Chemical Tools for Studying O-GlcNAc Glycosylation at the Systems Level

Thesis by

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For my family

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ABSTRACT

The addition of O-linked β-N-acetylglucosamine (O-GlcNAc) to intracellular serine and threonine residues is a ubiquitous post-translational modification (PTM) found in all higher eukaryotes. Like other PTMs, it is finely regulated in response to stimuli and dysregulated in multiple diseases. However, unlike other PTMs, methods to detect and profile the dynamics of O-GlcNAc glycosylation are still in their infancy. Herein, we discuss the background, development, and application of new chemical tools that have allowed for some of the first systems-level investigations of O-GlcNAcylation in different cells, organ systems, and disease states. We also significantly advance established techniques for the detection and monitoring of O-GlcNAc on proteins of interest. Using these new techniques, we first uncover a novel O-GlcNAcylation site on Cdk5 and show that this site can dynamically regulate Cdk5 activity in the context of neurodegenerative disease. Next, we apply novel chemical, mass spectrometric, and computational tools to, for the first time, uncover cellular networks engaged by O-GlcNAcylation in vivo. Finally, we undertake the systematic optimization of mass spectrometry based O-GlcNAcomics and use these new insights to significantly advance our understanding of O-GlcNAcylation dynamics in metabolic diseases of the liver. Overall, the techniques developed and data generated herein are closing the methodological and intellectual gaps between the study of O-GlcNAc glycosylation and that of other PTMs.

PUBLISHED CONTENT AND CONTRIBUTIONS

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Adapted for **Fig. 3.5** with permission from the Royal Society of Chemistry.

TABLE OF CONTENTS

LIST OF FIGURES AND TABLES

NOMENCLATURE

245AAA	T245A/T246A/S247A
46AA	S46A/S47A
Ablim	actin-binding LIM proteins
ACN	acetonitrile
AD	Alzheimer's disease
Add	adducin
AGC	automatic gain control
AKAP	A-kinase-anchoring proteins
AMPAR	α-amino-3-hydroxy-5-methyl-4-isoxazolepropionic acid receptor
ANKRD17	ankyrin repeat domain-containing protein 17
APP	amyloid precursor protein
ASH2L	Set1/Ash2 histone methyltransferase complex subunit ASH2
ASXL3	putative polycomb group protein ASXL3
Aβ	amyloid β
B	basic
BAP1	ubiquitin carboxyl-terminal hydrolase BAP1
BEMAD	β-elimination followed by Michael addition with dithiothreitol
Bhmt	Betaine--homocysteine S-methyltransferase 1
biotin-PC	photocleavable biotin tag
BP	biological process
BTTAA	2-(4-((Bis((1-(tert-butyl)-1H-1,2,3-triazol-4-yl)methyl)amino)methyl)-1H-1,2,3-triazol-1-yl)acetic acid
BUB3	mitotic checkpoint protein BUB3
CaMK	calcium-calmodulin dependent kinase
CARM1	histone-arginine methyltransferase CARM1
CD	charge-dependent
Cdk5	cyclin-dependent kinase 5
Ces3b	carboxylesterase 3B
ChREBP	carbohydrate responsive element binding protein
CID	collision-induced dissociation
cKO	conditional KO
CPEC	chemical/enzymatic photochemical cleavage
Cre	Cre recombinase
CREB	cyclic AMP-responsive element-binding protein
Creld2	protein disulfide isomerase CRELD2

CRTC2	CREB-regulated transcription coactivator 2
CTD110.6	O-GlcNAc antibody raised against the C-terminal domain of RNA polymerase II
Ctsf	cathespin F
CuAAC	copper-catalyzed azide-alkyne cycloaddition
Cyfip2	C-terminal domain of cytoplasmic FMR1-interacting protein 2
db/db	leptin receptor KO
DDB1	DNA damage-binding protein 1
Dde	1-(4,4-dimethyl-2,6-dioxocyclohex-1-ylidene)ethyl
ddH2O	doubly deionized H2O
DIV	days in vitro
Dlg1	disks large homolog 1
Dmpt	N,N’-dimethylpyrimidinetrione
DPY30	protein dpy-30 homolog
DTT	dithiothreitol
EDTA	ethylenediaminetetraacetic acid
Egfr	epidermal growth factor receptor
Elovl	elongation of very long chain fatty acid protein
Enah	protein enabled homolog
ER	endoplasmic reticulum
ETciD	ETD with collisional-induced dissociation
ETD	electron-transfer dissociation
EThcD	ETD with supplemental HCD activation
FAS	fatty acid synthase
Fmr1	synaptic functional regulator FMR1
fOGA	full-length OGA
FOXK1	forkhead box protein K1
FOXO1	forkhead box protein O1
GalNAz	N-azidoacetyl-D-galactosamine
GalT	β(1,4)-galactosyltransferase 1
GBD	GTPase protein binding
GFAT	glutamine:fructose-6-phosphate aminotransferase
GlcNAz	N-azidoacetylglucosamine
GNPNAT	glucosamine 6-phosphate N-acetyltransferase
GO	Gene Ontology
GPI	glucose-6-Phosphate isomerase
HBP	hexosamine biosynthesis pathway
HCD	higher-energy collisional dissociation
HCFC1	host cell factor 1

HEK	human embyonic kidney
HEPES	4-(2-hydroxyethyl)-1-piperazineethanesulfonic acid
HK	hexokinase
hnRNP	heterogeneous nuclear ribonucleoprotein
HpHRP	high pH reversed-phase
HPLC	high performance liquid chromatography
HSP	heat schok protein
IAA	iodoacetamide
IP	Immunoprecipitate
IR	insulin receptor
IsoTaG	isotope-targeted glycoproteomics
IT	Injection time
iTRAQ	isobaric tag for relative and absolute quantitation
KCNQ3	KQT member 3
KD	knockdown
KO	knocout
Kpna1	importin subunit alpha-5
LC	liquid chromatography
LTD	long-term depression
LTP	long-term potentiation
LXR-α	liver x receptor α
m/z	mass to charge
MAGUKs	membrane-associated guanylate kinases
MALDI-TOF	Matrix-assisted laser desorption/ionization time-of-flight
Manba	beta-mannosidase
MAPK	p38 mitogen-activated protein kinase
MeCP2	methyl CpG binding protein 2
MLL	mixed lineage leukemia
MOE	metabolic oligosaccharide engineering
mOGT	mitochondrial OGT
MS	mass spectrometry
mTOR	mammalian target of rapamycin
N2A	Neuro-2a
NAFLD	nonalcoholic fatty liver disease
Nckap1	Nck-associated protein 1
ncOGT	nucleocytoplasmic OGT
NFTs	neurofibrillary tangles
NMDAR	N-methyl-D-aspartate receptor
NOTISE	networking of O-GlcNAc transferase interactors and substrates

NR2A	NMDAR subunit 2A
NR2B	NMDAR subunit 2B
NSL	nonspecific lethal
NTSB	2-Nitro-5-(Sulfothio)-Benzoate
NUP153	nuclear pore complex protein Nup153
NUP62	nuclear pore glycoprotein p62
OGA	O-GlcNAcase
O-GlcNAc	O-linked β-*N*-acetylglucosamine
O-GlcNAcomics	O-GlcNAc proteomics
O-GlcNAcylation	O-GlcNAc glycosylation
OGT	O-GlcNAc transferase
OGT-FH	FLAG- and HA-tagged OGT
PBS	phosphate-buffered saline
PEG	poly(ethylene glycol)
PGC-1α	peroxisome proliferator activated receptor gamma coactivator 1 alpha
PGM3	phosphoglycerate mutase
PKA	protein kinase A
Plin	perilipin
PNGaseF	peptide:N-glycosidase F
Ppfia1	liprin-α1
PPI	protein-protein interaction
Ppt2	lysosomal thioesterase PPT2
PR-DUB	polycomb repressive deubiquitinase
PRMT5	protein arginine N-methyltransferase 5
PSD	postsynaptic density
PSM	peptide spectral match
PTM	post-translational modification
PUGNAc	O-(2-acetamido-2deoxy-D-glucopyranosylidene)amino-N-phenylcarbamate
QM	S46A/S47A and T245A/T246A/S247A
QUIC-Tag	quantitative isotopic and chemoenzymatic tagging
RBBP5	retinoblastoma-binding protein 5
Rbfox1	RNA binding protein fox-1 homolog 1
RL-2	O-GlcNAc antibody raised against pore complex-lamina fraction from rat liver nuclear envelopes
ROC	receptor-operated channels
ROS	reactive oxygen species
SA	supplemental activation
SDC	sodium deoxycholate

sDHB	super-DHB
SDM	site-directed mutagenesis
SDS-PAGE	sodium dodecyl sulfate polyacrylamide gel electrophoresis
SF1	splicing factor 1
SHANK	SH3 and multiple ankyrin repeat domains
SILAC	stable isotope labeling by amino acids in cell culture
SOC	store-operated channels
SOCE	store-operated calcium entry
sOGA	short OGA
sOGT	short OGT
SP1	transcription factor Sp1
SPS	synchronous precursor selection
SREBP1c	sterol regulatory element-binding protein 1c
SRSF5	serine/arginine-rich splicing factor 5
STIM1	stromal interaction molecule 1
SynGAP	synaptic Ras GTPase activating protein
T2DM	type 2 diabetes mellitus
TAMRA	5-carboxytetramethylrhodamine
tau	microtubule-associated protein tau
TCEP	Tris(2-carboxyethyl)phosphine
TEAB	triethylammonium bicarbonate buffer
TET2	ten-eleven-translocation 2
TFA	trifluoroacetic acid
TMG	thiamet G
TMT	tandem mass tag
TRAK	trafficking kinesin proteins
TRE	tetracycline-responsive element
Tris	tris(hydroxymethyl)aminomethane HCl
UAP1	UDP-N-acetylglucosamine pyrophosphorylase
UDP	uridine diphosphate
UDP-GalNAz	uridine 5’-diphospho-2-azidoacetylamino-2-deoxy-α-D-galactose
UDP-GlcNAc	uridine disphospho-N-acetylglucosamine
UDP-ketogal	uridine 5’-diphospho-2-acetonyl-2-deoxy-α-D-galactose
Ugta5	UDP-glucuronosyltransferase 1-5
VOC	voltage-operated channels
Wasf1	Wiskott-Aldrich syndrome protein family member 1
Wasl	neural Wiskott-Aldrich syndrome protein
WASP	Wiskott-Aldrich syndrome protein
WAVE1	WASP family verprolin homologous protein 1

WB	Western blotting
WDR5	WD repeat-containing protein 5
WGA	wheat-germ agglutinin
WNK1	serine/threonine-protein kinase WNK1
WRC	WAVE regulatory complexes
WT	wild-type
Y289L GalT	Y289L bovine β-1,4-galactosyltransferase 1
Ywhah	14-3-3 protein eta
τ	time constant

Chapter 1

The Role of O-GlcNAc Glycosylation in Neuronal Function and Metabolic Disease

1.1. Abstract.

The dynamic post-translational modification (PTM) O-linked β-*N*-acetyl glucosamine glycosylation (O-GlcNAcylation) is present on thousands of intracellular proteins. Similar to phosphorylation, O-GlcNAcylation is inducible and plays a myriad of functional roles in physiological and pathological processes. However, unlike phosphorylation, which is controlled by hundreds if not thousands of kinases and phosphatases, there are only two enzymes known to be responsible for O-GlcNAc cycling in higher eukaryotes, O-GlcNAc transferase (OGT) and O-GlcNAcase (OGA). This, along with the unique challenges of detecting this modification on proteins of interest, has provided a major challenge to understanding the functional roles of O-GlcNAc in biology. For instance, O-GlcNAc has long been hypothesized to serve as a metabolic sensor, yet a precise mechanism for how this occurs, and its implications, has yet to be firmly established. Accordingly, altered O-GlcNAcylation has been observed in metabolic diseases including type 2 diabetes mellitus (T2DM) and Alzheimer's (AD). Given the prevalence and alarming rise of these conditions, an explosion of research into the role of O-GlcNAc in these conditions has already begun. Here, we review the current understanding of the role of O-GlcNAc in metabolism and neuronal function. First, we discuss the role of O-GlcNAc in regulating glucose homeostasis and in responding to metabolic stimuli, with a particular focus on its role in the liver. Then, we explore the regulatory roles for O-GlcNAc in neurons and its role in neurodegenerative disease. Overall, it is becoming increasingly clear that, like phosphorylation, O-GlcNAcylation plays a major role in cell signaling and general protein function in both health and disease.

1.2. Introduction.

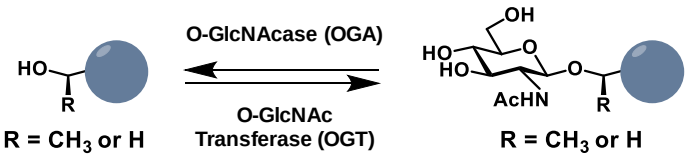

Fig. 1.1. O-GlcNAc Cycling by OGT and OGA

O-GlcNAcylation of serine or threonine residues is a dynamic, inducible PTM of intracellular proteins that regulates multiple physiological functions including insulin signaling,[1] transcription,[2] mitosis,[3] metabolism,[4] and neuronal homeostasis.[5] Unlike other forms of N- and O-glycosylation, which are often made up of extensive, intricately branching polymers, O-GlcNAcylation is never elaborated beyond the single GlcNAc monomer. To date, O-GlcNAcylation has been observed in all metazoans and over 1,000 O-GlcNAcylated proteins have been described in higher mammals and plants.[6,7]

Despite this incredible substrate diversity, there are only two enzymes known to be responsible for addition and removal of O-GlcNAc in mammals, OGT and OGA, respectively (**Fig. 1.1**).[6] Notably, OGT knockout (KO) is embryonically lethal in mice and is necessary for survival in dividing mammalian cells.[8,9] OGA KO is also perinatal lethal, although in rare cases mice survive to adulthood with profound metabolic abnormalities.[10-12] Given the widespread, critical, and specific regulatory nature of this modification, the fact that only two enzymes are responsible for its cycling suggests exquisite mechanisms for controlling the activity and targeting of these enzymes. Accordingly, dysregulation of O-GlcNAc cycling has been linked to numerous human diseases such as diabetes,[13] cancer,[14] and neurodegeneration.[15]

The *OGT* gene is located on the X-chromosome (Xq13.1 in humans) and is expressed as three distinct isoforms generated by alternative splicing: nucleocytoplasmic (ncOGT), mitochondrial (mOGT), and short (sOGT).[8,16 8,9] The three OGT isoforms are each composed of a conserved C-terminal catalytic domain and differ by the number of N-terminal tetratricopeptide

(TPR) repeats. OGA is encoded by *MGEA5* on chromosome 10 (10q23.1-23.4 in humans) and has two isoforms: full-length OGA (fOGA) and short (sOGA), which are predominantly localized to the cytosol and nucleus, respectively.[17-19] fOGA and sOGA differ by the presence or absence of a C-terminal histone acetyltransferase domain.[20] Crystal structures of both human OGT [21,22] and OGA [23-25] have been recently described, and insights into structure-function relationships have been reviewed elsewhere.[6,20,26-28]

Understanding the specifics of O-GlcNAc cycling on different substrates is key to understanding the overall functions of O-GlcNAc on a cellular and organismal scale. Moreover, it may lead to novel therapeutic interventions in human disease.[13,15] In higher mammals, O-GlcNAcylation and its cycling enzymes are most highly expressed in the pancreas and brain.[6,15] OGT activity was also shown to be 10-fold higher in the brain compared to other tissues,[29] and there have been thousands of O-GlcNAc sites identified on proteins intimately involved with neuronal function.[30-35] Importantly, there is also a strong association between aberrant O-GlcNAcylation and AD and other neurodegenerative diseases.[15] Thus, given the immense costs and rapidly increasing prevalence of AD, along with absence of disease-modifying treatments, understanding the function and regulation of O-GlcNAcylation in the brain is perhaps one of the most pressing issues in modern biomedical research.[36,37]

Within the brain, OGT and OGA expression exhibits temporal and spatial variability across substructures, with the highest levels occurring within the cortex, hippocampus, and cerebellum.[29,38-40] At the cellular level, OGT and OGA, along with O-GlcNAc, are highly enriched in the nuclear and synaptosomal fractions of neurons.[39,41,42] Interestingly, while O-GlcNAcylation and OGT are also enriched in the postsynaptic density (PSD), OGA is excluded.[43] Furthermore, O-GlcNAc and OGT/OGA expression have been observed in multiple types of excitatory and

inhibitory neurons as well as astrocytes, oligodendrocytes, and microglia.[40,44] Overall, the aforementioned observations have led to intense investigation of the role of O-GlcNAc in neuronal function, the results of which have recently been well-summarized previously.[12,45]

In some of the same studies, reporting aberrant O-GlcNAcylation in AD, alterations in O-GlcNAcylation were also found at earlier time points, including in individuals with mild cognitive impairment and T2DM.[46,47] O-GlcNAcylation has also been found to be elevated across multiple organ systems in T2DM, including peripheral fat tissue, muscle, liver, pancreas, and kidneys.[48-50] It has long been hypothesized that O-GlcNAc serves as a sensor for extracellular glucose concentrations and can direct intracellular response accordingly.[51] Importantly, elevated O-GlcNAcylation in response to hyperglycemia has been mechanistically linked to kidney, cardiac, and pancreatic complications of T2DM.[46,52-54] In the liver, increased O-GlcNAcylation has also been demonstrated to play a major role in maintaining organismal glucose homeostasis.[50] Moreover, T2DM has a strong epidemiological link with AD and other dementias,[55-58] and the changes in O-GlcNAcylation and associated dysfunction across organ systems seen with T2DM may potentially set the stage for the development of brain pathology.[15] Altogether, it is becoming increasingly clear that O-GlcNAcylation is intimately associated with cellular and organismal homeostasis and is likely a major player in the pathophysiology of metabolic and neurodegenerative diseases.

In spite of the wealth of information that has already been gathered on O-GlcNAcylation, many studies up to this point have almost exclusively taken a reductionist approach, trying to understand the role of O-GlcNAcylation on the function of a single protein[2] or exploring how modulating global O-GlcNAc levels affects a limited number of selected proteins or flux through a single signaling pathway.[42] However, unravelling exactly how O-GlcNAc cycling enzymes

recognize, discriminate, and act upon specific protein substrates in response to specific stimuli is critical to our understanding of the functions of O-GlcNAcylation in neurons, a task which has been largely ignored. For example, OGT has been shown to preferentially glycosylate neurofilament proteins in response to glucose deprivation; a preference arising from an increased affinity to p38 mitogen-activated protein kinase (MAPK).[59] Moreover, the observation that OGT interacts and participates in a functional complex with trafficking kinesin proteins (TRAKs) 1/2[60,61] led to the discovery that O-GlcNAcylation regulates mitochondrial motility in response to glucose availability in neurons.[62] In fact, it has been proposed that the interactions of OGT/OGA with various binding proteins, scaffolds, and lipids allow them to act specifically on coordinated groups of proteins to differentially respond to stimuli, known as the adaptor protein hypothesis.[27,63] Taken with the multitude of examples of a regulatory role for O-GlcNAcylation/OGT in multiprotein complexes, well-outlined in a recent review,[26] these data suggest that identifying and characterizing the dynamics of OGT/OGA interacting partners may provide critical insight into the functions of O-GlcNAc in neurons.

Herein, we will review the previous literature on the role of O-GlcNAcylation in metabolism and neuronal function, with a particular focus on the role of O-GlcNAcylation in maintaining glucose homeostasis in the liver and its role in neuronal signaling and neuroprotection. In the liver, we will outline the role of O-GlcNAcylation in insulin resistance, gluconeogenesis, and lipid metabolism. In neurons, we will discuss modulation of neuronal signaling, synaptic plasticity and cognition, neuroprotection, and neurodegenerative diseases as potential overarching functions of O-GlcNAc. Overall, the continued elucidation of the functional roles of O-GlcNAc in physiology and disease will undoubtedly lead to a deeper understanding across multiple fields of biology.

1.3. The Role of O-GlcNAc in Metabolic Homeostasis.

O-GlcNAc appears at the center of multiple metabolic signaling pathways as uridine disphospho-*N*-acetylglucosamine (UDP-GlcNAc), the end-product of the hexosamine biosynthesis pathway (HBP) serves as the high-energy donor substrate for OGT. The HBP (**Fig. 1.2**) integrates signals from amino acid, nucleotide, and fatty acid metabolism through multiple intermediates throughout the pathway. However, this pathway is primarily sensitive to extra- and intracellular glucose concentrations.[64] Interestingly, OGT has been shown to respond to changes in the levels of UDP-GlcNAc with changes in turnover rate and substrate specificity.[65] Taken together, it appears that O-GlcNAcylation is in a prime position to sense changes in glucose levels, and it has been postulated that the changes in O-GlcNAcylation also seen under varying levels of glucose represent the first steps towards restoring cellular homeostasis.[51] For example, modulating the levels of UDP-GlcNAc in a cell through inhibition of GFAT, the rate limiting step in the HBP, can prevent insulin resistance in the context of hyperglycemia.[66] Moreover, overexpression of GFAT can also directly lead to the development of insulin resistance in mice.[67] In both diabetic rats and multiple cells/tissues of humans with confirmed T2DM, there is an increase in O-GlcNAcylation concordant with insulin

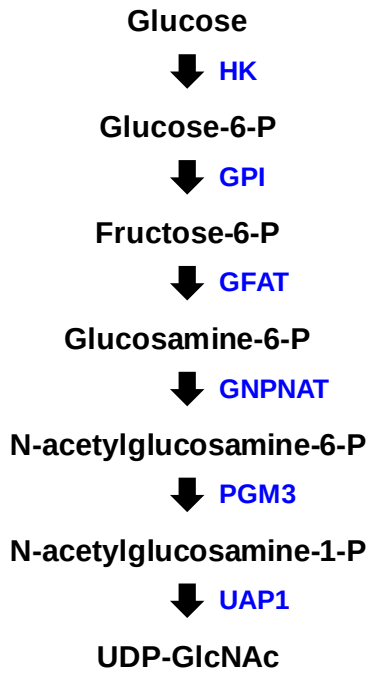

Fig. 1.2. The Hexosamine Biosynthesis Pathway.
HK: Hexokinase; GPI: Glucose-6-Phosphate isomerase; GFAT: Glutamine:fructose-6-phosphate aminotransferase; GNPNAT: Glucosamine 6-phosphate N-acetyltransferase; PGM3: Phosphoglycerate mutase; UAP1: UDP-N-acetylglucosamine pyrophosphorylase.

resistance.[49,53,68] Specifically, in the pancreas of rats and mice, elevated O-GlcNAcylation leads to a decrease of glucose-mediated secretion of insulin, which is a well-established feature of T2DM.[53,69] O-GlcNAcylation has also been directly implicated in insulin resistance in multiple cell types through its modification of multiple proteins in the insulin singling pathway, including the insulin receptor (IR) β subunit, IR substrate 1, 3-phosphoinositide-dependent protein kinase-1, protein kinase B, and phosphoinositide 3-kinase.[1]

O-GlcNAcylation has also been observed to impact lipid metabolism on multiple levels.[70] In adipocytes and skeletal myocytes, increased O-GlcNAcylation has also been shown to lead to insulin resistance.[66,71,72] However, in adipocytes, there has been some controversy with later studies showing that increased O-GlcNAcylation does not promote insulin resistance,[73] nor does reduction of OGT prevent insulin resistance.[74] Clearly, there is a complicated relationship between cell and tissue type, O-GlcNAc, and insulin signaling. On the organismal level, increased O-GlcNAcylation in ArgP neurons of the hypothalamus can suppress the browning of white fat, which on its own (or through other mechanisms) ultimately leads to increased insulin resistance and susceptibility to diet-induced obesity.[75] Moreover, blocking O-GlcNAcylation in adipocytes has been shown to reduce the production of signaling molecules that induce hyperphagia in the context of high-fat diet and promote intrinsic lipolysis.[76,77] Taken together, the direct relationship between extracellular glucose concentrations and O-GlcNAcylation of intracellular proteins can have wide range and deleterious consequences in T2DM.

Finally, O-GlcNAcylation has also been shown to play a major role in mitochondrial energy metabolism of both lipids and carbohydrates. In fact, multiple mitochondrial proteins, including many proteins in the electron transport chain and enzymes in the tricarboxylic acid cycle, are regulated by O-GlcNAcylation.[78] This has a major impact on cardiac myocyte function in

diabetes and heart failure, with increased O-GlcNAcylation leading to decreases in electron transport, ATP generation, and contractility.[78-80] Systemic manipulation of global O-GlcNAcylation through OGA hemizygosity also regulates organismal energy metabolism through changes in mitochondrial function.[11,81] Specifically, elevated O-GlcNAcylation as a result of either genetic or chemical means led to a marked shift toward carbohydrate-dependent metabolism. However, interestingly, OGA hemizygous mice exhibited weight gain, increased fat accumulation, and insulin resistance[11] while thiamet G (TMG), a potent OGA inhibitor,[82] treated did not.[81] It is possible that these conflicting results are due to different compensatory mechanisms, such as an increase in OGA expression in the TMG treated mice,[81,83] but future research into the roles of O-GlcNAc in regulating cellular and organismal metabolism will be important for resolving these and other long standing questions in the field. In summary, O-GlcNAcylation plays multiple roles throughout different signaling pathways and organ systems to regulate metabolism, and its dysregulation can have dramatic consequences for both the initial pathogenesis and prolonged disease progression in T2DM and other metabolic diseases.

1.4. O-GlcNAcylation in the Liver Controls Systemic Energy Homeostasis.

Having outlined the role of O-GlcNAc in metabolism, the following section will discuss its roles specifically in the liver. The liver is a central player in carbohydrate, lipid, and amino acid metabolism, storing, releasing, and interconverting carbohydrates and lipids to respond to systemic nutrient availability. Dysregulation of liver carbohydrate and lipid metabolism is also a key feature in metabolic diseases such as T2DM, metabolic syndrome, and nonalcoholic fatty liver disease (NAFLD) and nonalcoholic steatohepatitis. Under normal circumstances, the liver takes up glucose from the blood to make glycogen in the fed state which it slowly breaks down and releases

to maintain blood sugar in the fasted state. As this glycogen reserve is exhausted, i.e. with prolonged fasting, the liver will produce glucose from other sources, such as those derived from lipid metabolism or amino acids. Similarly, when there is a prolonged excess of carbohydrate and amino acid levels, the liver converts these molecules into fatty acids and triglycerides, which are then exported to and stored in adipose tissue throughout the body. The liver typically undertakes these functions in response to hormonal signals from the pancreas (and to a lesser extent, other organs). Briefly, in response to rising glucose levels, the pancreas excretes insulin which promotes uptake of glucose and glycogen and fatty acid synthesis by the liver (conversely inhibiting gluconeogenesis). Conversely, in response to falling glucose levels, the pancreas produces glucagon, which stimulates gluconeogenesis and glycogenolysis. Thus, the liver is the major organ responsible for maintaining systemic glucose homeostasis.

As mentioned in the previous sections, altered O-GlcNAcylation plays a central role in regulating insulin signaling, and this is no different in the liver.[1] However, as the liver is the major site of gluconeogenesis for the organism, insulin resistance in the liver can be particularly problematic due to the continued synthesis and export of glucose in the fed state (a major cause of diabetic hyperglycemia).[84] Therefore, understanding the molecular underpinnings of insulin-resistant gluconeogenesis in the liver would undoubtedly have important implications for therapeutic intervention in T2DM. Given the role of O-GlcNAcylation in insulin resistance generally, it is perhaps not surprising then that it also plays a major role in regulating hepatic gluconeogenesis. For instance, increased O-GlcNAcylation of cyclic AMP-responsive element-binding protein (CREB)-regulated transcription coactivator 2 (CRTC2) in response to hyperglycemia results in its nuclear localization, enhanced promoter binding at gluconeogenic genes, and increased expression of gluconeogenic enzymes.[85] Interestingly, CRTC2 is O-

GlcNAcylated at two protein kinase A (PKA) phosphorylation sites, sites that are known to sequester CRTC2 in the cytoplasm by engaging 14-3-3 proteins.[86] Thus, in addition to its role in stimulating aberrant gluconeogenesis, CRTC2 O-GlcNAcylation also highlights an important general function of O-GlcNAc in blocking phosphorylation (as they often share the same residues).

In addition to CRTC2, a master regulator of gluconeogenic gene expression, peroxisome proliferator activated receptor gamma coactivator 1 alpha (PGC-1α) is also O-GlcNAcylated in response to hyperglycemia.[87] Here, O-GlcNAcylation facilitates the binding of ubiquitin carboxyl-terminal hydrolase BAP1 (BAP1), which stabilizes PGC-1α through its potent deubiquitinase activity. The modification of PGC-1α is also interesting in that it is mediated through host cell factor 1 (HCFC1), which targets OGT to O-GlcNAcylate PGC-1α.[87] This is perhaps one of the most striking examples of the adaptor protein hypothesis (discussed in more detail in **Chapters 4**, **5**, and **7**). In addition to the aforementioned examples, there are also numerous others showing that increased O-GlcNAcylation of transcription factors, e.g. forkhead box protein O1 (FOXO1) whose O-GlcNAcylation is dependent on the PGC-1α-OGT interaction,[88] receptors, e.g. IR-β,[1] and proteins across multiple signaling cascades paradoxically lead to increased liver gluconeogenesis in hyperglycemic conditions.[50] Finally, at the organismal level, multiple studies have shown that decreasing liver O-GlcNAcylation through OGT knockdown[87] or OGA overexpression[85] can lead to increased insulin sensitivity and an improved metabolic profile in diabetic mice. Interestingly, hepatic OGT KO also decreases glucagon sensitivity, preventing autophagy and the subsequent production of glucose and ketone bodies in response to starvation.[89] Altogether, the O-GlcNAcylation of hepatic proteins is a critical PTM for regulating the homeostatic functions of the liver in both the fed and fasting states.

In addition to its role in hepatic gluconeogenesis, O-GlcNAcylation events have also been demonstrated to regulate hepatic lipid metabolism. For example, multiple lipogenic transcription factors are also O-GlcNAcylated in the liver, including two central regulators of lipogenesis enzyme expression carbohydrate responsive element binding protein (ChREBP) and liver x receptor α (LXR-α).[50] Like with CRTC2, ChREBP O-GlcNAcylation facilitates its nuclear localization and subsequent expression of lipogenic genes.[90] LXR-α O-GlcNAcylation also increases its promoter activity and subsequent expression of sterol regulatory element-binding protein 1c (SREBP1c).[91] SREBP1c directly promotes fatty acid synthase (FAS) expression and de novo lipogenesis.[92] Interestingly, this positive regulation of lipogenesis by O-GlcNAcylation may represent a resolution to a long standing paradox in T2DM, metabolic syndrome, and NAFLD, namely, that the increased insulin resistance seen in these diseases should result in *decreased* lipogenesis (however, in all cases, lipogenesis in the liver is elevated which is, at the very least, partially responsible for the fatty liver pathology seen in these diseases).[93] Despite marked insulin resistance, lipogenesis proceeds unhindered in the liver due to the hyperglycemia-induced upregulation of O-GlcNAcylation on lipogenic transcription factors, receptors, and other signaling proteins.[50] This hypothesis also bears out at organismal level where OGT overexpression (presumably leading to markedly upregulated O-GlcNAcylation of proteins promoting lipogenesis) results in increased circulating lipids in mice.[1]

Overall, the regulation of hepatic metabolism and systemic energy homeostasis depends intimately on O-GlcNAc. In many cases, O-GlcNAc serves as a nutrient sensor to fine tune hepatic responses to extracellular glucose and lipids. However, in metabolic disease, aberrantly increased O-GlcNAcylation can lead to a host of deleterious effects likely including the paradoxical gluconeogenesis and lipogenesis seen in T2DM, metabolic syndrome, and NAFLD. Future

investigations into the role of O-GlcNAc in these and other disorders, including elucidating the full landscape of O-GlcNAcylated proteins and how it changes in response to disease state, are thus likely to reveal new avenues for therapeutic intervention.

1.5. Roles for O-GlcNAc in Neuronal Function and Neurodegeneration.

To date, thousands of O-GlcNAc-modified proteins have been identified in the mammalian brain,[33-35] and O-GlcNAc has been shown to regulate many important neuronal functions, such as activity-dependent gene expression, α-amino-3-hydroxy-5-methyl-4-isoxazolepropionic acid receptor (AMPAR) trafficking, calcium signaling, and metabolism.[94] Notably, the modification may also contribute to higher-order brain functions. For instance, manipulating global O-GlcNAcylation levels profoundly alters synaptic plasticity, as well as learning and memory in vivo.[5,40,42,43,95-97] Moreover, O-GlcNAc regulates the function of numerous proteins critical for learning and memory, including AMPAR subunit 2,[40] protein kinase A,[95] and cAMP response CREB.[2] Remarkably, mutation of only a single O-GlcNAcylation site on CREB increased its transcriptional activity and accelerated long-term memory consolidation in mice.[2]

In addition to its physiological roles in the brain, aberrant O-GlcNAcylation and OGT/OGA expression have been linked to several neurodegenerative disorders such as Alzheimer's, Huntington's, and Parkinson's disease.[5,12,15,98] For instance, global levels of O-GlcNAcylation and neuronal OGT are significantly decreased in AD brains.[5,99,100] Moreover, conditional genetic deletion of OGT in excitatory neurons of the mouse forebrain recapitulates many of the pathological and behavioral hallmarks of AD, including progressive neuronal loss, increased production of hyperphosphorylated microtubule-associated protein tau (tau) and amyloidogenic amyloid β peptides, macroscopic plaque and tangle formation, and memory loss.[5]

Globally increasing O-GlcNAcylation has also been demonstrated to limit cognitive decline and neuronal pathology in mouse models of neurodegeneration.[15,83,101-103] Overall, it is becoming increasingly clear that O-GlcNAcylation plays a pivotal role in neuronal health and function, and modulating O-GlcNAc signaling may represent a promising neuroprotective strategy for neurodegenerative diseases.[12,15]

1.5.1. Modulation of Neuronal Signaling.

Given that a major function of neurons is to integrate, respond to, and relay extracellular signals, it is perhaps not surprising that many studies have uncovered a functional role for O-GlcNAcylation in this area. The regulation of protein phosphorylation, the canonical mode of signal transduction in neurons,[104-106] by O-GlcNAc is a common theme, especially in regards to interplay at the site and protein level.[6,107,108] In fact, a major function of O-GlcNAcylation in neuronal signaling may simply be to oppose phosphorylation. For instance, Hart and coworkers have long advanced the idea that O-GlcNAcylation and phosphorylation exist in a yin-yang relationship,[6,107-109] and there are numerous examples of direct yin-yang relationships between phosphorylation and O-GlcNAcylation in regulating the function, binding, and activity of individual proteins.[99,110-115] Moreover, inhibition or activation of multiple kinases and phosphatases were shown to, in general, reciprocally modulate global O-GlcNAcylation (i.e. treatments that generally increased global phosphorylation reduced, and treatments decreasing phosphorylation increased, O-GlcNAcylation) in cultured mouse cerebellar neurons, with the most significant effects seen in the cytoskeletal associated fraction.[116] However, proteome-wide analyses of O-GlcNAcylation and phosphorylation have revealed a more complicated picture. In an analysis of proteins isolated from mouse cortical homogenate, only 24% of all mapped O-

GlcNAc sites were either within 10 amino acids of or themselves a known phosphorylation site.[33] In another study which isolated both O-GlcNAcylated and phosphorylated proteins from murine synaptosomes, O-GlcNAcylation and phosphorylation sites were not correlated (outside of both being more common in disordered regions), and less than 7% of all O-GlcNAc sites were also phosphorylation sites.[34] In an in vitro, peptide glycosylation assay, OGT also did not recognize the proline-directed kinase motif, PX(S/T)P, which makes up ~40% of all known phosphorylation sites.[117] However, the same study described a well-defined "interplay motif," (pS/pT)P(V/A/T)(gS/gT), where O-GlcNAcylation is strongly inhibited by phosphorylation. Overall, while the above data suggest that while direct competition for the same or close by serine/threonine residues is likely a minor phenomenon on the scale of the phosphoproteome, there is clearly a certain subset of O-GlcNAcylation/phosphorylation events that exist in a yin-yang relationship.

At the protein level, virtually all O-GlcNAcylated proteins are known to also be phosphorylated, and the subset of O-GlcNAcylated proteins are enriched for kinases as a class.[33-35] Globally increasing O-GlcNAcylation also increases the phosphorylation of synapsin extracellular signal-regulated kinase (ERK) 1/2 in hippocampal slices.[42] Thus, O-GlcNAc may be playing a more active role in regulating functional aspects of neuronal kinases and signaling cascades. To date, many kinases heavily implicated in learning and memory, such as calcium-calmodulin dependent kinase (CaMK) II,[46] CaMKIV,[113] and PKA[95] have been shown to be functionally regulated by O-GlcNAcylation. We have also found that O-GlcNAcylation and phosphorylation occur simultaneously in distinct locations on CREB, and interestingly, phosphorylated CREB is preferentially O-GlcNAcylated in response to neuronal activity.[2] Taken together, these data suggest that O-GlcNAcylation may be playing a broader role in coordinating

the activity of multiple kinases and their substrates in ways other than directly opposing phosphorylation.

Next, we discuss examples of how O-GlcNAcylation regulates, and is regulated by, calcium signaling, a major subset of the neuronal signally machinery and absolutely required for long-term potentiation (LTP) and memory formation.[118-120] In neurons, calcium levels are mediated by the flux of calcium into the cell primarily through voltage-operated channels (VOCs), and the release of calcium from intracellular stores mediated by receptor-operated channels (ROCs) and store-operated channels (SOCs). Major targets of calcium signaling include the CaMKs, a family of serine/threonine kinases expressed throughout the brain and are involved in neuronal excitability and plasticity.[121] This class of kinases is activated by increases in the cytosolic concentration of calcium, resulting in phosphorylation of their substrates and activation of downstream signaling events. Increasing evidence suggests an intimate relationship between CaMK-mediated calcium signaling and O-GlcNAcylation.

In neuroblastoma cells, potassium chloride-induced depolarization across the membrane results in an increase in the activity of OGT, leading to an increase in O-GlcNAcylation of protein substrates.[122] Interestingly, this effect could be prevented by inhibition of voltage-operated calcium channels, indicating that these effects on O-GlcNAcylation were mediated by calcium signaling pathways.[122] Furthermore, inhibition of CaMKs also abolished the previously observed increase in O-GlcNAcylation indicating that CaMKs are involved in regulating the activity of OGT.[122] Of the CaMKs, CaMKIV activity was found to upregulate phosphorylation of OGT upon depolarization of cells, resulting in an increase in OGT activity. While CaMKIV may regulate OGT activity, evidence indicating a role for OGT in regulating the activity of CaMKIV has also emerged. In cells, CaMKIV can be O-GlcNAcylated in the active site, an event which opposes its

phosphorylation and activation [113]. Importantly, O-GlcNAcylation of CaMKIV also impeded activation of downstream signaling events such as activation of CREB, highlighting OGT as a regulator of CaMKIV-mediated calcium signaling pathways.

Similar interplay between calcium signaling and O-GlcNAcylation may also exist along a CaMKII-mediated axis. In 2013, it was demonstrated that diabetic hyperglycemia induced O-GlcNAcylation of CaMKII in the heart and brain, resulting in chronic activation of CaMKII-dependent pathways. In cardiomyocytes, these effects contributed to dysfunctional spontaneous release of calcium from intracellular stores, contributing to arrhythmias. Importantly, these effects were rescued by inhibition of O-GlcNAcylation, suggesting a regulatory role for O-GlcNAc in CaMKII-mediated calcium signaling.[46] More recently, it was demonstrated that CaMKII phosphorylates OGT and that this modification has some influence on substrate-specificity of OGT.[89] While performed in liver cells, this study highlights the role of calcium-signaling as a means through which O-GlcNAcylation levels are regulated and CaMKII-mediated activation of OGT may be important in excitable cells, similar to that observed of CaMKIV-mediated activation. Together, the above studies highlight a delicate interplay which is present in calcium-mediated and OGT-mediated signaling pathways and suggest there may exist feed-back mechanisms; however, future studies will be needed to probe CaMKII-OGT and CaMKIV-OGT regulatory axes in order to further explore these mechanisms.

A role for O-GlcNAcylation in regulating store-operated calcium signaling was highlighted by early studies demonstrating that increases in hexosamine biosynthesis pathway flux and increases in O-GlcNAc levels by treatment with extracellular glucosamine dampened store-operated calcium entry (SOCE) in excitable cells, such as cardiomyocytes.[123] Furthermore, the metabolic state of the cell exerts dramatic effects on SOCE; for example, hyperglycemia was found

to dampen SOCE and that concomitant inhibition of the hexosamine biosynthesis pathway by azaserine (a potent inhibitor of GFAT) restored SOCE.[123]

Recent studies aimed at identifying mechanisms through which O-GlcNAcylation may be mediating these effects have focused on the ER-membrane protein and calcium sensor stromal interaction molecule 1 (STIM1). Upon depletion of calcium stores in the ER, STIM1 adopts an extended, active conformation.[124-127] Active STIM1 oligomerizes and translocates to pre-existing endoplasmic reticulum (ER)-plasma membrane junctions,[128,129] leading to recruitment of ORAI1 and activation of SOCE.[127,130] These STIM1-ORAI1 complexes mediate calcium-selective influx of ions into the cell. Importantly, the O-GlcNAcylation of STIM1 was found to inhibit STIM1 mediated SOCE. O-GlcNAcylation may play a protective role in calcium signaling based on the findings that acute increases in O-GlcNAc levels prevent Ca overload induced by the calcium paradox characteristic of ischemia and reperfusion injuries [131].

1.5.2. Synaptic Plasticity and Cognition.

Having highlighted some examples of how O-GlcNAcylation may be involved in regulating neuronal signaling cascades, we next turn to the discussion of O-GlcNAc's roles in higher-order neuronal functions. We start on the synaptic level with the emerging role of O-GlcNAcylation in regulating AMPAR trafficking. We then move to the role of O-GlcNAcylation in LTP and long-term depression (LTD) of excitatory synapses, beyond its role in regulating AMPAR trafficking, the likely cellular correlates of memory formation and maintenance. Finally, we review the first evidence that site specific O-GlcNAcylation can influence memory formation and recall in vivo and discuss the other examples of how changes in global O-GlcNAcylation can affect behavior.

AMPAR are ligand-gated (glutamate) cation channels responsible for the majority of excitatory neurotransmission in the mammalian brain.[132] Moreover, they are intimately connected to learning and memory as their dynamic insertion into and removal from the postsynaptic membrane (trafficking) is thought to be the major means by which neurons potentiate or depress individual synapses.[132,133] Thus, the interesting observation by Vosseller and coworkers that inhibiting OGA/OGT enhanced/inhibited LTP (discussed further below),[42] strongly suggested that global modulation of O-GlcNAc levels likely has a strong effect on AMPAR trafficking. Shortly after the aforementioned observation, Din et al. hypothesized that O-GlcNAc may oppose known, functionally relevant phosphorylation events on AMPAR subunits GluA1 and GluA2 to maintain LTD and LTP respectively.[134] Thereafter, Kanno et al. reported that treatment with the OGT inhibitor alloxan resulted in the increased insertion of both GluA1 and GluA2 into the plasma membrane.[135] Another study reported that GluA2, but not GluA1, was O-GlcNAc modified, and that this modification was independent of S880 phosphorylation by PKC, a well-established mediator of AMPAR internalization.[40] Finally, culturing embryonic cortical neurons harvested from floxed-OGT mice[9] allowed Huganir and colleagues to assess the role of O-GlcNAcylation on AMPAR trafficking during synapse formation and development.[43] Interestingly, they found that conditional KO (cKO) of OGT, via transduction with Cre recombinase, decreased the synaptic expression of the GluA2 and GluA3, but not the GluA1 AMPAR subunits.[43]

Overall, these results clearly suggest a role for O-GlcNAc in the regulation of AMPAR trafficking, perhaps through the direct modification of GluA2, but we have yet to develop a mechanistic understanding of how this might occur. It will be interesting to see whether more sensitive techniques will be able to identify, map, and quantify the dynamics of individual AMPAR subunit O-GlcNAcylation. This information will facilitate the establishment of a casual role of

AMPAR O-GlcNAcylation in regulating trafficking by revealing how O-GlcNAcylation changes at individual sites in response to physiologically relevant stimuli and allowing for the investigation of the effects of expressing glycosylation-deficient AMPAR subunits. Alternatively, it is also possible that O-GlcNAcylation of AMPARs themselves is not responsible for the differences observed in AMPAR trafficking after global changes in O-GlcNAcylation. In fact, several large-scale proteomics studies of O-GlcNAcylated proteins isolated from mouse and human brains revealed multiple PDZ-domain-containing scaffold proteins, SH3 and multiple ankyrin repeat domains (SHANK) 1/2/3, multiple members of the membrane-associated guanylate kinases (MAGUKs), and synaptic Ras GTPase activating protein (SynGAP) 1, are O-GlcNAcylated.[30,33-35,136] PDZ-domain containing scaffolding proteins are known to regulate trafficking and clustering of AMPAR and play a pivotal role in organizing the postsynaptic density and its signaling machinery (also necessary for AMPAR trafficking).[137]

Thus, perhaps it is not altered AMPAR O-GlcNAcylation itself that is mediating the differences in trafficking outlined above, but rather altered synaptic organization (and hence AMPAR trafficking and clustering[132,137]) caused by gross perturbations in the O-GlcNAcylation state of many organizational and scaffolding proteins. This might at least partially explain the somewhat conflicting result that decreased O-GlcNAcylation can both increase[135] and decrease[43] AMPAR insertion into the postsynaptic membrane; if the above hypothesis is correct, small differences in the time course/length of inhibitor treatment, age of the neurons, etc… are likely to lead to large changes in synapse organization (that subsequently effect AMPAR trafficking).[132,138] Finally, regardless of whether AMPAR O-GlcNAcylation or changes in the O-GlcNAcylation of scaffolding proteins (certainly not mutually exclusive) are responsible for modulating AMPAR trafficking, it will be important for future studies to systematically and consistently investigate the

role of O-GlcNAcylation (either globally or site-specifically) on regulating AMPAR subunits (both individually and in concert) given the diverse roles of each subunit in different contexts.[132,139]

Closely related to AMPAR trafficking is LTP and LTD of excitatory synapses. In fact, many of the studies outlined above showed differences in LTP/LTD when O-GlcNAcylation levels were globally altered. As previously mentioned, Tallent et al. found that OGA inhibition increased LTP while the opposite was true with OGT inhibition.[42] However, Taylor et al. found that OGA inhibition rather caused severe LTD, and Kanno et al. found that OGT inhibition caused increased LTP, both in acute rat hippocampal slices.[40,135] Moreover, in an extensive characterization of OGA hemizygous mice, shown to have increased levels of O-GlcNAcylation in the brain, Suh and colleagues found that both LTP and LTD were attenuated in response to relevant stimuli in acute hippocampus slices.[140] Here, the authors suggest that these impairments may be due to the markedly altered phosphorylation dynamics of AMPAR subunit GluA1 at sites critical for LTP and LTD.[140] Interpreting these studies in relationship to one another is difficult given the in vivo[42,140] versus in vitro[40,135] modulation of O-GlcNAc levels and the use of different chemical[40,42,135] and genetic[140] tools. The result of this is a fairly significant difference in the time between enzyme inhibition and treatment, which is likely to engage differentially engage known compensatory mechanisms.[51,81,83] Moreover, the studies almost uniformly used different protocols to alter O-GlcNAcylation, assess LTP and LTD, and investigate mechanisms, further highlighting the need for more systematic studies on the role of O-GlcNAcylation in regulating synaptic plasticity. Last, an alternative explanation for the aforementioned conflicting results might be timescale/treatment dependent, differential reorganization of the global synaptic machinery (resulting from changes in O-GlcNAcylation of key scaffolding/organizational proteins, see above).

Another major aspect of LTP/LTD beyond AMPAR insertion in the postsynaptic membrane is modulation of glutamate release from the presynaptic neuron.[141-143] Interestingly, multiple O-GlcNAc sites have been identified on presynaptic proteins involved in regulating presynaptic vesicle trafficking, recycling, and release, e.g. bassoon, piccolo, and synapsin, in multiple large scale O-GlcNAc proteomics experiments.[30-35] Both Tallent et al. and Taylor et al. addressed potential presynaptic mechanisms, although they again reached different conclusions. Taylor et al. assessed whether glucosamine treatment (demonstrated to significantly increase global O-GlcNAcylation) changed the paired-pulse ratio, an indirect measure of presynaptic vesicle release, in hippocampal slices and found no effect.[40] On the other hand, Tallent et al. described a decrease in paired-pulse facilitation, increased short-term potentiation, and a marked increase in synapsin phosphorylation at multiple sites after OGA inhibition.[42] Synapsin, which generally serves to tether presynaptic, neurotransmitter containing vesicles to the neuronal cytoskeleton thereby preventing migration to and fusion with the presynaptic membrane (hence inhibiting neurotransmitter release), is dynamically regulated by phosphorylation in response to neuronal activity.[42,144] For example, phosphorylation at serine 9 blocks the association between synapsin and synaptic vesicles while phosphorylation at serine 603 induces a conformational change which decreases synapsin's affinity for both actin and synaptic vesicles, essentially "freeing" synaptic vesicles for neurotransmitter release.[144] An eloquent followup study by Vosseller and colleagues showed furthermore that O-GlcNAcylation of synapsin I itself, at the single site, Thr87, can directly disrupt the binding between synapsin and synaptic vesicles and decrease the amount of synapsin I localized to synapses.[145] Taken together, these studies indicate that O-GlcNAc is playing a key role in regulating synapsin phosphorylation and function to regulate presynaptic release probability and synaptic strength.

Finally, another way that O-GlcNAcylation could be involved in regulating LTP and LTD could be in modulating neuronal membrane potential (and thus controlling neuronal activity). An eloquent study by Yang and coworkers found that the activity of AgRP neurons in the hypothalamus was drastically reduced by OGT KO.[75] Two more recent studies by Huganir and colleagues arrived at similar conclusions for α-CaMKII positive neruons in the paraventricular nucleus of the hypothalamus and embryonic excitatory cortical neurons (although the defects here were attributed to impaired development of synaptic spines).[43,96] Yang and colleagues hypothesized that the loss of O-GlcNAcylation on potassium voltage-gated channel subfamily KQT member 3 (KCNQ3) may contribute to the decreased neuronal activity observed in OGT KO neurons,[75] presumably by changing the baseline excitability and responsiveness to synaptic input of these neurons.[146] Interestingly, a subsequent study also showed that increased O-GlcNAcylation also decreases spontaneous activity in excitatory neurons in hippocampal slices.[147] In summary, it is clear that changes in global O-GlcNAcylation can have marked effects on neuronal excitability and firing rate, perhaps by regulating the conductance of voltage gated potassium channels (or through other, as of yet unexplored, mechanisms), which would have drastic effects on LTP/LTP on the individual neuron, circuit, and organismal level.[146,148,149]

Although the evidence for the regulation of molecular and electrophysiological events by O-GlcNAc is being increasingly explored, there are relatively few studies investigating the role of O-GlcNAc in regulating neurobehavioral phenomenon.[2,5,40,95,96,140] First, hippocampal overexpression of glycosylation-deficient S40A CREB (versus wild-type CREB) significantly enhanced long-term memory consolidation in a cued auditory fear conditioning paradigm.[2] This study represents the potential, critical importance of *individual* O-GlcNAcylation events in coordinating neuronal signal transduction and gene expression to realize a specific behavior. Other

studies have focused on the behavioral consequences globally altering O-GlcNAcylation in neurons. Two groups studied the effects of OGT KO on memory acquisition and recall, overcoming the embryonic lethality of OGT KO by crossing floxed-OGT mice with mice expressing Cre recombinase, either constitutively[5] or inducibly[96], under the α-CaMKII promoter (which is not active until postnatal day 14-21). Interestingly, these studies both found very different behavioral phenotypes, hyperphagia[96] and increased anxiety and impaired contextual and cued fear leaning (discussed further in the neurodegeneration section below).[5] Similarly, Xie et al. showed that decreasing O-GlcNAcylation pharmacologically also impaired both contextual and cued fear conditioning in mice.[95] On the other hand, increased O-GlcNAcylation, due to OGA hemizygosity, also impaired spatial learning and memory in mice as assessed by the Barnes circular maze test and contextual fear conditioning.[140] However, increasing O-GlcNAcylation through pharmacological inhibition of OGA did not affect the performance of rats in a contextual fear learning task, although they did demonstrate profound defects in novel object recognition and novel object preference tasks.[40]

These comparable disruptions in learning and memory observed with decreasing and increasing O-GlcNAcylation suggest that dynamic O-GlcNAc cycling, rather than the presence or absence of the modification, on certain proteins is critical for neuronal function and cognition. Yet, outside of the study of glycosylation-deficient CREB mentioned above,[2] almost nothing is known about which specific O-GlcNAcylation events are most important for regulating behavioral phenomena or how they might act to do so. In summary, although we have only begun to explore the role of O-GlcNAc in regulating behavioral phenomena such as memory, appetite, and cognition, the few, exciting studies to date suggest that this is an area ripe for further exploration.

1.5.3. Neuroprotection.

When challenged by chemical, biological or thermal stress, O-GlcNAcylation of proteins is increased on a rapid and global scale across diverse cell types, suggesting that O-GlcNAcylation is involved in sensing and responding to a variety of stresses.[150] In neurons, O-GlcNAcylation has been hypothesized to serve neuroprotective functions by mediating responses to cell stress via mechanisms including: stabilization of protein integrity, regulation of protein degradation, inhibition of protein aggregation, and damping the effects of oxidative stress.[12,15]

Protein degradation by proteasomes is a main mechanism through which misfolded proteins are eliminated and concentrations of proteins are controlled.[151] Several studies have identified OGT as playing a central role in proteasomal regulation through its O-GlcNAcylation of the 19S regulatory particle of 26S proteasomes, thus inhibiting proteolysis by through inhibition of proteasomal ATPase activity.[152,153] In addition to regulating proteolytic activity of the proteasome, O-GlcNAcylation is also involved in regulating the susceptibility of proteins to degradation. For instance, O-GlcNAcylation of transcription factor Sp1 (SP1) appears to directly oppose its proteasomal degradation.[154] Moreover, loss of O-GlcNAc results in increased ubiquitination and subsequent degradation of nuclear pore protein p62.[155] O-GlcNAcylation has also been implicated in protein folding and in cellular responses to unfolded proteins. Studies have demonstrated that the unfolded protein response activates the hexosamine biosynthesis pathway, resulting in an increase of cellular O-GlcNAc levels.[156] A physiological role for this OGT-ER stress axis was also demonstrated in studies with mice lacking OGT in pancreatic β cells, which produce insulin.[157] These mice presented with massive β cell failure resulting from increased ER stress, ultimately leading to apoptosis triggered by accumulation of unfolded proteins. These findings highlight the role of OGT in protein folding and the unfolded protein response.

Another important neuroprotective function of O-GlcNAcylation includes inhibition of protein aggregation. Several aggregation prone proteins, such as tau and amyloid-precursor protein (APP), are abundant in neurons and the brain and heavily implicated in the pathogenesis of neurodegenerative disease. The microtubule-binding protein tau is an intrinsically disordered protein which is prone to aberrant oligomerization and fibril formation, a process characteristic of neurodegenerative diseases such as AD (discussed below). While long known to have the capacity to be extensively modified by OGT,[158] it was not until recently that O-GlcNAcylation of tau was found to inhibit fibril formation.[102] O-GlcNAcylation also inhibits the aggregation of another protein prone to forming fibrils, α-synuclein.[159] Furthermore, this protective role of O-GlcNAcylation is not unique to fibril-forming proteins; O-GlcNAcylation suppresses the aggregation of proteins which have been partially destabilized by thermal or chemical stress.[102,160] Recent studies of the polycomb protein polyhomeotic have also demonstrated that O-GlcNAcylation is essential to prevent aggregation of the native protein under physiological conditions.[161] These studies emphasize the expanding role of O-GlcNAcylation as a general protective mechanism against protein aggregation.

Finally, OGT may also impart protective functions by regulating cell response to oxidative stress and the generation of reactive oxygen species (ROS). Recent studies have demonstrated that global increases in O-GlcNAcylation result in decreased ROS production in cells,[81,162] and, similarly, that ROS increases O-GlcNAcylation in cells.[163] Interestingly, in response to oxidative stress, FAS appears to associate with and inhibit OGA, and FAS overexpression increased ROS-induced O-GlcNAcylation.[163] This also appears to be beneficial in the context of ischemic stroke, where (1) O-GlcNAcylation is upregulated in response to ischemia, and furthermore (2) that TMG treatment before or after stroke improves outcomes in mouse models of ischemic stroke.[164,165]

Multiple proteins involved in protecting against oxidative stress, e.g. NF-E2–related factor 2, nuclear factor erythroid 2-related factor, and FOXO1, are also known to be positively regulated by O-GlcNAcylation.[166] Thus, in addition to its direct roles in protein stability and homeostasis, O-GlcNAc can also regulate broad cellular responses to ROS, which may have important implications for disease of the nervous system such as ischemic stroke and amyotrophic lateral sclerosis.[15,167]

1.5.4. Neurodegenerative Diseases.

Focusing on neurodegeneration in the context of metabolic abnormalities is critically relevant given that T2DM is strongly associated with both AD and all-cause dementia.[57,168-171] Specifically, persistent hyperglycemia eventually leads to brain insulin resistance and decreased glucose metabolism, also the earliest known pathological feature of AD.[15,48,100,172] In fact, decreased cerebral glucose metabolism precedes mild cognitive impairment and neurodegeneration sometimes by many years, and further decreases correlate extremely well with further cognitive decline.[173-176] Because of the intimate link between glucose metabolism and O-GlcNAc,[6,15] a decrease in brain glucose metabolism is likely to lead to a concomitant decrease in O-GlcNAc levels. Thus, it is perhaps not surprising that there have been multiple reports of decreased O-GlcNAcylation in the brains of AD patients.[99,100,177] We also recently reported that neuronal OGT expression was decreased in tissue samples from Braak Stage V/VI AD patients.[5] Interestingly, there have also been several reports of increased O-GlcNAcylation in AD brains,[178-180] although they all use the CTD110.6 antibody (which does not specifically recognize O-GlcNAc in the presence of other N- or O-linked glycans),[181,182] and a recent study identified both increases and decreases in specific O-GlcNAcylation events in AD brains.[35] Overall, the regulation of

specific O-GlcNAcylation events in AD is likely to be more complex than a universal upregulation or downregulation. Thus, it will be extremely important for future studies to explore the mechanistic underpinnings of individual or function specific O-GlcNAcylation events in a systematic and standardized manner, especially given the current differences in detection techniques, post mortem delay, etc.[99,183]

However, there have been multiple studies that have shown detrimental effects of modulating global levels of O-GlcNAcylation on cellular, electrophysiological, and behavioral phenomenon relevant to AD (see also **Section 1.5.2**). Moreover, a protective effect of increased O-GlcNAcylation in mouse models of AD and other neurodegenerative diseases has been consistently demonstrated. The topic has been reviewed extensively elsewhere;[15,184-187] however, we note briefly here that OGA inhibition reduces the formation of both amyloid β (Aβ) plaques[101,103] and tangles of hyperphosphorylated tau[101,102], the two pathological hallmarks of AD.[15] Importantly, OGA inhibition also reduces overall neurodegeneration and attenuates the behavioral defects in these mouse models.[101-103] To understand whether decreased O-GlcNAcylation has a consistent phenotype, we recently generated a conditional KO of OGT in αCaMKII positive neurons, which, as mentioned previously, develop normally as OGT is expressed through postnatal day 14-21.[5] Consistent with a neuroprotective role of O-GlcNAcylation in the brain, these mice exhibited profound neurodegeneration and features of AD starting at 2 months of age. Specifically, we noted massive neuronal loss in the cortex and hippocampus, increased tau phosphorylation and amyloidogenic Aβ peptide levels, gliosis, the formation of plaques and aggregates, and significant memory defects.[5] Notably, the mouse recapitulates virtually all of the features of AD, including both of the pathological hallmarks, without expressing any exogenous, human proteins (as in all of the most common mouse

models).[188] Taken with the previous studies showing a neuroprotective effect of OGA inhibition, this study provides further, convincing evidence that O-GlcNAcylation may be protective in AD and that the decreased O-GlcNAcylation and OGT expression seen in human patients may be an important pathogenic mechanism.

As alluded to previously, Huagnir and coworkers also characterized a similar, conditional OGT KO mouse, but found a strikingly different phenotype, hyperphagia and extreme weight gain.[96] Moreover, they did not observe significant neuronal loss, although the time point examined was not specified.[5,96] Notably, their model employed the tamoxifen-inducible expression of Cre recombinase under the αCaMKII promoter, where ours was constitutively expressed, in floxed-OGT mice.[5,96] Notably, this results in a different time course of OGT KO; in their case OGT was universally deleted in αCaMKII neurons at ~6 weeks of age versus OGT deletion happening stochastically starting at ~2-3 weeks of age. Perhaps this difference in the time course is important for the phenotype, but it is difficult to say without definitive information about neuronal health in the tamoxifen-inducible conditional KO mouse over time (for instance, we also did not see significant neuronal loss at 1 month of age). Finally, differences in the spatial/cell-type distribution of Cre/loxP recombination due to the use of different αCaMKII-Cre founder lines may explain why we did not observe a hyperphagia phenotype (i.e. OGT may not have been deleted in the same subset of hypothalamic neurons regulating satiety in our mouse, although we did not assess this specifically); another possibility is that the hyperphagia phenotype was masked by the marked neurodegeneration.[5,189] It would be interesting to further characterize both mice to see whether and when the tamoxifen-inducible conditional OGT KO exhibits a neurodegenerative phenotype or other pathological changes associated with AD. If neurodegeneration is in fact absent, it would be extremely important to then determine the underlying, molecular or circuit level basis for this

difference. Regardless, future studies should aim to build a comprehensive understanding of how disruptions in O-GlcNAcylation play a role in neurodegenerative diseases. Moreover, as previous studies have mostly focused on the role of O-GlcNAcylation in regulating individual cellular pathologies, e.g. tau or α-synuclein aggregation, looking at the coordinated results of disrupted O-GlcNAcylation across multiple proteins, pathologies, and/or functions given the multifaceted and enigmatic nature of neurodegenerative disease. It would also be interesting to see whether there are certain, key O-GlcNAcylation events that can, on their own, attenuate or worsen neurodegeneration, as is the case for S40 CREB O-GlcNAcylation in fear memory.[2]

1.6. Conclusion and Outlook.

It is becoming increasing clear that O-GlcNAcylation is on par with phosphorylation for regulating the cellular response to metabolic, chemical, or electrical signals. UDP-GlcNAc, the high-energy donor substrate for OGT is synthesized from glucose through the HBP and is thus ideally suited to respond to changes in extracellular glucose concentrations. Accordingly, increased O-GlcNAcylation mobilizes metabolic machinery across the cell to attenuate glucose influx and, in the liver, stimulate lipogenesis. However, in the context of metabolic diseases like T2DM, sustained increases in O-GlcNAcylation can lead to the paradoxical elevation of gluconeogenesis, lipogenesis, and systemic insulin resistance as well as pancreatic β cell death. Understanding the physiological and pathological roles of O-GlcNAc is thus key to our understanding of metabolism and systemic energy homeostasis in general.

In the brain, O-GlcNAc has also been shown to regulate a wide range of functions. Like in metabolism, it regulates key transcriptional responses to extracellular signals and directly modulates the activity and flux through multiple signaling pathways, here involved primarily with

neuronal communication and survival. O-GlcNAcylation may also serve to regulate protein-protein interaction necessary for the assembly of synaptic signaling machinery as well as modify the properties of receptors and ion channels. Interplay with phosphorylation and regulation of calcium signaling are also major themes (as they are in the liver). O-GlcNAcylation also seems to be playing a major role in diseases of the nervous system. Especially in neurodegenerative diseases such as Parkinson's and AD, aberrant O-GlcNAcylation has been linked to disease pathogenesis and progression through its multiple neuroprotective properties and ability to prevent aggregation of pathologic proteins like α-synuclein and tau. This emerging theme of O-GlcNAcylation serving as a central regulator of neuronal function, homeostasis, and disease is ripe for further exploration.

Finally, although we have made significant strides in understanding the function of O-GlcNAc on multiple neuronal proteins individually, the chemical, genetic, and biotinformatic tools and model systems to study the neuron- or brain-wide functions of O-GlcNAcylation in an unbiased manner have only arisen in the last few years. Specifically, detecting and mapping O-GlcNAcylation events and sites, respectively, has been limited by the poor immunogenicity and chemical lability of O-GlcNAc, complicating the use of traditional biochemical techniques.[183] As a result, the kinds of systems-wide analyses of O-GlcNAcylation dynamics necessary for making unbiased functional hypotheses have been severely lacking. For example, to our knowledge, there have only been two attempts to quantify changes in O-GlcNAcylation after treatment with relevant stimuli or across different neuronal states (both discussed further in **Chapter 4**). First, building on our well-established chemoenzymatic labeling technique,[136,190] we developed a quantitative isotopic and chemoenzymatic tagging (QUIC-Tag) mass spectrometry (MS) method to explore the dynamics of O-GlcNAcylation in culture neurons and rat brains.[32] Ten years later, Wang et al. advanced the chemical/enzymatic photochemical cleavage (CEPC) method, developed by Hart

and coworkers,[191] to profile differences in O-GlcNAcylation in AD brains versus age-matched controls.[35] Although both of these studies represent a significant advance in our ability to profile dynamic O-GlcNAcylation events, they do not provide the amount of data necessary to truly provide an unbiased insight into the numerous, global functions of O-GlcNAcylation and lag far behind techniques for other PTMs, such as phosphorylation.[192,193] Thus, there is a critical need for improved chemical and MS techniques to explore the proteome-wide differences in O-GlcNAcylation in response to stimuli or across disease states. The development and application of such advanced tools would revolutionize the study of O-GlcNAcylation and shed new light on the intimate links between metabolism and neuronal function, cognition, and multiple devastating diseases including AD and T2DM.

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Chapter 2

Methods for the Detection, Study, and Dynamic Profiling of O-GlcNAc Glycosylation

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2.1. Abstract.

The addition of O-GlcNAc to serine/threonine residues of proteins is a ubiquitous PTM found in all multicellular organisms. Like phosphorylation, O-GlcNAcylation is inducible and regulates a myriad of physiological and pathological processes. However, understanding the diverse functions of O-GlcNAcylation is often challenging due to the difficulty of detecting and quantifying the modification. Thus, robust methods to study O-GlcNAcylation are essential to elucidate its key roles in the regulation of individual proteins, complex cellular processes, and disease. In this chapter, we describe a set of chemoenzymatic labeling methods to (1) detect O-GlcNAcylation on proteins of interest, (2) monitor changes in both the total levels of O-GlcNAcylation and its stoichiometry on proteins of interest, and (3) enable mapping of O-GlcNAc to specific serine/threonine residues within proteins to facilitate functional studies. First, we outline a procedure for the expression and purification of a multi-use mutant galactosyltransferase enzyme (Y289L GalT). We then describe the use of Y289L GalT to modify O-GlcNAc residues with a functional handle, *N*-azidoacetylgalactosamine (GalNAz). Finally, we discuss several applications of the copper-catalyzed azide-alkyne cycloaddition “click” reaction to attach various alkyne-containing chemical probes to GalNAz and demonstrate how this functionalization of O-GlcNAc-modified proteins can be used to realize (1) - (3) above. Overall, these methods, which utilize commercially available reagents and standard protein analytical tools, will serve to advance our understanding of the diverse and important functions of O-GlcNAcylation.

2.2. Introduction.

O-GlcNAcylation is a dynamic, inducible PTM found on thousands of intracellular proteins.[1] Only two are enzymes responsible for O-GlcNAc cycling in metazoans: OGT, which catalyzes the addition of O-GlcNAc, and OGA, which catalyzes its removal.[1] The O-GlcNAc modification plays a key role in many important cellular functions, including transcription,[2] nutrient sensing,[3] metabolism,[4] mitochondrial dynamics,[5] and autophagy.[6] Furthermore, dysregulation of O-GlcNAcylation has been strongly implicated in a number of human diseases such as diabetes,[7] cancer,[8] and neurodegenerative disorders.[9,10] However, the regulatory nature of the modification (e.g. dynamic, low cellular abundance) and its unique chemical characteristics (e.g. low immunogenicity of the neutral sugar, chemically labile) represent a central challenge in its detection and study. These features have necessitated the development of customized methods to visualize and quantify this PTM.[11]

One of the first techniques developed to detect O-GlcNAcylation used bovine milk galactosyltransferase to transfer [^{3}H]-galactose to terminal GlcNAc residues on proteins.[12] Along with metabolic labeling using [^{3}H]-glucosamine,[13] this method facilitated early studies of O-GlcNAcylated proteins. Another common detection method took advantage of the specificity of wheat-germ agglutinin (WGA) lectin, which binds to all terminal GlcNAc sugars as well as sialic acid.[14] Several antibodies have also been produced using various O-GlcNAcylated proteins and peptide fragments, including the C-terminal domain of RNA polymerase II (CTD110.6)[15] and the pore complex-lamina fraction from rat liver nuclear envelopes (RL-2).[16,17] A comprehensive list of O-GlcNAc-specific antibodies has been recently described in detail elsewhere.[18] However, the relatively poor immunogenicity of the neutral O-GlcNAc sugar has limited the availability of highly selective antibodies, and in particular, site-specific O-GlcNAc antibodies. Finally,

metabolic oligosaccharide engineering (MOE) has emerged as a powerful method to label cellular glycans, including O-GlcNAc.[19,20] Here, a non-natural, peracetylated sugar such as *N*-azidoacetylglucosamine[21] is incubated with live cells and incorporated into O-GlcNAcylated proteins by the cell's native biosynthetic machinery. The bioorthogonal azide group can then be used for downstream detection and enrichment.

Although many of these detection methods have been widely adopted, they have some key limitations. Labeling of proteins with bovine milk galactosyltransferase requires handling of expensive, radioactive materials and often necessitates exposure times of days to months.[22] While antibodies offer a convenient and faster means of detection, they exhibit a preference for specific sequence or structural motifs and thus only detect a subset of the O-GlcNAcylated proteins.[18] Moreover, like tritium-based methods, both antibody- and lectin-based techniques are often not sensitive enough to detect O-GlcNAc modifications in cases of low abundance or where sample is limiting. Additionally, the lack of specificity of some detection reagents like the CTD110.6 antibody can lead to misinterpreted results. For example, the increase in O-GlcNAc levels observed upon nutrient deprivation by Western blotting with CTD110.6 was later found to be due to an increase in truncated *N*-glycans.[23,24] O-GlcNAc detection using antibodies and lectins has also resulted in conflicting reports on the levels of total protein O-GlcNAcylation in similar systems. For example, an increase in O-GlcNAcylation in Alzheimer's disease brain tissue was observed by immunoblotting with the CTD110.6 antibody,[25] whereas the opposite finding was observed using the RL-2 antibody.[26] MOE methods also suffer from specificity issues, with reports of *N*-azidoacetylglucosamine incorporation into cell-surface *N*- and *O*-linked glycans[27] that have prompted efforts to develop more selective probes.[28,29] Furthermore, the addition of relatively high concentrations of monosaccharide precursors for MOE labeling may alter O-GlcNAc cycling and

artifically change physiological levels of O-GlcNAcylation in cells. Finally, MOE cannot achieve complete labeling due to competition with natural sugars, which limits its detection sensitivity and hinders the quantification of O-GlcNAc stoichiometry. Nevertheless, all of these methods can be effectively used for O-GlcNAc detection and remain key tools in the study of O-GlcNAcylation.

Given the above limitations, methods that are (1) highly sensitive and specific, (2) unbiased towards certain subsets of proteins, (3) able to easily and accurately assess changes in O-GlcNAcylation levels, and (4) compatible with traditional techniques for protein analysis are paramount to expanding our understanding of O-GlcNAcylation dynamics and function. Herein, we describe a chemoenzymatic labeling approach that utilizes engineered bovine β-1,4-galactosyltransferase 1 (Y289L GalT) to tag O-GlcNAcylated proteins with an GalNAz group (**Fig. 2.1a**). When combined with peptide:*N*-glycosidase F (PNGase F) treatment to remove GlcNAc-containing *N*-linked glycans,[30] this method allows for the specific, unbiased, and global labeling of O-GlcNAcylated proteins. The appended azide handle can subsequently be reacted with a wide variety of alkyne-modified chemical probes, facilitating multiple downstream analyses. Here, we describe four distinct workflows that take advantage of the copper-catalyzed azide-alkyne cycloaddition (CuAAC) “click” reaction to attach biotin, 5-

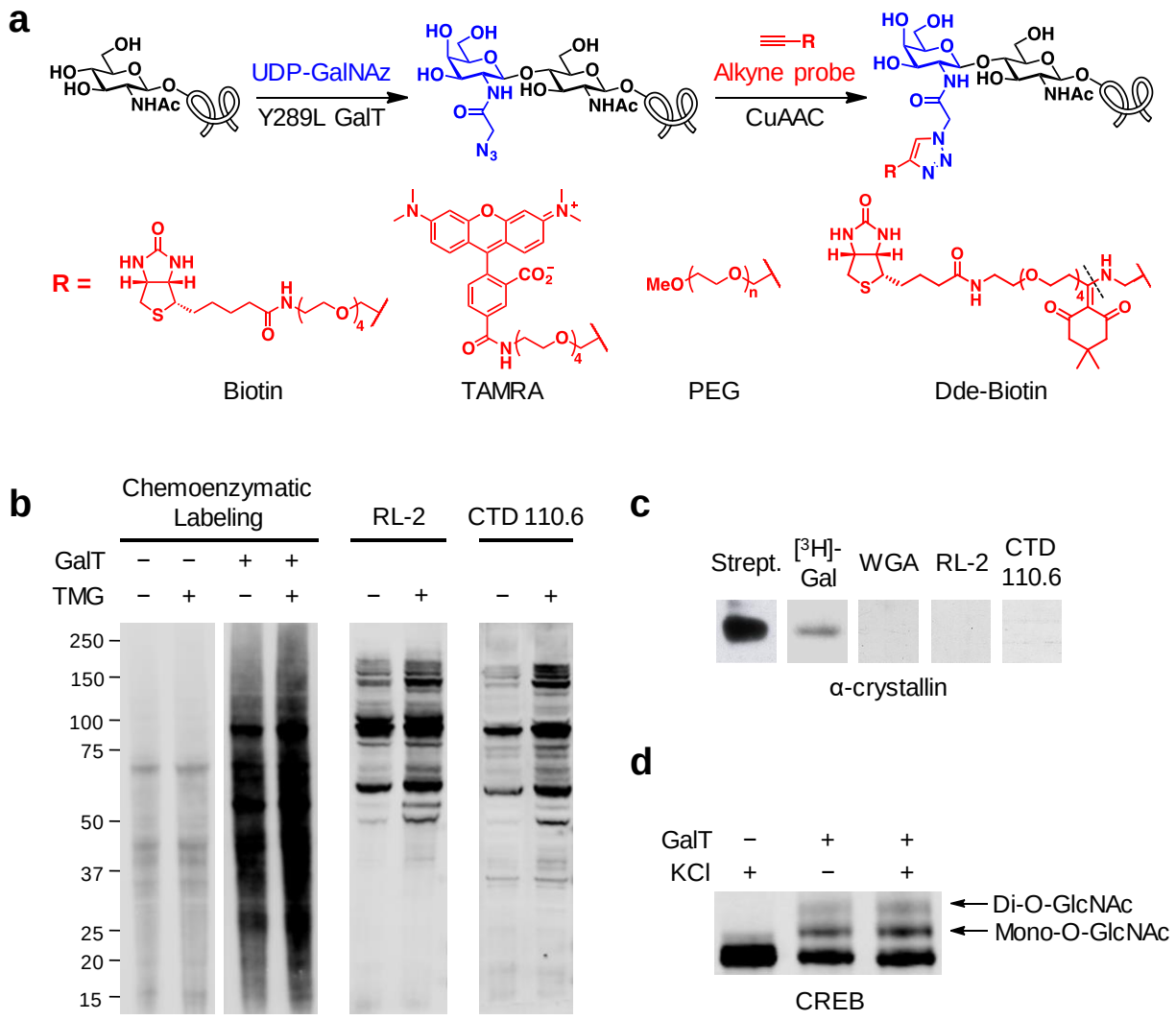

Fig. 2.1. See Caption on Next Page.

carboxytetramethylrhodamine (TAMRA), high-molecular-weight poly(ethylene glycol) (PEG), or cleavable Dde-biotin probes to O-GlcNAcylated proteins (**Fig. 2.1a**).

Biotinylation or TAMRA-labeling enables rapid, sensitive detection of O-GlcNAcylated proteins by Western/streptavidin blotting or direct in-gel fluorescence.[4,31] Importantly, these approaches allow for unbiased protein detection (**Fig. 2.1b**) and a significant enhancement in detection sensitivity (>380-fold relative to tritium labeling in the case of α-crystallin) compared to traditional methods (**Fig. 2.1c**).[22,31] Thus, detection of novel O-GlcNAcylated proteins is more

readily possible, such as CREB[2] and PFK1.[4] The biotin and TAMRA tags also allow for the selective enrichment of O-GlcNAcylated proteins by using streptavidin or anti-TAMRA antibody affinity chromatography. Such an enrichment step can greatly improve the detection of O-GlcNAcylated peptides by MS as the presence of unmodified peptides often suppresses the ionization of their O-GlcNAcylated counterparts.[32] To improve further the efficiency of enrichment and detection, we developed a chemically cleavable Dde-biotin probe (**Fig. 2.1a**).[33] This probe allows for the mild, quantitative elution of O-GlcNAcylated proteins from streptavidin beads and produces a positively charged amine upon cleavage to enhance ionization/MS-based detection.

Biotin or defined PEG mass tags can be used to monitor O-GlcNAcylation dynamics and stoichiometry by quantitative Western blotting. The ability to study changes in O-GlcNAcylation in response to cellular stimuli or across disease states is critical to understanding the specific

Fig. 2.1. Chemoenzymatic Labeling Strategies for the Study of O-GlcNAcylated Proteins. **(a)** Incubation of O-GlcNAcylated proteins with Y289L GalT and UDP-GalNAz installs a chemical handle that can be further functionalized with alkyne-containing biotin, TAMRA, PEG, or Dde-biotin probes using CuAAC. The Dde-biotin probe is cleaved by hydrazine to provide a positively charged amine at the site indicated (dotted line). **(b)** Attachment of either an alkynyl biotin or alkynyl TAMRA probe allows for the assessment of total O-GlcNAcylation dynamics in response to cellular stimuli. HEK 293T cells were treated for 6 hours with 50 μM of the OGA inhibitor thiamet-G (TMG) or vehicle and subjected to the workflow in **Sections 2.4 and 2.5**. Total O-GlcNAcylation levels were visualized by blotting with AlexaFluor 680-conjugated streptavidin. Robust, unbiased labeling of proteins is observed by chemoenzymatic labeling. Note the marked difference in the number and molecular weight of O-GlcNAcylated proteins detected as compared to the anti-O-GlcNAc antibodies RL-2 and CTD110.6. **(c)** Attempts to detect O-GlcNAcylated α-crystallin by various methods show the sensitivity advantage afforded by functionalization with biotin-PEG4-alkyne. In all cases, 0.75 μg of bovine lens α-crystallin was resolved on SDS-PAGE (after chemoenzymatic labeling, as described in **Section 2.4**, or tritium labeling, as described in (Khidekel et al., 2003)) and detected as indicated. **(d)** Labeling proteins with alkynyl PEG (2-kDa) allows for the observation of multiple O-GlcNAcylation states (mono-, di-O-GlcNAcylated, etc.) and their corresponding stoichiometries. Mouse primary cortical neurons were treated with 60 mM KCl for 2 hours and subjected to the workflow in **Sections 2.4 and 2.6** CREB O-GlcNAcylation was detected by immunoblotting with an anti-CREB antibody.

functions of the O-GlcNAc modification. Chemoenzymatic labeling with biotin enables the rapid, global assessment of O-GlcNAcylation and has the advantage of detecting many more proteins than antibody-based methods (**Fig. 2.1b**). Thus, it can be readily used to monitor changes in O-GlcNAcylation on either specific proteins or the total O-GlcNAcylated protein population in response to cellular stimuli. On the other hand, labeling with PEG tags of defined molecular mass provides the powerful ability to reveal O-GlcNAcylation states (i.e. mono-, di-O-GlcNAcylated, etc.) and quantify in vivo O-GlcNAcylation stoichiometries on proteins of interest (**Fig. 2.1d**). Such information cannot be readily obtained using other methods. When combined with site-directed mutagenesis, the PEG tagging approach can also determine O-GlcNAc occupancy levels and cycling at specific serine/threonine sites in a protein.[2,4,34] Quantitative comparisons of O-GlcNAcylation states and their stoichiometries following cellular stimulation or during disease progression are important for identifying the most physiologically relevant O-GlcNAcylation events.

We begin this chapter with an updated method for the purification of Y289L GalT (**Section 2.3**). We next describe how to use this enzyme to label O-GlcNAcylated proteins efficiently with GalNAz in a complex cellular lysate (**Section 2.4**). After attaching this azide handle, we outline a general method to install a variety of functional tags through CuAAC and detail how the four representative chemical probes can be used to detect, quantify, and measure the dynamics of O-GlcNAcylation both on individual proteins and on the total O-GlcNAcylated proteome (**Sections 2.5, 2.6, and 2.7**). Lastly, we briefly discuss methods to localize the O-GlcNAc modification to particular serine/threonine residues of proteins to facilitate in-depth functional analyses (**Section 2.8**).

2.3. Expression and Purification of Y289L GalT.

The first step of the chemoenzymatic approach is the selective labeling of O-GlcNAcylated proteins with GalNAz. This is achieved using Y289L GalT, which is robustly expressed in *E. coli*, purified from inclusion bodies, and refolded to obtain active enzyme.[35] The procedure below is a streamlined protocol for making large quantities of Y289L GalT. The enzyme can be stored for up to 1 year as the active protein or for several years in the unfolded form or cell pellet. We also describe procedures to test the purity and activity of the enzyme prior to its use. These checks are necessary before proceeding with the remaining techniques in this chapter.

2.3.1. Equipment.

1. 37°C incubator with shaker
2. UV-Vis spectrophotometer
3. Refrigerated centrifuge
4. Sonicator (Vibra-Cell VCX 130; Sonics & Materials)
5. Centricon Plus-70 Centrifugal Filter, 10-kDa nominal molecular weight limit (NMWL) (UFC700308, EMD Millipore)
6. Spectra/Por 4 Standard RC Dialysis Tubing, 12-14-kDa molecular weight cut-off (132706, Spectrum Labs)
7. Standard equipment for sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) and Coomassie staining
8. Matrix-assisted laser desorption/ionization time-of-flight (MALDI-TOF) MS instrumentation

a. Other MS methods such as liquid chromatography (LC)-electrospray ionization MS (Khidekel et al., 2003) also work well.

2.3.2. Materials.

1. Y289L GalT expressing plasmid (Ramakrishnan & Qasba, 2002)
2. 2-Nitro-5-(Sulfothio)-Benzoate (NTSB) (Thannhauser, Konishi, & Scheraga, 1984)
    a. To prepare 10 mL of NTSB, dissolve 0.1 g of 5,5'-dithiobis(2-nitrobenzoic acid) in 10 mL of 1 M Na_2SO_3 at 37°C. Adjust the pH to 7.5 with NaOH and bubble air through the solution until the color changes from deep orange-red to pale yellow (~1-2 hours).
    b. Make fresh or store at -20°C immediately after production.
3. Electro- or chemically competent BL21(DE3) *E. coli*
4. Luria-Bertani agar (LA) plates containing 100 μg/mL of ampicillin
5. Luria-Bertani (LB) broth containing 100 μg/mL of ampicillin
6. 100 mM Isopropyl β-D-1-thiogalactopyranoside (IPTG) in H_2O
7. Phosphate-buffered saline (PBS) pH 7.4 (10 mM Na_2HPO_4, 1.8 mM KH_2PO_4, 137 mM NaCl, 2.7 mM KCl), 1 mM ethylenediaminetetraacetic acid (EDTA)
8. 25% (w/v) Sucrose, 0.1% Triton-X100, and 1 mM EDTA in PBS pH 7.4
9. 5 M Guanidine hydrochloride in H_2O*
10. 5 M Guanidine hydrochloride and 0.3 M sodium sulfite in H_2O*
11. Refolding buffer: 50 mM tris(hydroxymethyl)aminomethane HCl (Tris) pH 8, 5 mM EDTA, 4 mM cysteamine, and 2 mM cystamine*

12. Dialysis buffer: 50 mM Tris pH 8, 5 mM EDTA, 4 mM cysteamine, and 2 mM cystamine*
13. 100 pmol/μL of Click-iT O-GlcNAc Peptide LC/MS Standard (Click-iT peptide) (C33374, Invitrogen)
14. 100 mM 4-(2-hydroxyethyl)-1-piperazineethanesulfonic acid (HEPES) pH 7.9
15. 10 mM uridine 5'-diphospho-2-acetonyl-2-deoxy-α-D-galactose (UDP-ketogal) (Khidekel et al., 2003) or 10 mM uridine 5'-diphospho-2-azidoacetylamino-2-deoxy-α-D-galactose (UDP-GalNAz)[36] in H_2O
    a. Store at -80°C and thaw on ice just before use.
16. 100 mM $MnCl_2$
17. C_{18} ZipTips (ZTC18M096, EMD Millipore)
18. MS grade acetonitrile (ACN)
19. MS grade H_2O
20. 1% trifluoroacetic acid (TFA) in H_2O
21. Super-DHB (sDHB) MALDI matrix (50862, Sigma-Aldrich)

    * Make fresh on the day of use.

