024276	-7.331868942	-6.397402459	-6.504393545	-6.684897966	-6.777516838	-7.22051894	-6.614286066	-6.584310182	-6.601448414	-6.847940951	-6.591472254	-6.908902756	-6.491648381	-6.864342884
OMG	P23515	LESLPAHLPR	-4.097282121	-4.400192954	-3.960640293	-3.336470424	-4.318934296	-3.497520275	-4.06939026	-4.076971657	-4.788425432	-3.566738767	-3.303294314	-3.831566188	-3.85339611	-4.585472215	-3.894193916	-3.81152674	-3.243372845	-4.286522694	-3.544989934	-3.736004904	-3.97991719	-4.121751186
PARK7	Q99497	ALVILAK	-8.36784994	-8.636631968	-8.604889138	-7.913966094	-8.903239278	-8.319805504	-9.112864381	-8.715667837	-9.444424509	-8.095266003	-8.593911866	-8.47648947	-8.652909359	-8.60624848	-8.93094612	-8.457553601	-7.621985192	-7.448017075	-8.326233639	-8.724417717	-8.460642904	-9.191462213
PEBP1	P30086	GNDISSGTVLSDYVGSGPPK	-5.226065359	-5.319027283	-4.822953621	-5.448304665	-5.600328917	-5.296624288	-5.395798679	-5.585333316	-6.037106061	-4.844792745	-4.84602616	-5.492203279	-4.895544232	-5.244802096	-5.341430827	-5.391958917	-4.222859847	-5.089409878	-4.97420388	-5.047356551	-4.972463415	-5.700496135
PEBP1	P30086	LYEQLSGK	-7.315525973	-7.720076406	-7.654614619	-7.257542199	-7.903919542	-7.793449852	-7.879970189	-8.263535196	-8.150697665	-7.608101622	-7.606160067	-7.675744251	-7.465677729	-7.582333219	-7.941713959	-7.860506506	-6.890001407	-7.156320605	-7.447962597	-7.48151771	-7.542854609	-7.987209257
PEBP1	P30086	VLTPTQVK	-6.696711996	-6.725871951	-6.591742436	-6.113706757	-7.034831908	-6.5410183	-6.872206374	-7.082989638	-7.514038282	-6.390422123	-6.495747714	-6.939895644	-6.514599647	-6.855641313	-6.689121951	-6.702100559	-5.753278109	-6.621473184	-6.504005433	-6.597434544	-6.628311272	-7.152839699
PGLYRP2	Q96PD5	TFTLLDPK	-3.910056052	-4.446460328	-4.399659654	-5.635693409	-5.02332571	-3.729355912	-4.66875802	-5.205922716	-5.227741894	-4.150073504	-4.874512868	-3.189141483	-4.727155634	-5.597742866	-5.27153464	-4.448385396	-5.037275555	-4.331569068	-4.7161521	-4.749871975	-4.686307851	-4.395718141
PKM	P14618	VVEVGSK	-7.703703928	-7.454802144	-7.314429525	-6.710005844	-8.070019024	-7.437066816	-7.739749181	-7.992421924	-7.944025643	-6.872970819	-7.20679517	-7.520163999	-7.505513885	-7.724223544	-7.569919842	-7.459977026	-6.366626333	-7.358119723	-7.067679246	-7.291656602	-7.393916319	-8.292030721
PKM	P14618	GVNLPGAAVDLPAVSEK	-7.247758155	-7.133783356	-7.136009797	-6.390598717	-7.537629979	-7.089542917	-7.474202634	-7.396347311	-7.914607838	-6.597964093	-6.915781907	-7.141763555	-6.834181631	-7.315372327	-7.057335305	-7.104764965	-5.977278871	-6.974892554	-6.725619504	-6.953402266	-6.91316019	-7.823894001
PKM	P14618	GDLGIEIPAEK	-8.018630167	-7.90973432	-7.937100281	-7.304364237	-8.31230517	-7.836536071	-8.167099514	-8.273345454	-8.476919155	-7.3524758	-7.755009231	-8.020509293	-7.845667828	-8.274296404	-7.946448712	-7.666779077	-6.761211795	-7.69240118	-7.5670894	-7.861722155	-7.821682711	-8.852791476
PKM	P14618	GDYPLEAVR	-6.433136173	-6.387974669	-6.488899445	-5.773129197	-6.934893898	-6.275434796	-6.905895243	-6.674573577	-7.190031576	-5.952572731	-6.357535234	-6.484604137	-6.138729343	-6.74533014	-6.470754192	-6.459961839	-5.484936399	-6.352092509	-6.122272231	-6.272821022	-6.237590144	-7.207324437
PKMisoform	NA	LFEELVR	-3.846239332	-3.670839824	-3.582135867	-3.072570418	-4.030790009	-3.547965284	-4.106660816	-4.120504288	-4.525313615	-3.322599298	-3.612746656	-3.854470676	-3.472568978	-3.954402158	-3.78869287	-3.675577685	-2.662050757	-3.712882571	-3.3290728	-3.499022519	-3.560165465	-4.637380537
PON1	P27169	LLIGTVFHK	-7.467852491	-8.133288019	-6.812987977	-8.143754281	-8.141676126	-6.748200117	-8.035291428	-9.483949605	-8.780748294	-7.637525832	-7.835000461	-5.679802126	-8.229336627	-9.261141365	-8.406603393	-7.214903737	-8.133288019	-7.861103108	-7.526728815	-7.680450643	-7.201726851	-7.537181223
PPIA	P62937	VSFELFADK	-8.672656769	-8.522880974	-9.179616758	-8.063892505	-9.021082754	-8.615415849	-8.992774325	-9.114948433	-8.939330883	-8.518246161	-8.970679622	-8.446852851	-9.186412904	-8.623043294	-9.043031328	-8.815932963	-8.36815838	-7.424068091	-8.474924486	-8.636256566	-8.828235383	-9.151817185
PRDX2	P32119	QITVNDLPVGR	-4.408638981	-4.802225193	-4.493854984	-4.034691423	-5.39401561	-4.666714219	-5.189291948	-4.856702113	-3.91078447	-4.707281143	-4.363378111	-3.371917094	-4.327677217	-4.830029068	-5.069429494	-4.532022805	-4.07036047	-0.472874041	-3.852789714	-4.876115164	-4.106458999	-5.263638735
PTPRZ1	P23471	AIIDGVESVSR	-6.47089713	-6.685770649	-6.463737338	-5.794709783	-6.647853127	-6.084309082	-6.734220321	-6.564039236	-7.007056512	-6.349161427	-5.97051961	-6.413048574	-6.332822297	-6.938715083	-6.218468131	-6.579219402	-5.77465193	-6.817039734	-6.129403775	-6.507709557	-6.491679186	-6.810336562
PTPRZ1	P23471	DIEEGAIVNPGR	-7.427097957	-7.687891486	-7.356708629	-6.718655119	-7.721792703	-6.842446512	-7.470490923	-7.572214371	-7.857042706	-7.020079187	-6.8722787	-7.583152866	-7.204827737	-8.078649252	-7.093750731	-7.464802466	-6.550387962	-7.671146246	-7.066964167	-7.533780207	-7.638527374	-7.606273563
SCG2	P13521	IESQTQEEVR	-7.626792132	-7.545622028	-8.151454122	-6.88836711	-8.708919334	-7.29810098	-7.786460345	-7.489945398	-8.327815136	-7.085751059	-7.073073371	-8.054847307	-7.924840154	-8.489602704	-6.890364589	-7.414654027	-6.301266176	-8.053264957	-7.901878876	-7.88817747	-7.210769642	-8.047540805
SCG2	P13521	SGQLGIQEEDLR	-9.722817238	-9.22519616	-9.542244992	-8.896725324	-10.07632526	-8.746086359	-9.768245686	-9.442402222	-10.80754946	-8.430800908	-8.938419037	-9.340848205	-9.476256753	-10.38208974	-9.401018751	-9.318810295	-7.733948094	-9.517360267	-9.42739999	-9.537006921	-9.579013927	-9.64040239
SMOC1	Q9H4F8	AQALEQAK	-7.035464462	-7.368898882	-7.357392557	-6.843641223	-7.714687303	-7.254962311	-7.782202926	-7.323089869	-8.689330409	-7.046409415	-7.781468535	-7.203757627	-7.158071523	-7.848067152	-7.654486345	-7.181337375	-5.576810716	-7.204357955	-6.685537306	-6.731756212	-7.421836438	-8.076524775
SOD1	P00441	AVC[+57]VLK	-2.158981526	-1.823369919	-2.181358235	-1.044884682	-2.008016378	-1.954311417	-1.938808469	-1.652560484	-2.594344505	-1.430393868	-1.231722782	-1.961113758	-1.812055664	-1.959339204	-1.515248219	-1.880609469	-0.669603671	-2.100504692	-1.58801996	-1.7364972	-1.889964932	-2.467203256
SOD1	P00441	GDGPVQGIINFEQK	-3.035629343	-2.535351978	-2.573496536	-1.810454514	-2.890691876	-2.517663623	-2.7243446	-2.688544392	-3.453774507	-2.029334976	-2.161465661	-2.528190147	-2.608983427	-3.004560808	-2.157866419	-2.35446065	-1.448714241	-2.939595236	-2.497107501	-2.614427943	-2.606078418	-3.056240968
SOD1	P00441	HVGDLGNVTADK	-5.146974832	-5.235720869	-5.072394506	-4.198561803	-5.240883325	-4.79501354	-5.023234995	-5.173603587	-5.726499688	-4.400581382	-4.469810353	-5.047187789	-4.87993531	-5.233307896	-4.481150548	-4.776140895	-3.781524994	-5.254283876	-4.706956226	-4.798643953	-5.052690428	-5.411373274
SPP1	P10451	GDSVVYGLR	-3.886305849	-3.692807876	-3.629339364	-2.904024046	-4.123406269	-2.987730964	-3.853784379	-3.891213875	-4.569558528	-4.352926839	-3.812646175	-3.42958979	-3.354122104	-3.690228479	-3.789865372	-3.298330228	-3.179240806	-3.65102674	-3.357566071	-3.536678235	-3.551523692	-4.630629744
SPP1	P10451	YPDAVATWLNPDPSQK	-2.020167527	-1.786760971	-2.016274487	-1.157239339	-2.300245414	-1.713293504	-2.12348656	-2.232033032	-2.761942689	-2.775744414	-2.259584225	-1.870628679	-2.026027175	-2.096805477	-1.968102507	-1.732052223	-1.211711737	-1.926844113	-1.671673705	-1.839238718	-2.153407726	-2.046973503
SPP1	P10451	QETLPSK	0.735798466	0.596409581	0.651523587	1.307854234	-0.019022482	0.867045787	0.314124703	0.119218807	-0.830582737	0.075977051	0.368565215	0.870793836	0.620206005	0.308382871	0.470036253	0.833613596	1.209238317	0.702467551	0.661711418	0.468410247	0.199784317	0.261315104
THY1	P04216	HVLFGTVGVPEHTYR	-4.357344817	-5.012162654	-4.232656221	-3.813065892	-5.410228807	-4.517445122	-5.208277434	-4.472209508	-5.657678722	-4.061033893	-4.077447613	-4.917659909	-4.493790644	-5.624388322	-4.524171151	-4.487129954	-3.233136455	-5.369797965	-4.47515051	-4.756173508	-4.048956015	-5.251935691
TPI1	P60174	IAVAAQNC[+57]YK	-9.745153846	-10.43178049	-9.230580673	-9.339811017	-10.65369056	-9.569235504	-10.55041262	-10.58829399	-10.354262	-10.10053753	-10.61020186	-9.650382819	-9.492221619	-10.73183868	-10.69596469	-10.37489648	-9.768815481	-8.685152205	-9.367636457	-10.3542002	-10.50076808	-11.03743927
VGF	O15240	EPVAGDAVPGPK	-6.02223362	-5.764940817	-6.143298227	-4.93547958	-6.880679467	-5.243069711	-5.854715738	-5.386690003	-6.65068052	-4.925558902	-5.034326422	-6.109158293	-5.980158638	-6.88778775	-5.10034159	-5.407683474	-3.753977278	-6.114270877	-5.907046816	-6.25092739	-5.224671836	-6.18804492
VGF	O15240	GLQEAAEER	-8.498143443	-8.259794957	-8.531310306	-7.33074675	-9.38718537	-7.437054237	-8.243638237	-7.917897278	-9.332299542	-7.138776534	-7.538173095	-8.526554353	-8.501866323	-9.564251531	-7.597151826	-8.078919695	-6.115136714	-8.398398706	-8.240744794	-8.592763296	-7.763150677	-8.635839776
VTN	P04004	GQYC[+57]YELDEK	-5.141554599	-5.345634204	-5.412289263	-5.839235947	-5.793546363	-4.845293388	-5.437367701	-6.25227399	-6.369681991	-5.302336634	-5.859478814	-4.174787906	-6.08298935	-6.66257027	-6.133983781	-5.475620565	-6.014595691	-5.929922316	-5.589699862	-6.012735745	-5.560444964	-5.308693062
VTN	P04004	DVWGIEGPIDAAFTR	-2.880908253	-2.730648224	-2.843188587	-3.341725835	-3.23145018	-2.271119296	-3.339048821	-4.107888558	-3.877819894	-2.820936852	-3.314445612	-1.459447265	-3.513106075	-4.186449759	-3.784123595	-2.996123907	-3.583887216	-3.403720727	-3.246645397	-3.471057336	-3.056059063	-2.971677146
YWHAB	P31946	NLLSVAYK	-6.87145093	-6.931534149	-6.97642049	-6.622594149	-7.165678807	-7.154322709	-7.488656129	-7.388506462	-7.660755149	-6.885930822	-7.118501176	-6.639461758	-6.794862589	-6.933645057	-7.414479593	-7.479772203	-6.270622795	-5.910394972	-6.299396966	-6.746527367	-7.318848879	-7.438492648
YWHAB	P31946	VISSIEQK	-7.752485447	-7.751505205	-7.935349504	-7.491080989	-7.947050491	-8.029720752	-7.988694726	-8.251240008	-8.239367756	-7.739270802	-7.94443265	-7.62563093	-7.710783429	-8.015161913	-8.347071272	-8.116575103	-7.135648697	-7.105433862	-7.387672601	-7.760468443	-7.920658815	-8.085783057
YWHAG	P61981	YLAEVATGEK	-9.370045809	-9.672713199	-9.576496686	-9.278655299	-10.00596812	-9.978491536	-10.21698042	-10.61424739	-10.30589472	-9.782481428	-10.02565232	-10.02574663	-9.298732725	-9.672319973	-10.22663319	-10.19062409	-8.739827394	-9.107569371	-9.089084825	-9.580840174	-10.21488287	-10.45652651
YWHAZ	P63104	VVSSIEQK	-6.07247902	-6.566586021	-6.03221515	-6.21322198	-6.6130397	-6.750517165	-6.653379966	-7.04111612	-7.689554416	-6.310138905	-6.73289761	-6.171626611	-6.492978593	-6.37143924	-6.997507998	-6.763173143	-5.90738489	-5.602593218	-5.558127643	-6.092341318	-6.840815199	-7.186233651