2.3.3. Procedure.

1. Transform 50 μL of electro- or chemically competent BL21(DE3) *E. coli* with 1 μL of Y289L GalT expressing plasmid (10 ng/μL), plate onto LA plates containing 100 μg/mL of ampicillin, and incubate overnight at 37°C.
2. Pick two colonies, add individually to 100 mL of LB containing 100 μg/mL of ampicillin, and incubate overnight with shaking (250 RPM) at 37°C.

3. Distribute the two 100-mL flasks equally between six 1-L volumes of LB containing 100 μg/mL of ampicillin.
4. Incubate with shaking (250 RPM) at 37°C until the optical density at 600 nm reaches 0.7.
5. Add IPTG to a final concentration of 1 mM to induce protein production.
6. Incubate with shaking (250 RPM) for another 4 hours at 37°C.
7. Harvest the cells by centrifugation at 8000 x *g* for 10 minutes.
    a. The bacterial pellets can be frozen at -80ºC for at least 2 years.
8. Resuspend bacteria from 1 L of culture medium in 10 mL of PBS containing 1 mM EDTA and sonicate thoroughly (10-15 x 30 seconds, with 10-second rest) at 40% amplitude on ice.
    a. From now on, the volumes correspond to the purification of Y289L GalT from 1 L of bacterial culture; we generally purify Y289L GalT from 1-2 L of bacterial culture at a time and save the remaining pellets for future purification. Alternatively, the purification can be performed up to step 2.3.19 below and frozen at -80°C for at least 2 years.
    b. Unless otherwise noted, all steps from this point onward should be performed on ice or at 4°C, and all reagents should be ice cold.
9. Dilute the bacterial lysate to 80 mL with PBS containing 1 mM EDTA and centrifuge at 14,000 x *g* for 30 minutes.
10. Discard the supernatant and resuspend the pellet in 25% (w/v) sucrose in PBS containing 1 mM EDTA and 0.1% Triton X-100.
11. Repeat the previous step 5 times.

   a. It is important to ensure that the pellet is completely resuspended with each wash step to ensure efficient purification of Y289L GalT. With repeated washes, the color of the pellet should change from yellow to ivory white.
   b. If necessary, the pellet can be stored overnight at 4°C at any point.

12. After the last centrifugation, resuspend the pellet in 50 mL of PBS containing 1 mM EDTA and centrifuge for 30 minutes at 14,000 x *g*.
13. Discard the supernatant, and repeat this step once more to remove any residual detergent.
14. Discard the supernatant, and resuspend the pellet in 20 mL of 5 M guanidine hydrochloride with 0.3 M sodium sulfite at room temperature.
15. Add 2 mL of S-sulfonating agent, NTSB, and stir the reaction vigorously until it has turned pale yellow in color.
    a. When NTSB (pale yellow) is added to the mixture, the solution should turn red-orange. The reaction is complete when the solution has turned back to pale yellow, which usually takes approximately 45 minutes.
16. Add 180 mL of ice-cold H_2O to precipitate the protein and centrifuge at 10,000 x *g* for 10 minutes.
17. Discard the supernatant, resuspend the pellet in 10 mL of H_2O, and centrifuge the sample at 10,000 x *g* for 10 minutes.
18. Repeat two more times to remove any remaining sulfonating agent.
19. Resuspend the pellet in 5 M guanidine hydrochloride to a protein concentration of 1 mg/mL (A_{280} ~ 2.0).

   a. We typically use absorbance at 280 nm on a NanoDrop® 2000 UV-Vis Spectrophotometer (ThermoFisher Scientific) to determine the protein concentration.
   b. If desired, the unfolded, sulfonated protein can be frozen and stored at -80°C for at least 2 years.

20. Dilute the protein solution 10-fold over the course of 15 minutes in refolding buffer.
   a. Add the refolding buffer in 10 portions over the course of 15 minutes while mixing the solution (by hand or with an orbital shaker).
   b. Some protein will precipitate as the refolding buffer is added.
21. Leave the protein undisturbed to refold at 4°C for 48 hours.
22. Centrifuge the solution at > 7,000 x *g* for 10 min to pellet any precipitate, and dialyze the supernatant 3 x 12 hours with 4 L of dialysis buffer.
   a. Some protein will precipitate during the dialysis process.
   b. Dialyzation using a stirred cell (e.g. UFSC05001, MilliporeSigma) or centrifugal concentrator is also possible, and we have observed no loss of activity using these methods. However, it is important in either case that the dialysis is closely monitored to avoid over-concentration and precipitation of the enzyme.
23. After dialysis, remove the precipitated protein by centrifugation at > 7,000 x *g* for 15 minutes.
24. Concentrate the Y289L GalT to 1 mg/mL (determined as previously described) using Centricon Plus-70 10-kDa NMWL Centrifugal Filter Units and store at 4°C.
   a. This typically requires more than 100-fold concentration.

b. Protein can be stored for at least 1 year at 4°C; use the assay described below to ensure activity of older protein stocks before use.

25. Check the quality of the Y289L GalT by performing SDS-PAGE followed by staining with Coomassie blue (**Fig. 2.2a**).
26. Check that the purified Y289L GalT labels an O-GlcNAcylated peptide using UDP-ketogal or UDP-GalNAz. Set up a dilution series of enzyme as follows:
    a. Add 0.75 µL of 100 mM $MnCl_2$; 1.5 µL of 100 mM HEPES (pH 7.9); 0, 0.375, or 0.75 µL of 2 mg/mL Y289L GalT; 0.75 µL of 10 mM UDP-ketogal or UDP-GalNAz; and 1.5 µL of 100 pmol/µL Click-iT peptide to 10.5, 10.125, or 9.75 µL of H_2O (pipetting up and down after each condition to mix). The final reaction conditions are outlined in **Table 2.1**.
    b. Incubate the above reactions at 4°C for 16 hours.

Table 2.1. Reaction Conditions for Testing Y289L GalT Activity.

Reaction Components[a]	Volume (µL)	Final Concentration
H_2O	10.5, 10.125, or 9.75	
100 mM $MnCl_2$	0.75	5 mM
100 mM HEPES pH 7.9	1.5	10 mM
2 mg/mL Y289L GalT	0, 0.375, or 0.75	0, 0.05, or 0.1 mg/mL
10 mM UDP-ketogal or UDP-GalNAz	0.75	500 µM
100 pmol/µL Click-iT Peptide	1.5	10 pmol/µL
Final Volume	15	

[a] Flick tubes to mix and spin down briefly after each addition.

27. After incubating for 16 hours, quench the reaction by adding 1.5 µL of 1% TFA and purify the peptides using ZipTips per the manufacturer's instructions.
28. Analyze the peptides from each reaction by MALDI-TOF MS using an sDHB matrix.[37]

29. After MALDI-TOF analysis, look for the complete conversion of the unlabeled peptide to the labeled peptide to confirm quantitative labeling (**Fig. 2.2b**).
    a. With UDP-ketogal, look for the labeled and unlabeled peptides at an *m/z* of 1320.5 and 1118.5 Da, respectively, in positive ionization mode. Often times their sodium adducts are also seen at 1342.5 and 1140.5 Da. If UDP-GalNAz is used, the labeled peptide will be observable at 1362.5 Da. A peak at [M-28], corresponding to the loss of N_2, is also usually observed. Note that using reflector mode detection may complicate analysis when using UDP-GalNAz.[38]

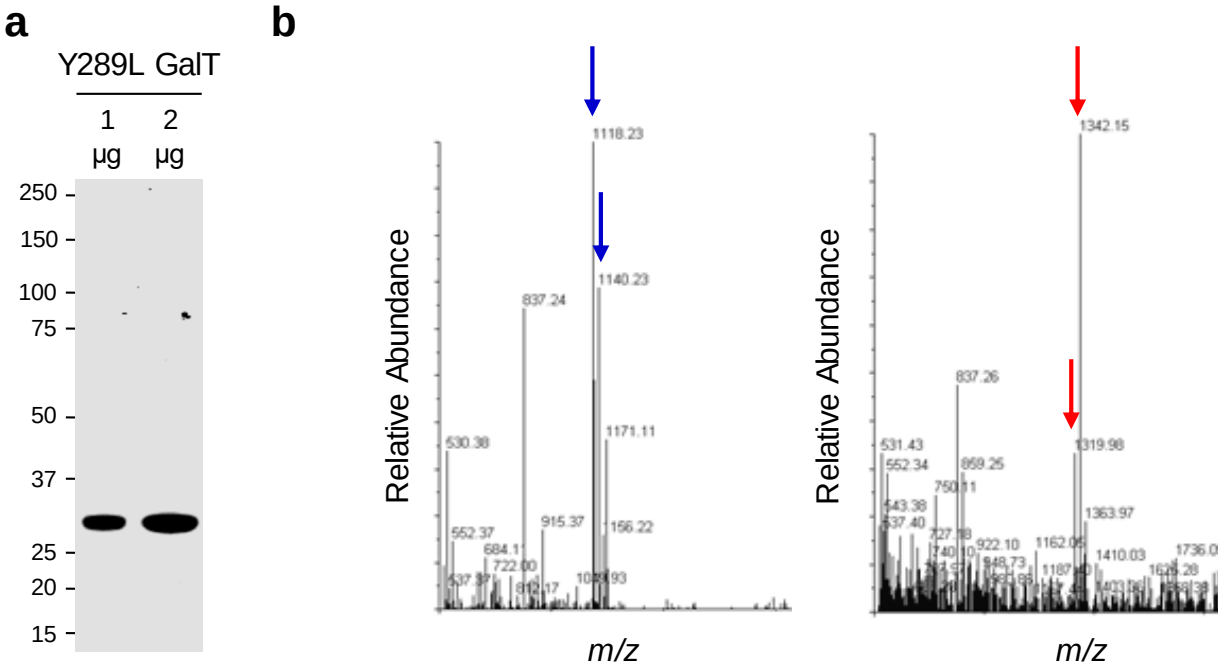

Fig. 2.2. GalT Characterization.
(a) Coomassie stained gel of purified Y289L GalT. **(b)** Representative MALDI-TOF spectra of the peptide labeling reaction with 0 mg/mL (left) or 0.1 mg/mL (right) Y289L GalT. The blue arrows indicate the unlabeled peptide (1118.23) and its sodium adduct (1140.23). The red arrows indicate the labeled peptide (1319.98) and its sodium adduct (1342.15).

2.3.4. Notes.

We usually obtain 5-10 mL of active Y289L GalT at a concentration of 2 mg/mL from the purification procedure described above. It is important to note that some protein will continue to precipitate over the first few days to weeks of storage. Although the precipitation of protein is usually not enough to significantly affect the concentration, it is important to re-check both the protein concentration and activity periodically to ensure consistent labeling in subsequent procedures. Overall, if stored properly at 4°C, the Y289L GalT should retain almost 100% of its activity for more than 1 year.

2.4. Labeling of O-GlcNAcylated Proteins with GalNAz.

The Y289L GalT (hereafter referred to as "GalT") produced in **Section 2.3** can be used to label O-GlcNAcylated proteins with UDP-ketogal or UDP-GalNAz. Here, we focus on the use of UDP-GalNAz to add an azide handle to O-GlcNAcylated proteins in cell lysates for further functionalization with an alkyne-modified chemical probe by CuAAC (**Sections 2.5-2.7**).

2.4.1. Equipment.

1. Centrifuge
2. Vortex mixer
3. End-over-end rotator
4. Spectrophotometer
5. Sonicator (Vibra-Cell VCX 130; Sonics & Materials)

2.4.2. Materials.

1. 20 mM TMG stock in DMSO
2. 50x cOmplete EDTA-free Protease Inhibitor Cocktail (11873580001, Sigma Aldrich) stock in H_2O
3. Lysate containing protein(s) of interest
    a. We generally use the following lysis buffer for most applications: 2% SDS, 100 mM Tris pH 8, 1x protease inhibitor cocktail, and 50 μM TMG.
    b. Other non-denaturing methods of lysis are also compatible with this protocol; however, it is important that OGA inhibitors, such as TMG,[39] be included at all steps until the protein is completely denatured to prevent the potential loss of protein O-GlcNAcylation.
    c. Purified protein obtained by recombinant expression or immunoprecipitated from cell lysate can also be used. In this case, reduce and alkylate the protein, and start at step 8 below.
4. Dithiothreitol (DTT)
5. Iodoacetamide (IAA)
6. IGEPAL CA-630 (I8896-50ML, Sigma-Aldrich)
7. Milli-Q (or equivalent) purified H_2O
8. PNGase F (glycerol-free) (P0705S, New England Biolabs)
9. BCA Protein Assay Kit (23225, ThermoFisher Scientific)
10. Methanol
11. Chloroform
12. 1% SDS in 20 mM HEPES pH 7.9

13. 2.5x GalT labeling buffer: 50 mM HEPES pH 7.9, 125 mM NaCl, 5% IGEPAL CA-630*
14. 100 mM $MnCl_2$ in H_2O*
15. 500 μM UDP-GalNAz in 10 mM HEPES pH 7.9*
    a. Store at -80°C and thaw on ice just before use.
16. 2 mg/mL GalT*
    a. Keep on ice.

* These materials are also commercially available as part of the Click-iT O-GlcNAc Enzymatic Labeling System (C33368, ThermoFisher Scientific).

2.4.3. Procedure.

1. Lyse the cells in boiling lysis buffer, boil for 5 minutes, and sonicate the lysate 3 x 10 seconds to sheer DNA.
2. Centrifuge the sample for 5 minutes at 21,130 x *g* and transfer the supernatant to clean 1.5-mL microcentrifuge tubes.
3. Measure the protein concentration of the sample using the BCA assay and dilute the sample to 1-2 mg/mL prior to reduction and alkylation.
4. Add 25 mM (final concentration) of DTT, boil for 5 minutes, and allow the sample to return to room temperature.
5. Add 80 mM (final concentration) of IAA and incubate with end-over-end rotation at room temperature in the dark for 60 minutes.
    a. Reduction and alkylation of the protein lysate is very important for preventing side reactions between free cysteine residues and the alkyne probes.[40-42] These

side reactions produce nonspecific background and artificially increase the O-GlcNAcylation stoichiometry.

6. Dilute cell lysate containing 150 μg of protein with H_2O to a total volume of 200 μL.
    a. This amount is a good starting point for detecting specific O-GlcNAcylated proteins of interest from cell lysates; however, the reaction can be easily scaled depending on the application.
7. Precipitate the protein to remove it from endogenous UDP-sugars in the cell lysate:
    a. Add 600 μL of methanol and vortex the sample.
    b. Add 200 μL of chloroform and vortex.
    c. Add 450 μL of H_2O, vortex, and centrifuge at 21,130 x *g* for 5 minutes to separate the aqueous and organic phases.
        i. The protein will be a thin solid layer at the aqueous-organic interface.
    d. Remove the top, aqueous layer carefully without disturbing the pellet.
    e. Add 450 μL of methanol and invert gently to produce a single organic layer.
    f. Remove all solvent and resuspend the pellet gently in another 450 μL of methanol.
8. Remove all solvent and resuspend the protein in 40 μL of 1% SDS, 20 mM HEPES pH 7.9 by boiling.
    a. Usually the protein will redissolve completely after ~1-2 minutes; however, care should be taken to ensure that the sample has completely redissolved as the protein pellet is often difficult to observe. The samples can be boiled or sonicated for up to 15 minutes if necessary.

9. After the protein has redissolved, add (in order) 49 µL of H_2O, 80 µL of 2.5x GalT labeling buffer, and 11 µL of 100 mM $MnCl_2$.
10. Vortex the sample to mix and transfer to ice before adding 10 µL of 500 µM UDP-GalNAz and 10 µL of 1 mg/mL GalT or H_2O. The final reaction components are outlined in **Table 2.2**.
    a. Adding H_2O in place of GalT or UDP-GalNaz is a suitable and important negative control for all of the workflows presented hereafter.
    b. If total O-GlcNAcylation levels or the O-GlcNAcylation level of a transmembrane protein is being measured, it is important to remove *N*-glycans as they may contain terminal GlcNAc residues that can be labeled by GalT. To achieve this for the reaction described above, add only 46 µL of H_2O and 3 µL of 500 U/µL PNGase F after adding GalT.
        i. Ovalbumin can serve as a useful positive control for PNGase F treatment.[30]

Table 2.2. Reaction Conditions for GalNAz Labeling.

Reaction Components	Volume (µL)	Final Concentration
Protein mixture (3.75 mg/mL in 1% SDS, 20 mM HEPES pH 7.9)	40	0.75 mg/mL
H_2O[a]	49	
2.5x GalT Labeling buffer[b]	80	1x
100 mM $MnCl_2$	11	5.5 mM
500 µM UDP-GalNAz	10	25 µM
2 mg/mL GalT[c]	10	0.1 mg/mL
Final Volume	200	

[a] If using PNGase F, add only 46 µL, and add 3 µL PNGase F (500 U/µL) after GalT.
[b] Vortex gently to mix after this step.
[c] Use H_2O for negative control.

11. Rotate the reaction end-over-end at 4°C for 1 hour.
    a. The reaction can also be left to proceed overnight if desired.
12. Precipitate the proteins using the methanol/chloroform/H_2O method as described above.
    a. If necessary, at this point, the pellets can be stored in methanol at -80°C for up to 1 year.

2.5. CuAAC "Click" Reaction with Small Molecule Alkyne Probes.

After labeling protein(s) with GalNAz, they are ready to be further functionalized with chemical probes and analyzed. In this section, we provide a workflow using CuAAC to append a biotin, TAMRA, or chemically cleavable biotin probe to GalNAz-labeled proteins. However, this general method can be used with a wide variety of alkyne-containing molecules with minimal modifications. Labeling of O-GlcNAcylated proteins with biotin or TAMRA provides a robust and sensitive method for quantifying the total levels of O-GlcNAcylation by streptavidin/Western blotting or direct in-gel fluorescence (**Section 2.5.4**). Moreover, biotin-labeled proteins of interest can be captured using streptavidin resin to determine the fraction of labeled proteins and approximate their O-GlcNAcylation stoichiometry (**Section 2.7.3.1**). TAMRA labeling followed by immunoprecipitation using an anti-TAMRA antibody can also be used for these same purposes (**Section 2.7.3.2**). Finally, labeling with Dde-biotin-alkyne provides a convenient method for the efficient capture and release of O-GlcNAcylated proteins under mild conditions; this may be especially useful for proteins whose O-GlcNAc sites have proven difficult to map (**Section 2.7.3.3**).

2.5.1. Equipment.

1. Centrifuge
2. Vortex mixer
3. End-over-end rotator
4. Standard equipment for SDS-PAGE and Western blotting

2.5.2. Materials.

1. GalNAz-labeled protein pellet (step 3.3.14)
2. 1% SDS, 20 mM HEPES pH 7.9
3. 50 mM $CuSO_4$-$5H_2O$ in H_2O*
4. 100 mM Tris(2-carboxyethyl)phosphine (TCEP) in H_2O*
    a. Prepare fresh immediately before use and protect from light.
5. Milli-Q (or equivalent) purified H_2O
6. Methanol
7. Chloroform
8. 10 X PBS pH 7.4 (100 mM Na_2HPO_4, 18 mM KH_2PO_4, 1.37 M NaCl, 27 mM KCl)*
9. Alkyne-functionalized chemical probe
    a. 5 mM Biotin-PEG4-alkyne in DMSO (TA105-25, Click Chemistry Tools) or
    b. 5 mM Dde-biotin-alkyne in DMSO (1137-10, Click Chemistry Tools)
    c. 5 mM TAMRA alkyne in DMSO (TA108-5, Click Chemistry Tools)
10. 10 mM 2-(4-((Bis((1-(tert-butyl)-1H-1,2,3-triazol-4-yl)methyl)amino)methyl)-1H-1,2,3-triazol-1-yl)acetic acid (BTTAA) in DMSO* (1236-100, Click Chemistry Tools)

11. SDS-PAGE loading buffer: 2% SDS, 50 mM Tris pH 6.8, 100 mM DTT, 0.1% (w/v) bromophenol blue, and 10% glycerol

* As an alternative, commercial kits are also available as the Click-iT Biotin or TAMRA Protein Analysis Detection Kits (C33372 and C33370, ThermoFisher Scientific). Furthermore, the Click-iT Protein Buffer Kit (C10276, ThermoFisher Scientific) provides all necessary components except for the alkyne probe for reaction customization.

2.5.3. Procedure.

1. Redissolve the protein pellet with 37.5 µL of 1% SDS, 20 mM HEPES pH 7.9 as described above.
2. After the protein is completely dissolved, add (in order) 87 µL of H_2O, 15 µL of 10x PBS, 3 µL of the 5 mM alkyne probe (if using other probes/volumes, adjust the volume of H_2O accordingly), 1.5 µL of 10 mM BTTAA, and 3 µL of 50 mM $CuSO_4$ with vortex mixing after each addition. Finally, add 3 µL of 100 mM TCEP and vortex to mix; the solution should change to a yellow-blue-green color before rapidly (less than 1 minute) retuning to clear. The final reaction conditions are outlined in **Table 2.3**.
    a. For multiple conditions, it is also possible to make a 'master mix' of the components as follows: (1) mix $CuSO_4$ and BTTAA together by gentle vortexing, (2) dilute the $CuSO_4$-BTTAA with H_2O, and (3) add the alkyne probe and vortex briefly. This master mix can then be added to multiple samples before vortex mixing and adding 3 µL of TCEP as described above.

Table 2.3. Reaction Conditions for CuAAC with Small Molecule Alkyne Probes.

Reaction Components[a]	Volume (μL)	Final Concentration
Protein mixture (4 mg/mL in 1% SDS, 20 mM HEPES pH 7.9)	37.5	1 mg/mL
H_2O	87	
10x PBS	15	1x
5 mM alkyne probe	3	100 μM
50 mM $CuSO_4$	3	1 mM
10 mM BTTAA	1.5	100 μM
100 mM TCEP	3	2 mM
Final Volume	150	

[a] Vortex briefly to mix after each addition.

3. Incubate the solution with end-over-end rotation for 1 hour at room temperature.
4. Precipitate the protein as previously described and wash three times with 1 mL of methanol to remove any unreacted alkyne probe.
5. Redissolve the pellet in 40 μL of 20 mM HEPES pH 7.9 containing 1% SDS.
    a. At this point, the redissolved, functionalized proteins can be frozen and stored for later analysis or subjected directly to SDS-PAGE (see **Section 2.5.4** below). Labeled proteins can also be enriched (**Section 2.7**) for further analysis and quantification.

2.5.4. Quantifying Total O-GlcNAcylation Levels.

After labeling O-GlcNAcylated proteins from a cellular lysate with biotin or TAMRA, the total levels of protein O-GlcNAcylation can be quantified. Typically, we resolve the labeled proteins (along with a negative control subjected to the same workflow but without the addition of

GalT) by SDS-PAGE, transfer the gel to a PVDF membrane, and blot with an anti-TAMRA antibody (A6397, ThermoFisher Scientific) or streptavidin-conjugated dye (S32358, ThermoFisher Scientific or 32230, LI-COR Biosciences). The total levels of O-GlcNAcylation can then be assessed using densitometry. Alternatively, TAMRA-labeled proteins can be resolved by SDS-PAGE and subjected to direct in-gel fluorescence analysis. These approaches are particularly useful for monitoring changes in protein O-GlcNAcylation in response to cellular stimuli (**Fig. 2.1b**). Moreover, the captured O-GlcNAcylated proteins can be excised from the gel, subjected to proteolytic digestion, and identified by MS analysis.[31] Together, these probes provide a robust, unbiased method for comparing total O-GlcNAcylation levels under various conditions and may avoid previously reported issues with O-GlcNAc antibodies.

2.6. CuAAC "Click" Reaction with PEG Alkyne.

Using a similar procedure to that described in **Section 2.5**, it is also possible to add an alkyne-functionalized PEG tag of defined molecular mass (e.g. 2-kDa or 5-kDa) to O-GlcNAcylated proteins. The PEG-labeled lysates can be resolved by SDS-PAGE and immunoblotted for specific proteins of interest (**Fig. 2.1d**). This provides a rapid, convenient way to monitor the O-GlcNAcylation state and stoichiometry across different conditions with minimal manipulation after labeling. Tagging O-GlcNAcylated proteins with alkynyl PEG is our method of choice for most applications, including: (a) monitoring O-GlcNAcylation in different tissues or in response to various treatments,[2,4] (b) confirming sites of O-GlcNAcylation,[2] and (c) detecting O-GlcNAc on proteins of interest in a more rapid, parallel fashion.[34]

2.6.1. Equipment.

1. Centrifuge
2. Vortex mixer
3. End-over-end rotator
4. 37°C incubator
5. Standard equipment for SDS-PAGE and Western blotting

2.6.2. Materials.

1. GalNAz labeled protein pellet (step 2.4.3.14)
2. 1% SDS, 50 mM Tris pH 8
3. Milli-Q (or equivalent) purified H_2O
4. Methanol
5. Chloroform
6. 50 mM $CuSO_4$ in H_2O
7. 100 mM TCEP in H_2O
    a. Prepare fresh immediately before use and protect from light.
8. 10 mM PEG alkyne in 200 mM Na_2HPO_4 pH 8
    a. We typically use 2-kDa or 5-kDa mPEG alkyne (PLS-2035 or PLS-2034, Creative PEGWorks).
    b. Prepare fresh immediately before use.
    c. For proteins with a very high molecular weight (MW), it may be possible to use a higher MW PEG.[43] Polymers up to 30-kDa are available from Creative PEGWorks. However, we find that longer reaction times and/or higher

temperatures are necessary for efficient labeling with larger PEG molecules. The precipitation of proteins labeled with 10-kDa or higher PEG molecules can also be problematic.

   d. Inspect the quality of any PEG compound prior to use by MALDI-TOF MS. High-quality PEG will present a narrow set of peaks centered on the reported MW.

9. 500 mM BTTAA in DMSO
10. SDS-PAGE loading buffer: 2% SDS, 50 mM Tris (pH 6.8), 100 mM DTT, 0.1% (w/v) bromophenol blue, and 10% glycerol

2.6.3. Procedure.

1. Redissolve the protein pellet in 50 µL of 1% SDS, 50 mM Tris pH 8 as described previously.
2. Add 46 µL of H_2O and vortex briefly.
3. Pre-mix BTTAA, $CuSO_4$, and PEG stock solutions:
   a. Add 0.5 µL of 500 mM BTTAA to 5 µL of 50 mM $CuSO_4$, mix, and incubate for 1-2 minutes.
   b. Add 100 µL of 10 mM PEG alkyne to the $CuSO_4$-BTTAA mixture and incubate for 1 minute.
4. Add (in order) 100 µL of the BTTAA-$CuSO_4$-PEG solution and 4 µL of 100 mM TCEP (vortex briefly to mix after each addition). The final reaction conditions are outlined in **Table 2.4**.

a. The solution should turn bright yellow after vortex mixing, but will turn back to clear over the next 1-2 minutes.

Table 2.4. Reaction Conditions for CuAAC with PEG Alkyne.

Reaction Components[a]	**Volume (µL)**	**Final Concentration**
Protein mixture (3 mg/mL in 1% SDS, 50 mM Tris pH 8)	50	0.75 mg/mL
H_2O	46	
PEG-$CuSO_4$-BTTAA mixture[b] **0.5 µL 500 mM THPTA** **5 µL 50 mM $CuSO_4$** **100 µL 10 mM PEG alkyne**	100	 1.2 mM 1.2 mM 4.75 mM
100 mM TCEP	4	2 mM
Final Volume	200	

[a] Vortex briefly to mix after each addition.
[b] Prepared according to instructions in text.

5. Incubate the reaction at 95°C for 1-2 minutes.
    a. Alternatively, the reaction can be left to rotate end-over-end at 37°C in the dark for 24 hours. If using 5-kDa PEG for 24 hour labeling at 37°C, sometimes incubating for an additional 24 hours (48 hours total) may improve labeling efficiency. Furthermore, for the potential use of higher MW PEG, we have found that many proteins are stable for at least 60 hours under these conditions.
    b. See also the recent protocol published by Pratt and colleagues.[44]
6. Precipitate the protein as previously described and wash three times with 1 mL of methanol to remove unreacted PEG.
7. Redissolve the protein in the desired volume of loading buffer for SDS-PAGE and analysis by Western blotting (see **Section 2.6.4** below).

2.6.4. Quantification of Protein O-GlcNAcylation Stoichiometry.

The lysates are resolved by SDS-PAGE and analyzed by Western blotting using antibodies against the protein(s) of interest. For standard cell lysates, we typically use 50 to 100 μg of total protein for analysis, depending on the abundance of the protein. For other applications, such as detecting O-GlcNAcylation of purified or overexpressed proteins, the amount needed depends on the O-GlcNAcylation stoichiometry and resolution capacity of the gel. Successful PEG labeling will reveal a mass-shifted band corresponding to the MW of the PEG tag for each O-GlcNAc group on the protein. The relative abundance of each O-GlcNAcylated form and the total O-GlcNAcylation stoichiometry can be obtained by quantifying the ratio of the signals for the mass shifted band(s) to the total, protein-specific band.[2,34] See **Fig. 2.1d** for typical results using an antibody against CREB (4820, Cell Signaling Technologies). In general, we have found that CREB serves as an excellent positive control that is expressed in many mammalian cell lines with an O-GlcNAcylation stoichiometry of approximately 20-30%. Although other well-characterized O-GlcNAcylated proteins can be used, we recommend against using highly O-GlcNAcylated proteins as a positive control because they often show a mass shift even when the labeling is incomplete. It is important that the labeling be complete for an accurate assessment of O-GlcNAcylation stoichiometry. Notably, this method can also be used to study the interplay between O-GlcNAcylation and other PTMs such as phosphorylation using phosphorylation state-specific antibodies.[2] Finally, in all of the above cases, it is important to employ a quantitative Western blotting system, such as the Odyssey Imaging System (LI-COR Biosciences). Overall, this method provides the only direct way to measure O-GlcNAcylation stoichiometries without the use of laborious MS methods. Moreover, this approach utilizes standard techniques for protein analysis without the need for advanced instrumentation or radiolabels.

2.7. Biotin/TAMRA Immunoprecipitation.

This section describes our workflow for streptavidin capture or TAMRA immunoprecipitation of O-GlcNAcylated protein(s) from a complex cell lysate. Upon release, the O-GlcNAcylated protein(s) can be subjected to detection and quantification (**Section 2.7.4**) or MS analysis (**Section 2.8**). These methods are most useful for initial detection of O-GlcNAcylation on a protein of interest or for MS-based detection and site-mapping of O-GlcNAcylated peptides (**Section 2.8**).

2.7.1. Equipment.

1. Centrifuge
2. Vortex mixer
3. End-over-end rotator
4. Magnetic separator
5. Standard equipment for SDS-PAGE and Western blotting

2.7.2. Materials.

1. Biotin or TAMRA-labeled proteins (step 2.5.3.5)
2. Neutralization buffer: 6% IGEPAL CA-630, 100 mM Na_2HPO_4 pH 8, 150 mM NaCl
3. Dilution buffer: 100 mM Na_2HPO_4 pH 8, 150 mM NaCl
4. Streptavidin magnetic beads or High Capacity NeutrAvidin Agarose (Pierce, for biotin IP)
5. Protein A/G magnetic beads (Pierce, for TAMRA IP)
6. TRITC polyclonal antibody (A-6397, ThermoFisher)

   a. Alternatively, a TAMRA monoclonal antibody (MA1-041, ThermoFisher) can also be used.

7. TAMRA wash buffer: 1% IGEPAL CA-630, 100 mM Na_2HPO_4 pH 8, 150 mM NaCl
8. Biotin low salt wash buffer: 100 mM Na_2HPO_4 pH 7.5, 150 mM NaCl, 1% Triton X-100, 0.5% sodium deoxycholate, 0.1% SDS
   a. While cleavage of the Dde-biotin-alkyne in buffers containing SDS has been previously reported,[45] we have found that it is stable in up to 1% SDS at room temperature.[33]
9. Biotin high salt wash buffer: 100 mM Na_2HPO_4 pH 7.5, 500 mM NaCl, 0.2% Triton X-100
10. Biotin elution buffer: 50 mM Tris pH 6.8, 2.5% SDS, 100 mM DTT, 10% glycerol, and 2 mM biotin (add 0.1% (w/v) bromophenol blue if to be used directly for Western blotting)
11. TAMRA wash buffer: 50 mM Tris pH 7.4, 150 mM NaCl, 1% Triton X-100
12. TAMRA elution buffer: 2% SDS, 50 mM Tris pH 6.8, 100 mM DTT, and 10% glycerol (add 0.1% (w/v) bromophenol blue if to be used directly for Western blotting)
13. PBS pH 7.4 (10 mM Na_2HPO_4, 1.8 mM KH_2PO_4, 137 mM NaCl, 2.7 mM KCl)
14. 2% (w/v) hydrazine monohydrate in H_2O
   a. Make this solution fresh immediately before use.
15. Acetone
16. 1% SDS in 20 mM HEPES pH 7.9

2.7.3. Procedure.

1. Save 1/10 (4 μL) of the biotin or TAMRA-labeled protein solution as input to confirm effective enrichment or to quantify the O-GlcNAcylation stoichiometry of labeled proteins.
2. To avoid denaturing proteins on the affinity resins, neutralize the SDS in the protein sample with an equivalent volume of neutralization buffer.
3. Dilute the sample to 500 μL with dilution buffer.
4. Wash the beads twice with 1 mL of wash buffer. Typically, we use the following amounts of beads for the applications discussed:
    a. 40 μL of streptavidin magnetic beads (**Section 2.7.3.1**)
    b. 50 μL of Protein A/G magnetic beads (**Section 2.7.3.2**)
    c. 25 μL of high capacity NeutrAvidin agarose (**Section 2.7.3.3**)
5. Add the diluted protein solution to the washed beads.

2.7.3.1. Non-Cleavable Biotin.

1. Rotate end-over-end for 2 hours at room temperature.
2. After the precipitation is complete, remove the flowthrough, resuspend the beads in 1 mL of biotin low salt wash buffer, and rotate end-over-end for 5 minutes at room temperature
    a. A portion of the flowthrough can be retained and analyzed to ensure complete precipitation by the affinity resin.
3. Remove the wash buffer and repeat four more times with 1 mL of low salt wash buffer and five times with 1 mL of high salt wash buffer to remove non-O-GlcNAcylated proteins.

   a. In applications where there tends to be high background (e.g. protein overexpression), the wash conditions can be made more stringent by replacing the low salt wash buffer with 100 mM Na_2HPO_4 pH 7.5, 150 mM NaCl, 1-3% SDS. However, this may elute some biotinylated proteins as well.

4. After the last wash, centrifuge the beads briefly (5-10 seconds) at 500 x *g* and remove any residual wash buffer.
5. Resuspend the beads with 30 µL of biotin elution buffer and boil for 15 minutes with occasional vortex mixing.
6. Centrifuge the tube briefly and transfer the elution buffer to a new tube.
   a. The eluent can be safely stored indefinitely at -80°C.
   b. For endogenous proteins, we typically resolve the entire eluent in a single gel lane. However, for overexpressed proteins, it is usually sufficient to run as little as 1/10 of the eluent.

2.7.3.2. TAMRA.

1. Add 10 µL of TRITC polyclonal antibody to the mixture.
2. Rotate end-over-end overnight at 4°C.
3. Remove the flow-through and wash the beads by rotating end-over-end for 5 minutes at 4°C with 1 mL of TAMRA wash buffer.
4. Remove the wash buffer and repeat four additional times.
5. After the final wash, elute TAMRA-labeled proteins by boiling with 30 µL of TAMRA elution buffer for 15 minutes and proceed as described for the biotin samples.

a. These conditions are used to quantitatively release TAMRA-labeled proteins, but they will also elute the antibody, which can interfere with Western blot quantification. We suggest the use of a conformation-specific secondary antibody for detection during Western blotting (e.g. 3678S, Cell Signaling Technology).
b. Alternatively, 100 mM glycine pH 2.5 can be used to elute the protein in cases where co-elution of TAMRA antibody is problematic and/or stoichiometric elution is not required.

2.7.3.3. Cleavable Dde-Biotin.

1. Rotate end-over-end for 2 hours at room temperature.
2. Transfer the beads to a spin filter and wash the beads as described for the non-cleavable biotin.
3. Wash the beads twice more with 0.5 mL of PBS.
4. Resuspend the beads with 50 µL of 2% (w/v) hydrazine monohydrate and incubate with end-over-rotation for 1 hour at room temperature.
5. Collect the eluent via centrifugation at 2,000 x *g* for 30 seconds.
6. Resuspend the beads in 50 µL of PBS and incubate with end-over-end rotation for 5 minutes at room temperature.
7. Collect this wash by centrifugation as before and combine with the eluent.
8. Precipitate the eluted proteins by the addition of 4 volumes (400 µL) of -20°C acetone and incubate for 2 hours to overnight at -20°C.

a. Do not use the methanol/chloroform/H_2O method here as it is extremely difficult to form a pellet with low quantities of protein. The precipitated proteins can be stored for up to 6 months in acetone at -80°C.

9. Centrifuge the precipitated proteins at 21,130 x *g* for 10 minutes at 4°C, remove the acetone, and dry the pellet as before.
10. For analysis by SDS-PAGE, resuspend the pellet in 40 μL of SDS-PAGE loading buffer.
    a. For direct analysis by MS, redissolve the proteins in a buffer compatible with an in-solution digestion method, such as 8 M urea, 50 mM Tris pH 8.

2.7.4. Detection and Quantification of Enriched O-GlcNAcylated Proteins.

Western blotting of the eluted solution can provide putative evidence for O-GlcNAcylation of specific proteins. It is important to run a negative control simultaneously in which GalT has been omitted from the GalNAz labeling step (as described earlier) to corroborate these results. Approximate O-GlcNAcylation stoichiometries can be determined following biotin labeling by resolving the eluted sample (step 2.7.3.1.6) by SDS-PAGE along with a portion of the retained input sample (step 2.7.3.1) and calculating the fraction of eluted O-GlcNAcylated protein to the total protein signal.[4] Furthermore, the method can be used to monitor changes in the O-GlcNAcylation levels of individual proteins across different physiological conditions. Although this method cannot reveal the presence of multiple O-GlcNAcylation sites, it does have some advantages over labeling proteins with PEG alkyne. Specifically, (1) enrichment allows for the detection of low O-GlcNAcylation stoichiometries, (2) O-GlcNAcylation of high MW proteins can be readily measured without relying on a mass shift, and (3) some antibodies may not recognize mass-shifted proteins. Regardless, after observing that a given protein is likely O-

GlcNAcylated, MS-based methods can be used as further, more definitive verification and to identify the exact site(s) of O-GlcNAcylation.

2.8. O-GlcNAc Site Identification.

The identification of specific serine/threonine residues that are modified by O-GlcNAc is often critical to interrogate its functional relevance. Accordingly, several techniques have been developed for this purpose. Originally, O-GlcNAcylated peptides were labeled with [^{3}H]-galactose and sequenced by Edman degradation.[30] However, with the rise of powerful MS-based methods for peptide/protein sequencing, many techniques have been developed to map O-GlcNAc sites on proteins;[32,33,46-49] a thorough review of current methods for O-GlcNAc site mapping can be found elsewhere.[18] Here we describe a general approach for O-GlcNAc site mapping and its enhancement using chemoenzymatic labeling. Unlike MS analysis of immunoprecipitated protein alone, chemoenzymatic labeling has the specific advantages of providing 1) an effective method for enrichment of O-GlcNAcylated peptides/proteins to greatly improve the detection sensitivity, 2) a positively charged amine left by the cleavable biotin tag to facilitate O-GlcNAc site mapping, and 3) a unique ion fragment signature upon MS/MS analysis for conclusive identification of the O-GlcNAc modification. Once modification sites are discovered, the tools outlined in the previous sections can be used to investigate how O-GlcNAcylation at individual sites changes in response to stimuli.

2.8.1. Mapping of O-GlcNAc Sites Using MS.

To map the O-GlcNAc sites on a protein of interest, a tagged form of the protein can be overexpressed in HEK 293T cells (or any other easily transfectable cell line). TMG can be added

to the cells to enhance the overall levels of O-GlcNAcylation. The protein of interest is then immunoprecipitated, subjected to SDS-PAGE, and excised from the gel. After reduction, alkylation, and proteolytic digestion in gel, the extracted peptides are analyzed by MS.[50] The use of electron-transfer dissociation tandem MS (ETD-MS/MS) has become a powerful technique for mapping O-GlcNAc sites due to its ability to fragment peptides without breaking the glycosidic linkage between serine/threonine residues and GlcNAc.[18] Indeed, we and others have used this workflow to successfully map O-GlcNAc sites on multiple occasions.[2,4,5,51]

Recently, we used a similar workflow in conjunction with a cleavable Dde-biotin-alkyne probe to identify two known and four novel O-GlcNAcylation sites on OGT.[33] The Dde-biotin moiety allows for efficient capture and release of O-GlcNAcylated peptides and generates a positively charged amine functionality on the glycopeptide to improve its ionization efficiency (**Fig. 2.1a**). We believe that this new probe has significant potential to facilitate the identification of O-GlcNAc sites. In this case, overexpressed, immunoprecipitated protein could be subjected to the workflow described in **Section 2.7.3** using Dde-biotin-alkyne as the azide-reactive probe. The eluted O-GlcNAcylated protein is then purified by SDS-PAGE and processed as outlined above. Alternatively, the eluent can be processed directly by in-solution digestion or with filter-aided sample preparation.[52]

Labeled O-GlcNAcylated peptides can be easily identified using higher-energy collisional dissociation (HCD) MS/MS fragmentation by the presence of up to three fragmented linker ions at 300.1, 318.1, and 503.2 *m/z*. These fragment ions correspond to cleavage of the glycosidic bond between GlcNAc and GalNAz and its water adduct (300.1 and 318.1 *m/z*, respectively) and cleavage between GlcNAc and the serine/threonine residue (503.2 *m/z*). For subsequent ETD-MS/MS analysis, we typically use LTQ-Velos, Orbitrap Elite, and/or Orbitrap Fusion instruments

(ThermoFisher Scientific), but any instrument capable of performing ETD-MS/MS would be sufficient. Regardless, it is important to account for the variable addition of the mass tag (502.202341 Daltons) to serine and threonine residues in the analysis.[33] In summary, we believe that the procedure outlined may aid in the detection of low-abundance or otherwise hard to identify O-GlcNAc sites.

2.9. Integrated Workflow for Discovery and Biological Assessment of Novel O-GlcNAcylated Proteins.

Together, chemoenzymatic tagging methods provide a powerful approach for the detection and analysis of novel O-GlcNAcylated proteins. In our lab, we follow an integrated workflow when assessing the importance of a putatively modified protein. First, we use biotin or TAMRA labeling followed by immunoprecipitation and Western blot detection (**Sections 2.5** and **2.7.3.1** or **2.7.3.2**) to provide direct evidence of protein O-GlcNAcylation. Importantly, we perform a negative control experiment without adding GalT to ensure that the observed signal is specific for the O-GlcNAcylated structure. Next, we map the modification site(s) by either direct MS analysis of a FLAG-tagged, immunoprecipitated protein of interest (**Section 2.8.1**) or labeling and enrichment with the Dde-biotin-alkyne probe prior to MS analysis (**Sections 2.5** and **2.7.3.3**). If the protein has multiple sites, expression of alanine mutants lacking specific O-GlcNAcylation sites in cells, followed by analysis of their stoichiometries using PEG or biotin labeling, can sometimes be used to determine the major sites (**Sections 2.7** and **2.8**). Moreover, these mutants can be expressed in the presence of TMG or other stimuli to uncover which sites are dynamic or rapidly cycled. Finally, cells with the endogenous protein or overexpressed mutants can be subjected to physiologically relevant treatments such as serum starvation, hypoxia, or KCl-

mediated depolarization followed by PEG labeling to measure changes in the levels of each O-GlcNAcylation state in response to biological stimuli. Again, we have found CREB to be an excellent positive control for the strategies outlined in this section. As an example, the increase in O-GlcNAcylation of CREB stimulated by TMG treatment can be seen in **Fig. 2.3** Using PEG labeling, mono-O-GlcNAcylation of CREB was also found to increase in neurons after KCl-induced depolarization (**Fig. 2.1d**). Ultimately, the collective results of this integrated workflow will provide strong evidence for novel O-GlcNAcylation events and guide subsequent functional studies.

2.10. Conclusions and Future Directions.

The O-GlcNAcylation of intracellular proteins is emerging as a major regulator of key cellular processes in both health and disease. Effective methods to characterize the presence and dynamics of this PTM will greatly propel studies of its functional significance. Traditional methods such as tritium labeling and the use of certain O-GlcNAc-specific antibodies suffer from a lack of sensitivity and specificity. Moreover, using such methods to detect changes in O-GlcNAcylation levels and stoichiometry reliably in a complex lysate can be very difficult or in some cases impossible. Although the rapid proliferation of MS-based techniques has alleviated some of these concerns, MS-based approaches require specialized expertise and access to expensive instrumentation. Thus, highly accessible, cost-effective approaches that can be readily performed in most laboratories on a routine basis remain vital to elucidate the physiological importance of O-GlcNAcylation.

The protocols above provide a practical platform that is easy to implement in many research settings. GalT labeling and the CuAAC reaction provide an efficient means to install a variety of functional tags for diverse downstream applications. The commercial availability of the reagents and the simplicity of the experimental approach should facilitate adoption of this methodology by non-specialists. In the future, further development of these techniques in conjunction with MS will pave the way for more quantitative, high-throughput methods to study O-GlcNAcylation dynamics on individual proteins as well as on a global scale. Combining the techniques with established methods such as stable isotope labeling by amino acids in cell culture (SILAC),[53] isobaric tag for relative and absolute quantitation (iTRAQ),[54] or tandem mass tags (TMT)[55] should allow for direct comparison of the O-GlcNAcome across diverse physiological conditions. Together, we hope that these advances will illuminate the broad importance of O-GlcNAcylation and lead to new discoveries at the frontiers of biology and human health.

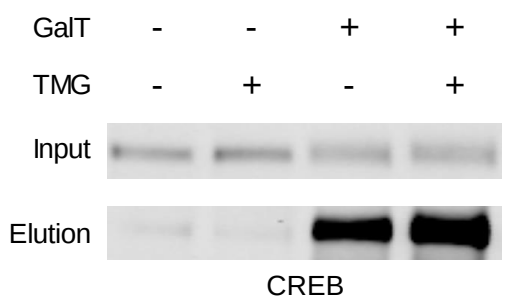

Fig. 2.3. Monitoring O-GlcNAc Dynamics with Biotin Labeling and Streptavidin Capture. Streptavidin capture of O-GlcNAcylated proteins labeled with biotin can allow for the detection and dynamic monitoring of novel O-GlcNAcylated proteins. HEK 293T cells were treated with 50 μM TMG or vehicle for 6 hours and subjected to the workflow outlined in **Sections 2.4 and 2.7**. Immunoblotting with an anti-CREB antibody revealed a robust increase in O-GlcNAcylation of CREB upon TMG treatment.

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Chapter 3

Studies into the Role of Cdk5 O-GlcNAcylation in Neuronal Function and Alzheimer's Disease

3.1. Abstract.

The prevalence of AD and other dementias has reached epidemic proportions. However, to date, not a single disease modifying therapeutic intervention has been developed. Furthermore, besides postmortem analysis of brain tissue, there are no consensus methods for AD diagnosis, especially in the early stages of the disease when preventing further cognitive decline is of utmost importance to patients and their families. It is highly likely that a more comprehensive understanding of the molecular underpinnings of AD will do much to remedy this unfortunate situation. Therefore, the studies in this chapter aim to address this lack of understanding through the investigation of two intracellular events that have emerged as potential, major drivers of AD pathogenesis: dysregulated cyclin-dependent kinase 5 (Cdk5) activity and aberrant modification of intracellular proteins by O-GlcNAc. Cdk5 is known to play a role in regulating, among others, two central intracellular events in AD: hyperphosphorylation of tau and amyloidogenic processing of APP. O-GlcNAc, on the other hand, is a dynamic, inducible PTM of proteins thought to regulate key cellular signaling pathways in response to a wide variety of stimuli such as stress, nutrient availability, and neuronal activity. Here, we report that Cdk5 activity is increased in the absence of OGT and dynamically regulated by O-GlcNAcylation. Moreover, we map specific O-GlcNAc sites on Cdk5 and show that blocking O-GlcNAcylation at two potential sites in Neuro-2a (N2A) cells is sufficient for increasing Cdk5 activity. Finally, we also develop a lentiviral knockdown (KD) and replacement strategy to facilitate the further study of Cdk5 O-GlcNAcylation in neurons and in vivo. Altogether, the data presented herein suggests a previously unappreciated link between the decreased levels of O-GlcNAc and dysregulated Cdk5 activity seen in AD.

3.2. Introduction.

In a progressively aging population, the prevalence of AD and other dementias has reached epidemic proportions. AD, which is characterized by the accumulation of senile plaques and neurofibrillary tangles (NFTs), striking neuronal loss, and a profound disruption of episodic memory, has an associated healthcare cost upwards of $172 billion per year in the United States alone.[1-3] Nevertheless, the pathogenesis of this devastating disease is poorly understood, and we lack both definitive diagnostic methods, beyond postmortem analysis of brain tissue, and any disease modifying treatment.[4,5] Thus, efforts to better understand the molecular underpinnings of AD are desperately needed. Here, we explore two promising paths toward unraveling the cellular mechanisms that underlie AD: understanding the role of (1) dysregulated Cdk5 activity and (2) aberrant modification of intracellular proteins by O-GlcNAc.

Cdk5 is a proline-directed serine/threonine kinase notable for its apparent lack of involvement in the cell cycle and its high activity in the brain.[6] Unlike other cyclin-dependent kinases, its activity does not depend on cyclins, but rather on two unique activator proteins, p35 and p39, and their calpain-mediated cleavage products, p25 and p29, respectively.[7] Cdk5 has been implicated in a huge variety of neuronal processes starting in early development (reviewed extensively by Tsai and colleagues[6]). For instance, KO of p35, the major of the two Cdk5 activator proteins, in mice results in severe cortical lamination defects due to the failure of newly generated neurons to correctly migrate past older neurons.[8] KO of Cdk5 itself is perinatally lethal with major disruptions to multiple nervous system structures.[9] Accordingly, during development, Cdk5 has been found to localize to the leading edge of migrating neurons as well as axonal growth cones where it seems to be playing a key role in regulating actin and other cytoskeletal dynamics.[10,11] This role in migration is preserved throughout adulthood with established roles for Cdk5 in

regulating dendritic spine development, again through the phosphorylation of substrates involved with actin dynamics such as Wiskott-Aldrich syndrome protein (WASP) family verprolin homologous protein 1 (WAVE1)[12] and serine/threonine-protein kinase PAK 1.[13]

As expected given the major role of actin dynamics in learning and memory,[14] inducible (to avoid the severe developmental phenotype) p35 KO mice show profound defects in learning and memory.[15-17] Consistent with this phenotype, Cdk5 is also known to modify multiple proteins directly involved in synaptic plasticity, LTP, and LTD in addition to regulating actin and cytoskeletal dynamics.[18] For instance, Cdk5 regulates both presynaptic vesicle release through its phosphorylation of multiple proteins, e.g. syntaxin-binding protein 1,[19,20] and the presence and function of receptors at the PSD, e.g. N-methyl-D-aspartate receptor (NMDAR) subunits 2A (NR2A)[21,22] and 2B (NR2B).[23] Interestingly, blocking the interaction between Cdk5 and NR2B actually improves synaptic transmission and memory formation in vivo, suggesting that Cdk5 activity also plays an inhibitory role in learning and memory.[24] Indeed, it has been suggested that Cdk5 activity is maintained in a fine balance where activity is necessary to promote memory formation but also inhibit prolonged neuronal activation which can lead to excitotoxicity and neuronal death, a key feature of many neurodegenerative diseases.[6]

Furthermore, one of the earliest identified substrates of Cdk5 was tau, which also suggests a role for Cdk5 in AD pathogenesis given that hyperphosphorylated tau is a major component of NFTs.[25,26] In addition, APP, the precursor to Aβ peptides, is also phosphorylated by Cdk5, and this phosphorylation is known to promote the formation of Aβ peptide species that have a higher propensity to form plaques.[27,28] Numerous subsequent studies have implicated dysregulated Cdk5 activity as a major driver of tau pathology,[29-32] neurodegeneration,[22,33,34] memory impairment,[22,35-39] β-amyloid plaque development,[27,28,40] and even human AD.[41-43] In fact, aberrant activation of

Cdk5 is sufficient to drive neurodegeneration and the accumulation of NFTs in mice.[44,45] Cdk5 overactivity also occurs in the context of ischemic stroke, and Cdk5 inhibitors as an adjuvant therapy for improving stroke outcomes are in active development.[46-49] Overall, Cdk5 overactivity seems to be driving the deleterious phenotypes across multiple neurological disorders. Thus, in AD specifically, we believe the following general conclusions are warranted: (a) increases in Cdk5 activity precipitate a host of neurodegenerative events, along with profound synaptic dysfunction,[6,24,50,51] and (b) pharmacological or other inhibition of Cdk5 has beneficial effects in models of neurodegeneration.[32,52-54] However, despite the strong body of literature implicating Cdk5 in AD and other neurodegenerative diseases, relatively little is known about how or why Cdk5 activity might increase in the context of AD. Here, we propose that this pathological increase in activity may be partially or wholly mediated by loss of O-GlcNAcylation on Cdk5.

O-GlcNAcylation is a dynamic, inducible PTM of intracellular proteins at serine and threonine residues. Interestingly, a decrease in the overall levels of neuronal O-GlcNAcylation has been strongly implicated in AD.[55-57] Moreover, as discussed in **Chapter 1**, O-GlcNAcylation has been shown to stabilize tau against aggregation and plays a host of neuroprotective roles. Recently, our lab created a forebrain-specific, conditional OGT KO (OGT cKO) mouse which exhibited a striking phenotype characterized by extensive neurodegeneration, formation of NFTs, and increases in the amyloidogenic 42-mer Aβ peptide.[58] Consistent with the profound neurodegeneration, these mice also showed defects in both cued and contextual freezing assays as well as increased anxiety. Interestingly, the deficits in cued freezing were apparent at only 2 months of age, before any detectable loss of neuronal thickness Moreover, we showed a marked decrease in OGT expression levels in the brains of AD patients, consistent with an overall decrease in the levels of O-GlcNAcylation in AD brains observed by others.[58-60] We also found that Cdk5

protein expression was markedly downregulated in neurons, yet genes involved in cell cycle arrest, another major function of Cdk5 in neurons,[6,58] were upregulated. Together, this suggests a reduction in Cdk5 expression or protein stability that may be a compensatory response to increased Cdk5 activity. Herein, we first confirm that Cdk5 activity is increased in the context of OGT KO. Subsequently, we demonstrate that Cdk5 is O-GlcNAcylated in neurons and furthermore that this modification is dynamic suggesting a regulatory versus structural role. Finally, we show that mutation of potential O-GlcNAc sites on Cdk5 in N2A cells is sufficient to increase its activity. Along with (1) the wealth of prior data demonstrating that increased Cdk5 activity is deleterious in neurons, and (2) the observation by multiple labs that O-GlcNAcylation is decreased globally in AD, these findings suggest that decreased O-GlcNAcylation of Cdk5 may at least in part contribute to AD pathogenesis.

3.3. OGT KO Increases Cdk5 Activity and p25/35 Binding.

To follow up on the possible causative link between Cdk5-specific defects and neurodegeneration in our OGT cKO mouse, we first set out to confirm whether neuronal Cdk5 activity was increased in the context of OGT KO. To simulate OGT KO in controlled neuronal culture conditions, we harvested embryonic cortical neurons from floxed-OGT mice and used a lentiviral system to deliver Cre recombinase (Cre). This system proved extremely robust and yielded approximately 97% KO of OGT (**Fig. 1a**). With an efficient method for generating OGT KO neurons in hand, we then prepared 6 neuronal cultures from floxed-OGT mice and treated them with either lentivirus delivering Cre or and mCherry control. After 14 days in vitro (DIV),

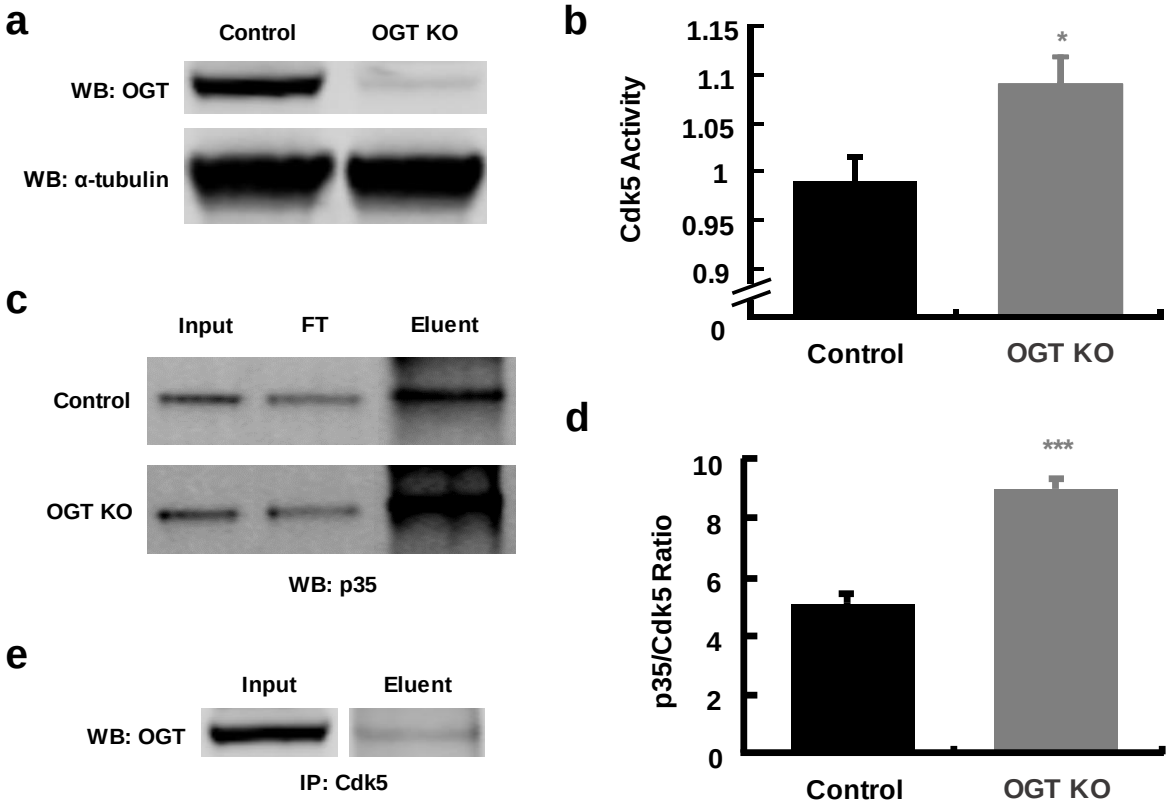

Fig. 3.1. OGT KO Increases Cdk5 Activity and Affinity for p35.
(a) Lentiviral transduction of floxed-OGT neurons with Cre results in efficient knockout of OGT versus an mCherry control. **(b)** Cdk5 activity is increased in primary mouse cortical neurons lacking OGT. Cdk5 from floxed-OGT neurons transduced with Cre or an mCherry control was IPed and activity was assessed using the ADP-Glo system. **(c)** Cdk5 co-IPs more p35 in floxed-OGT neurons transduced with Cre versus an mCherry control; p35 expression does not differ significantly between the two conditions. **(d)** Graph of the data in **(c)** with n=3 technical replicates from each of n=22 biological replicates. **(e)** OGT co-IPs with Cdk5 in mouse primary cortical neurons. Error bars are ± s.e.m., *$p < 0.05$, ***$p < 5e\text{-}5$ by unpaired Student's t-test.

these neurons were lysed, Cdk5 was immunoprecipitated (IPed), and Cdk5 activity was assayed using ADP-Glo (Promega, Madison, WI). Excitingly, we found Cdk5 IPed from OGT KO neurons exhibited significantly higher activity (**Fig. 3.1b**). To see whether this increased activity was a direct result of increased p35 binding, we also interrogated the amount of p35 co-IPed with Cdk5 by quantitative Western blotting (WB). Consistent with the increase in Cdk5 activity, we also found a concomitant increase in Cdk5-p35 binding (**Fig. 3.1c-d**). Interestingly, we also found that OGT IPs with Cdk5 confirming a direct interaction between the two proteins and suggesting that

Cdk5 may be a substrate of OGT (**Fig. 3e)**. In summary, these results confirm for the first time that globally decreased O-GlcNAcylation leads directly to an increase in Cdk5 activity in neurons, which may have important implications for AD and other neurodegenerative diseases.

3.4. Cdk5 is Dynamically O-GlcNAcylated in Neurons.

Having determined that the absence of OGT interacts with and increases Cdk5 activity, we next sought to investigate whether this was through direct modification of Cdk5 or some other mechanism. To our knowledge, Cdk5 O-GlcNAcylation has not been previously observed in large mouse or human O-GlcNAcomics data sets.[61-63] Thus, we used our well-established chemoenzymatic labeling technique (**Chapter 2**) to assess whether Cdk5 is O-GlcNAcylated in neurons. Briefly, O-GlcNAcylated proteins in neuronal lysate were labeled with an azido-containing nucleotide sugar analog (UDP-GalNAz) using Y289L GalT. Alkynyl biotin was then selectively added to O-GlcNAcylated proteins using CuAAC, and the O-GlcNAcylated proteins were captured using streptavidin resin.[64,65] The captured proteins were then subjected to SDS-PAGE and interrogated by WB with an anti-Cdk5 antibody. Using the above workflow, we found that Cdk5 is indeed O-GlcNAcylated in primary mouse cortical neurons. To see if this modification dynamically cycles in response to relevant physiological stimuli, we also compared Cdk5 O-GlcNAcylation levels between silenced and KCl depolarized neurons. Here, we noted a striking increase in Cdk5 O-GlcNAcylation after KCl-mediated depolarization (**Fig. 3.2a-b**), strongly suggesting that Cdk5 O-GlcNAcylation is playing a regulatory role in neurons.

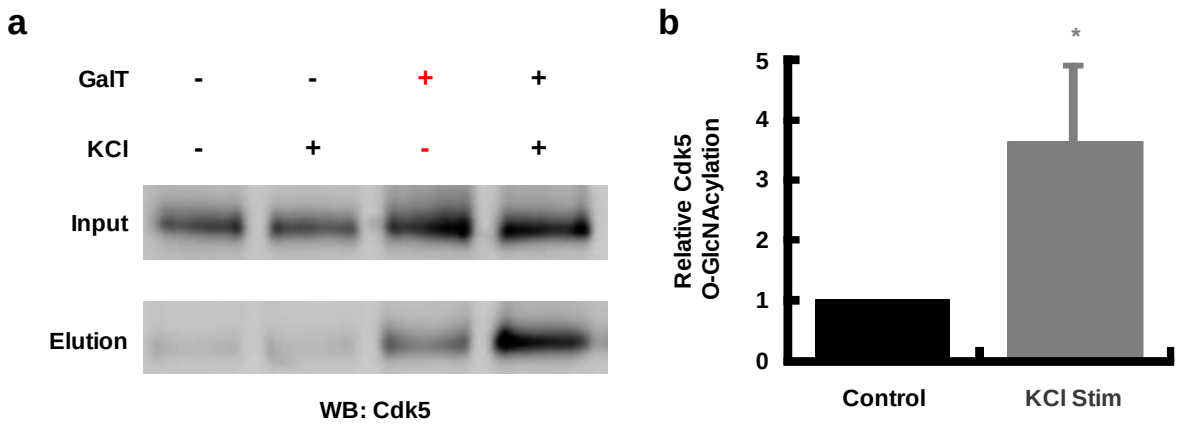

Fig. 3.2. Neuronal Depolarization Dynamically Induces Cdk5 O-GlcNAcylation.
(a) Primary mouse cortical neurons were lysed after treatment with 60 mM KCl or vehicle for 2 hours, and O-GlcNAcylated proteins were isolated using the chemoenzymatic labeling strategy described in the text. Immunoblotting with a Cdk5 antibody revealed increased signal in the elution for KCl simulated neurons. **(b)** Data were quantified as described in **Section 3.8.4**; each condition is the average of n=4 biological replicates. Error bars are ± s.e.m., *$p < 0.05$ by unpaired Student's t-test.

With direct evidence of Cdk5 O-GlcNAcylation, we next moved forward with using MS to map the O-GlcNAc sites on Cdk5. To prepare O-GlcNAcylated Cdk5 for site mapping experiments, we expressed FLAG-tagged Cdk5 in N2A cells. These cells were also co-transfected with OGT and treated with TMG and KCl to maximally increase Cdk5 O-GlcNAcylation stoichiometry and thus our chances of identifying O-GlcNAcylated peptides. Cdk5 was then purified from cell lysates over FLAG immunoaffinity gel (Sigma-Aldrich, St. Louis, MO). A portion of the FLAG eluent was also subjected to WGA affinity chromatography to further enriched O-GlcNAcylated from unmodified Cdk5. Both FLAG and WGA eluent were then gel purified, digested, and submitted for LC-MS/MS analysis. Excitingly, from the FLAG eluent, we were able to map O-GlcNAc to T245/T246/S247 in two separate trials using collision-induced dissociation (CID)/ETD and HCD fragmentation, respectively (see **Chapters 2** and **4** for in depth discussion on O-GlcNAc site mapping). During the course of these experiments, Ke and co-workers also identified this and an

additional site of Cdk5 at S46/S47.[66] Taken together, these studies provide the first evidence that Cdk5 is dynamically O-GlcNAcylated in neurons, potentially at multiple sites.

3.5. Mutation of Potential Cdk5 O-GlcNAcylation Sites Increases Cdk5 Activity in N2A Cells.

To help understand the potential effects of O-GlcNAcylation at each of the aforementioned sites, we used GLYCAM Web[67] to build a structural model of O-GlcNAcylated Cdk5. First, SWISS-MODEL[68] was used to build an optimized homology model of the mouse Cdk5/p25 complex from human Cdk5/p25 (PDB file 1H4L).[69] This model was then submitted to GLYCAM Web where an O-GlcNAc residue was modeled onto each known site (**Fig. 3.3a**). Interestingly, the model clearly shows that O-GlcNAcylation at S46 has the potential to disrupt binding of p25/p35 and

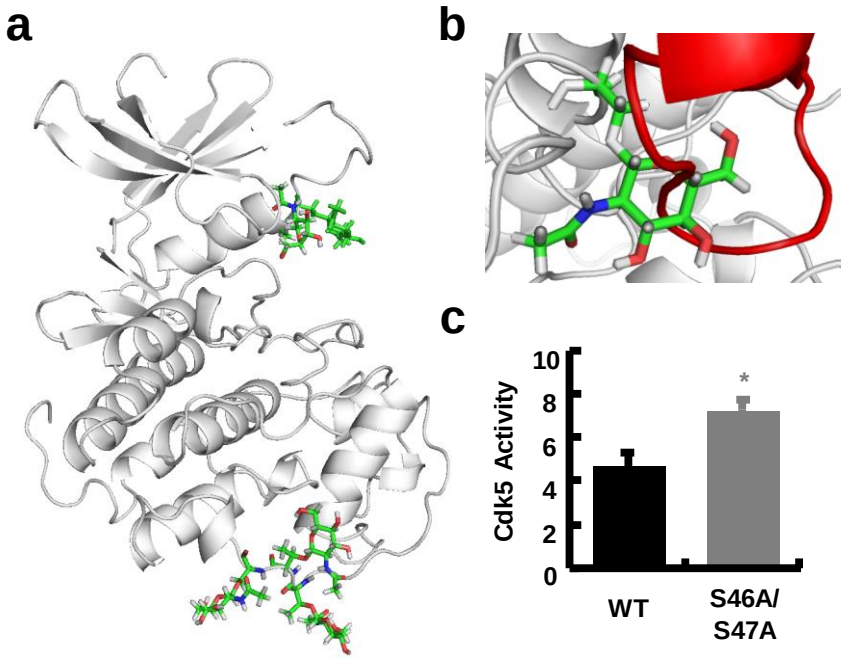

Fig. 3.3. O-GlcNAcylation of Cdk5 May Inhibit Its Activity through Inhibition of p25/35 Binding.
(a) Predicted crystal structure of O-GlcNAcylated Cdk5 at all known sites. **(b)** Magnified image of the environment sounding O-GlcNAcylated S46, highlighting that O-GlcNAcylation at S46 is likely to disrupt the interaction between Cdk5 (white) and p25 (red). **(c)** S46A/S47A Cdk5 has higher activity in N2A cells. Exogenous, FLAG-tagged WT and S46A/S47A Cdk5 were FLAG IPed from N2A cells, and the activity of each was quantified using the AD-Glo system. Each condition is the average of 3 technical replicates from each of 3 biological replicates. Error bars are ± s.e.m., *$p < 0.05$ by unpaired Student's t-test.

therefore inhibit Cdk5 activity (**Fig. 3.3b**). The role of T245/T246/S247 O-GlcNAcylation is less obvious, although it may affect substrate binding given its relative proximity to residues predicted to be involved in this function.[70] To test whether O-GlcNAcylation at S46/S47 might affect Cdk5 activity as suggested by the computational model, we used site-directed mutagenesis (SDM) to mutate both S46 and S47 to alanine and expressed either wild-type (WT) or S46A/S47A FLAG-tagged Cdk5 in N2A cells. The Cdk5 constructs were subsequently purified by FLAG IP and assayed for kinase activity as described above. Notably, the S46A/S47A mutant had significantly higher activity compared to WT Cdk5 (**Fig. 3.3c**). Thus, in summary, O-GlcNAcylation at S46/S47 likely inhibits the interaction between Cdk5 and its activator proteins and is thus a key mechanism for attenuating Cdk5 function in neurons. In the context of AD, reduced O-GlcNAcylation[59] may result in decreased Cdk5 O-GlcNAcylation at S46/S47 and explain the increased Cdk5 activity observed in this devastating disease[41]

3.6. Development of a Lentiviral Mediated Cdk5 KD and Replacement Strategy for Studying Cdk5 O-GlcNAcylation in Neurons and In Vivo.

Having confirmed that Cdk5 is O-GlcNAcylated at multiple sites and that the modification at S46/S47 is likely involved in regulating Cdk5 activity, we next turned to the development of new tools for interrogating the role of Cdk5 O-GlcNAcylation in neurons and in vivo. As transfection efficiencies in primary cortical neurons are known to be relatively low compared to other cell types,[71] we sought to develop a lentiviral delivery system to express mutant Cdk5 in neurons. To avoid any deleterious consequences of Cdk5 overexpression, we aimed to simultaneously KD endogenous Cdk5 and replace it with our mutants at a similar level of expression. Notably, lentiviral-mediated gene transfer is also an extremely efficient method for expressing exogenous

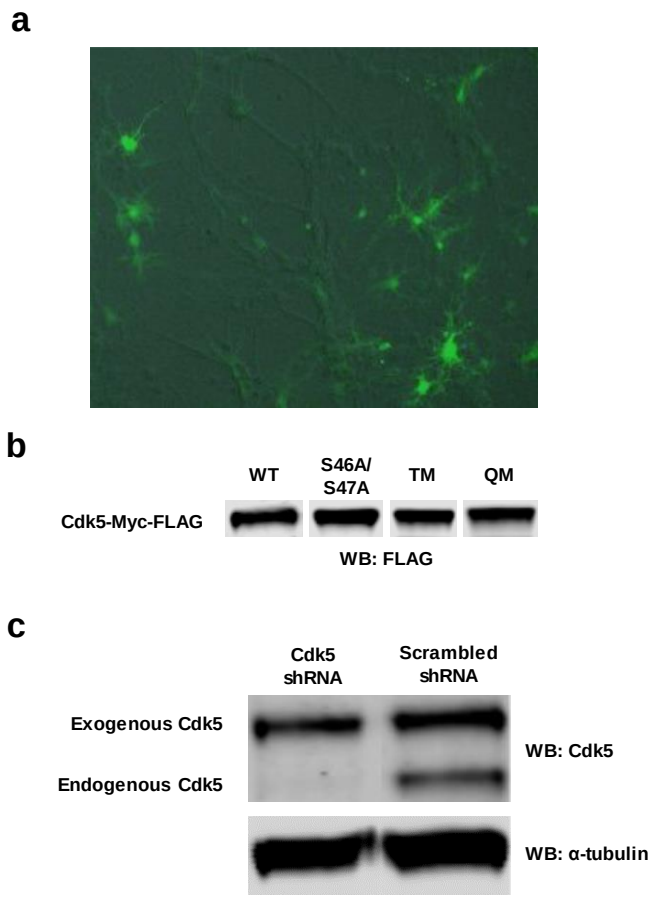

Fig. 3.4. Lentiviral Transduction of Neurons with shRNA-Resistant Cdk5 Allows for the Replacement of Endogenous Cdk5 with Glycosylation-Deficient Mutants.
(a) Fluorescence confocal microscopy confirms efficiency lentiviral transduction as determined by GFP expression. **(b)** All 4 shRNA-resistant Cdk5 constructs express at relatively equal levels in neurons even after co-transduction with Cdk5 shRNA. **(c)** WB showing the absence of Cdk5 after transduction with Cdk5 shRNA (KD efficiency >99%) but no effect after transduction with a scrambled shRNA control. Notably shRNA-resistant Cdk5 expression is present in both samples.

DNA in vivo.[72] The simultaneous delivery of short harpin (sh)RNA and shRNA resistant proteins of interest has proven to be a powerful method for targeted gene KD and replacement.[73] Therefore, we created four lentiviruses to deliver shRNA resistant, myc-FLAG-tagged Cdk5 mutants using SDM, S46A/S47A (46AA), T245A/T246A/S247A (T245AAA), an all known sites to alanine mutant (QM), and WT. These viruses were then used to transduce neurons that had also been co-transduced with Cdk5 shRNA. Notably, our Cdk5 vectors also delivered GFP for efficiency visualization of viral transduction. After 7 DIV, neurons were visualized with confocal microscopy (**Fig. 3.4a**), lysed, and subjected to WB with FLAG antibody. Excitingly, we were able to detect expression of all 4 constructs (**Fig. 3.4b**) at roughly the same level as endogenous Cdk5 (**Fig. 3.4c**). In future experiments, we hope to use this lentiviral KD and replacement system to confirm whether O-GlcNAc-deficient Cdk5 has increased activity in the

mammalian nervous system. Importantly, these studies may provide a unifying theory for decreased O-GlcNAcylation, increased Cdk5 activity, and the development of AD pathology.

3.7. Conclusion.

In this chapter, we have shown for the first time that Cdk5, an important kinase in both neuronal health and disease, activity is regulated by O-GlcNAcylation. The aforementioned studies strongly suggest that increased Cdk5 activity seen in the context of OGT KO is due to the absence of O-GlcNAcylation. This increase in activity may be responsible, at least in part, for the neurodegenerative phenotype observed in our OGT cKO mice and would be consistent with the well-established neurodegenerative effects of aberrant Cdk5 activity.[6] Moreover, combined with the fact that there are lower levels of both OGT and overall O-GlcNAcylation in AD, loss of Cdk5 O-GlcNAcylation may be an important contributor to AD pathogenesis in humans as well (**Fig. 3.5**). Future studies will be directed towards confirming whether loss of Cdk5 O-GlcNAcylation at S46/S47, specifically, contributes to increased Cdk5 activity and neurodegeneration in vivo. O-GlcNAc mimetic[74] Cdk5 constructs could also be used to replace endogenous Cdk5 with our lentiviral KD and replacement system to determine whether mimicking an increase in Cdk5 O-GlcNAcylation can attenuate the severe neurodegenerative phenotype in OGT cKO mice. In summary, the studies herein are beginning to (1) forge a critical new link between two cellular mediators of neurodegeneration previously thought to be unrelated, increased Cdk5 activity and decreased O-GlcNAc levels, and (2) suggest Cdk5 as a major agent through which disruptions in O-GlcNAcylation can lead to symptomatic AD.

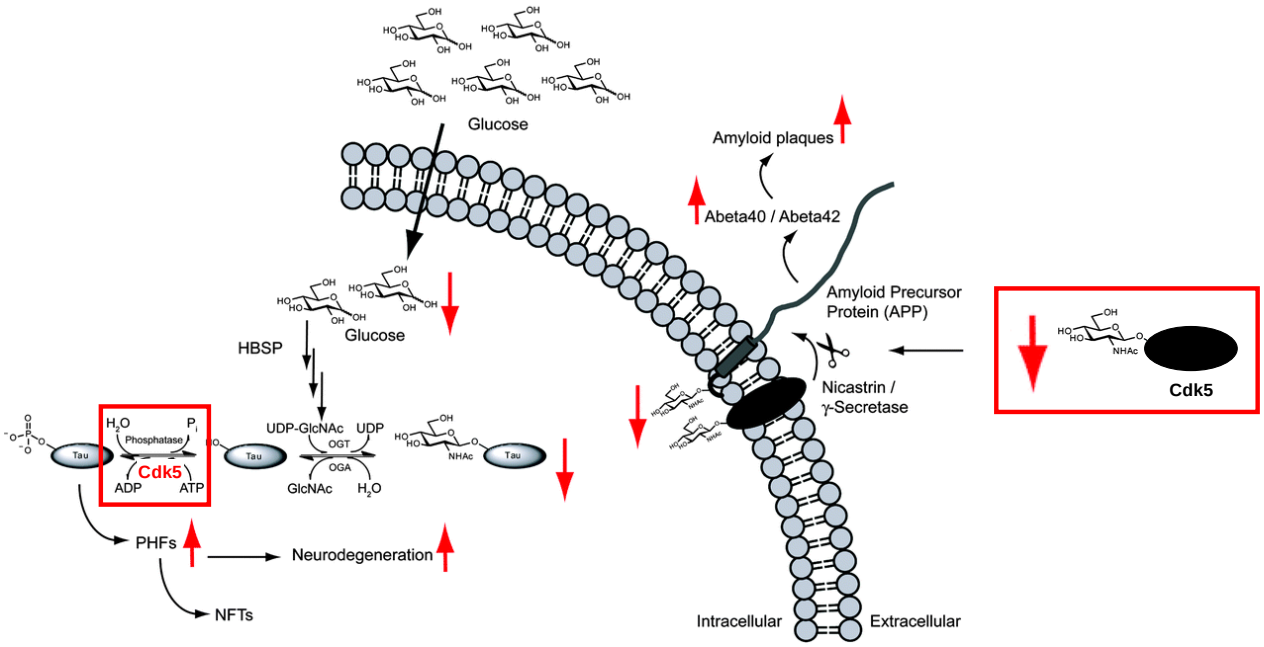

Fig. 3.5. Proposed Mechanism for the Role of Decreased Cdk5 O-GlcNAcylation in AD Pathogenesis.
Decreased O-GlcNAc on Cdk5 S46 may lead to an increased association of Cdk5 with activator proteins p25/35 and/or p29/39, resulting in higher activity. This, in turn, results in the increased phosphorylation of pathogenic proteins such as tau and APP which eventually leads to the formation of NFTs and Aβ plaques, respectively. Increases in phoshpo-tau and APP may have even more drastic effects in the context of decreased O-GlcNAcylation seen in AD, as O-GlcNAcylation is known to both oppose phosphorylation and stabilize proteins against aggregation. Adapted with permission from Yuzwa et al. 2014.[57]

3.8. Experimental Methods.

3.8.1. Reagents and Chemicals.

All chemicals were purchased from Sigma-Aldrich (St. Louis, MO), and all cell culture materials were purchased from ThermoFisher Scientific (Waltham, MA) unless otherwise noted. All primers were purchased from Integrated DNA Technologies (Coralville, IA), and all molecular biology supplies were purchased from New England Biolabs (NEB, Ipswich, MA) unless otherwise indicated.

3.8.2. Neuron and Cell Culture.

Primary mouse cortical neurons were harvested as previously described,[36] plated on poly-d-lysine coated plates, and cultured in Neurobasal medium with 1% penicillin-streptomycin (P/S), 2mM GlutaMAX Supplement, and GS-21 (MTI-GlobalStem, Gaithersburg, MD). Every 2-4 days, half of the media was changed for fresh culture media as outlined above. Neurons were allowed to grow for 7 days before transduction with lentivirus. Otherwise, they were cultured for the lengths indicated in the text. For KCl stimulation experiments, neuronal activity was first silenced by 24 hours treatment with 10 μM tetrodotoxin (Tocris Biosciences, Bristol UK) and 100 μM D-AP5 (Tocris Biosciences). Neurons were then treated with KCl (60 mM) or vehicle for 2 hours and subsequently lysed with either RIPA buffer (for IP experiments) or 2% SDS in HEPES pH 7.9 (for chemoenzymatic labeling experiments), containing Roche cOmplete protease inhibitor cocktail, 0.1 mM TMG, and 0.25 U/μL benzonase nuclease (Santa Cruz Biotechnology, Dallas, TX). In all cases, the protein concentration was measured using BCA assay (ThermoFisher).

N2A and HEK 293T cells were maintained in Dulbecco's Modified Eagle Medium with 100 U/mL P/S, and 10% FBS. Cells were split 1:8 every 2-3 days as necessary. N2A cell lysis was performed as described above for neurons.

3.8.3. Co-Immunoprecipitation.

Neuronal or N2A lysate, prepared as described above, was diluted to 0.5 mg/ml with Tris-buffered saline (TBS) buffer,[75] 0.1 mM TMG, and Roche cOmplete protease inhibitor cocktail. 30 μg of protein was saved as input. The remaining lysate was incubated with anti-FLAG magnetic beads (Sigma-Aldrich) or pre-incubated (1 hour) Cdk5 antibody (sc-173, Santa Cruz Biotechnology, 1:10 dilution) and Protein A/G magnetic beads (40 μL, ThermoFisher) at 4 °C

overnight or for 1 hour at room temperature with end-over-end rotation. The following day, beads were washed 3 times with 0.1% Triton-X-100 in TBS and eluted by boiling in 2% SDS in Tris, pH 8. For samples undergoing subsequent WGA affinity chromatography, elution was performed with 150 μg/mL 3xFLAG Peptide (Sigma-Aldrich) in TBS. Inputs and eluents were run on SDS-PAGE and subjected to WB as described below.

3.8.4. Wheat Germ Agglutinin Affinity Chromatography.

Cdk5 eluted from the FLAG resin was immediately incubated with WGA agarose (Vector Laboratories, Burlingame, CA) overnight with end-over-end rotation at 4 °C. The following day, the beads were washed 5 times with 0.1% Triton-X 100 in TBS and eluted with 0.5 M GlcNAc in 0.1% Triton-X 100 in TBS. The elution was then concentrated by vacuum centrifugation and subjected to SDS-PAGE.

3.8.5. Western Blotting.

Primary antibodies were all used at 1:1000 dilution, and secondary antibodies at 1:10000 unless otherwise specified. Samples were diluted with 4x SDS-PAGE buffer (200 mM Tris-HCl pH 6.8, 400 mM DTT, 8% SDS, 0.4% bromophenol blue, 40% glycerol), resolved on a NuPAGE 4-12% Bis-Tris protein gel (ThermoFisher Scientific), and transferred to Immobilion-FL PVDF membrane (MilliporeSigma, Burlington, MA). Blots were blocked for 1 h at RT with LiCor Odyssey Blocking Buffer (927-50003, LI-COR Biosciences, Lincoln NE) before probing overnight at 4 °C with the following antibodies diluted in blocking buffer: Cdk5 (DC-17, Santa Cruz Biotechnology), FLAG (1:5000, F3165, Sigma-Aldrich), p35 (2860S, Cell Signaling Technologies, Danvers, MA), OGT (DM-17, Sigma-Aldrich), and anti-α-tubulin (Sigma Aldrich,

T9026, 1:3000). Blots were rinsed three times with TBST and then probed with the appropriate secondary antibodies in blocking buffer: anti-mouse AlexaFluor 680 conjugate (A21057, ThermoFisher), anti-rabbit AlexaFluor 680 (A21109, ThermoFisher), anti-rabbit AlexaFluor 790 (A11369, ThermoFisher), or anti-mouse IgG DyLight 800 (A11357, ThermoFisher). Blots were washed 3 x 5 min with TBST and then imaged using an Odyssey Infrared Imaging System (LI-COR Biosciences). Images were processed using ImageStudio v5.2 (LI-COR Biosciences). To calculate O-GlcNAcylation stoichiometry, the ratios of eluents to inputs, weighted by proportion of the total protein in each lane, were used as previously described.[76]

3.8.6. Cdk5 Activity Assay.

Cdk5 activity was measured using ADP-Glo (Promega). Briefly, Cdk5 was IPed as described above, however, before elution from the FLAG beads, Cdk5 activity towards a well-characterized peptide substrate (sc-3066, Santa Cruz Biotechnology) was measured. Each kinase activity assay was performed in 40 mM Tris (pH 7.5), 20 mM $MgCl_2$, 0.1 mg BSA with the addition of 0.75 μL ultrapure ATP (ADP-Glo) and 0.1 mM Cdk5 substrate peptide (75 μL final volume). As a control, the Cdk5 substrate peptide was omitted or roscovitine (Cell Signaling Technologies), a potent Cdk5 inhibitor, was added. The kinase reaction was left to proceed for 45 min at room temperature with end-over-end rotation. The supernatant was then removed and the amount of ADP assayed with ADP-Glo according to the manufacture's protocol. Final luminescence values were normalized to the level of Cdk5 in each kinase reaction (after elution from the FLAG beads) as detected by WB.