SUPPLEMENTAL TABLE 11: SRM RATIO ABUNDANCES POST-REGRESSION

Gene ID	Protein ID	Peptide Sequence	S068_P1D09_53741	S069_P1E09_58595	S070_P1F09_72374	S071_P1G09_76348	S072_P1H09_66735	S073_P1A10_83459	S074_P1B10_49941	S075_P1C10_39138	S076_P1D10_46640	S077_P1E10_47232	S078_P1F10_67579	S079_P2A1_54179	S080_P2B1_73518	S081_P2C1_41483	S082_P2D1_51431	S083_P2E1_52154	S084_P2F1_55286	S085_P2G1_57502	S086_P2H1_70529	S087_P2A2_77792	S088_P2B2_86840	S089_P2C2_87070	S090_P2D2_48615
AHSG	P02765	EHAVEGDC[+57]DFQLLK	-4.741067108	-5.1079643	-4.708934126	-3.4477068	-5.197012687	-4.865416909	-4.582071612	-5.759569577	-4.788714777	-4.584959043	-4.675866359	-4.622941223	-5.192592426	-4.024702905	-5.125636321	-4.312292861	-4.966448233	-4.165923732	-4.833082322	-5.379090493	-3.833339661	-5.505783788	-4.561887193
ALB	P02768	LVNEVTEFAK	4.954382643	4.470387723	4.219682057	5.962136013	4.710769629	4.995903356	5.357163716	4.515502692	5.041062129	4.751603636	5.125807574	5.180659205	4.501734066	5.593656705	4.39782676	5.141988017	4.548573512	4.751477219	4.958176592	4.118743726	5.678020612	4.200111123	5.442955509
ALB	P02768	LVTDLTK	5.668212155	5.174264235	4.934029926	6.733143957	5.445900273	5.660495096	6.080027375	5.218291246	5.80826158	5.476803594	5.844469977	5.913612443	5.176489095	6.292459449	5.152092932	5.876653936	5.295153947	5.487741838	5.712634714	4.856764433	6.407824418	4.92113398	6.132461979
ALDOA	P04075	VLAAVYK	-6.811367954	-8.072356738	-7.871641935	-7.214034133	-7.724745245	-6.876640984	-7.398869047	-6.591496046	-7.189434115	-7.001310064	-6.717176142	-7.12211288	-6.830367789	-6.936871456	-7.251473551	-7.662783268	-7.844681087	-7.378324539	-7.597003243	-6.68527598	-6.144872108	-8.028862146	-6.551000598
APOA4	P06727	SLAPYAQDTQEK	-4.860665863	-5.615030012	-5.76365719	-3.722594533	-5.238624769	-5.218355511	-3.993164378	-5.645253042	-4.987911637	-5.522846815	-4.830260578	-5.137423226	-5.43961073	-4.799873419	-5.549975511	-5.229258999	-5.823690521	-4.984856279	-4.716283683	-5.777643415	-4.058854919	-5.750653562	-4.29345129
APOC1	P02654	QSELSAK	1.704474395	0.017095603	1.603731226	2.307314325	1.327209426	1.794032298	1.88464644	1.060888806	1.614572382	1.05211803	1.979618324	1.520362983	1.556071638	1.570872432	1.445409067	1.982902583	1.203980596	0.337458244	1.890973576	0.947631417	2.110514623	1.504338574	1.626427285
APOC2	P02655	TAAQNLYEK	-7.768533774	-8.28400425	-7.887268431	-6.803610502	-7.850037689	-7.654089387	-6.678374618	-8.564015549	-8.110241707	-7.912628911	-7.126432323	-7.316684665	-8.086015547	-7.005242899	-7.825762719	-6.483553469	-7.899972079	-8.265216887	-6.903771566	-8.600350284	-6.91993462	-8.745571105	-7.242478863
APOE	P02649	ELQAAQAR	-1.664315256	-2.613223899	-2.261015814	-2.437199361	-3.207503039	-2.303011985	-2.036565428	-1.941720244	-2.110167971	-2.258762007	-1.95370186	-1.918724793	-1.945271461	-1.909408677	-1.944206988	-1.950120164	-2.786028416	-2.533998039	-2.243158321	-2.056545462	-1.352515387	-2.843115303	-1.450727187
C9	P02748	TSNFNAAISLK	-8.316096322	-8.324732708	-8.565615964	-7.043389219	-8.269708513	-7.480760225	-7.594075746	-8.53152142	-7.817194087	-7.789713532	-7.48803201	-7.48208219	-8.378560769	-7.428898438	-8.922875239	-8.10524061	-8.398797965	-7.345021091	-8.092344481	-8.446221824	-6.990921799	-9.224335303	-7.302666379
C9	P02748	LSPIYNLVPVK	-7.536649769	-7.589720893	-7.857202937	-6.515646035	-7.548055383	-6.941915986	-6.945981174	-7.853520319	-6.912992195	-7.193691271	-6.829793189	-6.818464604	-8.011785971	-6.518309719	-8.18778909	-7.530566011	-7.559310713	-6.655145645	-7.28318842	-7.768764058	-6.381691579	-8.53888382	-6.799102322
CALM2	P0DP24	EAFSLFDK	-6.195016318	-7.220906087	-6.912622642	-6.525599519	-6.94256533	-6.117877987	-6.623357024	-5.895620626	-6.406099659	-6.436435285	-6.057618942	-6.592080815	-6.193910358	-6.280204484	-6.897735428	-6.94647616	-6.992895224	-6.779661719	-6.680729305	-6.138022403	-5.61306236	-7.168076614	-5.828631551
CD44	P16070	TEAADLC[+57]K	-9.700232286	-9.722616454	-9.546229753	-9.482099416	-9.483990532	-9.473413235	-10.24819309	-9.148199395	-9.812824479	-9.516622951	-9.297626587	-9.535842239	-9.815247131	-9.171213196	-9.508434205	-9.089641815	-10.0464275	-9.922203935	-9.66544923	-9.370909971	-9.147680377	-9.50811605	-9.356080732
CD44	P16070	ALSIGFETC[+57]R	-8.782271788	-9.777750865	-8.951650199	-8.674116223	-8.69131757	-9.022950634	-9.591471086	-8.81775686	-8.798777305	-9.024339625	-8.72034134	-9.405211056	-9.106440644	-9.264952716	-9.443093466	-9.099456199	-9.983523328	-9.424863648	-8.996085643	-9.175547861	-8.603726895	-8.956019448	-8.887458134
CHI3L1	P36222	IASNTQSR	-2.99938385	-3.875056707	-3.137820022	-2.675876456	-3.023840884	-2.517071682	-3.373675703	-2.106518035	-3.046902095	-2.286692297	-2.42142499	-3.645133376	-2.835567425	-2.516601209	-3.14725508	-3.030118307	-3.325910935	-4.139694864	-3.22779508	-3.053203156	-2.980755643	-3.438336436	-1.673084352
CHI3L1	P36222	GNQWVGYDDQESVK	-5.155531124	-5.899018588	-5.056611114	-4.713011227	-5.008835183	-4.726862383	-5.453595511	-4.177585605	-5.122227251	-4.354715127	-4.278385018	-5.649152797	-5.021088005	-4.725763726	-5.080869091	-5.138898945	-5.39751329	-6.346849083	-5.432992452	-5.017257697	-4.736243533	-5.510715438	-3.676413827
CHI3L1	P36222	QLLLSAALSAGK	-0.984525822	-1.797847125	-0.971369059	-0.304566043	-0.578026798	-0.08467265	-1.06767357	0.071568715	-0.615913072	-0.19986674	-0.204363079	-1.804118919	-0.52256815	-0.495003228	-1.025873235	-0.989421533	-1.14036595	-2.386039427	-1.110786031	-0.870535695	-0.763497804	-1.028833832	0.608764429
CP	P00450	EVGPTNADPVC[+57]LAK	-3.315518833	-4.121513645	-4.072081465	-3.209407981	-3.610377385	-2.952010114	-2.893635671	-3.661365455	-3.484740763	-3.861866233	-3.222647597	-3.174100246	-3.655679986	-2.825976595	-3.913720168	-3.099597789	-3.607657122	-2.594943427	-3.377863468	-4.002720092	-3.076513711	-4.081478446	-3.251982372
CP	P00450	GEFYIGSK	-4.524128818	-5.17552995	-5.446682297	-4.068170673	-4.84761205	-4.485304071	-4.313362673	-4.949066099	-4.594328177	-5.029740369	-4.496559179	-4.583468917	-5.298639353	-4.257442506	-5.309321663	-4.471533514	-5.182146991	-4.365634606	-4.871226745	-5.336327139	-4.141827715	-5.275287465	-4.338805819
CST3	P01034	ASNDM[+16]YHSR	-4.466001665	-5.392072703	-5.096136737	-4.769180574	-5.230403486	-4.798897524	-4.600681586	-3.779634073	-4.600451924	-4.74830455	-5.025152822	-4.551308554	-4.166633463	-4.293618181	-4.577864513	-4.734004627	-5.566130427	-5.496406859	-4.947721174	-4.550516734	-4.867078217	-5.054386856	-4.170176483
DCN	P07585	VDAASLK	-7.357781314	-7.258131143	-7.345382513	-7.010198322	-7.701614697	-7.29758245	-7.328698907	-7.286217426	-7.521976965	-7.400037902	-7.203048531	-7.265217194	-7.685526366	-7.324927468	-7.336125767	-7.053224969	-7.511767649	-7.095963893	-7.517912597	-7.436907589	-6.892016895	-7.21594214	-6.90340026
DDAH1	O94760	EFFVGLSK	-11.05043485	-11.5255096	-11.62627398	-10.94820208	-11.47253988	-10.80330309	-11.17132336	-10.59043919	-11.08253337	-10.68033284	-10.53187343	-11.1902888	-11.38765224	-10.89145632	-11.44845292	-11.50296551	-11.76653879	-11.18988565	-11.13917627	-10.72155473	-10.36323958	-11.34708473	-10.66577441
DKK3	Q9UBP4	DQDGEILLPR	-3.466459673	-4.58998237	-4.113200464	-3.73217082	-4.970295451	-4.165335569	-4.255014252	-3.425083448	-3.938458569	-4.191227733	-3.707929919	-4.198838093	-3.88108312	-3.390559533	-3.991768381	-4.426303737	-4.649066061	-4.510237656	-4.519812308	-3.838652905	-3.380534333	-4.839677351	-3.355587267
ENO1	P06733	IEEELGSK	-8.376464873	-9.5114366	-9.077292345	-8.736255427	-8.831418618	-8.269780166	-8.695897028	-8.327709396	-8.327733985	-8.383382134	-7.921109537	-8.544464876	-8.64959037	-8.25718634	-9.458096197	-8.622493616	-9.334106584	-9.552081552	-8.784913909	-8.252833756	-8.126201945	-9.274237568	-8.282824012
ENO1	P06733	LNVTEQEK	-8.561827131	-9.491270172	-9.286462343	-8.783962002	-9.034703158	-8.285041213	-8.939326843	-8.319469759	-8.555351002	-8.450540344	-7.887149591	-8.870725131	-8.693835444	-8.302263637	-9.056484861	-8.657201769	-9.309134029	-9.398763582	-8.6758769	-8.238803162	-8.013443849	-9.227349268	-8.142201193
ENO2	P09104	IEEELGDEAR	-6.256075048	-6.592018205	-6.618767641	-6.333886533	-7.112769919	-6.029566604	-6.547231234	-5.992919502	-6.22844639	-6.228238497	-5.707134358	-6.304659838	-6.010981756	-5.761093559	-6.172915223	-6.459757896	-6.777869476	-6.372087596	-6.379567905	-6.075118725	-5.371909979	-6.793948933	-5.836287423
F2	P00734	YTAC[+57]ETAR	-9.525715282	-8.829130135	-8.709716846	-7.8952725	-8.430339626	-8.27731397	-8.708083952	-9.895355336	-8.487220504	-9.312649	-8.456686429	-8.459373429	-8.775578918	-7.70554653	-9.250204022	-8.313954212	-9.261729367	-8.392184217	-8.97837079	-9.441625028	-8.01310899	-9.551931236	-8.610624501
F2	P00734	TATSEYQTFFNPR	-6.784549312	-7.005018637	-7.07953985	-5.772258531	-6.764513998	-6.215574423	-6.54739672	-7.410445212	-6.379354056	-6.769949217	-6.268777022	-6.201265834	-7.116401304	-5.719803857	-7.319902759	-6.535236839	-7.13072985	-6.331905031	-6.6605661	-7.331177734	-5.790033233	-7.511375152	-6.194678575
GAPDH	P04406	AAFNSGK	-9.616044347	-9.976289364	-9.3129603	-8.684929077	-9.343791246	-8.671085446	-9.25926061	-7.874800872	-8.510237793	-9.046175133	-7.329126231	-8.736983875	-8.895370633	-8.374698103	-9.248199659	-9.679368769	-9.819655024	-8.593952965	-9.145408405	-8.690911604	-7.602466917	-9.774531295	-8.548109731
GAPDH	P04406	YDNSLK	-11.68671897	-12.2243619	-11.7177017	-11.23227487	-11.94794172	-11.18690643	-11.29363644	-10.66712364	-11.2160775	-10.21683912	-9.840771747	-11.51095286	-10.95513817	-10.9132848	-11.69812812	-12.24561339	-11.99304996	-11.10850753	-11.37270684	-11.56321183	-10.33919008	-11.80203994	-10.91474767
GDA	Q9Y2T3	DHLLGVSDSGK	-9.060441867	-10.20870616	-9.538655212	-9.201620225	-9.921809823	-9.220029315	-9.495675447	-8.347894604	-9.315948925	-8.752753908	-8.426821141	-9.180069997	-8.713692802	-9.191159895	-9.681224434	-9.944790415	-9.7772236	-9.936287733	-9.663521493	-8.826440624	-8.360317971	-9.894556118	-8.982248916
GOT1	P17174	VGNLTVVGK	-7.26140245	-8.227967279	-8.445770538	-7.89055538	-8.6158421	-7.553531325	-8.112077243	-6.957316807	-7.744032622	-7.395982116	-7.252929544	-7.675383243	-7.394898418	-7.509425737	-7.865961704	-8.236402359	-8.639800384	-8.133968714	-8.134345363	-7.446457151	-6.841311861	-8.482949711	-7.138493191
GOT1	P17174	IGADFLAR	-9.516539282	-10.6316624	-10.36283007	-9.915371089	-10.50960135	-9.721463566	-10.0028388	-9.235786133	-9.544941251	-9.62194095	-9.8571459	-9.614348419	-9.596811891	-9.567057707	-10.07506973	-10.11918801	-10.6177088	-9.851792401	-10.07378655	-9.415670268	-9.067374182	-10.56397969	-9.370525989
GSN	P06396	AGALNSNDAFVLK	-3.914115368	-4.41317667	-4.375361749	-3.822820726	-4.37989691	-4.006477949	-3.955406701	-3.759129556	-3.933253902	-4.123271564	-4.026152285	-3.880723754	-4.179668859	-3.596447839	-4.044542316	-4.209795478	-4.846569185	-4.193172332	-4.266765274	-4.054769108	-3.572438357	-4.326379	-3.324853525
HBA1	P69905	FLASVSTVLTSK	-5.766132468	-9.777886798	-6.004945077	-9.023946039	-9.996172992	-3.923648319	-2.555139023	-3.043768117	-9.230379476	-8.915118797	-2.925976322	-6.238734908	-6.174287246	-3.830990608	-8.08621113	-8.653176484	-5.55374762	-1.127536098	-4.464052695	-8.613379073	-8.710788154	-10.00146187	-8.563928669
HBA1	P69905	VGAHAGEYGAEALER	-5.387531412	-12.93886455	-5.816321871	-12.45398179	-14.36166754	-3.583232137	-2.37442121	-2.662869547	-11.47005216	-10.86909844	-2.573549991	-6.206950607	-5.714993205	-3.490989412	-8.274742419	-9.611280807	-5.266095464	-0.809765528	-4.117816041	-8.759394581	-10.61748053	-13.56243931	-10.18707733
HBB	P68871	VNVDEVGGEALGR	-5.270748845	-11.23906393	-5.679299755	-9.614558864	-11.97033073	-3.370974303	-2.142940864	-2.472491601	-10.99144166	-10.6649047	-2.476545229	-5.778603065	-5.775161316	-3.345328669	-8.109160001	-8.787538857	-4.942375561	-0.564778141	-3.948482246	-9.085336528	-9.387788002	-10.7596259	-9.6071652
KNG1	P01042	EGDC[+57]PVQSGK	-9.202295496	-10.17709373	-9.677108793	-8.203177605	-9.474611206	-9.265635157	-9.281091722	-9.937021768	-9.581124697	-9.321965132	-9.239678426	-9.566974289	-10.27635664	-9.004215489	-9.923698971	-9.146739537	-10.31250462	-9.108882284	-9.618481164	-9.85972591	-8.802639675	-9.894079625	-9.812489553
KNG1	P01042	QVVAGLNFR	0.737403715	0.147238432	0.389207751	2.104388852	0.507088539	1.096736037	1.473048286	-0.058709546	1.350547753	1.05795854	0.807160663	1.252259629	0.692978514	1.761953469	0.391900565	0.911989342	0.251767067	1.191948118	1.107066823	0.017677561	1.28357573	0.210577192	1.044000929
KNG1	P01042	VQVVAGK	-5.315554186	-6.068719158	-5.81396999	-4.010508984	-5.890488461	-5.243775135	-5.058434056	-6.123255374	-5.225321489	-5.372690393	-5.156580881	-5.266698632	-5.977592524	-4.820566924	-5.954786144	-5.148652642	-6.291324974	-5.148650518	-5.345824109	-6.290151885	-4.719160297	-6.012597213	-5.250486789
L1CAM	P32004	GQLSFNLR	-5.138993613	-5.083761118	-4.843778396	-4.871334118	-5.244579983	-4.859389878	-4.683601466	-4.988336257	-4.657219549	-4.543080256	-4.56708541	-4.885850802	-4.842603584	-4.589237753	-5.064513158	-5.110666174	-4.725560572	-4.867949995	-5.150742795	-4.727272574	-4.517178861	-5.438558477	-4.50471928
LAMP1	P11279	VWVQAFK	-8.523832835	-9.3402319	-9.059853188	-8.287263684	-8.870286098	-8.835574579	-8.636166419	-8.255958162	-8.285754297	-8.269517924	-7.835229921	-8.179693934	-8.134997592	-8.034200446	-8.37183631	-8.706163909	-9.029822232	-8.973624441	-8.146506331	-8.54364298	-8.218550934	-8.726041061	-7.830674719
LAMP2	P13473	YLDFVFAVK	-8.265382192	-8.861485209	-8.746540611	-7.746540611	-8.483816616	-8.078786816	-7.900047246	-7.79768474	-7.866252415	-8.042645269	-7.690710952	-8.156176671	-8.043869084	-7.82703298	-7.875924535	-8.714414158	-8.780754629	-8.140334637	-8.381568453	-8.225366871	-7.392903656	-8.645075279	-7.89215887
LDHB	P07195	FIIPQIVK	-8.646288601	-9.563915892	-9.427879492	-9.117539371	-9.55253732	-8.800662691	-9.207305066	-8.421185714	-8.878309195	-8.795555437	-8.508190506	-8.9209712	-8.757070272	-8.612146484	-9.096524075	-9.402240432	-10.18328699	-9.018272229	-9.28928441	-8.714199567	-8.371295963	-9.846418814	-8.445169584
LDHC	P07864	VIGSGC[+57]NLDSAR	-9.622968633	-10.45369959	-10.1902223	-9.360147299	-9.593443549	-8.770410406	-9.915073654	-8.765510945	-8.996186228	-8.860250637	-8.321608998	-8.94857244	-9.305436962	-8.670240717	-9.956432082	-9.994317912	-10.09975862	-8.823859339	-9.326485186	-8.891927347	-8.038219204	-10.15710548	-8.546099973
MDH1	P40925	GEFVTTVQQR	-7.524374751	-8.303432119	-8.098980528	-7.67751676	-8.23405456	-7.378701264	-8.070919566	-6.849715867	-7.60634327	-7.331912734	-7.08872525	-7.577603696	-7.484557904	-7.311518752	-7.716729718	-8.13702071	-8.216511803	-8.04439784	-7.956825347	-7.215920741	-6.68716693	-8.253916784	-7.2738591
NCAM1	P13591	GLGEISAASEFK	-5.323150886	-6.33233171	-6.260903744	-5.699024856	-6.450264253	-5.88461499	-5.871691219	-5.143179341	-5.656613366	-5.770435621	-5.375324779	-6.02974632	-5.73189257	-5.508501575	-5.780355618	-6.107175179	-6.460850062	-6.204413363	-6.291383013	-5.517462541	-5.084746789	-6.528602302	-5.135054946
NPTX2	P47972	VAELEDEK	-8.689076869	-9.064886235	-9.297524972	-8.802760281	-10.25419489	-9.703741701	-9.456041251	-8.621749303	-9.885652312	-9.40487351	-9.032691552	-9.792082357	-9.050643133	-8.864059301	-9.186456269	-9.275810751	-9.755625053	-9.675674814	-9.713648968	-9.173573095	-9.056516873	-9.524322332	-8.996440502
NPTXR	O95502	ELDVLQGR	-1.843368841	-2.916703767	-2.465614122	-2.116398789	-3.316277052	-2.712509602	-2.568288279	-1.893604005	-2.722414641	-2.506825822	-2.197762558	-2.799472667	-2.337510551	-1.995077418	-2.276438357	-2.679318792	-2.765080617	-2.745748785	-2.964861288	-2.204300508	-1.967318771	-3.179540528	-1.99628503
NRXN1	P58400	LAIGFSTVQK	-6.913138495	-7.924779688	-7.703150262	-7.399144075	-8.156673148	-7.452181784	-7.088692135	-6.816813764	-7.964660831	-7.28579887	-6.691410249	-7.544949278	-7.103739744	-6.804202545	-7.430131316	-7.515737715	-8.096032217	-7.648106439	-7.692688619	-7.027638399	-6.391948574	-8.593402601	-6.689677127
OGN	P20774	LEGNPIVLGK	-6.658759294	-6.823141844	-7.09394464	-6.190159956	-7.00331146	-6.862931925	-6.830917429	-7.034907527	-6.391329307	-6.533165726	-6.835464406	-6.48903306	-6.809337897	-6.522828795	-7.238643138	-6.820893273	-7.343780305	-6.757914094	-7.056637375	-7.21204935	-6.240786029	-7.008389978	-6.12329125
OMG	P23515	LESLPAHLPR	-3.556461077	-4.42733889	-4.19812312	-3.921988102	-4.906754818	-4.752098575	-4.011823298	-3.520344762	-4.218149982	-3.811275511	-3.339019447	-3.85604556	-3.864037021	-3.442969521	-3.906581441	-4.173343347	-4.51017102	-4.525330053	-4.285011383	-4.110156139	-3.383033806	-4.867803412	-3.858054971
PARK7	Q99497	ALVILAK	-8.597146807	-9.474886587	-9.228113013	-8.728542003	-9.036783063	-8.197753279	-8.711940633	-8.231763902	-8.264046015	-8.365583915	-8.280214693	-8.591268848	-8.369530127	-8.365167898	-8.785274997	-9.039613388	-9.290817134	-8.565412416	-8.558564106	-8.311533816	-7.78231326	-9.262390297	-8.090074483
PEBP1	P30086	GNDISSGTVLSDYVGSGPPK	-4.67642695	-5.755775678	-5.400450212	-5.51592743	-5.653143387	-5.052608114	-5.280891261	-4.408289849	-4.99283723	-4.880244183	-5.0417693	-5.004004357	-5.010459417	-4.973614307	-5.187037431	-5.555226132	-5.939623327	-5.361752447	-5.476417159	-4.796369058	-4.436700738	-5.992911716	-4.481461307
PEBP1	P30086	LYEQLSGK	-7.321898262	-8.087353558	-8.228019125	-7.836828368	-7.958407404	-7.295007689	-7.794794037	-7.084143937	-7.321600438	-7.234715947	-7.204372775	-7.496038924	-7.641084704	-7.614626791	-7.730244668	-8.028905924	-8.313637665	-7.948933729	-7.74308253	-7.311692626	-6.929937772	-8.124184355	-7.095525966
PEBP1	P30086	VLTPTQVK	-6.247366481	-7.197387214	-7.013551563	-6.803516348	-7.165228222	-6.429362179	-6.800269122	-6.024293408	-6.427636323	-6.436043765	-6.24867825	-6.712656625	-6.564929444	-6.49856753	-6.684551867	-6.885375975	-7.269315695	-6.873999867	-6.88892655	-6.375240882	-6.002825156	-7.362042142	-6.084464162
PGLYRP2	Q96PD5	TFTLLDPK	-4.759781513	-5.251691448	-5.157062065	-4.029306518	-4.963443999	-5.137191777	-4.500966785	-5.324787455	-4.984427858	-5.033378803	-4.271736378	-4.896743385	-5.313406791	-4.157932576	-5.185162714	-5.035068976	-5.310551413	-4.707591336	-4.751511092	-5.726957518	-3.918404589	-5.63395896	-4.541130656
PKM	P14618	VVEVGSK	-7.241742823	-8.320429458	-7.942935338	-7.628826747	-8.066405581	-7.045041274	-7.703019669	-6.783596889	-7.506309973	-7.018804883	-6.989648196	-7.396935991	-7.27381811	-7.159345839	-7.716189844	-7.749080537	-8.536644745	-7.616949121	-7.850123505	-7.037832798	-6.390837471	-8.237782905	-6.664763333
PKM	P14618	GVNLPGAAVDLPAVSEK	-6.776403692	-8.011154808	-7.542997274	-7.439374643	-7.553288399	-6.770819641	-7.221423995	-6.380663019	-6.870743723	-6.66786553	-6.521081151	-7.081394475	-7.053912427	-6.82960852	-7.159870245	-7.371585661	-7.891750247	-7.454795828	-7.570013672	-6.574154895	-6.026123763	-7.811524623	-6.258448594
PKM	P14618	GDLGIEIPAEK	-7.52743964	-8.522526203	-8.327330872	-8.082218374	-8.374206679	-7.575184252	-8.065209735	-7.263641125	-7.733964101	-7.735385086	-7.475855651	-7.893764438	-7.991378577	-7.652249714	-8.147292994	-8.158418642	-8.739546932	-7.893965491	-8.485043647	-7.438411318	-6.834290861	-8.659849537	-7.086745356
PKM	P14618	GDYPLEAVR	-6.29784516	-7.161645734	-7.167151411	-6.49419243	-7.090243094	-6.310590798	-6.561086317	-5.803798893	-6.310667442	-6.211318152	-5.980511299	-6.432741755	-6.750448212	-6.249347517	-6.645063417	-6.928250322	-7.06029202	-6.6085565	-6.908376628	-6.083015134	-5.537519861	-7.228843821	-5.69730278
PKMisoform	NA	LFEELVR	-3.593795566	-4.614636283	-4.234649135	-4.025663372	-4.396568409	-3.396167433	-3.944095196	-3.121758145	-3.524977478	-3.426613817	-3.405486727	-3.612232611	-3.712786787	-3.359664576	-3.736068418	-4.087964099	-4.5751686	-3.903346097	-4.151766338	-3.293075724	-2.79964099	-4.516508719	-3.026799577
PON1	P27169	LLIGTVFHK	-8.971971859	-8.673032131	-8.488190191	-6.714466047	-8.440744514	-7.597170316	-7.26581857	-8.96585395	-7.758750034	-8.006494135	-7.521743061	-7.994533176	-8.350502038	-7.209442242	-8.772138794	-8.277944616	-7.980878239	-7.875345567	-7.600435988	-9.224586558	-7.194458988	-8.719513523	-7.733476572
PPIA	P62937	VSFELFADK	-8.819461098	-9.522170475	-8.842765434	-8.738428775	-8.74562047	-8.218334025	-9.001516579	-8.317201629	-8.761322246	-8.719873113	-8.467037043	-8.738487774	-8.48061327	-8.657679988	-9.128675931	-8.962896596	-9.237690838	-9.197265344	-9.129934738	-8.291584197	-8.210497219	-9.142955819	-8.319882248
PRDX2	P32119	QITVNDLPVGR	-4.223354301	-5.246127156	-4.7081411	-4.692776791	-5.603504825	-4.085650814	-4.237283538	-3.681512773	-4.651920669	-4.490794126	-3.480789641	-4.623325655	-4.709348779	-3.961363586	-4.811117112	-5.023662594	-4.928712657	-3.244242859	-4.51202046	-4.652380888	-3.874113378	-5.398896986	-4.375386428
PTPRZ1	P23471	AIIDGVESVSR	-6.201228805	-6.87986924	-6.661086762	-6.399645614	-6.840244714	-6.862325146	-6.614304673	-5.977283256	-6.250571802	-6.697797778	-6.100211879	-6.35282983	-6.395472088	-6.234838627	-6.384634445	-6.631665766	-7.026817861	-7.168851362	-6.94924237	-6.438425317	-5.646826069	-6.804782768	-5.963199696
PTPRZ1	P23471	DIEEGAIVNPGR	-6.914335218	-7.733292375	-7.643665335	-7.298168769	-7.907203949	-7.69519721	-7.491419582	-6.901801032	-7.2763309	-7.536585496	-7.1841387	-7.382426434	-7.419729176	-7.074858891	-7.502057669	-7.643936223	-8.174133615	-7.905999138	-7.883308785	-7.262055166	-6.593624652	-7.843041424	-6.898508155
SCG2	P13521	IESQTQEEVR	-6.789672635	-8.557299808	-7.747759751	-7.300300774	-8.919882147	-7.798048319	-7.826266767	-7.011982179	-8.279040301	-8.440894478	-7.924647958	-8.551774251	-7.371297654	-7.158655951	-7.483800467	-8.00224623	-8.04774983	-7.916370438	-8.508458941	-7.378830364	-7.187291813	-8.760615271	-7.322627677
SCG2	P13521	SGQLGIQEEDLR	-9.036314905	-10.44493185	-9.830629523	-9.000554525	-10.59821501	-9.511905933	-9.776003365	-8.705548741	-9.48291438	-9.838563876	-9.277893188	-9.875310628	-9.283880162	-8.858004561	-9.609779931	-10.44387391	-10.05857712	-10.20723007	-10.26513184	-9.104557385	-8.585517025	-10.78913105	-9.035031361
SMOC1	Q9H4F8	AQALEQAK	-6.788224074	-7.853801496	-7.688740448	-7.402831576	-7.961782634	-7.273738562	-7.270807134	-6.227408754	-6.990871464	-7.755855663	-6.61334278	-7.63739168	-7.200919108	-7.133815242	-7.639368746	-7.968241853	-8.314099394	-8.059050489	-7.640644113	-6.37987713	-6.347183547	-8.086018901	-6.224044423
SOD1	P00441	AVC[+57]VLK	-1.756032386	-2.226526134	-2.019090524	-2.021988958	-2.489273052	-1.888798545	-2.354082746	-1.272440843	-1.802781056	-1.44042158	-1.932555808	-1.659848053	-1.482248421	-0.906266861	-1.714298719	-1.693894983	-2.148025875	-2.028650562	-2.01000456	-0.975848699	-1.40238769	-2.353984193	-1.19005688
SOD1	P00441	GDGPVQGIINFEQK	-2.494167366	-3.253032508	-3.100157665	-2.644285622	-3.41611279	-2.683755191	-3.114638845	-2.380555202	-2.40662526	-2.444074781	-2.773623898	-2.445647524	-2.374232101	-1.749270925	-2.588373565	-2.280087677	-3.028783597	-3.112235333	-2.729902432	-2.218273629	-2.102292356	-3.248299818	-1.996247876
SOD1	P00441	HVGDLGNVTADK	-4.722817118	-5.425951992	-5.51025012	-5.008672514	-5.530608851	-5.218939152	-5.381971587	-4.552924778	-4.798188897	-4.686935049	-5.122499951	-4.776779194	-4.702585348	-4.113241813	-5.078667275	-4.889152827	-5.384907816	-5.149529598	-5.168196325	-4.316224368	-4.413592251	-5.68967427	-4.249429081
SPP1	P10451	GDSVVYGLR	-4.004355585	-4.221712897	-4.292445406	-4.120885622	-4.056474887	-3.608436474	-4.095430484	-3.405977836	-3.143335341	-3.292672385	-3.453724095	-3.328728838	-3.081184737	-2.917563831	-3.429882296	-3.90582176	-3.70353789	-3.506936717	-3.741855211	-3.649839252	-2.995014394	-3.873764303	-3.530323183
SPP1	P10451	YPDAVATWLNPDPSQK	-1.791883841	-2.06237746	-2.387298131	-2.113423034	-1.806427518	-2.017173472	-2.492686866	-1.443903348	-1.351289969	-1.726760925	-1.678734771	-1.415688309	-1.722051107	-1.845991883	-1.963805152	-2.395849011	-2.591030315	-1.914368973	-1.753247375	-2.100475694	-1.591894969	-2.141937085	-1.835734563
SPP1	P10451	QETLPSK	0.361944371	0.064357618	-0.081222247	0.738864251	0.534968467	0.706298826	0.199526413	0.712378665	0.903536047	0.685408775	0.99872909	0.679612553	0.750114521	0.653947971	0.343941251	-0.189065134	-0.006868732	0.13389093	0.476765761	0.528503626	1.183348759	0.071378357	0.741334851
THY1	P04216	HVLFGTVGVPEHTYR	-4.029001727	-5.442837617	-4.858800716	-4.572361706	-5.526427436	-5.248126946	-4.851797784	-4.170569532	-4.865658792	-4.704527586	-4.327922045	-5.269421264	-3.984541755	-4.12083712	-4.703889739	-5.041287792	-4.95186875	-4.748646469	-5.300740871	-4.394618069	-3.912600418	-5.729059981	-4.318820019
TPI1	P60174	IAVAAQNC[+57]YK	-9.942006444	-11.22657317	-10.88675458	-9.886754578	-10.98019399	-9.761916723	-10.62968654	-10.67208725	-10.4622652	-9.576386212	-9.533530121	-9.844133667	-10.24785141	-9.755075787	-10.66884131	-11.00778903	-10.51706862	-10.36804397	-9.935029119	-9.589302147	-8.886754578	-11.4037031	-10.03621091
VGF	O15240	EPVAGDAVPGPK	-4.738264073	-6.478325308	-5.907750203	-5.525190327	-7.185647993	-5.878598368	-5.750713683	-4.895748141	-6.261671878	-6.153321203	-6.066203171	-6.617023337	-5.740277172	-5.165646588	-5.646580114	-6.605699259	-6.126175029	-6.204344901	-7.038562624	-5.377646121	-5.264684748	-6.973152001	-5.093091287
VGF	O15240	GLQEAAEER	-7.419427903	-9.128440362	-8.481200892	-7.935766756	-9.689515166	-8.348820473	-8.383225006	-7.451899973	-8.568738744	-8.642587922	-8.553390316	-8.988318018	-8.27748313	-7.64080523	-8.254208727	-8.992928907	-8.56563458	-8.737114169	-9.718670039	-7.853919677	-7.624565067	-9.505422546	-7.621480872
VTN	P04004	GQYC[+57]YELDEK	-6.038391443	-6.388002101	-5.997046479	-4.498240622	-6.339900728	-5.911686138	-5.692392898	-6.81757246	-6.005840787	-5.774611018	-5.331235882	-5.796575126	-6.168104821	-6.734690322	-6.562187605	-5.736687578	-6.658459536	-5.517027925	-6.394304864	-6.802460722	-5.044875004	-6.766139205	-5.54575276
VTN	P04004	DVWGIEGPIDAAFTR	-4.131681792	-4.016816633	-3.808251919	-2.182787869	-3.650167044	-3.457856251	-3.125779741	-4.557073637	-3.400151382	-3.459369347	-3.191270614	-3.459135228	-3.731785473	-4.022657204	-4.204151571	-3.525600201	-3.825052115	-3.01215741	-3.856385433	-4.134675006	-2.813950524	-4.244518192	-3.171325434
YWHAB	P31946	NLLSVAYK	-7.106658386	-7.882517989	-7.631324479	-7.128824139	-7.010220556	-6.364327994	-7.439357638	-6.565842124	-6.928021516	-6.603179227	-6.094388089	-6.811944135	-6.585702794	-6.683503416	-7.634146994	-7.327514833	-7.699231448	-7.490305967	-6.958225619	-6.627145359	-5.968359466	-7.170252171	-6.318156743
YWHAB	P31946	VISSIEQK	-7.895581217	-8.425815418	-8.08255851	-8.032805475	-7.800504411	-6.977639538	-8.061416074	-7.281424438	-7.79522587	-7.60878814	-7.298202548	-7.833155353	-7.602258699	-7.418174093	-8.277182932	-8.186973244	-8.16876645	-8.265155877	-8.001948272	-7.496858113	-7.173981538	-8.05198941	-7.297454441
YWHAG	P61981	YLAEVATGEK	-9.872586928	-10.18266228	-10.00615444	-9.546722826	-9.484750125	-8.953946011	-10.24885272	-8.776492834	-9.167181642	-9.405148664	-8.843585974	-9.305046675	-9.16138977	-9.462436631	-10.45854974	-10.00327217	-10.38344124	-10.10673551	-9.746722232	-9.463082369	-8.876871428	-10.27772748	-8.938460699
YWHAZ	P63104	VVSSIEQK	-6.418041317	-7.302873814	-7.189600236	-6.545259188	-6.501316208	-5.460734888	-6.605361789	-5.547217782	-6.401573958	-6.505048978	-5.907591614	-6.395863382	-6.179016953	-5.991962374	-6.897395061	-6.738443748	-7.062751556	-7.074442328	-6.260899877	-6.162832882	-5.31292853	-6.883317002	-5.496647031