3.8.7. Chemoenzymatic Labeling.

O-GlcNAcylated proteins from neuronal lysates were labeled as previously described.[76] Briefly, lysate containing 150 µg of protein was diluted to 200 µL in water and proteins were precipitated by the addition of 3 volumes of methanol, 1 volume of chloroform, and 2.25 volumes of water followed by centrifugation at 21,130 x g for 5 minutes to reveal a disc-like protein pellet at the aqueous-organic interface. The aqueous layer was removed and the pellet washed three times with 2.25 volumes of methanol. Protein pellets were then resolubilized with 40 µL dissolution buffer (20 mM HEPES, 1% SDS, pH 7.9). Water (49 µL), 5.5 mM MnCl (11 µL), and 80 µL 2.5x GalT labeling buffer (50 mM HEPES, 125 mM NaCl, 5% IGEPAL CA-630, pH 7.9) were added and the solution was vortexed gently before adding 10 µL Y289L GalT (1 mg/mL), and 10 µL of UDP-GalNAz (0.5 mM in 10 mM HEPES, pH 7.9). The reaction was then left to rotate end-over-end at 4 °C overnight. Control experiments were carried out in parallel in the absence of UDP-GalNAz. The following day, proteins were precipitated as before and resolubilized in dissolution buffer (1% SDS in TBS pH 7.6). The following were added (in order) to the redissolved protein: 100 µL H2O, 2.5 µL BTTAA (10 mM, Click Chemistry Tools), 5 µL CuSO4 (50 mM), and 5 µL of biotin-PEG4-alkyne (5 mM, Click Chemistry Tools). The solutions were mixed by gentle vortexing and 4 µL of TCEP was added. The reaction was allowed to react for 1 hour with end-over-end rotation in the dark before being precipitated as before. Proteins were resolubilized in dissolution buffer as described, and 10% of the reaction volume was taken as input. The remaining volume was then incubated with streptavidin magnetic beads (ThermoFisher) for 1.5 hours in the dark. Beads were then washed 5 times with 0.5 ml of low salt buffer (100 mM Na2HPO4, 150 mM NaCl, 0.1% SDS, 1% Triton X-100, 0.5% sodium deoxycholate) and 5 times with 1 ml of high salt buffer (100 mM Na2HPO4, 500 mM NaCl, 0.2% Triton X-100). Biotinylated proteins were eluted

by boiling the resin in 50 mM Tris-HCl pH 6.8, 2.5% SDS, 100 mM DTT, 10% glycerol, and 2 mM biotin for 15 min with occasional vortexing.

3.8.8. In-Gel Digestion of Cdk5 for O-GlcNAc Site Mapping.

After SDS-PAGE, the gel was stained and visualized using Imperial protein staining reagent (ThermoFisher Scientific) and destained in doubly deionized H_2O (ddH_2O). The band corresponding to FLAG-tagged Cdk5 was then excised and stored at -80 °C until in-gel digestion as previously described.[77] Briefly, the gel piece was cut into 1 mm squares, reduced with 10 mM DTT for 1 h at 37 ºC, and alkylated with 50 mM iodoacetamide for 45 min at room temperature protected from light. The slices were dried and incubated with 20 ng/uL Pierce Trypsin, or Pierce Chymotrypsin, protease (ThermoFisher Scientific) solution in 100 mM NH_4HCO_3 (pH 8.0) overnight at 37 ºC. The peptides were recovered using sequential washes with 100 mM NH_4HCO_3, 1:1 v/v 100 mM NH_4HCO_3/CH_3CN, and 5% formic acid. The recovered peptides were dried and desalted with a C18 ZipTip pipette tip (MilliporeSigma). The desalted peptides were resuspended in 25 μL of 0.2% formic acid for LC-MS/MS analysis.

3.8.9. LC-MS/MS Analysis.

Cdk5 samples were analyzed on a nanoflow LC system, EASY-nLC 1000 (ThermoFisher Scientific), coupled to either a Q-Exactive or LTQ Velos (ThermoFisher Scientific) equipped with a Nanospray Flex ion source.

3.8.9.1. LTQ Velos Analysis (CID/ETD).

Cdk5 peptides (2 µL and 5 µL) were loaded onto a 360x100 µm precolumn (2cm Monitor C18, Waters Milford, MA) prior to separation on a 360x75µm column/tip (9cm BEH 1.7 µm) at 1µL/min at 600 bar constant pressure for 15 µL. The column was heated to 60 °C. The peptides were separated with a 145-min gradient at a flow rate of 250 nL/min. Solvent A consisted of 99.9% water and 0.1% formic acid, and Solvent B consisted of 80% acetonitrile, 19.9% water, and 0.1% formic acid. The gradient was as follows: 0-30% Solvent B (120 min), 30-90% B (2 min), and 90% B (13 min). Full spectra were acquired over *m/z* 350-1500 in the Orbitrap (60 K resolution at 200 *m/z*); automatic gain control (AGC) was set to accumulate 50,000 ions, with a maximum injection time of 50 ms. Data-dependent MS2 analysis was performed using a top 5 approach with alternating CID and ETD fragmentation.

3.8.9.2. Q-Exactive Analysis (HCD).

Cdk5 peptides (2 µL) were loaded onto a 360x100 µm precolumn prior (2cm Monitor C18, Waters) to separation on a 360x75µm column/tip (9cm BEH 1.7 µm, Waters) at 1µL/min at 600 bar constant pressure for 15 µL. The column was heated to 60 °C. The peptides were separated with a 77-min gradient at a flow rate of 250 nL/min. Solvent A consisted of 99.9% water and 0.1% formic acid, and Solvent B consisted of 80% acetonitrile, 19.9% water, and 0.1% formic acid. The gradient was as follows: 2% Solvent B (10 min), 2-35% B (60 min), 35-95% B (2 min), and 95% B (5 min). Full spectra were acquired over *m/z* 350-1500 in the Orbitrap (70 K resolution at 200 *m/z*); automatic gain control (AGC) was set to accumulate 1,000,000 ions, with a maximum injection time of 50 ms. Data-dependent MS2 analysis was performed as described

previously[78] using a top 12 approach with HCD fragmentation at 35 K resolution, a max injection time of 60 ms, and an intensity threshold of 100,000 ions.

3.8.10. LC-MS/MS Data Analysis.

The data was converted to MGF files for Mascot searching using Proteome Discoverer. ETD and CID spectra were extracted to separate MGF files for searching. The data was then searched against a custom database with the expected sequence of interest and a mouse slice of the UniProt database downloaded in April 2015 with fixed modifications of carbamidomethyl (C) and variable mods of O-GlcNAc (ST), and oxidation (M). Enzyme specificity was Trypsin with 2 missed cleavages and semichymotrypsin with 4 missed cleavages. Mass tolerances were 25 ppm and 0.8 Da for precursor and fragments ions, respectively. CID data and ETD data were searched with instrument parameters of ESI-trap or ETD-Trap, respectively. For HCD, mass tolerances were 25 ppm and 50 mmu for precursor and fragment ions, respectively. Data was then loaded into Scaffold (Proteome Software, Portland OR) and filtered for a 1% false discovery rate at the peptide level.

3.8.11. Lentiviral Plasmid Construction.

Cdk5 shRNA lentiviral plasmid (pLKO.1) was purchased from Sigma-Aldrich (TRCN0000278085). Cdk5-Myc-FLAG in pCMV6 (MR204021) was purchased from Origene (Rockville, MD). Mutations conferring shRNA resistance (1325-CCCTGAGATTGTGAAGTCATTC-1346 to CCCTGAaATTGTGAAGagtTTt) and all serine to alanine mutations were produced using the Q5 Site-Directed Mutagenesis Kit (NEB) according to the manufacturer's protocols. All primers were designed with the NEBaseChanger software.

shRNA resistant mutant or WT Cdk5 was then linearized by using the Q5 Hot Start High-Fidelity 2x master mix and the pEF-ENTRA A[73] entry vector was linearized by digestion with BamHI-HF and XbaI. Linear DNA was then gel purified using the Zymoclean gel DNA recovery kit (Zymo Research, Irvine, CA) and assembled with the NEBuilder HiFi DNA assembly kit according to the manufacturer's protocol. The Cdk5 entry vectors were then recombined with the pLENTI CMV GFP[73] destination vector using the Gateway LR Clonase II Enzyme mix (ThermoFisher) as described by the manufacturer. The final lentivectors were then amplified in Stable Competent *E. coli* (New England Biolabs), purified using ZymoPURE II Plasmid Kit (Zymo Research, Irvine, CA), sequenced (Laragen, Culver City, CA), and resolved by 1% agarose gel electrophoresis to ensure plasmid fidelity.

3.8.12. Lentivirus Production.

HEK 293T cells were transfected with the lentiviral plasmids produced above, as well as lentiviral packaging plasmids (ViraPower Lentiviral Packaging Mix, ThermoFisher), using Lipofectamine 3000 (ThermoFisher) at 90% confluency according to manufacturer's instructions. The virus was harvested by collecting media every 24 hours for 3 days. Lentiviral particles were concentrated approximately 50 fold at 4 °C using 15-mL 100 kDa MWCO Amicon concentrator tubes (MilliporeSigma), flash frozen immediately, and stored at -80 °C until use. Lentiviral titer was estimated by traducing neurons with a dilution series of lentivirus and estimating transfection efficiency by GFP fluorescence confocal microscopy or determining Cdk5 expression levels compared to endogenous by WB. In all cases, neurons were assayed at least 7 days after transduction.

3.9. References.

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Chapter 4

Chemical Tools for Site-Specific Quantitative O-GlcNAcomics

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4.1. Abstract.

The dynamic PTM, O-GlcNAcylation, is present on thousands of intracellular proteins. Like phosphorylation, O-GlcNAcylation is inducible and plays important functional roles in both physiology and disease. Recent advances in MS and bioconjugation methods are now enabling the mapping of O-GlcNAcylation events to individual sites in proteins. However, our understanding of which glycosylation events are necessary for regulating protein function and controlling specific processes, phenotypes, or diseases remains in its infancy. Given the sheer number of O-GlcNAc sites, methods are greatly needed to identify promising sites and prioritize them for time- and resource-intensive functional studies. Revealing sites that are dynamically altered by different stimuli or disease states will likely go a long way in this regard. Here, we describe advanced methods for identifying O-GlcNAc sites on individual proteins and across the proteome, and for determining their stoichiometry in vivo. We also highlight emerging technologies for quantitative, site-specific MS-based O-GlcNAc proteomics (O-GlcNAcomics), which allow proteome-wide tracking of O-GlcNAcylation dynamics at individual sites. These cutting-edge technologies are beginning to bridge the gap between the high-throughput cataloging of O-GlcNAcylated proteins and the relatively low-throughput study of individual proteins. By uncovering the O-GlcNAcylation events that change in specific physiological and disease contexts, these new approaches are providing key insights into the regulatory functions of O-GlcNAc.

4.2. Introduction.

Over the past decade, growing interest in O-GlcNAcylation has led to the discovery of many new functions (**Fig. 4.1**) for this modification and revealed its central importance for both

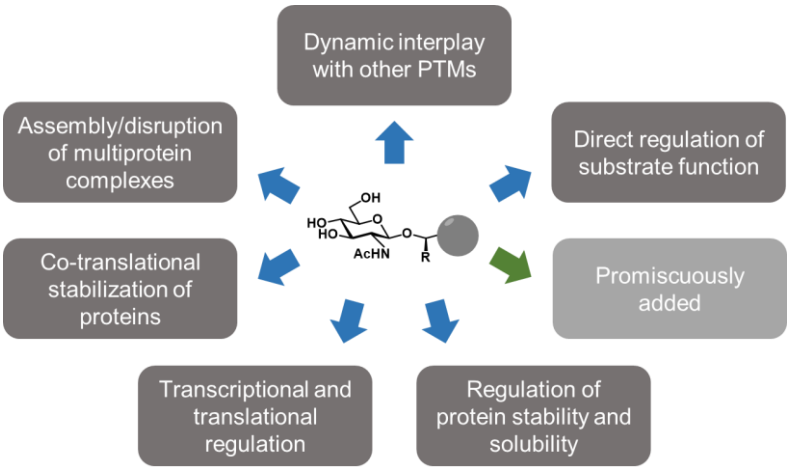

Fig. 4.1. Selected Functions of O-GlcNAc.
An explosion of studies has identified many new functions for O-GlcNAcylation. Yet, a central challenge remains in distinguishing the most functionally important sites in a given context from background or promiscuously added modifications.

physiology and pathology. However, the huge diversity of functions and substrates has created a major challenge for the field – namely, the prioritization of O-GlcNAcylation events for follow-up studies. Given the sheer number of O-GlcNAc modification sites, methods are greatly needed to identify promising sites and prioritize them for time- and resource-intensive functional studies. To address this challenge, it will be critical to move from a static picture of whether a protein is O-GlcNAcylated to a more dynamic view and identify context-specific changes in O-GlcNAcylation, such as sites that are induced by specific stimuli or altered during development or disease progression. Identifying these key sites and developing methods to selectively modulate their glycosylation status may also prove critical for therapeutic intervention in neurodegenerative disease, as globally altering O-GlcNAcylation levels could have deleterious, compensatory, or potentially unforeseen off-target effects.[1-5]

The importance of monitoring the dynamics of O-GlcNAcylation at specific sites is further underscored by the observation that OGT and OGA exhibit exquisite selectivity for particular

substrates, depending on the cellular context.[5-9] For instance, early quantitative proteomics studies by our laboratory showed that robust stimulation of excitatory neurons in vivo induces O-GlcNAcylation on only a subset of OGT substrates, while pharmacological inhibition of OGA affects almost an entirely different subset.[6] This suggests that OGT can discriminate among its various substrates in response to specific cellular signals. OGT can also exhibit exquisite selectivity for different sites within the same protein. For example, neuronal depolarization induces CREB glycosylation at only a single site, Ser40, while other glycosylation sites in CREB remain unchanged.[10] Thus, different sites within the same protein can show distinct temporal dynamics, which may enable O-GlcNAc to regulate various aspects of a protein's function. Finally, several studies have observed that changes in O-GlcNAcylation at the protein level often do not correlate with changes at individual sites. This is exemplified by the transcriptional repressor methyl CpG binding protein 2 (MeCP2), whose loss of function underlies Rett syndrome.[11] Although the O-GlcNAcylation level on the total MeCP2 population decreases upon neuronal depolarization, the O-GlcNAcylation level on the Ser80-

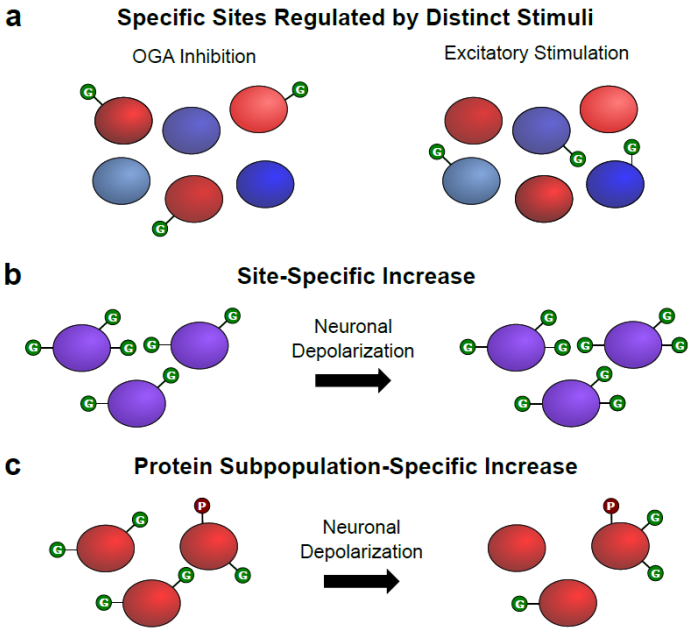

Fig. 4.2. O-GlcNAcylation Undergoes Complex Regulation and Site-Specific Dynamics in the Brain.
(a) Inhibition of OGA increases O-GlcNAcylation on a subset of OGT substrates (in red), whereas excitatory neuronal stimulation with kainic acid increases O-GlcNAcylation on a different subset (in blue). **(b)** Neuronal stimulation increases O-GlcNAcylation of CREB at S40, while the other two sites remain unchanged. **(c)** Overall O-GlcNAcylation of MeCP2 decreases upon neuronal depolarization; however, for a subset of phosphorylated MeCP2, O-GlcNAcylation increases.

phosphorylated subpopulation of MeCP2 significantly increases.[12] These examples clearly demonstrate that O-GlcNAcylation undergoes complex regulation and site-specific dynamics in neurons (**Fig. 4.2a-c**).

Herein, we will highlight state-of-the art technologies for identifying O-GlcNAc sites and tracking their context-specific dynamics. We will first focus on methods for mapping glycosylation sites within proteins and for quantifying site occupancy or stoichiometry. We will then describe emerging technologies for quantitative, MS-based O-GlcNAcomics and discuss how such approaches are providing new, systems-level insights into the site-specific dynamics of O-GlcNAc in response to different cellular or disease states. Our intention is to provide an overview of these technologies with an emphasis on their potential impact on the field of neurobiology. Overall, the development and implementation of quantitative O-GlcNAcomics methods should greatly accelerate the prioritization of O-GlcNAcylation sites for further study and are a critical next step toward advancing our understanding of the functions of O-GlcNAc in health and disease.

4.3. O-GlcNAc Site Identification on Individual Proteins.

The identification of O-GlcNAc sites is often crucial for elucidating the function of the modification in the context of specific proteins. However, this task can be challenging as there is no known consensus sequence for OGT, and the O-GlcNAc modification occurs substoichiometrically on many proteins. Moreover, the O-GlcNAc moiety is frequently found within a stretch of serine or threonine residues and is readily lost upon CID MS due to the lability of the O-glycosidic linkage.[13,14] As a result, O-GlcNAcylation sites are often ambiguous, difficult to localize to a single serine or threonine residue, or require confirmation with time-consuming site-directed mutagenesis studies.[15,16]

In response to these challenges, Hart and coworkers developed the BEMAD (β-elimination followed by Michael addition with dithiothreitol) approach,[17] which chemically converts O-GlcNAcylated serine and threonine residues to thiol-containing derivatives that are stable during CID. As other O-linked modifications such as phosphorylation are also derivatized in the process, this technique is not well suited for the selective mapping of O-GlcNAc sites unless it is combined with some form of enrichment for O-GlcNAcylated peptides.[15,18,19] Our laboratory has developed a chemoenzymatic labeling strategy that accomplishes this task.[16,20-23] The approach allows for selective, quantitative labeling of O-GlcNAcylated peptides or proteins with an unnatural azido- or ketone-containing galactose sugar GalNAz[22] or 2-acetonyl-2-deoxy-α-D-galactose[20] using an engineered β-1,4-galactosyltransferase (Y289L GalT).[24] The azide or ketone functionality enables the attachment of different reporter groups (e.g. biotin, fluorescent dyes) using bioorthogonal chemistry.[16,20,22,23] Thus, following labeling with biotin, O-GlcNAcylated proteins can be captured using streptavidin resin and then simultaneously derivatized and eluted using BEMAD (**Fig. 4.3a**). This dual chemoenzymatic labeling/BEMAD strategy has proven effective for mapping O-GlcNAcylation sites on individual proteins[15,18,19,25,26] and has been applied on a proteome-wide level,[18,26-28] albeit with less success in site identification compared to the methods discussed below. Using this approach, several residues near the active site of CaMKIV, an important kinase whose signaling functions have been linked to learning, memory, and neurodegeneration,[19,29-31] were identified.[19] Site-directed mutagenesis studies demonstrated that O-GlcNAcylation of these sites modulates the phosphorylation and subsequent activation of CaMKIV.[19,32] Overall, although

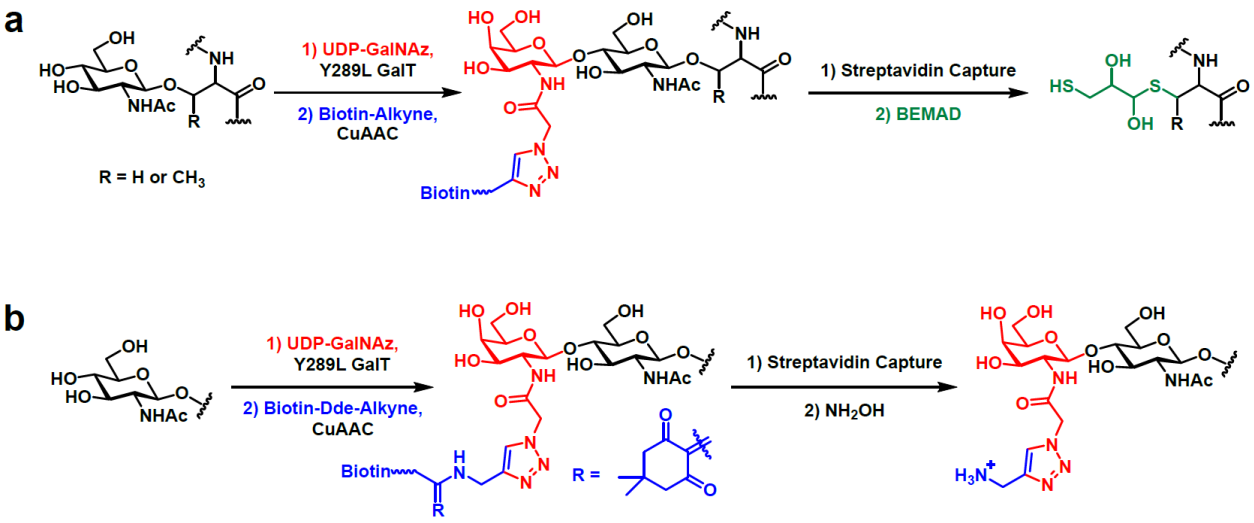

Fig. 4.3. Strategies for Mapping O-GlcNAc Sites.
(a) Chemoenzymatic labeling/BEMAD strategy. O-GlcNAcylated peptides are chemoenzymatically labeled with a biotin moiety, enriched by streptavidin capture, and then eluted using BEMAD prior to LC-MS/MS analysis. **(b)** Cleavable biotin-Dde-alkyne strategy. O-GlcNAcylated peptides are chemoenzymatically labeled with a biotin-Dde-alkyne derivative and enriched by streptavidin capture. Quantitative release of O-GlcNAcylated peptides is then achieved using hydroxylamine or hydrazine, which imparts an additional positive charge on the peptide and thereby facilitates LC-MS/MS analysis.

BEMAD has some limitations (such as being prone to false positives and causing peptide degradation[27,33]), it remains a useful method for mapping O-GlcNAc sites and is amenable to traditional MS workflows.

With advances in MS instrumentation, the direct mapping of O-GlcNAc sites, without chemical conversion of the labile O-GlcNAc moiety, has also become possible in some cases. ETD enables the observation of O-GlcNAcylated serine and threonine fragment ions in MS/MS spectra without O-glycosidic bond cleavage,[6,34] thereby localizing the exact modification site. Typically, O-GlcNAcylated proteins of interest are overexpressed, immunoprecipitated, and analyzed directly by LC-MS/MS following in-gel digestion.[10,16] We and others have successfully employed this approach to identify crucial, regulatory O-GlcNAcylation sites on neuronal proteins involved in learning and memory, signal transduction, and metabolism, including CREB and the mitochondrial motor-adaptor protein Milton.[10,35] Given the limitations of the BEMAD approach

discussed above, the use of ETD-MS/MS to map exact O-GlcNAc sites is generally preferred if appropriate instrumentation is available.

Difficult-to-detect or low-abundance O-GlcNAc sites on proteins require techniques for the highly efficient enrichment and release of O-GlcNAcylated peptides. While labeling O-GlcNAcylated peptides with a biotin tag provides an effective enrichment strategy,[6,18] the strength of the biotin-streptavidin interaction can hinder efficient release of the peptides from the resin. To overcome this problem, we recently developed a biotin tag containing a chemically cleavable 1-(4,4-dimethyl-2,6-dioxocyclohex-1-ylidene)ethyl (Dde) functionality to selectively capture O-GlcNAcylated peptides after chemoenzymatic labeling.[36] The O-GlcNAcylated peptides are then quantitatively released from streptavidin resin using hydrazine or hydroxylamine (**Fig. 4.3b**).[16] Importantly, this cleavage event leaves O-GlcNAcylated peptides with an additional positive charge that significantly improves their ETD fragmentation efficiency. Ultimately, this approach greatly increases the likelihood of successful identification and sequencing of O-GlcNAcylated peptides.[16,36-39] It is worth noting that an additional advantage of the biotin-Dde tag is that produces three signature ions upon fragmentation by HCD, which result from cleavage of the glycosidic bond between GlcNAc and GalNAz (300.1 *m/z*), the water adduct of the previous fragment (318.1 *m/z*), and cleavage between GlcNAc and the serine/threonine residue (503.2 *m/z*).[16] These signature ions enable unambiguous assignment of the modification at the peptide level, and the increased ETD fragmentation efficiency (due to the additional positive charge) increases the likelihood that an O-GlcNAcylation event can be definitively localized to a single residue. In fact, using this strategy, we identified four new O-GlcNAc sites on OGT that were previously undetectable by other methods, all of which were on tryptic peptides spanning multiple sites of O-GlcNAcylation.[36] We believe that this improved enrichment/release workflow will be widely

applicable for discovering low-abundance sites or sites that were previously ambiguous due to the lability of O-GlcNAc or poor glycopeptide ionization/fragmentation. Thus, the development of new chemoenzymatic labeling tags coupled with cutting-edge MS technologies has significantly reduced the barriers to the unambiguous assignment of O-GlcNAc sites, and in the future, the complete mapping of sites on nearly any protein of interest should become increasingly routine.

4.4. O-GlcNAc Site Mapping Across the Proteome.

The identification of O-GlcNAc sites across the proteome requires effective methods for the enrichment of O-GlcNAcylated proteins or peptides from complex biological samples. One powerful, widely used approach involves the chemoenzymatic tagging strategy described above. In early studies, we applied this strategy to enrich O-GlcNAcylated proteins from the mammalian brain and identified 34 O-GlcNAcylated peptides corresponding to 25 proteins. These proteins had a wide range of important neuronal functions, including the regulation of gene expression, neurotransmission, and synaptic plasticity.[18] Similar to the biotin-Dde tag described above, the biotin tag in this case also provided a unique fragmentation pattern upon MS/MS analysis that enabled us to conclusively identify the modification. This approach was subsequently improved through the development of a photocleavable biotin tag (biotin-PC)[40] and the chemically cleavable biotin-Dde tag described above (**Fig. 4.3b**).[36] Using the biotin-PC tag, Hart and colleagues identified 458 O-GlcNAc sites on 195 proteins in the brains of WT and 3xTg (a common mouse model of AD[41]) mice.[42] Impressively, 168 of the identified O-GlcNAcylated proteins had not been previously described and included multiple proteins involved in synaptic plasticity and neuronal signaling, cytoskeletal organization, and neuronal gene expression.[42] More recently, the chemically cleavable biotin-Dde tag has significantly improved our ability to comprehensively

map O-GlcNAc sites across the proteome. In a direct side-by-side comparison, the biotin-Dde tag outperformed the biotin-PC tag, enabling the identification of 414 unique O-GlcNAcylated peptides from human embryonic kidney 293T cells, as compared to the 227 unique O-GlcNAcylated peptides identified using the biotin-PC tag (unpublished). Building further on this approach, we have designed a next-generation, chemically cleavable tag that has greater thermal stability compared to biotin-Dde and has enabled the mapping of over 1,300 O-GlcNAc sites across ~600 proteins in 293T cells (manuscript in preparation).

An alternative to chemoenzymatic labeling strategies involves the use of lectin weak affinity chromatography with wheat germ agglutinin to enrich O-GlcNAcylated peptides. Using this approach combined with high-pH reversed-phase fractionation and ETD-MS/MS, Burlingame and coworkers identified 1,750 unique sites of O-GlcNAcylation from fractionated mouse synaptosomes, the most sites described thus far in a single experiment.[43] This study also interrogated the phosphoproteome on these same samples given the precedent for a high degree of crosstalk between these two modifications.[5,44] Interestingly, all but one of the extensively O-GlcNAcylated proteins were extensively phosphorylated. Moreover, protein kinases as a class were found to be more extensively O-GlcNAcylated in synaptosomes, suggesting an intriguing potential for crosstalk at the level of enzyme activity. However, at the site level, the number of O-GlcNAc sites that were also phosphorylation sites did not exceed what would be expected by chance, and there was no propensity for O-GlcNAc and phosphorylation sites to cluster in primary sequence or three-dimensional space.

Collectively, studies of the O-GlcNAcylated proteome have provided critical insights into the physiological functions of O-GlcNAc in the brain. For instance, these analyses have revealed a large number of pre- and postsynaptic scaffolding proteins, suggesting important roles for the

modification in synaptic communication and function.[45] Moreover, the unbiased identification of O-GlcNAc sites has facilitated follow-up studies to understand the function of O-GlcNAc in the context of specific proteins, as demonstrated by a recent study by Pratt and coworkers on the effects of site-specific O-GlcNAcylation on α-synuclein aggregation.[46,47] However, despite the power of O-GlcNAcomic approaches, these technologies provide only a static snapshot of the O-GlcNAcome, without regard for the stoichiometry or dynamics of specific sites. As described below, knowledge of the site occupancy and inducibility of specific sites can provide insights into the importance of specific glycosylation events and the cellular contexts in which they function.

4.5. Methods for Measuring Dynamic O-GlcNAc Stoichiometry.

Determining the stoichiometry of glycosylation on a protein, or at a specific site, is critical for assessing whether that glycosylation event is likely important. The modification is more likely to be functionally relevant and to operate in a regulatory capacity if a significant population of the protein is modified and the modification is dynamically cycled. Glycosylation stoichiometries can be challenging to quantify and thus are known for only a small fraction of the O-GlcNAcome. To quantify O-GlcNAc stoichiometries, large amounts of purified protein (e.g. for high-pH anion-exchange chromatography with pulsed amperometric detection)[48-50] or synthetic O-GlcNAcylated peptide standards encompassing the sites of interest are typically required. In order to overcome these challenges, we have developed two methods to detect and quantify the O-GlcNAc-modified subpopulation. The first approach employs the chemoenzymatic biotin/streptavidin enrichment

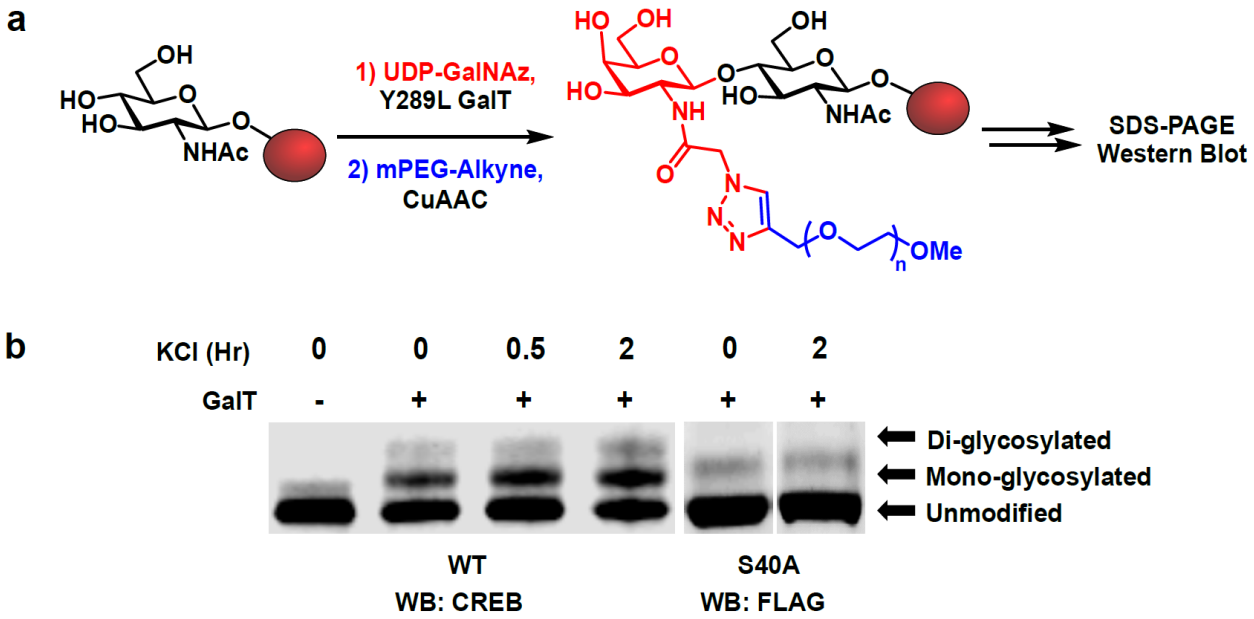

Fig. 4.4. Chemoenzymatic Labeling with PEG Tags to Determine O-GlcNAcylation Stoichiometry.
(a) A PEG tag of defined mass (2-kDa or 5-kDa) is installed on O-GlcNAcylated proteins in cell lysates using Y289L GalT and copper (I)-catalyzed azide-alkyne cycloaddition (CuAAC) chemistry. **(b)** Neurons expressing either WT or S40A CREB fused to a FLAG tag were depolarized with KCl for the times indicated before lysis and chemoenzymatic labeling with PEG. Labeled proteins were then subjected to SDS-PAGE and Western blotting for CREB or FLAG. Note the presence of two major CREB glycoforms, mono- and di-glycosylated, and the loss of KCl-induced O-GlcNAcylation upon mutation of Ser40.

strategy described above, in combination with immunoblotting to detect the protein of interest. The amount of a captured (i.e. O-GlcNAcylated) protein is quantified relative to the total amount of that protein to give an approximate measure of stoichiometry.[16,21,51] The second approach allows for direct visualization and quantification of the O-GlcNAc-modified subpopulation via chemoenzymatic labeling of the proteins with resolvable PEG tags (**Fig. 4.4a**). Specifically, O-GlcNAcylated proteins from cell lysates are labeled with a keto-galactose or azido-galactose sugar as described above and then reacted with an aminooxy-, alkyne-, or dibenzocyclooctyne-functionalized PEG tag of defined molecular mass (typically 2-kDa or 5-kDa). Importantly, the PEG tag shifts the molecular weight of the glycosylated species and allows them to be resolved from the non-glycosylated species by SDS-PAGE.[12,16,23,52] After immunoblotting to detect the

protein(s) of interest, simple inspection of the mass-shifted bands can rapidly establish whether a protein is singly, doubly, or multiply glycosylated. Moreover, in vivo glycosylation stoichiometries can be readily calculated by quantifying the relative intensities of each band. One caveat with chemoenzymatic labeling, however, is that GalT can also label complex glycans that contain a terminal GlcNAc sugar. For known membrane proteins, complex N-linked glycans can be removed using Peptide:N-glycosidase F.[16] In addition, it is possible that chemoenzymatic labeling may differ in efficiency for different sites, although the use of excess reagents ensures highly efficient labeling, and both of these methods have been consistently demonstrated to provide accurate measurements of the O-GlcNAcylation stoichiometry on a range of peptide and protein substrates.[12,16,23,36,53]

When used in combination with site-directed mutagenesis, this approach allows for rapid interrogation of O-GlcNAc stoichiometry at specific sites and across multiple conditions. For instance, we found that approximately 30% of CREB was mono-glycosylated in resting neurons. Upon KCl-mediated depolarization, glycosylation was induced specifically at a single site, Ser40 (**Fig. 4.4b**).[10,12] Strikingly, mutation of Ser40 to alanine resulted in increased CREB-dependent gene transcription, and significantly accelerated long-term memory formation in mice.[10] Overall, this powerful method enables the measurement of O-GlcNAcylation stoichiometries on endogenous proteins of interest without the need for protein purification, advanced instrumentation, or expensive radiolabels.

4.5. Quantitative O-GlcNAcomics.

Systems-level approaches to quantify site-specific changes in O-GlcNAcylation across the proteome can help find the “needle in the haystack” – namely, the glycosylation events that are

functionally important in a specific cellular or disease context. We will describe here three promising technologies for quantitative site-specific O-GlcNAcomics: QUIC-Tag, quantitative CEPC, and quantitative IsoTaG.

The QUIC-Tag method, developed in 2007, was the first quantitative O-GlcNAcomics approach.[6] This approach combines chemoenzymatic biotin tagging for O-GlcNAcylated peptide enrichment with stable isotope dimethyl labeling for quantitative proteomics (**Fig. 4a**). Using QUIC-Tag, we observed changes in O-GlcNAcylation at specific sites following stimulation of rats with kainic acid, a kainate-type glutamate receptor agonist that produces widespread excitatory stimulation of the brain.[6] These studies provided the first evidence that O-GlcNAcylation is

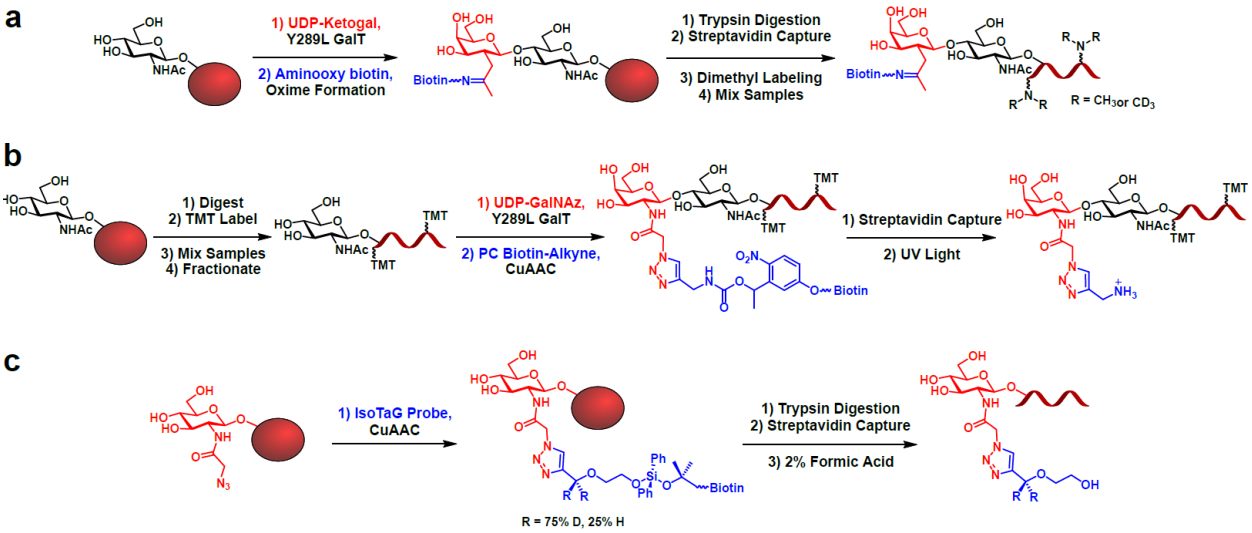

Fig. 4.5. Strategies for Quantitative O-GlcNAcomics.
(a) QUIC-Tag strategy. O-GlcNAcylated proteins are chemoenzymatically labeled with biotin, digested, captured, and subjected to isotopic dimethyl labeling before LC-MS/MS analysis. **(b)** Quantitative CEPC. O-GlcNAcylated proteins are digested, TMT labeled, and fractionated before chemoenzymatic labeling with a biotin-PC tag. The labeled peptides are then enriched, eluted from the beads by UV cleavage, and subjected to LC-MS/MS analysis. **(c)** Quantitative IsoTaG. Metabolically labeled O-GlcNAzylated proteins are functionalized with an acid-cleavable biotin linker containing an isotopic label (IsoTaG Probe) using CuAAC. Labeled proteins are then enriched, digested, eluted from the beads, and analyzed by LC-MS/MS. Importantly, glycopeptides can then be readily identified by their unique isotopic signature in MS1. In all cases, the relative O-GlcNAcylation levels on peptides derived from two or more samples can be calculated from the ratio between light and heavy isotopically-labeled peptides (QUIC-Tag and CEPC) or the ratio of intensities after label-free quantification (IsoTaG).

dynamically modulated in vivo by neuronal activity. Moreover, we found that different subsets of O-GlcNAc sites respond to different neuronal stimuli, with kainic acid affecting a distinct set of sites compared to the OGA inhibitor O-(2-acetamido-2deoxy-D-glucopyranosylidene)amino-*N*-phenylcarbamate (PUGNAc). Overall, our findings highlight key differences in the occupancy and temporal dynamics of specific sites in response to different stimuli and demonstrate the complex regulation of O-GlcNAcylation in neurons. With recent advances in MS instrumentation and the new chemoenzymatic tags described above, this strategy can now be adapted to enable more comprehensive, quantitative comparisons across many different functional states.

The quantitative CEPC strategy relies on isotopic labeling (e.g. SILAC) or isobaric labeling (e.g. TMTs) of peptides derived from cell lysates, followed by chemoenzymatic labeling using Y289L GalT and biotin-PC to enrich O-GlcNAcylated peptides (**Fig. 4b**).[54] Recently, Liu and coworkers exploited this technique to quantify site-specific differences in O-GlcNAcylation between AD and non-diseased brain tissue.[52] After TMT labeling followed by chemoenzymatic labeling, enrichment, and photochemical cleavage, they determined 623 ratios at the O-GlcNAcylated peptide level and mapped 1,094 sites. Twenty-four of these sites showed significant differences in O-GlcNAcylation between AD and control tissues that were not due to changes in protein expression. Most of the sites were found on proteins involved in pre- and post-synaptic organization and structure, such as synaptopodin, ankyrin-3, integrin beta-4, and neurofascin.[52] Overall, these quantitative O-GlcNAcomics studies show that dysregulated O-GlcNAcylation occurs on multiple, select neuronal proteins during the development of sporadic AD and identify several novel candidates for in-depth investigations into the mechanisms underlying AD pathogenesis.

Finally, Pitteri and colleagues have recently reported combining the isotope-targeted glycoproteomics (IsoTaG)[55,56] strategy with label-free quantification to profile changes in O-GlcNAcylation (Figure 4C).[57] This approach relies on metabolic incorporation of *N*-azidoacetylglucosamine (GlcNAz) into O-GlcNAcylated proteins.[58] Briefly, cells are incubated with peracetylated GalNAz, which is converted to uridine diphosphate (UDP)-GlcNAz by the UDP-galactose 4-epimerase pathway.[59] As OGT tolerates UDP-GlcNAz as a substrate, O-GlcNAcylated proteins can be labeled with GlcNAz and then conjugated to an acid-cleavable biotin-alkyne linker containing an isotopic label (IsoTaG Probe) using CuAAC. It is important to note, however, that other GlcNAc- and *N*-acetylgalactosamine-containing complex glycans will also be metabolically labeled,[56,58] and the incorporation of GlcNAz is substoichiometric, reducing the labeling efficiency compared to chemoenzymatic strategies. The labeled glycoproteins are enriched by streptavidin capture, proteolytically digested, and the resulting glycopeptides are released by cleavage of the linker and analyzed by LC-MS/MS. Importantly, the cleaved IsoTaG Probe imparts a readily detectable isotope pattern to the glycopeptides, which allows them to be definitively identified and targeted in subsequent LC-MS/MS runs.[56,57] Using this strategy, Woo et al. mapped 851 O-GlcNAc sites in primary human T cells across 77 MS runs.[57] They also quantified changes in O-GlcNAcylation in response to T cell activation using label-free quantification and identified differences in the levels of 518 O-linked glycopeptides, corresponding to 227 proteins, between resting and activated T cells. One caveat with such comparisons is that the non-natural GlcNAz sugar may or may not be incorporated into proteins with the same relative ratios as the endogenous O-GlcNAc modification, and thus the differences in O-GlcNAcylation at specific sites may not reflect physiological conditions. Nonetheless, diverse site-specific dynamics were observed on several highly O-GlcNAcylated proteins, including

CREB, nuclear pore complex protein Nup98, transcription factor jun-B, and protein phosphatase 1 regulatory subunit 12A. Given the interesting parallels between T cell and neuronal activation,[60] these results may also have important implications for neurons and shed light on common pathways and mechanisms shared by both cell types.

4.6. Conclusions and Future Directions.

Significant advances in O-GlcNAc detection, site mapping, and quantitative MS-based O-GlcNAcomics are uncovering key regulatory roles for O-GlcNAcylation in multiple aspects of cellular (patho)physiology. As these advanced methods develop and become widely available, the number of important discoveries will only continue to grow. We have focused here on the emergence of new MS-based O-GlcNAcomics technologies for profiling and monitoring the dynamics of O-GlcNAc at thousands of sites simultaneously. These technologies have the potential to revolutionize our understanding of the modification by providing unprecedented insight into the specificity and kinetics of glycosylation at particular sites, by facilitating the much-needed prioritization of O-GlcNAcylation sites for functional studies, and by revealing those sites that are important in specific physiological and disease contexts (**Fig. 4.6)**.

Chemoenzymatic labeling strategies are particularly well-suited for quantitative, site-specific O-GlcNAcomics because they provide highly specific, nearly quantitative labeling

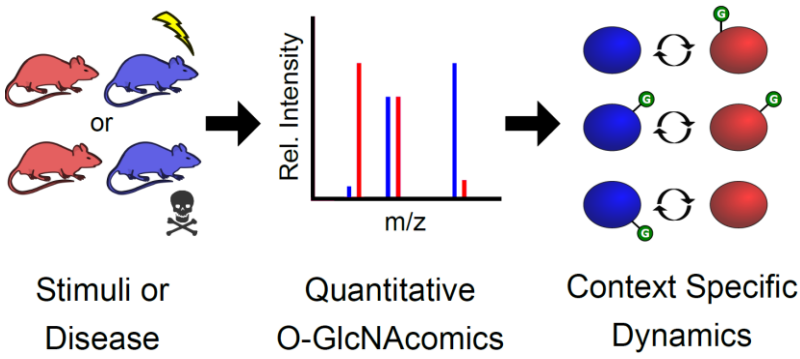

Fig. 4.6. Emerging Quantitative MS Technologies Can Help Prioritize O-GlcNAc Sites that Are Functionally Active in a Given Context.

and enrichment of low-abundance O-GlcNAcylated proteins or peptides. Bringing other advanced techniques for PTM profiling and quantitative proteomics to bear on the O-GlcNAc field would also open up even more exciting experimental possibilities. Moreover, with additional improvements in the design of new chemical tags and MS analysis workflows specially tuned for glycopeptides, we may soon find that the long-standing challenge of quantitative "shotgun O-GlcNAcomics" has become a thing of the past.

The continued development of quantitative, site-specific O-GlcNAcomics methods will also help to overcome key gaps in our understanding of O-GlcNAcylation. For instance, the ability to compare O-GlcNAcylation levels across different cell populations or regions of a tissue of interest should provide new insights into cell-specific roles for the modification and how aberrant O-GlcNAcylation at the cellular level may give rise to macroscopic, tissue-level pathology. Quantitative O-GlcNAcomics should also enable specific O-GlcNAcylation events to be monitored with unprecedented temporal resolution. As such, they could be used to track dynamic O-GlcNAc cycling at specific sites under a limitless set of important physiological and disease-relevant conditions. For example, while global changes in O-GlcNAcylation and expression of OGT/OGA are observed during development, aging,[61-64] and disease progression,[65-68] the site-specific changes in O-GlcNAcylation associated with these processes are largely uncharacterized.

In the future, the integration of quantitative O-GlcNAcomics data with other state-of-the-art "-omics" techniques (e.g. interactomics, phosphoproteomics, transcriptomics, proteomics) will also help uncover important correlations across biological systems and crosstalk between O-GlcNAcylation and other signaling networks. We expect that such multimodal approaches will prove particularly powerful for addressing questions such as how O-GlcNAcylation regulates protein-protein interactions, kinase signaling, and gene expression. In addition to revealing new

regulatory roles for O-GlcNAc, these efforts may shed light on long-standing questions regarding the complex regulation of OGT and OGA. Together, we believe that multimodal, systems-level approaches, coupled with rapidly emerging technologies for quantitative O-GlcNAcomics, will usher in a new era in our understanding of the functional roles played by O-GlcNAc.

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Chapter 5

A Network-Based Approach to Functional O-GlcNAcomics

This project was a collaboration, running title:

Functional Glycoproteomics by Integrated Network Assembly and Partitioning. **Thompson, J. W.**,* Griffin, M. E.,* Xiao, Y,.* Sweredoski M. J., Aksenfeld, R. B., Jensen, E. H., Koldobskaya, Y., Schacht, A. L., Kim, T. D., Choudhry, P. Moradian, A., Lomenick, B., Garbis, S. D.. Hsieh-Wilson, L. C. *Denotes equal contribution.

5.1. Abstract.

The PTM of proteins by O-GlcNAc is essential and widespread across both the proteome and lifespan of all multicellular organisms. However, nearly all functional studies have focused on the modification of individual proteins, overlooking the possibly thousands of other simultaneous O-GlcNAcylation events that may work in tandem to coordinate cellular activities. Here, we present **n**etworking of **O**-GlcNAc **t**ransferase **i**nteractors and **s**ubstrat**e**s (NOTISE), a novel systems-level approach to rapidly and comprehensively monitor O-GlcNAcylation events across the proteome in a given biological context. Our method integrates affinity purification mass spectrometry and site-specific chemoproteomics with network generation and unsupervised partitioning to organize potential upstream regulators and downstream targets of O-GlcNAcylation into functional clusters. Using a newly generated mouse model, we apply NOTISE to identify both conserved and tissue-specific activities of O-GlcNAcylation in the adult brain and liver. This holistic, networking approach provides a broadly applicable framework to delineate the roles of multifunctional PTMs across diverse tissue-types and biological states.

5.2. Introduction.

PTMs allow cells to rapidly and dynamically modulate protein function in response to biological stimuli. O-GlcNAcylation is the reversible addition of the monosaccharide β-*N*-acetyl-D-glucosamine to intracellular Ser and Thr residues. Unlike other classes of PTMs, this modification is catalyzed by a single O-GlcNAc transferase (OGT) and hydrolase (OGA) pair.[1] Nevertheless, O-GlcNAcylation occurs over thousands of proteins and is thought to function as a major integrating signal for the physiological status of the cell. The O-GlcNAc moiety incorporates metabolic information from synthetic pathways of all major biomolecules to produce its precursor

UDP-GlcNAc.[2] Cycling of the modification rapidly responds to many stimuli such as stress,[3] nutrient availability,[4] and extracellular signaling.[5] Accordingly, O-GlcNAcylation regulates many essential functions, including transcription,[5] translation,[6] metabolism,[7] protein homeostasis,[8] and signal transduction.[9,10] Altered O-GlcNAc levels have been implicated in multiple diseases including cardiovascular disease,[11] diabetes,[12] cancer,[13] and neurodegeneration.[14]

Recent methodological advances have improved the identification of O-GlcNAcylated proteins and peptides.[15] However, the vast majority of O-GlcNAcylation events remain functionally uncharacterized, and nearly all previous functional studies have focused only on individual modifications. Although critical advances, these studies do not encompass the full breadth of the role changes in O-GlcNAcylation plays in these contexts. For example, in cancer cells, changes in O-GlcNAcylation in response to nutrient and oxygen availability coordinate diverse responses from metabolic reprograming[16] to cytoskeletal reorganization,[17] ultimately significantly influencing tumor aggressiveness and metastatic potential. Moreover, in neurons, dynamic O-GlcNAcylation of proteins from the synapse to the nucleus occurs differentially in response to multiple stimuli.[5,18,19] In both of these cases, O-GlcNAcylation also cycles on multiple time scales to immediately regulate protein localization and stability as well as influence long-term genetic reprogramming through modulation of transcription factor recruitment and the epigenome. Interestingly, on the organismal level, O-GlcNAc has also been shown to respond differently to the same stimuli in different tissues[9,20] and even different cell types of the same tissue.[21] Thus, O-GlcNAcylation provides a unique challenge to understand how a single enzymatic pair can dynamically coordinate such broad cellular responses to intra- and extracellular stimuli.

To address this challenge, new systems-level methodologies are needed to provide a more holistic analysis of the many simultaneous O-GlcNAc events occurring in a given biological context. Furthermore, the sheer breadth of activity of O-GlcNAcylation highlights the difficulty in selecting or prioritizing individual sites for intensive, low throughput functional analyses. An integrated, bottom-up assembly of PTM sites and possible regulatory factors from a single biological condition would provide a thorough and contextualized view of PTM activity. This comprehensive approach may in turn inform on critical functions or sites for further investigation. In addition, the application of a standardized workflow to more completely identify and characterize PTM function across tissues and contexts could provide the first insights into cell-, tissue-, and stimulus-specific functions and regulatory networks of O-GlcNAc cycling enzymes. However, methods to generate, integrate, and deconvolute these data have not yet been developed.

A key hurdle to overcome for a systems-level interrogation of PTM function is the simultaneous discovery of coordinating or regulatory factors that are active in a given context. To discriminate between different stimuli, pleiotropic enzymes rely on a number of regulatory mechanisms to control and direct their activity. For example, intensive efforts have been made to define the mechanisms underlying the selectivity of OGT for its stimuli or tissue specific targets in a universe of thousands of potential modification sites. Emerging evidence suggests that OGT activity is controlled, at least in part, by adaptor proteins that target OGT to its cellular substrates.[2] This phenomenon is similar to A-kinase-anchoring proteins (AKAPs), which bind to the regulatory subunit of PKA to selectively direct its cellular activity.[22] Therefore, OGT interactors may provide the organizational basis for O-GlcNAcylation across the proteome that can be exploited not only to systematically organize OGT substrates but also provide unique insights into coordinated O-GlcNAc functions.

Here, we describe **n**etworking of **O**-GlcNAc **t**ransferase **i**nteractors and **s**ubstrat**e**s (NOTISE), a new approach to conduct comprehensive, systems-level analyses of PTM activity. Our method first ascertains potential upstream organizational determinants and downstream outcomes of OGT activity by identifying both OGT interacting proteins (**Fig. 5.1a**) and O-GlcNAcylated substrates (**Fig. 5.1b**). These elements are combined to produce a functional protein-protein interaction network that is then partitioned into process-specific subnetworks by unsupervised clustering (**Fig. 5.1c**). Together, this workflow produces a holistic, proteome-wide snapshot of the interactions and substrates of OGT for a given biological state. It also provides a physical framework for downstream functional interrogation. The approach can be applied to cells, tissues, or in vivo by utilizing a novel mouse model generated by CRISPR/Cas9 genome editing. Using NOTISE, we elucidate functional O-GlcNAc networks from the healthy adult brain and liver, revealing novel roles of O-GlcNAcylation in histone modification, mRNA processing, actin dynamics, and cytoskeletal organization. In total, these global analyses reveal for the first time both conserved and tissue-specific activities of O-GlcNAcylation in vivo.

5.3. Identification of OGT-Interacting Proteins.

To profile OGT interactors, we performed tandem affinity purification mass spectrometry (TAP-MS) using a dual FLAG- and HA-tagged OGT construct (OGT-FH; **Fig. 5.1a**). A stable HEK-293T cell line was generated that enabled inducible expression of OGT-FH under a

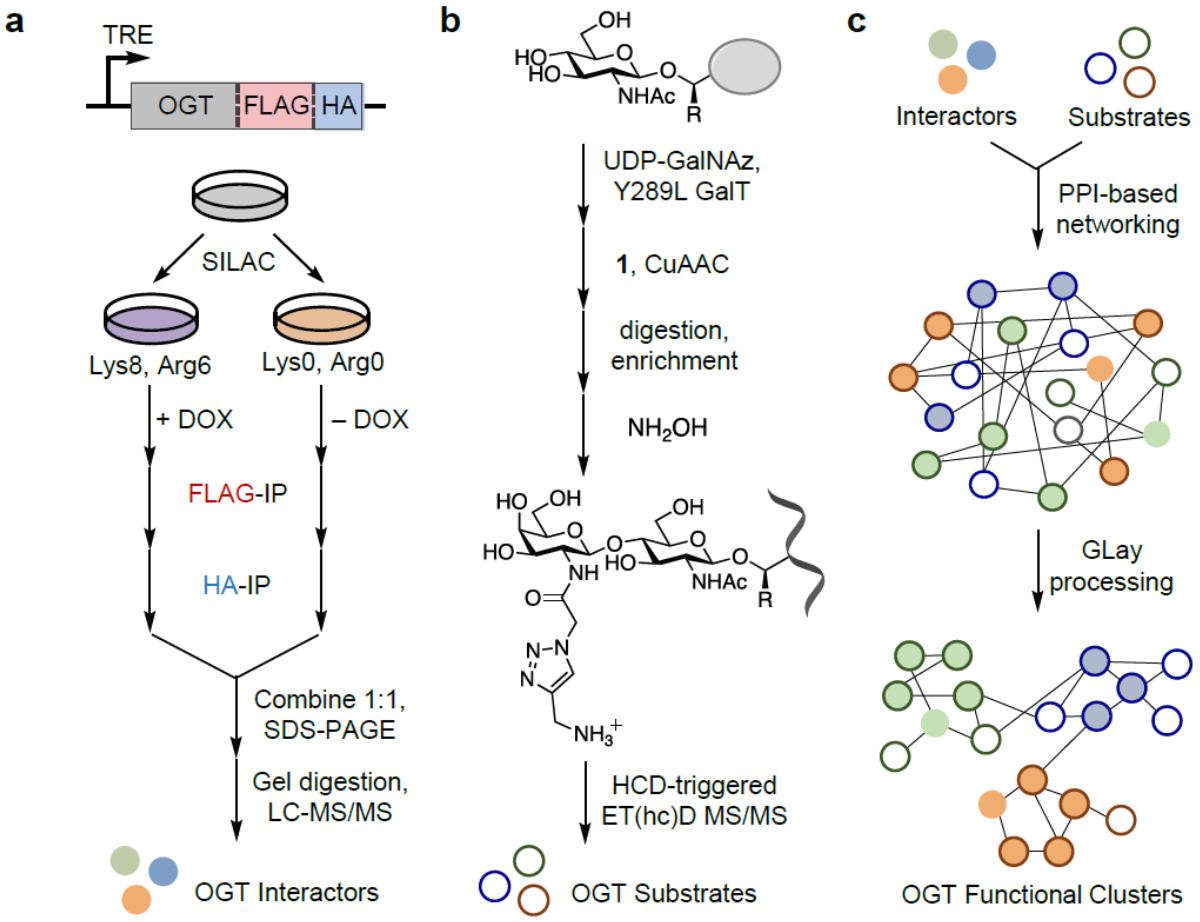

Fig. 5.1. The NOTISE Workflow.
(a) Tandem affinity purification of OGT interactors by sequential FLAG and HA immunoprecipitation. **(b)** Chemoenzymatic labeling and purification of O-GlcNAcylated peptides for chemoproteomic site identification. **(c)** Combination of interactor and substrate datasets via network generation and GLay community clustering to produce O-GlcNAc functional communities.

tetracycline-responsive element (TRE) promoter to ensure uniform, controllable levels of the dual-tagged OGT (**Fig. 5.2**). The appended FLAG and HA tags were then used to sequentially immunoprecipitate OGT and its associated proteins (**Fig. 5.3a**). Notably, our method confirms the stable interaction between OGT and retinoblastoma-binding protein 5 (RBBP5), nuclear pore glycoprotein p62 (NUP62), WD repeat-containing protein 5 (WDR5), and HCFC1 (**Fig. 5.3b**). Using TAP-MS combined with stable isotopic labeling with amino acids in cell culture (SILAC), we then compared OGT interacting proteins between HEK-293T cells treated with doxycycline

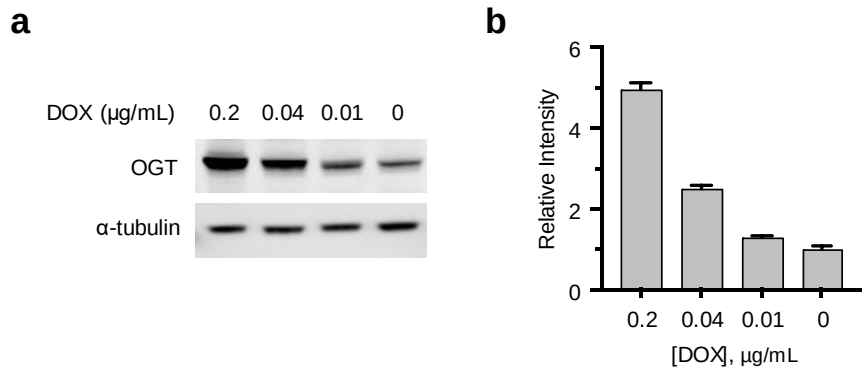

Fig. 5.2. Tunable Expression of OGTFH in HEK-293T-iOGTFH Cell Line.
(a) Cells were treated with different concentrations of doxycycline overnight, lysed, and immunoblotted for OGT levels. **(b)** Quantification of OGT expression in A (n = 3, mean ± S.E.M.).

(DOX) to untreated cells. This approach allowed us to construct the first statistically validated OGT interactome over background, identifying 519 high-confidence OGT interactors. Notably, many of the identified OGT interactors (**Fig. 5.3c**) represent significant advances in the O-GlcNAc literature, including HCFC1,[23,24] BAP1,[25] and ten-eleven-translocation 2 (TET2).[26] In addition, our studies identified 455 OGT interactors not found in protein-protein interaction (PPI) databases BioGRID[27] and IntAct[28] including DNA damage-binding protein 1 (DDB1), mitotic checkpoint protein BUB3 (BUB3), and serine/threonine-protein kinase WNK1 (WNK1), which play critical roles in DNA damage repair,[29] mitotic spindle assembly,[30] and ion homeostasis,[31] respectively. Our analysis was also extremely robust with 0 single-trial-interactors identified (**Fig. 5.3d**). Overall, these new findings demonstrate the importance of robust, targeted interactomic approaches for the comprehensive identification of OGT interacting partners needed for systems-level network analysis.

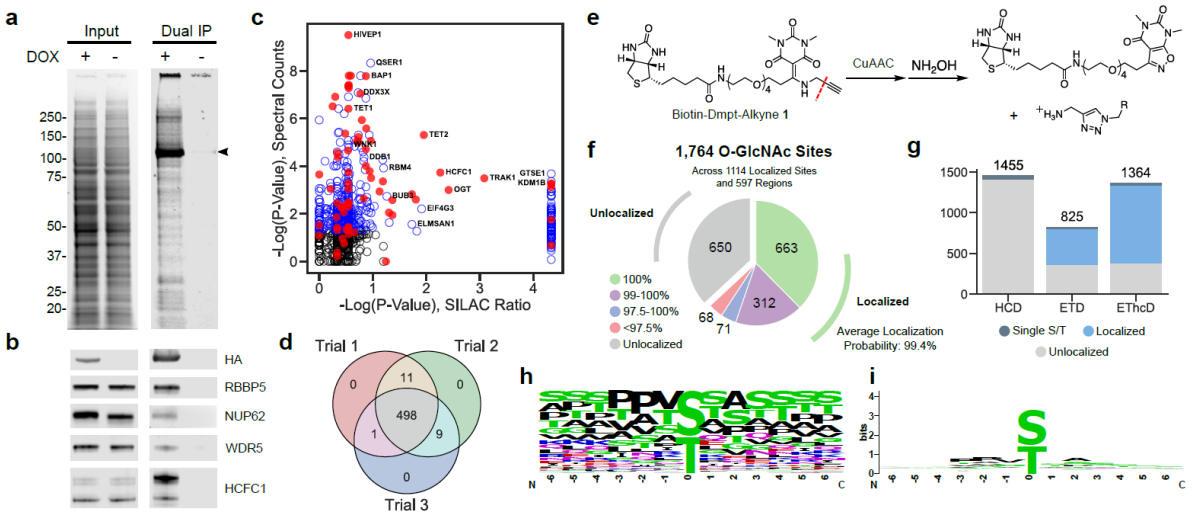

Fig. 5.3. OGT Interactor and Substrate Identification.
(a) Silver stain of cell lysates before and after tandem immunoprecipitation protocol. Arrow indicates OGTFH. DOX = doxycycline. **(b)** Validation of identified OGT interactors by immunoblotting. **(c)** Graph of p-values for limma-moderated t-test of SILAC ratios vs p-values for inverted beta-binomial test of spectral counts. True OGT interactors ($p < 0.05$ in either tests) are shown in blue. Filled red points represent known OGT interactors from the protein-protein interaction databases BioGRID and IntAct. **(d)** Reproducibility of identified OGT interactors across three independent experiments. **(e)** Chemical structure of biotin-Dmpt-alkyne **1** and cleavage product upon NH_2OH treatment. **(f)** Pie chart of localization probabilities for localized sites as calculated by ptmRS. **(g)** Breakdown of localized sites from each fragmentation method (note, all HCD sites were considered unlocalized). **(h)** Frequency plot of the region surrounding localized O-GlcNAc sites. **(i)** Enrichment plot of data in **h**.

5.4. Proteome-Wide Site Mapping of Protein O-GlcNAcylation.

To examine the output of OGT activity, we expanded on our previous chemoenzymatic approach to identify and map sites of protein O-GlcNAcylation across the proteome.[32,33] This method employs a mutant galactosyltransferase (Y289L GalT) to append the non-natural monosaccharide GalNAz onto O-GlcNAc-modified proteins as a handle for downstream functionalization and enrichment. Importantly, this approach has advantages over other existing methods using non-natural sugars, such as metabolic labeling.[34] Specifically, due to its higher specificity towards O-GlcNAcylated substrates, quantitative labeling, and lack of need for exogenous sugars, it provides enhanced detection sensitivity in a native context. To improve the

compatibility of our well-documented chemoenzymatic labeling techniques with downstream analysis by MS,[32,35] we developed a new chemically cleavable linker for facile capture-and-release of modified targets. The novel linker, biotin-Dmpt-alkyne **1** (**Fig. 5.3e**), is based on the *N,N'*-dimethylpyrimidinetrione (Dmpt) group, which exhibits higher chemical and thermal stability than the Dde scaffold used in our previous generation linker (**Fig. 5.4**). Importantly, the Dmpt group is stable under conditions used for trypsin-mediated protein digestion and can be quantitatively removed by treatment with dilute solutions of alpha nucleophiles like hydroxylamine, providing a versatile tag for targeted enrichment workflows. Once cleaved, the Dmpt group also leaves behind

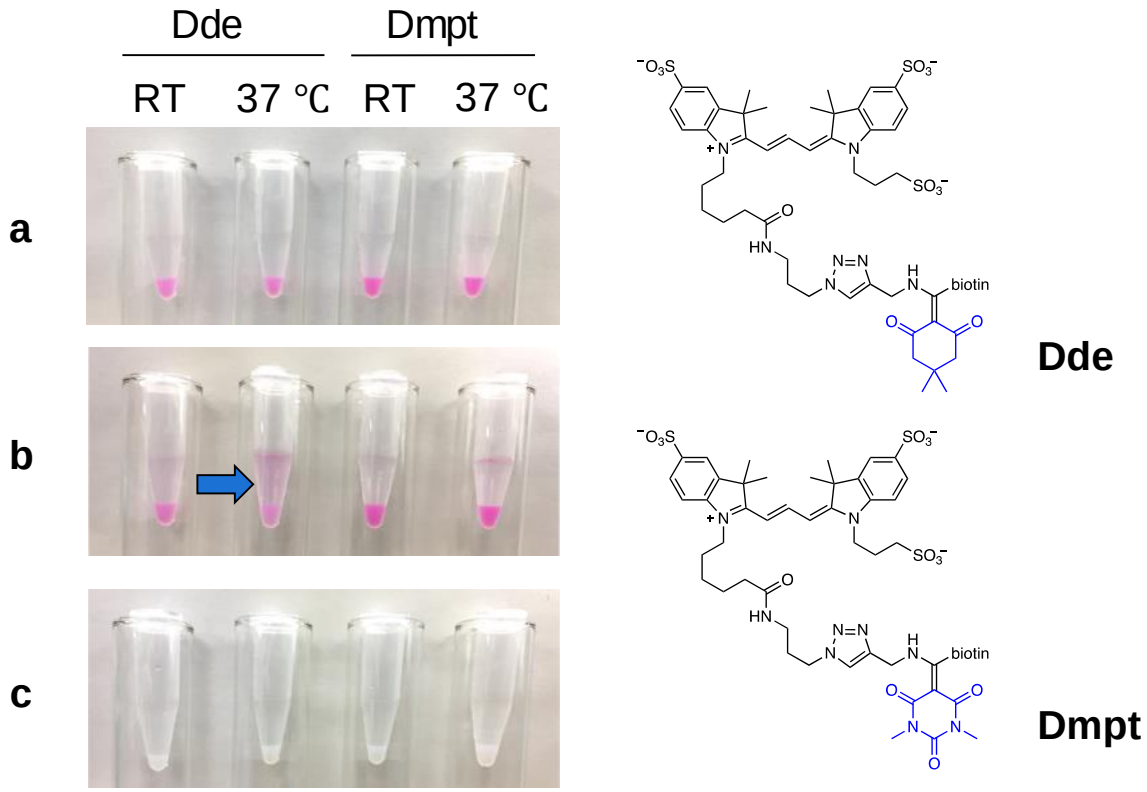

Fig. 5.4. Thermostability of the Second-Generation Dmpt-Based Linker.
(a) Alkyne-Dde-biotin or alkyne-Dmpt-biotin 1 was reacted with azido-Cy3 and immobilized onto high-capacity Neutravidin resin. **(b)** After overnight incubation in phosphate-buffered saline, the dye conjugated to the Dde linker showed leaching into the buffer at higher temperatures necessary for tryptic digestion. **(c)** Both linkers showed efficient release of the immobilized dye after treatment with NH_2OH.

a relatively small additional mass tag that contains primary amine, which can aid in peptide fragmentation through ETD by increasing the peptide charge density.[36] Tagged peptides also produce signature ions of 300.1 *m/z* during HCD,[32,37] allowing for the rapid identification of O-GlcNAcylated peptides during MS analysis.

We applied our state-of-the-art chemoenzymatic labeling and enrichment approach with the new biotin-Dmpt-alkyne linker to profile OGT substrates in the transduced HEK-293T cell line described previously. In this new workflow, we also take advantage of the unique signature ions produced by our biotin-Dmpt-alkyne tag to develop a novel MS method for identification, sequencing, and site mapping of O-GlcNAcylated peptides. Specifically, we employ both HCD product ion triggered electron-transfer dissociation ETD and EThcD using the 300.1 *m/z* fragment ions from the tag as the trigger. This approach significantly improves overall instrument cycle time while maximizing O-GlcNAcylated peptide identifications. Duplicate samples were then processed through the labeling and enrichment process, and each were analyzed by both HCD-triggered ETD and HCD-triggered EThcD. Finally, to map and quantify O-GlcNAc sites, we developed a novel bioinformatics workflow to rapidly identify non-redundant, localized "sites" versus unlocalized "regions" and calculate the total number of O-GlcNAc sites present in our dataset with maximum parsimony (**Fig. 5.5**). Unlike standard methods for counting PTM sites, this approach eliminates the counting of duplicate peptides/sites from missed cleavages or different charge states and provides a parsimonious enumeration of O-GlcNAcylation events at the site, rather than the modified peptide, level. Moreover, this general analysis is immediately applicable to any variable peptide modification including other PTMs such as phosphorylation, acetylation,

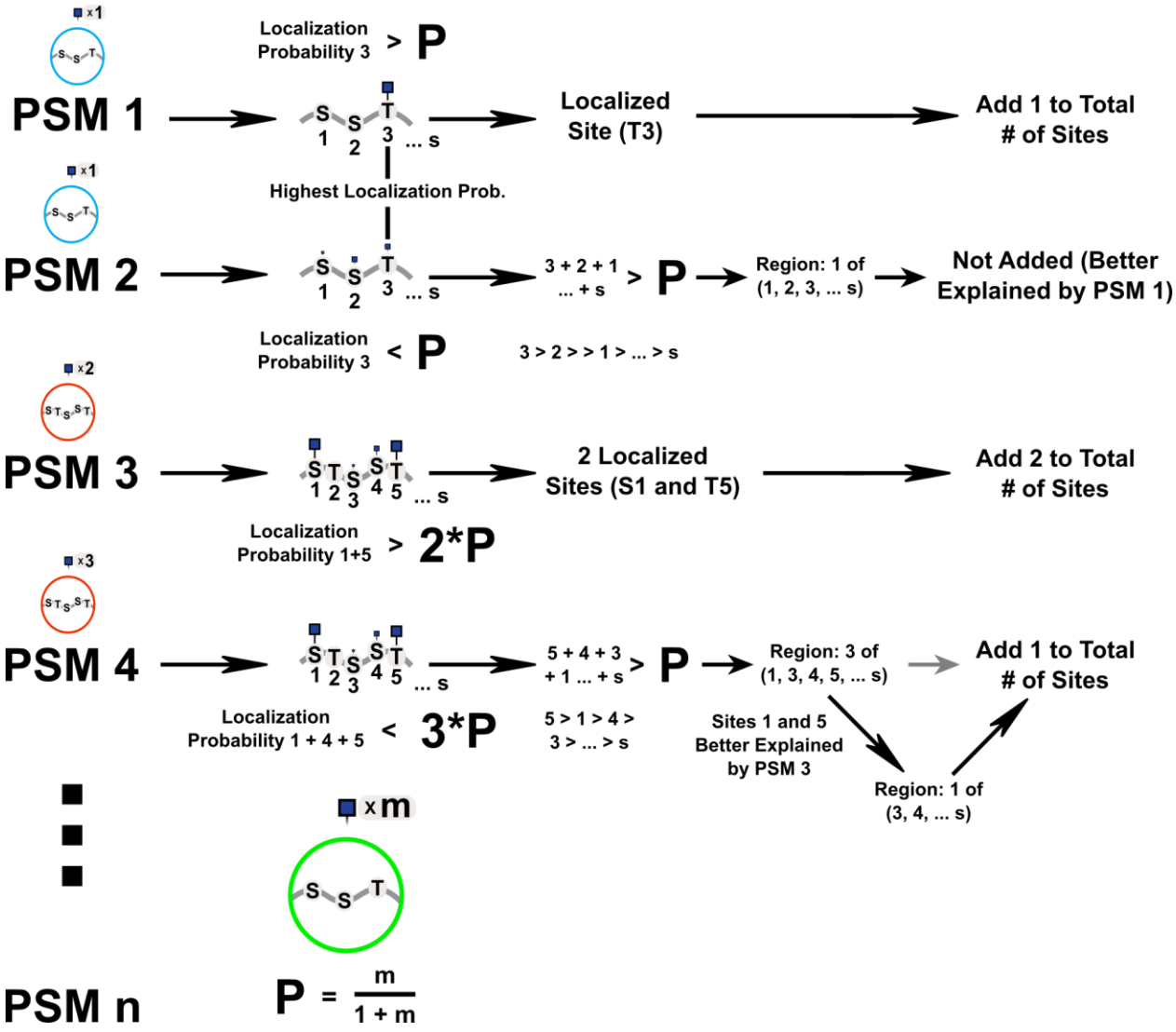

Fig. 5.5. Sites and Regions Workflow. See next page.

and ubiquitination. Together, these validation experiments yielded 1,764 unique O-GlcNAcylated sites across 646 proteins with a false discovery rate of 1%. Our methods were also able to produce highly efficient peptide fragmentation without loss of the glycan, allowing us to localize the O-GlcNAc modification to a single Ser/Thr residue for 63% of the sites (**Fig. 5.3f**). For example, strikingly, we found 67 localized sites (74 total) on HCFC1, including 47 that were not previously annotated in the PhosphoSitePlus database.[38] Splitting the identified peptides by fragmentation,

we found that that HCD identified the highest number of O-GlcNAcylated peptides followed by EThcD and ETD (all HCD identification were considered unlocalized due to essentially universal neutral loss of the glycan) (**Fig. 5.3g**). Finally, logo generation (**Fig. 5.3h**) and enrichment analysis (**Fig. 5.3i)** of sites using WebLogo,[39] revealed an overall lack of consensus sequence for OGT with a slight preference for proline, valine, and alanine in the -3 through -1 and +2 positions. O-GlcNAc sites were also more likely to be in the vicinity of multiple additional S/T residues.

5.5. Functional Networking of OGT Interactors and Substrates.

With comprehensive lists of interactors and substrates derived from the same biological source, we sought to integrate this information to better understand how substrates and interactors coordinate to affect cellular function. We obtained known PPIs either between two OGT interactors or between an OGT interactor and substrate as annotated in at least one of the PPI databases BioGRID or IntAct. An O-GlcNAc functional network with undirected edges defined

Fig. 5.5. Cont. Sites and Regions Workflow. O-GlcNAc sites are counted until all sites in every PSM are explained with max parsimony. O-GlcNAc sites are only localized if the localization probability (ptmRS) is greater than what would be expected by chance alone. In the example above, there are two proteins, denoted by the red and blue circles, each with two PSMs. In PSM 1 (1 O-GlcNAc), there is only one site with a localization probability of 1. Thus, 1 site is counted at position T3 in the first protein. In PSM 2 (1 O-GlcNAc), there are s sites all with localization probabilities less than 0.5. The localization probability is summed over all sites until it is greater than 0.5 in aggregate resulting in a single site region in (1, 2, 3, … s). However, this site is not counted in the total number of sites as PSM 1 would better explain this single site region. In PSM 3 (2 O-GlcNAcs), there are s sites, two of which combined have a localization probability greater than 1.333. Thus, 2 sites are counted at S1 and T5 in the red protein. Finally, in PSM 4 (3 O-GlcNAcs), there are s sites, of which no three have a combined localization probability of greater than 2.25. Again, the localization probabilities of sites 1 through s are then summed until the localization probability in aggregate exceeds 2.25 resulting in a 3 site region in (1, 3, 4, 5, … s). However sites S1 and T5 can already be explained by PSM 3 so they are removed from the region giving a single site region in (3, 4, … s). In cases where multiple amino acids have the same localization probability (e.g. in HCD spectra where the localization probability was set to equal on every S/T), they are taken together for a given region. PSM: peptide spectral match.

by these PPIs was then visualized with Cytoscape.[40] To better identify the individual functional cellular networks engaged by O-GlcNAcylation, we employed the community clustering algorithm GLay.[41,42] This program scores edge betweenness for node groups to extract local communities from a larger network. Importantly, this approach is inherently blind to protein identity, providing a functionally unbiased approach to network partitioning. Excitingly, Gene Ontology (GO)[43] biological process (BP) term analysis followed by GO term grouping in ClueGO[44] of the resulting communities (**Fig. 5.6a**) revealed five subnetworks enriched for distinct cellular functions: 1. (Regulation of) Transcription and Translation, 2. Chromatin Organization and Remodeling, 3. Nuclear and Organelle Transport, Cytoskeleton Organization, 4. RNA/DNA Synthesis and Metabolism, and 5. Translation and mRNA Splicing. Hierarchical clustering of all significant GO terms from the entire dataset also supported the functional segregation of clusters in biological process (**Fig. 5.6b**), molecular function (**Fig. 5.7a**), and cellular component (**Fig. 5.7b**) space, highlighting the power of GLay clustering to reveal and partition networks of functionally and spatially related proteins for further analysis. Interestingly, the interactors underlie a much more diverse set of biological functions, and the combined networking approach reveals functional and component information that would have been missed by analysis of interactors and substrates alone (e.g. in Cluster 3). Finally, the clusters were also highly enriched for distinct pathways (**Figs. 5.7c-e**), again revealing new pathways that would not have been discovered in the absence of our combined functional networking approach (e.g. in Clusters 3 and 4.

In addition to broad functional roles, the resulting network clusters directly offer protein candidates, complexes, and potential adaptor proteins that may underlie the biological activities of

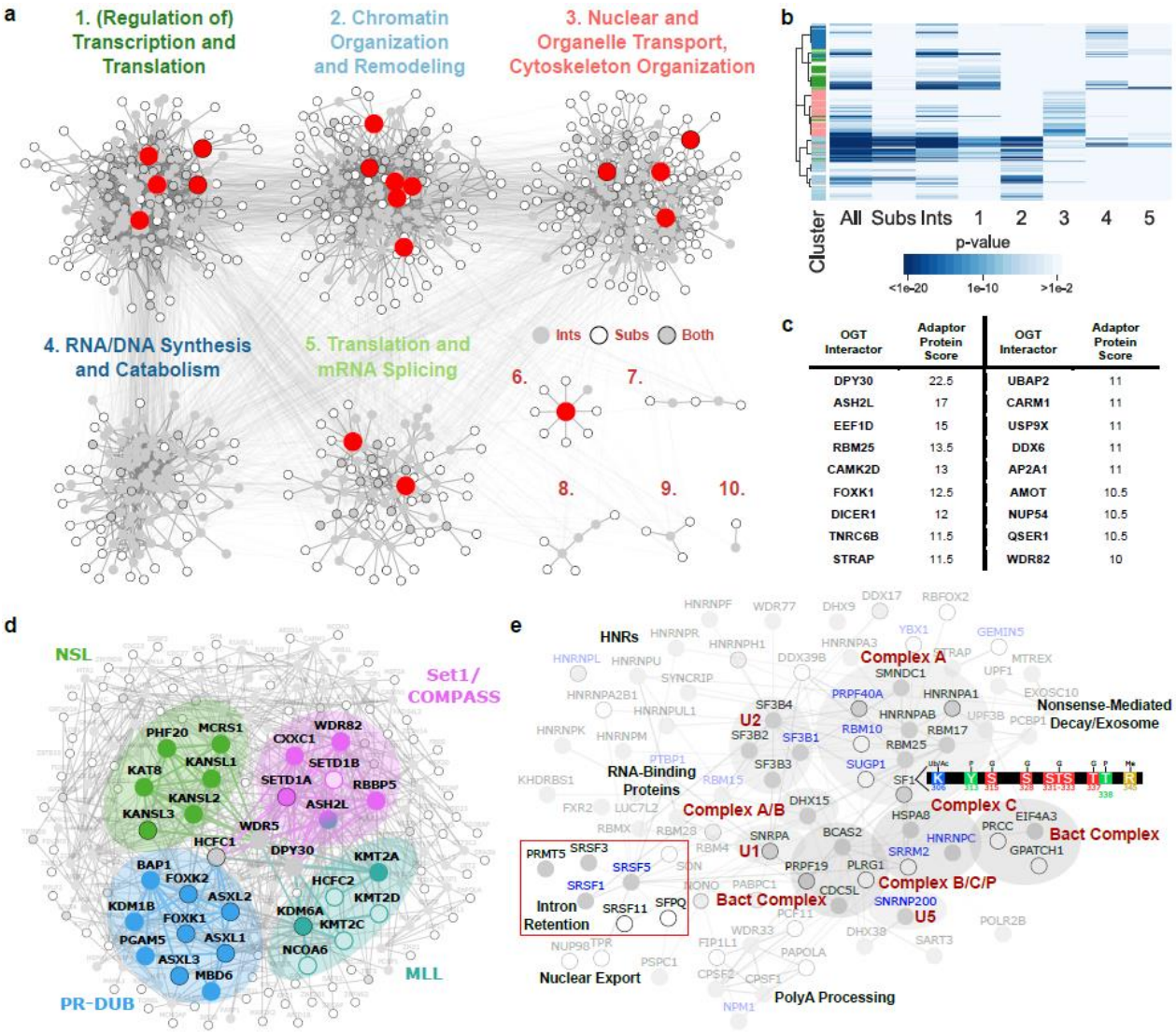

Fig. 5.6. NOTISE in 293T Cells. See next page.

O-GlcNAcylation. First, to find potentially undiscovered OGT adaptor proteins in our network, we developed a program to rank OGT interactors, rewarding them with 1 point for their connection to substrates and penalizing them 0.5 points for their connection to interactors (to avoid co-selecting members of large protein complexes), to find the most well-connected single proteins (**Fig. 5.6c**). Interestingly, protein dpy-30 homolog (DPY30) and Set1/Ash2 histone methyltransferase complex subunit ASH2 (ASH2L), core components of the Set1/mixed lineage

leukemia (MLL) complexes and known molecular scaffolds,[45-47] were our top two hits. Many of the other top hits are also known molecular scaffolds or adaptors, including histone-arginine methyltransferase CARM1 (CARM1) which has previously been suggested to function as an OGT adaptor protein.[48] Overall, the unique structural insight into the PPI networks associated with OGT provided by NOTISE is a key first step towards understanding how OGT might associate with molecular adaptors to facilitate its different regulatory roles in different contexts.