SUPPLEMENTAL TABLE 11: SRM RATIO ABUNDANCES POST-REGRESSION

Gene ID | Protein ID| Peptide Sequence	S091_P2E2_49087	S092_P2F2_48746	S093_P2G2_48316	S094_P2H2_50273	S095_P2A3_51264	S096_P2B3_51319	S097_P2C3_73786	S098_P2D3_76950	S099_P2E3_57056	S100_P2F3_66276	S101_P2G3_66827	S102_P2H3_46282	S103_P2A4_42570	S104_P2B4_77355	S105_P2C4_44511	S106_P2D4_57326	S107_P2E4_51023	S108_P2F4_52626	S109_P2G4_63982	S110_P2H4_68545	S111_P2A5_53398	S112_P2B5_85026	S113_P2C5_48786
AHSG | P02765 | EHAVEGDC[+57]DFQLLK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	-5.203530652	-4.260706784	-4.394529156	-4.060994616	-4.801037618	-4.801955756	-3.992216593	-5.20511896	-4.490354034	-5.199817998	-4.048937182	-4.338026031	-5.124184042	-4.554916824
ALB | P02768 | LVNEVTEFAK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	4.632969394	5.624475077	5.623677066	5.057606869	4.256374325	4.865179111	5.782055457	4.672630872	4.898994498	4.596528139	5.967482022	5.929191956	4.585453606	4.901446072
ALB | P02768 | LVTDLTK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	5.359213303	6.338557983	6.350391105	5.750835337	5.001437275	5.604798271	6.514899589	5.371814844	5.658821046	5.329724726	6.766793236	6.645214797	5.31816194	5.622181726
ALDOA | P04075 | VLAAVYK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	-7.537452703	-7.450682612	-6.755774215	-7.147445933	-6.887010779	-7.272133297	-6.592695183	-7.480334983	-6.959029734	-7.079898699	-6.955064549	-6.837650382	-7.548144193	-7.094145091
APOA4 | P06727 | SLAPYAQDTQEK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	-5.789501631	-4.401763327	-4.364020381	-4.549915135	-6.315033242	-5.459536614	-4.460389791	-4.839017592	-4.856876236	-5.590782209	-4.672224276	-4.809592406	-5.391320193	-5.081315529
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	0.903757258	2.114196377	2.568822372	1.355082607	1.395554589	1.0206846	2.092371246	1.552925258	1.640993179	1.496657723	2.595051085	2.239747731	0.540939278	1.235495646
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F2 | P00734 | YTAC[+57]ETAR	-9.751627866	-9.07187841	-8.389707307	-8.557848827	-8.373912613	-9.021900199	-8.664554542	-9.137106106	-9.163618435	-8.751552428	-8.391925247	-8.395081308	-8.606752238	-8.779497234	-8.65146691	-8.223573958	-9.090677327	-9.155004706	-9.168275313	-7.923217306	-8.556545817	-8.991805793	-8.679213924
F2 | P00734 | TATSEYQTFFNPR	-7.470479133	-6.759410093	-6.053344952	-6.59354336	-6.349157244	-7.058623035	-6.491075123	-6.95393446	-6.683638733	-6.78521602	-5.985069832	-5.928673891	-6.294554935	-6.827253588	-7.217643949	-5.985869561	-6.856888982	-6.681056609	-7.127455955	-5.606275795	-5.736228525	-6.829639855	-6.373101948
GAPDH | P04406 | AAFNSGK	-8.031895497	-8.234346898	-9.024738903	-8.802931914	-8.543257893	-10.17116826	-9.060541618	-9.320215639	-7.854573643	-8.788109623	-9.528250276	-7.196000896	-8.643309572	-7.657176963	-8.396019672	-8.382121943	-11.013006	-8.86057378	-8.527829546	-8.909524466	-8.222623579	-8.833804719	-9.095128231
GAPDH | P04406 | YDNSLK	-10.47617898	-11.03886455	-11.37308175	-11.03450567	-11.05943806	-12.48960763	-12.17673566	-11.96737869	-10.60331891	-11.26916994	-12.0121185	-9.972476451	-10.71837968	-10.19221427	-11.02443236	-10.62754697	-12.90031547	-11.28937502	-11.20308852	-11.52971471	-10.54412726	-11.08685924	-11.37308175
GDA | Q9Y2T3 | DHLLGVSDSGK	-9.424842436	-9.197862568	-9.397997779	-8.895956658	-8.821269734	-10.15611849	-8.748264551	-9.251794773	-8.300245264	-9.329056004	-10.28147804	-8.584450788	-9.509160213	-8.587433908	-8.933030266	-8.749881334	-9.105940201	-8.794973554	-8.92030808	-9.514445913	-8.922551227	-9.308947986	-9.054043378
GOT1 | P17174 | VGNLTVVGK	-7.741292321	-7.709286215	-7.601133799	-7.331869039	-7.410348872	-9.082306822	-7.368498161	-7.995152794	-6.994085574	-7.828759563	-8.041133232	-7.090242901	-7.624796232	-7.320925538	-7.759159506	-7.364565348	-8.042233192	-7.466196282	-7.688863287	-7.508252238	-7.413119456	-8.298805667	-7.493330509
GOT1 | P17174 | IGADFLAR	-9.995656757	-9.76688483	-9.779817802	-9.543299726	-9.738905673	-11.06378366	-9.749807286	-9.999760782	-9.120585416	-10.12098284	-10.03156698	-9.304651039	-9.838300164	-9.621794152	-9.979017188	-9.407358826	-9.973242802	-10.04223753	-9.41541296	-9.483296592	-9.382992085	-9.836402306	-9.578183941
GSN | P06396 | AGALNSNDAFVLK	-4.092980716	-4.201727542	-4.151756896	-3.800920834	-3.635447707	-4.934021462	-3.753089749	-4.218957336	-3.980759609	-4.245664979	-3.908447686	-3.527386811	-3.901125973	-4.44830808	-4.196489341	-3.603647433	-4.836901309	-3.730589535	-4.225144221	-3.711348715	-3.563196142	-4.625858003	-3.856006915
HBA1 | P69905 | FLASVSTVLTSK	-7.838578509	-7.944008516	-9.348719721	-0.947169074	-7.712720669	-4.278386664	-8.901169671	-9.216660782	-5.765728432	-8.540224549	-9.636270322	-8.902270997	-1.467521626	-8.925270529	-9.703380522	-8.725541963	-10.05331351	-9.236907196	-6.118050944	-3.011243734	-9.64676462	-5.765393771	-7.466645446
HBA1 | P69905 | VGAHAGEYGAEALER	-9.133349154	-7.673530622	-12.06625648	-0.609457831	-8.515451659	-3.878062358	-10.92077092	-13.59475797	-5.520945245	-10.3080831	-13.22676368	-10.20367361	-1.182833016	-11.64945663	-12.14740181	-9.896208152	-16.82162121	-11.58350957	-5.972748887	-2.711596092	-11.71179068	-5.383639484	-7.248633218
HBB | P68871 | VNVDEVGGEALGR	-7.796446985	-7.875908247	-9.995609127	-0.3634421	-8.141121778	-3.718793743	-10.55801543	-10.88699477	-5.468298808	-8.554272944	-10.23340723	-9.481524048	-0.874055296	-11.08688385	-10.64715117	-9.846716173	-11.95807632	-10.83862693	-5.767320784	-2.580291482	-10.68193815	-5.158783395	-7.071645019
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KNG1 | P01042 | QVVAGLNFR	0.57210106	0.751222828	1.528990982	1.481930199	0.921767155	0.784822315	0.901032599	0.506381365	0.850340516	0.711806287	1.43833307	1.492320516	1.017090195	0.478529458	0.696698123	1.30607916	0.634460223	0.608755764	0.82195142	2.272490861	2.13451453	0.965981344	1.013844592
KNG1 | P01042 | VQVVAGK	-5.911142314	-5.606815171	-4.738309244	-4.913355775	-5.476117196	-5.783314781	-5.268426969	-5.880191064	-5.180051322	-5.744612831	-4.81327121	-4.697782446	-5.233988645	-5.96876274	-5.679173479	-4.697730629	-5.799805952	-5.298279341	-5.647576191	-4.123657053	-4.32213321	-5.657261324	-5.270197629
L1CAM | P32004 | GQLSFNLR	-4.635341412	-4.789157949	-5.006232202	-4.767082304	-4.236638765	-4.889899107	-4.649638187	-5.033509712	-4.620958468	-4.85034139	-4.791014825	-4.62281209	-4.810438782	-4.822543477	-5.013953093	-4.643417409	-4.995437208	-4.901600826	-4.773687218	-4.662788631	-4.550370969	-5.007063723	-4.469756576
LAMP1 | P11279 | VWVQAFK	-8.206062651	-8.205648248	-8.227385775	-8.473268162	-7.872317826	-9.756614123	-8.186368539	-8.905412183	-7.987493393	-8.447222239	-8.169931324	-8.116403475	-8.206333667	-7.63898323	-8.455951897	-8.101451716	-8.847667271	-7.788024014	-8.159291292	-8.510532476	-8.157182688	-8.630767817	-8.694511786
LAMP2 | P13473 | YLDFVFAVK	-8.339058483	-7.933661114	-7.826001754	-7.708007891	-7.505623038	-9.16381905	-8.008745701	-8.370357974	-7.517206118	-8.374346419	-7.992731895	-7.536041416	-7.914690052	-7.43710106	-8.140602696	-7.856821478	-8.382591011	-7.991634441	-8.150846918	-7.536276757	-8.000371214	-8.859197931	-7.67597631
LDHB | P07195 | FIIPQIVK	-8.866622562	-9.147771431	-8.994787462	-8.943622794	-8.793078161	-10.19544802	-8.722842688	-9.332073553	-8.445374817	-9.454722512	-9.291260851	-8.436100649	-8.778907824	-8.836366502	-9.064010249	-8.376003408	-9.605970987	-9.048369093	-8.895792502	-8.658134431	-8.700460914	-9.374211205	-8.929199121
LDHC | P07864 | VIGSGC[+57]NLDSAR	-9.093309818	-9.125222222	-9.607852463	-9.287888054	-9.338835684	-10.9337895	-9.648806256	-9.323935905	-8.286761964	-9.714903541	-10.25650228	-8.44557257	-8.890241441	-8.688674661	-9.420139885	-8.487947489	-10.41304108	-10.17435572	-9.002751462	-9.257731583	-8.745551825	-9.625873108	-9.424988406
MDH1 | P40925 | GEFVTTVQQR	-7.448790568	-7.571893675	-7.628548831	-7.631679674	-7.120351162	-8.920899294	-7.543402771	-8.157555246	-6.962546022	-7.758325721	-8.082471032	-7.321354153	-7.667940237	-7.123461434	-7.668954283	-7.35663965	-7.972478719	-7.791627731	-7.452698929	-7.628229017	-7.267587968	-7.872553566	-7.628548831
NCAM1 | P13591 | GLGEISAASEFK	-5.772913505	-5.913785952	-5.681412272	-5.379821288	-5.229147533	-6.87483133	-5.17561094	-5.859100329	-5.430250761	-6.392787595	-5.839472325	-5.433126514	-5.801276525	-5.592284642	-5.817490135	-5.358437333	-5.909394117	-5.198344831	-5.586629608	-5.337007493	-5.606173558	-6.611075405	-5.541837823
NPTX2 | P47972 | VAELEDEK	-9.385606289	-9.211400843	-8.608422823	-8.644914556	-8.382017945	-9.642212573	-8.594591842	-9.157883386	-8.640271275	-9.479444917	-9.185803867	-8.719309043	-8.595630144	-8.526279272	-9.30192991	-8.907406836	-9.124937419	-8.132973073	-8.755555841	-8.759396827	-9.492532984	-9.591775576	-8.782452222
NPTXR | O95502 | ELDVLQGR	-2.683754506	-2.289244947	-1.848519766	-1.896363738	-1.842648296	-2.969234969	-1.667453337	-2.389360715	-1.938570098	-2.591887769	-2.572937057	-1.655111594	-2.007675496	-2.012181118	-2.172600854	-2.169245027	-2.221481381	-1.409418431	-1.820127987	-1.970989678	-2.420668177	-2.693511772	-1.8151025
NRXN1 | P58400 | LAIGFSTVQK	-7.287997679	-7.285971395	-6.96600196	-7.017995876	-6.346429857	-7.9876516	-6.558668885	-7.174855361	-6.791438779	-7.744267413	-7.372952503	-6.673317339	-7.024386678	-6.881051777	-7.049082085	-6.593834126	-7.468729361	-6.705669368	-6.894062609	-6.823763335	-6.856538657	-7.941234444	-6.92581287
OGN | P20774 | LEGNPIVLGK	-6.516321404	-6.708041612	-6.635293134	-6.425984706	-6.526278579	-7.852839189	-6.329760415	-6.992904348	-6.491932774	-6.9754872	-6.558889584	-6.192119604	-6.358207303	-7.172231442	-6.585935007	-6.392571671	-7.55129009	-6.620493956	-6.9282613	-6.656349009	-6.251507318	-7.089889584	-6.612023355
OMG | P23515 | LESLPAHLPR	-3.662076549	-4.041058948	-3.589131072	-3.703520503	-3.073276661	-4.932363537	-3.554831947	-4.336891927	-3.503012612	-3.964643042	-4.267645094	-3.421597442	-3.876598794	-3.443322744	-3.709999289	-3.801458318	-4.52253793	-3.20539733	-3.774268665	-3.93982089	-3.947438214	-4.406356331	-3.52346991
PARK7 | Q99497 | ALVILAK	-8.590182504	-8.503274021	-8.885238451	-8.5803707	-8.513310736	-9.739272225	-8.42431731	-8.796610764	-8.074006449	-8.805932376	-9.311241247	-8.169749107	-8.260387696	-8.239254254	-8.465923691	-8.256017148	-9.249248191	-8.569588252	-8.352616111	-8.332888916	-8.237605952	-9.297313883	-8.532936707
PEBP1 | P30086 | GNDISSGTVLSDYVGSGPPK	-6.281636244	-5.20370572	-5.208258966	-5.158180826	-4.722823137	-6.288358983	-4.809148057	-5.329756026	-4.597614811	-5.486066983	-5.289465894	-4.546432159	-4.987358915	-4.83904104	-5.938168751	-5.183831973	-5.183695012	-5.049558561	-5.100702271	-4.763169877	-5.016308609	-6.002624162	-4.941189047
PEBP1 | P30086 | LYEQLSGK	-7.713381978	-7.56123485	-7.577793068	-7.442946988	-7.626356605	-8.384689358	-7.422766316	-8.055672488	-7.036338287	-8.059658946	-7.87046125	-7.442508671	-7.450697216	-7.423603516	-8.017269151	-7.127820724	-7.858841586	-7.63792559	-7.59076204	-7.425514722	-7.246414833	-8.059739112	-7.589288707
PEBP1 | P30086 | VLTPTQVK	-6.885312358	-6.618250402	-6.737747222	-6.542331198	-6.310207385	-7.513109095	-6.281527775	-6.742690692	-6.175506477	-6.950234159	-6.842829572	-6.24802438	-6.584437345	-6.328835277	-6.767025977	-6.258419008	-6.931760478	-6.403829875	-6.505951962	-6.423971969	-6.425118316	-7.233815648	-6.463308053
PGLYRP2 | Q96PD5 | TFTLLDPK	-5.359456811	-5.735754764	-4.272718073	-4.813918398	-4.965148017	-6.189944846	-4.798001707	-4.905514223	-4.657423916	-5.318134467	-4.131740087	-4.350185556	-4.682851172	-5.850795292	-4.96497016	-4.358650801	-5.318925833	-4.556889321	-5.087295747	-4.184952033	-4.146938149	-6.070951159	-4.648096807
PKM | P14618 | VVEVGSK	-7.303586106	-7.50714545	-7.393885208	-7.166411653	-7.082473811	-8.764429134	-7.062127698	-7.581526718	-6.602233202	-7.626907006	-7.790517066	-6.762998097	-7.36295423	-7.401622523	-7.784610276	-6.706091727	-7.843514457	-7.435129179	-7.231986517	-7.205267369	-7.004354349	-7.799496489	-7.3540842
PKM | P14618 | GVNLPGAAVDLPAVSEK	-7.065669144	-7.090103631	-7.102589535	-6.73469618	-6.67695123	-8.371302742	-6.698365381	-7.377823047	-6.381178576	-7.193161267	-7.495832762	-6.556255249	-7.107777556	-6.819961565	-7.447471053	-6.318756618	-7.313787479	-6.88904843	-6.798454941	-6.940013315	-6.660107986	-7.350342163	-6.955748147
PKM | P14618 | GDLGIEIPAEK	-7.816375253	-8.049947582	-7.980491168	-7.613140583	-7.560081364	-9.206467249	-7.394199894	-8.060634844	-7.059380527	-8.114619378	-8.126524392	-7.327722563	-7.886841843	-7.647429128	-8.05063949	-7.252762899	-8.125943505	-7.725684898	-7.72023943	-7.669663381	-7.453273143	-8.39978532	-7.85763442
PKM | P14618 | GDYPLEAVR	-6.426748911	-6.575165475	-6.427026141	-6.265218527	-5.951897067	-7.656352544	-6.237634472	-6.670483102	-5.697732241	-6.648340979	-6.973014992	-5.915413535	-6.44076725	-6.118480846	-6.745028043	-5.908260599	-6.652855273	-6.366138088	-6.293997053	-6.161275372	-6.038241571	-6.691764143	-6.355040028
PKMisoform | NA | LFEELVR	-3.562830033	-3.727177039	-3.70893611	-3.457397637	-3.394320453	-4.836474612	-3.454529144	-3.847465867	-2.937938701	-3.954869305	-3.983938934	-3.227003292	-3.781098936	-3.431647409	-3.907066113	-3.111507323	-4.015532659	-3.656727017	-3.497500326	-3.588826584	-3.290982311	-3.934689939	-3.53508078
PON1 | P27169 | LLIGTVFHK	-8.492559105	-8.343970693	-6.898502153	-7.888408256	-7.950140568	-8.846875634	-8.261136671	-7.970184667	-7.691605357	-8.482847903	-6.802510163	-7.302833508	-7.835253925	-8.498285628	-7.953978777	-7.533535053	-8.261022495	-8.056369859	-8.225563404	-6.538960988	-6.770297846	-8.093284798	-9.220430248
PPIA | P62937 | VSFELFADK	-8.64181042	-8.719215879	-8.813986854	-8.271329011	-8.541396891	-9.537581238	-8.652178378	-8.755458684	-8.383873531	-9.014719857	-8.893369778	-8.6166947	-8.363964599	-8.214724375	-9.142955819	-7.882550763	-8.931080819	-8.836651708	-8.622790444	-8.608367128	-8.789007738	-9.347103073	-8.527105706
PRDX2 | P32119 | QITVNDLPVGR	-4.662204614	-4.561276715	-4.395818102	-2.757102643	-4.035863752	-5.128022906	-3.926815558	-5.003007922	-4.037205109	-4.74521107	-4.620196133	-4.200489912	-3.016863282	-4.353317835	-5.001176062	-3.840230357	-5.480121605	-4.491667707	-4.688980273	-4.519068083	-4.341425592	-4.945914348	-5.035843576
PTPRZ1 | P23471 | AIIDGVESVSR	-6.053543969	-6.564986403	-6.394892294	-6.196270383	-5.945481056	-7.52978265	-5.966650197	-6.308219182	-5.992532241	-6.727622974	-6.473700576	-6.020401225	-6.333499886	-6.097232527	-6.320583244	-6.099397088	-6.756265534	-5.865525849	-6.389381264	-6.360639147	-6.415181912	-6.978598374	-6.034560687
PTPRZ1 | P23471 | DIEEGAIVNPGR	-7.0533881	-7.572329107	-7.220879024	-7.299257454	-6.919779069	-8.077259048	-6.766345584	-7.273768573	-6.761418765	-7.762809986	-7.35273027	-7.0442034	-7.140382069	-7.102231882	-7.278256805	-6.757245081	-7.643459286	-6.743847484	-7.202568447	-7.28395371	-7.342789641	-8.094531271	-7.056649628
SCG2 | P13521 | IESQTQEEVR	-8.664403908	-7.949252582	-7.444553066	-7.037999015	-6.862978897	-8.569575961	-6.787857534	-7.38130504	-6.970436166	-8.103246538	-7.803677627	-6.939603951	-7.246350364	-7.770708798	-7.579008464	-7.466330378	-7.438496545	-6.676703	-7.091949939	-6.863795852	-8.29899703	-8.718995689	-7.103118657
SCG2 | P13521 | SGQLGIQEEDLR	-10.36263777	-9.541022436	-9.282228191	-9.045531512	-9.147627466	-10.35998664	-8.593342176	-9.316018197	-8.95944572	-10.37971727	-9.808276318	-8.776623352	-8.992103483	-9.481767904	-9.419897243	-9.045215718	-9.802316598	-8.848244281	-9.073472367	-8.670654272	-9.447384197	-10.22049133	-8.992721574
SMOC1 | Q9H4F8 | AQALEQAK	-6.982760696	-7.618191805	-7.336778623	-7.531892448	-7.647448557	-8.308364412	-7.103659001	-7.474846991	-6.3806648	-7.282346754	-8.155719822	-6.813461946	-7.13166058	-6.742681171	-7.153133096	-6.561154788	-7.823429278	-6.77406457	-7.107113132	-6.850074021	-7.085407225	-7.823029595	-6.969721153
SOD1 | P00441 | AVC[+57]VLK	-1.724033308	-1.803349384	-1.432778925	-1.627144576	-1.352449166	-2.516872267	-1.128199389	-1.744831306	-1.512321684	-2.036346226	-1.837185219	-1.298195625	-1.707055349	-1.902953834	-1.341290658	-1.714973775	-1.551260835	-1.209697738	-1.708307658	-1.454569487	-1.596935777	-1.995046809	-1.529005912
SOD1 | P00441 | GDGPVQGIINFEQK	-2.635080457	-2.510380968	-2.422156198	-2.443099454	-2.15900086	-3.280314319	-1.875124434	-2.655488322	-2.066939232	-2.662218506	-2.392885694	-1.833913882	-2.670822741	-2.700754345	-2.830017929	-2.265906092	-2.535597288	-1.865043236	-2.341950247	-2.021799057	-2.25940301	-2.777189793	-2.378979235
SOD1 | P00441 | HVGDLGNVTADK	-5.00904252	-4.871939438	-4.506616285	-4.721838168	-4.416615659	-5.64564909	-4.208407432	-4.937261365	-4.391779907	-5.278952369	-4.887159068	-4.315558249	-4.884097898	-5.096206569	-4.728234116	-4.394263354	-4.763245236	-4.193043938	-4.897010806	-4.506508052	-4.620614781	-5.096339941	-4.512474953
SPP1 | P10451 | GDSVVYGLR	-3.568928963	-3.789722937	-3.825700624	-3.641044601	-3.171337055	-4.069986387	-3.593840731	-3.610011769	-2.922400008	-3.696474014	-3.656846398	-3.570501647	-4.109235173	-2.62060058	-3.143205297	-3.266241427	-3.881400163	-3.514711755	-3.778790641	-4.120357701	-3.19105248	-3.507201885	-3.577132236
SPP1 | P10451 | YPDAVATWLNPDPSQK	-1.460882417	-2.026239137	-2.574159674	-2.290101601	-1.689193501	-3.009209538	-2.339949479	-1.790107362	-1.500729867	-1.693364271	-2.320141984	-1.719561407	-1.942334528	-1.537756706	-1.671372873	-1.656197269	-2.545070198	-1.884090733	-1.980274116	-2.218148941	-1.82594957	-1.989637005	-2.027117002
SPP1 | P10451 | QETLPSK	0.975188396	0.35812226	-0.298151079	0.089842359	0.390768303	-0.59649775	0.57882374	0.297855616	1.156456962	0.557329415	0.346165599	0.369439692	0.454415651	0.968757684	0.768108017	0.716883779	-0.357131249	0.714463371	0.285139476	0.228265349	1.125756905	0.496405672	0.3825468
THY1 | P04216 | HVLFGTVGVPEHTYR	-4.781135332	-4.589581098	-4.621828069	-3.99377643	-3.811298289	-5.292416925	-3.946938961	-4.620616998	-4.073800474	-5.122230764	-4.735757628	-4.041389065	-4.191131739	-4.333830727	-4.959098816	-4.833571322	-4.624630623	-4.119136365	-4.330504535	-4.034018385	-4.585930133	-5.14206831	-4.248300205
TPI1 | P60174 | IAVAAQNC[+57]YK	-10.49610711	-9.900627862	-10.15816754	-9.797146485	-9.781463205	-12.1156252	-9.674056827	-10.62623716	-9.48162131	-10.61595082	-9.728994945	-10.16966548	-9.63874325	-9.135171683	-9.963130513	-9.194425209	-11.3048209	-10.28412462	-9.760039359	-10.94654382	-9.526463241	-10.59180517	-10.15816754
VGF | O15240 | EPVAGDAVPGPK	-6.565129649	-5.958296976	-5.595154399	-5.102605	-5.215443509	-6.704401228	-4.59590917	-5.536515347	-5.142906295	-6.802876789	-6.133290482	-5.030841866	-5.238856353	-5.723976959	-6.058399288	-5.503337102	-5.401519669	-4.755976119	-5.020201326	-4.802161302	-6.470243629	-6.402474539	-5.101257714
VGF | O15240 | GLQEAAEER	-8.916916522	-8.428920823	-8.091161836	-7.647703933	-7.81368218	-8.906412114	-7.132687804	-8.101223924	-7.508579671	-9.309664238	-8.640069905	-7.514647781	-7.716590569	-8.127761052	-8.438751506	-8.06746897	-8.11697404	-7.315885021	-7.564495139	-7.404414412	-8.751101876	-8.832783918	-7.535725287
VTN | P04004 | GQYC[+57]YELDEK	-6.508691531	-5.59884303	-5.324333756	-5.54396469	-6.061638357	-6.485479731	-5.614707854	-6.154998946	-6.082835448	-5.834406555	-5.606175431	-5.527654158	-5.381109878	-6.113490363	-6.059335581	-5.61041949	-6.389279492	-5.877190674	-5.930382492	-5.164474972	-5.528802467	-6.276582565	-5.866591806
VTN | P04004 | DVWGIEGPIDAAFTR	-4.220117391	-3.549607637	-2.871864789	-3.213027172	-3.594866788	-3.661207327	-3.191040022	-3.820063477	-3.565360411	-3.717429777	-2.998289485	-3.170076722	-3.028561749	-4.118958704	-3.647986303	-3.175044948	-3.977326903	-3.715010998	-3.703248473	-2.340729192	-3.006415362	-3.902154836	-3.594466157
YWHAB | P31946 | NLLSVAYK	-6.582879824	-7.00151344	-7.383991696	-7.037884232	-6.927706683	-8.218071205	-6.929013815	-7.486650341	-6.468693049	-6.99385816	-7.357602257	-6.415965024	-7.020203964	-6.518294055	-7.094303317	-5.952340062	-7.600016244	-7.199379137	-6.757479912	-7.438882118	-6.616891228	-7.138969375	-6.922411611
YWHAB | P31946 | VISSIEQK	-7.761519185	-7.967176549	-8.144122678	-7.733207561	-7.881798173	-8.662478762	-7.690060967	-7.974143541	-7.298082926	-7.929992887	-8.37988185	-7.397179455	-7.507247503	-7.650540037	-8.092631394	-7.261219135	-7.889477086	-7.906783597	-7.639184144	-7.692699433	-7.414114416	-8.273078068	-7.826640488
YWHAG | P61981 | YLAEVATGEK	-9.239199952	-9.735123809	-9.909440396	-9.862555502	-9.687881841	-11.92880793	-9.329801435	-9.721153866	-9.193991787	-10.11500932	-10.20000097	-9.067619981	-9.573004044	-9.22978435	-9.972872901	-8.59365684	-10.15913628	-9.829460282	-9.517341014	-9.907935753	-9.15757371	-9.781196419	-9.909440396
YWHAZ | P63104 | VVSSIEQK	-6.314944344	-6.26011696	-6.499997978	-6.294805818	-6.328729207	-8.54895253	-6.110749545	-7.036084127	-5.70276529	-6.189043795	-6.601955965	-6.006114402	-6.660847096	-5.870550951	-6.477605295	-5.345027422	-6.707863706	-6.724281715	-6.233088694	-6.916008129	-6.002354315	-6.67821603	-6.412887314