In addition to single proteins, NOTISE also reconstructed multiple, well-characterized multi-protein complexes with statistical enrichment of 82 complexes across all clusters (**Fig. 5.7f**). Cluster 2, Chromatin Organization and Remodeling, was itself enriched for 44 complexes and almost completely reassembled four OGT-containing complexes: the SET1 histone methyltransferase complex,[49,50] the polycomb repressive deubiquitinase (PR-DUB) complex,[51] the nonspecific lethal (NSL) histone acetyltransferase complex,[52,53] and the MLL complex (**Fig. 5.6d**). Recent results from other groups have confirmed the regulatory roles of OGT/O-GlcNAcylation in SET1-mediated histone methylation,[49] NSL-mediated histone acetylation,[52] and MLL stability[54] that are implicated by our network analysis. O-GlcNAcylation is also known to coordinate

Fig. 5.6. Cont. NOTISE in 293T Cells.
(a) O-GlcNAc functional communities revealed by PPI networking and GLay clustering of OGT interactors and substrates. Grey fill indicates OGT interactors and black outline represents OGT substrates. Larger red nodes are interactors with an adaptor rank score > 10 (see also **(c)**). Edges opacity and thickness is varies for in-cluster (greater) vs out-of-cluster (less) connections. **(b)** Hierarchical clustering of all significant biological process GO terms in our dataset. Terms are color-coded based on the cluster in which their p value was lowest. **(c)** Proteins that had an adaptor rank score of 10 or higher in our network (shown in red in **a**). **(d)** A closer view of Cluster 2 highlighting the almost completely reassembly of the NSL, SET1/COMPASS, PR-DUB, and MLL complexes. **(e)** All proteins annotated with "splicing" in the Uniprot Knowledgebase (almost exclusively from Cluster 5) are shown with core components of the spliceosome and other RNA processing functions indicated. The red box highlights OGT interactors/substrates previously implicated in detained intron removal. PTMs from position 306 to 345 on SF1 are shown, including four O-GlcNAc sites at S315, S328, S/T/S331-333 (unlocalized), and T337.

transcriptional repression by the PR-DUB complex in *Drosophila*, and our results imply that this regulatory activity is conserved in mammalian cells.[55]

To better understand the functional implications of the proteins and sites present in our network, we also integrated data from the Uniprot[56] and PhosphositePlus databases into our

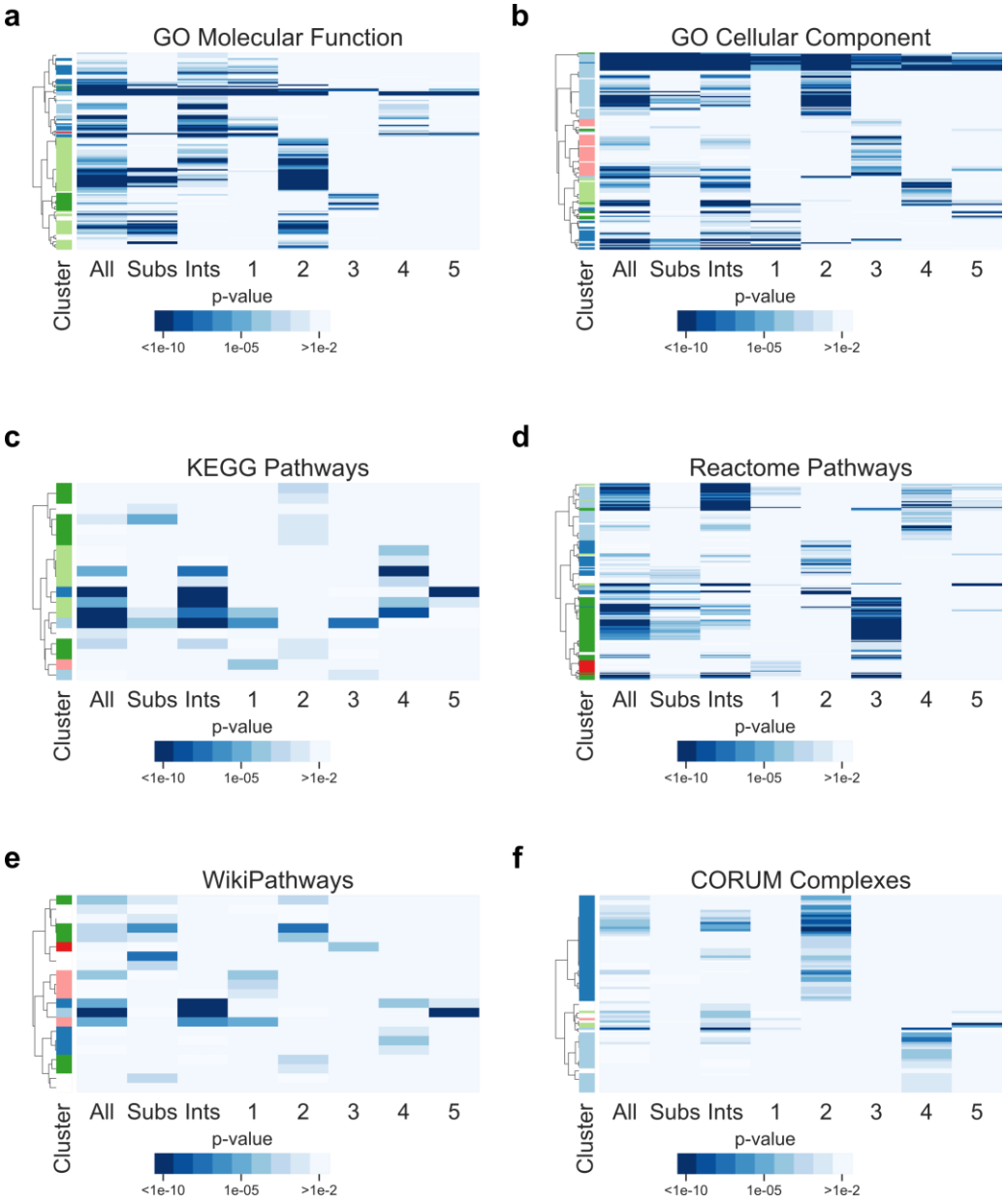

Fig. 5.7. Hierarchical Clustering of 293T Functional Communities.
Hierarchical clustering of Molecular Function **(a)** and Cellular Component **(b)** GO terms; KEGG **(c)**, Reactome **(d)**, and Wiki **(e)** Pathways; and CORUM complexes **(f)** reveals distinct roles for each functional community. Cluster colors correspond to those in **Fig. 5.6a**.

previously constructed Cytoscape network. This allows for the live interrogation and contextualization of a vast knowledge base of protein structure and function, including the ability to rapidly find O-GlcNAc sites in various PPI domains (**Fig. 5.8a**) or overlapping with other known PTMs (**Fig. 5.8b**). Strikingly, we found that roughly 65% of O-GlcNAc sites identified in the canonical SwissProt sequences were within 10 amino acids of a phosphorylation site in addition to hundreds within 10 amino acids of acetylation, methylation, and ubiquitination sites, indicating the interplay between O-GlcNAc and other PTMs is perhaps much more extensive than previously realized. As an example of a specific function, we focused on the previously uncharacterized role for O-GlcNAcylation in RNA splicing. Excitingly, during the preparation of this manuscript, Walker and coworkers identified a novel role for O-GlcNAcylation in regulating global splicing of detained introns.[57] Here, we find that OGT interacts with and modifies many components of the

a

Top Domains		Top Regions	
RID	7	11 X 5 AA approximate repeats	35
Peptidase A1	2	Interaction with ZBTB17	15
EGF-like 30; calcium-binding	2	Interaction with SIN3A	15
		Head	8
		18 X 4 AA approximate repeats	6
		Pore side	6
		11 X 3 AA approximate repeats	6
		Interaction with BRCA2	6
		Sufficient for interaction with AGO2	5
		Tail	5

b

Modification Type	Sites within 10 Amino Acids	Overlapping Sites
Acetylation	62	0
Methylation	103	0
OGalNAc	2	1
OGlcNAc	195	120
Phosphorylation	710	278
Sumoylation	29	0
Ubiquitination	186	0
Disease	8	2
Regulatory	32	6
PTMVar	46	1

Fig. 5.8. UniProt and PhosphoSitePlus Integrated Cytoscape Networks Allows for Rapid Integration of Site and Protein Features.
(a) Top domains and regions in which O-GlcNAc sites are found. **(b)** The number of O-GlcNAc sites that are within 10 amino acids or overlapping with annotated PTMs in the PhosphoSitePlus databased. PTMVar: PostTranslational Modifications (phosphorylation, ubiquitination, acetylation, methylation and succinylation) that overlap with genetic variants associated with diseases and genetic polymorphisms. In both cases, data was searched against the Swiss-Prot database to facilitate matching with PhosphoSitePlus.

spliceosome,[58] including many splicing factors that were differentially phosphorylated in response to OGT inhibition (**Fig. 5.6e**). Given our data, it is also tempting to speculate that OGT may modulate detained intron splicing through its interaction with or modification of protein arginine N-methyltransferase 5 (PRMT5) and various associated splicing factors, e.g. the highly-connected protein serine/arginine-rich splicing factor 5 (SRSF5), known to enhance removal of detained introns (red box).[59-61] It is also possible that O-GlcNAcylation of core spliceosome components regulate detained intron removal by changing their activities or molecular associations. For example, we found multiple O-GlcNAcylation sites on splicing factor 1 (SF1) that occur in a nexus of diverse PTMs (strongly suggesting a role for O-GlcNAcylation in regulating initial spliceosome assembly and function).[62] Altogether, the discovery of both established and possible new activities of O-GlcNAcylation through network analysis highlights the uniquely powerful capacity of NOTISE to generate new hypotheses regarding O-GlcNAc function and to provide a molecular foundation for future investigations via the underlying OGT interactors and substrates not possible with other high-throughput methods.

5.6. NOTISE-Driven, Selective Disruption of Protein O-GlcNAcylation.

We next aimed to determine if NOTISE could provide molecular insights into the OGT-adapter hypothesis and reveal specific regulatory proteins that could be targeted to disrupt O-GlcNAcylation events. We focused on the PR-DUB complex in Cluster 2 given (1) its extensive molecular characterization,[51] (2) a role of OGT/O-GlcNAcylation in regulating complex activity has not yet been described in mammals, and (3) and the presence of forkhead box protein K1 (FOXK1) near the top of our adapter rank list. Interestingly, we found that siRNA-mediated knockdown of BAP1 disrupted the association of FOXK1 with OGT without interfering with other

OGT-protein interactions in the SET1/COMPASS complex (**Fig. 5.9a**). To understand whether specifically disengaging OGT from FOXK1 can modulate its activity towards interacting substrates, we interrogated site-specific substrate O-GlcNAcylation in CRISPR/Cas9-generated BAP1 KO versus WT 293T cells. Specifically, we developed a novel quantitative O-GlcNAcomics workflow using TMT-synchronous precursor selection (SPS)-MS3 for site level quantification of O-GlcNAcylation (**Fig. 5.10**), the first of its kind. Because TMT labeling also modifies the primary amine installed on the O-GlcNAc residue after purification with our biotin-Dmpt-alkyne linker, we were able to take advantage of three new diagnostic ions at 732.4, 547.3, and 529.3 *m/z* (**Fig.**

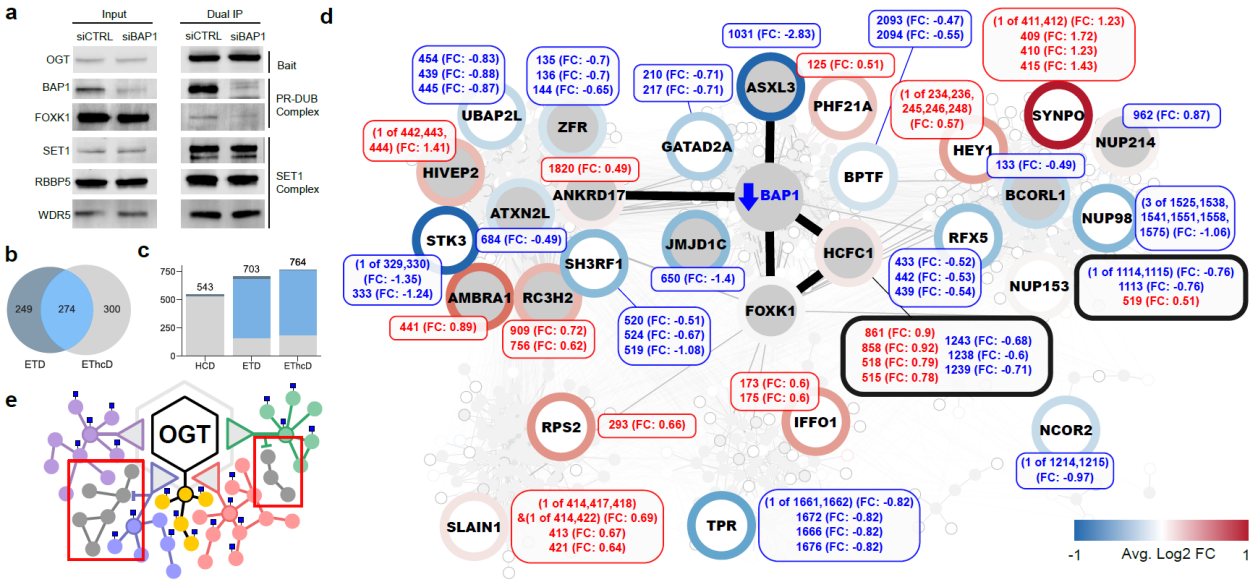

Fig. 5.9. NOTISE Driven Disruption of Protein O-GlcNAcylation.
(a) Validation of OGT decoupling from PR-DUB complex but not the SET1 complex by specific targeting of BAP1 by siRNA knockdown after OGT immunoprecipitation. **(b)** Venn diagram of localized sites identified by ETD and EThD with our novel quantitative MS workflow over n=3 biological samples. **(c)** Breakdown of all sites identified by each fragmentation method. **(d)** Significantly changing sites in the 293T PPI network. Interactions between BAP1/FOXK1 and other proteins are shown as black edges (with those between proteins with significantly changing sites shown thicker). Node boarders are colored based on the average log2 fold change of *all* O-GlcNAc sites on a given protein. Note the black outlines represent proteins with both up- and downregulated sites.

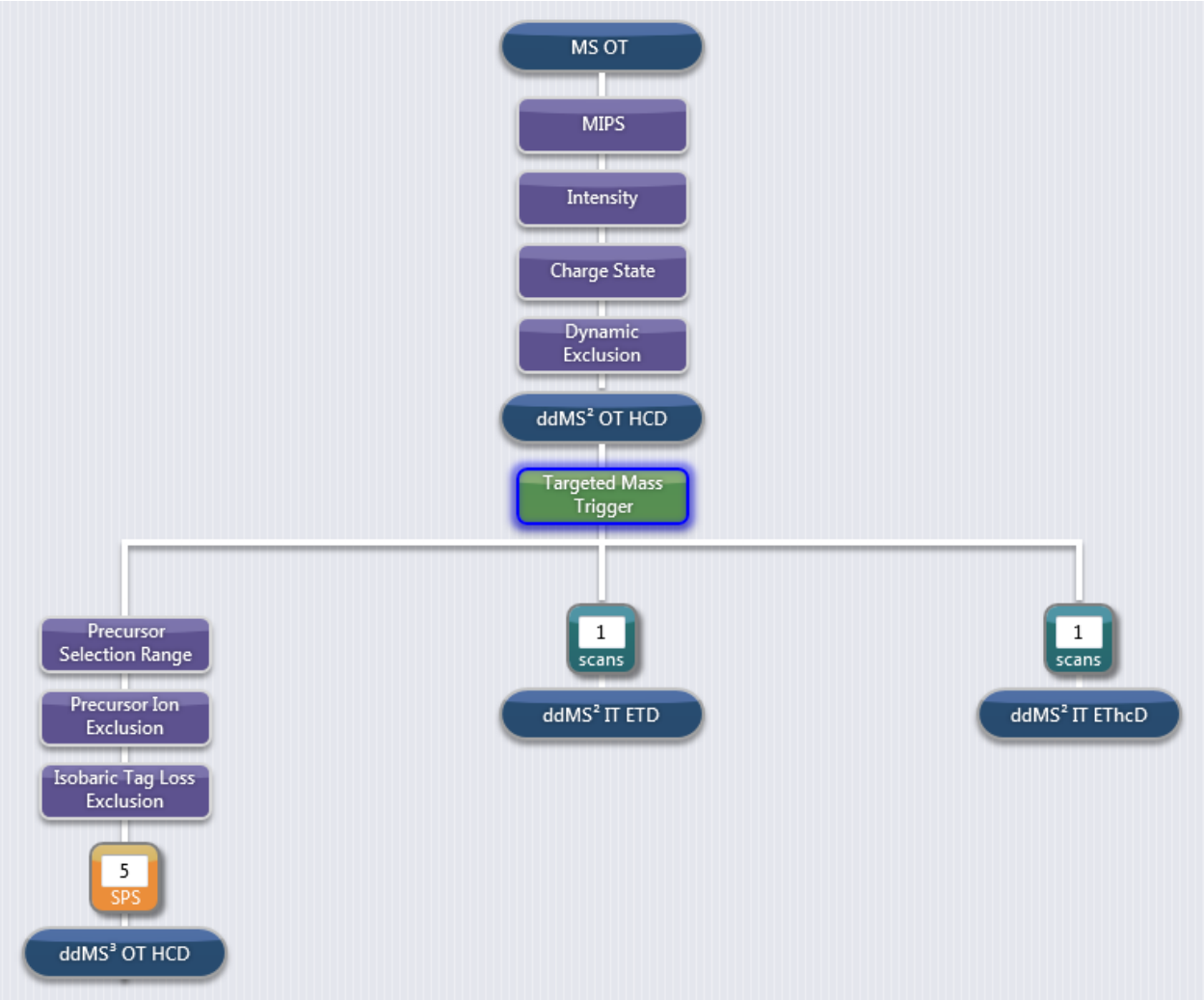

Fig. 5.10. Quantitative O-GlcNAcomics Workflow.
Precursor ions are fragmented by HCD to reveal tag specific fragment ions at 732.4, 547.3, and 529.3 *m/z*. If any of these ions are present in the top 30 most intense fragments, precursors are further subjected to SPS-HCD-MS3, ETD, and EThcD. Note ETD and EThcD spectra are acquired in the Ion Trap with all MS2 and MS3 HCD spectra acquired in the Orbitrap for optimal acquisition speed. Both top speed (5 sec cycle time) and top 10 versions of this method were used.

5.11) in HCD fragmentation as triggers for both ETD/EThcD and SPS-MS3. Notably, this new TMT-SPS-MS3 protocol also saved significant cycle time over standard SPS-MS3 fragmentation of all precursor ions. We combined top speed (5 sec) and top 10 data-dependent runs (**Fig. 5.12**) over three biological replicates to identify 1,087 sites (76 percent localized) across 365 unique proteins (**Appendix 5.1**). Importantly, our method allowed us to obtain quantitative information

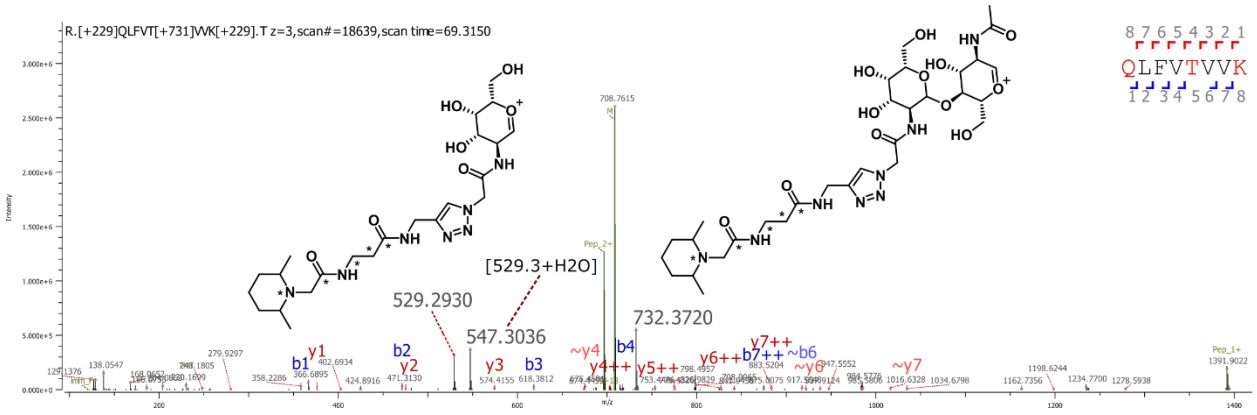

Fig. 5.11. TMT-Labeled Biotin-Dmpt-Alkyne Fragments.
HCD spectra of ANKRD17 O-GlcNAcylated at T2001. Note the three fragments from the full tag oxonium ion (732.3720), the tag after loss of GlcNAc (529.2930) and the water adduct of the later (547.3036). The TMT-127N tag is shown.

for *all* of these sites. We were also able to track the relative site occupancy on 935 sites across 290 proteins after normalizing for changes in protein expression (6,485 proteins quantified in total), the most protein-expression-corrected sites ever described. Interestingly, in this experiment, where every precursor was fragmented by both ETD and EThcD in the same run, we found that there was a large, non-overlapping set of localized sites only identified by either fragmentation method (**Fig. 5.9b**), with EThcD having only a slight advantage in the number of identified sites (**Fig. 5.9c**).

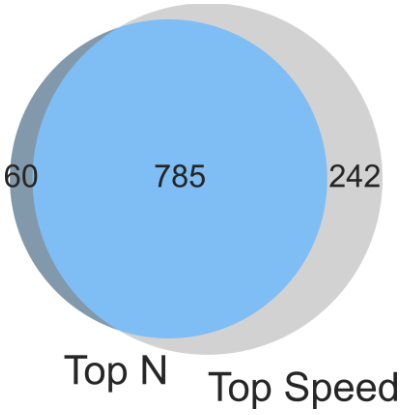

Fig. 5.12. Comparison of Sites Identified in Top N vs Top Speed Trials. Overlap between sites identified in the top 10 (n=2) versus the top speed (5 sec cycle time, n=3) MS methods.

To identify significantly changing sites, fold-change was then averaged across the top speed and top 10 runs, and significant differences were determined by limma-moderated t-test ($p < 0.05$). In total, there were 86 significantly changing sites/regions across 45 proteins, of which 27 were present in our previously generated PPI network (**Fig. 5.9d**). Interestingly,

although FOXK1 O-GlcANcylation remained unchanged, we found a striking decrease on in S1031 O-GlcNAcylation on the BAP1 interactor putative polycomb group protein ASXL3 (ASXL3). In our network, BAP1 is the only interactor with ASXL3 in the PR-DUB protein complex, suggesting that BAP1 may be serving as an adaptor protein between OGT and ASXL3. However, unfortunately, we did not quantify ASXL3 protein expression, so we are not able to rule out confounding changes in ASXL3 expression. Surprisingly, we also found an increase in S1820 O-GlcNAcylation on BAP1 interactor ankyrin repeat domain-containing protein 17 (ANKRD17) and *both* an increase and decrease on BAP1/FOXK1 interactor HCFC1 (in both of these cases we were able to quantify protein expression).

Throughout the network, we also found both increases and decreases in relative site occupancy on proteins that were relatively close to BAP1/FOXK1, including another example of both up and downregulated O-GlcNAcylation on nuclear pore complex protein Nup153 (NUP153). This suggests that BAP1 may not only be targeting OGT to various proteins, but also blocking access to certain sites potentially through interaction with either OGT or the target protein, a potentially unrecognized nuance of the adapter protein hypothesis (**Fig. 5.9e**). Overall, these studies represent the first successful attempt to modulate the O-GlcNAcylation on specific proteins at specific sites through disruption OGT-protein interactions. Moreover, our powerful new MS workflow is the first to quantify site-specific changes in O-GlcNAcylation on the same peptide (e.g. sites 1238-43 on HCFC1). Taken together, these studies provide the first tools to site-specifically modulate and monitor O-GlcNAcylation, and, as new technologies emerge to specifically inhibit protein-protein interactions, lay the ground work for future targeting of specific O-GlcNAc sites as a therapeutic strategy for neurodegenerative disease, cancer, diabetes, and other pathologies.

5.7. Defining Conserved and Tissue-Specific O-GlcNAc Regulatory Networks In Vivo.

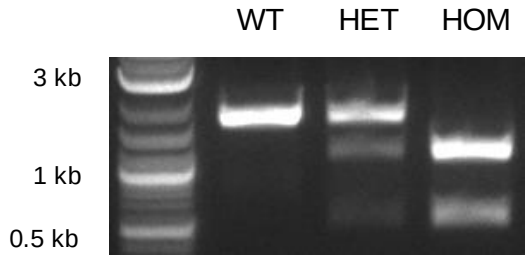

Fig. 5.13. OGT-FH Mouse Genotyping. Facile genotyping of the OGTFH mouse line was achieved by genomic amplification of the *C*-terminal region of OGT followed by digestion with BamHI, which cleaves genomic DNA amplicons that contain the tag insertion.

We next aimed to expand our method to the study of O-GlcNAcylation networks in vivo. To achieve this goal, we first generated a novel mouse model using CRISPR/Cas9 technology in which FLAG and HA tags were inserted at the C-terminus of the endogenous OGT gene (OGT-FH, **Fig. 5.13**, **Fig. 5.14a**). To ensure that the dual tags did not affect protein expression levels, we used Western blotting to confirm equivalent expression levels of tagged and untagged OGT in the major organs of both OGT-FH and WT adult mice (**Fig. 5.14b**). Moreover, the tagged OGT mouse line exhibited no obvious phenotypes through development to adulthood, and inheritance of the tagged OGT gene followed a normal Mendelian distribution (chi-square test, $P > 0.5$, **Fig. 5.15**).

Using our OGT-FH mouse model, OGT interacting partners were immunoprecipitated from the brains and livers of two-month-old animals by adapting our previously described workflow. Briefly, after tandem affinity purification, digested peptides of OGT interactors from each organ and control organs from age-matched C57BL/6J mice were subjected to reductive amination with isotopically defined formaldehyde in lieu of SILAC labeling prior to mixing and downstream mass spectrometric analysis (**Fig. S12**). Using the same analysis pipeline as for 293T cells, we found 993 and 643 high-confidence interactors (**Appendices 5.2** and **5.3**) and 2,219 and 1,150 O-GlcNAc sites (**Appendices 5.4** and **5.5**) across 810 and 492 proteins in the brain and liver, respectively. In total, we found 2,785 unique O-GlcNAc sites (62% localized) across both datasets,

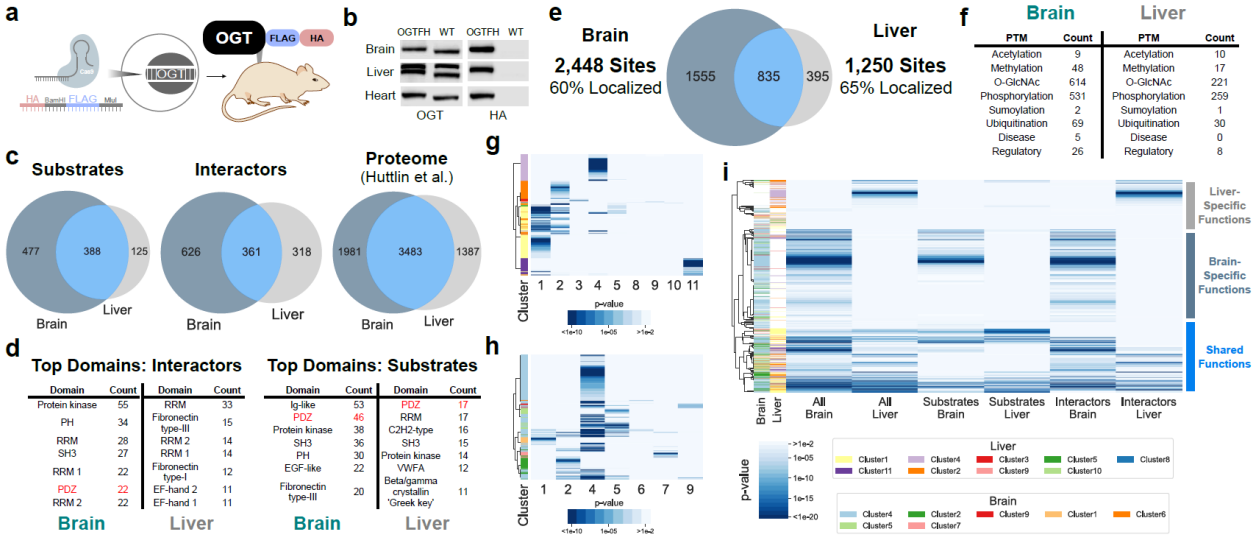

Fig. 5.14. In Vivo NOTISE Reveals both Tissue-Specific and Conserved Functions for O-GlcNAc in the Mouse Brain and Liver.
(a) CRISPR/Cas9-mediated genome editing for expressing tagged OGT in vivo. **(b)** Western blot profiling of OGT expression between various organs of wild-type and OGTFH mice. **(c)** Overlap between all substrates, interactors, and the full proteomes in the brain and liver. **(d)** The top domains identified in substrates in the liver and brain. **(e)** Site-level overlap between the brain and the liver. **(f)** Number of O-GlcNAcylation sites within 10 amino acids of other PTM sites as annotated in the PhosphoSitePlus database. **(g)** Hierarchical clustering of individual functional communities in the liver shows relatively distinct partitioning of functions into individual clusters. Terms are color-coded based on the cluster in which their p value was lowest. **(h)** Hierarchical clustering of individual functional communities in the brain as in (**g**). **(i)** Hierarchical clustering of all biological process GO terms in the combined brain and liver dataset. Note the distinct clusters for liver-specific, brain-specific, and shared function (indicated left). Terms are color coded as in (**g**) and (**h**).

significantly updating our understanding of the O-GlcNAcome and by far the most ever described. Interestingly, although the overlap between substrates was relatively consistent with that of the overall proteome,[63] the overlap between interactors was much more distinct (**Fig. 5.14c**), suggesting that the tissue specific roles of OGT may be driven by differences in OGT-protein interactions. As with 293T cells, we also built Uniprot/PhosphoSitePlus integrated Cytoscape files and enumerated the most common domains found in both the interactors and substrates (**Fig. 5.14d**). Interestingly, the PDZ domain, a well-known mediator of PPIs, was near the top of those domains found in brain interactors as well as those found in both brain and liver substrates. PDZ

domains are essential for organizing synaptic architecture,[64] and our data suggest that OGT interactions/O-GlcNAcylation may be playing an important role in regulating these domains. Thus, it is tempting to speculate that the well-established effects of modulating O-GlcNAcylation on LTP and LTD may also be mediated in part through altering the assembly and organization of the pre-/postsynaptic signaling.[10,65] We also calculated the site-level overlap between the brain and liver (**Fig. 5.14e**) and again identified numerous sites within 10 amino acids of other PTMs, including those known to have a regulatory or disease modifying role (**Fig. 5.14f**).

a

	X^{WT}	X^{FH}
X^{FH}	34	29
Y	34	46

$\chi^2 = 4.38$; df = 3; $P = 0.22$

b

	X^{WT}	X^{FH}
X^{WT}	34	34
Y	53	38

$\chi^2 = 6.16$; df = 3; $P = 0.10$

Fig. 5.15. Chi-square Analysis of OGTFH Gene Heritability. Offspring numbers for (a) $X^{FH}Y$ x $X^{WT}X^{FH}$ or (b) $X^{WT}Y$ x $X^{WT}X^{FH}$ crossings are presented as Punnett squares with chi-square (χ^2), degrees of freedom, and calculated *P*-values.

We then employed our PPI networking strategy and GLay clustering to construct brain and liver networks. Again, we found that individual clusters had relatively distinct functions for both the liver (**Fig. 5.14g**) and brain (**Fig. 5.14h**). We also performed hierarchical clustering on all biological process GO terms and found clear evidence of both conserved and brain-/liver-specific functions that were relatively separate by cluster in each organ (**Fig. 5.14i**). As with 293T cells, we also found distinct differences in molecular function, cellular component, complex, pathway, and human phenotype space (**Fig. 5.16**). Notably, this is the first systems-level evidence that O-GlcNAcylation has tissue-specific functions. Overall, NOTISE revealed eight functional communities in the brain and seven in the liver (**Fig. 5.17a**), enriched for a variety of processes from nervous system development to metabolism. Key processes that were shared between the tissues were chromatin organization, RNA processing, and cytoskeletal organization/dynamics.

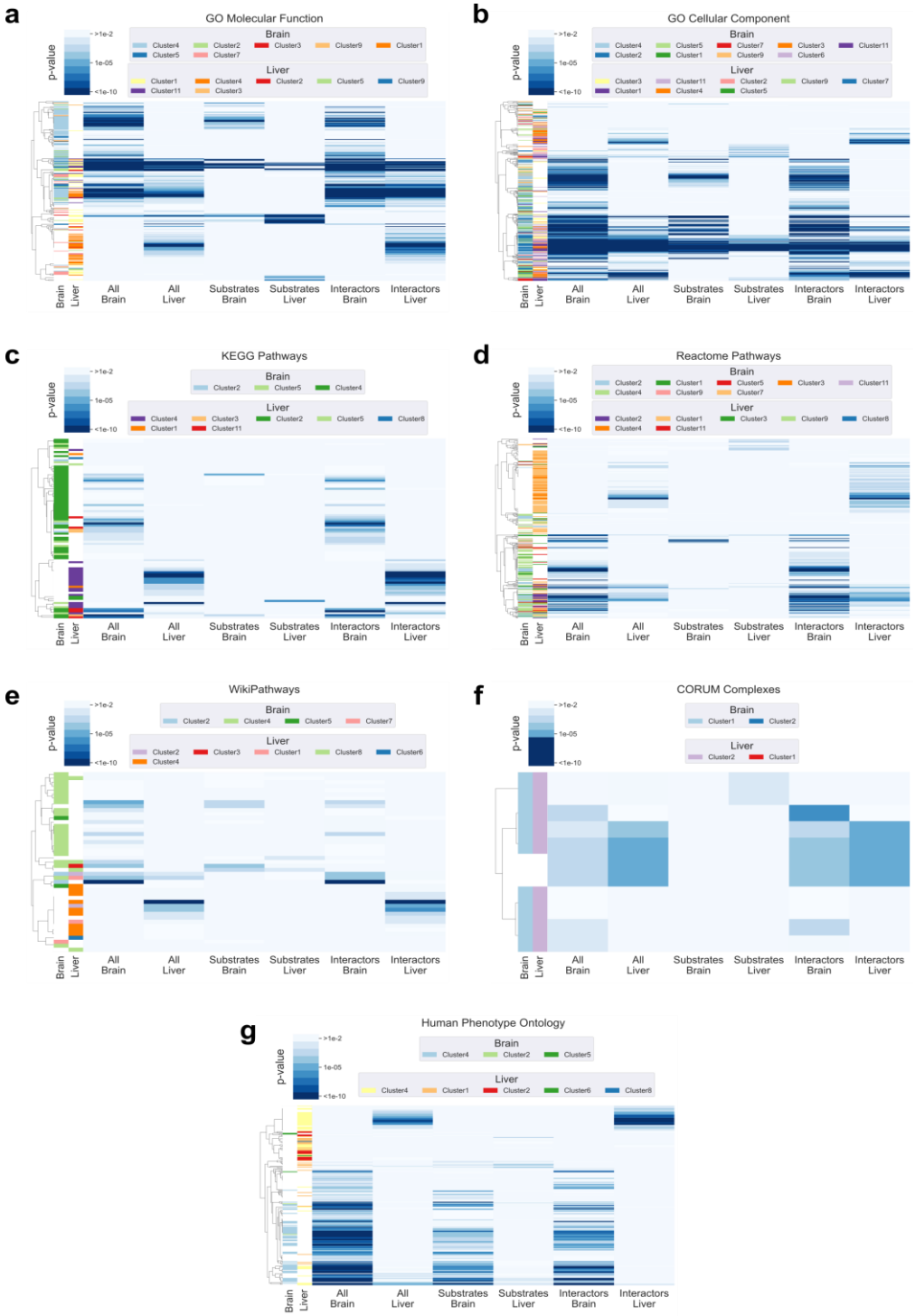

Fig. 5.16. Hierarchical Clustering of Brain and Liver Gene Ontologies, Pathways, and Protein Databases. See next page.

Interestingly, these processes are also shared with 293T cells, suggesting that they may represent more of a core, conserved subset of OGT functions. Finally, there was only 26% overlap between

the proteins in both networks, further suggesting that differences in the roles of OGT between the tissues goes beyond the differences in their proteomes.

As in 293T cells, we also used our adaptor rank program to find candidate OGT adaptor proteins (**Fig. 5.17b**). Here, RNA binding protein fox-1 homolog 1 (Rbfox1), a multifunctional proteins with molecular adaptor activity involved in alternative splicing, autism, and epilepsy was our top hit in the brain.[66] In the liver, 14-3-3 protein eta (Ywhah), a known adaptor protein and potential O-GlcNAc "reader" protein,[67] was far and away the top hit, further suggesting an important role for the interplay between phosphorylation and O-GlcNAcylation in the mammalian liver. Other proteins in these lists have known molecular adaptor activity and are involved in the assembly of the post synaptic density, e.g. disks large homolog 1 (Dlg1),[68] and nuclear import, e.g. importin subunit alpha-5 (Kpna1).[69]

Interestingly, actin dynamics appeared to be a common and, to our knowledge, as yet unrecognized function of OGT/O-GlcNAc in the liver and brain. Closer examination of the B5. Actin Cytoskeleton Organization and B4. Nervous System Development, Cell Signaling functional communities revealed multiple actin binding proteins and effectors including the complete Arp2/3 and WAVE regulatory complexes (WRC). A closer look at these complexes and associated proteins (**Fig. 6c**) revealed potential regulatory O-GlcNAcylation sites on neural Wiskott-Aldrich syndrome protein (Wasl), several members of the WAVE regulatory complex, and protein enabled homolog (Enah). For example, Wasl O-GlcNAcylation is positioned to close to the basic (B) and GTPase protein binding (GBD) domains, which could potentially disrupt auto-inhibition or

Fig. 5.16. Cont. Hierarchical Clustering of Brain and Liver Gene Ontologies, Pathways, and Protein Databases.
Hierarchical clustering of Molecular Function **(a)** and Cellular Component **(b)** GO terms; KEGG **(c)**, Reactome **(d)**, and Wiki **(e)** Pathways, CORUM complexes **(f)**, and Human Phenotype Ontology **(g)** reveals differences across tissues, substrates/interactors, and functional communities.

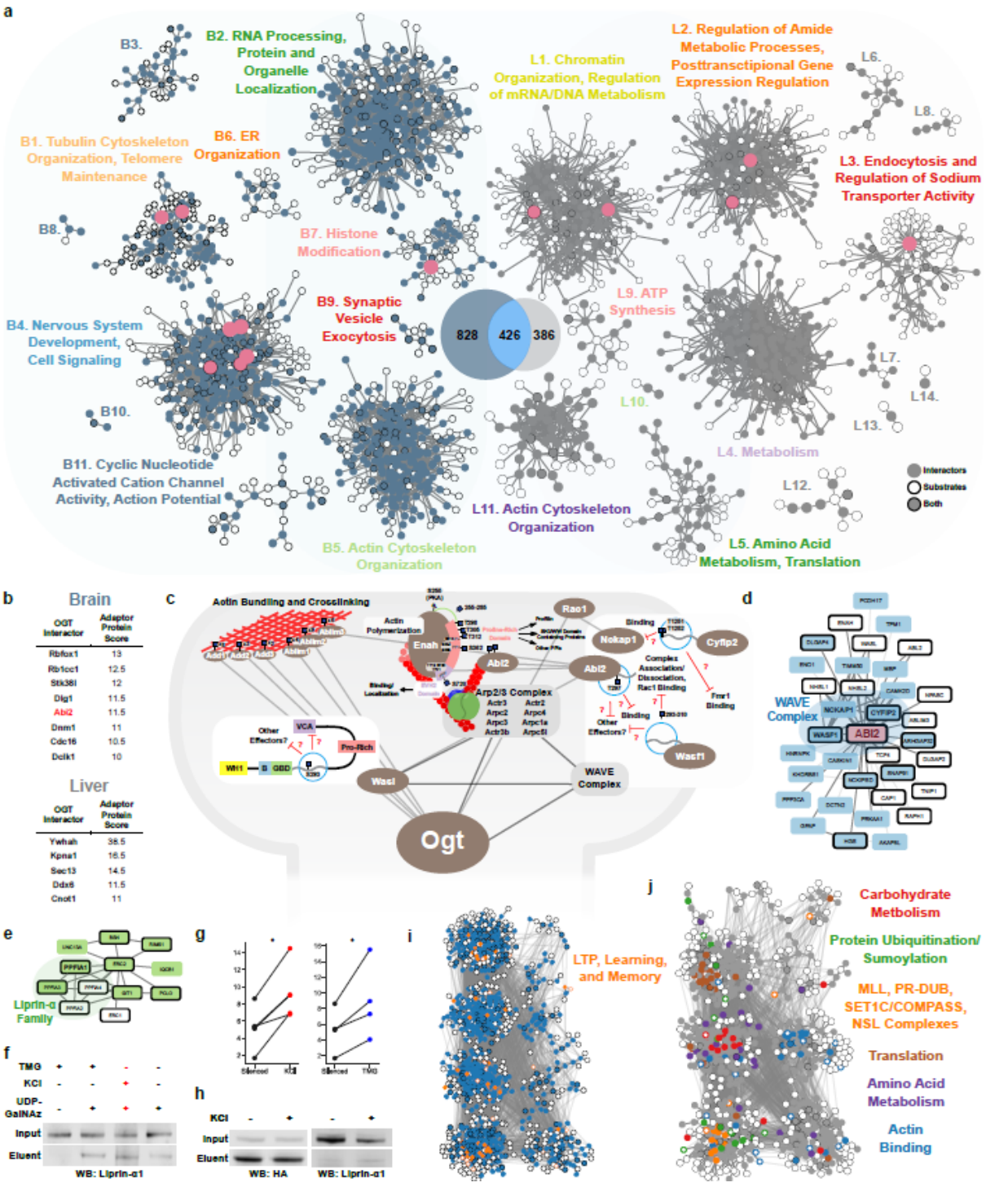

Fig. 5.17. NOTISE Enables Mechanistic Insights into the Tissue-Specific and Conserved Functions of OGT in the Liver and Brain. See next page.

effector binding.[70] The closely related protein and member of the WRC, Wiskott-Aldrich syndrome protein family member 1 (Wasf1) was also O-GlcNAcylated in the same region.

Although the Wasf1 inhibition is based on its interactions with other proteins in the WRC,[71] it is also possible that Wasf1 O-GlcANcylation or O-GlcNAcylation of other proteins in this complex could disrupt complex association and (de)activation or effector binding.[72,73] Specifically, we mapped two O-GlcNAc sites to the C-terminal domain of cytoplasmic FMR1-interacting protein 2 (Cyfip2), a key region for its interaction with Nck-associated protein 1 (Nckap1), and synaptic functional regulator FMR1 (Fmr1), a key RNA binding protein known to associated with upwards of 4% of neuronal mRNAs.[71,74,75] We also found extensive O-GlcNAcylation on known actin scaffolding proteins, actin-binding LIM proteins 1-3 (Ablim1-3), and adducin proteins (Add1-3), which play important roles in maintaining the cellular cortex as well as in spine development and maintenance and neurite outgrowth.[76-78] On Enah, we found multiple O-GlcNAc sites in close

Fig. 5.17. Cont. NOTISE Enables Mechanistic Insights into the Tissue-Specific and Conserved Functions of OGT in the Liver and Brain. (a) O-GlcNAc functional communities revealed by PPI networking and GLay clustering of OGT interactors and substrates in the liver and brain. Cluster name colors represent those displayed in Figs 5g, 5h, and 5i. Filled nodes (teal for the brain and grey for the liver) indicate OGT interactors while a black outline represents OGT substrates. Larger pink nodes are interactors with an adaptor rank score > 10 (see also b). Venn diagram represents the overlap of all proteins in each network. **(b)** Proteins with an adaptor rank score >10 in the brain and liver. **(c)** NOTISE provides extensive mechanistic insight into the potential roles of OGT in actin dynamics. Interactions between proteins (lighter) and complexes (darker) are indicated by grey lines. WH1: WASP homology 1 domain; B: basic domain; GBD: GTPase protein binding; EVH2: Ena/Vasp homology domain 1/2; VCA: Verprolin, cofilin, acidic domain; SH3: SRC Homology 3 Domain; WW: WWP repeating motif. **(d)** All primary interactors of Abi2 identified by NOTISE. **(e)** Subset of proteins involved in presynaptic vesicle exocytosis (from clusters B9 and B4). Note every member of the liprin-α family of proteins is present. **(f)** Chemoenzymatic labeling, streptavidin capture, and liprin-α1 immunoblotting identifies dynamic O-GlcNAcylation in response to KCl-mediated depolarization and TMG treatment in mouse primary cortical neurons. **(g)** Quantification of the data in f over n=5 or n=4 trials for KCl and TMG treatment, respectively. *$p < 0.05$ by paired Student's t-test and Holm-Bonferroni correction. **(h)** Liprin-α1 co-immunoprecipitates with OGT in OGT-FH mouse primary cortical neurons under both resting and stimulated conditions. **(i)** Interrogation of the brain network reveals multiple proteins (and their interrelationships) involved with learning, memory, and LTP. **(j)** Multiple pathways, functions, and memberships in multiprotein complexes can be rapidly mapped on to the networks provide unique insights into network structure/function, as shown here for the liver network. Note also the blue actin binding cluster also contains multiple members of the Arp2/3 complex.

proximity to important regulatory phosphorylation sites, including that of PKA at S255,[79] and in the proline-rich domain, a known mediator of PPIs important for actin dynamics.[80,81] Finally, Abi2 also looks well positioned as a key intermediary between OGT and multiple proteins involved in actin dynamics, synaptic spine formation, and neuronal signaling (**Fig. 5.17d**).

In addition to the potentially novel role of OGT in regulating actin dynamics, we were also intrigued by the many proteins involved in synaptic vesicle exocytosis. Global changes in O-GlcNAcylation have long been known to affect synaptic vesicle exocytosis,[82] and indeed previous experiments have identified numerous presynaptic proteins that are O-GlcNAcylated.[83] However, a clear mechanism for how O-GlcNAcylation is involved in this process has yet to be uncovered. Here we find every member of the liprin-α family of proteins is O-GlcNAcylated and tightly linked with multiple other proteins that regulate presynaptic function (a subset from clusters B9 and B4 is shown in **Fig. 5.17e**).[84] We sought to confirm whether the most well-studied member of the liprin-α family, liprin-α1 (Ppfia1) was dynamically O-GlcNAcylated in response to neuronal activity (suggesting a regulatory role for this modification). Indeed, using our well-established chemoenzymatic labeling assay,[33] we found this modification to be dynamic to both KCl-mediated depolarization and TMG treatment of cortical neurons, indicating that this site dynamically cycles in response to stimuli (**Figs. 5.17f** and **5.17g**). Interestingly, we also mapped the site to between amino acids 1233 and 1240, the C-terminal PDZ binding domain and an area where O-GlcNAcylation would likely block key binding events with glutamate receptor-interacting protein 1.[85] Combined with the abundance of PDZ domains identified in OGT interactors and substrates (**Fig. 5.14d**), it is again tempting to speculate that O-GlcNAcylation may play an important role in synaptic transmission through its regulation of pre- and postsynaptic signaling machinery. Finally,

we validate that Ppfia1 is indeed in OGT interactor in primary mouse cortical neurons, an experiment enabled by the generation of our novel tagged OGT mouse line (**Fig. 5.17h**).

Taken together, the two examples above only begin to scratch the surface of the powerful ability of NOTISE to reveal and outline hypotheses for the role of OGT in organ and cell-specific functions. In fact, NOTISE, along with our Uniprot/PhosphoSitePlus integrated tables, allows for rapid identification the key protein players, and their interrelationships, behind functions, pathways, etc. in isolation (e.g. learning, memory, and LTP in the brain, **Fig. 5.17i**) or altogether (e.g. in the liver network, **Fig. 5.17j**) regulated by OGT substrates and interactors. These data will undoubtedly provide a critical molecular foundation for multiple in-depth, functional studies of O-GlcNAc-mediated regulation.

5.8. Discussion.

We have developed a new systems-level approach to annotate the multiple functions of O-GlcNAc regulation in a given biological system by networking of O-GlcNAc transferase interactors and substrates (NOTISE). In contrast to current state-of-the-art approaches, the NOTISE method provides several new insights into the functional coordination of O-GlcNAcylation. First, our method integrates both possible upstream regulators and downstream effectors of OGT activity, providing a simultaneous, integrated analysis of protein O-GlcNAcylation across the proteome. The development of robust biological model systems, chemical tools, and enrichment and detection methods to, for the first time, obtain these comprehensive datasets provides a systematic process to integrate biological context-specific information. Therefore, this approach allows for the direct comparison of matched in vitro or in

vivo biospecimens, which is not currently possible from existing datasets collected from disparate sample types or biological contexts.

By organizing these datasets into networks and partitioning the data into district functional communities, NOTISE not only rapidly provides functional information, but also lays the groundwork for in-depth followup studies by revealing the PPI networks and modification sites that are most likely to be involved. As an initial proof-of-principle, our unbiased method recapitulated numerous instances of O-GlcNAc regulation that have previously been demonstrated in the literature including histone modification,[49,52] intracellular transport,[86] transcription and translation,[6,87] synaptic vesicle exocytosis,[65,82] and carbohydrate metabolism,[7] validating that our approach readily uncovers critical pathways of O-GlcNAc activity. Moreover, by utilizing the molecular-level data provided by approach, NOTISE also provided a systematic and unbiased approach for untangling the molecular mechanisms behind these functions, something that has long eluded researchers in the field given the complexity of OGT regulation. It is our hope that the vast array of new functions, substrates and their sites, interactors, and their molecular relationships provided herein will spur numerous productive investigations throughout the biological sciences.

Additionally, our results provide key insights into the adaptor protein hypothesis, showing the potential for interacting proteins to both facilitate and block O-GlcNAcylation on their interacting partners. The novel quantitative MS methods developed herein are also the first to demonstrate and quantify site-specific changes in O-GlcNAcylation on the same peptide and increase the scope of protein-expression-corrected, site-specific O-GlcNAc quantification by a factor of five. These powerful, new quantitative O-GlcNAcomics techniques have finally enabled the long-standing goal of interrogating truly site-specific O-GlcNAcylation dynamics in response to stimuli. Finally, our in vivo application of NOTISE provides the first direct, systems-level

comparison of conserved and tissue-specific of O-GlcNAc functions between the adult brain and liver.

In total, NOTISE provides a strong foundation for new studies to interrogate the activity of PTMs both in vitro and in vivo. As numerous other enrichment methods for other PTMs have been developed, our method could rapidly be generalized to other proteoform states. Although the current approach relies upon existing PPI databases, the advent of new, global interactome datasets, especially in the mouse, will undoubtedly improve both node connectivity within our network and resulting functional annotation. By applying the tools and methods developed herein, we envision that global analyses of upstream PTM regulators and downstream effectors could be rapidly generated for diverse biological contexts across individual tissues, developmental stages, and disease progression. Therefore, we believe that our approach towards the global functional annotation of PTMs will accelerate our current understanding of protein regulation and broaden our interrogation of coordinated PTM activities across the proteome well beyond the scope of current studies.

5.9. Experimental Methods.

5.9.1. Cell Culture Conditions.

The parental HEK-293T was obtained from American Type Culture Collection (Manassas, VA). All cell culture reagents were purchased from ThermoFisher Scientific (Waltham, MA) unless otherwise indicated. All cell lines were cultured in DMEM supplemented with high glucose, GlutaMAX, 10% fetal bovine serum (PBS), and 1x penicillin–streptomycin (P/S) (complete DMEM). To perform quantitative proteomics, cells were cultured for at least six passages in

SILAC medium. SILAC medium was produced using SILAC DMEM Flex media supplemented with high glucose, GlutaMAX, 10% dialyzed FBS, 1x P/S and either 0.80 mM L-lysine and 0.40 mM L-arginine (MilliporeSigma, St. Louis, MO; light; K0, R0) or 0.80 mM [U-$^{13}C_6$,$^{15}N_2$] L-lysine and 0.40 mM [U-$^{13}C_6$] L-arginine (Cambridge Isotope Laboratories, Tewksbury, MA; heavy; K8, R6).

5.9.2. Lentiviral Plasmid Construction.

Primers were purchased from Integrated DNA Technologies (Coralville, IA). All molecular biology supplies were purchased from New England Biolabs (Ipswich, MA) unless otherwise indicated. The OGT lentiviral vector was produced by first producing OGT with C-terminal FLAG and HA tags in the pCMV6 backbone (Origene, Rockville, MD) using the NEBuilder HiFi DNA assembly and Q5 site-directed mutagenesis kits according to the manufacturer's protocols. Both the tagged form of OGT (OGTFH) and pTRIPZ vector were linearized by amplification using the Q5 Hot Start High-Fidelity 2x master mix. Fragments were gel purified using the Zymoclean gel DNA recovery kit (Zymo Research, Irvine, CA) and assembled with the NEBuilder HiFi DNA assembly kit according to the manufacturer's protocol. The ligated plasmid was transformed into Stable Competent *E. Coli* (New England Biolabs), and colonies were picked and sequenced (Laragen, Culver City, CA) to ensure proper incorporation and no recombination. Bacterial cultures were stored as glycerol stocks (50%) at -80 °C, and maxiprep cultures (100 mL) of the plasmid-expressing bacteria were grown and purified by ZymoPure plasmid kits (Zymo Research). Each purification of pTRIPZ-OGTFH was resolved by 1% agarose gel to ensure no recombination occurred.

5.9.3. Cell Line Generation.

Transfection and cell culture reagents were purchased from ThermoFisher Scientific unless otherwise indicated. The lentiviral packaging plasmids pMD2.G and psPAX2 (Didier Trono; 12259, 12260) were obtained from Addgene (Cambridge, MA). Four 15-cm culture plates containing HEK-293T cells at 80% confluency were transfected with 8 μg pTRIPZ-OGTFH, 6 μg psPAX2, and 2 μg pMD2.G using Lipofectamine 3000 at a 2:1 lipid/DNA ratio according to the manufacturer's protocol in OptiMEM. The medium was replaced at 6 h post-transfection with complete DMEM containing only 2% FBS. Medium was harvested at 48 h and 72 h post-transfection, and lentiviral particles were concentrated using 15-mL 100 kDa MWCO Amicon concentrator tubes (MilliporeSigma). Lentiviral concentrate was used immediately. To a six-well plate containing HEK-293T cells at 80% confluency in complete DMEM containing 8 μg/mL hexadimethrine bromide (MilliporeSigma), 0-50 μL lentiviral concentrate was added. Medium was replaced with complete DMEM after 24 h. After 48 h, cells were passaged 1:4 into new six-well plates with complete DMEM containing 2 μg/mL puromycin. After selection for two weeks, cells treated with the least amount of lentiviral supernatant that survived were then split for clonal dilution. After 2-3 weeks, single clones were isolated and expanded. Clones were then tested for induction of OGTFH expression by incubating with complete DMEM containing 0.1 μg/mL doxycycline hyclate (MilliporeSigma) for 24 h followed by Western blotting. A single clone for the HEK-293T-iOGTFH cell line was chosen and used for subsequent experiments.

5.9.4. Mouse Line Generation and Genotyping.

All mouse procedures were performed in accordance to protocols approved and guidelines set by the Caltech Institutional Animal Care and Use Committee. All mice were obtained from

Jackson Laboratory (Bar Harbor, ME) or Charles River (Wilmington, MA). The OGTFH mouse model was generated and maintained with a C57BL/6 mice background. sgRNA candidates were designed using the CRISPR design (www.genome-engineering.org) and CHOPCHOP programs (chopchop.cbu.uib.no). Genomic DNA isolated from the tail tip of a wild-type C57BL/6J mouse using the DNEasy Blood and Tissue Kit (Qiagen, Hilden, Germany). The genomic *C*-terminal region of OGT was amplified using the Q5 Hot Start High Fidelity 2x master mix (New England Biolabs). The pCAG-EGxxFP plasmid (Addgene, Masahito Ikawa; 50716) was cut with BamHI and SalI, and the construct was assembled using the NEBuilder HiFi Assembly kit. sgRNA candidates were cloned into the pX330 plasmid (Addgene, Feng Zhang; 42230) according to the published protocol. The two plasmids were then transfected into HEK-293T cells at 80% confluency in a six-well plate using Lipofectamine 3000 at a 2:1 lipid/DNA ratio according to the manufacturer's protocol. After 48 h, cells were observed using an LSM 710 confocal microscope (Carl Zeiss AG, Oberkochen, Germany) for GFP^+ cells, indicating active sgRNA. The most active sgRNA found within 20 bp of the OGT stop codon was chosen for in vivo genomic editing (5'-CCTGAATAAAGACTGCGCAC-3').

The sgRNA was amplified from the pX330 plasmid and then transcribed and purified using the MEGAshortscript T7 transcription and clean-up kits (ThermoFisher Scientific), respectively. For homology-directed recombination, a single stranded oligodeoxynucleotide (ssODN) was synthesized as an Ultrimer oligonucleotide by Integrated DNA Technology containing an MluI cut site, FLAG tag, BamHI cut site, HA tag, and OGT stop codon flanked on either side by 60 nucleotides homologous to the genomic region surrounding the insertion site. The protospacer adjacent motif was mutated to prevent further nuclease activity after homology-directed recombination.

Zygotes from C57BL/6N mice from Charles River were produced, collected, cultured, and implanted as previously described.[88] Microinjection of embryos was performed using an inverted microscope (Carl Zeiss AG) equipped with a micromanipulator (Leica Microsystems, Wetzlar, Germany), CellTram (Eppendorf, Hamburg, Germany), and FemtoJet (Eppendorf). Injections were carried out as previously described.[89] Solutions containing 2.5 ng/μL sgRNA, 10 ng/μL ssODN, and 5 ng/μL Cas9 mRNA (System Biosciences, Palo Alto, CA) in 10 mM Tris-HCl pH 8.0, 0.1 mM EDTA were used for injection into the pronucleus of fertilized mouse zygotes. Following injection, the zygotes were cultured to the two-cell stage and implanted into pseudopregnant foster mothers at 0.5 days post coitum (up to 30 two-cell embryos per recipient). Approximately 19.5 days after implantation, the pups were delivered, and 3 weeks after birth the pups were tailed and separated by gender. Offspring were genotyped by restriction enzyme digestion using BamHI after purification of the genomic DNA from tail tips using the DNEasy Blood and Tissue kit and amplification of the genomic *C*-terminal region of OGT. A single heterozygous female was obtained containing the correct on-target inserted sequence. The line was then backcrossed for at least three generations with the C57BL/6J strain prior to experiments. Subsequent homozygous mice obtained from this founder exhibited no abnormalities in growth, behavior, or breeding and were indistinguishable from wild-type and heterozygous mice.

5.9.5. siRNA Knockdown.

The BAP1 RNA knockdown was performed with a set of 3 unique 27mer siRNA duplexes targeting BAP1 (Origene, SR305435) using siTrans 1.0 (Origene). Briefly, cells in six-well plates at 70% confluency were transfected with 20 nmol siRNA mixture according to the manufacturer's protocol. Cells were allowed to grow for three days prior to harvesting as described for cell lysates

above. Knockdown was validated by Western blotting. Co-immunoprecipitation experiments were carried out as described below for TAP-MS sample preparation.

5.9.6. CRISPR/Cas9-Mediated KO of BAP1.

BAP1 CRISPR/Cas9 KO Plasmid (h) (sc-400232), BAP1 HDR Plasmid (h) (sc- 400232-HDR), and Control CRISPR/Cas9 Plasmid (sc-418922) were purchased from Santa Cruz Biotechnology and prepared per the manufacturer's instructions. 293T cells at ~60-70% confluency (maintained as described above) in a 12-well tissue culture plate before were then transfected with 1 ug of BAP1 KO/HDR or control plasmid using Lipofectamine 3000 (ThermoFisher Scientific) at a 2:1 lipid/DNA ratio according to the manufacturer's protocol in OptiMEM. Once confluent, the cells were split 1:1 into media containing 10 μg/mL puromycin (ThermoFisher Scientific) or normal media for the control. Cells were then selected for 2 weeks replacing the media or splitting as necessary. BAP1 KO was confirmed by Western blotting (**Fig. 5.18**) before splitting the KO and WT cells into three 10 cm plates which were grown to confluency, lysed as described below, and subjected to chemoenzymatic labeling and enrichment as described below. 100 μg of lysate from each condition was also saved for quantitative proteomics.

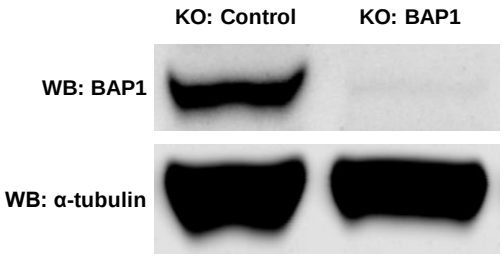

Fig. 5.18. BAP1 KO in 293T Cells. Transfection of BAP1-targeting gRNA, Cas9, and a homology directed repair template conferring puromycin resistance shows efficient KO after 2 weeks of puromycin selection compared to transfection with off-target control gRNA.

5.9.7. Cell Lysate Preparation.

To prepare HEK-293T cell lysate for immunoprecipitation or Western blotting, two 15-cm plates of heavy-labeled HEK-293T-iOGTFH cells at 60%

confluency were treated with freshly made 0.04 μg/mL doxycycline hyclate for 24 h. As a control, light-labeled HEK-293T-iOGTFH cells were left untreated. The cells were collected with a scraper and homogenized on ice in 10 mL of 50 mM Tris-HCl pH 7.4, 150 mM NaCl, 0.5% NP-40, 1x cOmplete EDTA-free protease inhibitor cocktail (Roche, Basel, Switzerland) using 30-40 strokes with a 20-mL Potter-Elvehjem tissue grinder (Wheaton, Millville, NJ) followed by centrifugation at 15,000 g for 10 min at 4 ºC. The protein concentration of the clarified supernatant was measured using the Pierce BCA Protein Assay Kit (ThermoFisher Scientific).

To prepare HEK-293T cell lysate for chemoenzymatic labeling, two 15-cm plates of HEK-293T-iOGTFH cells at 60% confluency were lysed in 5 mL of 1% SDS, 50 mM Tris-HCl pH 7.4, 150 mM NaCl, 1x cOmplete EDTA-free protease inhibitor cocktail, 10 μM Thiamet-G (MilliporeSigma) and probe sonicated to shear DNA. The protein concentration was measured as described above.

5.9.8. Affinity Purification from 293T Cells.

For each replicate, approximately 15 mg cell lysate from heavy- and light-labeled cells were subjected to immunoprecipitation with 200 μL settled volume of ANTI-FLAG M2 Affinity Agarose Gel (MilliporeSigma) overnight at 4 ºC. The beads were washed 3 x 5 min in wash buffer (50 mM Tris-HCl pH 7.4, 150 mM NaCl, 0.1% NP-40) and eluted with 150 μg/mL 3xFLAG peptide (MilliporeSigma) in wash buffer, followed by immunoprecipitation with 100 μL settled volume of anti-HA agarose beads (ThermoFisher Scientific) for 6 h at 4 ºC. The beads were washed with wash buffer and eluted with 3 M NaSCN. The eluates were acetone precipitated, re-dissolved in 1x SDS loading buffer (50 mM Tris-Cl pH 6.8, 100 mM dithiothreitol (DTT), 2% SDS, 0.1% bromophenol blue, 10% glycerol), and subjected to in-gel digestion.

The eluates from heavy- and light-labeled samples were mixed immediately before loading onto a NuPAGE 4-12% Bis-Tris protein gel (ThermoFisher Scientific). The gel was stained and visualized using Imperial protein staining reagent (ThermoFisher Scientific) and destained in doubly deionized H_2O (ddH_2O). The gel lane was cut into 30-40 gel slices. Each gel piece was reduced with 10 mM DTT (MilliporeSigma) for 1 h at 37 ºC and then alkylated with 50 mM iodoacetamide (MilliporeSigma) for 45 min at room temperature protected from light. The slices were dried and incubated with 20 ng/uL Pierce trypsin protease (ThermoFisher Scientific) solution in 100 mM NH_4HCO_3 (pH 8.0) with 1 mM $CaCl_2$ overnight at 37 ºC. The peptides were recovered using sequential washes with 100 mM NH_4HCO_3, 1:1 v/v 100 mM NH_4HCO_3/CH_3CN, and 5% formic acid. The recovered peptides were dried and desalted with a C18 ZipTip pipette tip (MilliporeSigma). The desalted peptides were resuspended in 0.2% formic acid for LC-MS/MS analysis.

5.9.9. Affinity Purification from Brain and Liver Tissue.

To prepare brain and liver tissue lysate, 2-month old OGTFH and WT mouse forebrains and livers were freshly dissected and rinsed with ice cold phosphate-buffered saline. One hemisphere or lobe was used per experiment. Lysate from each of OGT-FH and WT organs was harvested and homogenized on ice in 10 mL of 50 mM Tris-HCl pH 7.4, 150 mM NaCl, 0.5% NP-40, 1x cOmplete EDTA-free protease inhibitor cocktail using 30-40 strokes with a Potter-Elvehjem homogenizer followed by centrifugation at 15,000 g for 10 min at 4 ºC. Lysates from each mouse (15 mg) were subjected to immunoprecipitation using the same procedure outlined above followed by filter assisted sample preparation and dimethyl labeling.

The eluates were loaded onto 0.5 mL 10 kDa MWCO Amicon Ultra centrifugal filters (MilliporeSigma) and buffer exchanged into 100 mM TEAB pH 8.5 (MilliporeSigma). The samples were then reduced with 10 mM DTT for 1 h at 37 ºC and alkylated with 50 mM iodoacetamide for 45 min at room temperature protected from light. The proteins were digested with 50 ng/µL trypsin in 100 mM TEAB at 37 ºC overnight. The resulting peptides were recovered by washing the centrifugal filter with 100 mM TEAB three times for a final volume of 100 uL. To each peptide mixture, 4 uL of 4% v/v CH_2O (WT) or CD_2O (OGTFH) was added followed by 4 uL of 0.6 M $NaBH_3CN$. Samples were rotated end-over-end for 1 h at RT and then quenched with 16 uL of 1% v/v NH_3 followed by 8 uL formic acid. The differentially labeled samples from OGT-FH and WT mice were mixed and desalted by an Agilent 1100 Series HPLC system with a MicroTrap Cartridge (Michrom, 1x8 mm internal dimension, 5.0 µL bed volume, 20µg capacity, 1-1000 µL sample volume). Solvent A consisted of 99.8% H_2O and 0.2% formic acid and solvent B consisted of 99.8% ACN, and 0.2% formic acid. The gradient was as follows: 0% Solvent B (10 min), 0-85% Solvent B (2 min), 85% Solvent B (5 min), 85-90% B (1 min), 90% B (5 min), 90-100% B (1 min), and 100% B (6 min). Eluted peptide fractions were collected in 1 mL fractions, lyophilized, and resuspended in 0.2% formic acid for LC-MS/MS analysis.

5.9.10. Chemical Synthesis of Biotin-Dmpt-Alkyne 1.

Unless otherwise indicated, all chemical reagents were obtained from MilliporeSigma and used as provided. Reactions were performed in flame-dried glassware under Ar using freshly dried solvents passaged through an activated alumina column under Ar. Preparative HPLC was conducted using a 1260 Infinity II LC system (Agilent) with a custom Zorbax Eclipse XDB-C18 PrepHT column (Agilent, 21.2 x 250 mm, 5 µm) with a linear gradient of 5-50% MeCN/0.1% aq.

Formic acid over 70-85 min with a flow rate of 6 mL/min. ^{1}H and ^{13}C NMR experiments were recorded on a Bruker 400 spectrometer at the Caltech NMR facility. Spectra are reported in parts per million (δ) relative to $CDCl_3$ (7.26 ppm). Data are reported as chemical shift (ppm), multiplicity (s = singlet, d = doublet, t = triplet, q = quartet, p = pentet, m = multiplet, b = broad), coupling constant (Hz), and integration. Mass spectra were obtained using a Waters LCT Premier XE electrospray time of flight mass spectrometer at the Caltech Multi User Mass Spectrometry Laboratory.

5.9.11. 5-(3-(2-(2-(2-(2-(N-biotinyl)aminoethoxy)ethoxy)ethoxy)ethoxy)-1-hydroxypropylidene)-1,3-dimethylpyrimidine-2,4,6-trione (Biotin-Dmpt-OH, 2).

Biotin-PEG_4-CO_2H (BroadPharm, 400 mg, 0.814 mmol) and N,N'-dimethylbarbituric acid (164.8 mg, 1.3 eq) were suspended in 10 mL of dry DCM under Ar and cooled to 0 °C. Separately, EDC·HCl (202.7 mg, 1.3 eq), DMAP (9.9 mg, 0.1 eq), and TEA (170.1 μL, 1.5 eq) were dissolved in 5 mL of dry DCM. The coupling solution was added to the suspension dropwise. The reaction was allowed to warm to RT and stirred overnight. The solution was then concentrated to a yellow oil and redissolved in a minimal volume of 5% aq. MeCN. The product was then purified by preparative HPLC. Fractions were combined, concentrated, and lyophilized to afford the product as a light yellow powder (468.9 mg, 92% yield). ^{1}H NMR (500 MHz, $CDCl_3$): δ 7.33 (bs, 0.2H, O*H*), 6.73 (bt, *J* = 5.4 Hz, 0.8H, O*H*), 6.28 (s, 1H, N*H*), 5.43 (s, 1H, N*H*), 4.51 (t, *J* = 6.5 Hz, 1H, biotin-C*H*), 4.32 (dd, *J* = 7.6, 4.5 Hz, 1H, biotin-C*H*), 3.86 (t, *J* = 6.3 Hz, 2H, OCH_2), 3.68-3.59 (m, 12H, OCH_2), 3.55 (t, *J* = 5.1 Hz, 2H, CH_2), 3.48-3.27 (m, 10H, OCH_2, CH_3), 3.15 (dt, *J* = 12.0, 6.0 Hz, 1H, biotin-C*H*), 2.91 (dd, *J* = 12.7, 4.9 Hz, 1H, biotin-C*H*), 2.73 (d, *J* = 12.7 Hz, 1H, biotin-C*H*), 2.22 (td, *J* = 7.1, 3.4 Hz, 2H, biotin-CH_2), 1.82-1.57 (m, 4H, biotin-CH_2), 1.44 (p, *J* =

7.5 Hz, 2H, biotin-C*H*$_2$). ^{13}C NMR (100 MHz, $CDCl_3$): 196.88, 173.41, 169.85, 164.02, 150.45, 96.02, 77.36, 70.68, 70.57, 70.53, 70.34, 70.22, 70.08, 66.91, 61.91, 60.33, 55.55, 40.68, 39.29, 37.26, 35.96, 28.21, 25.65. ESI-HRMS (*m/z*): $[M+H]^+$ calc'd for $C_{27}H_{44}N_5O_{10}S^+$: 630.2803, found: 630.2791.

5.9.12. 5-(3-(2-(2-(2-(2-(N-biotinyl)aminoethoxy)ethoxy)ethoxy)ethoxy)-1-(N-propargyl)aminopropylidene)-1,3-dimethylpyrimidine-2,4,6-trione (Biotin-Dmpt-Alkyne, 1).

Compound 2 (50.0 mg, 0.079 mmol) was suspended in 2 mL of neat propargylamine and stirred at 50 °C for 4 h. The reaction was then concentrated, and the residue was diluted in DCM. The solution was extracted with H_2O, and the aqueous layer was back-extracted twice with DCM. The organic layers were combined, dried with $MgSO_4$, and concentrated. The residue was redissolved in a minimal volume of 5% aq. MeCN and then purified by preparative HPLC. Fractions were combined, concentrated, and lyophilized to afford the product as a light yellow powder (14.8 mg, 28% yield). ^{1}H NMR (400 MHz, $CDCl_3$): δ 12.87 (bt, *J* = 5.5 Hz, 1H, N*H*), 6.64 (bt, *J* = 5.6 Hz, 1H, N*H*), 6.20 (s, 1H, N*H*), 5.28 (s, 1H, N*H*), 4.50 (ddt, *J* = 7.5, 5.0, 1.2 Hz, 1H, biotin-C*H*), 4.45 (dd, *J* = 5.5, 2.6 Hz, 2H, NC*H*$_2$), 4.31 (ddd, *J* = 7.8, 4.6, 1.4 Hz, 1H, biotin-C*H*), 3.86 (t, *J* = 5.5 Hz, 2H, OC*H*$_2$), 3.67-3.53 (m, 14H, OC*H*$_2$), 3.51-3.40 (m, 4H, OC*H*$_2$), 3.33 (s, 3H, NC*H*$_3$), 3.29 (s, 3H, NC*H*$_3$), 3.14 (td, *J* = 7.4, 4.6 Hz, 1H, biotin-C*H*), 2.90 (dd, *J* = 12.8, 4.9 Hz, 1H, biotin-C*H*), 2.74 (d, *J* = 12.8 Hz, 1H, biotin-C*H*), 2.41 (t, *J* = 2.6 Hz, 1H, CC*H*), 2.22 (td, *J* = 7.3, 2.2 Hz, 2H, biotin-C*H*$_2$), 1.78-1.58 (m, 4H, biotin-C*H*$_2$), 1.44 (q, *J* = 7.6 Hz, 2H, biotin-C*H*$_2$). ^{13}C NMR (100 MHz, $CDCl_3$): δ 175.65, 173.30, 166.84, 163.79, 162.63, 151.35, 90.31, 77.86, 77.36, 73.87, 70.64, 70.62, 70.56, 70.52, 70.25, 70.12, 69.91, 61.88, 60.28, 55.56, 40.68, 39.28,

36.02, 33.97, 31.14, 28.25, 28.22, 28.14, 27.91, 25.67. ESI-HRMS (*m/z*): $[M+H]^+$ calc'd for $C_{30}H_{47}N_6O_9S^+$: 667.3120, found: 667.3133.

5.9.13. Chemoenzymatic Labeling and Enrichment for O-GlcNAcomics.

HEK-293T-iOGTFH cell lysate, brain, liver, or WT/BAP1 KO 293T cell lysate (5 mg) was diluted with 1% SDS, 20 mM HEPES pH 7.6 to 2.5 mg/mL. Samples were reduced using 20 mM DTT pH 7.6 for 45 min at 60 °C, cooled to room temperature, and alkylated with 80 mM iodoacetamide for 45 min at RT protected from light. Protein was then precipitated by the addition of 3 volumes of methanol, 1 volume of chloroform, and 2.25 volumes of water. The precipitated protein was pelleted by centrifugation at 7,068 x *g* for 35 min at 4 °C. Solvents were removed and the pellet washed twice with 3 volumes of methanol before redissolving at 5 mg/mL with 1 mL of 1% SDS, 20 mM HEPES pH 7.9 at 95 °C for 5 min. Samples were then diluted with 2 mL of 2.5x GalT labeling buffer (50 mM HEPES pH 7.9, 125 mM NaCl, 5% IGEPAL CA-630), 1.2 mL of ddH_2O, and 275 µL of 100 mM $MnCl_2$. The mixture was chilled on ice for 5 min, and then 250 µL of 0.1 mM UDP-GalNAz, 250 µL of 2 mg/mL Y289L GalT, 50 µL of 500 kU/mL PNGase F (New England Biolabs, 5 U/µg of protein), and 62.5 µL of Lambda Protein Phosphatase (New England Biolabs, 5 U/µg of protein) were added with gentle mixing after each addition. Sample was rotated end-over-end overnight at 4 °C. The following day, samples were then precipitated by the methanol/chloroform/water method described above. The protein pellet was redissolved at 5 mg/mL in 1 mL of 1% SDS, 20 mM HEPES pH 7.6 at 95 °C for 5 min. The solution was diluted with 2.85 mL of ddH_2O and 0.15 mL of 200 mM HEPES pH 7.6. In a separate tube, a 5x CuAAC mix was prepared by sequential addition of 885 µL of ddH_2O, 10 µL of 5 µL of 100 mM BTTAA (Click Chemistry Tools, Scottsdale, AZ) in DMSO, 100 µL of 50 mM $CuSO_4$ (freshly prepared),

and 50 mM **1** in DMSO. The 5x mix was then added directly to the protein sample and mixed gently before adding 100 µL of 100 mM TCEP (freshly prepared). The CuAAC reaction was allowed to proceed with end-over-end for 1 h at RT before the proteins were precipitated as described above. The protein was resuspended in 5 ml of 50 mM HEPES pH 7.6, 10 mM EDTA pH 8 to chelate residual Cu^{2+}. Then, 200 µg Pierce trypsin protease (1:25 w/w) was added, and the sample was rotated end-over-end for 20 hours at 37 °C. Two 15-mL 10 kDa MWCO Amicon concentrator tubes were rinsed with 2 x 5 mL of 50% MeOH and 2 x 5 mL of ddH_2O by centrifugation at 4,000 x *g* for 5 min. Tryptic solutions were then centrifuged in the rinsed concentrator tubes at 4,000 x *g* for 20 min. The remaining residue was rinsed 2 x 2.5 mL of H_2O by centrifugation, and the flowthrough fractions were combined. The sample was diluted two-fold with PBS. In a separate tube, 500 µL of a 50% slurry of high capacity Neutravidin agarose (ThermoFisher Scientific) was washed twice with 0.5 mL of PBS. The washed agarose resin was then added to the sample and rotated end-over-end for 1 h at RT. The resin was pelleted by centrifugation at 500 x *g* for 5 min and then transferred to a 900 µL spin filter (ThermoFisher Scientific) pre-rinsed twice with 50% MeOH and 50% ddH_2O. Beads were washed 5 min each with the following solutions: 5 x 0.5 mL of PBS, 5 x 0.5 mL of 1 M NaCl in PBS, and 5 x 0.5 mL of PBS. Captured peptides were eluted in twice with 0.75 mL of 2% v/v NH_2OH with end-over-end rotation for 1.5 h at 37 °C. Elution fractions were combined and concentrated to dryness with vacuum centrifugation before desalting as described for affinity purified peptides. For each pair of quantitative samples, dried peptides were resuspended in 50 µL of 100 mM TEAB pH 8.5 and labeled using two tags from the TMT10plex Isobaric Labeling Kit (ThermoFisher Scientific) per the manufacturer's instructions. Labeled peptides were then combined, desalted and dried as before, and resuspended in 10 µL of 0.2% formic acid for MS analysis.

5.9.14. Preparation of Peptides for Quantitative Proteomics Experiments.

100 μg of WT or BAP1 KO lysate (n=3 for each), prepared as described above, was precipitated using the methanol/chloroform/water method as described above except the samples were centrifuged at 21,130 x g for 5 min to pellet proteins. 100 ul of 100 mM TEAB pH 8.5 was then added to the pellets before adding 3 μg of Pierce MS Grade Trypsin Protease (ThermoFisher Scientific) (1:33 w/w enzyme:protein). The samples were then left to digest for 20 hours at 37 °C. The following day, peptides were labeled with the TMTsixplex Isobaric Labeling Kit (ThermoFisher Scientific) per the manufacturer's instructions. After labeling, peptides from all groups were combined and dried in a vacuum centrifuge. Peptides were then resuspended in 100 μL of 10 mM ammonium hydroxide and subjected to offline high pH reversed phase fractionation[90] using an Agilent Extend-C18; 5 μm, 2.1x150 mm on an Agilent 1100 HPLC (Santa Clara, CA) operating at 0.2 mL/min. Buffer A consisted of 10 mM ammonium hydroxide in water and buffer B consisted of 10 mM ammonium hydroxide in 90% acetonitrile. The combined 600 μg of peptides were injected onto the column and separated per the following gradient: 1% Solvent B (4 min), 1-30% B (50 min), 30-60% B (4 min), 60-70% B (2 min), and 70-90% B (5 min). 64 1 min fractions were collected into 96 deep-well plates, concatenated to 16, and dried by vacuum centrifugation. Each fraction was resuspended in 10 uL of 0.2% formic acid by bath sonication for MS analysis.

5.9.15. LC-MS/MS Analysis.

5.9.15.1. Affinity Purification from HEK293T Cells.

Affinity purified, in-gel digested samples from HEK293T cells were subjected to LC-MS/MS analysis on a nanoflow LC system, EASY-nLC II, (ThermoFisher Scientific) coupled to

a LTQ Orbitrap Elite mass spectrometer (ThermoFisher Scientific). For the EASY-nLC II system, solvent A consisted of 97.8% H_2O, 2% ACN, and 0.2% formic acid and solvent B consisted of 19.8% H_2O, 80% ACN, and 0.2% formic acid. Samples were directly loaded onto a 16-cm analytical HPLC column (50 µm ID) packed in-house with ReproSil-Pur C18AQ 3 µm resin (120 Å pore size, Dr. Maisch, Ammerbuch, Germany). The column was heated to 60 °C. The peptides were separated with a 60-min gradient at a flow rate of 220 nL/min. The gradient was as follows: 2-30% Solvent B (60 min), 30-100% B (1 min), and 100% B (9 min). Eluted peptides were then ionized using a Nanospray Flex ion source (ThermoFisher Scientific) and introduced into the mass spectrometer. The LTQ Orbitrap Elite was operated in a data-dependent mode, automatically alternating between a full-scan (*m/z* 400-1600, 120K resolution) in the Orbitrap and subsequent MS/MS scans of the 20 most abundant peaks in the linear ion trap (Top20 method).

5.9.15.2. Affinity Purification from Brain and Liver Tissue.

Affinity purified samples from brain tissue were subjected to LC-MS/MS analysis on a nanoflow LC system, EASY-nLC 1200, (ThermoFisher Scientific) coupled to a Q Exactive HF Orbitrap mass spectrometer (ThermoFisher Scientific) equipped with a Nanospray Flex ion source. Samples were directly loaded onto a PicoFrit column (New Objective, Woburn, MA) packed in house with ReproSil-Pur C18AQ 1.9 µm resin (120 Å pore size, Dr. Maisch, Ammerbuch, Germany). The 20 cm x 50 µm ID column was heated to 60 °C. The peptides were separated with a 120-min gradient at a flow rate of 220 nL/min. The gradient was as follows: 2-6% Solvent B (7.5 min), 6-25% B (82.5 min), and 25-40% B (30 min) and to 100% B (9 min). Solvent A and B were the same as described above. The Q Exactive HF Orbitrap was operated in data dependent mode. Full scan resolution was set to 60,000 at *m/z* 200. Full scan target was 3×10^6 with a maximum

injection time of 15 ms. Mass range was set to 300-1650 *m/z*. For data dependent MS2 scans the loop count was 12, target value was set at 1×10^5, and intensity threshold was kept at 1×10^5. Isolation width was set at 1.2 *m/z* and a fixed first mass of 100 was used. Normalized collision energy was set at 28%. Peptide match was set to off, and isotope exclusion was on.

5.9.15.3. O-GlcNAcomics Samples.

Chemoenzymatic labeled and enriched digested samples were analyzed on a nanoflow LC system, EASY-nLC 1000 (ThermoFisher Scientific), coupled to an Orbitrap Fusion Tribrid mass spectrometer (ThermoFisher Scientific) equipped with a Nanospray Flex ion source. Sample loading and LC separation was identical to the QE Orbitrap LC method mentioned above. Full spectra were acquired over *m/z* 350-1800 in the Orbitrap (120 K resolution at 200 *m/z*); automatic gain control (AGC) was set to accumulate 50,000 ions, with a maximum injection time of 50 ms. Data-dependent MS2 analysis was performed using a top-speed approach (cycle time of 5 s) with multiple fragmentation methods (see below). Dynamic exclusion set to exclude features after 1 time for 15 seconds with exclude isotopes turned on. The normalized collision energy was optimized at 28% for high collision dissociation (HCD) fragmentation. The intensity threshold for fragmentation was set to 25,000. HCD fragmentation spectra were collected in the Orbitrap operating at 30K resolution at 200 *m/z*. ETD/EThcD fragmentation was then performed for precursor ions that whose HCD spectra contained a fragment of mass 300.1303 *m/z* (15 ppm tolerance, within the top 30 ions). AGC was set to 50,000 with a maximum injection time set at 500 ms for the Orbitrap operating at 30K resolution. ETD reaction time was charge-dependent and supplemental activation (SA) energy was set to 20%.

5.9.15.4. Quantitative O-GlcNAcomics Samples.

Quantitative O-GlcNAcomics samples were analyzed on a nanoflow LC system, EASY-nLC 1000 (ThermoFisher Scientific), coupled to an Orbitrap Fusion Tribrid mass spectrometer (ThermoFisher Scientific) equipped with a Nanospray Flex ion source. ~4 μg of peptides per sample were loaded onto an Aurora 25cm x 75μm ID, 1.6μm C18 reversed phase column (Ion Opticks, Parkville, Victoria, Australia) and separated over 135 min at a flow rate of 350 nL/min with the following gradient: 2–6% Solvent B (7.5 min), 6-25% B (82.5 min), 25-40% B (30 min), 40-100% B (1 min), and 100% B (14 min). MS1 spectra were acquired at 120,000 resolution with a scan range from 350-1800 *m/z*; AGC was set to accumulate 50,000 ions, with a maximum injection time of 50 ms. Data-dependent MS2 analysis, either top speed (5 s) or top 10 was then performed in which features were filtered for monoisotopic peaks with a charge state of 3-8 and a minimum intensity of 25,000, with dynamic exclusion set to exclude features after 1 time for 15 seconds with a 10 ppm mass tolerance and exclude isotopes turned on. HCD fragmentation was performed with normalized collision energy of 28 after quadrupole isolation of features using an isolation window of 1.6 *m/z*, an AGC target of 1e5, and a maximum injection time of 100 ms. MS2 scans were then acquired at 30K resolution in Centroid mode with the scan range set to automatic. Detection of at least fragment of 732.3726, 547.3037, or 529.2931 *m/z* in the top 30 ions triggered three additional scans: (1) SPS-MS3 in the Orbitrap on the top 5 SPS precursors, an isolation window of 1.3 *m/z*, 65% normalized collision energy, a resolution of 50,000, an ACG target of 50,000, an automatic scan range, and a maximum injection time of 250 ms. Precursor selection range, ion exclusion and isobaric tag loss exclusion were all employed. (2) ETD-MS2 in the Ion Trap with an isolation window of 1.6 *m/z*, calibrated charge-dependent ETD parameters, rapid scan mode, automatic scan and mass range, an ACG target of 50,000, and a maximum injection time of

100 ms. (3) EThcD-MS2 was performed as described for (2) except with 20% supplemental activation energy.

5.9.15.5. BAP1 KO Protein Expression.

Liquid chromatography-mass spectrometry (LC-MS) analysis of native peptide fractions was carried out on an EASY-nLC 1000 (Thermo Fisher Scientific, San Jose, CA) coupled to an Orbitrap Eclipse Tribrid mass spectrometer (Thermo Fisher Scientific, San Jose, CA). 3 μL of each resuspended fraction was loaded onto a monolithic column (Capillary EX-Nano MonoCap C18 HighResolution 2000, 0.1 x 2000 mm, Merck, Darmstadt Germany) fitted with a silica coated PicoTip emitter (New Objective FS360-20-10-D) and separated over 180 min at a flow rate of 500 nL/min with the following gradient: 2–6% Solvent B (10 min), 6-40% B (140 min), 40-98% B (1 min), and 98% B (29 min). MS1 spectra were acquired in the Orbitrap at 120K resolution with a scan range from 400-1500 *m/z*, an AGC target of 4e5 and the maximum injection time set automatically. Features were filtered for monoisotopic peaks with a charge state of 2-5 and a minimum intensity of 5,000, with dynamic exclusion set to exclude features after 1 time for 60 seconds with a 10 ppm mass tolerance. Data-dependent MS2 analysis was performed using a top-speed approach (cycle time of 5 s). CID fragmentation was performed with normalized collision energy of 35% and an activation time of 10 ms with an activation Q of 0.25 after quadrupole isolation of features using an isolation window of 0.7 *m/z*. Scans were acquired in the Ion Trap using automatic scan range, a maximum injection time of 250 ms, and rapid scan mode. HCD-SPS-MS3 scans were also performed in Orbitrap on the top 10 SPS precursors, an isolation window of 0.7 *m/z*, 55% normalized collision energy, a resolution of 60,000, an ACG target of

150,000, a scan range of 100-500 *m/z*, and a maximum injection time of 118 ms. Precursor selection range, ion exclusion, and isobaric tag loss exclusion were all employed.

5.9.16. MS Data Analysis.

All raw files were searched using Proteome Discoverer 2.4.0.305 (ThermoFisher Scientific) with the Byonic (Protein Metrics, Cupertino, CA) search node v3.7.4. Search parameter files are provided in. Peak lists were searched against the species-specific complete UniProtKB databases and the UniprotKB/Swiss-Prot databases (Mus musculus, retrieved January 21, 2020; Homo sapiens, retrieved January 25, 2020) supplemented with database of frequently observed contaminants (245 sequences). The Swiss-Prot only searches were used to match O-GlcNAc sites with known PTMs in the PhosphoSitePlus database and for the BAP1 KO quantitative O-GlcNAcomics and proteomics experiment (to facilitate matching of O-GlcNAcylation peptides to their parent protein expression). For all searches the following parameters were set: MS1 tolerance of 5 ppm, MS2 tolerance of 10 ppm or 0.5 Da for Orbitrap and Ion Trap spectra, respectively, minimum peptide length of 6 amino acids, a maximum of three missed cleavages, carbamidomethylation of cysteine residues was set as a fixed modification, acetylation of the protein N-terminus and oxidation of methionine (common2) were set as a variable modifications, and the tagged O-GlcNAc was set as a variable modification (common 2), dimethylation or TMT labeling of lysines and peptide N-termini were set to fixed modification where appropriate, and phosphorylation was set as a variable modification for the protein expression samples. Data was filtered to a 1% false discovery rate on PSMs using the Percolator or target decoy algorithm in Proteome Discoverer. Localization of O-GlcNAc sites was performed using the ptmRS node. For

HCD spectra, equal localization probabilities were assigned to every serine/threonine due to neutral loss of the glycan.

5.9.17. Data Analysis.

5.9.17.1. General and Statistics.

All data analysis was performed using the Python language (Python Software Foundation. Python Language Reference, version 3.7.3. Available at http://www.python.org) with all Anaconda packages installed (Anaconda Software Distribution, version 4.8.3. Available at https://anaconda.com). Information from the Uniprot Knowledgebase[56] and PhosphoSitePlus[38] database used for the integrated Cytoscape tables was retrieved on April 22, 2020 and April 28, 2020, respectively. For the limma moderated t-test[91] (package, limma v3.42.2) and inverted beta binomial tests[92] (package, ibb v13.06) the R language (R Development Core Team, version 3.6.1. Available at https://www.R-project.org) was employed using the rpy2 (Laurent Gautier, v2.9.4) python package. Multiple hypothesis testing correction was performed with either the Benjamini-Hochberg method (interactomics and O-GlcNAcomics) or Holm- Bonferroni method (Western blotting). A p-value of less than 0.05 was considered significant. Code for all analyses and figures is in **Appendix 5.6.**

5.9.17.2. Bioinformatics Analysis of OGT Interactome and O-GlcNAcome.

The input for the network analysis included OGT interactors from TAP-MS and OGT substrates from chemoenzymatic labeling and proteomics generated in this project, and known interactions from PPI databases. Two sources of protein-protein interactions for were utilized: (1)

BioGRID (Homo sapiens-specific dataset, downloaded February 25, 2020) and (2) IntAct (human-human PPIs, downloaded February 25, 2020 and filtered for only multivalidated interactions). An in-house script was used to filter for interactions between an OGT interactor and other interactors or substrates to generate the edges of the O-GlcNAc network. Edges from individual OGT interactor baits with more than thirty connections to other protein prey within were removed to avoid biasing during community clustering. Examples of these proteins include ribosomal proteins, heterogeneous nuclear ribonucleoproteins (hnRNPs), and heat shock proteins (HSPs). In most cases, the eliminated edges coincided with interactions from proteins highly represented within the CRAPome, implying a high rate of non-specific interactions. However, edges generated in the reverse direction (e.g. from an interactor/substrate bait to a ribosomal protein prey) were retained. The nodes and edges were then used to build a network of OGT interactome and O-GlcNAcome, which was visualized and analyzed using Cytoscape version 3.7.2. To partition the network, we used the Community cluster (GLay) algorithm[42] in the Cytoscape plug-in clusterMaker2[93] (v1.3.1) which is a community clustering algorithm that implements the Girvan-Newman fast greedy algorithm.[41]

The protein names from the whole network or from each cluster were submitted for statistical overrepresentation testing using g:Profiler.[94] Only terms with a p-value of less than 0.01 with the g:SCS significance threshold were used and electronic GO annotations were excluded. To group GO terms and appropriately name clusters the Cytoscape plugin ClueGO[44] v2.5.6 was used. For each cluster, the proteins were submitted to ClueGO analysis with the GO Biological Processes (Downloaded February 17, 2020) without electronic annotation. GO term Fusion was used and only pathways with a p-value of less than 0.01 were considered significant. Network

specificity was set to medium with all dependent parameters left as default; GO Term grouping was employed.

5.9.18. Neuron Culture, Stimulation, and Lysis.

Primary mouse cortical neurons were prepared as previously described,[5] plated on poly-d-lysine (PDL) coated plates, and cultured in Neurobasal medium (ThermoFisher) with 1% penicillin-streptomycin (P/S, ThermoFisher), 2mM GlutaMAX Supplement (ThermoFisher), and B-27 Plus (ThermoFisher). Half of the media was changed every 2-4 days. After 20 DIV, neuronal activity was silenced using tetrodotoxin (TTX, 10 μM, Tocris Biosciences) and D-AP5 (100 μM, Tocris Biosciences), and a subset was also treated with Thiamet-G (TMG, 50 μM, Sigma Aldrich). The following day, silenced neurons were depolarized with KCl (60 mM) or vehicle for 2 hours and subsequently lysed with 2% SDS in HEPES pH 7.9, containing Roche cOmplete protease inhibitor cocktail (Sigma Aldrich) and TMG (0.1 mM), and protein concentration was measured using BCA assay (ThermoFisher). For the immunoprecipitation experiments, silenced and depolarized neurons were prepared as described and lysed with 1% Triton in TBS containing Roche cOmplete protease inhibitor cocktail (Sigma Aldrich), TMG (0.1 mM), and 0.25 U/μL benzonase nuclease (Santa Cruz Biotechnology).

5.9.19. Chemoenzymatic Labeling of Neuronal Lysates.

O-GlcNAcylated proteins from cell lysates (150 μg) were labeled as previously described.[95] Briefly, proteins were precipitated by the methanol/chloroform/water method described above. Protein pellets were then resolubilized with 40 μL dissolution buffer (20 mM HEPES, 1% SDS, pH 7.9) for 5 min at 95 °C. Water (49 μL), 5.5 mM MnCl (11 μL), and 80 μL

2.5x GalT labeling buffer (50 mM HEPES, 125 mM NaCl, 5% IGEPAL CA-630, pH 7.9) were added and the solution was vortexed gently before adding 10 µL Y289L GalT (1 mg/mL), and 10 µL of UDP-GalNAz (0.5 mM in 10 mM HEPES, pH 7.9). The reaction was then left to rotate end-over-end at 4 °C overnight. Control experiments were carried out in parallel in the absence of UDP-GalNAz. The following day, IAA was added (12.5 mM final concentration) to alkylate free cysteine residues, and the solution was left to rotate end-over-end in the dark at room temperature for 1 hour. Proteins were then precipitated as before and resolubilized by boiling in 199.6 µL of dissolution buffer (1% SDS in TBS pH 7.6). After allowing the redissolved proteins to cool to room temperature, 0.4 µL of 50 mM WS DBCO Biotin (Click Chemistry Tools) was added. The solution was allowed to react for 1 hour with end-over-end rotation in the dark before being precipitated as before. Proteins were again resolubilized by boiling in dissolution buffer and 10% of the reaction volume was taken as input. The remaining aliquot was then incubated with streptavidin magnetic beads (ThermoFisher) for 1.5 hours in the dark. Beads were then washed 5 times with 0.5 ml of low salt buffer (100 mM Na2HPO4, 150 mM NaCl, 0.1% SDS, 1% Triton X-100, 0.5% sodium deoxycholate) and 5 times with 1 ml of high salt buffer (100 mM Na2HPO4, 500 mM NaCl, 0.2% Triton X-100). Biotinylated proteins were eluted by boiling the resin in 50 mM Tris-HCl pH 6.8, 2.5% SDS, 100 mM DTT, 10% glycerol, and 2 mM biotin for 15 min with occasional vortexing.

5.9.20. Western Blotting.

Primary antibodies were obtained from Cell Signaling Technology (Danvers, MA), and secondary antibodies were obtained from ThermoFisher Scientific unless otherwise specified. Primary antibodies were all used at 1:1000 dilution and secondary antibodies at 1:10000 unless

otherwise specified. Cell lysates were diluted with 4x SDS-PAGE buffer (200 mM Tris-HCl pH 6.8, 400 mM DTT, 8% SDS, 0.4% bromophenol blue, 40% glycerol), resolved on a NuPAGE 4-12% Bis-Tris protein gel (ThermoFisher Scientific), and transferred to Immobilion-FL PVDF membrane (MilliporeSigma). Blots were blocked for 1 h at RT with LiCor Odyssey Blocking Buffer (LiCor, Lincoln NE, 927-50003) before probing overnight at 4 °C with the following antibodies diluted in blocking buffer: Rb anti-OGT (Proteintech, Rosemont, IL; 11576-2-AP), Rb anti-HA (C29F4), Ms anti-Nup62 (BD Biosciences, Franklin Lakes, NJ; 610498), Rb anti-HCFC1 (Bethyl Laboratories, A301-399A-M), Rb anti-SET1A (61702S), Rb anti-RBBP5 (61702S), Rb anti-BAP1 (Bethyl Laboratories, Montgomery, TX; A302-243A-M), Rb anti-WDR5 (13105S), Rb anti-FoxK1 (Bethyl Laboratories, A301-728A-M), Rb anti-FoxK2 (12008S), Rb anti-liprin-α1 (Proteintech, 14175-1-AP), Ms C-4 anti-BAP1 Antibody (Santa Cruz Biotechnology, sc-28383), or Ms anti-α-tubulin (Sigma Aldrich, T9026, 1:3000). Blots were rinsed three times with TBST and then probed with the appropriate secondary antibodies in blocking buffer: Gt anti-Ms AlexaFluor 680 conjugate (A21057), Gt anti-Rb AlexaFluor 680 (A21109), Gt anti-Rb AlexaFluor 790 (A11369), or Gt anti-Ms IgG DyLight 800 (ThermoFisher, A11357). Blots were washed 3 x 5 min with TBST and then imaged using an Odyssey Infrared Imaging System (LI-COR Biosciences, Lincoln, NE). Images were processed using ImageStudio v5.2 (LI-COR Biosciences). To calculate O-GlcNAcylation stoichiometry, the ratios of eluents to inputs, weighted by proportion of the total protein in each lane, were used as previously described.[33]

5.9.21. Co-Immunoprecipitation.

Neurons harvested from OGT-FH mice were grown and either silenced or KCl stimulated as described above. Cells were lysed after 21 days as previously described and 1 mg of protein

was diluted to 1 mL with TBS buffer, TMG (0.1 mM), and Roche cOmplete protease inhibitor cocktail (Sigma Aldrich). 15 μg of protein was saved as input. The remaining lysate was incubated with anti-FLAG magnetic beads (Sigma Aldrich) at 4°C overnight with end-over-end rotation. The following day, beads were washed with 3 times with 0.1% Triton-X-100 in TBS pH 7.9 and eluted by boiling in 2% SDS in Tris, pH 8. Inputs and eluents were run on SDS-PAGE and Western blotted for HA and liprin-α1.

5.10. References.

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Appendix 5.1. All Sites and Regions Quantified in WT and BAP1 KO 293T Cells.

Whether each site was identified in the top speed, top 10, or both runs is indicated by the "Experiment" column. logFC Protein: log2 fold change in protein expression. logFC_Corrected, and P-Val_Corrected are the log2 fold change, p-value (after correction for multiple comparisons using the Benjamini-Hochberg method). If protein expression could not be quantified, these values represent those calculated for the sites and regions alone (logFC, and P-Val).

Protein	Gene	Min Sites	Site ID Constraints	Type	Experiment	logFC	P-Val	logFC Protein	logFC_ Corrected	P-Val_ Corrected
A3KN83	SBNO1	1	130	Site	Both	0.2634	0.25765	0.16	0.103378705	0.7400405
A3KN83	SBNO1	1	135	Site	Both	0.4848	0.10288	0.16	0.324841051	0.31261988
A3KN83	SBNO1	1	138	Site	Both	0.4848	0.10288	0.16	0.324841051	0.31261988
A3KN83	SBNO1	1	112	Site	Both	0.2777	0.23985	0.16	0.117695545	0.70759286
A3KN83	SBNO1	1	113	Site	Both	0.0213	0.95725	0.16	-0.13871259	0.65957296
A3KN83	SBNO1	1	126	Site	Both	0.4043	0.08851	0.16	0.244318929	0.3509044
A3KN83	SBNO1	1	127	Site	Both	0.3775	0.11222	0.16	0.217494756	0.41239846
A5YKK6	CNOT1	1	(1 of 5,7,11,14,21)	Region	TopSpeed	0.4282	0.30747	-0.01	0.438155494	0.3509044
A5YKK6	CNOT1	1	1037	Site	Both	0.3432	0.15566	-0.01	0.353235846	0.17220996
A5YKK6	CNOT1	1	1038	Site	Both	0.2865	0.2284	-0.01	0.296521412	0.2501051
A5YKK6	CNOT1	1	1041	Site	Both	0.3642	0.13435	-0.01	0.374216885	0.15033071
A5YKK6	CNOT1	1	1042	Site	Both	0.3642	0.13435	-0.01	0.374216885	0.15033071
A5YKK6	CNOT1	1	1043	Site	Both	0.4498	0.05551	-0.01	0.459794992	0.05793284
A5YKK6	CNOT1	1	1044	Site	Both	0.4288	0.06881	-0.01	0.438813953	0.07316613
A5YKK6	CNOT1	1	1046	Site	Both	0.2912	0.22228	-0.01	0.301209739	0.24428434
A5YKK6	CNOT1	1	1051	Site	Both	-0.06	0.86659	-0.01	-0.05002103	0.90986391

A8CG34	POM121C	2	(2 of 532,536,538,540,542,545,546,549,551,553,559,561,564,565,570,571,577)	Region	Both	-0.043	0.92396		-0.04263184	0.92511993
A8CG34	POM121C	1	599	Site	Both	0.1142	0.714		0.114194512	0.70759286
A8CG34	POM121C	1	583	Site	Both	0.0808	0.79813		0.080833764	0.80312346
A8CG34	POM121C	1	663	Site	Both	-0.227	0.48597		-0.22722047	0.51842158
A8CG34	POM121C	1	665	Site	Both	-0.176	0.62736		-0.17640576	0.64364752
A8CG34	POM121C	1	603	Site	Both	0.1142	0.714		0.114194512	0.70759286
O00151	PDLIM1	1	128	Site	Both	-0.277	0.25669	-0.23	-0.04729067	0.90986391
O00268	TAF4	1	(1 of 709,712,714,715,723,725,728)	Region	TopN	0.2251	0.67242	0.02	0.205058211	0.70759286
O00268	TAF4	1	409	Site	Both	-0.089	0.83321	0.02	-0.10870175	0.7935387
O00512	BCL9	1	(1 of 315,318,321,323,324,325)	Region	TopSpeed	-0.316	0.30656	-0.06	-0.25551919	0.48282553
O00512	BCL9	1	(1 of 337,338,343,352)	Region	Both	-0.018	0.97709	-0.06	0.041900376	0.92511993
O00512	BCL9	1	1035	Site	TopSpeed	0.1881	0.73332	-0.06	0.248062426	0.65348486
O00584	RNASET2	1	103	Site	Both	0.1655	0.76807	-0.07	0.235548823	0.66993821
O14497	ARID1A	1	(1 of 263,264)	Region	Both	0.0202	0.96144	0.13	-0.10979539	0.73706765
O14497	ARID1A	1	265	Site	Both	0.0134	0.97926	0.13	-0.1165729	0.71796103
O14497	ARID1A	1	238	Site	Both	-0.012	0.97926	0.13	-0.14242844	0.66085936
O14497	ARID1A	1	241	Site	Both	-0.012	0.97926	0.13	-0.14242844	0.66085936
O14497	ARID1A	1	249	Site	Both	-0.012	0.97926	0.13	-0.14242844	0.66085936
O14497	ARID1A	1	255	Site	Both	0.0134	0.97926	0.13	-0.1165729	0.71796103
O14686	KMT2D	1	2402	Site	Both	0.3552	0.13477	0.31	0.045183147	0.90986391
O14686	KMT2D	1	2405	Site	Both	0.3552	0.13477	0.31	0.045183147	0.90986391
O14964	HGS	1	(1 of 299,300)	Region	Both	-0.125	0.70431	-0.23	0.10540641	0.74875917
O14964	HGS	1	297	Site	Both	-0.164	0.58701	-0.23	0.065983656	0.86597032
O14964	HGS	1	306	Site	Both	-0.378	0.11674	-0.23	-0.14817061	0.6241827
O14964	HGS	1	309	Site	Both	-0.311	0.18108	-0.23	-0.08091512	0.80292165
O14964	HGS	1	310	Site	Both	-0.283	0.22228	-0.23	-0.05345055	0.88767054
O14964	HGS	1	314	Site	Both	-0.259	0.25945	-0.23	-0.02861969	0.92831607
O14964	HGS	1	315	Site	Both	-0.239	0.30656	-0.23	-0.00872719	0.97975
O14974	PPP1R12A	2	(2 of 379,381,385,386,387,388,396,397)&(1 of 374,379,381,385,386,387,388,396,397,399,401,402,406,408,409)	Region	Both	-0.374	0.13319	-0.04	-0.33436101	0.20309052

O14974	PPP1R12A	1	(1 of 564,566,569,570,571,572,573,575,577,578)	Region	Both	-0.018	0.97709	-0.04	0.022394637	0.95760145
O14974	PPP1R12A	1	(1 of 659,660)	Region	Both	0.058	0.86036	-0.04	0.097965707	0.75083287
O14974	PPP1R12A	1	644	Site	Both	-0.079	0.80699	-0.04	-0.03869652	0.91823676
O14974	PPP1R12A	1	590	Site	Both	-0.115	0.76699	-0.04	-0.07537674	0.86597032
O14974	PPP1R12A	1	592	Site	Both	-0.115	0.76699	-0.04	-0.07537674	0.86597032
O14974	PPP1R12A	1	658	Site	Both	0.0423	0.89837	-0.04	0.08233485	0.79704572
O14974	PPP1R12A	1	565	Site	Both	-0.018	0.97709	-0.04	0.022394637	0.95760145
O14974	PPP1R12A	1	631	Site	Both	-0.011	0.97926	-0.04	0.028822912	0.92831607
O14974	PPP1R12A	1	637	Site	Both	-0.01	0.97938	-0.04	0.029781363	0.92831607
O15014	ZNF609	1	1196	Site	Both	-0.002	0.99326	0.32	-0.32177089	0.20896022
O15027	SEC16A	1	(1 of 2158,2159)	Region	Both	-0.286	0.24557	0.04	-0.32570797	0.22504717
O15372	EIF3H	1	8	Site	Both	-0.289	0.34289	-0.02	-0.2692201	0.43520501
O15372	EIF3H	1	10	Site	Both	-0.289	0.34289	-0.02	-0.2692201	0.43520501
O43151	TET3	1	(1 of 513,515,516,520)	Region	TopSpeed	-0.035	0.96144		-0.03472066	0.95269929
O43151	TET3	1	(1 of 431,439,441,445)	Region	Both	0.4431	0.13039		0.443106148	0.1578518
O43166	SIPA1L1	1	1408	Site	TopSpeed	0.1129	0.73082	0.09	0.022949152	0.94300057
O43312	MTSS1	1	491	Site	Both	-0.419	0.08291		-0.41940964	0.10146861
O43318	MAP3K7	1	(1 of 382,383)	Region	TopSpeed	-0.414	0.1724	0.02	-0.43442926	0.18280589
O43318	MAP3K7	1	378	Site	TopSpeed	-0.544	0.06693	0.02	-0.56356598	0.06661396
O43395	PRPF3	1	176	Site	TopSpeed	-0.477	0.24557	0.11	-0.58707126	0.1911075
O43424	GRID2	2	(2 of 599,601,602,603,604)	Region	TopN	-1.456	0.00077		-1.45612394	0.00124114
O43432	EIF4G3	2	(2 of 277,278,283,284,285,288,289,294,295)	Region	TopN	0.0592	0.92655	0.19	-0.13080781	0.83311173
O43432	EIF4G3	1	258	Site	Both	0.2944	0.20869	0.19	0.10435455	0.73706765
O43432	EIF4G3	1	251	Site	Both	0.2138	0.37511	0.19	0.02378505	0.94022854
O43432	EIF4G3	1	253	Site	Both	0.2445	0.29634	0.19	0.054547432	0.88667585
O43524	FOXO3	1	418	Site	Both	0.0324	0.92718	0.41	-0.37757893	0.1324731
O43670	ZNF207	2	(2 of 257,263,266,267,268,269,270,272,273,275,277,279,281,282)	Region	TopSpeed	0.2086	0.45523	-0.14	0.348625466	0.20309052
O43823	AKAP8	1	216	Site	TopSpeed	0.1493	0.69788	0.08	0.069334225	0.88425848
O60237	PPP1R12B	1	(1 of 543,547,548,551,552)	Region	TopSpeed	0.0832	0.8847	-0.03	0.113173737	0.86428932
O60318	MCM3AP	1	(1 of 114,116,117,123,124,125,137)	Region	Both	-0.14	0.637	0.09	-0.2300285	0.39591243

O60641	SNAP91	1	(1 of 305,306,309,310,312,313,316,317)	Region	TopSpeed	0.1556	0.77943	0.1	0.055617497	0.92831607
O60675	MAFK	1	153	Site	TopSpeed	0.459	0.12517	0.06	0.399029019	0.20309052
O60675	MAFK	1	156	Site	TopSpeed	0.459	0.12517	0.06	0.399029019	0.20309052
O60675	MAFK	1	133	Site	Both	0.5112	0.08291	0.06	0.45124976	0.15033071
O60675	MAFK	1	134	Site	Both	0.5112	0.08291	0.06	0.45124976	0.15033071
O75170	PPP6R2	1	899	Site	Both	0.408	0.08851	0.29	0.118040261	0.70710977
O75170	PPP6R2	1	887	Site	Both	0.3971	0.09827	0.29	0.107101138	0.73229249
O75170	PPP6R2	1	903	Site	Both	0.3595	0.12714	0.29	0.069518523	0.84513314
O75179	ANKRD17	1	(1 of 2041,2042,2044,2045,2047,2056)	Region	TopN	-0.042	0.94684	0.13	-0.17243844	0.75674684
O75179	ANKRD17	1	(1 of 1563,1566)	Region	TopSpeed	-0.486	0.24051	0.13	-0.61591879	0.17220996
O75179	ANKRD17	1	1825	Site	Both	0.2962	0.23195	0.13	0.166236225	0.60078955
O75179	ANKRD17	1	1826	Site	Both	0.4651	0.05551	0.13	0.335086668	0.19486577
O75179	ANKRD17	1	1830	Site	Both	0.2962	0.23195	0.13	0.166236225	0.60078955
O75179	ANKRD17	1	1831	Site	Both	0.3515	0.13469	0.13	0.221486479	0.41007524
O75179	ANKRD17	1	2001	Site	Both	0.1085	0.75105	0.13	-0.02145716	0.95269929
O75179	ANKRD17	1	1820	Site	Both	0.6201	0.01176	0.13	0.490145419	0.04891006
O75376	NCOR1	1	1487	Site	Both	0.0297	0.93293	0.24	-0.21027994	0.4557783
O75533	SF3B1	1	296	Site	Both	0.2968	0.53663	0.02	0.276810206	0.60078955
O75533	SF3B1	1	299	Site	Both	0.2968	0.53663	0.02	0.276810206	0.60078955
O75947	ATP5PD	1	37	Site	Both	0.124	0.84412	-0.29	0.414010355	0.41163169
O75947	ATP5PD	1	39	Site	Both	0.1495	0.78918	-0.29	0.439547796	0.3509044
O94832	MYO1D	1	240	Site	TopSpeed	0.028	0.97573	0.09	-0.06202952	0.92511993
O94880	PHF14	1	(1 of 139,141,147,151,152,155,156,162,163,165,168,169,170,171,173,178)	Region	TopSpeed	0.0528	0.93131	0.29	-0.23716402	0.6680228
O95382	MAP3K6	1	1285	Site	Both	0.4081	0.16314		0.40814701	0.19131351
O95382	MAP3K6	1	1286	Site	Both	0.3534	0.22767		0.353387251	0.2609852
O95487	SEC24B	1	347	Site	Both	-0.294	0.23195	-0.28	-0.01429667	0.97305303
O95487	SEC24B	1	310	Site	Both	-0.33	0.16065	-0.28	-0.05023136	0.89825847
O95487	SEC24B	1	311	Site	Both	-0.27	0.24051	-0.28	0.01012769	0.97877402
O95487	SEC24B	1	344	Site	Both	-0.294	0.23195	-0.28	-0.01429667	0.97305303
O95487	SEC24B	1	315	Site	Both	-0.32	0.17273	-0.28	-0.04043916	0.91559759
O95628	CNOT4	1	331	Site	TopSpeed	-0.095	0.86659	-0.02	-0.07466505	0.91381441
O95628	CNOT4	1	333	Site	TopSpeed	-0.092	0.87183	-0.02	-0.07168632	0.91559759
O95628	CNOT4	1	335	Site	TopSpeed	-0.092	0.87183	-0.02	-0.07168632	0.91559759

O95677	EYA4	2	(1 of 105,106,108,109,111)&(2 of 106,108,109,111,119,121,127,128,131)&(1 of 126,127,128)	Region	Both	-0.309	0.28953	-0.07	-0.239164	0.49091587
O95677	EYA4	1	112	Site	Both	-0.188	0.58701	-0.07	-0.11787429	0.76034174
O95677	EYA4	1	123	Site	Both	-0.164	0.65436	-0.07	-0.09354478	0.82382993
O95789	ZMYM6	1	615	Site	Both	0.0612	0.85398	0.04	0.021220457	0.94931495
O95817	BAG3	1	(1 of 144,145)	Region	TopSpeed	-0.408	0.22729	-0.14	-0.26845961	0.5100738
P02545	LMNA	1	(1 of 612,613)	Region	Both	-0.013	0.97926	0.25	-0.26313788	0.43085957
P02545	LMNA	1	615	Site	Both	-0.013	0.97926	0.25	-0.26313788	0.43085957
P04792	HSPB1	1	184	Site	TopSpeed	-0.243	0.438	-0.34	0.096926157	0.81537205
P05062	ALDOB	1	(1 of 160,161)	Region	TopSpeed	0.0946	0.86659		0.094611325	0.88875793
P05387	RPLP2	1	(1 of 64,74,79,86)	Region	TopSpeed	-0.132	0.81511	-0.21	0.077552052	0.91044412
P06576	ATP5F1B	1	405	Site	TopSpeed	0.1949	0.73082	0.03	0.164894815	0.76722608
P06748	NPM1	1	75	Site	Both	0.2405	0.3163	-0.06	0.300458111	0.24051635
P07197	NEFM	1	50	Site	Both	0.474	0.11047	0.49	-0.01601658	0.97340685
P07197	NEFM	1	47	Site	Both	0.5646	0.05342	0.49	0.074639285	0.86792234
P07339	CTSD	1	265	Site	TopSpeed	-0.482	0.24375	0.21	-0.69151582	0.12260258
P07711	CTSL	1	218	Site	Both	-0.048	0.88252	0.03	-0.07773968	0.81593663
P07711	CTSL	1	223	Site	Both	-0.048	0.88252	0.03	-0.07773968	0.81593663
P07902	GALT	1	377	Site	TopSpeed	-0.574	0.1724	-0.04	-0.5336392	0.23658316
P08651	NFIC	1	473	Site	Both	0.3759	0.11275	0.29	0.085863376	0.79074906
P08651	NFIC	1	462	Site	Both	0.541	0.02605	0.29	0.250985064	0.35679661
P08670	VIM	1	32	Site	Both	-0.211	0.38826	-0.31	0.099417475	0.74875917
P08670	VIM	1	33	Site	Both	-0.055	0.86134	-0.31	0.25488492	0.32418494
P08670	VIM	1	34	Site	Both	-0.455	0.0523	-0.31	-0.14516197	0.62861844
P08670	VIM	1	35	Site	Both	-0.096	0.76383	-0.31	0.213784417	0.43727997
P08670	VIM	1	7	Site	Both	-0.595	0.04462	-0.31	-0.2848734	0.39591243
P08670	VIM	1	20	Site	Both	-0.016	0.97703	-0.31	0.294353503	0.2609852
P08670	VIM	1	22	Site	Both	-0.164	0.62052	-0.31	0.145503903	0.6902866
P09012	SNRPA	1	131	Site	Both	0.0701	0.86086	-0.14	0.210118398	0.56656261
P09012	SNRPA	1	148	Site	Both	0.3165	0.29634	-0.14	0.456524016	0.16094902
P0C7T5	ATXN1L	1	22	Site	Both	0.1728	0.51124		0.172754828	0.54933658
P0C7T5	ATXN1L	1	23	Site	Both	0.1728	0.51124		0.172754828	0.54933658
P0CJ78	ZNF865	1	(1 of 94,95,96,97,98,99,100,101,102,103,104)	Region	Both	-0.14	0.63582		-0.13976111	0.65781223
P0CJ78	ZNF865	1	93	Site	Both	-0.232	0.34289		-0.23183599	0.39591243
P10071	GLI3	1	(1 of 78,79)&(1 of 77,78)	Region	Both	-0.325	0.317		-0.32527636	0.36895199
P10073	ZSCAN22	1	476	Site	Both	0.3314	0.4737		0.33137544	0.50795571

P10253	GAA	1	(1 of 142,143,144,149,151,153)	Region	TopSpeed	-0.071	0.90456	-0.14	0.068888477	0.91878967
P10253	GAA	1	884	Site	TopN	-0.235	0.65436	-0.14	-0.09521978	0.88772423
P11940	PABPC1	1	635	Site	Both	-0.151	0.60645	-0.06	-0.09133626	0.78573066
P11940	PABPC1	1	485	Site	TopSpeed	0.4164	0.08291	-0.06	0.476393117	0.05035599
P11940	PABPC1	1	486	Site	TopSpeed	0.2714	0.24051	-0.06	0.331426813	0.18623291
P11940	PABPC1	1	631	Site	Both	-0.151	0.60645	-0.06	-0.09133626	0.78573066
P12270	TPR	1	(1 of 1661,1662)	Region	Both	-0.74	0.01205	0.08	-0.81963063	0.00616466
P12270	TPR	1	1672	Site	Both	-0.74	0.01205	0.08	-0.81963063	0.00616466
P12270	TPR	1	1666	Site	Both	-0.74	0.01205	0.08	-0.81963063	0.00616466
P12270	TPR	1	1676	Site	Both	-0.74	0.01205	0.08	-0.81963063	0.00616466
P14859	POU2F1	1	267	Site	TopSpeed	-0.158	0.66876	-0.31	0.152329916	0.69740433
P14859	POU2F1	1	255	Site	TopSpeed	-0.158	0.66876	-0.31	0.152329916	0.69740433
P15336	ATF2	1	(1 of 283,290,294)	Region	TopSpeed	0.1863	0.73332	-0.19	0.376329078	0.43514761
P15822	HIVEP1	1	1633	Site	TopSpeed	0.1222	0.75105		0.122195485	0.75067469
P15822	HIVEP1	1	741	Site	TopSpeed	-0.32	0.49818		-0.32031838	0.52828118
P15822	HIVEP1	1	2325	Site	Both	0.3961	0.17803		0.396129358	0.20309052
P15822	HIVEP1	1	698	Site	TopSpeed	-0.135	0.73332		-0.13477281	0.73658347
P15822	HIVEP1	1	699	Site	TopSpeed	-0.135	0.73332		-0.13477281	0.73658347
P15880	RPS2	1	293	Site	Both	0.3265	0.1687	-0.33	0.656521619	0.00616466
P18583	SON	1	(1 of 303,305,309,310,312,314,321,322,323,324,325,331,332)	Region	TopSpeed	0.0906	0.87206	0.15	-0.05941887	0.92511993
P18583	SON	1	1097	Site	Both	0.1479	0.65395	0.15	-0.00214061	0.99576765
P18583	SON	1	265	Site	TopSpeed	0.274	0.37335	0.15	0.124046451	0.75179055
P18583	SON	1	244	Site	Both	0.3198	0.1857	0.15	0.169759363	0.58282978
P18583	SON	1	252	Site	Both	0.3237	0.18108	0.15	0.173655092	0.57129172
P18583	SON	1	253	Site	Both	0.2983	0.21998	0.15	0.148345204	0.6375374
P18846	ATF1	1	(1 of 183,184,186,188,189,193,197,198,201,203,204,206,207)	Region	TopSpeed	0.2082	0.53065	-0.01	0.218158639	0.54109863
P19419	ELK1	1	270	Site	TopSpeed	0.1711	0.637	0.22	-0.04894678	0.91692242
P20719	HOXA5	1	72	Site	TopN	-0.21	0.70431		-0.21018123	0.70495902
P22681	CBL	1	601	Site	Both	0.1765	0.50486	-0.14	0.316484714	0.20309052
P23246	SFPQ	1	660	Site	Both	0.1303	0.67048	-0.07	0.20030839	0.48282553
P23246	SFPQ	1	652	Site	Both	0.0907	0.78143	-0.07	0.1606535	0.60786377
P23769	GATA2	1	196	Site	Both	0.6792	0.02182		0.679198462	0.0242215
P25054	APC	1	2715	Site	TopSpeed	-0.282	0.56324	-0.17	-0.11217118	0.86428932
P27540	ARNT	1	642	Site	Both	0.3162	0.17833	0.21	0.106233867	0.73357459
P27540	ARNT	1	643	Site	Both	0.3785	0.1114	0.21	0.168521376	0.5649946

P27816	MAP4	1	793	Site	Both	-0.108	0.73332	-0.08	-0.02847438	0.92993035
P27816	MAP4	1	811	Site	TopSpeed	0.2008	0.72438	-0.08	0.280756324	0.60078955
P27816	MAP4	1	797	Site	Both	-0.074	0.83802	-0.08	0.00574355	0.98629216
P31629	HIVEP2	1	(1 of 442,443,444)	Region	TopSpeed	1.4092	0.00099		1.409219662	0.00143963
P31629	HIVEP2	1	1057	Site	TopSpeed	0.041	0.95052		0.040968591	0.94241548
P31629	HIVEP2	1	1936	Site	Both	0.0524	0.87183		0.05242962	0.89452881
P31629	HIVEP2	1	406	Site	Both	0.0563	0.86271		0.056327818	0.88667585
P31629	HIVEP2	1	1274	Site	TopSpeed	0.1252	0.83276		0.125194601	0.84495868
P31629	HIVEP2	1	251	Site	Both	0.259	0.39149		0.259026179	0.43727997
P31629	HIVEP2	1	1981	Site	TopSpeed	0.802	0.05597		0.802021943	0.06716852
P31942	HNRNPH3	1	(1 of 14,17)	Region	TopN	-0.382	0.37903	0.12	-0.50233338	0.2609852
P35453	HOXD13	1	(1 of 25,26,27,28,29,30,37)	Region	TopSpeed	-0.364	0.22246		-0.36444125	0.2560924
P35527	KRT9	1	85	Site	TopSpeed	0.4855	0.24051	-0.18	0.665469038	0.14452898
P35658	NUP214	1	(1 of 1556,1557,1558,1559,1564,1568,1571)&(1 of 1549,1551,1556,1557,1558,1559)	Region	Both	0.0335	0.92718	-0.1	0.133458847	0.67158708
P35658	NUP214	1	(1 of 1271,1272)	Region	Both	-0.093	0.7694	-0.1	0.007249102	0.98261543
P35658	NUP214	1	(1 of 1291,1292)	Region	Both	-0.126	0.67751	-0.1	-0.02589688	0.93373979
P35658	NUP214	1	(1 of 1137,1141,1142)	Region	Both	-0.048	0.88358	-0.1	0.051519989	0.89825847
P35658	NUP214	1	(1 of 592,597,598,601,602,603)	Region	Both	0.0435	0.89829	-0.1	0.14348877	0.63995712
P35658	NUP214	1	(1 of 518,519,521,526)	Region	TopSpeed	-0.208	0.40508	-0.1	-0.108489	0.73182451
P35658	NUP214	1	(1 of 1278,1279)	Region	Both	-0.093	0.7694	-0.1	0.007249102	0.98261543
P35658	NUP214	1	(1 of 439,440)	Region	Both	-0.482	0.04462	-0.1	-0.38164613	0.1432696
P35658	NUP214	1	1283	Site	Both	-0.091	0.7717	-0.1	0.008850902	0.97975
P35658	NUP214	1	1925	Site	Both	0.102	0.75105	-0.1	0.202038684	0.48282553
P35658	NUP214	1	1553	Site	Both	0.1641	0.54766	-0.1	0.264068719	0.30809545
P35658	NUP214	1	1301	Site	Both	0.0986	0.86134	-0.1	0.198565282	0.71678949
P35658	NUP214	1	1304	Site	Both	0.0986	0.86134	-0.1	0.198565282	0.71678949
P35658	NUP214	1	1305	Site	Both	0.0986	0.86134	-0.1	0.198565282	0.71678949
P35658	NUP214	1	1572	Site	Both	0.0443	0.89829	-0.1	0.144346574	0.64266867
P35658	NUP214	1	430	Site	Both	-0.482	0.04462	-0.1	-0.38164613	0.1432696
P35658	NUP214	1	1202	Site	Both	-0.025	0.95198	-0.1	0.074717547	0.85736486
P35658	NUP214	1	437	Site	Both	-0.482	0.04462	-0.1	-0.38164613	0.1432696
P35658	NUP214	1	962	Site	TopSpeed	0.7689	0.06881	-0.1	0.868897753	0.04333656
P35658	NUP214	1	579	Site	Both	0.0218	0.95524	-0.1	0.121826145	0.70052671

P35658	NUP214	1	580	Site	Both	0.0489	0.87853	-0.1	0.148873789	0.62022567
P35658	NUP214	1	966	Site	TopSpeed	-0.12	0.83909	-0.1	-0.02047024	0.97812544
P35658	NUP214	1	1354	Site	Both	-0.338	0.14727	-0.1	-0.2378977	0.36383611
P35658	NUP214	1	1355	Site	Both	-0.299	0.20372	-0.1	-0.19923821	0.46976784
P35658	NUP214	1	1356	Site	Both	-0.299	0.20372	-0.1	-0.19923821	0.46976784
P35658	NUP214	1	1358	Site	Both	0.0707	0.84721	-0.1	0.170719945	0.60078955
P35658	NUP214	1	1359	Site	Both	-0.008	0.98301	-0.1	0.09230139	0.80184027
P35658	NUP214	1	1360	Site	Both	-0.171	0.53798	-0.1	-0.07101564	0.84808137
P35658	NUP214	1	596	Site	Both	0.0172	0.96948	-0.1	0.117186691	0.70759286
P35658	NUP214	1	605	Site	Both	-0.067	0.84852	-0.1	0.033060094	0.92831607
P35658	NUP214	1	610	Site	Both	0.0327	0.93078	-0.1	0.132741218	0.69207847
P35658	NUP214	1	613	Site	Both	0.1233	0.69055	-0.1	0.223273715	0.40685096
P35658	NUP214	1	614	Site	Both	0.0896	0.77943	-0.1	0.189609236	0.50795571
P35658	NUP214	1	616	Site	Both	0.0038	0.98673	-0.1	0.10377368	0.74560734
P35658	NUP214	1	1134	Site	Both	0.0952	0.76133	-0.1	0.195229106	0.47797702
P35658	NUP214	1	496	Site	Both	-0.184	0.48832	-0.1	-0.08368789	0.79704572
P35658	NUP214	1	1905	Site	Both	0.102	0.75105	-0.1	0.202038684	0.48282553
P35658	NUP214	1	501	Site	Both	-0.109	0.73332	-0.1	-0.00913283	0.97975
P35658	NUP214	1	503	Site	Both	-0.176	0.52077	-0.1	-0.07571411	0.8319825
P35658	NUP214	1	1146	Site	Both	-0.18	0.51124	-0.1	-0.08021673	0.81537205
P35658	NUP214	1	1275	Site	Both	-0.093	0.7694	-0.1	0.007249102	0.98261543
P35658	NUP214	1	509	Site	Both	-0.22	0.37357	-0.1	-0.120074	0.70495902
P40222	TXLNA	1	(1 of 519,529,530,533,536,542,543)	Region	TopN	0.6932	0.10489	0.05	0.643243005	0.15352465
P40763	STAT3	1	(1 of 714,716,717,719,721,727)	Region	TopSpeed	-0.504	0.22708	-0.39	-0.11414456	0.86428932
P41235	HNF4A	1	(1 of 166,167,170)	Region	TopN	0.2915	0.54815		0.291460632	0.58728077
P42167	TMPO	1	264	Site	Both	-0.351	0.14727	-0.14	-0.21084197	0.45686225
P42167	TMPO	1	265	Site	Both	-0.47	0.06485	-0.14	-0.329539	0.22202586
P42857	NSG1	1	(1 of 130,137,138)	Region	TopSpeed					
P43694	GATA4	2	(1 of 330,335,337,339,344,347,348,350,351,354,355,356,357,358)&(2 of 344,348,350,351,354)	Region	Both	0.0427	0.89829		0.042717156	0.91129339
P48382	RFX5	1	433	Site	Both	-0.434	0.06946	0.09	-0.5238683	0.03105627
P48382	RFX5	1	442	Site	Both	-0.441	0.06827	0.09	-0.53074098	0.03028951
P48382	RFX5	1	439	Site	Both	-0.45	0.06179	0.09	-0.5396056	0.02674372
P48431	SOX2	1	246	Site	Both	-0.709	0.0054	-0.72	0.01124884	0.97877402
P48634	PRRC2A	1	2096	Site	TopSpeed	0.3057	0.52034	0.09	0.215708314	0.70101954

P48634	PRRC2A	1	1796	Site	Both	0.0916	0.77465	0.09	0.001641614	0.99576765
P48634	PRRC2A	1	1790	Site	Both	0.0601	0.85824	0.09	-0.02990007	0.92831607
P48634	PRRC2A	1	1788	Site	Both	0.0601	0.85824	0.09	-0.02990007	0.92831607
P49321	NASP	1	690	Site	Both	-0.297	0.3167	0.04	-0.33717117	0.29696117
P49321	NASP	1	677	Site	Both	-0.297	0.3167	0.04	-0.33717117	0.29696117
P49321	NASP	1	678	Site	Both	-0.244	0.45057	0.04	-0.28385408	0.4009486
P49336	CDK8	1	420	Site	Both	0.194	0.44512		0.194045694	0.48576359
P49336	CDK8	1	419	Site	Both	0.3019	0.1975		0.301947988	0.22504717
P49336	CDK8	1	411	Site	Both	0.0728	0.83276		0.072841649	0.84495868
P49336	CDK8	1	410	Site	Both	0.2427	0.30747		0.242736362	0.35793478
P49750	YLPM1	1	751	Site	TopSpeed	-0.186	0.73332	-0.03	-0.15611039	0.7882435
P49790	NUP153	1	(1 of 197,199)	Region	TopSpeed	0.2346	0.65473	0.06	0.174635259	0.75179055
P49790	NUP153	1	(1 of 1017,1018,1019, 1023,1026,1032, 1038,1041,1042)	Region	Both	0.0674	0.83909	0.06	0.007418259	0.98261543
P49790	NUP153	1	(1 of 776,778,780)	Region	Both	0.0881	0.82977	0.06	0.0281486	0.94241548
P49790	NUP153	1	(1 of 1178,1179)	Region	Both	0.2486	0.31176	0.06	0.188610023	0.52599901
P49790	NUP153	1	(1 of 1114,1115)	Region	Both	-0.696	0.01956	0.06	-0.75641094	0.0125797
P49790	NUP153	1	897	Site	Both	-0.085	0.88252	0.06	-0.14459536	0.80312346
P49790	NUP153	1	515	Site	Both	0.4832	0.05597	0.06	0.423159773	0.12136128
P49790	NUP153	1	771	Site	Both	0.0426	0.92396	0.06	-0.01744124	0.9722008
P49790	NUP153	1	1031	Site	Both	0.0602	0.85694	0.06	0.00017259	0.99908938
P49790	NUP153	1	520	Site	Both	0.3104	0.22708	0.06	0.250442561	0.39293271
P49790	NUP153	1	1159	Site	TopSpeed	0.1647	0.7694	0.06	0.104655886	0.87523489
P49790	NUP153	1	519	Site	Both	0.5734	0.01865	0.06	0.51342951	0.04036339
P49790	NUP153	1	908	Site	Both	-0.131	0.73332	0.06	-0.19073954	0.60786377
P49790	NUP153	1	909	Site	Both	-0.079	0.84852	0.06	-0.13858992	0.71678949
P49790	NUP153	1	783	Site	Both	0.0783	0.84852	0.06	0.018291545	0.97001968
P49790	NUP153	1	534	Site	Both	0.4046	0.11222	0.06	0.344556137	0.19530979
P49790	NUP153	1	535	Site	Both	0.5024	0.03892	0.06	0.442364767	0.08451531
P49790	NUP153	1	1177	Site	Both	0.2841	0.24051	0.06	0.224072364	0.42146519
P49790	NUP153	1	921	Site	Both	-0.085	0.83549	0.06	-0.14490984	0.70710977
P49790	NUP153	1	1180	Site	Both	0.2841	0.24051	0.06	0.224072364	0.42146519
P49790	NUP153	1	543	Site	Both	0.135	0.65532	0.06	0.074964041	0.83417348
P49790	NUP153	1	544	Site	Both	0.135	0.65532	0.06	0.074964041	0.83417348
P49790	NUP153	1	548	Site	Both	0.0868	0.78918	0.06	0.02683305	0.93373979
P49790	NUP153	1	550	Site	Both	0.1729	0.51992	0.06	0.112854704	0.71678949
P49790	NUP153	1	937	Site	Both	-0.039	0.90979	0.06	-0.09922357	0.75179055
P49790	NUP153	1	947	Site	Both	0.1483	0.59754	0.06	0.088342466	0.78573066
P49790	NUP153	1	1078	Site	TopSpeed	-0.223	0.49818	0.06	-0.28337146	0.39253732
P49790	NUP153	1	1113	Site	Both	-0.696	0.01956	0.06	-0.75641094	0.0125797

P49790	NUP153	1	624	Site	Both	-0.177	0.51686	0.06	-0.23742102	0.38360195
P49790	NUP153	1	115	Site	Both	0.6077	0.1456	0.06	0.547679511	0.22202586
P49790	NUP153	1	761	Site	Both	-0.094	0.81444	0.06	-0.15440366	0.69221229
P49790	NUP153	1	630	Site	Both	-0.122	0.70725	0.06	-0.18192196	0.54824901
P49790	NUP153	1	759	Site	Both	-0.094	0.81444	0.06	-0.15440366	0.69221229
P49790	NUP153	1	632	Site	Both	0.0543	0.86659	0.06	-0.00569009	0.9862528
P49790	NUP153	1	633	Site	Both	-0.025	0.94416	0.06	-0.08521236	0.79441218
P49790	NUP153	1	893	Site	Both	0.1233	0.83402	0.06	0.063330156	0.92400636
P49792	RANBP2	1	(1 of 1953,1954)	Region	TopSpeed	0.1637	0.76942	-0.06	0.223658076	0.69130082
P49792	RANBP2	1	(1 of 1039,1045,1047, 1048,1053,1061, 1063,1065,1071, 1072,1082)	Region	TopN	-0.101	0.86086	-0.06	-0.04055195	0.94241548
P49792	RANBP2	1	1894	Site	Both	-0.267	0.25172	-0.06	-0.20704984	0.45276858
P49792	RANBP2	1	1399	Site	Both	-0.101	0.75713	-0.06	-0.04064314	0.91692242
P49848	TAF6	1	(1 of 595,598)	Region	Both	-0.018	0.97703	0.13	-0.14837728	0.70101954
P49848	TAF6	1	481	Site	TopSpeed	0.335	0.4663	0.13	0.204965358	0.70759286
P49848	TAF6	1	594	Site	Both	-0.018	0.97703	0.13	-0.14837728	0.70101954
P49848	TAF6	1	587	Site	Both	-0.053	0.89829	0.13	-0.18344512	0.62321657
P50402	EMD	1	(1 of 49,52,53,54,57,58,60,62,66,67)	Region	TopSpeed	-0.41	0.08291	-0.01	-0.39962593	0.11121166
P50454	SERPINH1	1	122	Site	TopSpeed	0.1561	0.77943	0.1	0.056078791	0.92831607
P51003	PAPOLA	1	706	Site	TopN	-0.052	0.89886	0.14	-0.19206099	0.60078955
P51003	PAPOLA	1	709	Site	TopN	-0.052	0.89886	0.14	-0.19206099	0.60078955
P51610	HCFC1	2	(1 of 727,733,734,737,738,739,742,746)&(2 of 733,734,737,738,739)	Region	Both	0.0061	0.98301	0.08	-0.07387311	0.84621405
P51610	HCFC1	1	(1 of 427,441,457,458,459,460,466,470,471,473,476)	Region	Both	0.4815	0.24375	0.08	0.40152833	0.39591243
P51610	HCFC1	1	(1 of 666,669,674,678)	Region	TopSpeed	-0.319	0.49928	0.08	-0.3988956	0.4009486
P51610	HCFC1	1	(1 of 638,640,642,651,652)	Region	Both	0.3732	0.12517	0.08	0.293242219	0.25550595
P51610	HCFC1	1	(1 of 1485,1486,1488, 1490,1491,1497, 1507)	Region	Both	-0.174	0.63582	0.08	-0.25367277	0.4590033
P51610	HCFC1	1	(1 of 695,698)	Region	TopSpeed	0.7684	0.03462	0.08	0.688397988	0.06815382
P51610	HCFC1	1	1153	Site	Both	0.2709	0.24543	0.08	0.190887637	0.49565552
P51610	HCFC1	1	771	Site	Both	0.2159	0.37335	0.08	0.135945211	0.66085936
P51610	HCFC1	1	515	Site	Both	0.8629	0.00039	0.08	0.782884095	0.00143963

P51610	HCFC1	1	518	Site	Both	0.8747	0.00036	0.08	0.794678273	0.00138288
P51610	HCFC1	1	775	Site	Both	0.5331	0.04016	0.08	0.453052993	0.10340696
P51610	HCFC1	1	779	Site	Both	0.5099	0.05342	0.08	0.42991359	0.1277745
P51610	HCFC1	1	658	Site	Both	0.3732	0.12517	0.08	0.293242219	0.25550595
P51610	HCFC1	1	787	Site	Both	0.5436	0.03624	0.08	0.463628064	0.09202231
P51610	HCFC1	1	788	Site	Both	0.3688	0.12517	0.08	0.288799917	0.25580836
P51610	HCFC1	1	405	Site	Both	-0.076	0.85398	0.08	-0.15567815	0.69098468
P51610	HCFC1	1	660	Site	TopN	-0.236	0.65395	0.08	-0.31611791	0.53711129
P51610	HCFC1	1	797	Site	Both	0.1278	0.67468	0.08	0.047815737	0.90677977
P51610	HCFC1	1	800	Site	Both	0.0998	0.74963	0.08	0.019823147	0.95206316
P51610	HCFC1	1	801	Site	Both	0.1028	0.73531	0.08	0.022837842	0.94241548
P51610	HCFC1	1	419	Site	Both	-0.083	0.84025	0.08	-0.16286141	0.67158708
P51610	HCFC1	1	806	Site	Both	-0.007	0.98301	0.08	-0.08673132	0.79409661
P51610	HCFC1	1	808	Site	Both	0.1346	0.64952	0.08	0.054605187	0.88697434
P51610	HCFC1	1	685	Site	Both	0.241	0.3332	0.08	0.160953818	0.60434096
P51610	HCFC1	1	562	Site	Both	-0.139	0.63582	0.08	-0.21916793	0.41618591
P51610	HCFC1	1	563	Site	Both	-0.126	0.67542	0.08	-0.20591	0.45311328
P51610	HCFC1	1	566	Site	Both	-0.1	0.75105	0.08	-0.17992526	0.52819421
P51610	HCFC1	1	569	Site	Both	-0.122	0.69245	0.08	-0.20206357	0.46477752
P51610	HCFC1	1	446	Site	Both	0.4815	0.24375	0.08	0.40152833	0.39591243
P51610	HCFC1	1	703	Site	TopSpeed	0.7697	0.03441	0.08	0.689658664	0.06767492
P51610	HCFC1	1	574	Site	Both	-0.093	0.76984	0.08	-0.17254106	0.56143055
P51610	HCFC1	1	575	Site	Both	-0.131	0.65608	0.08	-0.2113882	0.43520501
P51610	HCFC1	1	579	Site	Both	0.5449	0.01893	0.08	0.464923365	0.05085475
P51610	HCFC1	1	586	Site	Both	0.2894	0.21736	0.08	0.209424944	0.43520501
P51610	HCFC1	1	587	Site	Both	0.1436	0.61976	0.08	0.06356562	0.86428932
P51610	HCFC1	1	588	Site	Both	0.1839	0.51124	0.08	0.103892731	0.75067469
P51610	HCFC1	1	848	Site	TopSpeed	0.0671	0.87961	0.08	-0.01288798	0.97975
P51610	HCFC1	1	1234	Site	Both	0.4319	0.12517	0.08	0.351901957	0.23715992
P51610	HCFC1	1	726	Site	Both	-0.037	0.91819	0.08	-0.11728657	0.71631465
P51610	HCFC1	1	1239	Site	Both	-0.635	0.00841	0.08	-0.71453363	0.00381407
P51610	HCFC1	1	1238	Site	Both	-0.515	0.0296	0.08	-0.59533246	0.0125797
P51610	HCFC1	1	858	Site	Both	1.003	0.00078	0.08	0.922995735	0.00248528
P51610	HCFC1	1	1243	Site	Both	-0.598	0.01937	0.08	-0.6784639	0.00886704
P51610	HCFC1	1	861	Site	Both	0.98	0.00099	0.08	0.899963929	0.00315997
P51610	HCFC1	1	1246	Site	Both	0.2755	0.35377	0.08	0.195460153	0.60078955
P51610	HCFC1	1	607	Site	Both	-0.671	0.11674	0.08	-0.75124756	0.09202231
P51610	HCFC1	1	480	Site	Both	0.1185	0.76383	0.08	0.038521447	0.92831607
P51610	HCFC1	1	870	Site	TopSpeed	0.2606	0.25987	0.08	0.18061222	0.52815702
P51610	HCFC1	1	490	Site	Both	0.2632	0.26438	0.08	0.183249811	0.52819421
P51610	HCFC1	1	619	Site	Both	0.3695	0.1272	0.08	0.289464076	0.26010785
P51610	HCFC1	1	620	Site	Both	0.5312	0.0278	0.08	0.451180812	0.07461082
P51610	HCFC1	1	622	Site	Both	0.5038	0.03624	0.08	0.423762568	0.09810077

P51610	HCFC1	1	495	Site	Both	-0.175	0.5556	0.08	-0.2548633	0.37870029
P51610	HCFC1	1	623	Site	Both	0.5038	0.03624	0.08	0.423762568	0.09810077
P51610	HCFC1	1	496	Site	Both	-0.137	0.65436	0.08	-0.21722021	0.4378204
P51610	HCFC1	1	498	Site	Both	-0.157	0.59356	0.08	-0.23676741	0.39591243
P51610	HCFC1	1	625	Site	Both	0.5055	0.03624	0.08	0.425513215	0.09810077
P51610	HCFC1	1	1150	Site	Both	0.2297	0.34289	0.08	0.14973261	0.6241827
P52594	AGFG1	1	362	Site	Both	0.0496	0.90456	-0.11	0.159553644	0.6806514
P52594	AGFG1	1	367	Site	Both	0.0403	0.92718	-0.11	0.150349468	0.70052671
P52594	AGFG1	1	359	Site	Both	0.0624	0.87352	-0.11	0.172409555	0.65348486
P52948	NUP98	3	(3 of 1525,1538,1541, 1551,1558,1575)	Region	TopSpeed	-1.053	0.01277	0.01	-1.06334025	0.0125797
P52948	NUP98	1	(1 of 1075,1081,1082, 1083,1084,1086, 1092,1093,1096, 1099)	Region	Both	-0.193	0.73332	0.01	-0.20264149	0.71329871
P54253	ATXN1	1	22	Site	Both	-0.411	0.10095		-0.41134357	0.12136128
P54725	RAD23A	1	(1 of 123,125,128,131 ,132,133,136,13 8,140,143,144,1 46,147)	Region	TopSpeed	-0.158	0.77669	-0.02	-0.13795793	0.81593663
P54727	RAD23B	3	(3 of 81,82,87,88,91,9 5,96,97,100,101, 102,103,104,105 ,106,112,120,12 1,122,125,127,1 30,132,134,135, 141)	Region	Both	-0.281	0.33282	0.02	-0.30120122	0.34894985
P55198	MLLT6	1	412	Site	Both	0.067	0.85694		0.067015024	0.87022092
P55198	MLLT6	1	413	Site	Both	0.1993	0.48128		0.199276697	0.51295544
P55198	MLLT6	1	414	Site	Both	0.1416	0.67242		0.14160748	0.6902866
P56270	MAZ	1	(1 of 141,152,155,162 ,168,169,170,17 8)	Region	TopSpeed	-0.759	0.02553	-0.02	-0.73857424	0.03549576
P57740	NUP107	1	(1 of 64,66)	Region	TopSpeed	-0.377	0.38874	0.15	-0.52672942	0.24428434
P78312	FAM193A	1	(1 of 707,708)	Region	Both	0.374	0.12132		0.374017556	0.14474479
P78312	FAM193A	1	709	Site	Both	0.3519	0.13469		0.351885388	0.16525791
P78337	PITX1	1	195	Site	Both	0.6962	0.10288		0.696245482	0.12136128
P78337	PITX1	1	188	Site	Both	0.6962	0.10288		0.696245482	0.12136128
P78344	EIF4G2	1	(1 of 506,508,514)	Region	TopSpeed	-0.016	0.98301	-0.09	0.073868264	0.914156
P78347	GTF2I	1	202	Site	TopSpeed	-0.12	0.76383	0.08	-0.20002076	0.60078955
P80192	MAP3K9	1	118	Site	TopSpeed	-1.008	0.0162		-1.00801526	0.01783221
P82979	SARNP	1	115	Site	TopN	-0.131	0.73332	0.04	-0.17053373	0.66085936
P85037	FOXK1	1	(1 of 541,542)	Region	Both	-0.038	0.91749	-0.04	0.002149967	0.99576765

P85037	FOXK1	2	(1 of 683,686,688,689,696,697)&(2 of 682,683,686,688)	Region	Both	0.0721	0.8305	-0.04	0.112092343	0.71917436
P85037	FOXK1	1	(1 of 530,531,534)	Region	Both	-0.013	0.97926	-0.04	0.026859541	0.93373979
P85037	FOXK1	1	549	Site	Both	-0.081	0.80863	-0.04	-0.04102832	0.91674426
P85037	FOXK1	1	679	Site	Both	-0.132	0.66876	-0.04	-0.09240613	0.78573066
P85037	FOXK1	1	681	Site	Both	-0.123	0.70131	-0.04	-0.08304899	0.80455849
P85037	FOXK1	1	562	Site	Both	-0.081	0.80863	-0.04	-0.04102832	0.91674426
P85037	FOXK1	1	691	Site	Both	-0.07	0.83321	-0.04	-0.03011871	0.92831607
P85037	FOXK1	1	695	Site	Both	0.1169	0.70725	-0.04	0.156931817	0.60078955
P98082	DAB2	1	(1 of 471,473,477)	Region	Both	-0.389	0.18539	0.02	-0.40920172	0.19131351
P98082	DAB2	1	464	Site	Both	-0.283	0.33696	0.02	-0.3032347	0.3509044
Q02078	MEF2A	1	280	Site	Both	-0.002	0.99326		-0.00165042	0.99576765
Q02078	MEF2A	1	281	Site	Both	-0.013	0.97884		-0.01340033	0.97305303
Q02086	SP2	1	(1 of 187,188,189,190,191,192,196)	Region	TopSpeed	0.1105	0.85197	0.07	0.040470518	0.94241548
Q02880	TOP2B	1	(1 of 788,799,813)	Region	TopSpeed	-0.509	0.22228	0.17	-0.67905884	0.1324731
Q02880	TOP2B	1	1466	Site	TopN	-2.287	#######	0.17	-2.45715473	2.45E-07
Q04637	EIF4G1	1	61	Site	Both	-0.325	0.26722	0.01	-0.33466987	0.30324723
Q04721	NOTCH2	1	1297	Site	Both	-0.475	0.04462	-0.23	-0.24547612	0.35176469
Q04724	TLE1	1	(1 of 296,297,298)	Region	Both	0.3565	0.13039	0.65	-0.29346717	0.24697571
Q04724	TLE1	1	290	Site	Both	0.335	0.15676	0.65	-0.31496169	0.20843731
Q04724	TLE1	1	284	Site	Both	0.2881	0.22708	0.65	-0.36193576	0.16010262
Q04724	TLE1	1	286	Site	Both	0.2881	0.22708	0.65	-0.36193576	0.16010262
Q04725	TLE2	1	334	Site	Both	0.273	0.23985		0.27303963	0.28033045
Q04726	TLE3	1	289	Site	Both	-0.014	0.97865	0.34	-0.35430995	0.17519547
Q04726	TLE3	1	293	Site	Both	0.0534	0.87183	0.34	-0.28661534	0.28012236
Q04726	TLE3	1	294	Site	Both	0.0317	0.93078	0.34	-0.30826805	0.23658316
Q04726	TLE3	1	295	Site	Both	0.0055	0.98301	0.34	-0.3345212	0.1911075
Q04726	TLE3	1	328	Site	TopSpeed	0.3043	0.29634	0.34	-0.03573367	0.92831607
Q04726	TLE3	1	296	Site	Both	0.0055	0.98301	0.34	-0.3345212	0.1911075
Q04726	TLE3	1	332	Site	TopSpeed	0.3043	0.29634	0.34	-0.03573367	0.92831607
Q04726	TLE3	1	333	Site	TopSpeed	0.3043	0.29634	0.34	-0.03573367	0.92831607
Q04726	TLE3	1	286	Site	Both	0.0283	0.93512	0.34	-0.31168198	0.22599199
Q04727	TLE4	1	(1 of 334,337)&(1 of 334,340)	Region	Both	0.3727	0.11817	0.06	0.312729424	0.20838287
Q04727	TLE4	1	321	Site	Both	-0.282	0.25706	0.06	-0.3419141	0.20309052
Q04727	TLE4	1	330	Site	Both	0.3719	0.11925	0.06	0.311906841	0.20843731
Q04727	TLE4	1	298	Site	Both	0.0221	0.96705	0.06	-0.03794937	0.92831607

Q04727	TLE4	1	318	Site	Both	-0.282	0.25706	0.06	-0.3419141	0.20309052
Q04743	EMX2	1	25	Site	Both	0.6476	0.02553		0.647576092	0.02945771
Q04743	EMX2	1	20	Site	Both	0.6476	0.02553		0.647576092	0.02945771
Q06330	RBPJ	1	(1 of 465,466,473,475,477,480,482,485,486,488,489,490,492,493,494,495,497,500)	Region	TopSpeed	0.1397	0.80863	0.13	0.009707716	0.9862528
Q06546	GABPA	1	264	Site	Both	0.2288	0.52697	0.16	0.068835888	0.89452881
Q06546	GABPA	1	278	Site	Both	0.2153	0.5556	0.16	0.055276238	0.914156
Q07912	TNK2	1	817	Site	Both	0.2249	0.35734		0.224890877	0.40655976
Q07912	TNK2	1	818	Site	Both	0.1937	0.4663		0.193706048	0.49907317
Q07912	TNK2	1	823	Site	Both	0.3403	0.14159		0.340301007	0.17354814
Q08211	DHX9	1	(1 of 77,87,92,94,97,98,107,108)	Region	Both	0.3688	0.12425	-0.04	0.408797496	0.10429034
Q0D2I5	IFFO1	1	183	Site	Both	0.5817	0.04711		0.581658753	0.05209999
Q0D2I5	IFFO1	1	173	Site	Both	0.5997	0.04016		0.599662231	0.04461592
Q0D2I5	IFFO1	1	175	Site	Both	0.5994	0.04016		0.599414009	0.04461592
Q12830	BPTF	2	(2 of 2052,2056,2057,2058,2059,2060,2062,2063,2064,2065,2066,2067,2068,2070)	Region	TopN	-1E-03	0.99808	0.23	-0.23096878	0.67805155
Q12830	BPTF	3	(3 of 2338,2342,2343,2345,2346,2348,2349,2350,2351,2352,2353,2355,2356,2357,2361)	Region	TopSpeed	-0.103	0.86075	0.23	-0.33260834	0.50549352
Q12830	BPTF	1	2081	Site	TopSpeed	-0.131	0.73657	0.23	-0.36134063	0.25763321
Q12830	BPTF	1	2093	Site	Both	-0.241	0.30217	0.23	-0.47132736	0.04862263
Q12830	BPTF	1	2094	Site	Both	-0.322	0.16929	0.23	-0.55169354	0.01961629
Q12830	BPTF	1	1709	Site	Both	0.1569	0.58701	0.23	-0.07313964	0.84490759
Q12830	BPTF	1	1712	Site	Both	0.098	0.77465	0.23	-0.1319771	0.70101954
Q12830	BPTF	1	1749	Site	Both	0.1344	0.64584	0.23	-0.09560922	0.75915012
Q12830	BPTF	1	1750	Site	Both	0.1415	0.63582	0.23	-0.08851561	0.79074906
Q12830	BPTF	1	1719	Site	Both	0.098	0.77465	0.23	-0.1319771	0.70101954
Q12830	BPTF	1	1752	Site	Both	0.1153	0.71246	0.23	-0.11467676	0.70759286
Q12830	BPTF	1	1753	Site	Both	0.0825	0.7987	0.23	-0.14752854	0.63222257
Q12830	BPTF	1	1754	Site	Both	0.0308	0.93078	0.23	-0.19921989	0.48356887
Q12830	BPTF	1	1755	Site	Both	0.1055	0.73332	0.23	-0.12448369	0.69740433
Q12830	BPTF	1	2230	Site	TopSpeed	0.1124	0.77152	0.23	-0.11758757	0.76034174
Q12830	BPTF	1	2237	Site	TopSpeed	0.1124	0.77152	0.23	-0.11758757	0.76034174
Q12857	NFIA	1	270	Site	TopSpeed	-0.186	0.73332		-0.18597741	0.73706765

Q12888	TP53BP1	1	(1 of 1631,1634,1635, 1638,1640,1642, 1643,1644,1645, 1646,1647,1648, 1650)	Region	TopSpeed	-0.43	0.30656	-0.14	-0.289946	0.58728077
Q12948	FOXC1	1	(1 of 329,330,335)	Region	Both	-0.574	0.01536	-0.2	-0.37363455	0.14474479
Q12948	FOXC1	1	(1 of 487,506)	Region	TopSpeed	0.4962	0.23195	-0.2	0.696246463	0.12136128
Q12948	FOXC1	1	339	Site	Both	-0.574	0.01536	-0.2	-0.37363455	0.14474479
Q12948	FOXC1	1	340	Site	Both	-0.574	0.01536	-0.2	-0.37363455	0.14474479
Q13188	STK3	1	(1 of 329,330)	Region	TopSpeed	-1.455	0.00077	-0.11	-1.34545449	0.0023022
Q13188	STK3	1	333	Site	TopSpeed	-1.347	0.0014	-0.11	-1.23726976	0.00441517
Q13283	G3BP1	1	(1 of 230,231,232,241)	Region	TopSpeed	-0.04	0.92796	-0.01	-0.03000793	0.94022854
Q13310	PABPC4	1	(1 of 643,644)	Region	Both	-0.058	0.86075	-0.07	0.0122177	0.9764823
Q13492	PICALM	1	297	Site	Both	-0.377	0.38874	-0.2	-0.17673113	0.75024933
Q14008	CKAP5	1	(1 of 1898,1899,1900, 1901,1904,1910, 1914,1916,1917, 1918,1920,1921, 1925,1933)	Region	TopSpeed	0.2384	0.46631	0.13	0.108356034	0.7935387
Q14119	VEZF1	1	110	Site	Both	0.3102	0.19579		0.310173439	0.22504717
Q14119	VEZF1	1	117	Site	Both	0.2598	0.28478		0.259826876	0.34122004
Q14119	VEZF1	1	118	Site	Both	0.2598	0.28478		0.259826876	0.34122004
Q14119	VEZF1	1	111	Site	Both	0.2505	0.30747		0.250510396	0.35793478
Q14157	UBAP2L	1	(1 of 291,293,294,299 ,300,305,309,31 7,319)	Region	TopSpeed	0.0799	0.8926	-0.07	0.149872023	0.79526178
Q14157	UBAP2L	1	(1 of 260,262,265,266 ,275,277)	Region	TopN	-0.047	0.94008	-0.07	0.023360684	0.97340685
Q14157	UBAP2L	1	(1 of 852,855,859,863)	Region	TopSpeed	-0.005	0.98673	-0.07	0.065277072	0.89043821
Q14157	UBAP2L	1	453	Site	Both	-0.111	0.73038	-0.07	-0.04129292	0.914156
Q14157	UBAP2L	1	454	Site	Both	-0.901	0.02821	-0.07	-0.83100091	0.04891006
Q14157	UBAP2L	1	783	Site	TopN	-0.466	0.25945	-0.07	-0.39571021	0.40541964
Q14157	UBAP2L	1	439	Site	Both	-0.953	0.01761	-0.07	-0.88286676	0.03189479
Q14157	UBAP2L	1	444	Site	Both	-0.165	0.53663	-0.07	-0.09534715	0.7587687
Q14157	UBAP2L	1	445	Site	Both	-0.938	0.01956	-0.07	-0.86839374	0.03735066
Q14157	UBAP2L	1	446	Site	Both	-0.147	0.60052	-0.07	-0.07656378	0.81593663
Q14247	CTTN	1	344	Site	TopN	0.0346	0.96144	0.03	0.004593925	0.99576765
Q14444	CAPRIN1	1	(1 of 478,479)	Region	Both	-0.323	0.40787	-0.05	-0.27296242	0.55702358
Q14444	CAPRIN1	1	497	Site	Both	-0.323	0.40787	-0.05	-0.27296242	0.55702358
Q14657	LAGE3	1	142	Site	Both	0.1582	0.56379	-0.16	0.318215114	0.20309052

Q14671	PUM1	1	(1 of 797,799,800,802,803,806,808,809,810,813,814,815)	Region	TopSpeed	0.0708	0.84614	0.14	-0.06915149	0.86428932
Q14684	RRP1B	1	736	Site	TopSpeed	0.2675	0.59117	0.09	0.177464549	0.74875917
Q14684	RRP1B	1	731	Site	TopSpeed	0.1014	0.86086	0.09	0.011404101	0.98322904
Q14684	RRP1B	1	735	Site	TopSpeed	0.2675	0.59117	0.09	0.177464549	0.74875917
Q14686	NCOA6	1	(1 of 1772,1777,1778,1783,1786,1787,1789,1790,1791,1794,1798,1800,1803,1804)	Region	Both	0.0146	0.97926	0.16	-0.14535495	0.70754983
Q14686	NCOA6	1	1641	Site	Both	-0.042	0.90087	0.16	-0.20192891	0.47797702
Q14686	NCOA6	1	1107	Site	TopSpeed	0.5935	0.15848	0.16	0.433475824	0.35176469
Q14686	NCOA6	1	1933	Site	Both	0.2269	0.38695	0.16	0.06692767	0.86428932
Q14686	NCOA6	1	1649	Site	Both	-0.033	0.92795	0.16	-0.19321073	0.49907317
Q14966	ZNF638	1	789	Site	Both	-0.005	0.98673	0.1	-0.10542768	0.7935387
Q14980	NUMA1	1	(1 of 2092,2093,2094,2096,2099,2106)	Region	Both	0.3852	0.18604	-0.1	0.485151346	0.12136128
Q14980	NUMA1	1	1844	Site	TopSpeed	-0.342	0.14074	-0.1	-0.24219947	0.35176469
Q15059	BRD3	1	(1 of 248,249,250,252,253,254,257,259)	Region	TopSpeed	0.2495	0.63227	0.33	-0.08050699	0.90986391
Q15061	WDR43	1	390	Site	TopSpeed	0.0357	0.96038	-0.05	0.085674292	0.90457041
Q15233	NONO	1	(1 of 410,418,424,428,431,432)	Region	TopSpeed	0.2766	0.57065	0	0.276649165	0.60078955
Q15418	RPS6KA1	1	734	Site	TopSpeed	0.3029	0.52697	0.19	0.112863293	0.86428932
Q15637	SF1	1	328	Site	Both	0.0594	0.86086	0.01	0.04941044	0.90473946
Q15637	SF1	1	331	Site	Both	0.088	0.78918	0.01	0.077975206	0.83189333
Q15637	SF1	1	333	Site	Both	0.0123	0.97926	0.01	0.002251456	0.99576765
Q15637	SF1	1	337	Site	Both	0.0978	0.75877	0.01	0.087787714	0.7898207
Q15637	SF1	1	338	Site	Both	0.0054	0.98301	0.01	-0.00463028	0.98815648
Q15637	SF1	1	342	Site	Both	-0.075	0.81814	0.01	-0.08514038	0.79704572
Q15637	SF1	1	315	Site	Both	0.1932	0.44818	0.01	0.183198879	0.51842158
Q15652	JMJD1C	1	1457	Site	Both	-0.298	0.20372	-0.1	-0.19766751	0.46976784
Q15652	JMJD1C	1	650	Site	TopSpeed	-1.498	0.00059	-0.1	-1.39831188	0.00147127
Q15652	JMJD1C	1	1453	Site	Both	-0.292	0.21005	-0.1	-0.19160086	0.48891404
Q15654	TRIP6	1	(1 of 133,135,142,147,153,156,158,159,161,162)	Region	TopSpeed	0.497	0.23195	0.31	0.186981288	0.73658347
Q15723	ELF2	1	378	Site	Both	0.2465	0.30448	0.03	0.216484188	0.43085957
Q15723	ELF2	1	380	Site	Both	0.2899	0.21821	0.03	0.259881991	0.31836649

Q15723	ELF2	1	374	Site	Both	0.2899	0.21821	0.03	0.259881991	0.31836649
Q15723	ELF2	1	375	Site	Both	0.2752	0.23985	0.03	0.245194097	0.3509044
Q15750	TAB1	1	(1 of 399,400)	Region	Both	-0.061	0.87667	-0.03	-0.03127127	0.93471134
Q15750	TAB1	1	395	Site	Both	-0.072	0.86075	-0.03	-0.04154887	0.92511993
Q15750	TAB1	1	396	Site	Both	-0.072	0.86075	-0.03	-0.04154887	0.92511993
Q15942	ZYX	1	170	Site	Both	-0.099	0.76383	0.22	-0.31880081	0.22504717
Q15942	ZYX	1	169	Site	Both	-0.099	0.76383	0.22	-0.31880081	0.22504717
Q15942	ZYX	1	258	Site	Both	0.0285	0.93452	0.22	-0.19151173	0.49566768
Q16186	ADRM1	1	225	Site	Both	-0.268	0.31873	-0.28	0.012099766	0.97877402
Q16186	ADRM1	1	213	Site	Both	-0.528	0.02433	-0.28	-0.24806466	0.3467146
Q16186	ADRM1	1	217	Site	Both	-0.235	0.32056	-0.28	0.045423283	0.90986391
Q16186	ADRM1	1	219	Site	Both	-0.271	0.25385	-0.28	0.009461637	0.97975
Q16186	ADRM1	1	221	Site	Both	-0.291	0.23987	-0.28	-0.011301	0.97877402
Q16186	ADRM1	1	222	Site	Both	-0.185	0.50057	-0.28	0.095410027	0.76863976
Q16204	CCDC6	1	(1 of 349,351,352,357,359,361,362,363)	Region	TopSpeed	0.17	0.76319	-0.12	0.289971045	0.58728077
Q2KHR2	RFX7	1	342	Site	Both	0.1635	0.54815		0.163453229	0.58728077
Q2KHR3	QSER1	1	(1 of 1263,1271,1272,1274,1277,1278,1280,1282,1283,1284,1285,1286,1287)	Region	TopSpeed	0.2013	0.54815	-0.05	0.251299495	0.45686225
Q2KHR3	QSER1	1	290	Site	Both	-0.429	0.16065	-0.05	-0.37853671	0.2501051
Q2KHR3	QSER1	1	105	Site	Both	0.0694	0.83511	-0.05	0.119353487	0.70495902
Q2KHR3	QSER1	1	558	Site	Both	-0.095	0.81411	-0.05	-0.04543834	0.92229001
Q2KHR3	QSER1	1	1270	Site	TopSpeed	0.2013	0.54815	-0.05	0.251299495	0.45686225
Q2KHR3	QSER1	1	282	Site	Both	-0.429	0.16065	-0.05	-0.37853671	0.2501051
Q2KHR3	QSER1	1	284	Site	Both	-0.429	0.16065	-0.05	-0.37853671	0.2501051
Q2KHR3	QSER1	1	285	Site	Both	-0.429	0.16065	-0.05	-0.37853671	0.2501051
Q2M2I8	AAK1	1	360	Site	TopSpeed	-0.175	0.63582	-0.21	0.034998897	0.92993035
Q2M2I8	AAK1	1	359	Site	TopSpeed	-0.175	0.63582	-0.21	0.034998897	0.92993035
Q2Q1W2	TRIM71	1	163	Site	TopSpeed	0.1488	0.78918		0.148784548	0.79694509
Q2TAL8	QRICH1	1	364	Site	TopSpeed	0.2439	0.30048	0.16	0.083921264	0.79609599
Q495X7	TRIM60	1	465	Site	TopSpeed	0.1679	0.76383		0.167890106	0.76207249
Q4KMP7	TBC1D10B	1	51	Site	Both	0.0068	0.98301	-0.05	0.05684767	0.88132546
Q4KMP7	TBC1D10B	1	43	Site	Both	0.0068	0.98301	-0.05	0.05684767	0.88132546
Q4KMP7	TBC1D10B	1	46	Site	Both	0.0068	0.98301	-0.05	0.05684767	0.88132546
Q4VCS5	AMOT	1	(1 of 182,185,186)	Region	TopN	-0.163	0.76996	0.36	-0.52260377	0.24840102
Q4VCS5	AMOT	1	195	Site	Both	0.4556	0.05342	0.36	0.095550495	0.7592459
Q4VCS5	AMOT	1	196	Site	Both	0.4136	0.08262	0.36	0.053646884	0.88767054
Q4VCS5	AMOT	1	774	Site	Both	0.6213	0.01516	0.36	0.261314361	0.35629934
Q4VCS5	AMOT	1	776	Site	Both	0.3611	0.1303	0.36	0.001075253	0.99722698

Q4VCS5	AMOT	1	780	Site	Both	0.4024	0.08938	0.36	0.042400415	0.91220682
Q4VCS5	AMOT	1	274	Site	Both	0.5964	0.01486	0.36	0.236427738	0.39128449
Q52LR7	EPC2	1	750	Site	Both	0.1384	0.73082		0.138400527	0.72107369
Q5H9F3	BCORL1	1	(1 of 529,530,532,534,535,536,537,551,552,555,557)	Region	Both	0.3228	0.29634	0.31	0.01279594	0.97975
Q5H9F3	BCORL1	1	133	Site	Both	-0.178	0.51686	0.31	-0.4875276	0.04862263
Q5H9F3	BCORL1	1	127	Site	Both	-0.123	0.68431	0.31	-0.43278712	0.07751725
Q5HYC2	KIAA2026	1	1452	Site	Both	0.0878	0.78632		0.087775176	0.79409661
Q5HYW2	NHSL2	1	350	Site	Both	0.2113	0.40866		0.211293614	0.45686225
Q5JSZ5	PRRC2B	1	(1 of 1984,1990)	Region	Both	-0.122	0.73332	-0.06	-0.06159262	0.88667585
Q5JSZ5	PRRC2B	1	1793	Site	Both	-0.194	0.43956	-0.06	-0.13436017	0.66352405
Q5JSZ5	PRRC2B	1	1796	Site	Both	-0.212	0.38951	-0.06	-0.15212105	0.61468324
Q5JSZ5	PRRC2B	1	1801	Site	Both	-0.181	0.49928	-0.06	-0.12141756	0.70101954
Q5JSZ5	PRRC2B	1	1808	Site	Both	-0.169	0.52811	-0.06	-0.10917434	0.72451182
Q5JSZ5	PRRC2B	1	1982	Site	Both	-0.122	0.73332	-0.06	-0.06159262	0.88667585
Q5JTW2	CEP78	1	(1 of 615,621,622,628,629,630,638)	Region	Both	-0.189	0.59117	-0.08	-0.10919225	0.79074906
Q5SW79	CEP170	1	1165	Site	TopN	-0.397	0.35377	-0.04	-0.35679226	0.46658124
Q5SW79	CEP170	1	1331	Site	Both	0.2536	0.29634	-0.04	0.293566484	0.25763321
Q5SW79	CEP170	1	1339	Site	Both	0.1937	0.4579	-0.04	0.233670095	0.38842528
Q5SW79	CEP170	1	1342	Site	Both	0.212	0.38941	-0.04	0.252042736	0.34100654
Q5SW79	CEP170	1	1343	Site	Both	0.2239	0.35377	-0.04	0.263914465	0.3122305
Q5T0B9	ZNF362	1	(1 of 217,220)	Region	TopSpeed			0.08		
Q5T0B9	ZNF362	4	(3 of 140,142,143,144,146,147,149,150,151,152,154)&(2 of 133,147,149,150)&(2 of 132,133,140,142,143,149)&(1 of 124,126,128,129,130,132,133,140,142,143,144,146,147,149,150,151,152,154)&(2 of 128,129,130,132,133,140,142,143)	Region	Both	0.3051	0.20318	0.08	0.225136019	0.40541964
Q5T0B9	ZNF362	1	(1 of 114,116)	Region	Both	0.2145	0.39149	0.08	0.134514909	0.67158708
Q5T0B9	ZNF362	1	408	Site	TopSpeed	0.6753	0.00462	0.08	0.595330914	0.01331913
Q5T0B9	ZNF362	1	113	Site	Both	0.2145	0.39149	0.08	0.134514909	0.67158708
Q5T0B9	ZNF362	1	138	Site	Both	0.4046	0.09528	0.08	0.324578479	0.20309052
Q5T1R4	HIVEP3	1	1401	Site	TopSpeed	0.2054	0.714		0.205363179	0.70759286