SUPPLEMENTAL TABLE 11: SRM RATIO ABUNDANCES POST-REGRESSION

Gene ID | Protein ID| Peptide Sequence	S114_P2D5_51123	S116_P2F5_47498	S117_P2G5_52945	S118_P2H5_47147	S119_P2A6_63141	S120_P2B6_78086	S121_P2C6_56326	S122_P2D6_51464	S123_P2E6_79243	S124_P2F6_80287	S125_P2G6_[illegible]	S126_P2H6_49903	S128_P2B7_47248	S129_P2C7_73621	S130_P2D7_74112	S131_P2E7_47480	S132_P2F7_52791	S133_P2G7_56007	S134_P2H7_57450	S135_P2A8_58815	S137_P2C8_45101	S138_P2D8_57251	S139_P2E8_53731	S140_P2F8_46008
AHSG | P02765 | EHAVEGDC[+57]DFQLLK	-4.852783548	-4.598561409	-5.47666071	-4.420065843	-4.678898944	-3.971175363	-4.772412486	-5.18851009	-4.866875741	-4.990858432	-4.600912	-4.135445036	-5.822308639	-4.311841493	-5.34319819	-5.194841808	-4.983753708	-5.009696671	-4.770045574	-5.224282581	-4.806236758	-4.775067516	-4.049476452	-4.627094182
ALB | P02768 | LVNEVTEFAK	4.789930999	4.639006901	4.410518543	5.274612796	5.097235352	4.428173575	5.164173493	4.490407863	4.467100353	4.414485764	4.63581131	5.738752444	4.196495922	5.18099282	4.744092107	4.629350581	4.643405421	5.169152542	4.581031601	4.303329613	4.580702079	4.705754443	5.451019883	5.261766048
ALB | P02768 | LVTDLTK	5.514990181	5.345148478	5.119351597	6.011887653	5.783534454	5.079070919	5.879482514	5.243263134	5.190941216	5.105507708	5.32485618	6.428125536	4.948679008	5.881131179	5.477268854	5.35736869	5.382532263	5.901829701	5.272536629	5.037020066	5.309563122	5.483637399	6.146013425	5.955453782
ALDOA | P04075 | VLAAVYK	-7.004126481	-6.647292973	-7.217886706	-6.94060585	-7.614989546	-7.755482964	-6.793447881	-7.059542134	-7.189420158	-6.432453	-6.5223273	-6.87971166	-7.26976462	-6.59291168	-7.406571015	-6.919326481	-8.358001188	-7.134142355	-7.370191378	-7.30967882	-6.858644836	-7.056196127	-7.617720593	-6.606731479
APOA4 | P06727 | SLAPYAQDTQEK	-5.124060055	-5.378953735	-6.559749809	-5.177208609	-5.24838038	-5.621008615	-4.560247725	-6.042740051	-5.47608646	-5.376953695	-5.0571812	-4.421492454	-5.885064789	-4.869599788	-5.903952986	-5.863701825	-5.661789163	-4.62881415	-5.282813305	-5.537166869	-5.141990759	-5.614318907	-4.986036874	-4.703507164

SUPPLEMENTAL TABLE 11: SRM RATIO ABUNDANCES POST-REGRESSION										
Gene ID | Protein ID| Peptide Sequence	S141_P2G8_47368	S142_P2H8_57498	S143_P2A9_82876	S144_P2B9_46103	S145_P2C9_52475	S146_P2D9_53705	S147_P2E9_42719	S148_P2F9_46743	S149_P2G9_45831	S150_P2H9_84217
AHSG | P02765 | EHAVEGDC[+57]DFQLLK	-3.48258077	-4.401788378	-5.09737431	-4.776902989	-4.676916991	-4.13161839	-4.650883231	-4.265254495	-4.261598285	-4.896379211
ALB | P02768 | LVNEVTEFAK	6.492457053	5.818919951	4.874573611	5.177282841	4.823789087	5.409556264	5.659118062	5.512356491	5.214005835	4.695630294
ALB | P02768 | LVTDLTK	7.163614418	6.545198388	5.618960002	5.896925244	5.529663364	6.10691086	6.399528484	6.259548286	6.002963205	5.421198567
ALDOA | P04075 | VLAAVYK	-7.59096463	-7.26931797	-7.235690724	-7.622568164	-6.831789122	-7.025675692	-7.042976309	-6.811056448	-7.045516203	-7.017202843
APOA4 | P06727 | SLAPYAQDTQEK	-3.871432543	-4.722948019	-5.181709535	-5.132277382	-4.739472669	-4.30626396	-4.361795832	-4.811759812	-5.751507493	-5.540022315
APOC1 | P02654 | QSELSAK	2.334065916	2.291734229	1.24330025	1.524982016	0.7778773	1.91868183	1.687183198	2.245788408	2.011679631	1.183932294
APOC2 | P02655 | TAAQNLYEK	-7.380326297	-7.013398376	-7.942291249	-7.442739177	-8.342775231	-7.225443593	-7.301143629	-7.119159844	-7.018744638	-7.619895769
APOE | P02649 | ELQAAQAR	-2.434742416	-2.26883999	-2.024358806	-2.659586148	-1.622964062	-1.770297136	-2.097501075	-1.599398089	-2.220836252	-2.233875194
C9 | P02748 | TSNFNAAISLK	-7.01197186	-8.123400564	-8.231351298	-7.499525298	-8.094454171	-7.722794612	-7.839184763	-7.225972335	-7.433785188	-8.484337997
C9 | P02748 | LSPIYNLVPVK	-6.380949532	-6.941417876	-7.676308224	-6.648333005	-7.393727745	-7.129434738	-7.097958221	-6.37298274	-6.699732037	-8.077034666
CALM2 | P0DP24 | EAFSLFDK	-6.25575865	-6.591690799	-6.476635971	-6.865520743	-5.98586179	-6.514462891	-6.487977749	-5.973067738	-6.384466283	-6.279125572
CD44 | P16070 | TEAADLC[+57]K	-10.13483996	-9.760489901	-9.509041074	-9.678823042	-9.601580853	-9.297596977	-9.498715049	-9.205725397	-9.398470393	-9.368695288
CD44 | P16070 | ALSIGFETC[+57]R	-9.23957189	-9.539331824	-9.489030954	-9.613390009	-9.103325135	-9.088239051	-9.12250389	-9.073052185	-9.474041128	-9.195487207
CHI3L1 | P36222 | IASNTQSR	-3.036792815	-3.259788046	-2.674694272	-3.537890631	-2.640251753	-2.92398215	-3.166805294	-2.404199401	-2.615642454	-2.876061155
CHI3L1 | P36222 | GNQWVGYDDQESVK	-5.118651683	-5.083209049	-4.757569511	-5.741962846	-4.434473703	-5.050772227	-5.313481573	-4.285117354	-4.857836215	-4.944046408
CHI3L1 | P36222 | QLLLSAALSAGK	-0.655296749	-0.55285942	-0.484197049	-1.337000338	-0.383504306	-0.739579774	-1.033414291	0.032065122	-0.693625209	-0.89712417
CP | P00450 | EVGPTNADPVC[+57]LAK	-3.550071288	-3.435008098	-3.414490255	-3.267216836	-3.586364918	-2.934864214	-3.328578962	-3.017044903	-3.759450355	-3.236340392
CP | P00450 | GEFYIGSK	-4.473659142	-4.507315859	-5.06208505	-4.325268556	-4.998766573	-4.144505769	-4.327361342	-3.990094756	-4.574007259	-4.771415332
CST3 | P01034 | ASNDM[+16]YHSR	-5.448750872	-4.868828247	-4.763084284	-5.060855883	-4.667029073	-4.948195237	-5.110981181	-4.386669696	-4.60554909	-4.793773928
DCN | P07585 | VDAASLK	-6.697466857	-7.218310454	-7.081915913	-6.939134378	-7.224555848	-7.202438424	-7.37887248	-7.317003549	-7.737660612	-6.844956489
DDAH1 | O94760 | EFFVGLSK	-10.92373787	-11.36577505	-11.06952735	-11.26214652	-10.84685979	-10.89191946	-10.90264011	-10.79175901	-11.00994382	-10.78461575
DKK3 | Q9UBP4 | DQDGEILLPR	-4.10786519	-4.443196611	-3.996879206	-4.382336227	-3.512322656	-3.600731111	-4.060248825	-3.386218132	-4.229605838	-4.024869942
ENO1 | P06733 | IEEELGSK	-8.210362634	-8.942462412	-9.016170836	-9.14285208	-8.724932296	-8.931638359	-8.603179061	-8.749088262	-8.590771359	-8.290427201
ENO1 | P06733 | LNVTEQEK	-8.259026011	-8.744382566	-8.635796007	-9.299125906	-8.481406621	-8.571910456	-8.360777873	-8.584604282	-8.64453919	-8.262316847
ENO2 | P09104 | IEEELGDEAR	-6.21550092	-6.29462702	-6.013750292	-6.53048444	-6.089886048	-6.025593795	-6.333070407	-5.784503633	-6.411315928	-6.173216144
F2 | P00734 | YTAC[+57]ETAR	-8.093901728	-8.439489625	-8.892668335	-8.515925428	-8.85385054	-8.01597871	-8.514926066	-8.204283374	-8.130444936	-8.482922001
F2 | P00734 | TATSEYQTFFNPR	-5.530533562	-5.996267782	-6.62350126	-6.107626925	-6.783471448	-6.054859451	-6.116946563	-5.98324436	-6.198482643	-6.543013542
GAPDH | P04406 | AAFNSGK	-8.377626079	-9.039532436	-9.039033324	-8.809157536	-8.881696103	-8.59012773	-9.023560857	-9.093147238	-8.69678329	-8.639699243
GAPDH | P04406 | YDNSLK	-10.68658237	-11.72058814	-11.48998254	-10.92773664	-11.120825	-11.28467045	-11.18432667	-11.21463428	-11.27014813	-11.04684589
GDA | Q9Y2T3 | DHLLGVSDSGK	-9.978418818	-9.088058057	-8.966543629	-9.686012057	-8.667789797	-9.119685662	-9.351466911	-8.400721274	-9.376105834	-9.090930631
GOT1 | P17174 | VGNLTVVGK	-7.982419881	-7.637182107	-7.708892508	-8.427966755	-7.387826792	-8.08509039	-7.697326159	-7.111193976	-7.676654937	-7.728046579
GOT1 | P17174 | IGADFLAR	-9.744933587	-9.917423102	-9.792534988	-10.08019976	-9.830861787	-9.830627921	-9.876006066	-9.608045582	-9.677198494	-9.579464203
GSN | P06396 | AGALNSNDAFVLK	-3.141597843	-3.639808588	-3.973103715	-3.983717708	-3.888944795	-3.535354034	-3.715747983	-3.462689616	-3.915409212	-4.128919538
HBA1 | P69905 | FLASVSTVLTSK	-1.589668217	-8.771394834	-7.121081783	-4.152946724	-0.423796413	-6.616319627	-4.493164857	-3.147292171	-3.54661335	-5.400680097
HBA1 | P69905 | VGAHAGEYGAEALER	-1.249092608	-10.94698491	-7.097592586	-3.920975132	-0.096534823	-6.748174384	-4.268969953	-2.796152541	-3.154124506	-4.909590042
HBB | P68871 | VNVDEVGGEALGR	-1.03965585	-9.448449662	-6.77579915	-3.649979328	0.025323195	-6.538173701	-3.995301482	-2.713117002	-2.952226854	-5.017278715
KNG1 | P01042 | EGDC[+57]PVQSGK	-8.189285506	-9.205324712	-9.491081409	-9.170074838	-9.510270161	-8.874922491	-8.795666256	-9.196722504	-9.366623809	-9.460084139
KNG1 | P01042 | QVVAGLNFR	2.769506789	1.590760765	0.718009641	1.506407625	0.57747406	1.546066973	1.556725701	1.243521285	0.927646433	0.914807361
KNG1 | P01042 | VQVVAGK	-3.865819119	-4.818906167	-5.500398497	-5.0239461	-5.540522678	-4.927874893	-4.934951394	-4.877799147	-5.312267285	-5.551934776
L1CAM | P32004 | GQLSFNLR	-4.798713913	-4.978890766	-4.619165912	-4.684872108	-4.410011527	-4.436897225	-5.112542145	-4.660387416	-4.464236065	-4.591364238
LAMP1 | P11279 | VWVQAFK	-8.086245039	-8.15433343	-8.708210551	-8.767580828	-8.371761175	-8.074322122	-8.36797228	-7.808630834	-8.851082563	-8.40031527
LAMP2 | P13473 | YLDFVFAVK	-7.274354713	-8.11152433	-8.159382424	-8.43589424	-8.398531842	-7.799805528	-7.931624864	-7.713042501	-8.301970691	-8.064518717
LDHB | P07195 | FIIPQIVK	-8.755177705	-8.904820366	-8.928234671	-9.38945051	-8.605657942	-9.107291167	-8.755935307	-8.59850319	-8.799791544	-8.909334896
LDHC | P07864 | VIGSGC[+57]NLDSAR	-8.638795216	-8.779301631	-8.755218863	-9.219490234	-9.1036019	-9.200921788	-8.83160214	-8.921371469	-9.004648935	-8.846877424
MDH1 | P40925 | GEFVTTVQQR	-7.602533328	-7.604929455	-7.440423291	-7.869507988	-7.426438405	-7.647955195	-7.506972008	-7.212838471	-7.456766389	-7.23984699
NCAM1 | P13591 | GLGEISAASEFK	-6.175566294	-6.082396542	-5.606475414	-6.310041186	-5.454470059	-5.563441494	-5.938193132	-5.157924992	-5.754920573	-5.906250559
NPTX2 | P47972 | VAELEDEK	-9.789304465	-9.671295071	-9.440368238	-9.294053065	-8.665744035	-8.514318758	-9.631372523	-8.328358303	-9.574914948	-9.761459894
NPTXR | O95502 | ELDVLQGR	-2.765861714	-2.662104161	-2.366820584	-2.547714939	-1.732287389	-1.778804745	-2.822793508	-1.634876516	-2.487292627	-2.425498843
NRXN1 | P58400 | LAIGFSTVQK	-7.361950277	-7.476044034	-6.928980487	-7.391936789	-6.687915809	-6.722902096	-7.393248147	-6.745619708	-7.179116183	-7.072968785
OGN | P20774 | LEGNPIVLGK	-6.120639495	-6.312501234	-6.383578162	-6.476423085	-6.715031787	-6.350617152	-6.351359337	-6.112065706	-6.371528865	-6.682221835
OMG | P23515 | LESLPAHLPR	-4.157815329	-4.235725802	-3.470365924	-4.186278649	-3.710088067	-3.565475703	-3.90990609	-3.37599677	-4.290719613	-3.976927277
PARK7 | Q99497 | ALVILAK	-8.237978503	-8.416733471	-8.297165353	-8.981382098	-8.680306676	-8.550817436	-8.465961411	-8.302591052	-8.447534863	-8.21111297
PEBP1 | P30086 | GNDISSGTVLSDYVGSGPPK	-5.300785221	-5.027364877	-6.109680403	-5.580293017	-4.793699102	-4.996451216	-5.081554747	-4.816519062	-5.224784547	-5.372452702
PEBP1 | P30086 | LYEQLSGK	-7.240841581	-7.592244594	-7.759757095	-7.980804918	-7.518924443	-7.569307799	-7.75503972	-7.218483304	-7.72927351	-7.398931486
PEBP1 | P30086 | VLTPTQVK	-6.720832093	-6.751763907	-6.874674323	-7.270325282	-6.349770113	-6.704176432	-6.623101698	-6.318803283	-6.70925742	-6.524998409
PGLYRP2 | Q96PD5 | TFTLLDPK	-3.498448536	-4.604617312	-5.60962317	-4.415928439	-4.938632153	-4.301313709	-4.42011363	-4.315519333	-4.688834712	-5.712219193
PKM | P14618 | VVEVGSK	-7.508643844	-7.746317062	-7.261923234	-7.94904834	-7.146546611	-7.61282346	-7.364444729	-7.033344606	-7.192332043	-7.194902656
PKM | P14618 | GVNLPGAAVDLPAVSEK	-7.18466747	-7.442483563	-6.934317704	-7.616773244	-6.738705574	-7.309767993	-6.977026823	-6.681199545	-6.861258076	-6.876539736
PKM | P14618 | GDLGIEIPAEK	-7.881336694	-7.955985284	-7.72550159	-8.395925911	-7.566202313	-7.895595046	-7.844804813	-7.50417015	-7.809947507	-7.767915097
PKM | P14618 | GDYPLEAVR	-6.341167381	-6.397557493	-6.176888181	-6.883951549	-6.179050376	-6.617820303	-6.394319427	-6.080930689	-6.148765544	-6.393106011
PKMisoform | NA | LFEELVR	-3.923573986	-3.75246229	-3.642219862	-4.050341765	-3.507558308	-3.784224528	-3.530521768	-3.366750059	-3.479150341	-3.476174734
PON1 | P27169 | LLIGTVFHK	-6.373835084	-7.919418304	-8.007438275	-7.29363025	-8.449649383	-8.58232635	-7.922143691	-7.103949721	-7.828425701	-8.356408057
PPIA | P62937 | VSFELFADK	-8.043060024	-8.644498104	-8.663450185	-9.174566962	-8.550691072	-8.908611066	-8.80372488	-8.54462609	-8.515074059	-8.558400011
PRDX2 | P32119 | QITVNDLPVGR	-3.316111971	-4.843961124	-4.879773686	-4.468424018	-2.452810432	-4.056397826	-4.363523269	-3.915243475	-4.030435784	-4.529786154
PTPRZ1 | P23471 | AIIDGVESVSR	-6.388915461	-6.721930892	-6.295684091	-6.769697946	-6.048526853	-6.151536442	-6.380688796	-6.000225809	-6.628420457	-6.495971766
PTPRZ1 | P23471 | DIEEGAIVNPGR	-7.356288399	-7.532432295	-7.222030739	-7.629141864	-6.995777609	-7.154966626	-7.502931413	-6.796814613	-7.682455588	-7.318934235
SCG2 | P13521 | IESQTQEEVR	-8.292676869	-8.336904225	-8.136069369	-7.978071177	-6.852204782	-7.325767207	-8.105030984	-7.233005967	-7.9332041	-7.995253881
SCG2 | P13521 | SGQLGIQEEDLR	-9.651252573	-10.13106738	-9.733357672	-9.715344274	-8.829124344	-9.113181579	-9.919099001	-8.771472174	-9.671776358	-9.553577845
SMOC1 | Q9H4F8 | AQALEQAK	-7.219508126	-8.295870655	-7.104016424	-7.966967211	-7.15703067	-7.217034855	-7.540830669	-6.595019875	-6.831401911	-7.026254383
SOD1 | P00441 | AVC[+57]VLK	-2.468721607	-1.791722698	-1.500650906	-2.182006298	-1.602012888	-2.391996489	-2.096983448	-1.520874636	-1.882414935	-1.461182495
SOD1 | P00441 | GDGPVQGIINFEQK	-3.021039818	-2.48291015	-2.429150433	-3.105990642	-2.584130181	-2.897605176	-2.582222631	-2.272396363	-2.378201541	-2.606036469
SOD1 | P00441 | HVGDLGNVTADK	-5.735947767	-4.755905412	-4.781616306	-5.52863168	-4.797160017	-5.361134688	-5.008377763	-4.552705541	-4.941879532	-4.906546022
SPP1 | P10451 | GDSVVYGLR	-3.322326063	-3.768703379	-3.283784993	-3.443585806	-3.624184563	-3.33661848	-3.16212585	-3.240758366	-3.768731441	-3.331899417
SPP1 | P10451 | YPDAVATWLNPDPSQK	-2.116740037	-1.913862801	-1.566608583	-2.368328778	-2.269356717	-2.069798365	-1.834379245	-1.507962909	-2.352803289	-1.847076122
SPP1 | P10451 | QETLPSK	0.738945338	0.513092916	1.020350309	0.33689986	0.112958244	0.526648133	0.689096969	1.184023567	0.48998551	0.51038402
THY1 | P04216 | HVLFGTVGVPEHTYR	-4.907465107	-4.964673895	-4.545966721	-4.672702146	-4.226411005	-4.112924756	-4.800886906	-4.235007657	-4.991478767	-4.672243178
TPI1 | P60174 | IAVAAQNC[+57]YK	-9.418634861	-9.982163569	-9.858983362	-11.13402189	-9.22883758	-9.428792626	-10.04994663	-10.3542002	-11.02733551	-10.19206383
VGF | O15240 | EPVAGDAVPGPK	-6.477476967	-7.015466335	-6.212489471	-6.038015938	-4.967219036	-5.166358165	-6.774315307	-4.997084297	-6.15555582	-6.152891478
VGF | O15240 | GLQEAAEER	-8.679274012	-9.172477875	-8.775700445	-8.615595964	-7.458759428	-7.609153014	-9.087857203	-7.507681795	-8.574038014	-8.554371072
VTN | P04004 | GQYC[+57]YELDEK	-4.742868758	-5.727086603	-6.025055964	-5.695316759	-5.863679839	-5.189640553	-5.741541277	-5.374780156	-5.482619303	-5.741483808
VTN | P04004 | DVWGIEGPIDAAFTR	-1.946553682	-3.019511767	-3.642709006	-3.144776768	-3.466847757	-2.915154107	-3.157702487	-3.173228598	-2.942941082	-3.399323002
YWHAB | P31946 | NLLSVAYK	-6.545603734	-6.759680427	-6.874555328	-7.307785924	-6.793689156	-7.347640167	-6.687717835	-6.977532918	-7.254230687	-6.673152561
YWHAB | P31946 | VISSIEQK	-7.411279466	-7.895490447	-7.906532781	-7.874401725	-7.601533573	-7.928451334	-7.702376283	-7.711558842	-7.885527902	-7.413678224
YWHAG | P61981 | YLAEVATGEK	-9.499985422	-9.616594957	-9.413454186	-9.813367883	-9.661132288	-10.05492264	-9.606329641	-9.291333557	-9.593755212	-9.312609564
YWHAZ | P63104 | VVSSIEQK	-6.236773697	-6.139109139	-6.59423683	-6.403494496	-6.195678159	-6.679731499	-6.165114995	-5.966077545	-6.504877687	-5.887492782