Q5T6F2	UBAP2	1	(1 of 789,790)	Region	TopSpeed	-0.198	0.73082	-0.02	-0.17753928	0.74875917
Q5T6F2	UBAP2	1	(1 of 519,526,530,543,546,548,552,555,556,559,565,568)	Region	Both	-0.511	0.22228	-0.02	-0.49123341	0.28012236
Q5T6F2	UBAP2	1	1006	Site	Both	0.0851	0.81444	-0.02	0.105138382	0.76243442
Q5T8P6	RBM26	1	691	Site	TopSpeed	-0.008	0.98301	0.08	-0.08788229	0.84495868
Q5T8P6	RBM26	1	692	Site	TopSpeed	-0.008	0.98301	0.08	-0.08788229	0.84495868
Q5VT52	RPRD2	1	(1 of 1233,1237,1241,1245)	Region	TopSpeed	0.1596	0.77465	0.08	0.079589268	0.90986391
Q5VT52	RPRD2	1	417	Site	Both	0.2186	0.38512	0.08	0.138568457	0.66528784
Q5VT52	RPRD2	1	422	Site	Both	0.2404	0.32626	0.08	0.160422834	0.60078955
Q5VT52	RPRD2	1	424	Site	Both	0.1164	0.73394	0.08	0.036407995	0.92657403
Q5VT52	RPRD2	1	396	Site	Both	0.1359	0.73082	0.08	0.055891788	0.90986391
Q5VT52	RPRD2	1	399	Site	Both	0.1359	0.73082	0.08	0.055891788	0.90986391
Q5VT52	RPRD2	1	593	Site	Both	-0.032	0.93078	0.08	-0.11234665	0.72645216
Q5VT52	RPRD2	1	596	Site	Both	-0.151	0.60052	0.08	-0.23104754	0.39591243
Q5VT52	RPRD2	1	597	Site	Both	-0.103	0.74963	0.08	-0.18284874	0.53246758
Q5VT52	RPRD2	1	404	Site	Both	-0.036	0.93284	0.08	-0.11591152	0.76243442
Q5VT52	RPRD2	1	407	Site	Both	-0.036	0.93284	0.08	-0.11591152	0.76243442
Q5VT52	RPRD2	1	602	Site	Both	-0.003	0.98679	0.08	-0.08342374	0.8081101
Q5VT52	RPRD2	1	603	Site	Both	0.004	0.98673	0.08	-0.07602774	0.83417348
Q5VT52	RPRD2	1	604	Site	Both	-0.032	0.93078	0.08	-0.11234665	0.72645216
Q5VT52	RPRD2	1	414	Site	Both	0.1112	0.75105	0.08	0.031195672	0.92993035
Q5VT52	RPRD2	1	415	Site	Both	0.0678	0.85197	0.08	-0.01218549	0.97846125
Q5VWN6	TASOR2	1	1097	Site	Both	-0.325	0.20701	0.27	-0.59517233	0.02357941
Q5VWN6	TASOR2	1	1098	Site	Both	-0.325	0.20701	0.27	-0.59517233	0.02357941
Q5VWN6	TASOR2	1	1099	Site	Both	-0.274	0.2807	0.27	-0.54438843	0.03735066
Q5VWN6	TASOR2	1	1593	Site	TopSpeed	-0.011	0.98301	0.27	-0.28111704	0.60078955
Q5VWN6	TASOR2	1	1595	Site	TopSpeed	-0.011	0.98301	0.27	-0.28111704	0.60078955
Q5VWN6	TASOR2	1	1150	Site	Both	0.2715	0.24375	0.27	0.001529204	0.99576765
Q5XG87	TENT4A	1	769	Site	TopSpeed	0.4079	0.33696		0.407925417	0.39128449
Q66K74	MAP1S	1	(1 of 782,785,786,788,790,793,795,797,809,813)	Region	Both	0.2788	0.56699	0.04	0.238770451	0.6680228
Q6AI39	BICRAL	1	590	Site	TopSpeed	-0.171	0.76133		-0.17127397	0.7587687
Q6MZP7	LIN54	1	106	Site	Both	-0.268	0.40384	-0.38	0.11152646	0.7935387
Q6MZP7	LIN54	1	235	Site	Both	-0.335	0.24557	-0.38	0.0454572	0.92229001
Q6MZP7	LIN54	1	238	Site	Both	-0.335	0.24557	-0.38	0.0454572	0.92229001
Q6MZP7	LIN54	1	243	Site	Both	-0.335	0.24557	-0.38	0.0454572	0.92229001
Q6MZP7	LIN54	1	276	Site	TopSpeed	-0.326	0.16736	-0.38	0.053825184	0.88767054

Q6P3W7	SCYL2	1	(1 of 720,722,728,729,731,732,734,736,737)	Region	Both	-0.113	0.77943	-0.06	-0.05272944	0.91559759
Q6P3W7	SCYL2	1	(1 of 740,741,743,744,745,747,748,751,759,760,762,765)	Region	TopSpeed	0.0607	0.92396	-0.06	0.120715705	0.85339519
Q6P4R8	NFRKB	1	1156	Site	Both	0.5752	0.01536	0.26	0.315203657	0.21242528
Q6P4R8	NFRKB	1	1030	Site	Both	-0.108	0.7819	0.26	-0.36757368	0.24697571
Q6P4R8	NFRKB	1	841	Site	TopN	-0.195	0.73082	0.26	-0.4552252	0.32647628
Q6P4R8	NFRKB	1	1291	Site	Both	0.0816	0.79813	0.26	-0.17841293	0.53711129
Q6P4R8	NFRKB	1	750	Site	Both	0.109	0.77943	0.26	-0.15095742	0.70101954
Q6P4R8	NFRKB	1	1141	Site	Both	0.4387	0.0892	0.26	0.178715654	0.58384107
Q6P4R8	NFRKB	1	1174	Site	Both	0.1838	0.59754	0.26	-0.07621936	0.86597032
Q6P4R8	NFRKB	1	1051	Site	TopSpeed	0.3691	0.39948	0.26	0.10911518	0.86597032
Q6P4R8	NFRKB	1	863	Site	TopN	-0.522	0.21204	0.26	-0.78227365	0.07461082
Q6PJT7	ZC3H14	1	(1 of 734,735)	Region	TopSpeed	0.4856	0.24051	0.15	0.33562007	0.49907317
Q6PJT7	ZC3H14	1	360	Site	TopSpeed	-0.008	0.98301	0.15	-0.15807985	0.68490254
Q6PJT7	ZC3H14	1	370	Site	Both	0.2756	0.24051	0.15	0.125626215	0.69526006
Q6PJT7	ZC3H14	1	365	Site	TopSpeed	0.1493	0.70431	0.15	-0.00068618	0.9980702
Q6PJT7	ZC3H14	1	374	Site	Both	0.3142	0.19504	0.15	0.164151668	0.59767111
Q6UN15	FIP1L1	1	253	Site	Both	-0.053	0.87051	0.22	-0.27291121	0.29540703
Q6UN15	FIP1L1	1	205	Site	Both	0.0272	0.93687	0.22	-0.19278331	0.49521567
Q6UN15	FIP1L1	1	206	Site	Both	-0.083	0.81019	0.22	-0.302619	0.25580836
Q6UN15	FIP1L1	1	207	Site	Both	-0.03	0.93452	0.22	-0.25037488	0.38169817
Q6VMQ6	ATF7IP	1	(1 of 706,708,712,715,719,721,722,723,727,733,734)	Region	TopSpeed	-0.034	0.94008	0.31	-0.34352819	0.29975916
Q6VMQ6	ATF7IP	1	(1 of 994,995,996)	Region	Both	0.3748	0.11664	0.31	0.064792775	0.86388013
Q6VMQ6	ATF7IP	1	992	Site	Both	0.2009	0.43056	0.31	-0.10910307	0.72881104
Q6VMQ6	ATF7IP	1	988	Site	Both	0.3705	0.14583	0.31	0.060524105	0.88578642
Q6W2J9	BCOR	1	453	Site	TopSpeed	0.5666	0.178	0.54	0.026614377	0.97001968
Q6W2J9	BCOR	1	366	Site	TopSpeed	0.3234	0.49198	0.54	-0.21658578	0.70052671
Q6Y7W6	GIGYF2	1	678	Site	Both	0.142	0.637	0.02	0.122002635	0.70495902
Q6ZNB6	NFXL1	1	41	Site	TopSpeed	0.1318	0.81619	-0.08	0.211833489	0.70495902
Q6ZNB6	NFXL1	1	228	Site	TopSpeed	-1.348	0.0014	-0.08	-1.26814054	0.00360272
Q6ZNB6	NFXL1	1	230	Site	TopSpeed	-1.348	0.0014	-0.08	-1.26814054	0.00360272
Q6ZQY2	LRRC74B	1	294	Site	TopN	0.2277	0.66876		0.227721626	0.68490254
Q6ZRI6	C15orf39	1	635	Site	Both	0.3232	0.18108	0.75	-0.4267629	0.09810077
Q6ZRS2	SRCAP	1	(1 of 2406,2412,2416,2420)	Region	TopSpeed	0.1551	0.77943	0.13	0.025058424	0.9722008
Q6ZU65	UBN2	1	1008	Site	Both	0.4536	0.05551	0.11	0.343630448	0.17519547

Q6ZU65	UBN2	1	1011	Site	Both	0.2732	0.24051	0.11	0.163174049	0.58728077
Q6ZU65	UBN2	1	1007	Site	Both	0.4331	0.06881	0.11	0.323101849	0.20197226
Q6ZW76	ANKS3	1	329	Site	TopN	0.1085	0.85398		0.108496341	0.86597032
Q6ZW76	ANKS3	1	333	Site	TopN	0.1085	0.85398		0.108496341	0.86597032
Q70E73	RAPH1	1	(1 of 805,807)	Region	Both	-0.056	0.86134	-0.03	-0.02557883	0.93373979
Q70E73	RAPH1	1	793	Site	Both	-0.056	0.86134	-0.03	-0.02557883	0.93373979
Q7KZ85	SUPT6H	1	1526	Site	Both	-0.221	0.37192	0.12	-0.34080978	0.18417863
Q7LBC6	KDM3B	1	(1 of 425,426)	Region	TopSpeed	0.1781	0.51124	0.14	0.038103145	0.92229001
Q7LBC6	KDM3B	1	1284	Site	TopSpeed	0.5537	0.18604	0.14	0.413742791	0.38169817
Q7LBC6	KDM3B	1	428	Site	TopSpeed	0.1781	0.51124	0.14	0.038103145	0.92229001
Q7LBC6	KDM3B	1	429	Site	TopSpeed	0.1781	0.51124	0.14	0.038103145	0.92229001
Q7Z3K3	POGZ	1	(1 of 361,362,363)	Region	Both	-0.118	0.84328	0.05	-0.16792283	0.76207249
Q7Z3K3	POGZ	1	(1 of 289,292,297,300,303)	Region	TopN	-0.741	0.08254	0.05	-0.79103418	0.07186233
Q7Z3K3	POGZ	1	(1 of 251,252,254,255,256,257,258,260,262,265,266,274,278,281,282)	Region	Both	-0.056	0.86086	0.05	-0.1062941	0.73229249
Q7Z3K3	POGZ	1	(1 of 699,703,704,707,710,719,720,721)	Region	Both	-0.127	0.66876	0.05	-0.17703816	0.53670439
Q7Z3K3	POGZ	1	434	Site	Both	-0.206	0.40049	0.05	-0.25575525	0.32395753
Q7Z3K3	POGZ	1	310	Site	TopSpeed	0.2674	0.59117	0.05	0.217382335	0.70052671
Q7Z417	NUFIP2	1	(1 of 374,376)	Region	Both	-0.371	0.13469	-0.17	-0.20053647	0.49565552
Q7Z417	NUFIP2	1	(1 of 382,384,385,386,387)&(1 of 384,385,386,387,390,392,394,395)	Region	Both	-0.371	0.13469	-0.17	-0.20053647	0.49565552
Q7Z417	NUFIP2	1	(1 of 408,410,411,415,423,437,438,442,444,447,448,450,452,458,460,461)	Region	TopN	-0.403	0.34289	-0.17	-0.23267705	0.67324247
Q7Z417	NUFIP2	1	380	Site	Both	-0.371	0.13469	-0.17	-0.20053647	0.49565552
Q7Z417	NUFIP2	1	396	Site	Both	-0.371	0.13469	-0.17	-0.20053647	0.49565552
Q7Z434	MAVS	1	(1 of 300,301,307)	Region	TopSpeed	-0.212	0.53065	-0.02	-0.19190006	0.60978896
Q7Z434	MAVS	1	354	Site	TopSpeed	0.0708	0.86086	-0.02	0.090798301	0.83417348
Q7Z434	MAVS	1	366	Site	Both	-0.103	0.79071	-0.02	-0.08282834	0.85736486
Q7Z460	CLASP1	1	578	Site	Both	-0.884	0.00235	-0.07	-0.81430515	0.00616466
Q7Z589	EMSY	1	(1 of 504,506)	Region	Both	-0.357	0.42251		-0.3569155	0.46658124
Q7Z589	EMSY	1	1120	Site	Both	-0.239	0.30656		-0.23943881	0.35679661
Q7Z589	EMSY	1	228	Site	Both	0.0032	0.98679		0.003197988	0.99342364

Q7Z589	EMSY	1	236	Site	TopSpeed	0.0299	0.93131		0.029862092	0.92831607
Q7Z589	EMSY	1	557	Site	Both	-0.078	0.84967		-0.07797854	0.86428932
Q7Z589	EMSY	1	534	Site	Both	0.1462	0.70431		0.146202259	0.70495902
Q7Z589	EMSY	1	535	Site	Both	0.1462	0.70431		0.146202259	0.70495902
Q7Z589	EMSY	1	502	Site	Both	-0.357	0.42251		-0.3569155	0.46658124
Q7Z589	EMSY	1	541	Site	Both	0.1462	0.70431		0.146202259	0.70495902
Q7Z6E9	RBBP6	1	98	Site	Both	-0.141	0.73082	0.03	-0.17056606	0.6680228
Q7Z6E9	RBBP6	1	99	Site	Both	-0.141	0.73082	0.03	-0.17056606	0.6680228
Q7Z6E9	RBBP6	1	92	Site	Both	-0.011	0.98301	0.03	-0.04079606	0.92831607
Q7Z6J0	SH3RF1	1	520	Site	Both	-0.331	0.16909	0.18	-0.51110069	0.03740923
Q7Z6J0	SH3RF1	1	505	Site	Both	-0.014	0.97926	0.18	-0.19356928	0.60078955
Q7Z6J0	SH3RF1	1	524	Site	Both	-0.486	0.04016	0.18	-0.66604472	0.00616466
Q7Z6J0	SH3RF1	1	519	Site	Both	-0.902	0.00059	0.18	-1.08181964	4.41E-05
Q7Z6Z7	HUWE1	2	(2 of 2764,2768,2773, 2776,2789,2796, 2797,2798)	Region	TopSpeed	0.1153	0.84725	0.05	0.065260979	0.92229001
Q7Z6Z7	HUWE1	1	2922	Site	Both	-0.364	0.13469	0.05	-0.41436267	0.11121166
Q7Z6Z7	HUWE1	1	2923	Site	Both	-0.299	0.22128	0.05	-0.34910488	0.18417863
Q7Z6Z7	HUWE1	1	2926	Site	Both	-0.308	0.20879	0.05	-0.35771159	0.17421552
Q7Z6Z7	HUWE1	1	2927	Site	Both	-0.301	0.22067	0.05	-0.35143401	0.18417863
Q7Z739	YTHDF3	1	(1 of 218,219)	Region	Both	0.0077	0.98301	0.02	-0.01228336	0.9772446
Q7Z739	YTHDF3	1	229	Site	Both	0.0265	0.94045	0.02	0.006549465	0.98322904
Q7Z739	YTHDF3	1	230	Site	Both	-0.086	0.78918	0.02	-0.10582048	0.73706765
Q7Z739	YTHDF3	1	201	Site	Both	0.1645	0.53987	0.02	0.144467134	0.62887819
Q7Z739	YTHDF3	1	205	Site	Both	0.2045	0.40698	0.02	0.184501355	0.51191244
Q7Z739	YTHDF3	1	213	Site	Both	0.0372	0.91819	0.02	0.017150554	0.96482269
Q7Z739	YTHDF3	1	215	Site	Both	0.0739	0.82577	0.02	0.053877895	0.89043821
Q7Z7K6	CENPV	1	98	Site	TopN	0.1384	0.81019	0.32	-0.18164787	0.74475012
Q86UE4	MTDH	1	(1 of 492,494,495,496)	Region	Both	-0.292	0.31873	0.19	-0.48153162	0.12183743
Q86UP3	ZFHX4	1	(1 of 2698,2699,2705, 2706,2708,2709, 2712)	Region	TopN	0.1555	0.77943	-0.03	0.185533945	0.73706765
Q86V15	CASZ1	1	(1 of 1067,1074,1078, 1085,1086,1093, 1094,1096,1098, 1099,1106,1109, 1112,1113,1115)	Region	Both	0.2597	0.39149	-0.16	0.419742063	0.1821957
Q86XN7	PROSER1	1	609	Site	TopSpeed	0.0923	0.81489	-0.26	0.352287383	0.2560924
Q86XN7	PROSER1	1	612	Site	TopSpeed	0.0923	0.81489	-0.26	0.352287383	0.2560924
Q86YP4	GATAD2A	1	581	Site	TopSpeed	0.124	0.83321	0.34	-0.21599559	0.70101954
Q86YP4	GATAD2A	1	329	Site	Both	-0.061	0.85694	0.34	-0.40135119	0.12136128

Q86YP4	GATAD2A	1	330	Site	Both	-0.061	0.85694	0.34	-0.40135119	0.12136128
Q86YP4	GATAD2A	1	333	Site	Both	-0.077	0.81489	0.34	-0.41655141	0.10496422
Q86YP4	GATAD2A	1	625	Site	Both	0.3122	0.19504	0.34	-0.02775749	0.93096088
Q86YP4	GATAD2A	1	210	Site	Both	-0.37	0.20372	0.34	-0.70957332	0.01539257
Q86YP4	GATAD2A	1	340	Site	Both	-0.077	0.81489	0.34	-0.41655141	0.10496422
Q86YP4	GATAD2A	1	217	Site	Both	-0.37	0.20372	0.34	-0.70957332	0.01539257
Q86Z02	HIPK1	1	(1 of 947,948,950)	Region	TopSpeed	0.0853	0.88252		0.085306253	0.90473946
Q86Z02	HIPK1	2	(1 of 670,696,700,703,705,711,718,720,728,730)&(2 of 696,700,703,705,711,718,720)	Region	Both	0.1411	0.72438		0.141139318	0.71533959
Q8IVW6	ARID3B	1	(1 of 556,557)	Region	Both	-0.664	0.00462	-0.51	-0.15441615	0.60078955
Q8IVW6	ARID3B	1	408	Site	TopSpeed	-0.341	0.14894	-0.51	0.168626857	0.57766052
Q8IVW6	ARID3B	1	560	Site	Both	-0.664	0.00462	-0.51	-0.15441615	0.60078955
Q8IVW6	ARID3B	1	395	Site	Both	-0.384	0.19579	-0.51	0.126193744	0.74875917
Q8IVW6	ARID3B	1	558	Site	Both	-0.664	0.00462	-0.51	-0.15441615	0.60078955
Q8IWB9	TEX2	1	(1 of 181,184)	Region	Both	-0.545	0.06263	-0.36	-0.18456821	0.62022567
Q8IWB9	TEX2	1	(1 of 178,179)	Region	Both	-0.572	0.05158	-0.36	-0.21184813	0.56131209
Q8IWB9	TEX2	1	180	Site	Both	-0.572	0.05158	-0.36	-0.21184813	0.56131209
Q8IWB9	TEX2	1	175	Site	Both	-0.545	0.06263	-0.36	-0.18456821	0.62022567
Q8IWI9	MGA	2	(2 of 1663,1664,1667,1668,1672)	Region	Both	0.3624	0.1272	0.21	0.152406249	0.61326319
Q8IWI9	MGA	1	1561	Site	Both	0.3109	0.20372	0.21	0.100915223	0.75674684
Q8IWI9	MGA	1	1557	Site	Both	0.3138	0.20146	0.21	0.103780668	0.74875917
Q8IWI9	MGA	1	1911	Site	Both	0.2567	0.27988	0.21	0.046687697	0.90986391
Q8IWP9	CCDC28A	1	(1 of 271,272,274)	Region	TopSpeed	0.5646	0.17833		0.564613462	0.203931
Q8IWX8	CHERP	1	(1 of 373,374)	Region	Both	0.2029	0.51124	0.03	0.172925688	0.62172767
Q8IWX8	CHERP	1	379	Site	Both	0.1596	0.637	0.03	0.129616574	0.71678949
Q8IWY8	ZSCAN29	1	(1 of 483,495)	Region	Both	0.1007	0.86086		0.100747737	0.88132546
Q8IWZ3	ANKHD1	2	(2 of 58,59,64,66)	Region	TopSpeed	-1.008	0.0162	0.05	-1.05766805	0.0125797
Q8IWZ3	ANKHD1	1	1813	Site	TopSpeed	0.9498	0.02427	0.05	0.899809573	0.03735066
Q8IWZ8	SUGP1	1	118	Site	Both	-0.387	0.18539	-0.1	-0.28730897	0.38360195
Q8IWZ8	SUGP1	1	108	Site	Both	-0.454	0.12565	-0.1	-0.3540138	0.25904595
Q8IWZ8	SUGP1	1	102	Site	Both	-0.395	0.17707	-0.1	-0.29516795	0.36539083
Q8IWZ8	SUGP1	1	103	Site	Both	-0.395	0.17707	-0.1	-0.29516795	0.36539083
Q8IX15	HOMEZ	1	291	Site	TopSpeed	-0.135	0.81444	-0.07	-0.06526393	0.92229001
Q8IZ21	PHACTR4	1	202	Site	Both	0.556	0.07405	-0.09	0.64600931	0.04036339
Q8IZ21	PHACTR4	1	203	Site	Both	0.556	0.07405	-0.09	0.64600931	0.04036339
Q8IZ21	PHACTR4	1	205	Site	Both	0.556	0.07405	-0.09	0.64600931	0.04036339
Q8IZ21	PHACTR4	1	206	Site	Both	0.556	0.07405	-0.09	0.64600931	0.04036339

Q8IZ21	PHACTR4	1	215	Site	Both	0.7063	0.02433	-0.09	0.796309128	0.0125797
Q8N122	RPTOR	1	696	Site	Both	-0.084	0.83909	-0.04	-0.04354863	0.92511993
Q8N122	RPTOR	1	700	Site	Both	-0.077	0.85197	-0.04	-0.03710292	0.92831607
Q8N122	RPTOR	1	704	Site	Both	-0.093	0.81489	-0.04	-0.05348012	0.91044412
Q8N1E2	LYG1	1	(1 of 119,120)	Region	TopN	-0.65	0.12517		-0.65003497	0.15033071
Q8N1E2	LYG1	1	115	Site	TopN	-0.65	0.12517		-0.65003497	0.15033071
Q8N1G0	ZNF687	1	(1 of 377,379)	Region	Both	-0.12	0.75883	0.07	-0.18984563	0.60594301
Q8N1G0	ZNF687	1	380	Site	Both	-0.107	0.77943	0.07	-0.17748224	0.6375374
Q8N1I0	DOCK4	1	1787	Site	TopSpeed	-0.154	0.78143	0.05	-0.20373377	0.71058792
Q8N3V7	SYNPO	1	(1 of 411,412)	Region	Both	1.2305	#######		1.230542408	1.02E-06
Q8N3V7	SYNPO	1	409	Site	Both	1.7164	#######		1.716373871	1.99E-08
Q8N3V7	SYNPO	1	410	Site	Both	1.2305	#######		1.230542408	1.02E-06
Q8N3V7	SYNPO	1	415	Site	Both	1.4271	#######		1.427074636	1.55E-07
Q8N3X1	FNBP4	1	797	Site	Both	-0.2	0.55175	0	-0.20012548	0.58903014
Q8N6T3	ARFGAP1	1	141	Site	Both	0.1283	0.76271	0.07	0.058325461	0.91044412
Q8N9U9	SPANXA2-OT1	1	120	Site	Both	-0.515	0.27029		-0.51521971	0.32418494
Q8N9U9	SPANXA2-OT1	1	122	Site	Both	-0.444	0.35734		-0.44411612	0.40655976
Q8ND82	ZNF280C	1	(1 of 213,214)	Region	TopN	-0.176	0.75105	0.09	-0.26605587	0.62022567
Q8ND83	SLAIN1	1	(1 of 414,417,418)&(1 of 414,422)	Region	Both	0.0192	0.96548	-0.67	0.689191669	0.00631517
Q8ND83	SLAIN1	1	293	Site	TopSpeed	-1.362	0.0014	-0.67	-0.69189237	0.12260258
Q8ND83	SLAIN1	1	292	Site	TopSpeed	-1.362	0.0014	-0.67	-0.69189237	0.12260258
Q8ND83	SLAIN1	1	413	Site	Both	0.004	0.98673	-0.67	0.674033899	0.00659634
Q8ND83	SLAIN1	1	421	Site	Both	-0.029	0.93512	-0.67	0.641114332	0.00923662
Q8NDV7	TNRC6A	1	(1 of 241,245,260,273,276)	Region	TopSpeed	-0.113	0.84852	0.26	-0.37313015	0.43727997
Q8NDV7	TNRC6A	1	1688	Site	Both	-0.156	0.67751	0.26	-0.41586578	0.18877354
Q8NDV7	TNRC6A	1	1666	Site	TopSpeed	0.1385	0.81019	0.26	-0.12151321	0.85168276
Q8NDV7	TNRC6A	1	1686	Site	Both	-0.156	0.67751	0.26	-0.41586578	0.18877354
Q8NDV7	TNRC6A	1	1687	Site	Both	-0.009	0.98301	0.26	-0.26873259	0.41618591
Q8NDX5	PHC3	1	283	Site	TopSpeed	-0.761	0.0722		-0.76142538	0.08564855
Q8NEM8	AGBL3	1	729	Site	Both	0.3302	0.15892		0.330197635	0.18877354
Q8NEM8	AGBL3	1	726	Site	Both	0.3302	0.15892		0.330197635	0.18877354
Q8NEZ4	KMT2C	1	2230	Site	Both	-0.338	0.26828		-0.33836706	0.32395753
Q8NFC6	BOD1L1	1	1540	Site	TopSpeed	0.0803	0.89207	-0.03	0.110334756	0.86597032
Q8NFH5	NUP35	1	298	Site	Both	-0.215	0.52697	-0.13	-0.0849761	0.85664364
Q8NFM7	IL17RD	1	(1 of 304,311)	Region	TopN	-0.097	0.86418		-0.09695052	0.88697434
Q8TDD1	DDX54	1	240	Site	TopN	0.1583	0.77645	-0.06	0.2183245	0.69996477
Q8TEQ6	GEMIN5	1	627	Site	Both	0.3574	0.13319	-0.01	0.367394713	0.15033071
Q8TEQ6	GEMIN5	1	620	Site	Both	0.3744	0.1207	-0.01	0.384404311	0.13225558

Q8WU79	SMAP2	1	(1 of 180,181,197,201)	Region	Both	-0.447	0.1303	-0.27	-0.17742491	0.64062732
Q8WUH6	TMEM263	1	(1 of 70,73,74,77)	Region	TopSpeed	0.6305	0.13435	-0.18	0.810539362	0.0635335
Q8WV99	ZFAND2B	1	150	Site	TopN	-0.422	0.3167		-0.42228931	0.36821502
Q8WVE6	TMEM171	1	266	Site	Both	-0.191	0.73332		-0.19064179	0.73150788
Q8WVJ2	NUDCD2	1	(1 of 137,142,146)	Region	TopSpeed	0.0235	0.97884	-0.04	0.063505196	0.92400636
Q8WWI1	LMO7	1	1584	Site	Both	0.1696	0.54815	0.25	-0.08042586	0.81593663
Q8WWM7	ATXN2L	3	(3 of 452,459,461,469,473,474,475,477,481,482,483,485,491,493,496)	Region	Both	-0.316	0.20869	-0.03	-0.28580882	0.29995112
Q8WWM7	ATXN2L	1	678	Site	Both	-0.496	0.03892	-0.03	-0.46611055	0.06087099
Q8WWM7	ATXN2L	1	680	Site	Both	-0.307	0.20426	-0.03	-0.27688651	0.29696117
Q8WWM7	ATXN2L	1	681	Site	Both	-0.038	0.91749	-0.03	-0.00765123	0.98261543
Q8WWM7	ATXN2L	1	683	Site	Both	-0.038	0.91749	-0.03	-0.00765123	0.98261543
Q8WWM7	ATXN2L	1	684	Site	Both	-0.523	0.02553	-0.03	-0.49269722	0.04036339
Q8WWM7	ATXN2L	1	268	Site	Both	0.035	0.93512	-0.03	0.065023074	0.89452881
Q8WXI9	GATAD2B	1	(1 of 287,288,289,302,303,304,305)	Region	Both	0.1923	0.73332	0.08	0.112302813	0.86428932
Q8WXI9	GATAD2B	1	584	Site	Both	-0.202	0.55729	0.08	-0.2815964	0.40347809
Q8WXI9	GATAD2B	1	525	Site	TopSpeed	-0.187	0.73332	0.08	-0.26656219	0.62022567
Q8WY36	BBX	1	(1 of 885,887,894,898)	Region	TopSpeed	-0.138	0.81179	-0.24	0.102410425	0.88132546
Q8WYP5	AHCTF1	1	1165	Site	Both	-0.219	0.51041	0.1	-0.3188713	0.32418494
Q92538	GBF1	1	(1 of 1788,1789)	Region	TopSpeed	-1.212	0.00453	-0.25	-0.96244856	0.0242215
Q92538	GBF1	1	(1 of 1850,1855,1856)	Region	TopN	-0.3	0.53065	-0.25	-0.05018958	0.92993035
Q92540	SMG7	1	624	Site	Both	-0.15	0.63756	0.02	-0.1696132	0.60078955
Q92540	SMG7	1	627	Site	Both	-0.246	0.33679	0.02	-0.26620012	0.3467146
Q92615	LARP4B	1	581	Site	Both	0.3239	0.17345	0.34	-0.01608623	0.9659325
Q92733	PRCC	1	(1 of 227,228)	Region	Both	0.2852	0.5556	0.06	0.225243099	0.6902866
Q92733	PRCC	1	226	Site	Both	0.2852	0.5556	0.06	0.225243099	0.6902866
Q92750	TAF4B	1	187	Site	Both	0.3753	0.20372	0.17	0.205281029	0.58552609
Q92750	TAF4B	1	190	Site	Both	0.3717	0.20372	0.17	0.201680501	0.58749894
Q92750	TAF4B	1	46	Site	Both	-0.013	0.97926	0.17	-0.18303889	0.62321657
Q92750	TAF4B	1	383	Site	TopSpeed	0.7117	0.09528	0.17	0.541703339	0.22504717
Q92841	DDX17	1	64	Site	Both	0.1649	0.54424	0.04	0.124877069	0.69221229
Q92841	DDX17	1	55	Site	Both	0.1464	0.61124	0.04	0.106368309	0.73658347
Q92945	KHSRP	1	144	Site	Both	-0.141	0.62736	-0.04	-0.1008171	0.74671998
Q92945	KHSRP	1	191	Site	TopSpeed	0.1304	0.73332	-0.04	0.17039893	0.65957296
Q92945	KHSRP	1	95	Site	TopSpeed	0.0138	0.97926	-0.04	0.053825744	0.91044412

Q93052	LPP	1	11	Site	Both	-0.364	0.21821	-0.37	0.005512601	0.98815648
Q93052	LPP	1	12	Site	Both	-0.364	0.21821	-0.37	0.005512601	0.98815648
Q96BD5	PHF21A	1	124	Site	Both	-0.369	0.13039	-0.57	0.201189116	0.48356887
Q96BD5	PHF21A	1	125	Site	Both	-0.065	0.8473	-0.57	0.505027119	0.03735066
Q96D46	NMD3	1	(1 of 240,241,243,258)	Region	TopSpeed	0.1629	0.76984	0.18	-0.01706091	0.97975
Q96DF8	ESS2	1	437	Site	TopN	0.6142	0.14074	0.18	0.434194905	0.35176469
Q96E09	FAM122A	1	(1 of 262,263,264,265,267,270,276,285,286)	Region	TopSpeed	-0.187	0.73332	-0.04	-0.14737055	0.797687
Q96HA1	POM121	1	(1 of 555,559,561,563,565,569,572,574,576,584,587,588,593,594,600)	Region	TopSpeed	-0.238	0.65016	0.14	-0.3778663	0.43296161
Q96HA7	TONSL	1	(1 of 912,915,918,919)	Region	TopN	-0.076	0.89829	-0.03	-0.04642662	0.93373979
Q96KM6	ZNF512B	1	(1 of 263,267,273,277,279)	Region	Both	0.3186	0.49928	0.04	0.278627309	0.60078955
Q96KM6	ZNF512B	1	225	Site	TopSpeed	-0.103	0.79045	0.04	-0.14273154	0.70759286
Q96KR1	ZFR	1	(1 of 165,167,180,184,188)	Region	TopSpeed	0.0642	0.91819	-0.02	0.084161002	0.90658075
Q96KR1	ZFR	1	(1 of 429,432)&(1 of 422,429)	Region	Both	0.1039	0.73889	-0.02	0.123905064	0.70019113
Q96KR1	ZFR	1	195	Site	Both	-0.361	0.13469	-0.02	-0.34137046	0.18918449
Q96KR1	ZFR	1	135	Site	Both	-0.724	0.00462	-0.02	-0.70395354	0.00659634
Q96KR1	ZFR	1	136	Site	Both	-0.724	0.00462	-0.02	-0.70395354	0.00659634
Q96KR1	ZFR	1	423	Site	Both	0.1641	0.55244	-0.02	0.184063713	0.52599901
Q96KR1	ZFR	1	202	Site	Both	-0.361	0.13469	-0.02	-0.34137046	0.18918449
Q96KR1	ZFR	1	142	Site	Both	-0.429	0.08291	-0.02	-0.40882187	0.12136128
Q96KR1	ZFR	1	144	Site	Both	-0.674	0.01058	-0.02	-0.65408057	0.0125797
Q96KR1	ZFR	1	434	Site	Both	0.2034	0.41228	-0.02	0.223448352	0.40347809
Q96KR1	ZFR	1	532	Site	Both	0.146	0.60707	-0.02	0.165985849	0.58079224
Q96KR1	ZFR	1	533	Site	Both	0.146	0.60707	-0.02	0.165985849	0.58079224
Q96KR1	ZFR	1	149	Site	TopSpeed	-0.31	0.28579	-0.02	-0.2895806	0.37837942
Q96L91	EP400	1	2689	Site	Both	0.0686	0.85763	0.05	0.018637286	0.96545905
Q96L91	EP400	1	2691	Site	Both	0.0964	0.75883	0.05	0.046355546	0.90863054
Q96L91	EP400	1	2696	Site	Both	-0.123	0.71306	0.05	-0.17306941	0.58728077
Q96L91	EP400	1	2699	Site	Both	0.1395	0.63582	0.05	0.089500677	0.78573066
Q96L91	EP400	1	2700	Site	Both	-0.039	0.90979	0.05	-0.08877451	0.78573066
Q96L91	EP400	1	2604	Site	Both	0.1073	0.73332	0.05	0.057283773	0.88132546
Q96L91	EP400	1	1488	Site	TopSpeed	0.1129	0.72438	0.05	0.062866405	0.86428932
Q96L91	EP400	1	2608	Site	Both	0.1073	0.73332	0.05	0.057283773	0.88132546

Q96L91	EP400	1	1495	Site	TopSpeed	0.1129	0.72438	0.05	0.062866405	0.86428932
Q96L91	EP400	1	2712	Site	TopSpeed	0.6656	0.11948	0.05	0.615629535	0.17220996
Q96L91	EP400	1	2686	Site	Both	0.2017	0.46113	0.05	0.1516742	0.63995712
Q96M27	PRRC1	1	(1 of 152,157,159,162,164,169,172,176,178,179,184,186,187,188,191)	Region	Both	-0.237	0.51124	-0.15	-0.08717574	0.86428932
Q96MY1	NOL4L	1	375	Site	Both	0.6373	0.00701		0.637264826	0.00722461
Q96N67	DOCK7	1	14	Site	TopSpeed	0.1175	0.84355	-0.22	0.337544275	0.49566768
Q96P48	ARAP1	1	(1 of 91,97,104,105,106)	Region	Both	0.3678	0.20701	0.41	-0.04220113	0.92511993
Q96PK6	RBM14	1	(1 of 225,231,236)	Region	TopSpeed	0.228	0.49818	-0.06	0.287951697	0.39348757
Q96PK6	RBM14	1	256	Site	Both	0.0486	0.882	-0.06	0.108605532	0.72881104
Q96PK6	RBM14	1	244	Site	Both	-0.155	0.56699	-0.06	-0.09525019	0.7587687
Q96PK6	RBM14	1	278	Site	Both	-0.113	0.73036	-0.06	-0.05299425	0.89061809
Q96PK6	RBM14	1	280	Site	Both	-0.219	0.36761	-0.06	-0.15908225	0.60078955
Q96PK6	RBM14	1	254	Site	Both	0.0062	0.98301	-0.06	0.066224198	0.86428932
Q96RK0	CIC	1	(1 of 1143,1145,1149,1150,1154,1156,1159,1161,1163)	Region	TopSpeed	0.0367	0.95813		0.036700316	0.95080035
Q96RK0	CIC	1	(1 of 1000,1001,1002)	Region	TopSpeed	-0.082	0.88826		-0.08179017	0.90986391
Q96RK0	CIC	1	132	Site	Both	0.3845	0.18664		0.384520227	0.21589723
Q96RK0	CIC	1	127	Site	Both	0.3845	0.18664		0.384520227	0.21589723
Q96RN5	MED15	1	405	Site	Both	0.4712	0.07856	0.18	0.291203614	0.32115861
Q96RT1	ERBIN	1	1070	Site	Both	-0.785	0.0296	0.17	-0.95473365	0.00901228
Q96T58	SPEN	1	(1 of 2452,2456,2460,2463,2466,2471,2474,2476)	Region	Both	0.1921	0.57065	0.2	-0.00788737	0.98322904
Q96T58	SPEN	1	(1 of 2586,2591,2594,2599)	Region	TopN	0.1356	0.81444	0.2	-0.06437736	0.92257958
Q96T58	SPEN	1	(1 of 3461,3462,3463,3466,3467,3476)	Region	TopSpeed	0.3175	0.50076	0.2	0.117472573	0.85936701
Q96T58	SPEN	1	2529	Site	Both	0.0193	0.96144	0.2	-0.18071218	0.52819421
Q96T58	SPEN	1	2530	Site	Both	-0.034	0.92396	0.2	-0.23445534	0.37449508
Q96T58	SPEN	1	2531	Site	Both	-0.166	0.55309	0.2	-0.36572514	0.15933894
Q96T58	SPEN	1	2522	Site	Both	0.3509	0.14159	0.2	0.150939178	0.6241827
Q96T58	SPEN	1	2619	Site	Both	-0.05	0.87459	0.2	-0.25017446	0.34187785
Q96T58	SPEN	1	2525	Site	Both	0.0386	0.91151	0.2	-0.16139323	0.59767111
Q96T58	SPEN	1	2811	Site	Both	-0.124	0.68002	0.2	-0.32394733	0.19486577

Q99550	MPHOSPH9	1	(1 of 511,513)	Region	TopN	0.1133	0.84852	0.35	-0.23667043	0.6680228
Q99550	MPHOSPH9	1	(1 of 977,980,984)	Region	TopSpeed	0.7768	0.06671	0.35	0.42680919	0.36102741
Q99700	ATXN2	1	(1 of 202,207,213,215,216,217,218,220,221,222,223,225,228,229,234,235)	Region	TopN	-0.564	0.17833	-0.15	-0.41408615	0.38169817
Q99700	ATXN2	1	666	Site	TopN	0.0004	0.99876	-0.15	0.150418062	0.79441218
Q99856	ARID3A	1	408	Site	Both	0.0871	0.83321	0.1	-0.01287465	0.97877402
Q9BQC3	DPH2	1	470	Site	Both	0.0419	0.89954	-0.07	0.111901942	0.71678949
Q9BR26	OCSTAMP	1	(1 of 385,386)	Region	TopN	-0.012	0.98301		-0.01165269	0.98322904
Q9BTC0	DIDO1	2	(2 of 1277,1278,1285,1288,1291,1292,1297,1298,1301,1302,1303,1305,1306,1308)	Region	Both	-0.163	0.55025	0	-0.16266714	0.58749894
Q9BWF3	RBM4	1	(1 of 199,202,204,208)	Region	TopSpeed	-0.006	0.98673	0.08	-0.08638122	0.90425011
Q9BXB4	OSBPL11	1	(1 of 742,743)	Region	Both	0.2938	0.31873	-0.24	0.533820284	0.08457958
Q9BYJ9	YTHDF1	1	196	Site	Both	-0.395	0.09528	-0.76	0.364688756	0.15020879
Q9BYJ9	YTHDF1	1	198	Site	Both	-0.35	0.13469	-0.76	0.410334164	0.10146861
Q9BYP7	WNK3	1	(1 of 974,976,977,978,980,981,982,983)	Region	TopSpeed	0.05	0.93452		0.049997574	0.92993035
Q9BYP7	WNK3	1	1312	Site	TopSpeed	0.0521	0.87144		0.052110399	0.89160973
Q9BYP7	WNK3	1	709	Site	TopSpeed	-0.153	0.78246		-0.15269994	0.7935387
Q9BZA8	PCDH11Y	1	713	Site	TopSpeed	1.0267	0.01536		1.026719098	0.01539257
Q9C0A1	ZFHX2	1	(1 of 2563,2564,2565,2566,2567,2568)	Region	Both	0.4911	0.04052		0.491135077	0.0457197
Q9C0C7	AMBRA1	1	441	Site	TopSpeed	0.9159	0.02893	0.03	0.885876261	0.04036339
Q9C0F0	ASXL3	1	1031	Site	Both	-2.864	#######		-2.86433827	6.29E-12
Q9H0E9	BRD8	1	284	Site	Both	-0.123	0.75105	0.13	-0.25271561	0.4557783
Q9H0W8	SMG9	1	(1 of 114,117,118,122)	Region	TopSpeed	-0.018	0.97938	0.18	-0.19797461	0.71777261
Q9H2Y7	ZNF106	1	(1 of 1492,1496,1498,1501,1502)	Region	Both	-0.015	0.97703	0.34	-0.35518895	0.17220996
Q9H3P2	NELFA	1	(1 of 312,321,322,323,327,328,330,335,336,340,341,343,348,349)	Region	TopSpeed	0.2513	0.62736	0.07	0.181282208	0.74496687

Q9H3S7	PTPN23	1	(1 of 1506,1515,1519, 1533,1537,1538, 1542,1543,1544, 1549,1550)	Region	TopSpeed	-0.448	0.28298	-0.11	-0.33797649	0.49565552
Q9H4A3	WNK1	1	1849	Site	TopN	-0.132	0.73332	0.04	-0.17175119	0.65896254
Q9H4A3	WNK1	1	1950	Site	TopSpeed	0.0258	0.95813	0.04	-0.01422783	0.97812544
Q9H4A3	WNK1	1	1951	Site	TopSpeed	0.0166	0.97884	0.04	-0.02336926	0.95631267
Q9H6L5	RETREG1	2	(2 of 390,392,397,402 ,405)	Region	TopN	0.0543	0.93078		0.054286837	0.92831607
Q9H7P9	PLEKHG2	1	1314	Site	TopSpeed	0.1918	0.73332		0.19179229	0.72881104
Q9H7S9	ZNF703	1	(1 of 180,181,182)	Region	Both	-0.27	0.24706	0.04	-0.31022131	0.22202586
Q9H7S9	ZNF703	1	259	Site	Both	-0.055	0.87202	0.04	-0.09483631	0.78573066
Q9H7S9	ZNF703	1	170	Site	Both	-0.335	0.16027	0.04	-0.37524996	0.14474479
Q9H7S9	ZNF703	1	172	Site	Both	-0.332	0.17291	0.04	-0.37195079	0.15457126
Q9H7S9	ZNF703	1	173	Site	Both	-0.315	0.19579	0.04	-0.35521922	0.17220996
Q9H7S9	ZNF703	1	174	Site	Both	-0.31	0.20146	0.04	-0.3495109	0.17519547
Q9H7S9	ZNF703	1	177	Site	Both	-0.294	0.21821	0.04	-0.3336451	0.1911075
Q9H7S9	ZNF703	1	179	Site	Both	-0.292	0.22228	0.04	-0.33151834	0.19418349
Q9H7S9	ZNF703	1	184	Site	Both	-0.32	0.18108	0.04	-0.360492	0.16199967
Q9H7S9	ZNF703	1	252	Site	Both	-0.044	0.90087	0.04	-0.08394283	0.81537205
Q9H8Y8	GORASP2	1	424	Site	Both	-0.239	0.34227	-0.12	-0.11920483	0.71533959
Q9H8Y8	GORASP2	1	367	Site	TopSpeed	-0.735	0.08291	-0.12	-0.61498228	0.17220996
Q9HAP2	MLXIP	1	602	Site	Both	0.2237	0.34572	0.24	-0.01634719	0.96482269
Q9HAP2	MLXIP	1	603	Site	Both	0.2823	0.22708	0.24	0.042291806	0.91220682
Q9HAP2	MLXIP	1	607	Site	Both	0.2887	0.22228	0.24	0.048708485	0.90457041
Q9HAU0	PLEKHA5	1	382	Site	Both	0.0491	0.91175	-0.3	0.349137192	0.29539138
Q9HBD1	RC3H2	1	897	Site	TopSpeed	0.3388	0.45828		0.338807689	0.49565552
Q9HBD1	RC3H2	1	482	Site	TopSpeed	0.3227	0.25945		0.322659319	0.31349934
Q9HBD1	RC3H2	1	483	Site	TopSpeed	0.3227	0.25945		0.322659319	0.31349934
Q9HBD1	RC3H2	1	770	Site	TopSpeed	0.7884	0.06223		0.788399354	0.07282391
Q9HBD1	RC3H2	1	478	Site	TopSpeed	0.3313	0.24557		0.331258543	0.29696117
Q9HBD1	RC3H2	1	909	Site	Both	0.7207	0.00192		0.720722212	0.00280956
Q9HBD1	RC3H2	1	468	Site	TopSpeed	0.1949	0.56699		0.194862986	0.60078955
Q9HBD1	RC3H2	1	756	Site	Both	0.6184	0.00841		0.618439323	0.00886704
Q9HBD1	RC3H2	1	470	Site	TopSpeed	0.3313	0.24557		0.331258543	0.29696117
Q9HBD1	RC3H2	1	471	Site	TopSpeed	0.3313	0.24557		0.331258543	0.29696117
Q9HBD1	RC3H2	1	574	Site	TopSpeed	0.4483	0.12714		0.448290194	0.15189114
Q9HBM6	TAF9B	1	152	Site	Both	0.4077	0.1724		0.407696117	0.20019143
Q9HCJ0	TNRC6C	1	(1 of 547,548)	Region	TopSpeed	-0.054	0.93078		-0.05383715	0.92831607
Q9HCJ0	TNRC6C	1	542	Site	TopSpeed	-0.054	0.93078		-0.05383715	0.92831607
Q9HCK8	CHD8	1	2522	Site	Both	0.2608	0.26124	0.31	-0.04917738	0.90255635
Q9HCK8	CHD8	1	2519	Site	Both	0.2608	0.26124	0.31	-0.04917738	0.90255635

Q9HCM7	FBRSL1	1	(1 of 989,1004,1010)	Region	TopSpeed	0.1436	0.79945		0.143573522	0.8045802
Q9HDC9	APMAP	1	162	Site	Both	0.1479	0.70288	-0.06	0.207894594	0.57422616
Q9NPF5	DMAP1	1	(1 of 409,412,418,424)	Region	TopN	0.1971	0.73082	0.12	0.077082688	0.91044412
Q9NQC3	RTN4	1	160	Site	Both	0.0134	0.97926	-0.31	0.323417741	0.3370957
Q9NQX3	GPHN	1	260	Site	Both	-0.292	0.3576	0.02	-0.3122891	0.3695296
Q9NR09	BIRC6	1	(1 of 1586,1587,1591, 1598,1601,1619, 1621)	Region	TopSpeed	-0.11	0.85197	0.12	-0.23028352	0.67932235
Q9NR12	PDLIM7	1	(1 of 203,204,205,214 ,217,219)	Region	Both	0.8121	0.05348	0.23	0.582149109	0.1936142
Q9NR12	PDLIM7	1	89	Site	TopSpeed	0.081	0.84852	0.23	-0.14897549	0.70754983
Q9NR12	PDLIM7	1	196	Site	Both	0.5758	0.17156	0.23	0.345773946	0.48516346
Q9NRA8	EIF4ENIF1	1	(1 of 768,769,772)	Region	TopSpeed	-0.53	0.20577	0.09	-0.61972505	0.17056868
Q9NSI2	FAM207A	1	39	Site	TopSpeed	0.0139	0.98301	-0.17	0.183887797	0.73910336
Q9NTZ6	RBM12	1	111	Site	Both	-0.397	0.12961	0	-0.39684991	0.15457126
Q9NUQ6	SPATS2L	1	(1 of 543,544,550,555)	Region	TopN	-0.373	0.20403	-0.07	-0.30318887	0.35483335
Q9NXV6	CDKN2AIP	1	323	Site	TopSpeed	0.1738	0.63587	-0.19	0.363770158	0.25195289
Q9NYJ8	TAB2	1	456	Site	Both	-0.083	0.84102	-0.13	0.04698471	0.92229001
Q9NYV4	CDK12	1	592	Site	TopSpeed	0.4582	0.12091	0.07	0.388215829	0.20838287
Q9NYV4	CDK12	1	593	Site	TopSpeed	0.4582	0.12091	0.07	0.388215829	0.20838287
Q9P2B4	CTTNBP2NL	1	(1 of 637,638,639)	Region	TopSpeed	-0.62	0.00841	-0.27	-0.34976538	0.16525791
Q9P2N5	RBM27	1	(1 of 539,546,549,552)	Region	TopSpeed	0.0192	0.96548	0.02	-0.00082661	0.99778642
Q9P2N6	KANSL3	1	860	Site	Both	0.4076	0.16314		0.407564126	0.19131351
Q9P2P6	STARD9	1	3937	Site	TopSpeed	0.7181	0.09169		0.718109757	0.11065661
Q9P2R6	RERE	1	1237	Site	Both	0.3901	0.11047	-0.05	0.440059034	0.08031377
Q9P2R6	RERE	1	1238	Site	Both	0.1835	0.49928	-0.05	0.233497741	0.39293271
Q9UHD9	UBQLN2	1	(1 of 116,124)&(1 of 124,125,127,128)	Region	Both	-0.119	0.73332	0.02	-0.13857632	0.69130082
Q9UHD9	UBQLN2	1	112	Site	Both	-0.261	0.33696	0.02	-0.28134191	0.3509044
Q9UHD9	UBQLN2	1	113	Site	Both	-0.261	0.33696	0.02	-0.28134191	0.3509044
Q9UHD9	UBQLN2	1	123	Site	Both	-0.028	0.94675	0.02	-0.04755437	0.914156
Q9UHD9	UBQLN2	1	121	Site	Both	-0.261	0.33696	0.02	-0.28134191	0.3509044
Q9UHR5	SAP30BP	1	231	Site	Both	0.1836	0.48429	0.09	0.093578674	0.76243442
Q9UHR5	SAP30BP	1	232	Site	Both	0.3428	0.14074	0.09	0.25275918	0.33206844
Q9UHR5	SAP30BP	1	233	Site	Both	0.3043	0.19504	0.09	0.214292899	0.42146519
Q9UHR5	SAP30BP	1	237	Site	Both	0.1566	0.57018	0.09	0.066572715	0.85896869

Q9UHR5	SAP30BP	1	245	Site	Both	0.1551	0.58145	0.09	0.065085095	0.86428932
Q9UHY1	NRBP1	1	(1 of 532,534,535)	Region	Both	0.1602	0.56379	-0.13	0.290229661	0.25580836
Q9UHY1	NRBP1	1	528	Site	Both	0.1602	0.56379	-0.13	0.290229661	0.25580836
Q9UHY1	NRBP1	1	150	Site	TopN	0.177	0.75105	-0.13	0.306968665	0.557488
Q9UIF8	BAZ2B	2	(2 of 9,10,13,14,15,16,18,19,20,21,22,24,27,30)	Region	TopN	-0.494	0.09528		-0.49381305	0.1161024
Q9UK61	TASOR	1	(1 of 1124,1125,1126)	Region	TopSpeed	-0.352	0.43444	0.13	-0.48179117	0.29539138
Q9UKD1	GMEB2	1	404	Site	Both	0.0855	0.78918	-0.15	0.235471978	0.38431317
Q9UKD1	GMEB2	1	407	Site	Both	0.1053	0.73487	-0.15	0.255265804	0.33838036
Q9UKY1	ZHX1	1	(1 of 429,437,440,444,449,450,452)	Region	Both	-0.162	0.66876	0.1	-0.26245561	0.44935957
Q9UKY1	ZHX1	1	232	Site	Both	0.3744	0.11948	0.1	0.274367565	0.28724519
Q9UKY1	ZHX1	1	227	Site	Both	0.3428	0.14074	0.1	0.242758611	0.35176469
Q9UKY1	ZHX1	1	228	Site	Both	0.3428	0.14074	0.1	0.242758611	0.35176469
Q9UKY7	CDV3	1	(1 of 144,157,159,165,166)	Region	TopSpeed	0.2733	0.24098	0.07	0.203289073	0.46104916
Q9ULH7	MRTFB	1	(1 of 209,211)	Region	Both	-0.26	0.38973	-0.08	-0.17986893	0.62887819
Q9ULH7	MRTFB	1	207	Site	Both	-0.26	0.38973	-0.08	-0.17986893	0.62887819
Q9ULH7	MRTFB	1	223	Site	Both	-0.26	0.38973	-0.08	-0.17986893	0.62887819
Q9ULM3	YEATS2	1	723	Site	TopSpeed	-0.345	0.44512	0.09	-0.43523607	0.35176469
Q9ULM3	YEATS2	1	389	Site	Both	-0.285	0.23985	0.09	-0.37521841	0.15189114
Q9ULM3	YEATS2	1	935	Site	Both	-0.147	0.79071	0.09	-0.23746513	0.6680228
Q9ULT8	HECTD1	1	(1 of 1342,1345,1350,1351,1352,1354,1356,1357,1359,1361,1362)	Region	TopN	0.5634	0.17833	0.6	-0.03656186	0.95080035
Q9ULU4	ZMYND8	2	(2 of 766,767,770,771,776,778,779,780,781,782,783,784,786,788,795,797)	Region	Both	0.1777	0.51796	-0.12	0.297654624	0.25195289
Q9ULU4	ZMYND8	1	(1 of 756,760)	Region	Both	-0.283	0.23195	-0.12	-0.1633565	0.59767111
Q9ULU4	ZMYND8	1	746	Site	Both	-0.255	0.2807	-0.12	-0.13489632	0.6680228
Q9ULU4	ZMYND8	1	750	Site	Both	-0.255	0.2807	-0.12	-0.13489632	0.6680228
Q9ULU4	ZMYND8	1	751	Site	Both	-0.255	0.2807	-0.12	-0.13489632	0.6680228
Q9UMR5	PPT2	1	208	Site	Both	0.1329	0.81489		0.132873669	0.82909303
Q9UMS4	PRPF19	1	(1 of 133,148,149,152,169)	Region	Both	-0.131	0.66876	0.04	-0.17109962	0.57766052
Q9UN86	G3BP2	1	235	Site	Both	-0.01	0.98301	0.17	-0.17987617	0.63788757

Q9UPA5	BSN	1	(1 of 2313,2314,2315)	Region	Both	0.46	0.12517		0.459988189	0.15033071
Q9UPN6	SCAF8	1	(1 of 617,619)	Region	TopSpeed	0.0686	0.86418	0.11	-0.04137163	0.92657403
Q9UPN6	SCAF8	2	(2 of 533,534,536)	Region	TopN	-0.333	0.47087	0.11	-0.44269654	0.3467146
Q9UPN6	SCAF8	1	615	Site	TopSpeed	0.0686	0.86418	0.11	-0.04137163	0.92657403
Q9UPX8	SHANK2	1	1288	Site	Both	0.3376	0.26828		0.337636644	0.32395753
Q9UQ35	SRRM2	1	(1 of 111,119,121)	Region	TopSpeed	0.2591	0.6078	0.12	0.1391044	0.81537205
Q9UQ35	SRRM2	1	2236	Site	TopSpeed	-0.065	0.91749	0.12	-0.18478065	0.73706765
Q9Y253	POLH	1	457	Site	TopSpeed	-0.199	0.56379		-0.19900761	0.60078955
Q9Y2K5	R3HDM2	1	345	Site	Both	0.5629	0.01536	0.23	0.332876857	0.18417863
Q9Y2X9	ZNF281	1	(1 of 883,884)	Region	Both	-0.025	0.94526	-0.38	0.355179049	0.16525791
Q9Y2X9	ZNF281	1	872	Site	Both	-0.025	0.94526	-0.38	0.355179049	0.16525791
Q9Y2X9	ZNF281	1	876	Site	Both	-0.031	0.93078	-0.38	0.348953899	0.17220996
Q9Y2X9	ZNF281	1	879	Site	Both	-0.043	0.89886	-0.38	0.336828854	0.19033394
Q9Y2X9	ZNF281	1	891	Site	Both	-0.752	0.00224	-0.38	-0.37190448	0.16010262
Q9Y2X9	ZNF281	1	61	Site	Both	-0.202	0.43985	-0.38	0.177786386	0.55949039
Q9Y3S1	WNK2	1	(1 of 1605,1606)	Region	Both	0.384	0.10547	0.6	-0.21604236	0.41618591
Q9Y3S1	WNK2	1	1608	Site	Both	0.384	0.10547	0.6	-0.21604236	0.41618591
Q9Y3S1	WNK2	1	1611	Site	Both	0.384	0.10547	0.6	-0.21604236	0.41618591
Q9Y467	SALL2	1	531	Site	TopSpeed	0.0414	0.90087	0.34	-0.29862717	0.24051635
Q9Y467	SALL2	1	253	Site	TopSpeed	-0.133	0.81489	0.34	-0.47280904	0.30392115
Q9Y467	SALL2	1	527	Site	TopSpeed	0.0414	0.90087	0.34	-0.29862717	0.24051635
Q9Y4B4	RAD54L2	2	(2 of 1084,1085,1086)	Region	Both	0.1314	0.73332	0.09	0.041428367	0.92511993
Q9Y4B4	RAD54L2	1	1074	Site	Both	0.1314	0.73332	0.09	0.041428367	0.92511993
Q9Y4B4	RAD54L2	1	1075	Site	Both	0.1314	0.73332	0.09	0.041428367	0.92511993
Q9Y4B4	RAD54L2	1	1012	Site	TopN	0.0095	0.98301	0.09	-0.08047481	0.90986391
Q9Y4B4	RAD54L2	1	983	Site	Both	0.1503	0.58701	0.09	0.060330907	0.86597032
Q9Y4L1	HYOU1	1	933	Site	Both	0.1176	0.71306	0	0.117638878	0.70759286
Q9Y4L1	HYOU1	1	935	Site	Both	0.1371	0.64275	0	0.137123605	0.6622578
Q9Y4X4	KLF12	2	(1 of 114,115,116,117,118)&(2 of 109,111,112,113,114)&(1 of 113,114,115)	Region	Both	0.1318	0.65532		0.131763777	0.67158708
Q9Y4X4	KLF12	1	(1 of 97,98,99,102)	Region	Both	-0.047	0.89829		-0.0470728	0.91044412
Q9Y4X4	KLF12	1	106	Site	Both	-0.037	0.92396		-0.0369753	0.92511993
Q9Y520	PRRC2C	1	(1 of 2149,2150,2154,2155)	Region	TopSpeed	-0.319	0.29634	-0.09	-0.22919452	0.53880758
Q9Y520	PRRC2C	1	2176	Site	Both	-0.449	0.12517	-0.09	-0.35945674	0.2501051
Q9Y520	PRRC2C	1	2181	Site	Both	-0.431	0.13493	-0.09	-0.34086803	0.28012236

Q9Y520	PRRC2C	1	2192	Site	Both	-0.292	0.2284	-0.09	-0.20212004	0.4850436
Q9Y520	PRRC2C	1	2196	Site	Both	-0.306	0.20372	-0.09	-0.21645872	0.43514761
Q9Y520	PRRC2C	1	2200	Site	Both	-0.281	0.22708	-0.09	-0.19096522	0.4936985
Q9Y520	PRRC2C	1	2203	Site	Both	-0.236	0.32929	-0.09	-0.14563296	0.6375374
Q9Y520	PRRC2C	1	2211	Site	Both	-0.368	0.22228	-0.09	-0.27778642	0.42146519
Q9Y520	PRRC2C	1	2221	Site	Both	-0.368	0.22228	-0.09	-0.27778642	0.42146519
Q9Y520	PRRC2C	1	2229	Site	Both	-0.502	0.03655	-0.09	-0.41167691	0.11000914
Q9Y520	PRRC2C	1	2682	Site	Both	-0.235	0.36991	-0.09	-0.14453134	0.6680228
Q9Y520	PRRC2C	1	2233	Site	Both	-0.248	0.32521	-0.09	-0.15755908	0.62172767
Q9Y520	PRRC2C	1	2238	Site	Both	-0.495	0.05342	-0.09	-0.40467838	0.14474479
Q9Y520	PRRC2C	1	2243	Site	Both	-0.391	0.11948	-0.09	-0.30148241	0.25550595
Q9Y520	PRRC2C	1	2245	Site	Both	-0.481	0.05342	-0.09	-0.3905221	0.14474479
Q9Y520	PRRC2C	1	2165	Site	Both	-0.449	0.12517	-0.09	-0.35945674	0.2501051
Q9Y520	PRRC2C	1	2681	Site	Both	-0.11	0.73082	-0.09	-0.02021436	0.95199371
Q9Y520	PRRC2C	1	2170	Site	Both	-0.493	0.09528	-0.09	-0.4032777	0.19409839
Q9Y520	PRRC2C	1	2685	Site	Both	-0.364	0.13469	-0.09	-0.2736026	0.31033822
Q9Y520	PRRC2C	1	2175	Site	Both	-0.47	0.11275	-0.09	-0.37968846	0.22202586
Q9Y5J3	HEY1	1	(1 of 234,236,245,246,248)	Region	Both	0.9322	0.00027	0.36	0.57217617	0.02084017
Q9Y618	NCOR2	1	(1 of 1214,1215)	Region	TopSpeed	-0.618	0.13822	0.35	-0.96844092	0.02372115
Q9Y618	NCOR2	1	1561	Site	Both	0.1984	0.43956	0.35	-0.15161698	0.62022567
Q9Y618	NCOR2	1	1562	Site	Both	0.2061	0.43956	0.35	-0.14386954	0.66085936
Q9Y618	NCOR2	1	1517	Site	TopSpeed	0.5638	0.17833	0.35	0.213831608	0.70101954
Q9Y618	NCOR2	1	1558	Site	Both	0.0218	0.95724	0.35	-0.32816019	0.20309052
Q9Y692	GMEB1	1	453	Site	TopN	-0.105	0.85824	0.19	-0.29499915	0.58079224
Q9Y6X8	ZHX2	1	265	Site	Both	0.1176	0.76383	0.33	-0.21238036	0.56028578
Q9Y6Y8	SEC23IP	1	136	Site	Both	0.1408	0.64435	-0.16	0.300842898	0.25195289
Q9Y6Y8	SEC23IP	1	118	Site	Both	0.1408	0.64435	-0.16	0.300842898	0.25195289
Q9Y6Y8	SEC23IP	1	134	Site	Both	0.1408	0.64435	-0.16	0.300842898	0.25195289
Q9Y6Y8	SEC23IP	1	126	Site	Both	0.1998	0.44511	-0.16	0.359800566	0.16525791

Appendix 5.2. All Significant OGT Interactors Identified in the Mouse Brain.

Table of all proteins with a value of less than 0.05 in either the limma moderated t-test (limmapVal) or inverted beta binomial test (ibbpVal) after correcting for multiple comparisons using the Benjamini-Hochberg method. FC: log2 fold change, B: limma B statistic.

Accession	Gene	limmaFC	limmapVal	limmaB	ibbFC	ibbpVal

Q8VDD5	MYH9	1.88	0.2044	-4.565	-11.47	0.00015
P14873	MAP1B	3.5133	0.0081	0.7929	-7.912	0.00033
Q8CGY8	OGT	6.64	0.0008	1.9925	-29.69	1.98E-07
Q3UHF7	HIVEP2	5.2267	0.0119	0.4132	-1E+05	8.67E-11
O88737	BSN	3.0533	0.0321	-1.011	-1E+05	9.07E-11
Q68FD5	CLTC	2.2667	0.0587	-2.022	-5.704	0.00131
Q61879	MYH10	2.42	0.2396	-4.911	-4	0.00131
Q61191	HCFC1	6.0567	0.0244	-0.531	-1E+05	9.21E-11
P20357	MAP2	4.1733	0.0161	0.0779	-14.07	2.83E-05
P60710	ACTB	3.5667	0.1735	-4.291	-3.003	0.01344
E9Q557	DSP	0.8267	0.4732	-6.663	-3.271	0.04052
A3KGU9	SPTAN1	2.6233	0.031	-0.905	-8.757	0.0001
Q03172	HIVEP1	1.5433	0.076	-2.633	-1E+05	2.54E-08
Q8R0Y6	ALDH1L1	1.5933	0.0947	-3.088	-13	0.03379
D3YZ62	MYO5A	3.19	0.0613	-2.129	-1E+05	4.71E-10
Q61768	KIF5B	6.0567	0.0025	1.5961	-1E+05	1.48E-09
Q9QYX7	PCLO	1.61	0.2276	-4.812	-1E+05	1.48E-09
A2ARP8	MAP1A	3.2933	0.0134	0.2967	-1E+05	1.32E-09
Q6PD31	TRAK1	6.4133	0.0017	1.7484	-1E+05	1.29E-09
Q6P9N8	TRAK2	4.43	0.03	-0.849	-1E+05	3.99E-09
E9Q6J5	BOD1L	3.51	0.018	-0.08	-1E+05	1.08E-08
B1ASP2	JAK1	1.47	0.2304	-4.835	-6.654	0.00208
P63017	HSPA8	4.6833	0.0323	-1.06	-16.04	2.92E-05
Q62261	SPTBN1	2.6933	0.0137	0.2592	-19.76	1.51E-05
P33175	KIF5A	5.0433	0.0613	-2.137	-1E+05	4.62E-09
A2A884	HIVEP3	0.9933	0.2498	-5.327	-1E+05	1.08E-08
P46735	MYO1B	0.82	0.474	-6.667	-1E+05	8.55E-05
Q02257	JUP	1.3467	0.2143	-4.668	-4	0.02055
Q7TSJ2	MAP6	4.11	0.0314	-0.942	-1E+05	6.22E-09
F7DCH5	CLASP2	4.0333	0.0046	1.2463	-1E+05	8.34E-09
Q9JMH9	MYO18A	2.2633	0.0789	-2.73	-7.41	0.00062
E9Q175	MYO6	3.1667	0.0278	-0.746	-1E+05	7.18E-07
Q7TMY8	HUWE1	1.1433	0.3251	-5.896	-1E+05	5.15E-06
Q8CAQ8	IMMT	2.7567	0.033	-1.096	-1E+05	8.78E-07
Q8K010	OPLAH	1.8733	0.1255	-3.61	-1E+05	0.00023
A0A0R4J049	PRMT5	3.21	0.167	-4.22	-3.797	0.01993
Q8BTI8	SRRM2	2.34	0.2195	-4.718	-1E+05	4.02E-07
Q61781	KRT14	1.9267	0.3864	-6.201	-8.25	0.00372
Q6PIC6	ATP1A3	4.1233	0.0275	-0.717	-39.33	4.65E-06
Q8BG87	TET3	3.7367	0.0507	-1.78	-1E+05	4.05E-07
A0A571BDG0	SRCIN1	3.7633	0.0632	-2.219	-1E+05	3.08E-08
E9PYH6	SETD1A	3.4833	0.0637	-2.257	-1E+05	5.12E-08

Q9DBR7	PPP1R12A	3.9533	0.0436	-1.554	-1E+05	5.82E-08
Q8C9B9	DIDO1	1.8467	0.0974	-3.138	-1E+05	2.71E-07
Q9QXS6	DBN1	3.56	0.0744	-2.584	-7.72	0.0008
P62702	RPS4X	1.6433	0.4172	-6.325	-3.9	0.02058
P13020	GSN	3.3	0.076	-2.635	-5.25	0.00806
Q9WTI7	MYO1C	0.5567	0.4967	-6.722	-96349	0.0067
Q6NZL0	SOGA3	1.6933	0.1784	-4.336	-3.552	0.01528
P27659	RPL3	3.05	0.2473	-5.078	-1E+05	1.49E-05
Q9D8E6	RPL4	3.4867	0.0581	-2.003	-14.34	0.00067
P20029	HSPA5	3.01	0.0317	-0.983	-1E+05	5.63E-05
Q5SVJ0	CAMK2B	5.71	0.0593	-2.075	-1E+05	2.54E-08
P38647	HSPA9	2.52	0.1398	-3.858	-1E+05	4.09E-06
Q7TMM9	TUBB2A	5.46	0.0099	0.6025	-11.78	0.00013
P83741	WNK1	3.1167	0.1351	-3.767	-1E+05	1.27E-07
P28665	MUG1	0.44	0.7573	-7.133	-25	0.01074
P10126	EEF1A1	3.0133	0.1181	-3.501	-14.93	0.00043
Q7TPH6	MYCBP2	2.1167	0.1255	-3.61	-1E+05	2.04E-07
P12970	RPL7A	3.0367	0.0757	-2.623	-8.511	0.00105
Q9DBG3	AP2B1	2.9733	0.0186	-0.165	-9.509	0.00081
Q6ZPE2	SBF1	2.8133	0.0322	-1.037	-40.88	7.36E-06
P97351	RPS3A	2.1033	0.3423	-6	-4.082	0.01362
P62908	RPS3	2.4867	0.0836	-2.867	-7.2	0.00177
P28738	KIF5C	3.0433	0.1432	-3.902	-1E+05	1.62E-07
A0A0A0MQF6	GAPDH	5.23	0.0637	-2.245	-11.92	0.00028
P14148	RPL7	3.1067	0.1523	-4.038	-10	0.00205
P46460	NSF	4.61	0.0351	-1.216	-1E+05	1.27E-07
P61979	HNRNPK	3.3167	0.0561	-1.934	-18.63	0.00021
A0A0A0MQA5	TUBA4A	4.26	0.0246	-0.559	-8.921	0.00056
P16330	CNP	3.2767	0.0589	-2.042	-5.228	0.00546
P25444	RPS2	2.5467	0.2473	-5.105	-10.25	0.00076
A2AQ25	SKT	3.26	0.0162	0.0652	-1E+05	3.71E-07
Q3U7K7	TRIM21	0.3767	0.4457	-6.56	-13	0.03379
Q80VC9	CAMSAP3	1.9867	0.0412	-1.451	-1E+05	6.14E-07
Q9CWW7	CXXC1	5.3867	0.0336	-1.129	-1E+05	7.89E-07
Q99NF7	PPM1B	3.0633	0.0321	-1.016	-9.091	0.0067
Q8BGD9	EIF4B	2.6967	0.1021	-3.218	-32.03	0.00016
P15105	GLUL	3.4567	0.0314	-0.946	-12.58	0.00064
P17426	AP2A1	2.65	0.0246	-0.561	-34.66	1.75E-05
Q03265	ATP5F1A	3.2	0.058	-1.994	-18.11	0.00044
Q4JK59	TET2	1.2533	0.2102	-4.638	-99548	0.00043
Q61699	HSPH1	2.0967	0.1788	-4.341	-1E+05	9.40E-07

Q80WJ7	MTDH	0.7733	0.4449	-6.448	-5.806	0.01694
P47738	ALDH2	1.5067	0.1374	-3.806	-97206	0.00276
Q91YI0	ASL	0.8533	0.22	-4.731	-5.252	0.01496
A0A1D5RM83	IQSEC1	3.0967	0.0185	-0.152	-1E+05	9.94E-07
P17427	AP2A2	2.0267	0.131	-3.694	-1E+05	4.87E-05
P47911	RPL6	2.4533	0.2473	-5.062	-4.87	0.01408
A2RSY1	KANSL3	3.39	0.0071	0.918	-1E+05	1.35E-05
Q00623	APOA1	0.3967	0.6866	-7.057	-3	0.04448
Q5XJF6	RPL10A	3.1433	0.1335	-3.729	-10.16	0.00235
P29341	PABPC1	2.4667	0.1314	-3.7	-1E+05	6.30E-06
Q9JHJ0	TMOD3	2.1867	0.2219	-4.753	-99261	0.0006
P70398	USP9X	2.4533	0.1081	-3.334	-1E+05	8.05E-07
Q8CFE4	SCYL2	1.0267	0.2473	-5.069	-4.786	0.01363
Q9ESK9	RB1CC1	1.5167	0.4449	-6.499	-1E+05	1.04E-06
P11499	HSP90AB1	2.2933	0.1682	-4.239	-10.67	0.00127
P62270	RPS18	1.89	0.2473	-5.086	-5.846	0.005
Q62167	DDX3X	3.8467	0.0618	-2.158	-1E+05	2.13E-05
F7BQW7	SYNJ1	2.5067	0.208	-4.604	-1E+05	1.99E-06
Q9Z1R2	BAG6	2.4567	0.0137	0.2553	-1E+05	3.40E-06
Q99J09	WDR77	2.0367	0.1808	-4.376	-11.33	0.00096
Q61656	DDX5	2.9533	0.0183	-0.127	-1E+05	4.09E-06
Q8BFR5	TUFM	4.0467	0.0697	-2.449	-1E+05	9.85E-06
Q3UHD9	AGAP2	2.9567	0.0979	-3.15	-1E+05	1.22E-06
P63318	PRKCG	5.5367	0.0779	-2.695	-1E+05	6.14E-07
P63038	HSPD1	2.69	0.0473	-1.675	-1E+05	5.63E-05
P58252	EEF2	1.26	0.1108	-3.373	-98641	0.00083
P68372	TUBB4B	5.53	0.0035	1.4109	-12	0.00586
Q8VDM4	PSMD2	0.6367	0.4732	-6.664	-98310	0.00137
Q80U49	CEP170B	1.51	0.2473	-5.065	-1E+05	1.31E-06
Q3U1J4	DDB1	1.81	0.2671	-5.506	-1E+05	0.0002
S4R2K9	ANK3	1.4867	0.3879	-6.209	-1E+05	5.20E-06
E9QAQ5	GSK3B	5.6533	0.0214	-0.363	-1E+05	4.09E-06
P68254	YWHAQ	4.67	0.0747	-2.602	-1E+05	3.36E-06
P51881	SLC25A5	4.2	0.1179	-3.491	-8.5	0.00521
Q9CZM2	RPL15	2.41	0.0561	-1.929	-1E+05	7.73E-05
Q91X20	ASH2L	4.3933	0.0503	-1.766	-1E+05	6.30E-06
Q6A0A9	FAM120A	1.96	0.0783	-2.708	-1E+05	9.18E-06
O08553	DPYSL2	5.3333	0.0275	-0.724	-1E+05	1.16E-06
Q8VDJ3	HDLBP	0.8833	0.2597	-5.441	-95353	0.01528
P62281	RPS11	3.1433	0.2483	-5.312	-4	0.02779
P35700	PRDX1	2.8733	0.1319	-3.711	-6.25	0.00457

A0A0G2JGS4	CAMK2D	4.4167	0.0453	-1.611	-1E+05	3.71E-06
P05213	TUBA1B	5.19	0.0079	0.8262	-98956	0.00074
P62754	RPS6	2.2967	0.0306	-0.885	-24	0.00062
E9QM73	WNK2	3.95	0.062	-2.166	-1E+05	5.88E-06
A0A0R4J2B6	RBBP5	4.9267	0.0071	0.9274	-1E+05	7.18E-06
P11798	CAMK2A	6.61	0.0008	1.9855	-1E+05	5.55E-06
Q91VR2	ATP5F1C	2.8233	0.0317	-0.986	-6.223	0.00853
P62301	RPS13	2.2667	0.1472	-3.967	-4.6	0.01324
P62918	RPL8	3.69	0.2473	-5.182	-17.03	0.00213
Q8K2B3	SDHA	2.4567	0.1358	-3.78	-1E+05	5.52E-05
P62983	RPS27A	2.9167	0.0909	-3.011	-7.626	0.00183
Q91VR5	DDX1	2.1533	0.0617	-2.151	-1E+05	0.00016
Q9EPU0	UPF1	1.6933	0.2152	-4.678	-1E+05	2.83E-05
P51410	RPL9	0.98	0.2094	-4.619	-9	0.02346
P63328	PPP3CA	5.99	0.0173	-0.015	-1E+05	3.16E-07
Q8CJG0	AGO2	1.9933	0.0257	-0.619	-1E+05	0.00011
A8DUK4	HBB-BS	2.33	0.2597	-5.44	-94143	0.0412
Q8CGF6	WDR47	2.2433	0.1808	-4.373	-1E+05	3.52E-06
Q68FG2	SPTBN2	1.8033	0.2508	-5.333	-1E+05	2.74E-05
D3YUP1	CARM1	4.4233	0.042	-1.495	-1E+05	7.73E-06
Q8BGH2	SAMM50	0.8867	0.598	-6.925	-99261	0.0006
Q99PU7	BAP1	3.0967	0.1895	-4.45	-1E+05	1.49E-05
D3YXZ3	KLC2	3.7867	0.0236	-0.484	-1E+05	4.09E-06
Q3UQ44	IQGAP2	-0.177	0.779	-7.153	-99548	0.00062
P62717	RPL18A	2.7833	0.0347	-1.195	-8.591	0.00448
P17751	TPI1	3.45	0.018	-0.074	-10.14	0.00361
H3BJU7	ARHGEF2	3.1867	0.008	0.8175	-1E+05	3.32E-06
Q9Z0H8	CLIP2	2.15	0.1086	-3.345	-1E+05	5.88E-06
Q9JJ28	FLII	2.8467	0.0344	-1.166	-1E+05	5.11E-05
P0C090	RC3H2	3.4667	0.0589	-2.045	-1E+05	1.62E-05
Q8BG51	RHOT1	4.6033	0.0602	-2.099	-1E+05	1.56E-06
Q91V55	RPS5	2.2233	0.2832	-5.616	-15	0.02345
Q925I1	ATAD3	2.2733	0.2212	-4.744	-1E+05	2.09E-05
P62242	RPS8	3.52	0.0535	-1.855	-5.333	0.01735
Q06890	CLU	1.74	0.0589	-2.049	-4.43	0.03411
E9PZ43	MAP4	4.36	0.0172	0.0005	-1E+05	6.35E-06
G5E829	ATP2B1	2.8367	0.2473	-5.012	-1E+05	5.34E-06
P47963	RPL13	3.6133	0.0637	-2.262	-22	0.00103
Q6ZWN5	RPS9	3.4467	0.0356	-1.241	-1E+05	6.19E-05
Q9CR57	RPL14	3.0033	0.1523	-4.044	-4.47	0.02105
P62830	RPL23	3.26	0.0744	-2.588	-9.107	0.00494
Q9WV92	EPB41L3	2.5533	0.0632	-2.228	-1E+05	6.43E-06

Q9EQQ9	OGA	2.9	0.2473	-5.008	-1E+05	5.43E-06
P60469	PPFIA3	1.96	0.1318	-3.708	-1E+05	4.38E-06
Q8R326	PSPC1	3.3933	0.0302	-0.864	-1E+05	8.55E-05
P46096	SYT1	1.0567	0.1383	-3.817	-2.6	0.02949
P17182	ENO1	1.5733	0.1441	-3.919	-1E+05	8.12E-05
Q9JHU4	DYNC1H1	2.1867	0.1528	-4.066	-1E+05	6.30E-06
Q8K3E5	AHI1	2.0533	0.2597	-5.432	-1E+05	1.56E-05
Q811P8	ARHGAP32	3.12	0.1335	-3.737	-1E+05	1.19E-05
P47857	PFKM	3.55	0.0228	-0.441	-1E+05	5.88E-06
Q61805	LBP	1.5933	0.0427	-1.524	-3	0.04448
P84091	AP2M1	3.15	0.0845	-2.885	-22	0.00012
Q8VEK3	HNRNPU	3.0333	0.0136	0.2772	-36	0.00013
Q8BH59	SLC25A12	2.89	0.2473	-5.174	-1E+05	3.71E-06
A2ADM8	ZFP831	2.3467	0.4449	-6.433	-1E+05	1.39E-05
O08788	DCTN1	2.7267	0.2057	-4.58	-1E+05	1.28E-05
P46660	INA	4	0.0706	-2.486	-1E+05	4.42E-06
S4R2F3	ANK2	2.23	0.237	-4.893	-1E+05	1.32E-05
P35980	RPL18	2.9933	0.1138	-3.426	-5.5	0.00741
P42669	PURA	3.68	0.0998	-3.185	-13.06	0.00039
Q9CPR4	RPL17	2.8467	0.2276	-4.817	-5.5	0.02691
Q3UKW2	CALM1	5.3133	0.0161	0.0766	-11.94	0.00126
A2AJI0	MAP7D1	3.17	0.0501	-1.755	-1E+05	1.49E-05
Q9R1L5	MAST1	1.1667	0.1467	-3.955	-1E+05	1.62E-05
Q9D0E1	HNRNPM	1.7833	0.2975	-5.721	-1E+05	2.88E-05
Q571I4	PRAG1	5.3	0.1131	-3.412	-1E+05	1.49E-05
Q8BPN8	DMXL2	0.2033	0.9349	-7.242	-1E+05	1.20E-05
P61965	WDR5	5.2633	0.0501	-1.757	-1E+05	2.84E-05
A2AUK5	EPB41L1	2.0833	0.0649	-2.32	-1E+05	1.23E-05
Q3U2G2	HSPA4	0.4533	0.8595	-7.209	-1E+05	8.64E-05
Q6ZQ08	CNOT1	1.8033	0.3352	-5.958	-98957	0.00061
E9QPE7	MYH11	1.3867	0.1369	-3.799	-1E+05	4.03E-05
E9PWM3	ARMCX4	2.6467	0.3708	-6.135	-1E+05	2.92E-05
Q3UVC0	KSR2	2.97	0.2328	-4.859	-1E+05	1.30E-05
O35668	HAP1	1.52	0.2473	-5.166	-1E+05	1.15E-05
A0A0R4J227	MARK2	3.3067	0.0185	-0.153	-1E+05	1.52E-05
P62259	YWHAE	4.66	0.2019	-4.543	-25	0.00058
Q9JME5	AP3B2	2.0767	0.0885	-2.968	-43	4.06E-05
P99027	RPLP2	2.3333	0.0397	-1.4	-4	0.02957
A0A2I3BQP6	CAMK2G	5.1833	0.004	1.3283	-1E+05	3.36E-05
Q9QYJ0	DNAJA2	2.5567	0.4449	-6.514	-99829	0.0006

P62911	RPL32	2.6967	0.2473	-5.031	-8.063	0.00874
P62960	YBX1	0.6133	0.4831	-6.691	-95871	0.00938
Q9WUM4	CORO1C	2.77	0.0316	-0.96	-7.236	0.0026
Q80XP9	WNK3	3.76	0.2473	-5.045	-1E+05	2.92E-05
P59759	MRTFB	2.0633	0.0829	-2.851	-1E+05	2.09E-05
P62245	RPS15A	3.0433	0.0644	-2.289	-5.441	0.01408
P47754	CAPZA2	3.4667	0.0632	-2.205	-6	0.01004
B1AQW2	MAPT	2.8733	0.3364	-5.966	-1E+05	2.20E-05
Q5SQX6	CYFIP2	1.9533	0.2349	-4.876	-1E+05	1.19E-05
Q99LF4	RTCB	1.6733	0.1384	-3.82	-98956	0.00064
D3Z4U5	JAKMIP1	2.84	0.0079	0.8296	-1E+05	2.04E-05
Q8CDG3	VCPIP1	0.4633	0.5464	-6.837	-1E+05	1.22E-05
P61514	RPL37A	2.3933	0.2473	-5.004	-3.794	0.0498
E9Q3L2	PI4KA	1.83	0.2358	-4.883	-1E+05	1.49E-05
P08226	APOE	1.4733	0.0647	-2.299	-25	0.00673
Q6PIE5	ATP1A2	0.7833	0.5635	-6.868	-1E+05	2.37E-05
Q91W50	CSDE1	1.67	0.091	-3.021	-1E+05	0.00013
O35295	PURB	1.4767	0.5407	-6.822	-4.18	0.02063
Q99K48	NONO	3.7567	0.0818	-2.82	-1E+05	0.00017
E9Q1S3	SEC23A	1.7267	0.3886	-6.215	-1E+05	7.44E-05
Q6P9K8	CASKIN1	5.0167	0.1608	-4.154	-1E+05	7.73E-05
Q76MZ3	PPP2R1A	3.39	0.0807	-2.779	-1E+05	1.39E-05
Q6ZWV3	RPL10	4.0433	0.2548	-5.39	-98310	0.00124
Q62073	MAP3K7	2.17	0.0317	-0.974	-1E+05	2.67E-05
Q6DFV3	ARHGAP21	4.85	0.0704	-2.475	-1E+05	3.15E-05
Q8CBB6	HIST1H2BQ	1.6767	0.1614	-4.163	-98956	0.00077
Q68FF6	GIT1	0.82	0.4506	-6.587	-1E+05	1.17E-05
Q99JY9	ACTR3	2.35	0.074	-2.568	-99827	0.00029
P28660	NCKAP1	3.5867	0.1393	-3.837	-1E+05	1.51E-05
Q9QXS1	PLEC	0.6433	0.2975	-5.723	-1E+05	2.68E-05
Q9EPN1	NBEA	1.19	0.4449	-6.541	-1E+05	1.75E-05
P62889	RPL30	3.2633	0.1287	-3.662	-99827	0.00046
Q80TV8	CLASP1	2.29	0.0772	-2.667	-1E+05	1.75E-05
Q8QZT1	ACAT1	2.2	0.1021	-3.225	-1E+05	0.00025
P43006	SLC1A2	5.64	0.0278	-0.743	-1E+05	1.97E-05
Q9DB20	ATP5PO	1.0967	0.2541	-5.38	-8	0.02998
Q9JLM8	DCLK1	3.69	0.0538	-1.873	-1E+05	6.33E-06
O55143	ATP2A2	-0.467	0.6978	-7.07	-1E+05	6.26E-05
P62852	RPS25	1.3267	0.3333	-5.941	-3.333	0.02695
P03995	GFAP	2.98	0.2323	-4.854	-1E+05	2.27E-05
P48453	PPP3CB	5.1067	0.0715	-2.51	-1E+05	1.15E-05
Q9D8N0	EEF1G	3.6533	0.2276	-4.81	-99548	0.00049