Gene ID | Protein ID| Peptide Sequence	S152_P2B10_48937	S153_P2C10_51175	S154_P2D10_56580	S155_P2E10_45918	S156_P2F10_48222	S157_P3A1_46043	S158_P3B1_46233	S159_P3C1_51760	S160_P3D1_45128	S161_P3E1_45739	S162_P3F1_49545	S163_P3G1_56582	S164_P3H1_76896
AHSG | P02765 | EHAVEGDC[+57]DFQLLK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
ALB | P02768 | LVNEVTEFAK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
ALB | P02768 | LVTDLTK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
ALDOA | P04075 | VLAAVYK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
APOA4 | P06727 | SLAPYAQDTQEK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
APOC1 | P02654 | QSELSAK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
APOC2 | P02655 | TAAQNLYEK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
APOE | P02649 | ELQAAQAR	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
C9 | P02748 | TSNFNAAISLK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
C9 | P02748 | LSPIYNLVPVK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
CALM2 | P0DP24 | EAFSLFDK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
CD44 | P16070 | TEAADLC[+57]K	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
CD44 | P16070 | ALSIGFETC[+57]R	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
CHI3L1 | P36222 | IASNTQSR	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
CHI3L1 | P36222 | GNQWVGYDDQESVK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
CHI3L1 | P36222 | QLLLSAALSAGK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
CP | P00450 | EVGPTNADPVC[+57]LAK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
CP | P00450 | GEFYIGSK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
CST3 | P01034 | ASNDM[+16]YHSR	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
DCN | P07585 | VDAASLK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
DDAH1 | O94760 | EFFVGLSK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
DKK3 | Q9UBP4 | DQDGEILLPR	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
ENO1 | P06733 | IEEELGSK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
ENO1 | P06733 | LNVTEQEK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
ENO2 | P09104 | IEEELGDEAR	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
F2 | P00734 | YTAC[+57]ETAR	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
F2 | P00734 | TATSEYQTFFNPR	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GAPDH | P04406 | AAFNSGK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GAPDH | P04406 | YDNSLK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GDA | Q9Y2T3 | DHLLGVSDSGK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GOT1 | P17174 | VGNLTVVGK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GOT1 | P17174 | IGADFLAR	-9.445988959	-9.709023365	-10.4161824	-10.09866788	-10.12161142	-9.379760046	-9.129878198	-10.06620708	-9.807237611	-10.15545657	-9.447470648	-9.67001645	-9.539726941
GSN | P06396 | AGALNSNDAFVLK	-3.764850201	-4.238476669	-4.123162313	-4.199271404	-3.506314517	-3.119049769	-3.737571261	-4.200591151	-3.985796593	-4.186005046	-3.665032162	-3.748169125	-3.675275335
HBA1 | P69905 | FLASVSTVLTSK	-2.803606347	-8.620299133	-7.638730852	-9.53591265	-4.566578701	-5.427088125	-8.186165115	-7.944604993	-3.454798252	-6.437632137	-9.278506132	-4.608696657	-4.88136621
HBA1 | P69905 | VGAHAGEYGAEALER	-2.472613987	-10.42636274	-7.880891508	-13.63985454	-4.354951394	-5.352499379	-9.645772211	-8.041353106	-3.219059314	-6.356600114	-10.95263697	-4.051326247	-4.590520866
HBB | P68871 | VNVDEVGGEALGR	-2.251295099	-10.03022928	-7.356930129	-10.01077074	-4.103843375	-4.950695812	-8.802207978	-7.818326268	-2.969820746	-6.081953825	-10.99233204	-4.049888909	-4.476728194
KNG1 | P01042 | EGDC[+57]PVQSGK	-9.408050884	-10.77062096	-9.202418862	-9.400902908	-8.43512141	-8.237189034	-9.532886635	-9.578783378	-9.505767956	-9.010782491	-8.645147059	-9.511112027	-9.874441186
KNG1 | P01042 | QVVAGLNFR	1.056975231	-0.587361777	1.160695795	1.445429502	2.229659964	2.890756715	1.026154314	1.361023658	1.008290216	1.194134468	1.977998626	0.889505753	0.953487855
KNG1 | P01042 | VQVVAGK	-5.216406899	-6.484895735	-5.173125729	-5.122490409	-4.283590326	-3.55861246	-5.239673532	-5.21866732	-5.244463605	-4.983017362	-4.42796543	-5.180116553	-5.367426083
L1CAM | P32004 | GQLSFNLR	-4.782218207	-4.654044219	-5.035159665	-5.059862103	-4.730837685	-4.568386365	-4.627758491	-4.887697102	-5.368866653	-4.975643838	-4.557147103	-4.622539361	-4.742067628
LAMP1 | P11279 | VWVQAFK	-7.87669972	-8.342363292	-8.510532476	-8.873027774	-8.430697047	-8.095155486	-7.951005614	-8.871731717	-8.712942964	-8.595750373	-8.614918429	-7.691956484	-7.910800601
LAMP2 | P13473 | YLDFVFAVK	-7.84509289	-7.84509289	-8.364510409	-8.654653848	-7.872049893	-6.892451009	-7.596467071	-8.169451691	-8.06113074	-8.417501784	-7.787673767	-7.622145698	-7.778808814
LDHB | P07195 | FIIPQIVK	-8.793656081	-9.069290524	-9.757670105	-9.329074846	-8.98031186	-8.506807461	-8.446659701	-9.503121651	-8.858746234	-9.294585971	-8.56201749	-8.530945646	-8.647791402
LDHC | P07864 | VIGSGC[+57]NLDSAR	-8.947354646	-9.768384505	-10.29725995	-9.453578575	-9.019633748	-8.56462572	-8.706178564	-10.0036365	-8.944764761	-9.227106881	-8.336689575	-8.87288307	-9.12096623
MDH1 | P40925 | GEFVTTVQQR	-7.310013583	-7.71297825	-8.08543597	-7.96127009	-7.57039097	-7.428935396	-7.078145943	-8.321848077	-7.447949424	-7.974728147	-6.969980562	-6.884191247	-6.956569121
NCAM1 | P13591 | GLGEISAASEFK	-5.383182439	-5.474578767	-5.990417344	-6.513628713	-6.158383118	-5.232309883	-4.835340655	-6.214541807	-5.821028104	-6.230498015	-5.342242726	-5.267398877	-5.282074328
NPTX2 | P47972 | VAELEDEK	-8.613391432	-8.2777884	-9.103351228	-10.15826186	-9.206769111	-8.839487201	-8.109900111	-9.101549907	-9.054515969	-9.645783094	-9.565624294	-9.04777816	-8.808933164
NPTXR | O95502 | ELDVLQGR	-1.82553626	-1.601535462	-2.24937059	-3.069423718	-2.843753956	-1.943959758	-1.395474192	-2.896005582	-2.462766361	-2.680202101	-2.277141603	-1.922573581	-2.062445536
NRXN1 | P58400 | LAIGFSTVQK	-6.633139262	-6.640092023	-7.778534081	-8.279511324	-7.465847449	-6.709677087	-6.458910858	-7.689219952	-7.327685512	-7.475336857	-7.165742305	-6.821697418	-6.780264456
OGN | P20774 | LEGNPIVLGK	-6.22828412	-6.977476016	-6.772758502	-6.71837828	-6.218233301	-6.374061367	-6.573484104	-6.486341297	-6.613665539	-6.893413348	-6.663140375	-6.466423968	-6.382109799
OMG | P23515 | LESLPAHLPR	-3.646442902	-3.416934352	-3.88449901	-4.758176573	-4.356773741	-3.592918598	-3.345393698	-4.947714921	-3.907492166	-4.388224844	-3.709357874	-3.413258797	-3.34165283
PARK7 | Q99497 | ALVILAK	-8.311723727	-8.606171085	-9.16577893	-8.975798477	-8.601607663	-8.299122396	-8.060277275	-9.208517815	-8.456669419	-8.80081997	-8.138367348	-8.177421418	-8.205666941
PEBP1 | P30086 | GNDISSGTVLSDYVGSGPPK	-4.922496221	-4.903415479	-5.480624647	-5.900949912	-5.676884975	-4.829924718	-4.520047438	-5.669298947	-5.014392043	-5.598841779	-4.834026554	-4.503323065	-4.993516575
PEBP1 | P30086 | LYEQLSGK	-7.352251145	-7.795857797	-8.137169228	-7.906201193	-7.577743404	-7.340054639	-7.511514466	-7.92042185	-7.783383369	-7.835728441	-7.31371472	-7.21650918	-7.556286801
PEBP1 | P30086 | VLTPTQVK	-6.330303343	-6.434222294	-7.019130237	-7.055115268	-7.067797423	-6.370223852	-6.098395613	-7.089552366	-6.505821164	-7.095474511	-6.217894042	-6.221570146	-6.487394971
PGLYRP2 | Q96PD5 | TFTLLDPK	-5.038681279	-5.131221685	-4.512082443	-4.474643843	-4.797028611	-3.2662193	-4.750132232	-4.686582615	-5.62657865	-4.395478774	-4.204610245	-4.458390393	-4.830662485
PKM | P14618 | VVEVGSK	-7.191313357	-7.191313357	-8.238690371	-7.94886476	-7.681135849	-7.043170517	-6.648436488	-7.949968857	-7.154089244	-7.785858705	-6.823181976	-6.884321508	-7.170099644
PKM | P14618 | GVNLPGAAVDLPAVSEK	-6.88780332	-6.953020979	-7.735474558	-7.670064615	-7.45189506	-7.002831676	-6.28344289	-7.474869415	-6.919067122	-7.578686755	-6.471233808	-6.508971386	-6.915185209
PKM | P14618 | GDLGIEIPAEK	-7.572705915	-7.612234279	-8.637954521	-8.359244917	-8.358171531	-7.557676981	-7.036286773	-8.300485555	-7.727945375	-8.309776821	-7.3375538	-7.256130437	-7.675533862
PKM | P14618 | GDYPLEAVR	-6.140585436	-6.380536228	-7.255251521	-6.858838764	-6.548705062	-6.090042158	-5.594608833	-6.942132469	-6.487273402	-7.018111924	-5.760325907	-5.902913686	-6.168058842
PKMisoform | NA | LFEELVR	-3.532745641	-3.630419399	-4.347086957	-4.058081026	-3.943057461	-3.322794244	-2.879809579	-4.086628261	-3.445691182	-4.249301429	-3.072564781	-3.261895446	-3.480696226
PON1 | P27169 | LLIGTVFHK	-7.759372984	-8.759372984	-8.287899224	-7.939431691	-7.046997195	-5.977156585	-8.294391848	-8.030965712	-8.555581795	-8.020003164	-7.11039457	-8.177819916	-7.950590632
PPIA | P62937 | VSFELFADK	-8.586810246	-8.726987904	-8.966821099	-9.130865154	-8.725043262	-8.778638286	-8.68603811	-8.822592033	-8.688813726	-9.42929456	-8.854178126	-8.313466644	-8.486821907
PRDX2 | P32119 | QITVNDLPVGR	-3.72303111	-4.393798214	-4.984554604	-5.415451877	-4.782618461	-4.347376124	-4.161790634	-4.594401457	-4.197630265	-5.38393813	-4.307181262	-4.156092486	-3.895901919
PTPRZ1 | P23471 | AIIDGVESVSR	-6.161195765	-6.149173237	-6.760879645	-7.062746826	-6.754825937	-6.193613597	-6.117926723	-6.818652157	-6.522187827	-6.888861479	-6.181013075	-5.821642802	-5.796316508
PTPRZ1 | P23471 | DIEEGAIVNPGR	-7.079160963	-7.129787036	-7.65371033	-7.91307991	-7.865981248	-7.053457177	-6.762744237	-7.804577685	-7.277992588	-8.093019228	-7.07623529	-6.678993923	-6.83519879
SCG2 | P13521 | IESQTQEEVR	-7.248347202	-6.795554781	-7.520063387	-8.28778848	-8.290798224	-7.196711463	-5.938133346	-8.038722203	-7.622951627	-8.342845268	-7.367426466	-7.720886527	-7.832667607
SCG2 | P13521 | SGQLGIQEEDLR	-8.64468646	-8.979105499	-9.960160889	-10.44468023	-10.45226233	-8.764253875	-8.296507941	-9.622603574	-9.196774946	-10.08094533	-9.165350543	-9.136940226	-9.530124625
SMOC1 | Q9H4F8 | AQALEQAK	-7.400081651	-7.430138885	-7.429742222	-7.615411768	-7.151018667	-6.977614455	-6.875547783	-7.631487966	-6.996448485	-7.485726873	-6.335646626	-6.539010003	-6.616206648
SOD1 | P00441 | AVC[+57]VLK	-1.271567411	-1.158834648	-2.184321009	-2.344320716	-2.481800222	-1.439135841	-1.211908328	-2.015570125	-1.678435899	-2.551306887	-1.521384981	-1.068964963	-0.879229372
SOD1 | P00441 | GDGPVQGIINFEQK	-2.115519737	-2.15207547	-2.822716381	-3.109613312	-2.745859816	-2.317205514	-2.048201041	-3.027680841	-2.476282178	-3.338352921	-2.273938073	-2.104901633	-1.929722026
SOD1 | P00441 | HVGDLGNVTADK	-4.437338812	-4.542533586	-5.234834728	-5.66132384	-5.417874014	-4.423449443	-4.208428433	-5.116730047	-4.674139523	-5.806670091	-4.561979685	-4.231268461	-4.096929345
SPP1 | P10451 | GDSVVYGLR	-3.461927833	-3.053051318	-3.691693242	-4.299390423	-3.895096748	-3.194885083	-3.225965264	-3.784208389	-3.088921173	-3.643304972	-3.203036031	-3.18583291	-3.125229836
SPP1 | P10451 | YPDAVATWLNPDPSQK	-2.201580023	-1.427116062	-2.146535467	-2.197188895	-2.038188143	-2.012314526	-1.893871148	-2.568785881	-1.80170625	-2.132319624	-1.59133029	-1.505970767	-1.332675019
SPP1 | P10451 | QETLPSK	0.008952248	0.918404205	0.206093167	0.308374925	0.84918166	0.538234826	0.916521145	-0.321352846	0.675066575	0.482091828	0.706287215	1.046726696	1.197966721
THY1 | P04216 | HVLFGTVGVPEHTYR	-4.191899167	-3.991561112	-4.982488084	-5.628588664	-4.902909784	-4.076103068	-3.323789341	-5.564005219	-4.577688806	-5.418413015	-4.179990663	-4.042173936	-3.920408635
TPI1 | P60174 | IAVAAQNC[+57]YK	-9.830904308	-10.3783921	-11.1391889	-11.34736324	-10.19897814	-10.04655905	-9.27565301	-11.62231614	-10.34040269	-10.06834332	-9.661157153	-9.604249457	-9.687854344
VGF | O15240 | EPVAGDAVPGPK	-4.945984568	-4.710749946	-5.923906574	-6.563252826	-6.922047809	-5.195364827	-4.115997068	-6.031762771	-5.782468627	-6.405121871	-5.682715002	-5.538843809	-5.771781726
VGF | O15240 | GLQEAAEER	-7.39958089	-7.344509508	-8.526898419	-8.855008908	-9.298278734	-7.528834653	-6.6810836	-8.675546474	-8.131991841	-8.812971709	-8.115324047	-7.882353251	-8.334926246
VTN | P04004 | GQYC[+57]YELDEK	-5.521051081	-6.180395778	-5.82275415	-6.007269759	-5.209546238	-3.884511787	-5.452400445	-5.729178113	-5.518793572	-5.575361952	-4.974401158	-5.757645874	-6.125495799
VTN | P04004 | DVWGIEGPIDAAFTR	-3.264788582	-4.065884513	-3.458478728	-3.415597483	-2.726002228	-1.195241835	-3.250197602	-3.124419177	-3.246539183	-3.324741175	-2.583916504	-3.274643516	-3.389130385
YWHAB | P31946 | NLLSVAYK	-7.098323206	-7.129801438	-7.637661982	-7.244402245	-6.804223086	-6.707637019	-6.919533167	-7.464911915	-6.977964604	-7.19430321	-6.460274815	-6.319444414	-6.666988258
YWHAB | P31946 | VISSIEQK	-7.640411114	-7.873901244	-8.000821729	-8.329985873	-7.755352561	-7.69824477	-7.509188204	-7.953324104	-7.649794713	-7.968568909	-7.630722743	-7.165598921	-7.474513775
YWHAG | P61981 | YLAEVATGEK	-9.884680967	-9.814291639	-9.907935753	-10.12769592	-9.626005108	-9.46544458	-8.939239061	-10.2677479	-9.675323877	-9.684976649	-9.161710612	-8.695133752	-9.509847777
YWHAZ | P63104 | VVSSIEQK	-6.40650671	-6.760479058	-7.369519776	-6.687200569	-6.767719855	-6.59287186	-6.004742989	-6.751486336	-6.017915168	-6.431020139	-5.637264906	-5.72285629	-5.967270073

SUPPLEMENTAL TABLE 11: SRM RATIO ABUNDANCES POST-REGRESSION					
Gene ID | Protein ID| Peptide Sequence	S165_P3A2_50502	S166_P3B2_55838	S167_P3C2_86092	S168_P3D2_46246	S169_P3E2_73152
AHSG | P02765 | EHAVEGDC[+57]DFQLLK	-5.057283886	-4.537019308	-4.78847371	-5.600417415	-4.716526923
ALB | P02768 | LVNEVTEFAK	4.693761398	5.29328388	4.597114204	4.336407579	5.03269641
ALB | P02768 | LVTDLTK	5.427619026	6.011200042	5.33195466	5.091056271	5.817698957
ALDOA | P04075 | VLAAVYK	-7.709609176	-6.917369221	-7.312500085	-7.358995046	-8.284335913
APOA4 | P06727 | SLAPYAQDTQEK	-5.81147989	-5.203609011	-5.729027189	-6.159274577	-5.357147544
APOC1 | P02654 | QSELSAK	1.579183741	2.451639409	1.152359	0.608124424	1.987880882
APOC2 | P02655 | TAAQNLYEK	-7.748414625	-7.428108667	-8.164332128	-7.815683169	-7.672211727
APOE | P02649 | ELQAAQAR	-2.108957241	-1.661974425	-1.783712978	-2.092712939	-3.532176757
C9 | P02748 | TSNFNAAISLK	-8.880792359	-7.560183255	-8.252636576	-8.195573684	-8.652395333
C9 | P02748 | LSPIYNLVPVK	-7.844448643	-7.128533926	-7.628892048	-7.512650284	-8.126491562
CALM2 | P0DP24 | EAFSLFDK	-7.057626041	-6.164930946	-6.563610299	-6.556000737	-7.238914347
CD44 | P16070 | TEAADLC[+57]K	-10.31137719	-9.629214283	-9.605075822	-9.532221271	-10.1624779
CD44 | P16070 | ALSIGFETC[+57]R	-10.14914039	-9.163907838	-9.402924444	-9.114411384	-10.15334078
CHI3L1 | P36222 | IASNTQSR	-3.732621537	-2.712312606	-3.272601756	-3.043595997	-3.527806051
CHI3L1 | P36222 | GNQWVGYDDQESVK	-6.065446647	-4.494924718	-5.095259872	-4.868062333	-5.722203452
CHI3L1 | P36222 | QLLLSAALSAGK	-1.4423502	-0.662751079	-0.877413787	-0.575441847	-1.56264005
CP | P00450 | EVGPTNADPVC[+57]LAK	-3.272929198	-3.074088487	-3.920513876	-3.70338588	-3.901447938
CP | P00450 | GEFYIGSK	-4.828887477	-4.402175451	-5.257070773	-5.067363986	-4.794286734
CST3 | P01034 | ASNDM[+16]YHSR	-4.113617981	-4.458198644	-4.715977261	-4.756034812	-5.681925786
DCN | P07585 | VDAASLK	-7.162154485	-7.264249237	-7.237545567	-7.593780916	-7.36375611
DDAH1 | O94760 | EFFVGLSK	-11.75259371	-11.21650807	-11.13324075	-11.32426551	-11.91524098
DKK3 | Q9UBP4 | DQDGEILLPR	-4.190360768	-3.401607422	-3.884265371	-3.988020522	-5.388809584
ENO1 | P06733 | IEEELGSK	-8.986826492	-8.639047951	-8.846879149	-8.783049235	-9.425864296
ENO1 | P06733 | LNVTEQEK	-8.940666155	-8.481185028	-8.372849531	-8.637816973	-9.449977816
ENO2 | P09104 | IEEELGDEAR	-6.295413478	-5.976429847	-6.014784839	-6.344378311	-7.003053797
F2 | P00734 | YTAC[+57]ETAR	-9.095353293	-8.75961343	-8.809585939	-8.80529244	-8.746370516
F2 | P00734 | TATSEYQTFFNPR	-6.752603478	-6.305489145	-6.726766058	-6.821663377	-6.568936613
GAPDH | P04406 | AAFNSGK	-9.954612688	-8.755711632	-8.236511628	-8.774102168	-9.603535252
GAPDH | P04406 | YDNSLK	-11.97717455	-11.29081824	-10.86104547	-11.12398529	-11.68017799
GDA | Q9Y2T3 | DHLLGVSDSGK	-9.413053874	-9.185877597	-9.195875077	-9.171051877	-10.06124737
GOT1 | P17174 | VGNLTVVGK	-8.018622687	-7.341147116	-7.694028938	-8.178717417	-9.115025548
GOT1 | P17174 | IGADFLAR	-10.34338832	-9.721335441	-9.816105647	-9.960549074	-10.62566052
GSN | P06396 | AGALNSNDAFVLK	-4.479573757	-3.760038716	-4.13798519	-4.109102499	-4.724515645
HBA1 | P69905 | FLASVSTVLTSK	-6.826703797	-8.907749569	-8.540039249	-4.261963548	-3.046526763
HBA1 | P69905 | VGAHAGEYGAEALER	-6.551590595	-13.75722272	-10.84629041	-3.879236166	-2.793520205
HBB | P68871 | VNVDEVGGEALGR	-6.325392466	-9.953269445	-8.997733395	-3.750842318	-2.509916382
KNG1 | P01042 | EGDC[+57]PVQSGK	-9.470620527	-9.590858528	-9.753129632	-10.36018249	-9.912230806
KNG1 | P01042 | QVVAGLNFR	0.866518669	0.470670532	0.143969924	0.518260341	0.986551965
KNG1 | P01042 | VQVVAGK	-5.529969608	-5.372634093	-5.80733537	-6.029219229	-5.477516515
L1CAM | P32004 | GQLSFNLR	-5.174604155	-4.728870354	-5.00783057	-5.015024629	-5.17603902
LAMP1 | P11279 | VWVQAFK	-8.418211299	-7.935550821	-8.248385751	-8.553238846	-9.042032293
LAMP2 | P13473 | YLDFVFAVK	-8.004518806	-7.817754554	-8.294514848	-8.349177555	-8.978197696
LDHB | P07195 | FIIPQIVK	-9.522877528	-8.875844537	-9.062706622	-9.253734461	-9.862684757
LDHC | P07864 | VIGSGC[+57]NLDSAR	-10.01000185	-9.530051095	-9.347796801	-9.351379531	-10.05870096
MDH1 | P40925 | GEFVTTVQQR	-8.253203699	-7.348715143	-7.489820256	-7.910615915	-8.351901709
NCAM1 | P13591 | GLGEISAASEFK	-6.065432774	-5.379507547	-5.647825292	-5.813006196	-6.881660375
NPTX2 | P47972 | VAELEDEK	-9.108287865	-8.401806939	-8.751552627	-9.338185438	-9.926184491
NPTXR | O95502 | ELDVLQGR	-2.419366136	-1.765811885	-1.892565433	-2.668988993	-3.149438256
NRXN1 | P58400 | LAIGFSTVQK	-7.293792333	-6.707119057	-6.712374037	-7.408109607	-8.757380841
OGN | P20774 | LEGNPIVLGK	-7.006339377	-7.000861321	-6.674929509	-6.665632586	-7.367939531
OMG | P23515 | LESLPAHLPR	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
PARK7 | Q99497 | ALVILAK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
PEBP1 | P30086 | GNDISSGTVLSDYVGSGPPK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
PEBP1 | P30086 | LYEQLSGK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
PEBP1 | P30086 | VLTPTQVK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
PGLYRP2 | Q96PD5 | TFTLLDPK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
PKM | P14618 | VVEVGSK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
PKM | P14618 | GVNLPGAAVDLPAVSEK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
PKM | P14618 | GDLGIEIPAEK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
PKM | P14618 | GDYPLEAVR	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
PKMisoform | NA | LFEELVR	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
PON1 | P27169 | LLIGTVFHK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
PPIA | P62937 | VSFELFADK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
PRDX2 | P32119 | QITVNDLPVGR	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
PTPRZ1 | P23471 | AIIDGVESVSR	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
PTPRZ1 | P23471 | DIEEGAIVNPGR	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
SCG2 | P13521 | IESQTQEEVR	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
SCG2 | P13521 | SGQLGIQEEDLR	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
SMOC1 | Q9H4F8 | AQALEQAK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
SOD1 | P00441 | AVC[+57]VLK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
SOD1 | P00441 | GDGPVQGIINFEQK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
SOD1 | P00441 | HVGDLGNVTADK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
SPP1 | P10451 | GDSVVYGLR	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
SPP1 | P10451 | YPDAVATWLNPDPSQK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
SPP1 | P10451 | QETLPSK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
THY1 | P04216 | HVLFGTVGVPEHTYR	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
TPI1 | P60174 | IAVAAQNC[+57]YK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
VGF | O15240 | EPVAGDAVPGPK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
VGF | O15240 | GLQEAAEER	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
VTN | P04004 | GQYC[+57]YELDEK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
VTN | P04004 | DVWGIEGPIDAAFTR	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
YWHAB | P31946 | NLLSVAYK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
YWHAB | P31946 | VISSIEQK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
YWHAG | P61981 | YLAEVATGEK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
YWHAZ | P63104 | VVSSIEQK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]