P19253	RPL13A	2.48	0.1349	-3.763	-1E+05	0.0001
Q8BFQ4	WDR82	3.0933	0.0807	-2.777	-1E+05	2.10E-05
P41105	RPL28	2.39	0.3238	-5.888	-42.99	0.00168
F8VPU2	FARP1	2.1267	0.1444	-3.924	-1E+05	4.68E-05
A2A690	TANC2	1.03	0.3218	-5.877	-1E+05	2.59E-05
Q01853	VCP	-0.01	1	-7.257	-95352	0.01528
Q9JKK7	TMOD2	3.25	0.0872	-2.943	-5.6	0.00926
G3X928	SEC23IP	4.7167	0.2253	-4.793	-11	0.04484
P47757	CAPZB	2.8567	0.0138	0.2454	-1E+05	1.75E-05
H7BX08	CAMSAP2	2.3967	0.0647	-2.311	-1E+05	2.46E-05
A0A1B0GSX0	LDHA	2.1033	0.0185	-0.151	-96349	0.0067
Q9ES97	RTN3	1.86	0.1138	-3.427	-1E+05	3.55E-05
A1BN54	ACTN1	2.7567	0.0581	-2.005	-1E+05	6.71E-05
P18872	GNAO1	3.1233	0.0816	-2.809	-1E+05	1.34E-05
P61255	RPL26	3.0133	0.0632	-2.226	-4.739	0.02345
Q8K0U4	HSPA12A	2.3867	0.1681	-4.236	-1E+05	2.37E-05
P48962	SLC25A4	4.28	0.058	-1.992	-11.33	0.00144
Q9EQZ6	RAPGEF4	0.35	0.5409	-6.823	-1E+05	4.99E-05
B7ZNF6	CTNND2	0.5533	0.3013	-5.744	-1E+05	5.94E-05
P18760	CFL1	3.1733	0.0275	-0.709	-1E+05	9.19E-05
A2A5Y4	KANSL1	1.67	0.2102	-4.638	-1E+05	0.00017
O70161	PIP5K1C	3.1933	0.0102	0.5623	-1E+05	2.68E-05
P61358	RPL27	2.67	0.2226	-4.763	-10	0.00291
Q920I9	WDR7	4.6233	0.1468	-3.958	-1E+05	2.83E-05
P42932	CCT8	2.6267	0.2219	-4.751	-1E+05	7.10E-05
A0A338P769	5-Sep	2.21	0.2829	-5.611	-1E+05	1.56E-05
P70333	HNRNPH2	3.2833	0.1452	-3.939	-1E+05	6.07E-05
P63101	YWHAZ	4.5567	0.0968	-3.126	-20	0.00139
Q9DBN5	LONP2	6.64	0.0008	1.9925	1	0.50437
Q3UHL1	CAMKV	3.8967	0.1119	-3.39	-1E+05	2.74E-05
O35129	PHB2	2.6933	0.2597	-5.439	-10	0.00309
A0A2R8VHH2	SYNGAP1	2.2833	0.0356	-1.245	-1E+05	6.43E-05
P59598	ASXL1	4.9367	0.1335	-3.741	-1E+05	0.00013
P56399	USP5	2.0733	0.2473	-5.189	-99827	0.00042
D3YZU1	SHANK1	-0.677	0.7568	-7.132	-1E+05	6.88E-05
P09405	NCL	2.2367	0.2473	-5.111	-5.089	0.04269
Q571K4	TAB3	2.3267	0.1142	-3.436	-1E+05	0.00027
Q5DTN8	JAKMIP3	1.5	0.0647	-2.31	-1E+05	6.74E-05
Q5PRE5	PROSER1	2.8	0.0189	-0.199	-98310	0.00117
O54774	AP3D1	1.4033	0.2878	-5.659	-1E+05	6.71E-05

Q9QYC0	ADD1	3.63	0.247	-4.961	-1E+05	3.87E-05
Q9CVB6	ARPC2	2.7	0.131	-3.693	-7.274	0.00689
Q8BP67	RPL24	3.4167	0.0316	-0.966	-3	0.08524
Q9CRB9	CHCHD3	1.2433	0.5411	-6.825	-99828	0.00043
P80315	CCT4	1.5067	0.2403	-4.921	-98958	0.00064
O09167	RPL21	2.0267	0.1895	-4.449	-98312	0.00105
Q91VA7	IDH3B	3.2933	0.1803	-4.366	-26	0.00043
P62267	RPS23	3.3433	0.0589	-2.049	-9	0.02345
Q80TE7	LRRC7	1.4633	0.4367	-6.397	-1E+05	3.04E-05
Q8R570	SNAP47	3.46	0.2473	-5.117	-1E+05	7.10E-05
Q8VEM8	SLC25A3	2.9167	0.0855	-2.907	-1E+05	6.43E-05
Q9ERU9	RANBP2	0.61	0.4269	-6.36	-1E+05	0.00058
Q5SRY7	FBXW11	1.55	0.4422	-6.413	-1E+05	9.19E-05
P80318	CCT3	1.2367	0.4826	-6.689	-1E+05	0.0001
P56480	ATP5F1B	1.5267	0.2473	-5.268	-97595	0.00205
A0A498WGS3	MBP	6.2433	0.0117	0.4338	-1E+05	7.36E-06
Q8CC35	SYNPO	1.38	0.3093	-5.793	-1E+05	0.00019
A0A0A0MQ79	PRRC2C	1.0033	0.3071	-5.781	-46.99	0.00154
Q5RJI5	BRSK1	2.6867	0.3701	-6.128	-1E+05	0.00016
Q80XN0	BDH1	4.3567	0.0983	-3.162	-98641	0.00081
Q8VDN2	ATP1A1	2.5533	0.1803	-4.362	-1E+05	7.10E-05
Q6A065	CEP170	2.0067	0.5069	-6.75	-1E+05	8.78E-05
E9Q1G8	7-Sep	4.4867	0.1181	-3.499	-1E+05	3.87E-05
P17225	PTBP1	-0.453	0.7332	-7.111	-95873	0.00938
P68404	PRKCB	2.1367	0.22	-4.728	-1E+05	8.55E-05
P48722	HSPA4L	2.4267	0.4251	-6.352	-1E+05	0.00012
Q80YA9	CNKSR2	2.4033	0.0322	-1.035	-1E+05	6.43E-05
P14094	ATP1B1	2.14	0.2053	-4.574	-7	0.00637
P12382	PFKL	3.47	0.0706	-2.488	-1E+05	8.64E-05
Q569Z6	THRAP3	-1.3	0.6868	-7.058	-17	0.02102
Q922B2	DARS	1.34	0.2721	-5.538	-96795	0.00416
P80317	CCT6A	1.7167	0.2967	-5.709	-98312	0.00107
D3YXK0	JAKMIP2	1.7633	0.2044	-4.561	-1E+05	6.71E-05
P17156	HSPA2	1.3733	0.284	-5.624	-1E+05	7.90E-05
P84099	RPL19	2.5233	0.2079	-4.601	-98956	0.00076
P67778	PHB	0.7767	0.4449	-6.445	-4.75	0.017
P80314	CCT2	2.01	0.0717	-2.523	-98641	0.001
P80316	CCT5	2.1733	0.4449	-6.436	-98957	0.00068
A0A0J9YUN4	DNM1	1.8133	0.0747	-2.601	-1E+05	2.74E-05
Q9WU78	PDCD6IP	3.42	0.2529	-5.366	-1E+05	0.00016
P80313	CCT7	1.5033	0.4449	-6.522	-97598	0.00243

Q9Z2C4	MTMR1	3.2533	0.1144	-3.442	-1E+05	3.83E-05
E9Q455	TPM1	0.9867	0.3879	-6.208	-99548	0.00043
Q0KL02	TRIO	0.7367	0.3725	-6.143	-1E+05	9.82E-05
Q63810	PPP3R1	4.4367	0.1526	-4.055	-1E+05	4.18E-05
Q9Z1W9	STK39	3.4167	0.1692	-4.251	-1E+05	6.88E-05
Q9ES28	ARHGEF7	2.3667	0.1549	-4.1	-1E+05	0.00026
Q9WUA3	PFKP	2.8167	0.2473	-5.099	-1E+05	0.00016
Q9R1R2	TRIM3	4.02	0.1739	-4.296	-1E+05	0.00012
Q8BH44	CORO2B	3.5933	0.1052	-3.279	-13.37	0.00141
Q80U63	MFN2	1.2267	0.4449	-6.541	-1E+05	0.00023
Q7TQH0	ATXN2L	0.6967	0.3344	-5.951	-1E+05	8.55E-05
Q80SW1	AHCYL1	2.81	0.0637	-2.258	-1E+05	6.60E-05
P20152	VIM	3.0167	0.2993	-5.733	-98957	0.00068
P63037	DNAJA1	4.5	0.0089	0.7087	-99258	0.00081
P62900	RPL31	2.82	0.0637	-2.257	-98956	0.00076
P35486	PDHA1	4.7133	0.0862	-2.924	-1E+05	6.19E-05
O70305	ATXN2	3.41	0.2767	-5.579	-1E+05	0.00019
Q8BG05	HNRNPA3	0.65	0.7847	-7.158	-99259	0.00064
P29788	VTN	0.6233	0.4337	-6.387	-94785	0.02345
P60335	PCBP1	5.69	0.0345	-1.18	-1E+05	0.00011
Q3UHK6	TENM4	0.8633	0.4601	-6.62	-1E+05	0.00019
Q8BJH1	ZC2HC1A	3.4667	0.0704	-2.466	-1E+05	0.0001
P61161	ACTR2	3.6267	0.0671	-2.377	-21	0.00105
D3YWN7	MAP7	2.03	0.0776	-2.681	-1E+05	0.00023
H7BX95	SRSF1	2.8067	0.0981	-3.156	-1E+05	0.00033
Q3TES0	IQSEC3	1.6433	0.339	-5.978	-1E+05	0.00027
Q8BUV3	GPHN	2.59	0.0704	-2.474	-1E+05	0.00015
Q8BGR3	CAMK4	2.1333	0.2493	-5.323	-1E+05	0.00015
P61164	ACTR1A	2.9767	0.2473	-4.981	-1E+05	0.0001
P62849	RPS24	3.8133	0.042	-1.49	-96792	0.00393
Q80ZX0	SEC24B	3.38	0.2473	-5.235	-1E+05	0.0002
E9Q7C9	KLC1	2.8933	0.3425	-6.008	-1E+05	0.0001
A0A087WPK3	LRRFIP1	1.54	0.167	-4.222	-1E+05	0.00017
P06837	GAP43	4.75	0.0783	-2.714	-39	0.00201
P63085	MAPK1	3.2533	0.2578	-5.417	-1E+05	5.73E-05
Q9D6M3	SLC25A22	4.8067	0.0101	0.5766	-1E+05	0.00015
P59764	DOCK4	1.26	0.2546	-5.384	-1E+05	0.00017
Q8CIE6	COPA	-1.077	0.2768	-5.581	-94144	0.0412
Q3UMP4	SERBP1	4.4267	0.2473	-5.302	-27	0.00549
A2AHJ7	DGKZ	0.95	0.4095	-6.292	-1E+05	0.00019
Q6ZWZ4	RPL36	1.4233	0.0606	-2.112	-6.338	0.0256

Q9QY01	ULK2	1.3933	0.2473	-5.089	-1E+05	0.00019
P11983	TCP1	3.0267	0.3278	-5.912	-98641	0.00083
Q9QVP9	PTK2B	2.83	0.3423	-6.003	-1E+05	0.00017
Q8C3Q5	SHISA7	1.9567	0.3706	-6.131	-1E+05	0.00012
E9Q6E0	MAPK8IP3	3.1133	0.3664	-6.107	-1E+05	0.0002
E9Q828	ATP2B4	1.8467	0.2634	-5.47	-1E+05	0.00019
Q9CQA3	SDHB	5.49	0.0829	-2.849	-1E+05	0.00023
A0A0R4J0B4	CMAS	2.55	0.4124	-6.303	-96795	0.00416
P62141	PPP1CB	3.0033	0.3194	-5.858	-98310	0.00117
P83882	RPL36A	2.6733	0.2508	-5.342	-21	0.01035
P47753	CAPZA1	2.71	0.3743	-6.152	-95351	0.01408
Q7TMK9	SYNCRIP	1.69	0.066	-2.348	-97597	0.00208
Q9WUM5	SUCLG1	0.12	0.9749	-7.252	-97962	0.00142
Q6NS52	DGKB	2.11	0.1608	-4.156	-1E+05	0.00018
Q3UHU5	MTCL1	0.44	0.4282	-6.366	-1E+05	0.00019
P68510	YWHAH	3.0567	0.2226	-4.767	-1E+05	0.0003
B2RXT3	OGDHL	3.8867	0.211	-4.646	-1E+05	7.33E-05
P14115	RPL27A	3.7767	0.0322	-1.046	-12	0.00932
Q8BG95	PPP1R12B	5.2333	0.1255	-3.608	-99827	0.00029
O70325	GPX4	2.6	0.1824	-4.392	-1E+05	7.33E-05
A2ATK9	FAM171A1	2.2767	0.0925	-3.049	-1E+05	0.00019
P10639	TXN	3.91	0.1981	-4.517	-96795	0.00393
P48318	GAD1	1.71	0.2851	-5.636	-1E+05	0.00033
Q8VHJ5	MARK1	3.6267	0.1142	-3.437	-1E+05	0.0001
Q3TUQ7	PRKAA1	1.7467	0.4478	-6.573	-98641	0.00081
Q8CCJ9	PHF20L1	6.64	0.0008	1.9925	1	0.50437
A0A0N4SW73	RAB11FIP5	1.9267	0.21	-4.629	-99548	0.00049
P28656	NAP1L1	4.2967	0.1335	-3.741	-97962	0.00154
E9PU87	SIK3	0.65	0.2699	-5.524	-1E+05	0.00014
A0A1B0GS91	SVIL	6.64	0.0008	1.9925	1	0.50437
Q6PB44	PTPN23	0.5133	0.3726	-6.145	-1E+05	0.00012
D6REV1	ASXL2	2.68	0.1397	-3.851	-96350	0.00643
Q99KJ8	DCTN2	6.0967	0.0213	-0.351	-1E+05	0.00023
O55142	RPL35A	3.1667	0.3106	-5.806	-25	0.00673
A0A0G2JEG8	AMPH	2.8467	0.0105	0.5351	-1E+05	0.00023
Q3UNH4	GPRIN1	0.28	0.7197	-7.096	-35	0.00324
F8WJE3	KANSL2	2.0633	0.2742	-5.56	-97966	0.00147
P43277	H1-3	2.3733	0.2749	-5.565	-6.982	0.01276
Q62095	DDX3Y	1.99	0.0179	-0.062	-7	0.09747

Q6R891	PPP1R9B	1.1533	0.1452	-3.936	-99827	0.00053
A0A1Y7VNZ6	MARK3	3.3	0.2621	-5.459	-1E+05	0.00023
Q60598	CTTN	1.8333	0.1448	-3.93	-1E+05	0.00017
Q7TPV2	DZIP3	1.2567	0.2887	-5.665	-1E+05	0.0001
Q2M3X8	PHACTR1	0.24	0.6947	-7.066	-33	0.0031
A0A494BB75	WDR26	2.7933	0.3932	-6.23	-97206	0.00276
Q6ZPQ6	PITPNM2	4.7333	0.2226	-4.76	-1E+05	0.00011
Q60865	CAPRIN1	2.9433	0.3106	-5.807	-97598	0.00208
Q61937	NPM1	2.1933	0.4449	-6.462	-27	0.00582
Q9JI90	RNF14	1.2567	0.2637	-5.481	-1E+05	0.00021
P99024	TUBB5	5.98	0.0314	-0.927	-37	0.00239
P60202	PLP1	5.5933	0.0379	-1.342	-6	0.01344
Q9Z2X1	HNRNPF	2.9033	0.2473	-5.235	-95351	0.01408
Q8K0T0	RTN1	1.4533	0.4454	-6.55	-99259	0.00053
Q61171	PRDX2	1.9567	0.1537	-4.081	-11	0.01347
G3UW85	ERH	4.7467	0.22	-4.734	-94144	0.0412
Q5DTY9	KCTD16	3.3667	0.2276	-4.811	-1E+05	0.0002
Q3U741	DDX17	3.9333	0.1796	-4.349	-99550	0.00049
Q9Z2I9	SUCLA2	2.1333	0.1179	-3.494	-98641	0.001
B1AZP2	DLGAP4	2.4033	0.4435	-6.419	-1E+05	0.00033
O08919	NUMBL	3.1833	0.2975	-5.721	-99827	0.0003
P63011	RAB3A	1.57	0.4251	-6.352	-1E+05	0.00011
Q3UHB8	CCDC177	5.31	0.1121	-3.395	-99548	0.00051
Q5SSL4	ABR	0.3167	0.6723	-7.029	-1E+05	0.00033
Q6PCP5	MFF	5.4867	0.0833	-2.859	-98957	0.00068
Q60749	KHDRBS1	2.1767	0.4478	-6.573	-99548	0.00059
Q8CCF0	PRPF31	1.3	0.3423	-6.004	-97595	0.00243
Q6ZWV7	RPL35	2.8633	0.339	-5.981	-7	0.03868
S4R1C4	ATP2B2	5.27	0.1184	-3.508	-99549	0.00049
Q6PAJ1	BCR	4.28	0.2699	-5.525	-99548	0.00068
Q80U23	SNPH	5.67	0.0632	-2.226	-99259	0.00053
Q8C1B7	SEPTIN11	5.7333	0.058	-1.985	-99827	0.00053
G5E8J2	ANK1	2.9667	0.0589	-2.036	-99827	0.00029
P28740	KIF2A	1.9833	0.3952	-6.238	-1E+05	0.00013
A0A0A6YWI6	DCLK2	4.1	0.1656	-4.204	-99259	0.00057
E9Q456	TPM1	1.5367	0.0263	-0.65	1	0.50437
Q9D2G2	DLST	1.6933	0.464	-6.635	-97206	0.00276
O88196	TTC3	3.31	0.0642	-2.278	-1E+05	0.0002
Q3UMT1	PPP1R12C	1.18	0.273	-5.543	-99827	0.00056
Q9D1M0	SEC13	4.2567	0.2742	-5.559	-94144	0.0412

P23242	GJA1	1.8267	0.0341	-1.149	-4.019	0.09383
Q60960	KPNA1	3.3133	0.2529	-5.359	-99259	0.00053
O70503	HSD17B12	5.9567	0.0322	-1.036	1	0.50437
Q91V61	SFXN3	1.8467	0.5299	-6.801	-99548	0.00043
Q9ERD7	TUBB3	3.66	0.0055	1.1221	-1E+05	3.21E-05
Q812A2	SRGAP3	1.6767	0.2473	-5.087	-99548	0.00044
Q8BFU3	RNF214	4.9767	0.1689	-4.246	-98313	0.00107
A0A338P6K9	QSER1	6.64	0.0008	1.9925	-98642	0.00137
O54950	PRKAG1	5.9767	0.0314	-0.943	-9	0.06498
A0A494B9F0	NEDD4L	1.09	0.3882	-6.213	-99827	0.0003
P21126	UBL4A	6.1133	0.0199	-0.265	-97962	0.00142
Q9JM52	MINK1	0.7267	0.6623	-7.017	-99258	0.00062
Q80YN3	BCAS1	2.3167	0.0322	-1.042	-1E+05	0.00027
Q6ZQ58	LARP1	-2.487	0.3423	-5.997	-25	0.00878
P84078	ARF1	2.14	0.0457	-1.624	-96350	0.00643
Q8C2Q7	HNRNPH1	6.64	0.0008	1.9925	1	0.50437
G3X972	SEC24C	1.9067	0.5118	-6.762	-96353	0.0067
Q8K4G5	ABLIM1	2.5167	0.1431	-3.899	-98642	0.00079
Q8CI32	BAG5	4.2533	0.1337	-3.748	-98641	0.00083
P61982	YWHAG	3.5133	0.2473	-5.052	-98310	0.00147
Q61548	SNAP91	-0.563	0.8535	-7.206	-99259	0.00057
Q3UG20	KMT2E	4.06	0.3132	-5.821	-25	0.00741
E9PZP8	HERC1	2.2167	0.3482	-6.033	-1E+05	0.00027
Q9R111	GDA	0.28	0.6863	-7.056	-98958	0.00064
Q9D1R9	RPL34	2.9633	0.1337	-3.749	-4.333	0.02826
Q9EQF5	DPYS	6.64	0.0008	1.9925	1	0.50437
E9Q9Y4	TET1	1.4367	0.22	-4.736	-98956	0.00064
Q9JIS5	SV2A	1.1633	0.4454	-6.551	-29	0.00657
Q9Z0E0	NCDN	-0.927	0.2575	-5.412	-98641	0.00119
P63330	PPP2CA	2.4967	0.2361	-4.887	-1E+05	0.00016
P27671	RASGRF1	3.3333	0.2637	-5.476	-99260	0.00079
Q9R0Q6	ARPC1A	2.79	0.2412	-4.927	-99827	0.00033
Q9CT10	RANBP3	-1.18	0.7068	-7.082	-1E+05	0.00023
Q8CF89	TAB1	3.3633	0.3365	-5.968	-1E+05	0.00025
P08553	NEFM	2.25	0.2322	-4.851	-1E+05	0.0001
O08539	BIN1	2.99	0.3327	-5.935	-99260	0.00052
Q99L90	MCRS1	2.7867	0.3498	-6.04	-97965	0.00165
Q5SNZ0	CCDC88A	2.5133	0.407	-6.281	-31	0.0048
Q9D415	DLGAP1	0.19	0.53	-6.802	-98956	0.00081
Q9JJV2	PFN2	3.5167	0.1549	-4.101	-11	0.01049

Q9CR62	SLC25A11	2.43	0.2153	-4.68	-98642	0.00079
Q6ZPJ3	UBE2O	5.3467	0.1058	-3.289	-1E+05	0.00023
A2AG50	MAP7D2	0.7433	0.4457	-6.555	-99827	0.00033
O54781	SRPK2	2.0767	0.0644	-2.285	-98956	0.00076
P08551	NEFL	6.3633	0.0057	1.0885	-99259	0.00053
Q8K310	MATR3	0.4933	0.4963	-6.72	-99548	0.00043
A0A0N4SVL0	EIF4G3	6.64	0.0008	1.9925	-97966	0.00147
Q8VBU5	PDE4B	4.6733	0.1189	-3.516	-1E+05	0.00023
Q62318	TRIM28	2.83	0.1803	-4.36	-99548	0.00044
B1AXZ5	ELAVL2	0.6167	0.8031	-7.173	-99259	0.00053
E9Q3M9	2010300C02RIK	3.47	0.2473	-5.115	-99259	0.00057
E9Q4K0	ABLIM2	4.2133	0.1395	-3.843	-99828	0.00029
P07901	HSP90AA1	0.63	0.7791	-7.154	-98641	0.00083
Q5U4C1	GPRASP1	1.6167	0.2831	-5.614	-99827	0.00056
Q61584	FXR1	0.8033	0.4251	-6.349	-95351	0.01408
Q14BB9	MAP6D1	6.14	0.0183	-0.125	-98310	0.00137
Q6P1F6	PPP2R2A	2.9667	0.3238	-5.888	-98310	0.0012
Q14CH0	FAM171B	4.9233	0.1803	-4.366	-99259	0.00057
Q62425	NDUFA4	4.5567	0.0822	-2.829	-12	0.00885
A2A9M4	DOCK7	3.7567	0.2573	-5.41	-98312	0.00208
Q64332	SYN2	0.68	0.7231	-7.1	-98310	0.00137
P59999	ARPC4	2.7367	0.0766	-2.654	-98312	0.00105
A2AWI7	SH3GLB2	2.7633	0.1537	-4.079	-98313	0.00117
Q8JZU2	SLC25A1	6.06	0.0244	-0.537	-95871	0.01096
P70392	RASGRF2	6.64	0.0008	1.9925	-97962	0.0034
P99029	PRDX5	4.08	0.0213	-0.348	-97962	0.00193
Q8CBY8	DCTN4	1.88	0.2637	-5.474	-98641	0.00094
Q8BIZ1	ANKS1B	1.1267	0.3423	-6.006	-99261	0.00057
P23927	CRYAB	2.5	0.3314	-5.929	-9.823	0.01312
Q8C2Q3	RBM14	2.6233	0.3781	-6.169	-13	0.03379
B2RQC6	CAD	0.83	0.2602	-5.446	-25	0.01074
Q9DD20	METTL7B	6.64	0.0008	1.9925	1	0.50437
P47708	RPH3A	3.6933	0.2276	-4.818	-98312	0.00154
P97765	WBP2	4.2433	0.0345	-1.172	-1E+05	0.00016
Q9QYJ3	DNAJB1	5.2767	0.1123	-3.4	-99259	0.00049
Q8R5H1	USP15	0.4533	0.4449	-6.521	-97962	0.00154
P97457	MYLPF	6.64	0.0008	1.9925	1	0.50437
Q9R0P5	DSTN	4.19	0.1523	-4.043	-98310	0.00107
Q9D1H7	GET4	0.9833	0.3731	-6.147	-97962	0.00208
P60879	SNAP25	1.1767	0.3503	-6.043	-99260	0.00052

Q6GT24	PRDX6	0.38	0.7981	-7.169	-96793	0.00416
Q8BX10	PGAM5	3.7467	0.22	-4.734	-98956	0.00064
Q8R2R9	AP3M2	4.65	0.0949	-3.095	-98641	0.00119
P54823	DDX6	2.0367	0.2403	-4.918	-97598	0.00208
Q6PHQ9	PABPC4	3.3033	0.2597	-5.442	-19	0.01427
Q61151	PPP2R5E	2.1467	0.0362	-1.27	-98641	0.00079
Q9WTX5	SKP1	3.1267	0.0417	-1.469	-97962	0.00165
Q8C7M3	TRIM9	3.6267	0.2336	-4.867	-99259	0.00052
P55937	GOLGA3	6.64	0.0008	1.9925	1	0.50437
P62196	PSMC5	6.64	0.0008	1.9925	-96349	0.00586
Q9CQV8	YWHAB	4.18	0.1824	-4.391	-97962	0.00154
Q8CI94	PYGB	2.12	0.0197	-0.251	-98310	0.00137
Q8C0T5	SIPA1L1	3.32	0.2843	-5.627	-97598	0.00208
E9Q804	ANKRD17	0.8167	0.3037	-5.763	-97595	0.00193
Q99PU8	DHX30	3.8233	0.208	-4.606	-98641	0.00081
P58871	TNKS1BP1	2.57	0.3969	-6.244	-13	0.03379
D3Z2H9	TPM3-RS7	1.26	0.2637	-5.485	-11	0.04484
A2AGT5	CKAP5	2.7967	0.2473	-5.009	-97962	0.00154
G5E924	HNRNPL	2.57	0.3932	-6.231	-95873	0.00938
Q8VIJ6	SFPQ	3.79	0.2155	-4.683	-95871	0.01096
Q8C3F2	FAM120C	3.1767	0.2845	-5.632	-97598	0.00243
A0A0G2JFT8	RUFY3	3.04	0.018	-0.089	-98957	0.00068
P68040	RACK1	3.29	0.2865	-5.647	-95352	0.01528
Q99KB8	HAGH	2.0167	0.1391	-3.83	-96792	0.00454
A0A0B4J1E7	KPNA4	6.64	0.0008	1.9925	1	0.50437
Q6URW6	MYH14	2.9167	0.0789	-2.734	-99258	0.00077
E9QKR0	GNB2	2.16	0.2473	-5.232	-98958	0.00064
P63168	DYNLL1	5.3133	0.0909	-3.017	-98957	0.00061
P62814	ATP6V1B2	-0.477	0.4506	-6.586	-97963	0.00154
Q61097	KSR1	5.0833	0.1494	-3.994	-97962	0.00208
Q5DTT2	PSD	6.64	0.0008	1.9925	-97596	0.00261
Q9QXZ0	MACF1	0.9567	0.407	-6.28	-98641	0.00178
Q8BHJ5	TBL1XR1	1.1733	0.0378	-1.328	-97962	0.00147
E9QMC2	GRM5	0.7967	0.4974	-6.724	-97208	0.00504
Q8R4U7	LUZP1	1.35	0.3882	-6.212	-97962	0.00154
P63089	PTN	1.56	0.0314	-0.941	-97598	0.00208
Q6A4J8	USP7	2.1367	0.4528	-6.595	-97966	0.00147
D3YTQ9	RPS15	2.0867	0.4752	-6.671	-97962	0.00165
Q8K0S0	PHYHIP	6.64	0.0008	1.9925	-98642	0.00094
P97427	CRMP1	5.6133	0.0693	-2.431	-99259	0.00053

Q8BXK8	AGAP1	0.4767	0.4506	-6.586	-98310	0.00147
D6RI62	ASXL2	5.36	0.1034	-3.25	-97962	0.00193
A0A0A6YWM5	RAB3GAP2	4.3133	0.1303	-3.681	-97962	0.00195
Q8C0M9	ASRGL1	5.3933	0.0979	-3.151	-97206	0.00276
Q8R5H6	WASF1	-0.16	0.8494	-7.203	-97962	0.00154
Q5F4T0	TRPM3	3.1833	0.2975	-5.721	-23	0.01255
P50516	ATP6V1A	5.06	0.1525	-4.051	-97965	0.00165
Q7TPW1	NEXN	-0.243	0.6601	-7.013	-98642	0.00147
H3BIV5	AKAP5	1.1433	0.2556	-5.397	-98310	0.00107
D3YZC9	SF1	3.3333	0.249	-5.319	-97965	0.00165
Q99JN2	KLHL22	3.0933	0.3002	-5.739	-98310	0.00107
P62869	ELOB	1.8867	0.2762	-5.574	-95873	0.00938
Q8BHL5	ELMO2	4.9967	0.0909	-3.015	-98641	0.00083
Q8CIP4	MARK4	3.8867	0.2102	-4.633	-98641	0.00147
P31650	SLC6A11	3.6333	0.2637	-5.475	-97210	0.00342
P97315	CSRP1	1.13	0.5826	-6.902	-97962	0.00165
O88935	SYN1	0.3733	0.4485	-6.577	-97595	0.00243
Q5SSM3	ARHGAP44	5.6733	0.0632	-2.213	-98641	0.00083
Q7TME0	PLPPR4	6.64	0.0008	1.9925	-98311	0.00154
Q9CQU5	ZWINT	1.53	0.2088	-4.612	-97965	0.00165
Q9JM76	ARPC3	4.4267	0.2473	-5.302	-96349	0.00586
P62631	EEF1A2	5.5	0.0451	-1.599	-97962	0.00193
Q8CI08	SLAIN2	4.1767	0.2893	-5.67	-97602	0.00243
S4R1Y1	CUL9	1.7567	0.2525	-5.355	-97598	0.00208
Q68FH0	PKP4	6.64	0.0008	1.9925	-97962	0.00154
Q3TEA8	HP1BP3	2.38	0.2096	-4.624	-96795	0.00416
Q9DCB4	ARPP21	6.64	0.0008	1.9925	-97962	0.00142
Q9QYG0	NDRG2	3.4533	0.253	-5.368	-95351	0.01408
O55022	PGRMC1	6.64	0.0008	1.9925	1	0.50437
A0A0R4J0A6	SLC17A6	2.74	0.249	-5.32	-98957	0.00062
E9PXF8	SBF2	4.4033	0.2508	-5.339	-97595	0.00193
Q9D6F9	TUBB4A	4.86	0.0697	-2.446	-98312	0.00107
A2AEW9	GRIPAP1	1.89	0.5233	-6.785	-97208	0.00504
Q9CXS4	CENPV	3.5	0.2473	-5.286	-96792	0.00454
Q9Z1S5	SEPTIN3	1.11	0.4449	-6.532	-98310	0.00124
Q04447	CKB	5.25	0.1227	-3.563	-97206	0.00276
P04627	ARAF	3.1667	0.2767	-5.579	-98311	0.00107
H3BIW6	PLCH2	3.09	0.3619	-6.09	-97595	0.00193
A6ZI47	ALDOART2	1.83	0.6022	-6.932	-19	0.0136
A0A5H1ZRL1	SPIRE1	2.5533	0.4449	-6.43	-97963	0.00142

Q60930	VDAC2	4.1267	0.1523	-4.04	-96351	0.0067
A0A1Y7VL44	TTC7B	0.0833	0.6863	-7.056	-97962	0.00154
Q8C570	RAE1	3.4933	0.2958	-5.704	-98311	0.00107
Q9Z268	RASAL1	0.4933	0.3197	-5.862	-97598	0.00208
Q80T41	GABBR2	4.95	0.1751	-4.307	-98311	0.00137
Q921F2	TARDBP	-2.483	0.4114	-6.298	-11	0.04484
Q6PER3	MAPRE3	3.0767	0.0149	0.1677	-98641	0.00094
V9GXM1	ARFGAP1	3.4267	0.4449	-6.453	-19	0.017
P28741	KIF3A	-0.687	0.274	-5.553	-98311	0.00159
P10922	H1-0	4.83	0.2044	-4.566	-96349	0.0067
A2A699	FAM171A2	2.6733	0.0807	-2.788	-96792	0.00454
P60843	EIF4A1	6.64	0.0008	1.9925	1	0.50437
H3BKQ7	PPP1R9A	6.64	0.0008	1.9925	-96792	0.00454
D3YYK8	MAPRE2	3.17	0.2742	-5.559	-21	0.01074
P70372	ELAVL1	0.3867	0.4576	-6.611	-94785	0.02345
Q8K212	PACS1	2.3067	0.4449	-6.457	-97595	0.00205
A0A1D5RMH7	PSD3	3.59	0.2637	-5.478	-97962	0.00252
G3UXL2	PRPS1L3	4.7267	0.223	-4.773	-97206	0.00393
Q9D1P2	KAT8	6.64	0.0008	1.9925	-17	0.01784
F6RJV6	LANCL2	2.9633	0.1358	-3.78	-97962	0.00142
Q9DBE7	STAU1	6.64	0.0008	1.9925	1	0.50437
A0A087WNT1	ELOC	3.3967	0.2473	-5.262	-96795	0.00393
E9Q4Z6	DZANK1	1.4367	0.2634	-5.47	-97598	0.00208
A0A0G2JGW6	CDKL5	2.88	0.3218	-5.876	-97962	0.00165
Q3UID0	SMARCC2	2.9133	0.3782	-6.171	-97595	0.00193
O35465	FKBP8	2.3267	0.4449	-6.441	-15	0.02345
B9EJA2	CTTNBP2	2.5233	0.3101	-5.799	-97206	0.00262
Q542V3	SRSF4	4.38	0.1216	-3.548	-21	0.01035
A0A0R4J1F4	MADD	4.4267	0.2473	-5.302	-21	0.01427
P68181	PRKACB	5.51	0.0807	-2.783	-97595	0.00193
Q3TLP8	RAC1	2.0533	0.0591	-2.061	-97595	0.00261
Q80UG5	SEPTIN9	1.05	0.3681	-6.116	-94785	0.02345
Q8CG76	AKR7A2	6.64	0.0008	1.9925	1	0.50437
P62317	SNRPD2	0.1733	0.8093	-7.178	-95871	0.00938
P49615	CDK5	2.7067	0.018	-0.093	-99548	0.0005
Q7TNC4	LUC7L2	3.2367	0.2676	-5.511	-13	0.03379
O88685	PSMC3	2.8333	0.3333	-5.94	-95351	0.01528
P31324	PRKAR2B	3.3033	0.268	-5.514	-97595	0.00243
A0A2R8VK79	RBFOX1	5.3167	0.0669	-2.369	-97962	0.00142

Q60737	CSNK2A1	2.95	0.3093	-5.793	-96792	0.00393
P12849	PRKAR1B	6.3033	0.0084	0.7643	-97595	0.00261
P16054	PRKCE	1.7667	0.2525	-5.353	-19	0.02345
Q9R0P9	UCHL1	4.1267	0.1526	-4.062	-97598	0.00243
G3X932	ARHGAP39	2.03	0.4761	-6.675	-97206	0.00276
O54962	BANF1	1.5633	0.3423	-5.998	-9	0.01867
Q8R071	ITPKA	2.92	0.3218	-5.877	-96351	0.00586
P62743	AP2S1	2.51	0.1397	-3.852	-9	0.01867
P33173	KIF1A	3.23	0.2618	-5.455	-97595	0.00261
Q9D898	ARPC5L	5.37	0.1021	-3.221	-96349	0.00586
E0CXB9	CTNNA2	5.66	0.0637	-2.262	-97595	0.00261
Q9DB41	SLC25A18	2.7533	0.3562	-6.069	-97598	0.00208
Q62189	SNRPA	0.54	0.8614	-7.21	-13	0.0317
Q9CXY6	ILF2	1.5467	0.3093	-5.793	-97206	0.00276
P31938	MAP2K1	3.0233	0.3174	-5.842	-98311	0.00159
A0A286YCV9	KIF13B	6.64	0.0008	1.9925	1	0.50437
P49025	CIT	2.71	0.0092	0.6676	-19	0.017
Q9CQ69	UQCRQ	2.9	0.0744	-2.589	-96349	0.00586
Q9QY76	VAPB	1.1967	0.3128	-5.819	-97597	0.00208
O70251	EEF1B	-0.103	0.9852	-7.254	-96349	0.00586
Q69ZH9	ARHGAP23	5.94	0.0333	-1.113	-96795	0.00393
B2RRE7	OTUD4	5.4533	0.0885	-2.966	-96349	0.00838
Q9ESJ4	NCKIPSD	1.64	0.2508	-5.337	-97595	0.00261
Q8VEG4	EXD2	1.0033	0.3194	-5.858	-97206	0.00276
B7ZBV9	KCNQ2	1.7833	0.5452	-6.835	-96795	0.00393
Q9Z2D6	MECP2	3.4267	0.2473	-5.162	-15	0.02345
P62897	CYCS	-0.477	0.4594	-6.617	-94144	0.0412
Q8BLG0	PHF20	6.64	0.0008	1.9925	-15	0.02345
Q9JLJ2	ALDH9A1	6.64	0.0008	1.9925	1	0.50437
Q9EP53	TSC1	2.2967	0.2906	-5.679	-17	0.02102
S4R2G0	DGKI	5.7333	0.058	-1.985	-96795	0.00393
Q78ZA7	NAP1L4	4.3667	0.1257	-3.617	-96351	0.00643
Q5SVG5	AP1B1	6.64	0.0008	1.9925	-5	0.1741
Q9DCL9	PAICS	6.64	0.0008	1.9925	1	0.50437
Q8CCT4	TCEAL5	5	0.1645	-4.193	-97598	0.00243
Q8BK64	AHSA1	2.8	0.3425	-6.008	-96792	0.00416
Q922P9	GLYR1	2.7767	0.3423	-5.995	-19	0.0136
O35344	KPNA3	2.2133	0.6797	-7.047	-95352	0.01528
Q80TK0	KIAA1107	0.7833	0.3423	-6.003	-96792	0.00454
Q99KI0	ACO2	6.0233	0.0275	-0.719	-97207	0.00342

G5E8Z3	2310050C09RIK	1.9433	0.5409	-6.824	-96349	0.0067
Q920P5	AK5	4.8133	0.2079	-4.6	-97596	0.00261
Q9WV69	DMTN	4.4267	0.2473	-5.302	-97206	0.00262
Q8BP92	RCN2	5.2433	0.042	-1.498	-97210	0.00342
Q5PR73	DIRAS2	5.9533	0.0322	-1.052	-97206	0.00393
Q8VHQ9	ACOT11	-0.537	0.3444	-6.016	-97962	0.00142
Q9R0L7	AKAP8L	3.8067	0.216	-4.689	-96350	0.00643
Q9QYB8	ADD2	2.5867	0.4449	-6.502	-96350	0.0067
A2AL85	ASPH	6.64	0.0008	1.9925	1	0.50437
D3Z2H2	CTNND1	6.64	0.0008	1.9925	1	0.50437
P62334	PSMC6	1.21	0.4449	-6.541	-94144	0.0412
Q91WG5	PRKAG2	6.64	0.0008	1.9925	-96351	0.00643
Q80X90	FLNB	6.64	0.0008	1.9925	1	0.50437
P62881	GNB5	5.5133	0.0807	-2.772	-17	0.01784
Q8K341	ATAT1	4.4667	0.1081	-3.331	-97206	0.00311
O54946	DNAJB6	5.9967	0.03	-0.848	-96792	0.00454
Q8VHH5	AGAP3	1.5533	0.2473	-5.167	-97598	0.00208
Q9JKC6	CEND1	1.6033	0.2742	-5.557	-19	0.0136
P58404	STRN4	3.1033	0.2844	-5.629	-96792	0.00504
E9PW37	RASAL2	3.3767	0.3331	-5.937	-97962	0.00208
Q8BKI2	TNRC6B	0.7033	0.4457	-6.558	-94144	0.0412
Q61990	PCBP2	0.0167	1	-7.258	-97595	0.00193
Q60972	RBBP4	1.4667	0.3338	-5.944	-99260	0.00091
A0A5F8MQC8	TECR	6.64	0.0008	1.9925	-7	0.09747
P62821	RAB1A	3.96	0.2191	-4.713	-95871	0.00938
Q61753	PHGDH	2.8667	0.2473	-5.15	-95351	0.01408
Q63844	MAPK3	2.68	0.4149	-6.316	-97206	0.00262
P08752	GNAI2	4.46	0.1081	-3.335	-97595	0.00261
O88703	HCN2	2.4767	0.4267	-6.359	-17	0.02102
P84104	SRSF3	4.68	0.2332	-4.862	-96349	0.0067
P56564	SLC1A3	5.5367	0.0779	-2.695	-95872	0.00938
P81122	IRS2	1.55	0.4449	-6.537	-17	0.017
O35098	DPYSL4	2.2467	0.4619	-6.626	-96350	0.0067
Q62418	DBNL	-1.157	0.5005	-6.733	-13	0.0419
Q8R191	SYNGR3	0.29	0.8761	-7.219	-97598	0.00205
Q6AXD2	ABI2	6.64	0.0008	1.9925	-96795	0.00393
P60122	RUVBL1	6.64	0.0008	1.9925	-95872	0.00938
Q02248	CTNNB1	4.4267	0.2473	-5.302	-15	0.02576
Q9WTM5	RUVBL2	4.7267	0.223	-4.773	-95351	0.01408
Q9ET77	JPH3	5.1633	0.1366	-3.793	-96792	0.00454
Q9Z2Y3	HOMER1	4.06	0.2276	-4.814	-15	0.02345

A0A5F8MQ25	PPP6R2	0.3333	0.4638	-6.634	-95871	0.01096
Q8K4P8	HECW1	4.3867	0.2529	-5.365	-96795	0.00416
E9Q401	RYR2	3.4667	0.2473	-5.093	-15	0.03379
Q8R349	CDC16	2.76	0.0318	-0.997	-15	0.02345
J3QMG3	VDAC3	4.2133	0.2834	-5.62	-95352	0.01528
E9QP99	GOLGA3	2.3733	0.4374	-6.4	-15	0.02345
H7BWY4	DLG1	5.34	0.1069	-3.309	-96792	0.00393
Q8C163	EXOG	3.05	0.3173	-5.839	-13	0.03379
Q9WV55	VAPA	1.59	0.6125	-6.948	-96349	0.00586
Q9JJD0	THAP11	1.8967	0.5213	-6.78	-95872	0.00938
Q9D823	RPL37	4.33	0.1272	-3.642	-15	0.03379
A2A7S7	YARS	2.5033	0.4091	-6.289	-13	0.03379
O89053	CORO1A	2.43	0.0942	-3.078	-97210	0.00342
P35802	GPM6A	4.7767	0.1269	-3.633	-97206	0.00276
Q8VDP4	CCAR2	0.67	0.4732	-6.665	-17	0.01784
E9PX29	SPTBN4	2.8867	0.3467	-6.025	-13	0.03379
Q9D051	PDHB	4.0233	0.2473	-5.052	-98310	0.00107
A0A0R4J008	HDAC2	4.1467	0.1641	-4.188	-96349	0.00586
Q8BH66	ATL1	4.75	0.22	-4.728	-96792	0.00454
A2AH22	AMBRA1	3.0533	0.3057	-5.775	-95871	0.01096
O70589	CASK	2.68	0.3647	-6.1	-7	0.03868
Q64336	TBR1	0.2533	0.4834	-6.692	-96349	0.0067
Q8C729	FAM126B	3.1467	0.3018	-5.747	-95872	0.00938
P26645	MARCKS	6.64	0.0008	1.9925	-7	0.09747
A2ARS0	ANKRD63	3.2867	0.2529	-5.365	-95872	0.00938
Q8BP00	IQCB1	5.5067	0.0809	-2.794	-96349	0.0067
Q52KI8	SRRM1	3.1067	0.287	-5.65	-96793	0.00504
D3YYH0	PEX5L	4.64	0.2427	-4.937	-96350	0.00643
Q8BL97	SRSF7	3.0867	0.3174	-5.843	-95873	0.00938
P58281	OPA1	1.4933	0.2473	-5.239	-95353	0.01528
Q6PH08	ERC2	-0.507	0.7062	-7.081	-13	0.0419
G3XA57	RAB11FIP2	-0.007	1	-7.258	-96349	0.00586
Q9JJC6	RILPL1	2.9033	0.3352	-5.958	-15	0.02576
Q9CWZ7	NAPG	2.2133	0.4449	-6.54	-96795	0.00393
Q80Z38	SHANK2	2.6767	0.371	-6.137	-96792	0.00504
Q5F2E7	NUFIP2	0.2667	0.5007	-6.733	-11	0.04484
Q62093	SRSF2	3.8467	0.2861	-5.642	-97206	0.00276
Q64337	SQSTM1	6.64	0.0008	1.9925	1	0.50437
Q6P5B5	FXR2	2.17	0.4474	-6.569	-95873	0.00938
Q8CHG7	RAPGEF2	1.1667	0.7261	-7.104	-96793	0.00454
O88712	CTBP1	3.59	0.2597	-5.441	-95873	0.00938

Q9JMK2	CSNK1E	3.51	0.2473	-5.039	-96792	0.00393
E0CYQ0	KCTD17	6.64	0.0008	1.9925	-95871	0.01096
A0A2R8VJW4	CLIP4	6.64	0.0008	1.9925	-13	0.0419
Q8K596	SLC8A2	1.94	0.5026	-6.739	-95871	0.01096
O88952	LIN7C	3.2567	0.2893	-5.669	-19	0.017
Q80TZ3	DNAJC6	4.5767	0.2473	-5.051	-95873	0.00938
Q61037	TSC2	4.73	0.2226	-4.767	-96792	0.00454
O70172	PIP4K2A	4.4267	0.2473	-5.302	-11	0.04484
Q9CYI4	LUC7L	6.64	0.0008	1.9925	1	0.50437
Q80Y24	PRICKLE2	-0.58	0.7546	-7.13	-96792	0.00504
A0A571BGH0	KCNAB2	4.4067	0.1145	-3.447	-96792	0.00504
Q4KUS2	UNC13A	0.49	0.9141	-7.236	-95871	0.00885
Q7TQD2	TPPP	3.1467	0.2739	-5.549	-95872	0.00938
Q9D7M1	GID8	5.8533	0.042	-1.496	-95351	0.01408
P02772	AFP	6.64	0.0008	1.9925	1	0.50437
D3YZZ4	TSC22D4	6.06	0.0244	-0.537	-15	0.02576
G3X920	ARMC8	3.55	0.2473	-4.97	-95872	0.00938
Q6AXB7	FMR1	6.64	0.0008	1.9925	-94785	0.02345
Q60854	SERPINB6	0.0867	0.6797	-7.045	-96351	0.00586
Q8K3B1	FBXO45	1.25	0.2597	-5.44	-95351	0.01408
Q3UHD6	SNX27	4.8567	0.1975	-4.51	-96792	0.00504
Q5SRX1	TOM1L2	6.64	0.0008	1.9925	-95353	0.01528
Q9QYB5	ADD3	5.5967	0.0706	-2.49	-96349	0.0067
Q8C052	MAP1S	-0.627	0.3352	-5.958	-96353	0.0067
Q99KH2	CYTH2	2.4533	0.4251	-6.35	-96795	0.00416
Q8CCJ4	AMER2	6.64	0.0008	1.9925	-11	0.05327
P10852	SLC3A2	6.64	0.0008	1.9925	-95351	0.01408
Q9QYH6	MAGED1	2.5533	0.397	-6.246	-95871	0.01096
A0A0G2JDC3	MAP11	0.3467	0.4065	-6.277	-13	0.0419
Q61553	FSCN1	4.8033	0.2094	-4.621	-95871	0.00938
A0A087WNU5	ANK3	0.2867	0.4732	-6.664	-11	0.04484
Q7TSE6	STK38L	1.31	0.2529	-5.361	-13	0.0317
Q8VE33	GDAP1L1	1.8067	0.5411	-6.827	-11	0.04484
Q9D0E3	LYSMD1	6.64	0.0008	1.9925	-95871	0.00885
P67871	CSNK2B	1.12	0.2226	-4.762	-96797	0.00393
Q9WTX2	PRKRA	2.2867	0.0226	-0.424	-95873	0.00938
Q8R307	VPS18	5.5867	0.0717	-2.524	-97598	0.00208
P16627	HSPA1L	0	1	-7.258	-95352	0.01528
Q8C419	GPR158	1.55	0.504	-6.742	-96349	0.0067
Q3U0M1	TRAPPC9	1.3767	0.2524	-5.351	-95873	0.00938

B1AXH1	NHSL2	2.09	0.4729	-6.66	-96792	0.00416
Q80ZM5	H1F10	2.9467	0.316	-5.833	-95871	0.00938
P21279	GNAQ	-0.547	0.4478	-6.574	-95351	0.01408
D3Z6D2	STAU2	6.64	0.0008	1.9925	-9	0.07001
P62812	GABRA1	4.4267	0.2473	-5.302	-15	0.02576
O35326	SRSF5	3.3467	0.2573	-5.408	-13	0.03379
O55091	IMPACT	4.1733	0.2901	-5.674	-95871	0.01096
Q80U93	NUP214	6.64	0.0008	1.9925	-95351	0.01408
O89112	LANCL1	4.55	0.2473	-5.097	-95871	0.00938
G3UZJ2	MAP2	4.8967	0.0716	-2.514	-6	0.04962
A0A5F8MP75	MAPK10	4.5333	0.2473	-5.126	-95873	0.00938
Q64521	GPD2	0.2833	0.8627	-7.211	-95871	0.00938
Q7TT50	CDC42BPB	6.64	0.0008	1.9925	-95351	0.01408
Q91WG7	DGKG	2.94	0.3277	-5.91	-96349	0.0067
Q9DBE8	ALG2	-1.063	0.4449	-6.543	-13	0.0419
Q3UGS4	MCRIP1	3.4467	0.2739	-5.551	-11	0.04484
E9PVU7	PDE4D	6.64	0.0008	1.9925	-95351	0.01528
B1AVH5	CORO2A	2.4933	0.2573	-5.409	-97598	0.00208
Q0KK55	KNDC1	2.24	0.4449	-6.513	-95871	0.01096
P84096	RHOG	0.1133	0.6179	-6.956	-96795	0.00416
E9PWE8	DPYSL3	6.64	0.0008	1.9925	-94785	0.02345
A0A1D5RM97	MAST3	6.64	0.0008	1.9925	-95353	0.01528
Q8R0S4	CACNB4	6.64	0.0008	1.9925	-95353	0.01528
Q61771	KIF3B	2.6867	0.3701	-6.128	-13	0.0419
Q00PI9	HNRNPUL2	6.64	0.0008	1.9925	-95353	0.01528
P19246	NEFH	0.5167	0.3725	-6.143	-17	0.01784
Q3UHH1	ZSWIM8	5.4933	0.0825	-2.838	-95871	0.01096
Q8R4E6	PURG	1.8433	0.0807	-2.784	-96349	0.0067
Q8BSZ2	AP3S2	3.2633	0.2548	-5.389	-13	0.03379
O70492	SNX3	1.4867	0.6385	-6.986	-96349	0.0067
P56942	PMCH	6.64	0.0008	1.9925	-96795	0.00393
A0A076FR46	SLC12A5	3.45	0.2473	-5.149	-95351	0.01408
Q99P72	RTN4	2.75	0.5581	-6.859	-95351	0.01408
Q8VHR5	GATAD2B	4.4033	0.2508	-5.339	-95351	0.01408
O35127	GRCC10	6.64	0.0008	1.9925	-94143	0.0412
Q8K4Q0	RPTOR	4.5233	0.2473	-5.143	-13	0.0419
P58854	TUBGCP3	0.41	0.4457	-6.554	-95351	0.01408
Q80TL4	PHF24	5.9133	0.0355	-1.234	-9	0.07001
Q8CHT1	NGEF	6.64	0.0008	1.9925	-9	0.07001
O35099	MAP3K5	-0.943	0.7981	-7.169	-96792	0.00504

A0A0R4J102	CPEB3	3.7767	0.2102	-4.637	-96351	0.00586
P97300	NPTN	2.9267	0.2473	-5.03	-96351	0.0067
Q6PEB6	MOB4	6.64	0.0008	1.9925	-95872	0.00938
Q8VEJ9	VPS4A	6.64	0.0008	1.9925	-95871	0.00885
A0JP53	DGKH	3.3733	0.2473	-5.273	-94785	0.02345
O55013	TRAPPC3	0.6867	0.3802	-6.18	-15	0.02345
Q9D883	U2AF1	-0.463	0.9207	-7.238	-11	0.04484
D3YWF6	OTUB1	6.64	0.0008	1.9925	-11	0.04484
Q80X85	MRPS7	3.21	0.2911	-5.682	-11	0.04484
Q8CI43	MYL6B	0.6467	0.9058	-7.233	-95871	0.00938
Q99K46	USP11	0.4333	0.4457	-6.561	-95871	0.01096
Q8CHG3	GCC2	4.5267	0.2473	-5.137	-96795	0.00393
Q8R404	MICOS13	6.64	0.0008	1.9925	1	0.50437
O88343	SLC4A4	2.7633	0.3538	-6.061	-94785	0.02345
E9PUD2	DNM1L	5.61	0.0697	-2.443	-94785	0.02345
Q62426	CSTB	3.78	0.2473	-5.14	-13	0.0317
B1AZ46	BAIAP2	1.3467	0.3818	-6.186	-95872	0.00938
Q61666	HIRA	1.34	0.4449	-6.539	-95351	0.01408
Q8K0D0	CDK17	6.64	0.0008	1.9925	-11	0.05327
P46471	PSMC2	6.64	0.0008	1.9925	-96797	0.00393
Q9D0R8	LSM12	6.64	0.0008	1.9925	-95873	0.00938
O55106	STRN	0.9367	0.5726	-6.885	-95871	0.00938
P16125	LDHB	3.5467	0.266	-5.499	-95351	0.01408
G3UX72	MCF2L	-1.007	0.7847	-7.158	-15	0.02345
Q9DB29	IAH1	6.64	0.0008	1.9925	1	0.50437
Q9D832	DNAJB4	6.64	0.0008	1.9925	-94785	0.02345
Q5HZI2	C2CD4CC2CD4 FAMILY	2.22	0.4457	-6.56	-96349	0.0067
G8JL68	MYEF2	6.64	0.0008	1.9925	-96351	0.00838
P62137	PPP1CA	5.1867	0.1335	-3.732	-95351	0.01528
Q8CH77	NAV1	6.64	0.0008	1.9925	-9	0.07001
Q3THS6	MAT2A	6.64	0.0008	1.9925	1	0.50437
P35278	RAB5C	5.6467	0.0647	-2.311	-94785	0.02345
Q0VGU4	VGF	2.3167	0.3189	-5.852	-95351	0.01408
A0A286YDR2	RAB3C	3.8367	0.225	-4.789	-11	0.04484
E9Q450	TPM1	6.64	0.0008	1.9925	1	0.50437
Q80XK6	ATG2B	6.64	0.0008	1.9925	-11	0.05327
D3YZI9	PGBD5	4.91	0.0779	-2.697	-94785	0.02345
Q9R1T4	SEPTIN6	6.64	0.0008	1.9925	-95351	0.01408
A0A286YDL6	CAMK2G	3.3467	0.3503	-6.045	-95871	0.00885
F7ASU3	RHOT1	3.4867	0.2855	-5.639	-96349	0.00586

Q9QXD1	ACOX2	6.64	0.0008	1.9925	1	0.50437
Q5M8N0	CNRIP1	4.15	0.1469	-3.961	-95352	0.01528
Q920Q4	VPS16	4.43	0.2473	-5.297	-95351	0.01408
Q62277	SYP	5.4567	0.0326	-1.076	-95871	0.00885
Q6P5D3	DHX57	4.2567	0.1397	-3.855	-95351	0.01408
B8XCJ6	UNC80	5.0433	0.1546	-4.091	-94785	0.02345
Q6QWF9	CAMK2N1	6.64	0.0008	1.9925	-11	0.05327
Q9QYS2	GRM3	-1.047	0.7995	-7.171	-17	0.01784
Q7TNM2	TRIM46	5.1433	0.1395	-3.844	-95873	0.00938
P70188	KIFAP3	4.4267	0.2473	-5.302	-95351	0.01408
G3UYV7	RPS28	6.64	0.0008	1.9925	1	0.50437
Q641P0	ACTR3B	5.36	0.1034	-3.25	-94785	0.02345
B1AR13	CISD3	6.64	0.0008	1.9925	-95351	0.01408
Q80YQ8	RMND5A	6.64	0.0008	1.9925	-5	0.1741
Q9WTP6	AK2	6.64	0.0008	1.9925	1	0.50437
Q9WUD1	STUB1	6.64	0.0008	1.9925	-95871	0.01096
Q99LI8	HGS	2.2133	0.4449	-6.535	-95871	0.00885
Q91YI1	ATG13	6.64	0.0008	1.9925	-95351	0.01408
A0A0A0MQE5	CAMSAP1	6.64	0.0008	1.9925	-9	0.07001
O88643	PAK1	2.7967	0.3482	-6.032	-11	0.04484
A2A841	EPB41	6.64	0.0008	1.9925	1	0.50437
Q80U95	UBE3C	6.64	0.0008	1.9925	-9	0.07001
Q9CPW4	ARPC5	6.64	0.0008	1.9925	1	0.50437
M0QWZ1	FAM193A	6.64	0.0008	1.9925	-3	0.22705
Q9D154	SERPINB1A	2.7767	0.3509	-6.049	-95351	0.01528
Q6NXL6	SENP5	1.9067	0.5419	-6.829	-94785	0.02345
Q60676	PPP5C	2.2133	0.6797	-7.047	-94144	0.0412
Q9Z1S3	RASGRP1	3.4967	0.4367	-6.397	-94785	0.02345
O09172	GCLM	6.64	0.0008	1.9925	1	0.50437
E9Q6Y8	USP31	6.64	0.0008	1.9925	-94785	0.02345
Q791V5	MTCH2	6.64	0.0008	1.9925	1	0.50437
F2Z471	VDAC1	4.1833	0.2486	-5.315	-95351	0.01408
P12025	MDK	6.64	0.0008	1.9925	-94785	0.02345
Q9QUG9	RASGRP2	6.64	0.0008	1.9925	-7	0.09747
Q7TSC1	PRRC2A	5.3367	0.1075	-3.319	-95873	0.00938
Q7TSY6	CELF4	6.13	0.0186	-0.178	-95351	0.01408
Q9CQZ1	HSBP1	5.9233	0.0346	-1.189	-11	0.04484
Q9R1V6	ADAM22	4.4267	0.2473	-5.302	-94144	0.0412
Q05816	FABP5	2.5533	0.3978	-6.249	-94143	0.0412
Q5U3K5	RABL6	5.28	0.1172	-3.48	-11	0.04484
B2RSH2	GNAI1	6.64	0.0008	1.9925	-95351	0.01408

Q8C078	CAMKK2	5.42	0.0938	-3.069	-95351	0.01408
A0A498WGK2	NARS	6.64	0.0008	1.9925	-94785	0.02345
Q9CX86	HNRNPA0	6.64	0.0008	1.9925	-94144	0.0412
P60766	CDC42	6.64	0.0008	1.9925	-9	0.06498
Q6PD03	PPP2R5A	6.64	0.0008	1.9925	-7	0.09747
Q9JKS5	HABP4	3.6467	0.2473	-5.127	-11	0.04484
Q9Z2D1	MTMR2	2.4667	0.4162	-6.321	-94144	0.0412
A0A1B0GRU0	SLC17A7	6.64	0.0008	1.9925	-94144	0.0412
A0A140LHA2	BUB3	6.64	0.0008	1.9925	-5	0.13692
Q60829	PPP1R1B	3.59	0.2508	-5.34	-94785	0.02345
Q9WVK8	CYP46A1	6.64	0.0008	1.9925	-94785	0.02345
S4R1M9	OSBPL10	6.64	0.0008	1.9925	-94144	0.0412
P53994	RAB2A	4.3733	0.1243	-3.586	-11	0.04484
A0A0A6YWB0	MBNL1	6.64	0.0008	1.9925	-7	0.09747
Q78IK2	ATP5MD	6.1433	0.0182	-0.108	-9	0.06498
Q3TDK6	ROGDI	6.64	0.0008	1.9925	-7	0.09747
Q3U0V1	KHSRP	5.89	0.0379	-1.337	-15	0.02576
Q62108	DLG4	6.64	0.0008	1.9925	-7	0.09747
Q9EPW0	INPP4A	3.18	0.2975	-5.723	-94144	0.0412
Q920M5	CORO6	6.64	0.0008	1.9925	-7	0.09747
E9PXF0	PCDH17	-1.42	0.6589	-7.012	-11	0.04484
Q9D880	TIMM50	-2.16	0.4511	-6.588	-11	0.04484
E9QAQ3	ARHGAP26	6.64	0.0008	1.9925	-5	0.13692
Q5SUT0	EWSR1	3.23	0.2597	-5.435	-95351	0.01408
Q61425	HADH	6.64	0.0008	1.9925	1	0.50437
O35737	HNRNPH1	4.4267	0.2473	-5.302	-94785	0.02345
Q61081	CDC37	6.64	0.0008	1.9925	-94144	0.0412
A0A1Y7VJN9	DTNA	2.2367	0.4449	-6.516	-11	0.04484
Q8C5L3	CNOT2	6.64	0.0008	1.9925	1	0.50437
O88532	ZFR	6.64	0.0008	1.9925	-5	0.1741
Q920Q8	IVNS1ABP	6.64	0.0008	1.9925	1	0.50437
P63213	GNG2	5.8167	0.0465	-1.651	-7	0.09747
Q3TQB2	FOXRED1	6.64	0.0008	1.9925	-94785	0.02345
Q60631	GRB2	0.56	0.53	-6.802	-94785	0.02345
P47809	MAP2K4	6.0133	0.0282	-0.768	-95353	0.01528
Q8CE90	MAP2K7	2	0.2637	-5.484	-15	0.02576
Q9D289	TRAPPC6B	4.7633	0.2176	-4.701	-11	0.04484
Q8JZW5	SH2D5	6.64	0.0008	1.9925	-5	0.1741

G3UZH5	TRAK2	6.64	0.0008	1.9925	-94144	0.0412
P58391	KCNN3	-1.957	0.4986	-6.727	-11	0.04484
P63141	KCNA2	6.0467	0.0255	-0.604	-94785	0.02345
Q80UE6	WNK4	6.64	0.0008	1.9925	1	0.50437
Q8VHI6	WASF3	6.64	0.0008	1.9925	-9	0.07001
Q61029	TMPO	2.4967	0.4251	-6.353	-94144	0.0412
Q9D9V3	ECHDC1	6.2867	0.0092	0.6727	1	0.50437
Q80TJ1	CADPS	6.64	0.0008	1.9925	-7	0.09747
Q99KX1	MLF2	6.64	0.0008	1.9925	-7	0.09747
P10637	MAPT	4.61	0.1051	-3.274	-15	0.02345
F6U2S8	WNK1	6.13	0.0186	-0.178	-9	0.07001
J3QPR1	ATXN1	6.64	0.0008	1.9925	-5	0.1741
Q9DCR2	AP3S1	6.64	0.0008	1.9925	-5	0.1741
Q91Z61	DIRAS1	6.64	0.0008	1.9925	-7	0.09747
Q6NSW3	SPHKAP	6.64	0.0008	1.9925	-3	0.22705
Q9D1C8	VPS28	6.64	0.0008	1.9925	-9	0.07001
Q99PU5	ACSBG1	6.64	0.0008	1.9925	-9	0.07001
Q3U8Y1	MRPS11	5.4033	0.0966	-3.12	-94144	0.0412

Appendix 5.3. All Significant OGT Interactors Identified in the Mouse Liver.

Columns are as described in Appendix 5.2.

Accession	Gene	limmaFC	limmapVal	limmaB	ibbFC	ibbpVal
Q8VDD5	MYH9	0.8533333	0.26557447	-6.40882	-1.5609	0.04135129
Q8CGY8	OGT	6.64	4.12E-05	4.662049	-91.624	6.92E-09
Q3UHF7	HIVEP2	2.3466667	0.01153018	-0.59452	-100000	2.01E-08
Q61191	HCFC1	5.7766667	0.00128624	2.59425	-100000	1.22E-10
Q8C196	CPS1	2.7666667	0.01009419	-0.36349	-4.3059	0.01063668
P60710	ACTB	0.8133333	0.02668156	-2.05412	-1.5238	0.03247181
A3KGU9	SPTAN1	1.2133333	0.01009419	-0.36447	1	0.52199355
Q03172	HIVEP1	2.9633333	0.00891163	-0.12785	-100000	3.12E-09
Q8R0Y6	ALDH1L1	2.7533333	0.01675747	-1.22154	-5.8631	0.00427884
Q61768	KIF5B	2.57	0.01079824	-0.48081	-100000	5.16E-08
Q6PD31	TRAK1	2.73	0.11642269	-4.74578	-100000	5.99E-07
Q6P9N8	TRAK2	4.45	0.0202417	-1.55718	-100000	1.04E-08
E9Q6J5	BOD1L	1.96	0.07695555	-3.99415	-100000	4.21E-06
B1ASP2	JAK1	0.8433333	0.02804449	-2.1529	-1.507	0.03592652
P63017	HSPA8	3.3433333	0.00399756	1.111258	-6.8947	0.00082695
Q62261	SPTBN1	0.6666667	0.06082359	-3.58198	-100000	0.00018216
A2A884	HIVEP3	-1	0.32680901	-6.95514	-97206	0.00624931
P46735	MYO1B	1.7066667	0.00908761	-0.17139	-2.6595	0.00524808
Q9JMH9	MYO18A	0.7766667	0.34554081	-7.04796	-3.5384	0.0157958
E9Q175	MYO6	1.16	0.09773122	-4.43896	-2.311	0.04808187
O35490	BHMT	3.0566667	0.00039486	3.687559	-3.0909	0.00996301
Q7TMY8	HUWE1	1.59	0.01773568	-1.32363	-100000	2.23E-08
Q8CAQ8	IMMT	5.0266667	0.00070083	3.219153	-100000	2.66E-08
Q8K010	OPLAH	1.6333333	0.02419371	-1.87083	-4.842	0.00589535
A0A0R4J049	PRMT5	1.6266667	0.05464446	-3.39796	-2.125	0.03671901
Q8BTI8	SRRM2	1.1833333	0.12979472	-4.94773	-17.001	0.00093661
P16460	ASS1	2.74	0.00247277	1.772051	-2.4723	0.01363853
Q8BMS1	HADHA	1.7133333	0.00759805	0.1364	-2.5862	0.01194503
Q91X77	CYP2C50	1.7	0.02577721	-1.99089	-1.7255	0.03454146
Q8BG87	TET3	2.4466667	0.01053282	-0.4364	-100000	1.21E-07
E9PYH6	SETD1A	1.6766667	0.03933283	-2.80515	-100000	2.00E-06
Q9DBR7	PPP1R12A	1.42	0.06586981	-3.72051	-100000	2.90E-06
Q8C9B9	DIDO1	1.09	0.08751501	-4.22161	-100000	1.09E-05
P13020	GSN	1.1533333	0.04795323	-3.17703	-1.6667	0.10426026
Q9WTI7	MYO1C	1.3666667	0.0368443	-2.66692	-2.5972	0.0356184
Q9QWL7	KRT17	0.87	0.6152919	-8.08361	-7.3288	0.00353512

Q9D8E6	RPL4	0.82	0.16063148	-5.31452	-2.0333	0.03101856
P20029	HSPA5	2.0333333	0.00944931	-0.23483	-1.7428	0.03958913
A0A0R4J135	SELENBP2	3.0166667	0.00107503	2.801134	-4.1578	0.0039124
Q5SVJ0	CAMK2B	2.4666667	0.03843975	-2.7578	1	0.52199355
P38647	HSPA9	2.79	0.02567503	-1.97701	-9.9424	0.00111666
Q7TMM9	TUBB2A	2.0433333	0.02642579	-2.03652	-95353	0.02763432
P83741	WNK1	1.5033333	0.1938357	-5.72005	-99827	0.00097107
P10126	EEF1A1	2.2966667	0.00897423	-0.14302	-1.9032	0.02948305
Q7TPH6	MYCBP2	1.63	0.03843975	-2.75986	1	0.52199355
P12970	RPL7A	0.66	0.26557447	-6.51467	-1.7812	0.03711631
P16546	SPTAN1	2.2433333	0.09104932	-4.28753	-100000	1.38E-06
A0A0A0MQF6	GAPDH	2.0433333	0.03692363	-2.68154	-2.7894	0.01357397
P61979	HNRNPK	1.67	0.00876718	-0.08446	-2.3684	0.02456875
A0A0A0MQA5	TUBA4A	2.2066667	0.00961371	-0.27381	-8.9999	0.03344923
Q3UPL0	SEC31A	2.97	0.02688339	-2.06884	-100000	4.71E-07
P25444	RPS2	1.02	0.12947556	-4.93961	-2.0476	0.03558977
Q9CWW7	CXXC1	3.24	0.01153018	-0.58659	-100000	3.77E-06
Q99NF7	PPM1B	0.5833333	0.03463485	-2.55438	-1.8276	0.04091465
Q8BGD9	EIF4B	1.8333333	0.00222101	1.929944	-3.1539	0.01722796
P15105	GLUL	2.7833333	0.00068231	3.24815	-4.0589	0.00668249
P17426	AP2A1	0.8633333	0.19606344	-5.74984	-32.995	0.01725639
Q03265	ATP5F1A	2.24	0.00114336	2.733396	-11	0.00094125
Q4JK59	TET2	1.42	0.18109362	-5.589	-100000	1.18E-06
Q61699	HSPH1	1.27	0.23054183	-6.03718	-100000	0.00074443
P47738	ALDH2	2.91	0.00668011	0.366728	-3.375	0.01363853
Q8BWT1	ACAA2	2.66	0.02331766	-1.79321	-8.9999	0.00122229
P17427	AP2A2	0.85	0.16915499	-5.4445	-3.3637	0.02195606
Q9ERG0	LIMA1	1.3866667	0.03321037	-2.47261	-4.1333	0.00624931
A2RSY1	KANSL3	2.2366667	0.03108513	-2.34073	-100000	2.95E-06
Q9QXD6	FBP1	1.8666667	0.06499087	-3.68741	-7.8336	0.00251997
P24270	CAT	1.1566667	0.11957992	-4.79009	-2.4	0.02661912
P29341	PABPC1	1.7066667	0.06420655	-3.66617	-5.2223	0.00688348
Q4LDG0	SLC27A5	2.0066667	0.00229487	1.878908	-4.6705	0.01634454
P11499	HSP90AB1	1.6	0.00466194	0.905287	-3.6666	0.01134556
O35488	SLC27A2	2.0466667	0.00293192	1.536826	-4.9673	0.01410674
Q62167	DDX3X	1.4433333	0.09405296	-4.34066	-54.994	6.61E-05
Q9Z1R2	BAG6	2.25	0.07704952	-3.99891	-100000	8.54E-05
Q99J09	WDR77	1.4066667	0.06190286	-3.61273	-2.5	0.03379989
Q569X9	CYP2C67	2.2933333	0.12015145	-4.81175	-3.8461	0.01348947
P54869	HMGCS2	3.0266667	0.00743387	0.181193	-4.3066	0.0107389
Q3UNX5	ACSM3	1.18	0.02461634	-1.89908	-2.1875	0.04091465

Q8BFR5	TUFM	2.8033333	0.02801646	-2.14716	-11.604	0.00158051
P24549	ALDH1A1	2.3233333	0.0101466	-0.38093	-7.2	0.00430638
Q9R0H0	ACOX1	2.4966667	0.00693167	0.281043	-13.235	0.00117728
P63038	HSPD1	3.05	0.00368777	1.229168	-5.2671	0.00873342
P58252	EEF2	1.5433333	0.02180485	-1.67359	-6.6327	0.00732276
P68372	TUBB4B	2.1866667	0.00680833	0.3231	-6.3925	0.00643242
Q8VDM4	PSMD2	2.09	0.00869119	-0.05274	-12	0.00160202
Q3ULD5	MCCC2	1.7833333	0.03852999	-2.76688	-9.3998	0.00270001
Q3U1J4	DDB1	1.8233333	0.02200465	-1.70435	-19	0.00072302
Q6P5E4	UGGT1	1.5933333	0.17102978	-5.47283	-11.332	0.00772892
E9QAQ5	GSK3B	2.6433333	0.07074181	-3.84432	-100000	1.30E-05
P68254	YWHAQ	3.0933333	0.00299178	1.505948	-100000	4.56E-05
P51881	SLC25A5	2.4166667	0.00194414	2.101522	-2.7333	0.01791661
P00186	CYP1A2	2.0833333	0.01991843	-1.52563	-4.3001	0.0106781
P34914	EPHX2	1.5333333	0.14245045	-5.10156	-100000	6.63E-05
Q91X20	ASH2L	2.1666667	0.21871601	-5.93894	-100000	8.38E-05
P19096	FASN	1.96	0.0282766	-2.17279	-100000	7.39E-06
G3X982	AOX3	3.0866667	0.00246235	1.784301	-100000	2.96E-06
Q6A0A9	FAM120A	1.29	0.10823452	-4.61965	-9.0003	0.0044352
Q8VDJ3	HDLBP	0.9366667	0.04635299	-3.11628	-3.1819	0.01961088
G5E8R3	PCX	1.63	0.25990283	-6.27405	-13.903	0.00132147
E9Q634	MYO1E	1.2166667	0.15473108	-5.24981	-5.5712	0.0073464
P35700	PRDX1	2.6633333	0.01153018	-0.59616	-2.0588	0.04784266
A0A0G2JGS4	CAMK2D	1.38	0.03618115	-2.6358	-100000	3.94E-05
P05213	TUBA1B	1.66	0.02640562	-2.03104	-2.9333	0.01518533
A0A0R4J2B6	RBBP5	2.61	0.04153623	-2.91863	-100000	5.38E-05
Q91VR2	ATP5F1C	1.45	0.01689477	-1.24267	-1.4074	0.21177926
Q8K2B3	SDHA	2.52	0.0052593	0.7297	-100000	7.70E-05
P62983	RPS27A	0.9066667	0.15698191	-5.27887	-4	0.01135746
Q91VR5	DDX1	1.51	0.0598876	-3.55073	-7.4999	0.00658736
Q9EPU0	UPF1	1.3666667	0.10513373	-4.5636	-100000	0.000106
P63328	PPP3CA	1.3033333	0.13469423	-5.00307	-96792	0.0085431
A8DUK4	HBB-BS	1.17	0.12047424	-4.82127	-7.1841	0.00762802
Q68FG2	SPTBN2	0.8366667	0.26557447	-6.40237	-100000	0.00020329
D3YUP1	CARM1	0.33	0.71121362	-8.23335	-98642	0.00183098
Q8BGH2	SAMM50	3.7166667	0.02356161	-1.81627	-100000	6.13E-06
Q99PU7	BAP1	0.87	0.08396336	-4.14701	-100000	4.49E-05
P00329	ADH1	2.0966667	0.00342283	1.329213	-3.5455	0.016215
Q3UQ44	IQGAP2	1.4466667	0.04091178	-2.89414	-7.7499	0.00568843
P17751	TPI1	2.3466667	0.01343203	-0.85514	-2.4166	0.051979
Q9JJ28	FLII	1.1033333	0.16475095	-5.39082	-10.999	0.01833596
P0C090	RC3H2	0.0433333	1	-8.43181	-100000	0.00066742

Q8BG51	RHOT1	2.7033333	0.07236415	-3.88489	-100000	0.00056591
Q925I1	ATAD3	2.5466667	0.02181133	-1.68752	-100000	9.08E-05
P11352	GPX1	2.2666667	0.01178289	-0.6307	-3.3571	0.01223336
Q3UH59	MYH10	0.59	0.38984787	-7.27812	-100000	7.95E-05
Q9EQQ9	OGA	1.3933333	0.04783712	-3.16667	-97595	0.00589535
Q8R326	PSPC1	3.9633333	0.03933283	-2.80357	-100000	7.39E-06
Q9JHU4	DYNC1H1	0.3333333	0.53473354	-7.91332	-94785	0.04091465
O09012	PEX5	2.2466667	0.03989753	-2.84486	-100000	0.00014102
O08788	DCTN1	2.23	0.00088817	2.997754	1	0.52199355
Q91VB8	HBA-A1	0.4666667	0.36127075	-7.13004	-100000	0.00018328
P42669	PURA	1.4133333	0.06586981	-3.72082	-12	0.00341058
P16015	CA3	1.5733333	0.02801646	-2.14721	-3	0.04307201
Q922D8	MTHFD1	3.02	0.02412333	-1.8531	-100000	4.10E-05
Q91X83	MAT1A	3.3933333	0.01682079	-1.23169	-3.8	0.01992088
O88844	IDH1	1.1833333	0.16076563	-5.34404	-5.8332	0.01498441
Q99JY0	HADHB	1.6933333	0.02577721	-1.99362	-2.0833	0.08347261
P11725	OTC	2.5166667	0.01256825	-0.74969	-5.7144	0.00646197
A2AN08	UBR4	0.8	0.15698191	-5.27824	-100000	2.97E-05
Q3UKW2	CALM1	1.2266667	0.03783811	-2.71902	-1.8889	0.15689585
P53395	DBT	0.8	0.47805356	-7.6409	-4.6666	0.02713591
Q91Y97	ALDOB	1.7766667	0.05120701	-3.28813	-7.0005	0.00490976
Q9D0E1	HNRNPM	1.83	0.20346267	-5.80713	-100000	0.00099254
Q571I4	PRAG1	6.64	4.12E-05	4.662049	1	0.52199355
P61965	WDR5	3.3533333	0.04298631	-2.98383	-100000	5.65E-05
Q3U2G2	HSPA4	0.8066667	0.59018396	-8.03111	-100000	0.00104526
Q6ZQ08	CNOT1	1.82	0.11106463	-4.67104	-100000	1.72E-05
E9QPE7	MYH11	1.0433333	0.16076563	-5.34199	-100000	0.00074443
P55096	ABCD3	2.0666667	0.01312265	-0.81422	-5.1666	0.01162608
Q9WVL0	GSTZ1	2.6133333	0.00250224	1.745053	-100000	7.13E-05
P62259	YWHAE	2.8366667	0.00904388	-0.15914	-2.6667	0.04153344
A0A2I3BQP6	CAMK2G	0.8533333	0.26557447	-6.38259	-100000	0.00065747
Q9QYJ0	DNAJA2	1.8433333	0.00649858	0.415221	-7.0847	0.01992088
P62960	YBX1	0.6066667	0.01583496	-1.12951	-1.7273	0.18165123
D3Z041	ACSL1	2.4766667	0.01453057	-0.9718	-100000	2.40E-05
Q8K182	C8A	0.5133333	0.03824431	-2.73754	-1.9167	0.09380016
P59759	MRTFB	0.24	0.52307375	-7.88457	-14.999	0.04391494
P47754	CAPZA2	1.7066667	0.07369872	-3.91936	-8.9999	0.04091465
Q99LF4	RTCB	1.5933333	0.00693167	0.286913	-6.9998	0.01217264
Q8BGL3	SULT2A8	3.2433333	0.01773568	-1.31977	-38.998	0.00018216
Q99MR8	MCCC1	2.2466667	0.0108209	-0.48915	-16.499	0.0013216
Q91W50	CSDE1	1.3866667	0.0921803	-4.30734	-100000	0.00104526
Q99K48	NONO	3.1433333	0.00784244	0.088736	-100000	8.87E-05

E9Q1S3	SEC23A	0.9666667	0.38049905	-7.2414	-100000	0.0007704
Q9EP89	LACTB	1.9433333	0.07312492	-3.90551	-5.2	0.01291602
Q99JY9	ACTR3	0.8866667	0.22624459	-6.00315	-4.0001	0.04391494
Q8VC30	TKFC	3.3033333	0.01245781	-0.73249	-100000	4.61E-05
Q8VCW8	ACSF2	2.17	0.07309126	-3.90174	-11.7	0.00362301
Q8CGC7	EPRS	0.38	0.76656113	-8.29403	-5.2	0.01455336
Q8VCB3	GYS2	2.5033333	0.02080449	-1.59936	-100000	0.00012559
Q9D8N0	EEF1G	1.8533333	0.00665028	0.378897	-10.5	0.00643242
P19253	RPL13A	0.6	0.34495564	-7.04446	-100000	0.00018844
Q8BFQ4	WDR82	0.54	0.13954641	-5.06625	-97208	0.01015707
F8VPU2	FARP1	0.91	0.27185299	-6.59536	-16.999	0.03671901
Q01853	VCP	0.9566667	0.26557447	-6.52617	-100000	0.00027588
G3X928	SEC23IP	1.3833333	0.29541247	-6.7773	-100000	6.63E-05
G3X9T7	LGALS9	1.37	0.00876718	-0.07977	-2.7499	0.05568397
Q9QXE0	HACL1	2.95	0.00129084	2.584239	-100000	0.00022415
A0A1B0GSX0	LDHA	1.84	0.00946993	-0.24351	-2.875	0.04638834
Q8BTM8	FLNA	0.9833333	0.1008434	-4.49294	-100000	0.00019797
Q6XVG2	CYP2C54	1.85	0.01568888	-1.11185	-5.7999	0.01148581
Q91X75	CYP2A5	1.5633333	0.08135896	-4.08263	-8.6663	0.0071733
P18760	CFL1	1.14	0.26557447	-6.32129	-98310	0.0027158
A2A5Y4	KANSL1	0.9933333	0.15209648	-5.21943	-100000	0.00051681
Q3TXS7	PSMD1	0.0966667	0.97462879	-8.42527	-7.0001	0.01156507
Q920I9	WDR7	6.64	4.12E-05	4.662049	1	0.52199355
P42932	CCT8	1.9833333	0.00179572	2.203502	-100000	0.00041739
A0A494B908	GSTP1	2.7866667	0.3817673	-7.2469	-100000	0.00033563
P70333	HNRNPH2	1.9333333	0.01210718	-0.68338	1	0.52199355
Q64458	CYP2C29	1.86	0.05874362	-3.51756	-5.6666	0.01950182
P63101	YWHAZ	2.2766667	0.01840073	-1.38851	-9.4997	0.008081
Q9DBN5	LONP2	1.6966667	0.44848644	-7.48764	-100000	6.61E-05
Q8CC88	VWA8	2.7233333	0.38555763	-7.26258	-100000	0.00021581
Q99K67	AASS	1.6866667	0.03363112	-2.49797	-100000	0.0009278
P56399	USP5	2.1866667	0.33540823	-6.99303	-96793	0.01015707
Q8JZN7	RHOT2	0.67	0.60572174	-8.0669	-100000	0.0001475
Q9DBF1	ALDH7A1	2.2666667	0.03154909	-2.37351	-100000	7.72E-05
Q5PRE5	PROSER1	1.6866667	0.08131375	-4.07881	-100000	0.00018328
Q9QXF8	GNMT	2.3666667	0.00171195	2.269416	-4.9998	0.03379068
A2AMW0	CAPZB	1.5933333	0.04698088	-3.13832	-5	0.01632804
Q9CRB9	CHCHD3	5.22	0.09476445	-4.35968	-100000	3.87E-05
Q9R112	SQOR	2.1266667	0.01560858	-1.09301	-100000	0.00038392
P80315	CCT4	1.63	0.04998867	-3.24811	-6	0.03558977
P97872	FMO5	1.9666667	0.01810557	-1.35665	-100000	3.47E-05
Q61510	TRIM25	1.3733333	0.03520421	-2.59261	-7.4996	0.04646419