Gene ID | Protein ID| Peptide Sequence	S170_P3F2_45487	S171_P3G2_52538	S172_P3H2_70714	S173_P3A3_46306	S174_P3B3_43738	S175_P3C3_45238	S176_P3D3_48358	S177_P3E3_47135	S178_P3F3_47351	S180_P3H3_72191	S181_P3A4_83798	S182_P3B4_50259	S183_P3C4_42947	S184_P3D4_53030	S185_P3E4_74682	S186_P3F4_76615	S187_P3G4_44820	S188_P3H4_86780
AHSG | P02765 | EHAVEGDC[+57]DFQLLK	-5.260502669	-4.963967969	-4.698272241	-4.418134532	-4.158888294	-5.054458648	-4.602281937	-4.548624305	-4.989375608	-4.710084508	-4.253764701	-4.197627264	-3.990835018	-4.956562561	-4.849885556	-6.012239633	-4.471149554	-5.765753454
ALB | P02768 | LVNEVTEFAK	4.685357106	4.808095382	4.859125438	5.292398979	5.704594716	3.99856875	4.83945887	5.216413085	4.720103421	4.868919968	5.763104631	5.857262407	5.586248635	4.768614363	5.209518152	3.727603443	5.173195413	4.342333084
ALB | P02768 | LVTDLTK	5.488764618	5.510139973	5.575553625	6.014429302	6.469808118	4.760183368	5.629762334	5.952995448	5.434427009	5.648026027	6.520462946	6.601301055	6.352024612	5.534031006	5.977102055	4.425906909	5.93090772	5.062268593
ALDOA | P04075 | VLAAVYK	-6.724170267	-7.03419438	-7.153509605	-7.787060649	-7.133418093	-7.175927929	-7.0421865	-5.889744553	-6.710913681	-6.753524269	-7.357530683	-5.958571211	-6.722037109	-7.106307284	-7.277143683	-7.524989787	-6.895966085	-6.765480528
APOA4 | P06727 | SLAPYAQDTQEK	-5.574350915	-5.259708987	-5.205671953	-4.788868001	-4.437300148	-6.238738845	-5.1665272	-4.395178042	-5.19093957	-4.943039345	-5.216836092	-4.294535918	-4.327974331	-5.009371811	-4.556444166	-6.280786844	-4.971054846	-5.047379715
APOC1 | P02654 | QSELSAK	1.638763865	1.420328348	1.127608451	2.124645767	1.957904943	0.768327295	1.565563367	1.743013397	1.305963901	1.447844558	2.170038434	2.953104987	2.049507487	1.338336882	2.221018159	0.181966066	1.224017095	0.840590307
APOC2 | P02655 | TAAQNLYEK	-8.00521826	-7.511764811	-8.320632294	-7.541150301	-7.034272963	-8.790947115	-7.485294031	-7.639633904	-8.26740434	-8.023436281	-7.359237105	-6.723816724	-7.022856244	-7.635660044	-7.75423174	-9.305706452	-7.829501604	-8.169547736
APOE | P02649 | ELQAAQAR	-1.898295674	-1.712978131	-2.040348247	-2.758957265	-2.424851722	-2.203200171	-1.644544794	-1.100637607	-2.301432418	-1.707036045	-2.121663694	-1.34698711	-1.407060531	-2.28830022	-2.26713366	-2.806580947	-1.974305733	-1.941033249
C9 | P02748 | TSNFNAAISLK	-8.359506342	-7.723816137	-8.346911151	-7.968675438	-7.839584216	-8.09094342	-7.977410677	-7.834272438	-7.7097546	-9.196368115	-7.469575106	-7.523205132	-7.407322504	-7.947397173	-7.703631368	-9.512584164	-8.57746837	-8.154213225
C9 | P02748 | LSPIYNLVPVK	-7.659342495	-7.255497466	-7.35608636	-7.059536249	-6.850444595	-7.120093994	-7.558362428	-7.12556176	-6.944579324	-7.789316231	-6.377970285	-6.678285194	-6.888272387	-7.158583111	-7.172464973	-8.501284373	-7.859613471	-7.473163654
CALM2 | P0DP24 | EAFSLFDK	-6.030124675	-6.283614717	-6.472847708	-7.020178233	-6.562878542	-6.312876197	-6.249002558	-5.303996369	-6.222766294	-6.123833729	-6.756426735	-5.271029179	-5.965406799	-6.446503864	-6.659362169	-6.768928214	-6.454505552	-5.741892586
CD44 | P16070 | TEAADLC[+57]K	-9.81075185	-9.703397166	-9.756768395	-10.28763267	-9.995239053	-9.166665404	-9.406821351	-9.226875257	-10.22005816	-9.508281817	-9.771889383	-9.09012266	-9.396444859	-9.962587319	-9.591573487	-9.785596586	-9.741197605	-9.119739679
CD44 | P16070 | ALSIGFETC[+57]R	-9.471322004	-9.099536977	-9.608669499	-9.882879395	-9.551368232	-8.789569651	-9.342163589	-8.715623764	-9.242291014	-9.214521079	-9.293541617	-9.1752597	-8.831352483	-9.821699094	-9.257739443	-10.07852676	-8.935335451	-8.692962359
CHI3L1 | P36222 | IASNTQSR	-2.111163894	-2.734971252	-3.221892932	-2.780931325	-3.515111833	-3.272418556	-2.813960033	-2.350309152	-2.849505788	-2.680291332	-3.670841698	-2.244862015	-2.122758053	-3.459253037	-2.961101091	-3.45345418	-2.921798494	-2.596683929
CHI3L1 | P36222 | GNQWVGYDDQESVK	-4.070871965	-4.763964001	-5.21247212	-4.697803062	-5.571381775	-5.299775379	-4.817883082	-4.277444343	-4.858365933	-4.980775594	-5.889561241	-4.380279724	-4.179221924	-5.478373297	-4.887635635	-5.542407988	-4.991989665	-4.485909077
CHI3L1 | P36222 | QLLLSAALSAGK	-0.043736014	-0.49382286	-1.142519041	-0.806362072	-1.365823182	-1.149141511	-0.825011164	-0.108151587	-0.735591527	-0.721410753	-1.727984605	0.01335045	-0.120950726	-1.408081344	-0.880081085	-1.551569163	-0.54266042	-0.104459904
CP | P00450 | EVGPTNADPVC[+57]LAK	-3.45195977	-3.783986256	-3.219170671	-3.318646919	-3.17266169	-3.862346275	-3.745410292	-3.974031539	-3.700371758	-3.662616573	-2.571293895	-2.923455266	-3.131402018	-3.56384323	-3.724331017	-4.56650664	-3.746415347	-3.253524021
CP | P00450 | GEFYIGSK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
CST3 | P01034 | ASNDM[+16]YHSR	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
DCN | P07585 | VDAASLK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
DDAH1 | O94760 | EFFVGLSK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
DKK3 | Q9UBP4 | DQDGEILLPR	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
ENO1 | P06733 | IEEELGSK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
ENO1 | P06733 | LNVTEQEK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
ENO2 | P09104 | IEEELGDEAR	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
F2 | P00734 | YTAC[+57]ETAR	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
F2 | P00734 | TATSEYQTFFNPR	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GAPDH | P04406 | AAFNSGK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GAPDH | P04406 | YDNSLK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GDA | Q9Y2T3 | DHLLGVSDSGK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GOT1 | P17174 | VGNLTVVGK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GOT1 | P17174 | IGADFLAR	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
GSN | P06396 | AGALNSNDAFVLK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
HBA1 | P69905 | FLASVSTVLTSK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
HBA1 | P69905 | VGAHAGEYGAEALER	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
HBB | P68871 | VNVDEVGGEALGR	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
KNG1 | P01042 | EGDC[+57]PVQSGK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
KNG1 | P01042 | QVVAGLNFR	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
KNG1 | P01042 | VQVVAGK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
L1CAM | P32004 | GQLSFNLR	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
LAMP1 | P11279 | VWVQAFK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
LAMP2 | P13473 | YLDFVFAVK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
LDHB | P07195 | FIIPQIVK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
LDHC | P07864 | VIGSGC[+57]NLDSAR	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
MDH1 | P40925 | GEFVTTVQQR	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
NCAM1 | P13591 | GLGEISAASEFK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
NPTX2 | P47972 | VAELEDEK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
NPTXR | O95502 | ELDVLQGR	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
NRXN1 | P58400 | LAIGFSTVQK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
OGN | P20774 | LEGNPIVLGK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
OMG | P23515 | LESLPAHLPR	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
PARK7 | Q99497 | ALVILAK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
PEBP1 | P30086 | GNDISSGTVLSDYVGSGPPK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
PEBP1 | P30086 | LYEQLSGK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
PEBP1 | P30086 | VLTPTQVK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
PGLYRP2 | Q96PD5 | TFTLLDPK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
PKM | P14618 | VVEVGSK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
PKM | P14618 | GVNLPGAAVDLPAVSEK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
PKM | P14618 | GDLGIEIPAEK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
PKM | P14618 | GDYPLEAVR	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
PKMisoform | NA | LFEELVR	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
PON1 | P27169 | LLIGTVFHK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
PPIA | P62937 | VSFELFADK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
PRDX2 | P32119 | QITVNDLPVGR	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
PTPRZ1 | P23471 | AIIDGVESVSR	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
PTPRZ1 | P23471 | DIEEGAIVNPGR	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
SCG2 | P13521 | IESQTQEEVR	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
SCG2 | P13521 | SGQLGIQEEDLR	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
SMOC1 | Q9H4F8 | AQALEQAK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
SOD1 | P00441 | AVC[+57]VLK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
SOD1 | P00441 | GDGPVQGIINFEQK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
SOD1 | P00441 | HVGDLGNVTADK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
SPP1 | P10451 | GDSVVYGLR	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
SPP1 | P10451 | YPDAVATWLNPDPSQK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
SPP1 | P10451 | QETLPSK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
THY1 | P04216 | HVLFGTVGVPEHTYR	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
TPI1 | P60174 | IAVAAQNC[+57]YK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
VGF | O15240 | EPVAGDAVPGPK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
VGF | O15240 | GLQEAAEER	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
VTN | P04004 | GQYC[+57]YELDEK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
VTN | P04004 | DVWGIEGPIDAAFTR	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
YWHAB | P31946 | NLLSVAYK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
YWHAB | P31946 | VISSIEQK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
YWHAG | P61981 | YLAEVATGEK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
YWHAZ | P63104 | VVSSIEQK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]

SUPPLEMENTAL TABLE 11: SRM RATIO ABUNDANCES POST-REGRESSION

Gene ID | Protein ID| Peptide Sequence	S189_P3A5_87124	S192_P3D5_44707	S193_P3E5_64149	S194_P3F5_77501	S195_P3G5_85961	S196_P3H5_54601	S197_P3A6_43820	S198_P3B6_44893	S199_P3C6_50409	S200_P3D6_51224	S201_P3E6_49450	S202_P3F6_83314	S204_P3H6_47251
AHSG | P02765 | EHAVEGDC[+57]DFQLLK	-4.44404982	-4.312005165	-5.016927463	-4.660188409	-4.522022466	-4.700471647	-4.674494314	-5.222271895	-3.77432928	-5.19092956	-5.160201352	-4.93559664	-4.045975481
ALB | P02768 | LVNEVTEFAK	5.104517057	5.048396543	4.308075958	5.42360123	5.115218139	4.634237897	4.981326336	4.578726143	6.459230856	4.622956033	4.373383635	4.675239741	5.561892211
ALB | P02768 | LVTDLTK	5.886843624	5.793818183	5.046023341	6.170837236	5.855820001	5.408390095	5.774475601	5.29035751	7.238046599	5.350001095	5.166864085	5.444734794	6.331026651
ALDOA | P04075 | VLAAVYK	-7.128867188	-6.695725674	-7.251185131	-7.108333917	-6.955945351	-7.061538205	-7.849950219	-7.672412033	-7.05207668	-7.374456415	-6.093311062	-7.272133297	-6.658809963
APOA4 | P06727 | SLAPYAQDTQEK	-4.510185763	-4.828695123	-5.4133233	-4.185478652	-5.160089626	-5.072831447	-5.142796083	-5.787382567	-3.08696108	-5.431534467	-5.848000874	-5.453754262	-4.43966992
APOC1 | P02654 | QSELSAK	1.597064023	1.360228928	0.86531898	2.113079682	2.200825489	1.338275261	1.673293165	1.213138826	2.877202315	1.310900834	0.77443226	1.566276395	2.148444354
APOC2 | P02655 | TAAQNLYEK	-7.653479783	-7.495574123	-8.5620729	-6.569156202	-7.094246146	-8.390030034	-8.466928083	-8.466928083	-5.477000109	-8.741186032	-8.489913008	-8.160608604	-7.126155881
APOE | P02649 | ELQAAQAR	-2.130273341	-1.736119559	-2.394479063	-1.65800067	-2.138638519	-2.488222199	-3.065561696	-2.767881147	-2.432615914	-2.182085056	-1.961128397	-2.47376928	-1.828381233
C9 | P02748 | TSNFNAAISLK	-8.016611662	-7.945704179	-8.352367486	-8.041212508	-8.089638868	-7.949665349	-7.651937809	-8.093942356	-7.363813695	-8.645065354	-8.924271546	-8.590463202	-7.622827339
C9 | P02748 | LSPIYNLVPVK	-7.175771308	-7.337677519	-7.742756502	-7.287177096	-7.515625961	-7.068006615	-6.99966888	-7.235736238	-6.447493496	-7.728961569	-8.184027537	-7.661367826	-6.549617916
CALM2 | P0DP24 | EAFSLFDK	-6.467637396	-5.853876938	-6.615598995	-6.413410459	-6.591181994	-6.489832302	-7.267198104	-7.157015187	-6.479687785	-6.692425051	-5.443300604	-6.3867169	-5.85325599
CD44 | P16070 | TEAADLC[+57]K	-9.712301947	-9.482281414	-9.664958168	-9.444474792	-10.46984961	-9.745301446	-9.730957588	-9.383034285	-9.603031882	-9.952034833	-9.746346076	-9.607651724	-9.127251203
CD44 | P16070 | ALSIGFETC[+57]R	-9.527737587	-9.700888822	-9.170109612	-9.326975165	-9.752949026	-9.21572071	-9.667296603	-9.268747227	-10.18247027	-9.602780096	-9.32386475	-9.441446275	-8.870059116
CHI3L1 | P36222 | IASNTQSR	-2.690742248	-2.486856979	-2.658244126	-2.285207815	-3.1048146	-3.072260957	-3.189840382	-3.871409731	-2.992757637	-3.506975486	-2.488064216	-3.284767806	-2.242288654
CHI3L1 | P36222 | GNQWVGYDDQESVK	-4.618075037	-4.500473346	-4.594405077	-4.339876386	-5.123637981	-5.128040849	-5.357740505	-6.135020459	-4.792641157	-5.691964308	-4.447632761	-5.238094984	-4.329437354
CHI3L1 | P36222 | QLLLSAALSAGK	-0.520548997	-0.665811615	-0.829297376	0.00148076	-0.980031243	-1.050206661	-0.947912857	-1.707388307	-0.782434639	-1.066394186	-0.358949504	-1.217759315	-0.22613555
CP | P00450 | EVGPTNADPVC[+57]LAK	-3.29926142	-3.667876612	-3.803142453	-3.566073516	-3.61247827	-2.994418775	-3.177050399	-3.393321915	-2.952806536	-4.060138894	-4.090942643	-3.609617378	-2.832877112
CP | P00450 | GEFYIGSK	-4.637582808	-4.588133951	-5.15699493	-4.682661213	-4.673055297	-4.672118426	-4.618134161	-4.80761196	-3.787383571	-5.295645144	-5.259524206	-4.957232379	-4.107902853
CST3 | P01034 | ASNDMYH[+16]YHSR	-4.616284157	-3.789935335	-4.589029154	-2.83152645	-3.587907526	-4.804814509	-5.018674625	-5.338971634	-4.96593585	-4.527122267	-4.08483141	-4.421727613	-4.46703495
DCN | P07585 | VDAASLK	-7.260101397	-7.416279184	-7.34165622	-7.53946885	-7.309106227	-7.539111458	-7.211963093	-7.627000592	-7.605284788	-7.452131344	-7.277307251	-7.417576001	-7.13687487
DDAH1 | O94760 | EFFVGLSK	-11.01235424	-10.70174986	-10.97951819	-10.92868376	-11.22031128	-11.02041437	-11.33308908	-11.33308908	-11.19242112	-11.31959773	-10.32426551	-11.02515664	-10.74186364
DKK3 | Q9UBP4 | DQDGEILLPR	-3.801952286	-3.549753295	-4.585611412	-4.039299455	-3.80937563	-3.881761552	-4.648583071	-4.520733116	-4.034321472	-4.033997109	-3.632296263	-4.133048455	-3.417093308
ENO1 | P06733 | IEEELGSK	-8.406557254	-8.038839617	-8.585655309	-8.29233353	-8.76858922	-8.484621417	-9.388915208	-9.014519693	-8.876683239	-8.963217769	-7.894694591	-8.935435655	-8.099444447
ENO1 | P06733 | LNVTEQEK	-8.450935054	-8.415790715	-8.649359183	-8.34724333	-8.821581124	-8.500452901	-9.355069175	-8.869642347	-8.722932415	-9.029396931	-7.894592388	-9.011620577	-8.1458125
ENO2 | P09104 | IEEELGDEAR	-5.913758103	-6.223113046	-6.307867539	-6.483788245	-5.679296594	-5.846746122	-6.74628473	-6.634536373	-6.189508715	-6.464007714	-5.800057795	-6.049787838	-5.860002704
F2 | P00734 | YTAC[+57]ETAR	-9.141032303	-8.48805606	-9.352012586	-8.353491409	-8.650194318	-9.278028841	-8.847663657	-9.283762771	-7.692819299	-9.321543163	-9.127220535	-8.551931236	-8.267737801
F2 | P00734 | TATSEYQTFFNPR	-6.605590092	-6.410081922	-7.392074412	-6.42447932	-6.551839972	-6.874619002	-6.810237901	-7.048397638	-5.227393509	-7.23792045	-6.851107155	-6.684211749	-5.825709305
GAPDH | P04406 | AAFNSGK	-9.659637143	-8.869377769	-9.139906334	-8.939172963	-8.464889062	-7.818750728	-9.33554655	-9.717417185	-9.173561248	-10.00297909	-7.98268879	-8.653515894	-8.434093226
GAPDH | P04406 | YDNSLK	-11.61442139	-10.96016259	-11.38751395	-11.15659881	-11.65771797	-10.73032224	-12.05222197	-12.05222197	-11.26339706	-12.24312376	-10.19109948	-11.14996324	-10.98399298
GDA | Q9Y2T3 | DHLLGVSDSGK	-9.374149236	-8.488015249	-9.584450788	-9.147453877	-8.798803653	-8.882007094	-9.816482111	-9.664479018	-8.896382607	-9.462162084	-8.633395091	-9.098089512	-8.640050873
GOT1 | P17174 | VGNLTVVGK	-7.734609798	-7.355468379	-7.874034351	-7.578417322	-7.69251931	-7.498289157	-8.53068822	-8.452685708	-8.098461046	-7.947689117	-6.786399994	-8.051610399	-7.127952548
GOT1 | P17174 | IGADFLAR	-9.767633851	-9.40966825	-9.864078447	-9.699917432	-9.72441346	-9.770301383	-10.39674065	-10.39674065	-9.853844414	-9.966928579	-8.77292207	-9.827014094	-9.445988959
GSN | P06396 | AGALNSNDAFVLK	-4.069775359	-3.89411974	-4.421077909	-3.833238347	-3.925744637	-4.193001395	-4.465566022	-4.35663163	-3.818142782	-4.258907199	-3.760557478	-4.393021341	-3.603115754
HBA1 | P69905 | FLASVSTVLTSK	-6.530794654	-6.477608792	-5.55649616	-9.072503167	-7.932216563	-7.417342339	-9.352744397	-9.820523359	-4.530108015	-8.390366167	-0.039199958	-3.759771704	-1.625992454
HBA1 | P69905 | VGAHAGEYGAEALER	-6.023765707	-6.397899445	-5.167892625	-10.88136314	-7.520659645	-7.461310746	-15.52993999	-16.52993999	-4.13450115	-9.225609768	0.296282496	-3.432726983	-1.406201919
HBB | P68871 | VNVDEVGGEALGR	-6.042242349	-6.244447899	-5.01809936	-10.93935592	-7.563565116	-7.300466252	-9.765747375	-10.9881362	-3.95391902	-8.712542668	0.541276736	-3.23500477	-1.101163882
KNG1 | P01042 | EGDC[+57]PVQSGK	-9.239944487	-9.705462701	-10.07782412	-9.098700622	-10.13464757	-9.592650969	-9.2785178	-10.20451722	-8.285058791	-9.910942008	-10.87475566	-9.894079625	-8.823088383
KNG1 | P01042 | QVVAGLNFR	1.692636707	0.882584266	0.408103724	1.218308194	0.96328012	1.254710099	1.368433457	0.96045967	2.561803514	0.805668783	0.252651024	0.472454016	1.790378969
KNG1 | P01042 | VQVVAGK	-4.973544494	-5.314878276	-5.758666488	-4.847265449	-5.312256728	-5.280604739	-5.096834529	-5.498932972	-3.771680037	-5.767066674	-6.152733766	-5.804704361	-4.871078372
L1CAM | P32004 | GGLSFNLK	-4.765659587	-4.883721638	-4.936159653	-5.104729756	-5.005365701	-5.071827982	-5.101390504	-4.891697945	-4.753096748	-5.264399744	-4.753357059	-4.699400036	-4.865718203
LAMP1 | P11279 | VWVQAFK	-8.232546333	-8.333701329	-8.788828817	-8.357233679	-8.130252156	-8.19076822	-8.794890006	-8.89442568	-8.303618027	-8.612176753	-8.15731017	-8.643578901	-8.00676026
LAMP2 | P13473 | YLDFVFAVK	-7.744528429	-7.833809157	-8.779966999	-8.625349943	-8.169298318	-8.169068313	-8.589226151	-8.289665869	-7.676180477	-8.694309813	-7.859792714	-8.213359038	-7.628774983
LDHB | P07195 | FIIPQIVK	-9.085192024	-8.441906288	-9.009835894	-8.671763783	-9.091863171	-8.804571879	-9.601129374	-9.437630642	-8.914366712	-9.19645573	-7.987454395	-9.097957581	-8.459237042
LDHC | P07864 | VIGSGC[+57]NLDSAR	-9.286846851	-8.978040791	-9.16546465	-8.508543376	-9.751955035	-8.665841981	-9.932614926	-9.821583614	-9.753975591	-9.562921163	-8.106757162	-9.130633267	-8.40848856
MDH1 | P40925 | GEFVTTVQQR	-7.865092606	-7.14003039	-7.855690581	-7.353766361	-7.494721537	-7.548161829	-8.503981092	-8.081748092	-7.552663522	-7.924008394	-6.73504435	-7.881948006	-7.149548911
NCAM1 | P13591 | GLGEISAASEFK	-5.973249119	-5.293852053	-6.070556434	-5.613016506	-5.973444771	-5.718110629	-6.53912698	-6.292066392	-5.844443724	-5.888825984	-5.240785364	-5.734838955	-5.262659677
NPTX2 | P47972 | VAELEDEK	-9.348342755	-9.100912662	-9.684543625	-9.409193384	-8.559787146	-8.799699763	-9.503045524	-8.753023777	-8.607086807	-9.025968751	-9.508110439	-9.35439733	-9.035112544
NPTXR | O95502 | ELDVLQGR	-2.585540785	-2.209696002	-2.678307251	-2.401047513	-2.355846069	-2.033752099	-2.63244563	-2.472811735	-1.901581281	-2.341186224	-2.316327771	-2.475243893	-1.986386241
NRXN1 | P58400 | LAIGFSTVQK	-7.267439528	-7.019761449	-7.553286635	-7.345789465	-7.145870947	-7.29752302	-7.942065821	-7.605782433	-7.143522068	-7.07748139	-6.660417607	-7.196512449	-6.78668452
OGN | P20774 | LEGNPIVLGK	-6.499752974	-6.744477156	-6.84297004	-6.512582547	-6.760649235	-6.35033381	-7.178315714	-6.732059484	-6.214541341	-6.893687797	-6.508907082	-7.0234032	-6.532064868
OMG | P23515 | LESLPAHLPR	-4.031752848	-3.741734313	-4.461165962	-4.045568217	-3.693715871	-3.957728246	-4.222713602	-4.141587899	-3.998488299	-4.118779865	-3.793513331	-3.957232956	-3.522956302
PARK7 | Q99497 | ALVILAK	-8.333825581	-7.951220181	-8.622261312	-8.303076353	-8.713221385	-8.270258401	-9.173073385	-9.051082861	-9.113911357	-8.909845317	-7.714550243	-8.603427215	-8.030310791
PEBP1 | P30086 | GNDISSGTVLSDYVGSGPPK	-5.367591705	-4.732675563	-5.339071351	-4.968057659	-5.441587108	-4.941944866	-6.113125753	-5.484492781	-5.512165551	-5.346883857	-4.207679612	-5.371224086	-4.763042823
PEBP1 | P30086 | LYEQLSGK	-7.906841302	-7.117702468	-7.617595378	-7.421649496	-7.657437109	-7.318212228	-8.130645553	-8.272001402	-8.199192208	-8.072561988	-6.694994746	-7.917733478	-7.259804896
PEBP1 | P30086 | VLTPTQVK	-6.623871671	-6.145178895	-6.746093711	-6.469102826	-6.777454834	-6.381279136	-7.519263357	-7.03574612	-7.023588563	-6.770401063	-5.655349401	-6.807667961	-6.270296033
PGLYRP2 | Q96PD5 | TFTLLDPK	-4.726695121	-4.523083951	-5.099862201	-4.352870254	-4.530145655	-4.903112727	-4.920017646	-5.137703065	-3.637722364	-5.048205169	-5.229895869	-4.813726579	-4.220392195
PKM | P14618 | VVEVGSK	-7.460149848	-6.853780647	-7.221624865	-7.134884425	-7.486855658	-7.147453272	-8.315183673	-8.150124427	-7.633207472	-7.605039281	-6.199347237	-7.430427983	-6.846783833
PKM | P14618 | GVNLPGAAVDLPAVSEK	-7.060551556	-6.375741858	-6.910538718	-6.699495509	-7.098083154	-6.91067224	-8.225572278	-7.8536035	-7.36554073	-7.283342007	-5.916380023	-7.090678695	-6.47475987
PKM | P14618 | GDLGIEIPAEK	-7.901303683	-7.240380163	-7.872884056	-7.50211275	-7.820140626	-7.686985879	-8.739334681	-8.512563819	-7.998895032	-8.087784865	-6.773576257	-7.884281104	-7.301032591
PKM | P14618 | GDYPLEAVR	-6.309111064	-5.82413253	-6.564824743	-6.05784091	-6.248081959	-6.181093547	-7.324579884	-6.940793319	-6.782840698	-6.55959774	-5.227720614	-6.408664858	-5.875613225
PKMisoform | NA | LFEELVR	-3.557839517	-3.064477178	-3.709985794	-3.344308138	-3.546097299	-3.479316164	-4.505531966	-4.329078922	-3.921161153	-3.856125804	-2.573882725	-3.723950798	-3.181613637
PON1 | P27169 | LLIGTVFHK	-7.510994211	-8.065997471	-9.221399041	-7.661325178	-7.841828686	-7.944501599	-7.783596925	-8.258162788	-6.361366152	-8.626265489	-8.714169696	-8.58201	-7.25241295
PPIA | P62937 | VSFELFADK	-8.890184016	-8.257657518	-8.982822599	-8.813035847	-8.94068197	-8.62821618	-9.737339064	-9.216506901	-9.52255997	-8.975769162	-7.80453475	-9.109008487	-8.275608557
PRDX2 | P32119 | QITVNDLPVGR	-4.860925592	-4.644136152	-4.952874907	-5.505843556	-4.14773875	-5.14361501	-5.364325048	-5.005664402	-4.283387558	-5.108533189	-2.233705567	-4.399697816	-3.267377054
PTPRZ1 | P23471 | AIDGVESVSR	-6.520887014	-6.295863948	-6.679094114	-6.42005466	-6.443051555	-6.639955594	-6.99447179	-7.028419122	-6.325922437	-6.672741941	-6.170339319	-6.66571873	-6.102060641
PTPRZ1 | P23471 | DIEEGAIVNPGR	-7.652072699	-7.20181454	-7.606935953	-7.398614861	-7.435614855	-7.356353474	-7.959739833	-7.866630428	-7.294590811	-7.573683361	-6.893767461	-7.439319238	-7.039901532
SCG2 | P13521 | IESQTDEEVR	-8.261376524	-7.07735042	-7.923950687	-7.742549627	-8.076178607	-7.260794964	-8.301603037	-7.766109213	-7.713319797	-7.386543256	-6.895654175	-7.988884259	-6.743277502
SCG2 | P13521 | SGQLGLQEEDLR	-9.728337044	-9.026723053	-9.699455492	-9.394006848	-9.839592554	-9.130558358	-9.968062541	-9.682660323	-9.288833328	-9.510481551	-8.821461133	-9.59273384	-8.548471145
SMOC1 | Q9H4F8 | AQALEQAK	-7.31055804	-6.368649745	-7.170723114	-6.66020675	-7.0749911	-6.677320653	-7.755734376	-7.259058408	-6.969688162	-7.56273603	-6.155803375	-6.911244499	-6.484294655
SOD1 | P00441 | AVC[+57]VLK	-1.294196821	-1.444975255	-2.321604512	-1.909559019	-1.993930636	-1.370131796	-2.064958143	-2.003472387	-2.267924557	-1.641602204	-1.32945842	-2.173177035	-1.150357368
SOD1 | P00441 | GDGPVQGIINFEQK	-2.264188607	-2.25357925	-3.497613053	-2.62646683	-2.835583166	-2.647458363	-3.319688589	-2.987071731	-2.688001587	-2.646521613	-2.347870362	-3.192889973	-2.167987157
SOD1 | P00441 | HVGDLGNVTADK	-4.555152964	-4.494677652	-5.354100925	-4.740862748	-4.958339174	-4.827553966	-5.40332929	-5.217194061	-4.901743023	-4.745883611	-4.398223025	-5.357005676	-4.428414896
SPP1 | P10451 | GDSVVYGLR	-2.900397747	-2.87988463	-4.178184224	-4.076116278	-3.503639183	-3.906628727	-3.841922046	-3.320472694	-3.723212244	-3.555160925	-3.166322867	-3.77989738	-2.806460353
SPP1 | P10451 | YPDAVATWLNPDPSQK	-1.525218925	-1.354020604	-2.234870837	-2.102254551	-1.633006314	-1.861505478	-2.364451042	-2.309057408	-1.851917416	-2.187307645	-1.50740181	-2.330234174	-1.741868786
SPP1 | P10451 | QETLPSK	0.96745127	1.24379814	0.036060598	0.131057131	0.548153732	0.678827442	0.167015809	0.300547793	0.646239721	0.115720592	0.815995736	0.22887879	0.905402812
THY1 | P04216 | HVLFGTVGVPEHTYR	-4.898775044	-4.599659593	-5.184310676	-5.113207402	-4.69658488	-4.528420712	-4.808719461	-4.751139481	-4.471239684	-4.510756421	-4.07065392	-4.891267325	-4.12943508
TPI1 | P60174 | IAVAAQNC[+57]YK	-10.73965683	-10.49495732	-10.71023386	-9.985698581	-10.09607872	-9.858437545	-11.02364175	-10.43867925	-11.07078327	-11.0488754	-9.730930132	-10.04113303	-9.619400203
VGF | O15240 | EPVAGDAVPGPK	-6.249465175	-5.206012056	-6.220402111	-5.753969775	-5.957694245	-5.410885604	-6.326492277	-5.827776282	-5.746189084	-5.370025488	-5.214938228	-5.749794566	-4.777656604
VGF | O15240 | GLQEAAEER	-8.720957449	-7.675436876	-8.687198252	-8.17586246	-8.275672239	-7.901195772	-8.800218246	-8.275951677	-8.176902567	-7.880512626	-7.71220944	-8.383959034	-7.35535689
VTN | P04004 | GQYC[+57]YELDEK	-5.402777591	-5.874608166	-6.159567073	-5.51413698	-5.90699312	-5.681176251	-5.573976443	-5.976347531	-4.489210663	-6.006209057	-6.167613386	-6.16468581	-5.180395778
VTN | P04004 | DVWGIEGPIDAAFTR	-2.834158863	-3.454114898	-4.006815451	-3.197652479	-3.404590881	-3.425154438	-3.043397357	-3.514667934	-2.062304365	-3.580023169	-3.969032268	-3.78825803	-2.893879202
YWHAB | P31946 | NLLSVAYK	-6.948148775	-6.479587677	-7.179107241	-6.684996618	-6.746599173	-7.055030903	-7.690031092	-8.127094898	-7.230096627	-7.315918413	-5.882604734	-7.004666105	-6.384374265
YWHAB | P31946 | VISSIEQK	-7.798495051	-7.323450455	-7.838689166	-7.576369378	-7.658484131	-7.955753723	-8.440558452	-8.667968949	-8.097640611	-8.0192457	-6.896446042	-7.936512192	-7.21298989
YWHAG | P61981 | YLAEVATGEK	-9.431037047	-8.81155623	-9.730584993	-9.509950194	-9.526853856	-9.745975281	-10.97049362	-10.680987	-10.02703129	-10.50014914	-8.667943567	-9.195265323	-9.077326045
YWHAZ | P63104 | VVSSIEQK	-6.401792687	-5.786732303	-6.362089978	-6.101360455	-6.330311299	-6.608308096	-7.094421264	-7.351329567	-7.087215854	-7.670676528	-5.368241665	-6.2786587	-5.927995151

Appendix Table 6.6: Correlation Values Between SRM and TMT-MS

Gene ID | Protein ID| Peptide Sequence	bicor	p
AHSG | P02765 | EHAVEGDC[+57]DFQLLK	0.7623983	1.14E-35
ALB | P02768 | LVNEVTEFAK	0.77247034	3.87E-37
ALB | P02768 | LVTDLTK	0.77556186	1.33E-37
ALDOA | P04075 | VLAAVYK	0.71463278	1.37E-29
APOA4 | P06727 | SLAPYAQDTQEK	0.78931886	9.04E-40
APOC1 | P02654 | QSELSAK	0.81232011	8.85E-44
APOC2 | P02655 | TAAQNLYEK	0.84048111	1.63E-49
APOE | P02649 | ELQAAQAR	0.6667207	1.25E-24
C9 | P02748 | TSNFNAAISLK	0.77327779	2.93E-37
C9 | P02748 | LSPIYNLVPVK	0.77415659	2.16E-37
CD44 | P16070 | TEAADLC[+57]K	0.33081839	5.40E-06
CD44 | P16070 | ALSIGFETC[+57]R	0.31900572	1.20E-05
CHI3L1 | P36222 | IASNTQSR	0.71941149	3.84E-30
CHI3L1 | P36222 | GNQWVGYDDQESVK	0.72160382	2.13E-30
CHI3L1 | P36222 | QLLLSAALSAGK	0.71404577	1.59E-29
CP | P00450 | EVGPTNADPVC[+57]LAK	0.69862608	7.98E-28
CP | P00450 | GEFYIGSK	0.70157352	3.85E-28
CST3 | P01034 | ASNDM[+16]YHSR	0.71430865	1.49E-29
DCN | P07585 | VDAASLK	0.34992095	1.37E-06
DDAH1 | O94760 | EFFVGLSK	0.48536443	4.36E-12
DKK3 | Q9UBP4 | DQDGEILLPR	0.64903925	5.04E-23
ENO1 | P06733 | IEEELGSK	0.41121196	8.90E-09
ENO1 | P06733 | LNVTEQEK	0.39346754	4.26E-08
ENO2 | P09104 | IEEELGDEAR	0.47383191	1.61E-11
F2 | P00734 | YTAC[+57]ETAR	0.66718198	1.13E-24
F2 | P00734 | TATSEYQTFFNPR	0.7185046	4.90E-30
GAPDH | P04406 | AAFNSGK	0.82854423	5.90E-47
GAPDH | P04406 | YDNSLK	0.8186034	5.68E-45
GDA | Q9Y2T3 | DHLLGVSDSGK	0.78616363	2.93E-39
GOT1 | P17174 | VGNLTVVGK	0.76070551	1.97E-35
GOT1 | P17174 | IGADFLAR	0.71338808	1.89E-29
GSN | P06396 | AGALNSNDAFVLK	0.32361528	8.84E-06
HBA1 | P69905 | FLASVSTVLTSK	0.83492507	2.68E-48
HBA1 | P69905 | VGAHAGEYGAEALER	0.76278902	1.00E-35
HBB | P68871 | VNVDEVGGEALGR	0.80742692	6.99E-43
KNG1 | P01042 | EGDC[+57]PVQSGK	0.75355351	1.93E-34
KNG1 | P01042 | QVVAGLNFR	0.8176424	8.71E-45
KNG1 | P01042 | VQVVAGK	0.79004004	6.89E-40
L1CAM | P32004 | GQLSFNLR	0.41209368	8.22E-09
LAMP1 | P11279 | VWVQAFK	0.38645987	7.72E-08
LAMP2 | P13473 | YLDFVFAVK	0.26890252	0.00025192
LDHB | P07195 | FIIPQIVK	0.58318093	7.04E-18
MDH1 | P40925 | GEFVTTVQQR	0.71399458	1.62E-29
NCAM1 | P13591 | GLGEISAASEFK	0.76507851	4.70E-36
NPTX2 | P47972 | VAELEDEK	0.82254472	9.61E-46
NPTXR | O95502 | ELDVLQGR	0.86521236	1.48E-55
NRXN1 | P58400 | LAIGFSTVQK	0.50862443	2.67E-13
OGN | P20774 | LEGNPIVLGK	0.2992511	4.27E-05
OMG | P23515 | LESLPAHLPR	0.70425667	1.97E-28
PARK7 | Q99497 | ALVILAK	0.68806487	1.01E-26
PEBP1 | P30086 | GNDISSGTVLSDYVGSGPPK	0.61326383	4.43E-20
PEBP1 | P30086 | LYEQLSGK	0.5461355	1.84E-15
PEBP1 | P30086 | VLTPTQVK	0.62020993	1.27E-20
PGLYRP2 | Q96PD5 | TFTLLDPK	0.75042625	5.11E-34
PKM | P14618 | VVEVGSK	0.79626334	6.31E-41
PKM | P14618 | GVNLPGAAVDLPAVSEK	0.81283689	7.09E-44
PKM | P14618 | GDLGIEIPAEK	0.7631657	8.84E-36
PKM | P14618 | GDYPLEAVR	0.74440429	3.20E-33
PON1 | P27169 | LLIGTVFHK	0.85372793	1.30E-52
PPIA | P62937 | VSFELFADK	0.42243149	3.15E-09
PRDX2 | P32119 | QITVNDLPVGR	0.5266618	2.63E-14
PTPRZ1 | P23471 | AIIDGVESVSR	0.59743528	6.82E-19
PTPRZ1 | P23471 | DIEEGAIVNPGR	0.55556383	4.76E-16
SCG2 | P13521 | IESQTQEEVR	0.83392878	4.38E-48
SCG2 | P13521 | SGQLGIQEEDLR	0.69455479	2.15E-27
SMOC1 | Q9H4F8 | AQALEQAK	0.60304712	2.63E-19
SOD1 | P00441 | AVC[+57]VLK	0.64804803	6.15E-23
SOD1 | P00441 | GDGPVQGIINFEQK	0.52708324	2.49E-14
SOD1 | P00441 | HVGDLGNVTADK	0.60438204	2.09E-19
SPP1 | P10451 | GDSVVYGLR	0.40604161	1.42E-08
SPP1 | P10451 | YPDAVATWLNPDPSQK	0.57766062	1.69E-17
SPP1 | P10451 | QETLPSK	0.53791195	5.78E-15
THY1 | P04216 | HVLFGTVGVPEHTYR	0.55672045	4.02E-16
TPI1 | P60174 | IAVAAQNC[+57]YK	0.36815258	3.42E-07
VGF | O15240 | EPVAGDAVPGPK	0.91564949	9.22E-73
VGF | O15240 | GLQEAAEER	0.89844556	6.87E-66
VTN | P04004 | GQYC[+57]YELDEK	0.73038636	1.88E-31
VTN | P04004 | DVWGIEGPIDAAFTR	0.79647096	5.82E-41
YWHAB | P31946 | NLLSVAYK	0.45898158	8.12E-11
YWHAB | P31946 | VISSIEQK	0.41491193	6.35E-09
YWHAG | P61981 | YLAEVATGEK	0.6193641	1.48E-20
YWHAZ | P63104 | VVSSIEQK	0.61819486	1.83E-20

Appendix Table 6.7: SRM Culled Protein List

Gene ID | Protein ID| Peptide Sequence	Short Name
AHSG | P02765 | EHAVEGDC[+57]DFQLLK	AHSG
ALB | P02768 | LVTDLTK	ALB
ALDOA | P04075 | VLAAVYK	ALDOA
APOA4 | P06727 | SLAPYAQDTQEK	APOA4
APOC1 | P02654 | QSELSAK	APOC1
APOC2 | P02655 | TAAQNLYEK	APOC2
APOE | P02649 | ELQAAQAR	APOE
C9 | P02748 | LSPIYNLVPVK	C9
CALM2 | P0DP24 | EAFSLFDK	CALM2
CD44 | P16070 | TEAADLC[+57]K	CD44
CHI3L1 | P36222 | GNQWVGYDDQESVK	CHI3L1
CP | P00450 | GEFYIGSK	CP
CST3 | P01034 | ASNDM[+16]YHSR	CST3
DCN | P07585 | VDAASLK	DCN
DDAH1 | O94760 | EFFVGLSK	DDAH1
DKK3 | Q9UBP4 | DQDGEILLPR	DKK3
ENO1 | P06733 | IEEELGSK	ENO1
ENO2 | P09104 | IEEELGDEAR	ENO2
F2 | P00734 | TATSEYQTFFNPR	F2
GAPDH | P04406 | AAFNSGK	GAPDH
GDA | Q9Y2T3 | DHLLGVSDSGK	GDA
GOT1 | P17174 | VGNLTVVGK	GOT1
GSN | P06396 | AGALNSNDAFVLK	GSN
HBA1 | P69905 | FLASVSTVLTSK	HBA1
HBB | P68871 | VNVDEVGGEALGR	HBB
KNG1 | P01042 | QVVAGLNFR	KNG1
L1CAM | P32004 | GQLSFNLR	L1CAM
LAMP1 | P11279 | VWVQAFK	LAMP1
LAMP2 | P13473 | YLDFVFAVK	LAMP2
LDHB | P07195 | FIIPQIVK	LDHB
LDHC | P07864 | VIGSGC[+57]NLDSAR	LDHC
MDH1 | P40925 | GEFVTTVQQR	MDH1
NCAM1 | P13591 | GLGEISAASEFK	NCAM1
NPTX2 | P47972 | VAELEDEK	NPTX2
NPTXR | O95502 | ELDVLQGR	NPTXR
NRXN1 | P58400 | LAIGFSTVQK	NRXN1
OGN | P20774 | LEGNPIVLGK	OGN
OMG | P23515 | LESLPAHLPR	OMG
PARK7 | Q99497 | ALVILAK	PARK7
PEBP1 | P30086 | VLTPTQVK	PEBP1
PGLYRP2 | Q96PD5 | TFTLLDPK	PGLYRP2
PKM | P14618 | GVNLPGAAVDLPAVSEK	PKM
PKMisoform | NA | LFEELVR	PKMisoform
PON1 | P27169 | LLIGTVFHK	PON1
PPIA | P62937 | VSFELFADK	PPIA
PRDX2 | P32119 | QITVNDLPVGR	PRDX2
PTPRZ1 | P23471 | AIIDGVESVSR	PTPRZ1
SCG2 | P13521 | IESQTQEEVR	SCG2
SMOC1 | Q9H4F8 | AQALEQAK	SMOC1
SOD1 | P00441 | AVC[+57]VLK	SOD1
SPP1 | P10451 | YPDAVATWLNPDPSQK	SPP1
THY1 | P04216 | HVLFGTVGVPEHTYR	THY1
TPI1 | P60174 | IAVAAQNC[+57]YK	TPI1
VGF | O15240 | EPVAGDAVPGPK	VGF
VTN | P04004 | DVWGIEGPIDAAFTR	VTN
YWHAB | P31946 | NLLSVAYK	YWHAB
YWHAG | P61981 | YLAEVATGEK	YWHAG
YWHAZ | P63104 | VVSSIEQK	YWHAZ

Appendix Table 6.8: SRM ANOVA Table

			ANOVA p -values with Tukey Adjustment						Difference (AD - CT)					
Gene ID | Protein ID| Peptide Sequence	F-Value	Pr(>F)	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA	AD-Cau vs AD-AA	CT-AA vs AD-AA	CT-Cau vs AD-AA	CT-AA vs AD-Cau	CT-Cau vs AD-Cau	CT-Cau vs CT-AA
AHSG | P02765 | EHAVEGDC[+57]DFQLLK	1.3396216	0.2628129	0.474086776	0.567944286	0.231890054	0.998878903	0.974327169	0.940159403	0.160646479	0.144026653	0.208064464	-0.016619826	0.047417985	0.064037811
ALB | P02768 | LVTDLTK	1.4734736	0.2231127	0.560749882	0.999833888	0.386011551	0.52910704	0.993836008	0.361096177	0.151464229	-0.008969364	0.181759163	-0.160433593	0.030294934	0.190728526
ALDOA | P04075 | VLAAVYK	10.174229	3.01E-06	0.017180245	0.05510928	0.891608328	1.06E-06	0.001827786	0.25670715	0.254410371	-0.218243155	-0.060023526	-0.472653526	-0.314433898	0.158219629
APOA4 | P06727 | SLAPYAQDTQEK	7.068182	0.0001573	0.001073693	0.682409995	0.001938129	0.043786257	0.99626835	0.06896345	0.487403173	0.142354234	0.459208662	-0.345048939	-0.028194511	0.316854428
APOC1 | P02654 | QSELSAK	4.7228839	0.0033382	0.023895768	0.604700618	0.005179218	0.383820323	0.971300003	0.169970479	0.32883891	0.141953217	0.379702922	-0.186885693	0.050864012	0.237749705
APOC2 | P02655 | TAAQNLYEK	4.0879524	0.0076726	0.055752971	0.220193185	0.005539559	0.92884694	0.883475114	0.530546559	0.355718941	0.268897924	0.458573753	-0.086821017	0.102854812	0.189675828
APOE | P02649 | ELQAAQAR	5.4560937	0.0012788	0.015879176	0.999320335	0.022145615	0.026818767	0.998585772	0.036804745	0.25881093	0.010664937	0.245113456	-0.248145993	-0.013697474	0.234448519
C9 | P02748 | LSPIYNLVPVK	0.3538492	0.7864062	0.797378492	0.991450105	0.999989941	0.928382144	0.815237848	0.993873772	0.110681286	0.035160214	0.003615085	-0.075521072	-0.107066201	-0.031545129
CALM2 | P0DP24 | EAFSLFDK	9.8850152	4.33E-06	0.008035563	0.13775141	0.923610412	2.09E-06	0.001020972	0.416682532	0.265238542	-0.177851995	-0.050690164	-0.443090538	-0.315928707	0.127161831
CD44 | P16070 | TEAADLC[+57]K	3.6944437	0.012848	0.044301701	0.955066897	0.896731038	0.012139633	0.215171448	0.627379969	0.172513572	-0.033772955	0.045092249	-0.206286527	-0.127421323	0.078865204
CHI3L1 | P36222 | GNQWVGYDDQESVK	16.294013	1.80E-09	0.035954989	0.000155743	0.631102228	4.93E-10	0.000842457	0.011343493	0.27185023	-0.430802889	-0.117652276	-0.702653119	-0.389502506	0.313150612
CP | P00450 | GEFYIGSK	0.5886242	0.6231626	0.553090124	0.943543602	0.878079104	0.880110799	0.938062504	0.998145304	0.135882844	0.057830795	0.075790988	-0.078052049	-0.060091856	0.017960193
CST3 | P01034 | ASNDM[+16]YHSR	6.2114283	0.0004776	0.001854471	0.999845797	0.108796562	0.003097524	0.490328835	0.141738964	0.320772007	0.006611731	0.195918623	-0.314160275	-0.124853383	0.189306892
DCN | P07585 | VDAASLK	0.8397242	0.4736246	0.641646728	0.999388245	0.628956628	0.727773387	0.999999999	0.71754541	-0.05695656	-0.005778465	-0.057018131	0.051178095	-6.16E-05	-0.051239666
DDAH1 | O94760 | EFFVGLSK	8.7911555	1.73E-05	0.030486889	0.076283343	0.98165867	4.93E-06	0.01070231	0.176587153	0.198120554	-0.172840243	-0.026491617	-0.370960797	-0.224612171	0.146348626
DKK3 | Q9UBP4 | DQDGEILLPR	4.1153167	0.0074023	0.018359658	0.94923062	0.065689771	0.087007876	0.957243976	0.233183281	0.276084605	0.05042026	0.228441757	-0.225664345	-0.047642847	0.178021497
ENO1 | P06733 | IEEELGSK	17.030119	7.64E-10	0.794881612	3.32E-06	0.000751516	6.49E-08	2.48E-05	0.543841784	0.069798944	-0.39360421	-0.291935805	-0.463403154	-0.361734749	0.101668405
ENO2 | P09104 | IEEELGDEAR	5.7336845	0.00089	0.53270156	0.040546901	0.570576895	0.000652094	0.048143582	0.503654161	0.097334969	-0.192713168	-0.091566684	-0.290048137	-0.188901654	0.101146484
F2 | P00734 | TATSEYQTFFNPR	0.1261265	0.9445471	0.94197397	0.999667166	0.99956457	0.967708979	0.967787788	0.999999851	0.064195398	0.011052583	0.011900774	-0.053142815	-0.052294624	0.000848191
GAPDH | P04406 | AAFNSGK	18.541109	1.34E-10	0.586856703	1.65E-05	9.17E-05	6.66E-08	4.39E-07	0.96662968	0.156500701	-0.597993413	-0.540178962	-0.754494114	-0.696679663	0.057814451
GDA | Q9Y2T3 | DHLLGVSDSGK	14.390617	1.72E-08	0.00285772	0.012872102	0.884685982	4.63E-09	0.000207764	0.092110587	0.33830207	-0.294112343	-0.068828278	-0.632414413	-0.407130348	0.225284064
GOT1 | P17174 | VGNLTVVGK	8.5114058	2.46E-05	0.042023181	0.07647602	0.924504692	8.45E-06	0.007251447	0.276858489	0.245745412	-0.223849661	-0.05671559	-0.469595073	-0.302461002	0.167134071
GSN | P06396 | AGALNSNDAFVLK	3.6466483	0.0136775	0.066301657	0.884672384	0.929398722	0.010244588	0.243378466	0.54948093	0.181281559	-0.053412143	0.043753808	-0.234693703	-0.137527751	0.097165951
HBA1 | P69905 | FLASVSTVLTSK	1.8404758	0.1412143	0.688225108	0.99826558	0.237292623	0.597738457	0.876431725	0.185494127	-0.600484676	0.09224722	-1.010991307	0.692731896	-0.410506631	-1.103238527
HBB | P68871 | VNVDEVGGEALGR	2.32807	0.0759095	0.471441228	0.999654801	0.154500976	0.43019762	0.924425675	0.137614742	-0.974579116	0.066439448	-1.396414228	1.041018564	-0.421835112	-1.462853676
KNG1 | P01042 | QVVAGLNFR	0.5385811	0.6564125	0.820225454	0.99799112	0.877461765	0.733563444	0.999148893	0.799653101	-0.113986756	0.023313687	-0.096423811	0.137300443	0.017562945	-0.119737498
L1CAM | P32004 | GQLSFNLR	0.093145	0.9637523	0.999912402	0.985270534	0.998071967	0.992183337	0.995469588	0.954191413	0.003282144	0.018388678	-0.009084311	0.015106534	-0.012366455	-0.027472989
LAMP1 | P11279 | VWVQAFK	5.3514801	0.0014662	0.132341239	0.234292876	0.987903909	0.000534872	0.253359955	0.125649981	0.158505253	-0.137629474	0.023387568	-0.296134728	-0.135117686	0.161017042
LAMP2 | P13473 | YLDFVFAVK	2.3746803	0.0714969	0.345176041	0.841812692	0.709686326	0.072737613	0.928418795	0.245171595	0.138832849	-0.068927313	0.087620352	-0.207760162	-0.051212497	0.156547665
LDHB | P07195 | FIIPQIVK	10.870453	1.26E-06	0.102383459	0.024141047	0.088702791	5.98E-06	4.59E-05	0.950273544	0.189724271	-0.236247714	-0.191794518	-0.425971985	-0.381518788	0.044453197
LDHC | P07864 | VIGSGC[+57]NLDSAR	26.440708	2.38E-14	0.313834644	2.04E-05	8.98E-08	7.92E-09	1.31E-11	0.728779159	0.182827987	-0.507006002	-0.617322064	-0.689833989	-0.800150051	-0.110316062
MDH1 | P40925 | GEFVTTVQQR	17.570267	4.09E-10	0.052687709	0.000269633	0.022401892	2.28E-09	1.25E-06	0.550298699	0.207863584	-0.336972635	-0.229624758	-0.544836219	-0.437488342	0.107347877
NCAM1 | P13591 | GLGEISAASEFK	9.6567936	5.77E-06	0.000205891	0.999998366	0.004881501	0.000306986	0.800774727	0.006464913	0.369088176	0.001441961	0.289622508	-0.367646214	-0.079465667	0.288180547
NPTX2 | P47972 | VAELEDEK	14.320392	1.87E-08	0.002246385	3.24E-05	1.28E-08	0.718761312	0.052388836	0.4364647	0.318446168	0.41332353	0.546955533	0.094877361	0.228509364	0.133632003
NPTXR | O95502 | ELDVLQGR	11.374712	6.74E-07	0.002975649	0.009208332	1.77E-07	0.986983258	0.138725346	0.063263917	0.289343027	0.261256179	0.467467578	-0.028086848	0.178124551	0.206211399
NRXN1 | P58400 | LAIGFSTVQK	4.3790295	0.0052388	0.012728391	0.873131688	0.038550944	0.108061632	0.973889804	0.239546117	0.293541207	0.072319195	0.252659369	-0.221222011	-0.040881838	0.180340174
OGN | P20774 | LEGNPIVLGK	1.3252112	0.2674555	0.971176757	0.82314577	0.511753895	0.57672992	0.27948397	0.960333897	0.029861415	-0.05847352	-0.092052756	-0.088334935	-0.121914171	-0.033579236
OMG | P23515 | LESLPAHLPR	7.1426892	0.0001428	0.011393561	0.999947435	0.003000718	0.016066064	0.985147457	0.00457736	0.278102215	0.00470359	0.309589204	-0.273398625	0.031486989	0.304885614
PARK7 | Q99497 | ALVILAK	15.790007	3.26E-09	0.443539456	0.000865847	0.000183232	2.36E-06	3.21E-07	0.987579629	0.121302854	-0.314064558	-0.340988963	-0.435367412	-0.462291818	-0.026924406
PEBP1 | P30086 | VLTPTQVK	8.8334042	1.64E-05	0.031720403	0.085660362	0.88176623	6.56E-06	0.003547763	0.358837809	0.213046555	-0.183073685	-0.05599928	-0.396120241	-0.269045835	0.127074406
PGLYRP2 | Q96PD5 | TFTLLDPK	6.5011868	0.0003278	0.000324031	0.049125468	0.00481251	0.443481747	0.858830524	0.886566143	0.495458115	0.312335988	0.400024045	-0.183122127	-0.09543407	0.087688057
PKM | P14618 | GVNLPGAAVDLPAVSEK	16.384755	1.62E-09	0.008241931	0.002054457	0.27652835	1.29E-09	9.04E-06	0.254039124	0.293431272	-0.331099983	-0.1616406	-0.624531255	-0.455071872	0.169459383
PKMisoform | NA | LFEELVR	12.429408	1.84E-07	0.083047304	0.00453063	0.146173467	3.09E-07	8.00E-05	0.568463751	0.202033174	-0.2877427	-0.177769226	-0.489775874	-0.379802399	0.109973475
PON1 | P27169 | LLIGTVFHK	0.0470855	0.9864194	0.995886864	0.989097202	0.987424468	0.999762047	0.999651238	0.999999578	0.033217628	0.046251968	0.047803852	0.013034339	0.014586224	0.001551884
PPIA | P62937 | VSFELFADK	13.936988	2.96E-08	0.79090781	0.000348451	0.000302146	1.05E-05	8.52E-06	0.999991365	0.068196327	-0.302190515	-0.300057591	-0.370386842	-0.368253918	0.002132924
PRDX2 | P32119 | QITVNDLPVGR	0.2401885	0.8682331	0.984968071	0.998648294	0.965758153	0.997463739	0.849693359	0.927358961	0.05207842	0.023039908	-0.068259202	-0.029038511	-0.120337621	-0.09129911
PTPRZ1 | P23471 | AIIDGVESVSR	9.1786459	1.06E-05	0.001394099	0.797703029	0.05013076	5.40E-05	0.639316624	0.003861135	0.27026657	-0.066060796	0.18441715	-0.336327366	-0.085849421	0.250477945
SCG2 | P13521 | IESQTQEEVR	11.717683	4.42E-07	0.004065574	0.00067309	1.78E-07	0.960908419	0.114335644	0.301663141	0.410032442	0.469947613	0.679866002	0.059915171	0.26983356	0.209918389
SMOC1 | Q9H4F8 | AQALEQAK	26.504979	2.23E-14	0.000487828	8.39E-05	0.02751479	7.22E-14	1.01E-09	0.338657408	0.385011458	-0.42690301	-0.265408394	-0.811914468	-0.650419852	0.161494616
SOD1 | P00441 | AVC[+57]VLK	1.7527405	0.1576797	0.259590964	0.999981904	0.547333631	0.259684358	0.952128706	0.541228261	0.173750354	-0.003490753	0.123521778	-0.177241106	-0.050228576	0.12701253
SPP1 | P10451 | YPDAVATWLNPDPSQK	21.003884	8.38E-12	0.54333901	7.93E-07	0.000164722	1.54E-09	6.23E-07	0.59529202	0.089618866	-0.368560908	-0.284034592	-0.458179774	-0.373653457	0.084526317
THY1 | P04216 | HVLFGTVGVPEHTYR	3.8131617	0.0109981	0.091339153	0.099771975	0.008541983	0.999980942	0.852359194	0.834136911	0.252454514	0.248334327	0.339405098	-0.004120187	0.086950584	0.091070771
TPI1 | P60174 | IAVAAQNC[+57]YK	5.8046053	0.0008114	0.359068399	0.139351895	0.322584487	0.001479566	0.006205254	0.964821241	0.188801899	-0.248347978	-0.193554437	-0.437149877	-0.382356336	0.054793541
VGF | O15240 | EPVAGDAVPGPK	13.011929	9.05E-08	0.000872829	5.51E-05	8.59E-08	0.906086836	0.207849997	0.582304446	0.521596368	0.61468769	0.787116551	0.093091322	0.265520183	0.172428861
VTN | P04004 | DVWGIEGPIDAAFTR	0.5773351	0.6305721	0.844691371	0.59135582	0.787885212	0.973640038	0.999682221	0.986612724	0.101776386	0.155920235	0.113738851	0.054143849	0.011962465	-0.042181384
YWHAB | P31946 | NLLSVAYK	45.256124	3.85E-22	0.100491254	2.03E-11	2.21E-09	0	0	0.79209038	0.185016851	-0.59697659	-0.522458644	-0.781993441	-0.707475495	0.074517946
YWHAG | P61981 | YLAEVATGEK	41.4635	1.11E-20	0.001947683	2.20E-09	3.03E-05	0	1.41E-13	0.197143145	0.334380251	-0.606854618	-0.423812263	-0.941234869	-0.758192513	0.183042355
YWHAZ | P63104 | VVSSIEQK	39.610775	5.97E-20	0.023466511	5.36E-09	1.88E-07	0	0	0.869276264	0.268051883	-0.60246889	-0.530498223	-0.870520774	-0.798550106	0.071970668

Appendix Table 6.9: ROC-AUC Analysis Table

	AUC			P Value			AUC 95% Confidence Interval (CI)			Accuracy			Sensitivity			Specificity		
Gene ID | Protein ID| Peptide Sequence	Cau ADvsCT	AA ADvsCT	ADvsCT	Cau ADvsCT	AA ADvsCT	ADvsCT	Cau ADvsCT	AA ADvsCT	ADvsCT	Cau ADvsCT	AA ADvsCT	ADvsCT	Cau ADvsCT	AA ADvsCT	ADvsCT	Cau ADvsCT	AA ADvsCT	ADvsCT
AHSG | P02765 | EHAVEGDC[+57]DFQLLK	51.74%	58.41%	45.95%	0.617745687	0.076453495	0.164582231	0.4-0.6349	0.4686-0.6995	0.3782-0.5408	0.567	0.622	0.518	0.681	0.902	0.98	0.46	0.319	0.052
ALB | P02768 | LVTDLTK	49.15%	49.90%	48.70%	0.444029899	0.494326325	0.376979717	0.3751-0.6079	0.3811-0.6168	0.4052-0.5687	0.526	0.582	0.533	0.574	0.804	0.949	0.48	0.34	0.113
ALDOA | P04075 | VLAAVYK	71.11%	66.37%	66.79%	0.000173953	0.002655286	2.57E-05	0.6052-0.817	0.555-0.7725	0.5924-0.7434	0.711	0.653	0.631	0.532	0.804	0.439	0.88	0.489	0.825
APOA4 | P06727 | SLAPYAQDTQEK	55.02%	56.70%	47.75%	0.198172405	0.127605798	0.29396845	0.4332-0.6672	0.4505-0.6834	0.3961-0.5589	0.608	0.602	0.508	0.638	0.647	0.408	0.58	0.553	0.608
APOC1 | P02654 | QSELSAK	51.49%	57.82%	54.33%	0.601122951	0.091794971	0.148168722	0.3974-0.6323	0.4638-0.6926	0.4619-0.6248	0.577	0.582	0.559	0.532	0.667	0.469	0.62	0.489	0.649
APOC2 | P02655 | TAAQNLYEK	53.36%	59.91%	57.68%	0.2854767	0.045961561	0.032059364	0.4171-0.6501	0.4846-0.7136	0.4964-0.6572	0.577	0.602	0.585	0.383	0.569	0.5	0.76	0.638	0.67
APOE | P02649 | ELQAAQAR	49.79%	48.52%	50.19%	0.487043435	0.601024933	0.482287941	0.3816-0.6141	0.3693-0.6011	0.4203-0.5835	0.526	0.551	0.533	0.617	0.961	0.827	0.44	0.106	0.237
C9 | P02748 | LSPIYNLVPVK	58%	51.98%	52.54%	0.087954609	0.36910549	0.270814996	0.4633-0.6967	0.4035-0.6362	0.4438-0.6069	0.639	0.571	0.554	0.362	0.843	0.337	0.9	0.277	0.773
CALM2 | P0DP24 | EAFSLFDK	71.45%	64.96%	66.26%	0.000139267	0.005451587	4.39E-05	0.6096-0.8193	0.5373-0.7619	0.5866-0.7387	0.722	0.673	0.636	0.596	0.725	0.745	0.84	0.617	0.526
CD44 | P16070 | TEAADLC[+57]K	65.74%	48.02%	56.15%	0.003824131	0.36910549	0.068988653	0.5464-0.7685	0.3596-0.6008	0.4806-0.6424	0.649	0.592	0.574	0.468	0.902	0.898	0.82	0.255	0.247
CHI3L1 | P36222 | GNQWVGYDDQESVK	71.40%	75.80%	72.39%	0.000143218	5.55E-06	3.35E-08	0.6121-0.816	0.66-0.8561	0.6526-0.7951	0.68	0.735	0.692	0.511	0.627	0.714	0.84	0.851	0.67
CP | P00450 | GEFYIGSK	54.17%	51.69%	50.47%	0.240779168	0.388034514	0.545964324	0.4257-0.6577	0.3974-0.6364	0.4225-0.587	0.557	0.612	0.559	0.638	0.863	0.857	0.48	0.34	0.258
CST3 | P01034 | ASNDM[+16]YHSR	57.06%	50.73%	51.75%	0.116111384	0.550925694	0.33723835	0.4549-0.6864	0.3883-0.6263	0.4359-0.599	0.588	0.582	0.544	0.553	0.725	0.704	0.62	0.426	0.381
DCN | P07585 | VDAASLK	49.02%	52.19%	49.42%	0.567350796	0.646872408	0.556005755	0.3726-0.6078	0.4035-0.6403	0.4125-0.5759	0.577	0.612	0.528	0.255	0.745	0.551	0.88	0.468	0.505
DDAH1 | O94760 | EFFVGLSK	69.70%	63.41%	65.72%	0.000421113	0.011224766	7.52E-05	0.5899-0.8041	0.5222-0.7461	0.5803-0.7341	0.68	0.633	0.636	0.681	0.784	0.663	0.68	0.468	0.608
DKK3 | Q9UBP4 | DQDGEILLPR	54.47%	48.69%	49.72%	0.225326295	0.412762212	0.5278198	0.4274-0.6619	0.3687-0.605	0.4155-0.5788	0.598	0.571	0.528	0.383	0.745	0.602	0.8	0.383	0.454
ENO1 | P06733 | IEEELGSK	75.96%	78.06%	76.38%	5.42E-06	8.82E-07	9.85E-11	0.6631-0.8561	0.6893-0.8718	0.6977-0.8299	0.732	0.735	0.708	0.532	0.725	0.684	0.92	0.745	0.732
ENO2 | P09104 | IEEELGDEAR	64.98%	67.29%	65.20%	0.005585823	0.001619945	0.000123233	0.5379-0.7617	0.5631-0.7827	0.5748-0.7292	0.66	0.673	0.631	0.596	0.745	0.52	0.72	0.596	0.742
F2 | P00734 | TATSEYQTFFNPR	55.23%	51.23%	51.42%	0.188278068	0.418308379	0.366424179	0.436-0.6687	0.3946-0.63	0.4326-0.5958	0.588	0.561	0.544	0.553	0.804	0.816	0.62	0.298	0.268
GAPDH | P04406 | AAFNSGK	79.91%	77.14%	78.25%	1.98E-07	1.90E-06	4.79E-12	0.712-0.8863	0.6768-0.866	0.7187-0.8462	0.732	0.724	0.718	0.596	0.745	0.735	0.86	0.702	0.701
GDA | Q9Y2T3 | DHLLGVSDSGK	73.23%	72.38%	69.82%	4.11E-05	6.90E-05	8.76E-07	0.629-0.8357	0.6199-0.8277	0.6244-0.772	0.701	0.724	0.677	0.723	0.784	0.816	0.68	0.66	0.536
GOT1 | P17174 | VGNLTVVGK	70.34%	65.71%	66.05%	0.000283626	0.00375	5.41E-05	0.595-0.8118	0.5451-0.769	0.5842-0.7368	0.711	0.673	0.641	0.489	0.765	0.765	0.92	0.574	0.515
GSN | P06396 | AGALNSNDAFVLK	62.13%	51.98%	55.82%	0.020004905	0.36910549	0.080434512	0.5083-0.7343	0.4023-0.6373	0.4773-0.6391	0.619	0.582	0.559	0.745	0.941	0.622	0.5	0.191	0.495
HBA1 | P69905 | FLASVSTVLTSK	54.72%	50.06%	52.71%	0.212540245	0.505673675	0.256719262	0.4305-0.664	0.3836-0.6176	0.4455-0.6088	0.588	0.571	0.549	0.404	1	0.48	0.76	0.106	0.619
HBB | P68871 | VNVDEVGGEALGR	53.62%	50.06%	52.35%	0.270944614	0.505673675	0.286149571	0.4185-0.6539	0.3837-0.6175	0.4417-0.6052	0.588	0.551	0.549	0.404	0.647	0.561	0.76	0.447	0.536
KNG1 | P01042 | QVVAGLNFR	51.02%	51.73%	50.04%	0.570187641	0.385312834	0.504555928	0.3927-0.6277	0.3997-0.6349	0.4185-0.5823	0.577	0.571	0.538	0.66	0.902	0.643	0.5	0.213	0.433
L1CAM | P32004 | GQLSFNLR	52.09%	49.94%	51.30%	0.363133858	0.497163091	0.623983822	0.4036-0.6381	0.3825-0.6163	0.4313-0.5948	0.577	0.541	0.549	0.362	0.51	0.5	0.78	0.574	0.598
LAMP1 | P11279 | VWVQAFK	62.38%	60.03%	59.57%	0.017998634	0.043941449	0.010494997	0.5107-0.737	0.4857-0.715	0.5162-0.6752	0.629	0.612	0.585	0.532	0.667	0.592	0.72	0.553	0.577
LAMP2 | P13473 | YLDFVFAVK	54.98%	54.03%	46.29%	0.200187522	0.247407982	0.185843017	0.4333-0.6663	0.4228-0.6577	0.3816-0.5443	0.577	0.592	0.518	0.596	0.843	1	0.56	0.319	0.031
LDHB | P07195 | FIIPQIVK	75.19%	67.08%	70.85%	9.79E-06	0.001816098	2.47E-07	0.6531-0.8507	0.5608-0.7809	0.636-0.781	0.722	0.684	0.687	0.638	0.745	0.765	0.8	0.617	0.608
LDHC | P07864 | VIGSGC[+57]NLDSAR	86.72%	73.51%	80.63%	2.39E-10	3.12E-05	7.40E-14	0.7952-0.9393	0.6319-0.8383	0.7445-0.8682	0.814	0.724	0.754	0.851	0.882	0.735	0.78	0.553	0.773
MDH1 | P40925 | GEFVTTVQQR	77.28%	76.39%	75.37%	1.89E-06	3.49E-06	4.68E-10	0.6777-0.8679	0.6669-0.8608	0.6863-0.8211	0.763	0.714	0.692	0.66	0.686	0.612	0.86	0.745	0.773
NCAM1 | P13591 | GLGEISAASEFK	56.34%	52.23%	51.85%	0.141873696	0.649511282	0.328018842	0.4471-0.6797	0.4045-0.6402	0.437-0.6	0.588	0.582	0.533	0.596	0.804	0.541	0.58	0.34	0.526
NPTX2 | P47972 | VAELEDEK	63.32%	76.28%	69.73%	0.012042705	3.79E-06	9.69E-07	0.5216-0.7448	0.6657-0.8599	0.6235-0.7712	0.629	0.765	0.672	0.617	0.765	0.531	0.64	0.766	0.814
NPTXR | O95502 | ELDVLQGR	61.62%	68.21%	65.19%	0.024590091	0.000966116	0.000124461	0.5029-0.7295	0.5747-0.7895	0.575-0.7288	0.619	0.663	0.626	0.745	0.863	0.714	0.5	0.447	0.536
NRXN1 | P58400 | LAIGFSTVQK	53.70%	51.98%	50.55%	0.266183941	0.36910549	0.448006873	0.4197-0.6543	0.4028-0.6369	0.4237-0.5872	0.588	0.571	0.538	0.447	0.784	0.49	0.72	0.34	0.588
OGN | P20774 | LEGNPIVLGK	60.38%	53.40%	56.76%	0.039400019	0.282306899	0.051491516	0.491-0.7166	0.4178-0.6502	0.487-0.6483	0.588	0.561	0.574	0.511	0.451	0.449	0.66	0.681	0.701
OMG | P23515 | LESLPAHLPR	50.34%	51.81%	50.79%	0.478412474	0.622817883	0.425019432	0.3862-0.6206	0.4005-0.6358	0.4261-0.5897	0.577	0.582	0.549	0.191	0.647	0.684	0.94	0.511	0.412
PARK7 | Q99497 | ALVILAK	82.09%	69.96%	76.40%	2.68E-08	0.000338011	9.53E-11	0.7359-0.9058	0.5939-0.8054	0.6971-0.831	0.784	0.704	0.708	0.745	0.863	0.847	0.82	0.532	0.567
PEBP1 | P30086 | VLTPTQVK	69.15%	66.92%	66.03%	0.000587891	0.001988311	5.52E-05	0.5834-0.7996	0.5584-0.7799	0.5841-0.7366	0.711	0.673	0.631	0.553	0.706	0.735	0.86	0.638	0.526
PGLYRP2 | Q96PD5 | TFTLLDPK	57.02%	62.08%	53.65%	0.117528197	0.019933784	0.189602939	0.4546-0.6858	0.5091-0.7325	0.455-0.618	0.608	0.602	0.564	0.66	0.373	0.224	0.56	0.851	0.907
PKM | P14618 | GVNLPGAAVDLPAVSEK	75.49%	73.34%	72.24%	7.79E-06	3.52E-05	4.08E-08	0.6547-0.8551	0.6319-0.835	0.6515-0.7933	0.753	0.714	0.667	0.532	0.843	0.694	0.96	0.574	0.639
PKMisoform | NA | LFEELVR	74.21%	72.38%	71.94%	2.03E-05	6.90E-05	6.03E-08	0.6386-0.8456	0.6206-0.827	0.6477-0.7912	0.732	0.714	0.677	0.702	0.941	0.755	0.76	0.468	0.598
PON1 | P27169 | LLIGTVFHK	51.66%	54.23%	51.48%	0.612227182	0.236309352	0.361183389	0.3997-0.6335	0.4251-0.6596	0.4331-0.5965	0.546	0.592	0.549	0.681	0.667	0.847	0.42	0.511	0.247
PPIA | P62937 | VSFELFADK	76.89%	72.92%	74.94%	2.58E-06	4.73E-05	8.94E-10	0.6707-0.8672	0.6275-0.831	0.6809-0.818	0.773	0.724	0.713	0.617	0.725	0.704	0.92	0.723	0.722
PRDX2 | P32119 | QITVNDLPVGR	59.70%	47.02%	55.14%	0.05027467	0.695675132	0.107537037	0.4813-0.7128	0.3528-0.5875	0.4701-0.6328	0.639	0.571	0.574	0.404	0.922	0.857	0.86	0.191	0.289
PTPRZ1 | P23471 | AIIDGVESVSR	57.53%	56.74%	44.83%	0.101321865	0.12612675	0.106600997	0.4599-0.6908	0.4503-0.6845	0.3672-0.5295	0.598	0.633	0.513	0.532	0.843	0.49	0.66	0.404	0.536
SCG2 | P13521 | IESQTQEEVR	63.06%	71.71%	67.82%	0.013467676	0.000108742	8.62E-06	0.5171-0.7442	0.6155-0.8188	0.6029-0.7535	0.67	0.684	0.656	0.447	0.843	0.541	0.88	0.511	0.773
SMOC1 | Q9H4F8 | AQALEQAK	82.55%	76.18%	77.60%	1.71E-08	4.12E-06	1.39E-11	0.7421-0.909	0.666-0.8576	0.7113-0.8408	0.773	0.724	0.733	0.83	0.686	0.694	0.72	0.766	0.773
SOD1 | P00441 | AVC[+57]VLK	53.53%	54.19%	52.46%	0.275747394	0.238506909	0.2767295	0.4179-0.6527	0.4244-0.6595	0.4431-0.6062	0.588	0.602	0.559	0.553	0.608	0.429	0.62	0.596	0.691
SPP1 | P10451 | YPDAVATWLNPDPSQK	77.49%	81.10%	79.29%	1.58E-06	5.86E-08	8.08E-13	0.6825-0.8673	0.7243-0.8978	0.7307-0.855	0.732	0.745	0.738	0.681	0.627	0.643	0.78	0.872	0.835
THY1 | P04216 | HVLFGTVGVPEHTYR	45.02%	62.62%	59.28%	0.200188296	0.015874236	0.012639801	0.3339-0.5666	0.5145-0.7379	0.513-0.6725	0.546	0.643	0.579	0.064	0.882	0.745	1	0.383	0.412
TPI1 | P60174 | IAVAAQNC[+57]YK	72%	61.03%	65.82%	9.64E-05	0.030235754	6.79E-05	0.6165-0.8235	0.4984-0.7223	0.5816-0.7348	0.711	0.592	0.641	0.745	0.412	0.622	0.68	0.787	0.66
VGF | O15240 | EPVAGDAVPGPK	60.30%	75.93%	68.43%	0.040644587	5.03E-06	4.39E-06	0.4887-0.7173	0.6634-0.8552	0.6093-0.7593	0.629	0.714	0.662	0.404	0.745	0.541	0.84	0.681	0.784
VTN | P04004 | DVWGIEGPIDAAFTR	51.91%	55.94%	52.38%	0.628710215	0.156300024	0.283565408	0.4022-0.6361	0.4439-0.675	0.4421-0.6055	0.557	0.592	0.564	0.702	0.765	0.765	0.42	0.404	0.361
YWHAB | P31946 | NLLSVAYK	89.32%	86.65%	87.82%	1.31E-11	2.14E-10	3.68E-20	0.8308-0.9556	0.7912-0.9418	0.8304-0.926	0.825	0.827	0.821	0.66	0.824	0.837	0.98	0.83	0.804
YWHAG | P61981 | YLAEVATGEK	88.38%	84.02%	84.98%	3.82E-11	3.40E-09	1.63E-17	0.8155-0.9521	0.7586-0.9218	0.7966-0.903	0.814	0.806	0.81	0.872	0.765	0.816	0.76	0.851	0.804
YWHAZ | P63104 | VVSSIEQK	90.21%	82.94%	85.94%	4.62E-12	1.01E-08	2.20E-18	0.8434-0.9608	0.743-0.9157	0.8077-0.911	0.825	0.796	0.8	0.915	0.843	0.776	0.74	0.745	0.825