Q8R570	SNAP47	6.64	4.12E-05	4.662049	-11	0.08613925
A0A0R4IZY2	CYP2D26	2.48	0.04041605	-2.8737	-100000	0.00027414
Q8CHR6	DPYD	0.0966667	0.99327983	-8.43007	-46.992	0.00299409
Q8VEM8	SLC25A3	1.58	0.29449945	-6.77174	-99259	0.00122229
Q9ERU9	RANBP2	0.7933333	0.47805356	-7.58068	-98310	0.00275368
Q9EQ20	ALDH6A1	2.7733333	0.00247859	1.762742	-100000	9.81E-05
Q5SRY7	FBXW11	1.43	0.02992316	-2.26744	-97595	0.00558987
P80318	CCT3	1.9366667	0.0017347	2.248312	-97206	0.00668249
P56480	ATP5F1B	1.1033333	0.00876718	-0.08838	-9.0001	0.00929561
Q80XN0	BDH1	3.0733333	0.00975918	-0.30646	-100000	0.00022415
Q05421	CYP2E1	2.0066667	0.01773568	-1.31979	-100000	0.00020329
A0A0A0MQ68	GCDH	2.18	0.00224616	1.910338	-5	0.03781598
P17225	PTBP1	1.3	0.2349259	-6.08336	-7.9998	0.01791661
P32020	SCP2	2.0733333	0.00961371	-0.27506	-3.6667	0.03507164
P12382	PFKL	6.0433333	0.00591385	0.562776	1	0.52199355
Q569Z6	THRAP3	0.9366667	0.02852226	-2.18893	-1.5555	0.33386831
Q9CY58	SERBP1	0.9433333	0.01939469	-1.47966	-100000	0.00062433
Q922B2	DARS	1.18	0.07461502	-3.94253	-100000	0.00062433
P80317	CCT6A	1.7333333	0.00674401	0.342751	-100000	0.00041739
Q921H8	ACAA1A	4.3133333	0.1228738	-4.85582	-100000	0.0003896
Q5YD48	A1CF	1.8733333	0.0319485	-2.39808	-10.333	0.02114943
P80314	CCT2	2.0866667	0.03278935	-2.44289	-98642	0.00310589
B1AU25	AIFM1	1.75	0.26557447	-6.3304	-100000	0.00040786
P80316	CCT5	1.5533333	0.10746502	-4.60721	-97597	0.00668249
P48776	TDO2	2.44	0.04389845	-3.02752	-7.3573	0.0166
Q9WU78	PDCD6IP	0.97	0.2672631	-6.55103	-14.999	0.04091465
P80313	CCT7	0.96	0.5485502	-7.94809	-100000	0.00054794
O88451	RDH7	3.7	0.015069	-1.03665	-100000	7.13E-05
P26443	GLUD1	1.73	0.02200465	-1.70893	-28.996	0.02114943
Q8BVQ9	PSMC2	2.02	0.01079824	-0.47682	-100000	0.00033327
P20152	VIM	1.1166667	0.26557447	-6.5106	-98641	0.00219055
P63037	DNAJA1	1.9333333	0.0052593	0.726123	-7.4998	0.01722796
Q8BG05	HNRNPA3	0.8133333	0.03836604	-2.74576	-4.3334	0.04341826
P29788	VTN	0.81	0.04041605	-2.87328	-2.3333	0.1076925
P23116	EIF3A	0.4666667	0.67033637	-8.1737	-11.666	0.02467716
Q9CW42	1-Mar	2.13	0.00433924	1.002156	-8.9999	0.00568843
P60335	PCBP1	2.0733333	0.0580735	-3.49172	-98310	0.00247938
P61161	ACTR2	1.1033333	0.47805356	-7.67403	-96349	0.01291602
H7BX95	SRSF1	1.41	0.015069	-1.02946	-3.3333	0.13281593
Q64459	CYP3A11	1.4466667	0.0398377	-2.83908	-99260	0.00157768
P11714	CYP2D9	2.28	0.00246235	1.783578	-8.0001	0.01410674
Q8CIE6	COPA	1.3933333	0.01638707	-1.18615	-99258	0.00413812

Q01279	EGFR	2.52	0.00910187	-0.1793	-100000	0.00040786
Q3UMP4	SERBP1	6.64	4.12E-05	4.662049	1	0.52199355
A2AS03	HELZ2	0.0266667	1	-8.43414	-42.992	0.01217264
P11983	TCP1	1.0466667	0.10007783	-4.47694	-99550	0.00094125
O09173	HGD	2.84	0.02461983	-1.90381	-100000	0.00094125
Q9CQA3	SDHB	2.2366667	0.04160557	-2.92503	-100000	0.00062433
A0A0R4J0B4	CMAS	1.3033333	0.02567503	-1.97926	-99827	0.00080344
P62141	PPP1CB	1.7033333	0.30894414	-6.8514	-97597	0.00668249
P24456	CYP2D10	2.1633333	0.01991843	-1.52104	-100000	0.00071431
Q9JLV1	BAG3	3.9466667	0.17985419	-5.56891	-100000	0.00040786
A0A0R4J0I1	SERPINA3K	-0.053333	0.98962034	-8.42916	-100000	0.0002828
Q7TMK9	SYNCRIP	0.5266667	0.40089488	-7.32053	-97962	0.00568843
O70475	UGDH	2.12	0.00743387	0.177285	-100000	0.00099254
P68510	YWHAH	2.4966667	0.32391254	-6.9392	-95353	0.02763432
Q5SYD0	MYO1D	1.2266667	0.06148184	-3.60006	-100000	0.0013216
Q8BG95	PPP1R12B	6.64	4.12E-05	4.662049	1	0.52199355
O70325	GPX4	2.14	0.03363112	-2.49597	-97962	0.0033964
Q3TUQ7	PRKAA1	3.1766667	0.03387284	-2.51584	-99259	0.0011878
Q8CCJ9	PHF20L1	-0.386667	0.83627173	-8.35558	-100000	0.00040786
P62827	RAN	0.3533333	0.04820073	-3.18761	-2.2	0.16793858
A0A1B0GS91	SVIL	1.2333333	0.18585927	-5.63657	-100000	0.00062433
D6REV1	ASXL2	-0.2	0.90543071	-8.40031	-99259	0.0012034
P50247	AHCY	0.93	0.16070491	-5.33511	-11	0.00489983
Q91ZJ5	UGP2	0.6466667	0.64056326	-8.12637	-22.998	0.02238739
F8WJE3	KANSL2	3.11	0.3386165	-7.00844	-97962	0.00327471
P43277	H1-3	0.6433333	0.47494682	-7.56645	-97602	0.00558987
Q62095	DDX3Y	1.6333333	0.03198109	-2.40453	100000	0.99998586
Q60598	CTTN	1.2533333	0.01827017	-1.3739	-95872	0.01722796
A0A494BB75	WDR26	1.67	0.28321197	-6.68787	-18.999	0.03055265
Q61937	NPM1	0.7466667	0.0110361	-0.52103	1	0.52199355
Q9JI90	RNF14	2.8033333	0.37087101	-7.20038	-96792	0.01015707
P99024	TUBB5	1.6133333	0.03287831	-2.45068	-97966	0.0033964
Q9Z2X1	HNRNPF	1.5333333	0.02419371	-1.87009	-1.8333	0.26057561
Q8K0T0	RTN1	6.64	4.12E-05	4.662049	1	0.52199355
Q8BH95	ECHS1	2.3466667	0.01855649	-1.40488	-6.6666	0.01304322
Q61171	PRDX2	1.6833333	0.03372194	-2.5057	-6.4999	0.02763432
Q99P30	NUDT7	3.0866667	0.00967833	-0.28969	-23.999	0.00122229
Q78JT3	HAAO	1.92	0.07228374	-3.88021	-100000	0.00078846
Q3U741	DDX17	0.0233333	0.99584046	-8.43066	-14.999	0.04391494
Q9Z2I9	SUCLA2	3.68	0.1250633	-4.88752	-98310	0.00275368
Q91VJ4	STK38	0.6433333	0.05649186	-3.44703	-5.5944	0.04036221

Q9QXX4	SLC25A13	0.48	0.88338888	-8.38659	-100000	0.0002828
Q3UHB8	CCDC177	6.64	4.12E-05	4.662049	1	0.52199355
O88962	CYP8B1	3.1	0.0806797	-4.06502	-100000	0.00030463
Q6PAJ1	BCR	6.64	4.12E-05	4.662049	1	0.52199355
Q80U23	SNPH	6.64	4.12E-05	4.662049	1	0.52199355
Q9D826	PIPOX	2.44	0.01565022	-1.10338	-98957	0.00146248
O88587	COMT	0.74	0.67326995	-8.17844	-5.5	0.04212434
E9Q456	TPM1	0.9266667	0.18905079	-5.67206	-100000	0.00037822
Q9D2G2	DLST	2.2433333	0.04795323	-3.17549	-100000	0.00040786
Q3UMT1	PPP1R12C	1.9033333	0.00122278	2.658984	-95353	0.02763432
Q3UZ39	LRRFIP1	1.2166667	0.02109085	-1.62277	-7.9997	0.02082518
Q9D1M0	SEC13	2.2433333	0.01911364	-1.45492	-99828	0.00099254
Q9DBM2	EHHADH	-1.16	0.59875679	-8.04913	-30.996	0.01148581
Q60960	KPNA1	1.41	0.34554081	-7.04929	-96792	0.0085431
O70503	HSD17B12	1.1333333	0.015069	-1.03151	-100000	0.00040786
Q8BFU3	RNF214	6.64	4.12E-05	4.662049	1	0.52199355
A0A338P6K9	QSER1	6.64	4.12E-05	4.662049	1	0.52199355
O54950	PRKAG1	2.1933333	0.10862188	-4.62724	-99550	0.00094125
A0A0R4J1E2	EEF1D	1.32	0.04357798	-3.01001	-2.4	0.138805
Q9WV68	DECR2	2.5633333	0.00200092	2.062412	-99827	0.00080344
G3UZ26	SHMT1	1.3666667	0.00747301	0.164269	-26.997	0.01410674
P21126	UBL4A	5.32	0.10678643	-4.59585	-98956	0.00153041
Q9JM52	MINK1	6.64	4.12E-05	4.662049	1	0.52199355
A0A1L1SV25	ACTN4	1.3233333	0.08253479	-4.11174	-100000	0.00074443
Q9CQE8	RTRAF	1.2666667	0.09660182	-4.39457	-13.999	0.01148581
O54749	CYP2J5	1.7133333	0.05811395	-3.49605	-98957	0.00288779
Q8C2Q7	HNRNPH1	-1.136667	0.5485502	-7.94875	-100000	0.00074443
G3X972	SEC24C	0.7266667	0.41800276	-7.37967	-99827	0.00078061
Q8CI32	BAG5	3.0866667	0.03321037	-2.47031	1	0.52199355
P61982	YWHAG	3.3566667	0.00518932	0.756224	-99259	0.00113133
Q3UG20	KMT2E	6.64	4.12E-05	4.662049	-4.9999	0.26057561
Q9EQF5	DPYS	-0.533333	0.74957403	-8.27625	-100000	0.00023968
D3YVL0	MOV10	1.33	0.02515812	-1.94244	-99260	0.00157768
P49429	HPD	1.38	0.17992616	-5.57383	-11	0.01876614
P08113	HSP90B1	1.26	0.00277081	1.611098	-99548	0.00157768
Q61694	HSD3B5	2.64	0.0009922	2.885872	-15	0.00700417
O70194	EIF3D	-0.433333	0.81656796	-8.33951	-98957	0.00353512
Q99L90	MCRS1	0.2833333	0.75006331	-8.27713	-96350	0.01291602
Q9JJV2	PFN2	6.64	4.12E-05	4.662049	1	0.52199355
Q9CZ13	UQCRC1	0.3666667	0.60235132	-8.05758	-99550	0.00094125
Q9CR62	SLC25A11	1.97	0.37087101	-7.19977	-95353	0.02763432

Q3U3J1	BCKDHA	1.32	0.19385777	-5.72231	-24.997	0.01950182
G5E8G6	MYO5B	0.7466667	0.47805356	-7.59759	-99553	0.00116811
P70694	AKR1C6	1.36	0.00200647	2.0527	-99827	0.00157768
P97742	CPT1A	2.21	0.00399756	1.116195	-100000	0.00040786
P38060	HMGCL	1.42	0.26557447	-6.47972	-98641	0.00296581
Q9WV32	ARPC1B	-0.66	0.67033637	-8.17338	-9.9996	0.02763432
A0A0N4SVL0	EIF4G3	6.64	4.12E-05	4.662049	1	0.52199355
Q62318	TRIM28	0.98	0.36849719	-7.18258	-95871	0.01722796
P50544	ACADVL	1.3033333	0.16504449	-5.39782	-98311	0.00362301
P07901	HSP90AA1	1.0833333	0.12015145	-4.81502	-96795	0.0085431
Q5U4C1	GPRASP1	6.64	4.12E-05	4.662049	1	0.52199355
Q61584	FXR1	1.01	0.23193459	-6.05318	-18.999	0.03055265
A2AG10	NUP62CL	1.1766667	0.18767487	-5.6538	-99259	0.00113133
Q9CQF3	NUDT21	0.4433333	0.69068436	-8.20402	-98642	0.00296581
Q14CH0	FAM171B	6.64	4.12E-05	4.662049	1	0.52199355
Q62425	NDUFA4	1.6433333	0.01857555	-1.41117	-1.8571	0.21555176
A2A9M4	DOCK7	6.64	4.12E-05	4.662049	1	0.52199355
A0A452J8A5	ECI1	3.7733333	0.20743072	-5.8545	-7.0001	0.019885
Q8JZU2	SLC25A1	2.3533333	0.00368777	1.224394	-12	0.01721898
P70392	RASGRF2	6.64	4.12E-05	4.662049	1	0.52199355
P99029	PRDX5	2.3466667	0.0052702	0.717014	-97965	0.00372498
Q8CBY8	DCTN4	6.64	4.12E-05	4.662049	-2	0.52199355
O88441	MTX2	0.79	0.15163189	-5.21287	-100000	0.00034199
Q61696	HSPA1A	2.3133333	0.03154909	-2.37214	-98641	0.00219055
K3W4R2	MYH14	0.3733333	0.46354024	-7.53165	-98641	0.00262189
Q9DD20	METTL7B	4.07	0.16070491	-5.32479	-97962	0.0071848
P97765	WBP2	1.04	0.47810397	-7.74083	-97965	0.00372498
Q78PY7	SND1	0.24	0.60083806	-8.05348	-99548	0.00128004
Q9R0P5	DSTN	1.73	0.27774406	-6.64801	-94785	0.04091465
Q9D1H7	GET4	2.6866667	0.00693167	0.282303	-20.999	0.01879409
Q6GT24	PRDX6	0.7933333	0.55928242	-7.9721	-98310	0.00310589
Q8BX10	PGAM5	0.6533333	0.47805356	-7.72495	-96349	0.01291602
E9Q509	PKLR	1.0166667	0.32204954	-6.92651	-98641	0.00219055
Q6PHQ9	PABPC4	1.1866667	0.20470983	-5.82277	-97206	0.00668249
P68033	ACTC1	1.7833333	0.19548469	-5.74176	-97595	0.00430638
Q8QZR5	GPT	1.7666667	0.00890243	-0.12056	-99259	0.00113133
Q8VCQ8	CALD1	1.46	0.16848167	-5.43232	-99550	0.00094125
Q9WTX5	SKP1	2.4933333	0.02867896	-2.20071	-97595	0.00589535
P55937	GOLGA3	1.2933333	0.28876457	-6.72595	-98956	0.0018932
P62196	PSMC5	2.4166667	0.00648153	0.425027	-99548	0.00094125
Q9CQV8	YWHAB	1.6533333	0.23513967	-6.08645	-96349	0.01148581
Q9DCS2	METTL26	2.5333333	0.00674401	0.341725	-98310	0.0027158

Q99PU8	DHX30	1.0733333	0.3703385	-7.19304	-94785	0.04091465
O54754	AOX1	1.0466667	0.26557447	-6.34611	-97595	0.00845527
P58871	TNKS1BP1	-1.836667	0.44148275	-7.4648	-96792	0.00929561
D3Z2H9	TPM3-RS7	1.2433333	0.03688522	-2.67623	-97214	0.00624931
Q9Z2I8	SUCLG2	2.0033333	0.03074504	-2.31726	-99259	0.00113133
Q8R086	SUOX	0.5566667	0.55874876	-7.96987	-98641	0.00219055
Q7TNV0	DEK	0.16	0.83201079	-8.35145	-22.998	0.03043969
A0A1L1SVH5	RBPMS2	2.3933333	0.01312265	-0.81844	-97962	0.00372498
P68040	RACK1	1.0666667	0.06082359	-3.57978	-97206	0.00814964
Q99KB8	HAGH	0.3933333	0.60433795	-8.06296	-13	0.01223336
A0A0B4J1E7	KPNA4	4.4533333	0.10974754	-4.65212	-98310	0.00256543
P16331	PAH	1.3266667	0.13780348	-5.04172	-99827	0.00078061
P63168	DYNLL1	1.8333333	0.03618115	-2.63806	1	0.52199355
Q8BGQ7	AARS	0.74	0.14431985	-5.12661	-98311	0.00362301
Q5DTT2	PSD	6.64	4.12E-05	4.662049	1	0.52199355
E9QMC2	GRM5	6.64	4.12E-05	4.662049	1	0.52199355
E9PVC6	EIF4G1	-0.366667	0.58005316	-8.01011	-97595	0.00845527
Q6ZWY3	RPS27L	1.6733333	0.00876764	-0.09442	-1.6667	0.34133733
Q8K0S0	PHYHIP	6.64	4.12E-05	4.662049	1	0.52199355
A0A494BA32	GPAM	0.32	0.47805356	-7.61383	-98311	0.00310589
D3YZC9	SF1	6.64	4.12E-05	4.662049	1	0.52199355
Q8VH51	RBM39	0.1466667	0.90363518	-8.39779	-96792	0.01015707
Q63886	UGT1A1	2.5766667	0.03133241	-2.35576	-98311	0.00353512
Q91V92	ACLY	-0.023333	0.98059073	-8.42703	-97962	0.00568843
P35505	FAH	1.12	0.16504449	-5.39588	-97206	0.00814964
P07310	CKM	6.64	4.12E-05	4.662049	-18.999	0.03055265
Q9D1I2	CARD19	2.9733333	0.09009915	-4.27026	-98956	0.00175067
Q8CI08	SLAIN2	6.64	4.12E-05	4.662049	1	0.52199355
Q68FH0	PKP4	6.64	4.12E-05	4.662049	1	0.52199355
Q91W43	GLDC	1.0066667	0.27075117	-6.5803	-98310	0.0033964
A0A494B923	PAPSS2	1.3833333	0.29083666	-6.74574	-97595	0.00589535
Q8QZY1	EIF3L	3.3733333	0.26557447	-6.46635	-97597	0.00668249
Q8VC28	AKR1C13	3.3833333	0.26557447	-6.50931	-97208	0.01015707
Q9DCB4	ARPP21	6.64	4.12E-05	4.662049	1	0.52199355
Q9QYG0	NDRG2	2.0733333	0.02181133	-1.68664	-97206	0.00814964
Q9WU79	PRODH	3.6766667	0.24463762	-6.16254	-98642	0.00183098
O55022	PGRMC1	1.86	0.03933283	-2.80657	-98310	0.00310589
Q3UEL5	UROC1	-0.873333	0.27355023	-6.60626	-97962	0.00568843
O35945	ALDH1A7	2.02	0.03952797	-2.82088	-6.9997	0.15689585
Q6P3A8	BCKDHB	1.38	0.23123598	-6.04537	-97206	0.00814964
P33267	CYP2F2	3.0233333	0.35550866	-7.0958	-97597	0.00668249

A8Y5N4	HSD17B13	1.9333333	0.00499494	0.81134	-98641	0.0019049
D3Z5I1	ZC3HAV1	0.5666667	0.48770796	-7.7816	-97208	0.01015707
Q9Z1S5	SEPTIN3	2.05	0.03010895	-2.28016	1	0.52199355
Q91WT9	CBS	4.4433333	0.10624409	-4.58617	-98310	0.00256543
Q9ET01	PYGL	0.5333333	0.47805356	-7.73356	-18.999	0.03055265
Q60930	VDAC2	3.8466667	0.19386991	-5.72449	-95871	0.01722796
A0A1Y7VL44	TTC7B	6.64	4.12E-05	4.662049	1	0.52199355
Q80T41	GABBR2	6.64	4.12E-05	4.662049	1	0.52199355
Q921F2	TARDBP	0.3166667	0.83627173	-8.35527	-95871	0.01722796
Q9DBL1	ACADSB	2.1033333	0.49714453	-7.81442	-97207	0.00698254
Q91WT7	AKR1C14	2.29	0.04389845	-3.02534	-16.999	0.04646419
P14685	PSMD3	5.0166667	0.16470583	-5.38814	-96349	0.01148581
Q3TJZ6	FAM98A	1.62	0.10414467	-4.54518	-14.999	0.04391494
A0A1W2P7A1	RPS12	1.4333333	0.03430709	-2.53733	-3	0.09355795
P60843	EIF4A1	1.6766667	0.01009419	-0.36841	-97962	0.00430638
H3BKQ7	PPP1R9A	6.64	4.12E-05	4.662049	1	0.52199355
Q8VBT2	SDS	3.6733333	0.23166827	-6.04974	-97962	0.00372498
P70372	ELAVL1	1.5233333	0.04277601	-2.97001	-95871	0.01722796
E9QM77	ATXN2	1.3233333	0.18108524	-5.58676	-98641	0.00262189
G3UXL2	PRPS1L3	6.64	4.12E-05	4.662049	1	0.52199355
Q9D1P2	KAT8	6.64	4.12E-05	4.662049	-4.9999	0.26057561
Q8JZR0	ACSL5	2.4666667	0.08253479	-4.11446	-97210	0.00721975
P10649	GSTM1	0.5833333	0.32204954	-6.92706	-98310	0.00275368
A0A0R4J1F4	MADD	6.64	4.12E-05	4.662049	1	0.52199355
P68181	PRKACB	6.64	4.12E-05	4.662049	1	0.52199355
A2AAN2	SRP68	0.59	0.03688522	-2.67387	-16.999	0.03202093
Q80UG5	SEPTIN9	1.59	0.00621919	0.491375	-16.999	0.03671901
Q8CG76	AKR7A2	1.8533333	0.26557447	-6.3582	-97206	0.00668249
Q5BL07	PEX1	6.64	4.12E-05	4.662049	1	0.52199355
P05784	KRT18	0.7	0.23539391	-6.09109	-98641	0.00262189
P12849	PRKAR1B	6.64	4.12E-05	4.662049	1	0.52199355
D3Z139	ESRP2	1.5	0.10921019	-4.64063	-16.999	0.03671901
O54962	BANF1	6.64	4.12E-05	4.662049	1	0.52199355
P62743	AP2S1	0.2366667	0.70068823	-8.21792	-96351	0.01291602
Q922Q1	2-Mar	1.8033333	0.04864419	-3.20717	-11	0.01722796
P54775	PSMC4	1.95	0.08362646	-4.13849	-96792	0.01015707
Q62189	SNRPA	0.1333333	0.87087963	-8.37865	-96792	0.00929561
A0A286YCV9	KIF13B	0.95	0.40240785	-7.32706	-97206	0.00624931
Q8BH00	ALDH8A1	5.01	0.16548508	-5.4037	-97206	0.00814964
Q9CQ69	UQCRQ	0.7333333	0.36005889	-7.12248	-96353	0.01291602
P62192	PSMC1	2.6366667	0.03506913	-2.58338	-97598	0.00458577

Q91WL5	CYP4A12A	1.9133333	0.26557447	-6.33132	-97210	0.00721975
O70251	EEF1B	1.3833333	0.04848607	-3.19921	-2.3333	0.24116815
P60229	EIF3E	-1.753333	0.35331732	-7.08549	-97206	0.00814964
Q80X98	DHX38	0.5366667	0.60572174	-8.06637	-14.999	0.04391494
Q61133	GSTT2	1.8033333	0.11520085	-4.72878	-16.999	0.03671901
Q05915	GCH1	1.5666667	0.26557447	-6.35473	-97595	0.00668249
Q9DAW9	CNN3	6.64	4.12E-05	4.662049	-3.9999	0.2579867
P26369	U2AF2	0.93	0.02501794	-1.93029	-96349	0.01291602
Q91V41	RAB14	0.99	0.03104349	-2.33471	-8.9997	0.10426026
Q9JLJ2	ALDH9A1	0.8033333	0.49202264	-7.80081	-96793	0.01015707
S4R2G0	DGKI	6.64	4.12E-05	4.662049	1	0.52199355
Q9R190	MTA2	0.4633333	0.05386555	-3.36799	-97595	0.0047905
Q91XD4	FTCD	1.0566667	0.36127075	-7.12963	-96349	0.0157301
E9QAT4	SEC16A	-0.14	0.84252854	-8.36019	-97962	0.00430638
Q61817	CREB3	1.8266667	0.05456044	-3.39244	-97595	0.00430638
Q9DCL9	PAICS	5.0333333	0.16082603	-5.34893	-18.999	0.026492
Q9CZS1	ALDH1B1	2.07	0.10000413	-4.47312	-97206	0.00624931
E9PVP0	STARD10	0.9266667	0.24868362	-6.19314	-98957	0.00157768
Q8BK64	AHSA1	6.64	4.12E-05	4.662049	1	0.52199355
P10605	CTSB	2.6033333	0.42543772	-7.40823	-96349	0.01291602
O35344	KPNA3	6.64	4.12E-05	4.662049	-94785	0.04091465
P32233	DRG1	0.93	0.08616354	-4.19139	-16.999	0.03671901
E9QNL5	SULT1A1	2.4033333	0.02331766	-1.79742	-16.999	0.03671901
Q810B6	ANKFY1	2.0066667	0.52307375	-7.88422	-95353	0.02763432
Q9WV69	DMTN	6.64	4.12E-05	4.662049	1	0.52199355
Q8CHT0	ALDH4A1	1.8166667	0.20622198	-5.83724	-97962	0.00353512
Q9R0L7	AKAP8L	6.64	4.12E-05	4.662049	1	0.52199355
D3Z2H2	CTNND1	1.4	0.02787677	-2.12901	-97965	0.00372498
Q9JIK5	DDX21	2.2566667	0.47810397	-7.73793	-14.999	0.04391494
Q91WG5	PRKAG2	6.64	4.12E-05	4.662049	1	0.52199355
Q80X90	FLNB	-1.21	0.17885918	-5.55269	-97206	0.00668249
Q61990	PCBP2	3.1666667	0.29024431	-6.73779	-95351	0.02613381
A0A0R4J0G4	RANBP10	1.5833333	0.04540077	-3.08421	-12.999	0.0533588
Q60972	RBBP4	-0.493333	0.78021462	-8.30767	-95871	0.01722796
A0A5F8MQC8	TECR	2.3633333	0.08453009	-4.16187	-96792	0.00814964
Q63844	MAPK3	6.64	4.12E-05	4.662049	1	0.52199355
P08752	GNAI2	6.64	4.12E-05	4.662049	1	0.52199355
Q61233	LCP1	2.0566667	0.01186193	-0.6451	-96792	0.00814964
P84104	SRSF3	1.71	0.0319485	-2.39903	1	0.52199355
Q6AXD2	ABI2	6.64	4.12E-05	4.662049	1	0.52199355
P60122	RUVBL1	6.64	4.12E-05	4.662049	-94144	0.06862082
Q8K0L9	ZBTB20	1.4966667	0.03468295	-2.56026	-97962	0.00353512

Q5F2F2	ABHD15	4.4266667	0.26557447	-6.5253	-14.999	0.04391494
Q99LX0	PARK7	0.9133333	0.06553018	-3.70398	-16.999	0.03202093
Q9D6Y7	MSRA	3.5866667	0.24055695	-6.13504	-96349	0.01148581
J3QMG3	VDAC3	4.8766667	0.19188661	-5.70032	-94785	0.04091465
Q9WV55	VAPA	6.64	4.12E-05	4.662049	1	0.52199355
Q9JJD0	THAP11	1.42	0.11470985	-4.7203	-96349	0.01148581
Q9QZD8	SLC25A10	-1.873333	0.26557447	-6.4395	-14.999	0.04091465
Q8K0E8	FGB	0.36	0.32158861	-6.92276	-95871	0.019885
Q9CRB3	URAH	3.3966667	0.00647032	0.433702	-98957	0.00157768
P14152	MDH1	0.6066667	0.40571105	-7.3387	-95871	0.019885
Q8VDP4	CCAR2	6.64	4.12E-05	4.662049	1	0.52199355
O09061	PSMB1	1.0433333	0.02180485	-1.6777	-6.9999	0.0738844
E9Q616	AHNAK	2.42	0.29212642	-6.75531	-96349	0.01291602
Q9EQ32	PIK3AP1	4.8233333	0.20383635	-5.81162	-16.999	0.03202093
Q9D0I9	RARS	2.26	0.0295548	-2.24621	-12.999	0.05568397
D3YYH0	PEX5L	6.64	4.12E-05	4.662049	1	0.52199355
Q62093	SRSF2	1.3466667	0.03046466	-2.30049	1	0.52199355
Q64337	SQSTM1	4.9533333	0.1768368	-5.53308	-14.999	0.04391494
P61620	SEC61A1	1.1166667	0.31402562	-6.88315	-96349	0.01291602
Q9JMK2	CSNK1E	6.64	4.12E-05	4.662049	1	0.52199355
A0A2R8VJW4	CLIP4	6.64	4.12E-05	4.662049	1	0.52199355
Q7TNG8	LDHD	1.6666667	0.16070491	-5.33785	-95871	0.01640025
Q61037	TSC2	6.64	4.12E-05	4.662049	1	0.52199355
Q9D819	PPA1	3.0133333	0.32741295	-6.95865	-95353	0.02763432
Q9D7M1	GID8	6.64	4.12E-05	4.662049	-3	0.33386831
Q9D1Q6	ERP44	0.29	0.69843168	-8.215	-95871	0.01640025
P55264	ADK	1.8066667	0.10362516	-4.53559	-96792	0.00929561
Q6AXB7	FMR1	6.64	4.12E-05	4.662049	1	0.52199355
Q9DBS5	KLC4	-0.416667	0.76563806	-8.29264	-96349	0.01148581
Q5SRX1	TOM1L2	6.64	4.12E-05	4.662049	1	0.52199355
D3Z7C6	PTGES3	1.58	0.04540077	-3.08352	-12.999	0.06953933
Q8CCJ4	AMER2	6.64	4.12E-05	4.662049	1	0.52199355
Q91YQ5	RPN1	0.7733333	0.27036519	-6.57393	-95871	0.01640025
Q5HZI1	MTUS1	1.1233333	0.37109004	-7.20557	-95873	0.01722796
Q78IK4	APOOL	2.4466667	0.46369672	-7.53301	-97598	0.0047905
A6ZI44	ALDOA	0.95	0.29449945	-6.77128	-95872	0.01722796
P62835	RAP1A	2.7833333	0.37109004	-7.20482	-95353	0.02763432
Q9D0E3	LYSMD1	6.64	4.12E-05	4.662049	1	0.52199355
Q8R307	VPS18	6.64	4.12E-05	4.662049	1	0.52199355
Q80ZM5	H1F10	6.64	4.12E-05	4.662049	1	0.52199355
P21279	GNAQ	6.64	4.12E-05	4.662049	1	0.52199355
Q9D0M5	DYNLL2	3.1533333	0.30377278	-6.82261	-94785	0.04091465

D3Z6D2	STAU2	6.64	4.12E-05	4.662049	1	0.52199355
P62812	GABRA1	6.64	4.12E-05	4.662049	1	0.52199355
Q80U93	NUP214	6.64	4.12E-05	4.662049	1	0.52199355
A0A5F8MP75	MAPK10	6.64	4.12E-05	4.662049	1	0.52199355
P53996	CNBP	0.9933333	0.26337304	-6.2947	-95872	0.01722796
Q7TT50	CDC42BPB	6.64	4.12E-05	4.662049	1	0.52199355
Q91WG7	DGKG	6.64	4.12E-05	4.662049	1	0.52199355
E9PVU7	PDE4D	6.64	4.12E-05	4.662049	1	0.52199355
A0A2I3BQW0	ASXL1	6.64	4.12E-05	4.662049	-96795	0.0085431
Q8BGT5	GPT2	0.0933333	0.98448066	-8.42813	-96349	0.01291602
Q8BI84	MIA3	-0.993333	0.42606419	-7.41199	-95871	0.019885
Q8BFY6	PEF1	2.7033333	0.39103474	-7.28367	-95873	0.01722796
P26150	HSD3B3	0.5866667	0.07428911	-3.93341	-96792	0.00814964
E9PWE8	DPYSL3	6.64	4.12E-05	4.662049	1	0.52199355
Q8BFW7	LPP	6.64	4.12E-05	4.662049	-94785	0.04091465
Q8R0S4	CACNB4	6.64	4.12E-05	4.662049	1	0.52199355
Q00PI9	HNRNPUL2	6.64	4.12E-05	4.662049	1	0.52199355
P10518	ALAD	-2.006667	0.00124447	2.634648	-2	0.43157443
Q8CGK3	LONP1	4.5233333	0.09744718	-4.41583	-95871	0.019885
P11679	KRT8	2.4233333	0.47494682	-7.56651	-96792	0.01015707
A0A286YCT4	SSR1	1.1266667	0.04325203	-2.99609	-1.4	0.52199355
A2AS89	AGMAT	2.0166667	0.03952797	-2.81994	-96349	0.0157301
Q8BRK8	PRKAA2	0.3266667	0.49142719	-7.79426	-95872	0.01722796
D3Z6I8	TPM3	1.55	0.04160557	-2.92823	-2	0.52199355
P97300	NPTN	6.64	4.12E-05	4.662049	1	0.52199355
P26231	CTNNA1	2.2533333	0.47805356	-7.70027	-95351	0.02763432
Q6PEB6	MOB4	6.64	4.12E-05	4.662049	1	0.52199355
Q8VEJ9	VPS4A	6.64	4.12E-05	4.662049	1	0.52199355
Q9D8W5	PSMD12	6.64	4.12E-05	4.662049	-11	0.08613925
Q9DBK0	ACOT12	6.64	4.12E-05	4.662049	-96349	0.01148581
Q9D2R8	MRPS33	6.4466667	0.00194291	2.10884	1	0.52199355
Q9D883	U2AF1	1.5333333	0.14018664	-5.07744	-94785	0.04091465
A0A0R4J0I6	ACAD11	6.64	4.12E-05	4.662049	-95871	0.01722796
Q99L04	DHRS1	2.29	0.00135204	2.529549	-96350	0.01245573
Q60936	COQ8A	0.5966667	0.66506216	-8.1649	-95353	0.02763432
Q8R404	MICOS13	5.4366667	0.08848591	-4.23965	-95353	0.02763432
Q8BJY1	PSMD5	4.9966667	0.16848167	-5.4346	-95351	0.02613381
P63158	HMGB1	-0.056667	0.90474388	-8.39909	-95871	0.01640025
Q9D0R8	LSM12	6.64	4.12E-05	4.662049	1	0.52199355
Q9DB29	IAH1	0.5166667	0.36171853	-7.1327	-14.999	0.04391494

Q9D832	DNAJB4	6.64	4.12E-05	4.662049	1	0.52199355
G8JL68	MYEF2	6.64	4.12E-05	4.662049	1	0.52199355
Q543K9	PNP	1.8366667	0.04298631	-2.984	-12.999	0.05568397
G3UY93	VARS	2.2233333	0.47805356	-7.72461	-95353	0.02763432
Q3UMU9	HDGFL2	6.64	4.12E-05	4.662049	1	0.52199355
Q9DBR0	AKAP8	2.7266667	0.38475871	-7.25829	-95871	0.01640025
Q3THS6	MAT2A	3.3	0.27360311	-6.61119	-95873	0.01722796
P56593	CYP2A12	4.9233333	0.18223793	-5.59957	-95871	0.019885
Q9JK92	HSPB8	0.0166667	1	-8.43406	-95353	0.02763432
P14602	HSPB1	0.8866667	0.24171578	-6.14317	-95352	0.02763432
E9Q450	TPM1	6.64	4.12E-05	4.662049	-3.9999	0.2579867
Q80XK6	ATG2B	6.64	4.12E-05	4.662049	1	0.52199355
Q9DCW4	ETFB	1.69	0.10921019	-4.64274	-95871	0.01722796
Q9DBG1	CYP27A1	0.66	0.47805356	-7.61954	-96349	0.01148581
Q9QXD1	ACOX2	6.64	4.12E-05	4.662049	-14.999	0.04391494
B1AT82	PRPSAP1	6.64	4.12E-05	4.662049	-3.9999	0.2579867
Q920Q4	VPS16	6.64	4.12E-05	4.662049	1	0.52199355
Q7TMQ7	WDR91	-0.456667	0.23350213	-6.06776	-95353	0.02763432
Q9JIA7	SPHK2	6.64	4.12E-05	4.662049	-2	0.52199355
Q6QWF9	CAMK2N1	6.64	4.12E-05	4.662049	1	0.52199355
B1AR34	ASGR1	1.1233333	0.36849719	-7.18213	-96349	0.01291602
Q9WUR2	ECI2	5.3466667	0.10245202	-4.51729	-96792	0.00929561
Q91WT8	RBM47	0.5766667	0.56791702	-7.98915	-96793	0.01015707
A0A1Y7VN70	GLRX5	6.64	4.12E-05	4.662049	-94144	0.06862082
P70188	KIFAP3	6.64	4.12E-05	4.662049	1	0.52199355
G3UYV7	RPS28	2.21	0.01638707	-1.18487	-95871	0.01640025
Q641P0	ACTR3B	6.64	4.12E-05	4.662049	1	0.52199355
Q9Z1D1	EIF3G	1.1566667	0.02017651	-1.54799	-6.9998	0.15689585
B2RQE8	ARHGAP42	1.21	0.08227595	-4.10238	-95871	0.01722796
Q6IR34	GPSM1	6.64	4.12E-05	4.662049	1	0.52199355
A2ADA6	ACAP3	6.64	4.12E-05	4.662049	1	0.52199355
B1AR13	CISD3	6.64	4.12E-05	4.662049	1	0.52199355
Q9WUD1	STUB1	6.64	4.12E-05	4.662049	1	0.52199355
Q91XE9	CREB3L3	6.64	4.12E-05	4.662049	-8.9997	0.10426026
P68369	TUBA1A	2.1033333	0.0398377	-2.8358	1	0.52199355
A2A841	EPB41	0.31	0.49922224	-7.82091	-95351	0.02613381
Q80U95	UBE3C	6.64	4.12E-05	4.662049	1	0.52199355
P23475	XRCC6	6.64	4.12E-05	4.662049	1	0.52199355
Q5XG73	ACBD5	1.2433333	0.03843975	-2.75984	-95351	0.02613381
M0QWZ1	FAM193A	6.64	4.12E-05	4.662049	-2	0.52199355
Q7TPV4	MYBBP1A	0.29	0.27980743	-6.66294	-94785	0.04091465
O09172	GCLM	6.64	4.12E-05	4.662049	-8.9997	0.10426026

Q8K2C9	HACD3	1.68	0.10513404	-4.56912	-95353	0.02763432
Q791V5	MTCH2	2.09	0.08362646	-4.13832	-96349	0.01148581
Q80U04	PJA2	6.64	4.12E-05	4.662049	1	0.52199355
E9Q3V2	SLC35A3	0.76	0.26557447	-6.40791	-95351	0.02613381
Q7TSY6	CELF4	6.64	4.12E-05	4.662049	1	0.52199355
Q99KK2	CMAS	1.8333333	0.02419371	-1.86789	6.9998	0.95168916
Q9CQZ1	HSBP1	6.64	4.12E-05	4.662049	1	0.52199355
Q5U3K5	RABL6	6.64	4.12E-05	4.662049	1	0.52199355
B2RSH2	GNAI1	6.64	4.12E-05	4.662049	1	0.52199355
A0A498WGK2	NARS	6.64	4.12E-05	4.662049	1	0.52199355
P40124	CAP1	6.64	4.12E-05	4.662049	1	0.52199355
Q9CX86	HNRNPA0	6.64	4.12E-05	4.662049	1	0.52199355
Q6ZWU9	RPS27	2.2333333	0.01560858	-1.09463	-6.9998	0.15689585
A0A140LHA2	BUB3	6.64	4.12E-05	4.662049	1	0.52199355
F6WHQ7	GSTM1	0.6166667	0.0275432	-2.10645	4.9999	0.92709827
S4R1M9	OSBPL10	6.64	4.12E-05	4.662049	1	0.52199355
Q920M5	CORO6	6.64	4.12E-05	4.662049	1	0.52199355
E9PXF0	PCDH17	6.64	4.12E-05	4.662049	1	0.52199355
E9QAQ3	ARHGAP26	6.64	4.12E-05	4.662049	1	0.52199355
Q61425	HADH	-2.87	0.02817268	-2.16345	-3.9999	0.2579867
Q99JI4	PSMD6	1.75	0.03478411	-2.56822	-94785	0.04091465
Q9EQQ2	YIPF5	6.64	4.12E-05	4.662049	-6.9998	0.15689585
Q9D7N3	MRPS9	6.64	4.12E-05	4.662049	-2	0.52199355
Q61081	CDC37	6.64	4.12E-05	4.662049	1	0.52199355
Q8C5L3	CNOT2	6.64	4.12E-05	4.662049	-94785	0.04091465
E9Q4D5	REM2	6.64	4.12E-05	4.662049	1	0.52199355
Q3TQB2	FOXRED1	6.64	4.12E-05	4.662049	1	0.52199355
A0A0R4J094	FAHD2A	6.64	4.12E-05	4.662049	-3	0.33386831
G3UX79	MRPS18B	6.64	4.12E-05	4.662049	1	0.52199355
S4R2A9	SEC31A	6.64	4.12E-05	4.662049	-8.9997	0.11265511
B2RXQ2	PPFIA1	6.64	4.12E-05	4.662049	1	0.52199355
G3UZH5	TRAK2	6.64	4.12E-05	4.662049	-2	0.52199355
P58391	KCNN3	5.95	0.02787677	-2.13168	1	0.52199355
A0A2R8VK76	CPSF1	6.64	4.12E-05	4.662049	-4.9999	0.26057561
A0A1B0GS70	PSMA1	0.3666667	0.4160534	-7.37209	-95352	0.02763432
B1AZS9	PRDX4	2.7933333	0.37109004	-7.20388	-95352	0.02763432
A0A1B0GR85	2900026A02RIK	1.8466667	0.01449795	-0.96351	-96795	0.0085431
Q8R4H2	ARHGEF12	6.64	4.12E-05	4.662049	1	0.52199355
P0C027	NUDT10	6.64	4.12E-05	4.662049	1	0.52199355
Q8VHI6	WASF3	6.64	4.12E-05	4.662049	1	0.52199355

Q62392	PHLDA1	6.64	4.12E-05	4.662049	-6.9998	0.15689585
Q9D9V3	ECHDC1	3.4733333	0.26482644	-6.30549	-95351	0.02613381
Q8VHW2	CACNG8	6.64	4.12E-05	4.662049	1	0.52199355
Q80TJ1	CADPS	6.64	4.12E-05	4.662049	1	0.52199355
P10637	MAPT	6.3966667	0.00313607	1.442439	1	0.52199355
Q8BGZ2	FAM168A	6.64	4.12E-05	4.662049	1	0.52199355
Q9DC71	MRPS15	6.64	4.12E-05	4.662049	-3	0.33386831
F6U2S8	WNK1	6.64	4.12E-05	4.662049	1	0.52199355
Q9Z140	CPNE6	0.82	0.04389845	-3.03083	1	0.52199355
P70266	PFKFB1	-1.956667	0.5348154	-7.91484	-94785	0.04091465
E9QQ25	SPEG	4.28	0.29083666	-6.74447	-95872	0.01722796
Q9D8X5	CNOT8	6.64	4.12E-05	4.662049	-4.9999	0.26057561
P48758	CBR1	6.64	4.12E-05	4.662049	1	0.52199355
Q61187	TSG101	6.64	4.12E-05	4.662049	-3	0.33386831
Q91Z61	DIRAS1	6.64	4.12E-05	4.662049	1	0.52199355
Q8K019	BCLAF1	0.4766667	0.53473354	-7.91399	-94785	0.04091465
I7HPV9	PREX1	6.64	4.12E-05	4.662049	1	0.52199355
E9Q3B9	MGLL	6.64	4.12E-05	4.662049	1	0.52199355
Q60973	RBBP7	6.64	4.12E-05	4.662049	1	0.52199355
Q9D1C8	VPS28	6.64	4.12E-05	4.662049	1	0.52199355
Q91W64	CYP2C70	6.64	4.12E-05	4.662049	-94785	0.04091465
A0A1B0GR60	FTL1	6.64	4.12E-05	4.662049	-4.9999	0.26057561

Appendix 5.4. O-GlcNAc Sites and Regions Identified in the Mouse Brain.

See also **Fig. 5.5**.

Protein	Min Sites	Site ID Constraints
A0A075B6D7	1	304
A0A075B6D7	1	164
A0A087WNU5	1	(1 of 268,269)
A0A087WNU5	1	(1 of 2278,2280,2283,2284,2286,2287)
A0A087WNU5	1	(1 of 224,226,227,231)
A0A087WNU5	1	(1 of 578,580)
A0A087WNU5	1	261
A0A087WNU5	1	401
A0A087WNU5	1	274
A0A087WNU5	1	275
A0A087WNU5	1	273
A0A087WNU5	1	276
A0A087WNU5	1	407
A0A087WNU5	1	280
A0A087WNU5	1	408
A0A087WNU5	1	412
A0A087WNU5	1	321
A0A087WNU5	1	323
A0A087WNU5	1	206
A0A087WNU5	1	210
A0A087WNU5	1	470
A0A087WNU5	1	471
A0A087WNU5	1	345
A0A087WNU5	1	346
A0A087WNU5	1	474
A0A087WNU5	1	349
A0A087WNU5	1	357
A0A087WNU5	1	486
A0A087WNU5	1	487
A0A087WNU5	1	871
A0A087WNU5	1	238
A0A087WNU5	1	369
A0A087WNU5	1	243
A0A087WNU5	1	500
A0A087WNU5	1	372
A0A087WNU5	1	379
A0A087WNU5	1	382

A0A087WNU5	1	383
A0A087WNV1	1	(1 of 267,269,270)
A0A087WNV1	1	322
A0A087WNV1	1	258
A0A087WNV1	1	260
A0A087WNV1	1	262
A0A087WNV1	1	327
A0A087WNV1	1	251
A0A087WP54	1	536
A0A087WPX3	1	975
A0A087WQC5	1	191
A0A087WSE3	1	(1 of 2550,2552,2553,2557,2565,2568,2569,2571,2573,2574,2575,2576,2578,2584,2585)
A0A087WSE3	1	(1 of 2625,2630,2632,2634,2636,2637,2638,2647,2648,2649,2650,2655,2656,2659,2676)
A0A0A0MQC7	1	(1 of 704,705,706,708,714,719)
A0A0A0MQC7	1	688
A0A0A0MQC7	1	555
A0A0A0MQC7	1	725
A0A0A0MQE5	1	387
A0A0A6YVZ3	2	(2 of 120,122,123,124,126,129,130,131,133,134,137,138,141,145)
A0A0A6YWC8	1	33
A0A0A6YWG7	1	(1 of 727,729,731,732,733,740)
A0A0A6YWG7	1	1313
A0A0A6YWG7	1	1512
A0A0A6YWG7	1	1513
A0A0A6YWG7	1	1356
A0A0A6YWG7	1	1589
A0A0A6YXG1	3	(3 of 2010,2011,2015,2016,2017,2018,2019,2020,2021,2025)&(2 of 2005,2007,2010,2011,2015,2016,2017,2018,2019,2020,2021,2025)&(1 of 2005,2007,2010,2011,2015,2016,2017,2018,2019,2020,2021,2025,2028,2029)
A0A0A6YXG1	1	2009
A0A0A6YY91	1	(1 of 986,987,990)
A0A0A6YY91	1	(1 of 920,924,926,932,942)
A0A0A6YY91	1	(1 of 771,776,777,780,788,789,791,798,800,801,803,804,806,808,810,812,815,819,821,822,824,825,826,828,829,830,836,837,841,843,850,852)
A0A0A6YY91	1	(1 of 1019,1024,1027,1031,1036,1037,1040)
A0A0A6YY91	1	(1 of 858,859)
A0A0A6YY91	1	(1 of 875,877,879,880,883,885,888,889,890,900,902,903,906,910,911)
A0A0A6YY91	1	856
A0A0G2JDK2	1	290
A0A0G2JDK2	1	71
A0A0G2JEG6	1	(1 of 702,705,706,708)
A0A0G2JEG6	1	1075
A0A0G2JEG8	1	336
A0A0G2JEG8	1	335

A0A0G2JER6	1	108
A0A0G2JER6	1	111
A0A0G2JGK8	1	(1 of 82,88,89,90,93,94)
A0A0J9YU75	1	(1 of 134,137,139,140,145,146,151,152)
A0A0J9YUN4	1	(1 of 740,747,748,749,751,752,761,767)
A0A0N4SW73	1	(1 of 1211,1212,1214,1215,1218,1219)
A0A0N4SW73	1	(1 of 1226,1228,1229,1234,1239,1243,1244,1247)
A0A0N4SW73	1	(1 of 702,705,711,712,713,715,722,723,725,728,729)
A0A0R4J060	1	(1 of 592,593,601,608,612,618,619,623,625,627,629,630,632,637,638)
A0A0R4J060	1	280
A0A0R4J060	1	320
A0A0R4J060	1	279
A0A0R4J092	1	91
A0A0R4J0B3	1	(1 of 746,747,754,757,760,763,767,768)
A0A0R4J0W7	1	1280
A0A0R4J0W7	1	535
A0A0R4J102	1	219
A0A0R4J138	1	(1 of 165,173,178,187,191)
A0A0R4J1F4	1	(1 of 699,700,701,702,703,704,706,707,708,710,711,715,718,723,724)
A0A0R4J1F4	1	(1 of 828,829,832,833,835,838,839,847,850,851)
A0A0R4J274	1	(1 of 217,220,223,226,227,229,233,234,237)
A0A0R4J2A2	1	398
A0A0R4J2B5	1	348
A0A0U1RPA0	1	(1 of 35,36,39,41,42,43,46,47,48,49)
A0A0U1RPL0	1	(1 of 266,267)
A0A0U1RPL0	2	(2 of 450,457,459,467,471,472,474,478,479,480)
A0A0U1RPL0	1	680
A0A0U1RPL0	1	675
A0A0U1RPL0	1	676
A0A0U1RPL0	1	437
A0A140LHQ8	1	(1 of 343,344)
A0A140LHQ8	1	(1 of 381,382,388,396,399,403)
A0A140LHQ8	2	(2 of 236,237,239,240,243,246,247,248,254,262,263,265,266,267,269,270,271)
A0A140LHQ8	1	(1 of 346,348,356,358,365,366,375)
A0A140LHQ8	1	(1 of 416,421,422,436,437,442,444)
A0A140LHQ8	1	337
A0A140LIW3	1	708
A0A140T8S0	1	346
A0A1B0GRV3	1	248
A0A1B0GSU0	1	(1 of 607,608)
A0A1B0GT88	1	(1 of 470,473,476)
A0A1C7ZMY3	1	(1 of 341,343,345,348)
A0A1C7ZMY3	1	(1 of 1077,1078,1079,1081,1083)

A0A1C7ZMY3	1	(1 of 452,453,456,457,465,475,477,479,480)
A0A1C7ZMY3	1	(1 of 188,196)
A0A1C7ZMY3	1	(1 of 902,903,904,910,911,912,913,915,916,918,919,921,922,924,925,930,933,935)
A0A1C7ZMY3	1	1065
A0A1C7ZMY3	1	1070
A0A1C7ZMY3	1	1135
A0A1C7ZMY3	1	1071
A0A1C7ZMY3	1	1075
A0A1C7ZMY3	1	759
A0A1C7ZMY3	1	183
A0A1C7ZMY3	1	669
A0A1D5RLD8	1	208
A0A1D5RLN6	1	355
A0A1D5RLV3	1	(1 of 2919,2920,2922,2923,2926,2927,2928,2929)
A0A1D5RLV7	1	2254
A0A1D5RLY6	1	(1 of 694,701,704,705,707,709,712,714,716,724,730,732)
A0A1D5RM55	1	118
A0A1D5RM83	1	(1 of 287,289,293,301,307)
A0A1L1SR84	2	(2 of 896,907,908,917,920,921,922,925,933)
A0A1L1SR84	1	(1 of 1326,1327,1330,1331)
A0A1L1SR84	1	1123
A0A1W2P6Y4	1	390
A0A1W2P7D7	1	(1 of 144,149,152)
A0A1W2P7D7	1	153
A0A1W2P7K6	1	(1 of 16,18,19,30,34,35,36,38)
A0A1W2P882	1	(1 of 242,245,251,254,255,257,262,263,264,265,267,268,269,274,279)
A0A1Y7VIR0	1	45
A0A1Y7VJH3	1	(1 of 382,389,390)
A0A1Y7VNM3	1	167
A0A286YDC8	1	(1 of 219,220,229,235,242,247,253,254,259,262,266)
A0A286YDC8	1	(1 of 273,275,279,283,285,292,293)
A0A286YDC8	1	343
A0A286YDY4	2	(2 of 480,482,483,487,489)
A0A2I3BPN6	1	486
A0A2I3BQ43	1	(1 of 540,541,542,544,550,556,558,566,567)
A0A2R8VKG2	1	(1 of 1926,1931,1933,1938)
A0A2R8VKG2	1	1896
A0A2R8VKG2	1	1921
A0A2R8VKG2	1	1501
A0A2R8VKG2	1	1838
A0A338P689	1	(1 of 310,315,331,332)
A0A338P6P6	1	554
A0A338P7L8	1	76

A0A494B9T4	1	(1 of 36,37,42,43,46,47)
A0A498WGM0	1	(1 of 191,196,197,199,200,202,203,206,209,210)
A0A498WGM0	1	(1 of 242,245,246,247,249,259,263)
A0A498WGM0	1	58
A0A498WGM0	1	52
A0A498WGM0	1	55
A0A571BDM4	1	43
A0A571BDM4	1	37
A0A571BDN3	1	709
A0A571BET0	1	(1 of 1082,1087,1092,1093,1094)
A0A571BET0	1	(1 of 2212,2216,2220,2223,2225,2226,2228,2233)
A0A571BEZ4	1	376
A0A5F8MPJ2	1	(1 of 229,230,231,233,240,241,242,246,248,254,255)
A0A5F8MPJ2	1	861
A0A5F8MPY3	1	392
A0A5F8MQ25	1	(1 of 876,879,881)
A0A5F8MQ25	1	(1 of 840,843)
A0A5F8MQ25	1	852
A0A5F8MQ25	1	886
A2A468	1	(1 of 641,642,644,646,647,649,652,653,654,655,656,658,660,661,662,663,668)
A2A484	1	(1 of 755,756,757,758,763,767,771)
A2A654	1	(1 of 2058,2059,2060,2061,2066,2067,2068,2069,2071)
A2A654	1	(1 of 1739,1742,1743,1744)
A2A654	1	(1 of 1750,1751,1753,1754,1755,1756,1757,1758,1760)
A2A654	1	1713
A2A690	1	(1 of 163,168,169,171,172,173,176)
A2A690	1	(1 of 129,132,133,135,136,137,138,140,144,145,148,149,154,155)
A2A690	1	(1 of 268,272,273,274)
A2A690	1	(1 of 1871,1875,1876,1879,1882,1884,1885,1894,1896,1899,1900,1902)
A2A690	1	1643
A2A690	1	1651
A2A690	1	1956
A2A690	1	1943
A2A6H0	1	77
A2A841	1	(1 of 769,771,777,780,791,794,796,797,799,800,801,802,803,804,805,806,809)
A2A841	1	765
A2A884	1	(1 of 1465,1467,1468,1470,1471,1474)
A2A884	1	(1 of 390,392,398,402)
A2A884	1	(1 of 1527,1536,1537,1541,1543,1544)
A2A884	1	984
A2A884	1	1074
A2A884	1	1070
A2AC24	1	140

A2ADM8	1	(1 of 1512,1516,1521,1522,1525,1526,1528,1529)
A2ADY9	1	(1 of 115,120,121,127,128)
A2AFG7	1	(1 of 574,578,584,588,589,596)
A2AFG7	1	667
A2AG50	1	(1 of 184,187,193,196,197,198,203,205,206,207,212,213)
A2AGT5	1	(1 of 1914,1916,1917,1918,1920,1921)
A2AGT5	1	1904
A2AGT5	1	1925
A2AGT5	1	1910
A2AH22	1	(1 of 322,329,334)
A2AH22	1	441
A2AH22	1	442
A2AH25	1	20
A2AJA9	1	(1 of 100,105,109)
A2AJA9	1	349
A2AKB4	1	1215
A2AKB9	1	(1 of 357,358,361,362,363)
A2AKB9	1	364
A2ALK6	1	535
A2ALS5	1	(1 of 606,610,611,616,618,619,620,621,624,625,629)
A2ALS5	1	(1 of 454,456,457,458,460,462,464)
A2AMI6	1	(1 of 187,188,190,196,202,208,211,217,218,221,224)
A2API8	1	(1 of 459,461,463,473)
A2AQ25	1	(1 of 359,361,363,365)
A2AQ25	1	(1 of 1716,1731,1732,1734,1737)
A2AQ25	2	(2 of 1893,1894,1895,1896,1897,1898,1899,1902,1905,1907,1908)
A2AQ25	1	(1 of 1814,1815,1816,1819,1821,1824,1825,1833,1836,1839,1840,1843)
A2AQ25	1	1348
A2AQ25	1	357
A2AQ25	1	1070
A2AQH4	1	646
A2ARP8	1	(1 of 2021,2027,2032)
A2ARP8	1	(1 of 2632,2633,2639,2641,2642,2653)
A2ARP8	1	(1 of 1007,1008,1009,1013,1024,1026,1029,1034,1035,1036)
A2ARP8	1	(1 of 1076,1077,1080,1081,1087,1090,1092,1096,1099)
A2ARP8	1	(1 of 1038,1044,1047,1064,1065,1067,1068,1070)
A2ARP8	1	(1 of 808,809,814,819)
A2ARP8	1	(1 of 2464,2468,2471,2472,2473,2476,2477,2481,2482)
A2ARP8	1	(1 of 1472,1479,1485,1487,1489,1492,1502,1505,1513,1514,1516,1518,1521)
A2ARP8	1	2433
A2ARP8	1	2147
A2ARP8	1	1115
A2AUD5	1	121

A2AUX5	1	(1 of 728,734)
A2AUY4	1	(1 of 277,285,287,289,295)
A2AW73	1	1014
A2AWI9	1	(1 of 263,267,268,272,276,277,278,279,281,282,283,286,292,314,316)
A2BH40	1	(1 of 127,128,129,130,139)
A2BH40	1	256
A2RSY1	1	534
A6H619	1	(1 of 1359,1363,1364,1365,1366,1368,1369,1376)
B0QZH6	1	(1 of 332,339,342,349)
B0R0Y8	1	(1 of 84,85,87)
B1AQX6	1	(1 of 670,671)
B1AQX6	1	(1 of 333,336,340,341,342,349,353,357,359,361)
B1AQX6	1	(1 of 563,564,566,568,569,575)
B1AQX6	1	320
B1AQX6	1	1057
B1AQX6	1	516
B1AQX6	1	1065
B1AQX6	1	662
B1AQX6	1	989
B1ARU4	1	(1 of 533,534,541,542,544,545,546)
B1ATU4	1	(1 of 489,490)
B1AUB8	1	(1 of 200,203,204,206,208,210,211,212,215,218)
B1AUB8	2	(1 of 327,331,332,333,334,340,342,343,345,348,351,352)&(2 of 327,331,332,333,334)
B1AUB8	1	347
B1AUB8	1	350
B1AUC0	1	(1 of 456,460,461,462,463,469,471,472)
B1AV60	1	(1 of 1472,1473,1474,1475,1476,1479,1481,1482,1484,1485,1488,1491,1492)
B1AVN9	1	208
B1AWN6	1	1970
B1AXH1	1	(1 of 359,361,368,374,377,378,383,385,386,388,389,390)
B1AXH1	2	(2 of 309,311,312,319)
B1AXH1	1	443
B1AZP2	1	(1 of 259,260,261,264,275,278,283,285)
B1B0C7	1	3059
B1B0C7	1	847
B2RRI2	1	125
B2RUJ2	1	1068
B2RUQ2	1	(1 of 361,364,366,367,369)
B2RXW8	1	(1 of 1233,1235,1238,1240)
B7ZCA7	1	258
B7ZCJ0	1	(1 of 313,314,315,318,321,328,329,331)
B7ZCJ0	1	(1 of 1561,1565,1569,1570,1571,1572,1575,1576,1577,1578,1579,1580,1581,1584,1585,1588,1589)
B7ZCJ0	1	354

B7ZCJ0	1	355
B7ZCJ0	1	356
B7ZCJ0	1	228
B7ZCJ0	1	307
B7ZCJ0	1	628
B8JJI7	1	(1 of 1003,1004,1011,1015,1016,1017,1019,1021,1022,1024,1026,1027)
B8QI36	1	1184
B9EIX2	1	(1 of 1312,1314,1321,1324,1325,1327)
B9EJA2	1	580
B9EKS2	2	(2 of 410,415,421,426,427,429,430,431,433,434)
B9EKS2	1	(1 of 648,651,652,655,658,660,661,662,663,665,666,668,669)
D3YTS3	1	1517
D3YU15	1	158
D3YUC9	1	11
D3YUI2	1	449
D3YUI2	1	450
D3YUL8	1	184
D3YUV1	1	540
D3YUV1	1	543
D3YYH0	1	(1 of 55,63,64,66,70,71,79,83,85,87)
D3YYY8	1	252
D3YZU1	1	(1 of 1064,1066,1067,1071,1073,1076,1077,1078,1081,1082)
D3YZU1	1	(1 of 1960,1962,1965,1966,1967,1968,1975,1976,1978,1980,1981,1983,1985,1986)
D3YZU1	1	(1 of 919,921,925,934,935,942,943,948,949,950)
D3YZU1	1	1891
D3YZU1	1	1796
D3YZU1	1	933
D3YZU1	1	1862
D3YZU1	1	973
D3YZU1	1	1137
D3Z197	1	(1 of 265,266,269,270,272,273,274)
D3Z1S6	1	210
D3Z3F8	1	478
D3Z3U7	1	328
D3Z3U7	1	324
D3Z3U7	1	327
D3Z4J9	1	95
D3Z5K8	1	769
D3Z6L3	2	(2 of 373,374,375,378)
D3Z6Q4	1	(1 of 477,478)
D3Z6Q4	1	(1 of 423,425,428,431,435,437,438,440,444,447,451,454,455,456,457,460)
D3Z752	1	58
D3Z768	1	(1 of 253,254,255,256,257,258)

D3Z768	1	545
E0CXP6	1	(1 of 38,39,44,49)
E0CZ72	1	(1 of 555,557,562,567,572,574,581,583,585)
E0CZD9	1	(1 of 142,150,151,154,157,158,162,163,164,165)
E9PU87	1	(1 of 950,952,953,955,957,958,965)
E9PU87	1	7
E9PUF4	1	(1 of 645,647,648,655,657,658,665,666,667,668,671)
E9PV14	1	(1 of 1166,1168,1169)
E9PV14	1	(1 of 1482,1483)
E9PV14	1	(1 of 1152,1153)
E9PV14	1	(1 of 1479,1480)
E9PV14	1	1409
E9PV14	1	1470
E9PV14	1	1477
E9PV14	1	1481
E9PV14	1	1417
E9PV14	1	1450
E9PV14	1	1453
E9PV14	1	1424
E9PV14	1	1457
E9PV14	1	1426
E9PV14	1	1430
E9PV14	1	1398
E9PV14	1	988
E9PV14	1	1469
E9PV14	1	1150
E9PV26	2	(2 of 531,532,534,544,548,549,550,551,552,554,559,560,561,564)
E9PV26	1	74
E9PV69	1	111
E9PV73	1	175
E9PWM3	1	(1 of 828,831,836,837)
E9PWM3	1	(1 of 595,599,601,602,603,604,607,610,611,612,616,617)
E9PWM3	1	(1 of 866,874,875)
E9PWM3	1	210
E9PX52	1	(1 of 837,838,839,843,844,845)
E9PX52	2	(2 of 756,762,768,770,773,774,776,780,781,782,783)
E9PX52	1	(1 of 853,854,856,864)
E9PXL0	1	(1 of 155,156,157,158,168,171)
E9PYK3	1	(1 of 1229,1239,1241,1242,1249)
E9PYL2	1	(1 of 993,995,999,1014,1015,1026,1031,1046)
E9PZ12	1	(1 of 702,705,706,709,710,715,717)
E9PZ12	1	(1 of 860,861,864,867)
E9PZ12	1	877

E9PZ43	1	(1 of 631,632,634,635,638,639,642,643)
E9PZ43	1	(1 of 161,173,175,183,184,192,194,196,201)
E9PZ43	1	(1 of 468,470,472,475,481)
E9PZ43	1	333
E9Q0A7	1	(1 of 355,356,359,360,362,365,367,373,375,377,378)
E9Q0A7	1	167
E9Q0A7	1	182
E9Q0A7	1	183
E9Q160	1	(1 of 189,192,197,200,203,205,207,208)
E9Q1M1	1	(1 of 1379,1384,1388,1389,1392,1394,1396,1397,1399,1402)
E9Q1M1	1	1030
E9Q1M6	1	(1 of 1786,1789,1792,1793,1797,1798,1800,1801,1802)
E9Q1M6	1	(1 of 2085,2088,2091,2098,2100,2104,2107)
E9Q1M6	1	1816
E9Q1M6	1	2096
E9Q2B2	1	(1 of 2022,2025,2026,2027,2028,2031,2032,2034,2037,2038,2039)
E9Q2B2	1	(1 of 2,3,4,14,15,18)
E9Q2B2	1	(1 of 1827,1834,1835,1839)
E9Q2B2	1	(1 of 2165,2166,2171,2180,2189,2190,2191,2195,2196)
E9Q2B2	1	(1 of 1969,1973,1975,1985,1986,1988)
E9Q2B2	1	(1 of 1847,1851)
E9Q2B2	1	1833
E9Q2B2	1	51
E9Q2B2	1	1429
E9Q2K2	1	69
E9Q323	1	(1 of 92,93)
E9Q3C1	1	395
E9Q3G8	1	(1 of 925,926,927,929,931,932)
E9Q3G8	2	(2 of 1158,1165,1167,1168,1169)
E9Q3G8	1	(1 of 554,557,559,561,562,563,565,568,569,570,575,579,580,581)
E9Q3G8	1	(1 of 1123,1127,1130,1134,1135,1138,1140,1142,1147)
E9Q3G8	1	705
E9Q3G8	1	513
E9Q3G8	1	899
E9Q3G8	1	934
E9Q3G8	1	1101
E9Q3G8	1	1102
E9Q3G8	1	627
E9Q3G8	1	1044
E9Q3G8	1	628
E9Q3G8	1	1046
E9Q3M9	1	(1 of 337,338,342,346,352,355,358,360,364,365,372)
E9Q3W4	1	(1 of 344,347,350,351)

E9Q3W4	1	2457
E9Q4K0	1	(1 of 449,450,452,454,457,459,463,464,465)
E9Q4K0	1	(1 of 397,399)
E9Q4K0	1	(1 of 297,298)
E9Q4K0	1	392
E9Q4K0	1	304
E9Q4K0	1	308
E9Q4K0	1	309
E9Q4K0	1	382
E9Q4K0	1	383
E9Q5Z1	1	(1 of 6,7,10,13)
E9Q616	1	(1 of 5376,5377,5378,5383,5384)
E9Q6H8	1	(1 of 483,484)
E9Q6H8	1	389
E9Q6R4	1	(1 of 1580,1583,1584,1587)
E9Q6R4	1	(1 of 745,749,752,756,765,767,769,770,771,776,778)
E9Q6Y8	1	(1 of 1161,1163,1164,1165,1166,1167,1168,1171,1172)
E9Q777	1	(1 of 689,691,701,703,706,708,709)
E9Q7E9	1	(1 of 415,417,422,423)
E9Q7M2	1	(1 of 113,121,128,130,131,135,136,138,140,145,147,148)
E9Q7M2	1	(1 of 743,744,745)
E9Q7M2	1	(1 of 539,540,541,548,554,556,559,560,564,567,571,573,583)
E9Q7M2	1	(1 of 767,768)
E9Q7M2	1	758
E9Q804	1	(1 of 2372,2375,2378,2381,2382,2384,2387,2391,2393,2394)
E9Q804	1	(1 of 1833,1834,1838,1839,1840,1841,1843,1845,1848,1853,1854,1856,1857)
E9Q804	1	(1 of 2185,2191,2192,2193,2195)
E9Q804	1	1825
E9Q804	1	1826
E9Q804	1	1996
E9Q804	1	1820
E9Q804	1	1821
E9Q828	1	(1 of 1135,1136,1138,1143)
E9Q828	1	1155
E9Q828	1	1125
E9Q828	1	1151
E9Q828; F7AAP4	1	(1 of 1135,1136)
E9Q828; F7AAP4	1	1125
E9Q842	1	1532
E9Q842	1	1285
E9Q9C4	1	(1 of 381,383,385,387)
E9Q9C4	1	(1 of 402,403,404)

E9Q9C4	1	414
E9Q9C4	1	303
E9QA68	2	(2 of 111,116,117,119,120,123,125,127,128,129,131,132,134,135,136,137,139)
E9QA68	1	115
E9QAT4	1	(1 of 1087,1094,1099,1103,1106,1110,1112,1119,1122,1125,1136,1137,1139,1141,1142,1143,1145,1146)
E9QAT4	1	(1 of 2027,2028,2030,2034)
E9QAT4	1	2013
E9QAT4	1	69
E9QAT4	1	70
E9QAT4	1	127
E9QKB1	1	(1 of 159,161,162,163,164,165,166,169,174,178,179)
E9QKW9	1	(1 of 130,132,135,138,139)
E9QKW9	1	(1 of 279,281,282,285,286,289)
E9QKW9	1	(1 of 86,117,123,125,127)
E9QKW9	1	133
E9QLT6	1	(1 of 545,547,551)
E9QLZ1	1	(1 of 1033,1036,1049,1051,1055,1056,1061,1062,1070,1073,1075,1076)
E9QLZ1	1	444
E9QM73	1	(1 of 1514,1523,1524,1525,1527,1530,1535,1540,1550,1553,1556,1558,1560,1563,1566)
E9QM73	1	(1 of 1018,1019,1023,1028,1030,1035,1036,1037,1042,1048,1072,1082,1083,1085,1089,1092,1093)
E9QM73	1	1698
E9QM73	1	1917
E9QM73	1	1918
E9QMN5	1	178
E9QMN5	1	326
E9QN14	1	(1 of 982,983,987,991)
E9QNF7	1	(1 of 75,77,79)
E9QP99	1	207
F2Z3U3	1	(1 of 763,767,775,777,789,793,795,796)
F2Z3U3	1	197
F2Z3U3	1	614
F6R6F1	1	245
F6RXJ8	1	(1 of 187,188,198)
F6SEU4	1	(1 of 907,912,913)
F6SEU4	1	(1 of 816,817,822,823,824,825,828)
F6SEU4	1	(1 of 1070,1074,1076)
F6SEU4	1	(1 of 892,895,897,898,900)
F6SEU4	1	809
F6SEU4	1	1137
F6SEU4	1	1140
F6SEU4	1	983
F6SEU4	1	1144
F6SEU4	1	1307

F6TAR7	1	(1 of 101,103,104,105,106,108,112,114,115,126,127,128)
F6TYF8	1	(1 of 124,125,132)
F6TYF8	1	(1 of 159,161,162,163,164,165,166,168,169,170,171,173,177,182,188)
F6U2S8	1	(1 of 246,247,248,249,251,255,257,258,269,270,271)
F6VBT9	1	(1 of 241,243,246,247,251,252,255,257)
F6W0G8	1	119
F6WMD1	1	(1 of 62,66)
F6Y6L6	1	132
F6Y6L6	1	127
F6YR19	2	(2 of 4,17,20,21,22,26,27,31)
F6YTL8	1	(1 of 483,487,495,497,498,501)
F6Z9T5	1	(1 of 139,155,156,159)
F6Z9T5	1	(1 of 104,110)
F6ZKM7	1	(1 of 65,66)
F7AAP4	1	(1 of 1146,1149,1151,1152,1155,1156,1159,1160,1165)
F7B4D5	1	(1 of 55,57,58,63,65,67,68,69)
F7BE84	1	(1 of 1157,1158,1159,1160,1161,1163,1166,1171,1174,1176,1178,1185)
F7BE84	1	1297
F7BJK1	1	(1 of 879,881,883,884,893,896,900,905,907,909,910)
F7BJK1	1	(1 of 1044,1046,1053,1055,1056,1061,1063,1066,1069)
F7CC56	1	(1 of 521,522,523,526,529,532)
F7CPX0	1	156
F7D291	1	199
F7D3N3	1	327
F7D4S5	1	(1 of 379,380,382,385,386,392,395)
F7D4S5	1	364
F8VPJ6	1	439
F8VPM9	1	(1 of 1565,1566,1583)
F8VPM9	1	1706
F8VPM9	1	1771
F8VPP8	1	(1 of 960,961,964,972,974,977,978,979,980)
F8VPZ9	1	(1 of 431,432,433,435,445)
F8VPZ9	1	1225
F8VQJ3	1	1216
F8VQJ3	1	1241
F8VQJ3	1	1106
F8WHT3	1	(1 of 2119,2126,2127)
F8WHT3	1	1984
F8WHT3	1	1803
F8WIK5	1	310
G3UX48	1	(1 of 42,43,46,47,53,59,61,64)
G3UX48	1	(1 of 616,625,631)
G3UX80	1	(1 of 128,129,130)

G3UZM1	1	(1 of 1428,1431)
G3UZX7	1	(1 of 494,501,503)
G3X8R8	1	(1 of 627,630,631,637,642,643,649,654,660,661,663,665)
G3X8R8	1	(1 of 849,850,862,866,869)
G3X8R8	1	256
G3X8R8	1	225
G3X8R8	1	218
G3X8R8	1	248
G3X932	1	(1 of 498,504,505,506,507,508,521)
G3X972	1	(1 of 65,66,72,81,82,96,97,98)
G3X9H5	1	1154
G3X9H5	1	1158
G3X9J0	1	(1 of 1550,1553,1556,1563,1568,1569,1570,1572,1575,1576,1577)
G3X9V4	1	(1 of 1353,1354,1356,1357,1367,1372)
G3X9V4	1	(1 of 1255,1259,1273,1274,1277,1278,1279)
G3X9V4	1	1030
G3X9Z4	1	(1 of 169,174,175,178,181,182,184,186,187)
G5E832	1	(1 of 2081,2083,2086,2089,2090,2095)
G5E8D8	1	(1 of 607,608,610,612,618,622)
G5E8J9	1	(1 of 622,630,631,632,635)
G5E8J9	1	(1 of 727,728)
G5E8J9	1	(1 of 750,751)
G5E8J9	1	731
G5E8J9	1	740
G5E8J9	1	758
G5E8J9	1	735
G5E8T6	1	(1 of 824,829)
G5E8T6	1	266
H3BJL2	1	(1 of 779,780)
H3BJY2	1	(1 of 815,819,820,825,827,828,829,831,832,833,835)
H3BKJ6	1	(1 of 83,90,97,103,108,110,112)
H3BKQ7	1	(1 of 195,199,201,203,206,212,219,220)
H9KV15	1	(1 of 1086,1089,1090,1092)
H9KV15	1	(1 of 256,262,264)
H9KV15	1	250
H9KV15	1	251
H9KV15	1	1614
I7HIP8	1	(1 of 404,408,409,412,413,417,418)
J3KMT7	1	(1 of 339,342,343,344,345)
J3KMT7	1	(1 of 296,297,300,303,304,305,306,307,309,310)
J3QNM3	1	(1 of 240,245,246,248,249,251,252,259,260,265,270)
J3QNM3	1	290
J3QNM3	1	707

J3QNM3	1	297
J3QNM3	1	283
J3QNM3	1	347
J3QPR1	1	23
K3W4L3	1	82
K3W4L3	1	459
K3W4L3	1	213
M0QWN7	1	(1 of 419,420)
O08553	1	507
O08579	1	(1 of 176,177,181,185,186,187,188,189,190,192,193,194,195,196,197,199,200,203)
O08599	1	(1 of 506,507,509,511,512,513,516)
O08599	1	504
O08715	1	(1 of 351,356,359,360,365,366,370,371)
O08785	1	446
O08789	1	158
O08919	1	(1 of 345,354,357,365,368,369,370,373,379,385,386,388,389,395)
O08919	1	(1 of 263,265,268,269,270)
O08919	1	285
O09117	1	(1 of 238,239,242,244,246,247,249,251,258,259)
O35126	1	(1 of 353,357,365,366,367)
O35607	1	(1 of 547,548,549,550,555,559,561)
O35633	1	15
O35738	1	(1 of 91,92,94,97,98,99,102,104,106,108,109,111,112,113,114,115,116,117,118,119,120,121)
O35927	1	(1 of 452,453,454,457,458,463)
O35927	1	(1 of 329,330,333,336,337,339,340,341,347,348,349,352,355,357,359)
O35927	1	320
O35927	1	447
O35927	1	267
O35927	1	268
O35927	1	269
O35927	1	435
O35927	1	307
O35927	1	437
O35927	1	319
O35954	1	1226
O54818	1	(1 of 156,157)
O55042	1	64
O55042	1	72
O55042	1	81
O55042	1	53
O55042	1	54
O55042	1	59
O70161	1	(1 of 495,498,511,514,519,520,522,525,526,528,529,530,531,533)

O70305	1	(1 of 382,383,386,387,389,390,392)
O70305	1	(1 of 635,636,641,643,644,647)
O70305	1	(1 of 778,779,780,781,783,789)
O70305	1	(1 of 812,816,817,818,819,820,821,824,825,827,828)
O70305	2	(2 of 174,175,182,186,187,189,200,201,202)
O70305	1	745
O70305	1	852
O70318	1	(1 of 886,888,891,902,907,910,912,913,915,917,918,919,920,921,922,925)
O70400	1	128
O70400	1	135
O70507	1	1022
O88492	1	354
O88492	1	189
O88492	1	222
O88531	1	(1 of 234,241)
O88531	1	199
O88532	1	(1 of 102,111,114,116,121)
O88532	1	(1 of 9,11,15)
O88532	1	(1 of 458,459)
O88532	1	(1 of 443,445,447,448,452,455)
O88532	1	195
O88532	1	422
O88532	1	135
O88532	1	136
O88532	1	167
O88532	1	202
O88532	1	423
O88532	1	300
O88532	1	429
O88532	1	148
O88532	1	180
O88704	1	(1 of 791,792,798,801)
O88704	2	(2 of 634,639,640,641,642,643,644,646,647)
O88712	1	(1 of 357,360,364,380)
O88735	1	(1 of 452,453,456,457,463)
O88737	1	(1 of 2671,2672,2677,2679)
O88737	1	(1 of 689,692,694,696,699,700,704,705,706,708,711,723,727,733,735)
O88737	1	(1 of 283,284,289)
O88737	1	(1 of 2649,2651,2656)
O88737	1	(1 of 3175,3181,3182,3187)
O88737	1	(1 of 1921,1927)
O88737	1	(1 of 1932,1934,1936)
O88737	1	(1 of 1586,1588,1590,1593,1594,1596,1598,1600,1601)&(1 of 1593,1594,1596,1598,1600,1601,1604)

O88737	1	(1 of 1623,1626,1644)
O88737	1	(1 of 301,307,308,311,312)
O88737	1	(1 of 3710,3711,3715,3717,3718)
O88737	1	(1 of 1525,1530)
O88737	1	(1 of 3254,3256)
O88737	1	(1 of 3509,3512,3516,3519)
O88737	1	(1 of 2542,2544,2547,2550)
O88737	1	(1 of 3225,3227,3230,3231)
O88737	1	(1 of 2022,2023)
O88737	1	(1 of 990,991,992,996,997,999,1001,1002,1004,1005,1007,1008,1010,1011,1016,1018,1019,1021)
O88737	1	(1 of 1423,1429,1430)&(1 of 1429,1430,1435)
O88737	3	(3 of 1711,1712,1727,1729,1733,1735,1736,1738,1740,1743,1744)
O88737	1	(1 of 3787,3810)
O88737	1	(1 of 2858,2860,2866,2868,2872)
O88737	1	(1 of 1159,1161,1170,1173,1175,1177,1179,1181,1182,1183,1184,1186,1187)
O88737	1	(1 of 2905,2908,2924,2930)
O88737	1	(1 of 742,743,747,756,760,765,766,767,768)
O88737	1	(1 of 3825,3830)
O88737	1	(1 of 2165,2180)
O88737	1	(1 of 912,913,920,928,930,931)
O88737	1	(1 of 3573,3578,3580,3590)
O88737	1	(1 of 3768,3772,3773)
O88737	1	(1 of 3739,3742)
O88737	1	(1 of 326,328,329,332,340,345)
O88737	1	(1 of 2046,2048)
O88737	1	1537
O88737	1	2058
O88737	1	1554
O88737	1	2067
O88737	1	2068
O88737	1	2070
O88737	1	2074
O88737	1	1563
O88737	1	1566
O88737	1	2091
O88737	1	1582
O88737	1	2096
O88737	1	2098
O88737	1	2099
O88737	1	2112
O88737	1	1606
O88737	1	2122
O88737	1	3158

O88737	1	2141
O88737	1	2658
O88737	1	2659
O88737	1	2660
O88737	1	2661
O88737	1	2662
O88737	1	1131
O88737	1	3179
O88737	1	2158
O88737	1	1649
O88737	1	1650
O88737	1	3190
O88737	1	1655
O88737	1	1654
O88737	1	2682
O88737	1	3195
O88737	1	2685
O88737	1	3197
O88737	1	640
O88737	1	2177
O88737	1	1666
O88737	1	2694
O88737	1	2188
O88737	1	2189
O88737	1	2700
O88737	1	2703
O88737	1	3216
O88737	1	1683
O88737	1	3222
O88737	1	1690
O88737	1	2714
O88737	1	1691
O88737	1	1707
O88737	1	3250
O88737	1	1233
O88737	1	2787
O88737	1	1258
O88737	1	1259
O88737	1	3818
O88737	1	3822
O88737	1	2295
O88737	1	1274
O88737	1	1788

O88737	1	3841
O88737	1	2818
O88737	1	2819
O88737	1	3842
O88737	1	2316
O88737	1	2317
O88737	1	2318
O88737	1	2841
O88737	1	1824
O88737	1	292
O88737	1	1828
O88737	1	3878
O88737	1	1324
O88737	1	1326
O88737	1	2352
O88737	1	2354
O88737	1	1337
O88737	1	3902
O88737	1	3401
O88737	1	1354
O88737	1	3403
O88737	1	3928
O88737	1	3932
O88737	1	1373
O88737	1	1374
O88737	1	1375
O88737	1	1378
O88737	1	1384
O88737	1	1386
O88737	1	1391
O88737	1	1394
O88737	1	1395
O88737	1	1916
O88737	1	1917
O88737	1	2941
O88737	1	1919
O88737	1	1407
O88737	1	2945
O88737	1	1404
O88737	1	387
O88737	1	1417
O88737	1	1418
O88737	1	1420

O88737	1	1942
O88737	1	1943
O88737	1	1437
O88737	1	1445
O88737	1	1962
O88737	1	1460
O88737	1	2488
O88737	1	1464
O88737	1	2493
O88737	1	1472
O88737	1	1987
O88737	1	1988
O88737	1	2501
O88737	1	1990
O88737	1	1488
O88737	1	2514
O88737	1	2524
O88737	1	2017
O88737	1	1506
O88737	1	1510
O88737	1	1511
O88737	1	3047
O88737	1	2027
O88737	1	1517
O88737	1	2541
O88737	1	2029
O88845	1	(1 of 194,197,198,200)
O88878	1	(1 of 117,120,125,128,130,132,135,136,137,139)
O88935	1	(1 of 436,437,438,443)
O88935	1	(1 of 448,449)
O88935	1	(1 of 9,11,23,36,39,43,46,48,50)
O88935	1	518
O88935	1	71
O88935	1	70
O88935	1	262
O88935	1	618
O88935	1	650
O88935	1	523
O88935	1	332
O88935	1	526
O88935	1	664
O88935	1	432
O88935	1	434

O88935	1	87
O88935	1	55
O88935	1	568
O88935	1	94
O88935	1	575
P04627	1	10
P05064	1	354
P06537	1	(1 of 268,271,274,275,277,278)
P06537	1	43
P06837	1	(1 of 86,88,89,95,96)
P06837	1	166
P08046	1	117
P08113	1	64
P08113	1	219
P08414	1	(1 of 5,8,11,12,15,16,18,20,21,33)
P08551	1	(1 of 402,404,405)
P08551	1	38
P08551	1	41
P08551	1	48
P08551	1	27
P08551	1	414
P08553	1	845
P08553	1	430
P08553	1	47
P08553	1	49
P08553	1	50
P08553	1	28
P09055	1	(1 of 586,588,593,596,602)
P0C090	1	(1 of 789,792,793,794,799,801,803,806,810)
P0C090	1	(1 of 492,493,497,499,501,502,504)
P0C090	2	(2 of 552,555,560,561,565,569,573)
P0C090	1	907
P0C090	1	592
P0C090	1	754
P0C090	1	471
P0C090	1	472
P0C090	1	895
P0C7T6	1	(1 of 201,202,203,205,206,215,217)
P0C7T6	2	(1 of 29,30,31,33,34,37,39,40,43,46)&(2 of 29,30,31,33)
P0C7T6	1	22
P0C7T6	1	23
P0CG14	1	(1 of 291,293,295,297,300,305,309,311)
P10605	1	194

P11531	1	(1 of 2425,2426,2427,2430,2432,2434,2436,2439,2441,2444)
P11881	1	2500
P12960	1	(1 of 468,475)
P14231	1	120
P14602	1	(1 of 63,71,78)
P14869	1	(1 of 273,285,286)
P14873	1	(1 of 1702,1706,1708,1714,1718,1720,1725,1727,1728,1729,1730,1733,1735,1739,1745,1747)
P14873	1	1778
P14873	1	794
P14873	1	2028
P16951	1	(1 of 287,289,292,296,302,303,304,305,307,310,314,315,318,321,322)
P16951	1	272
P17426	1	(1 of 635,636,637,647,649,650,652,653,655,657)
P19246	1	54
P20029	1	(1 of 638,644,649,650)
P20357	1	(1 of 496,500,506,511,512)
P20357	1	(1 of 1057,1064)
P20357	1	(1 of 1176,1186,1191,1192)
P20357	1	(1 of 1289,1292,1299,1303,1304,1305,1310,1312,1314)
P20357	1	777
P20357	1	1034
P20357	1	361
P20357	1	239
P20357	1	787
P20357	1	472
P25444	1	(1 of 281,285,292,293)
P27612	1	(1 of 481,482,485,487,490,495)
P27671	1	807
P28652	1	(1 of 331,333,334)
P28652	1	(1 of 306,307,311)
P28652	1	320
P28652	1	328
P28652	1	325
P28652	1	327
P29341	1	531
P31361	1	(1 of 3,6,14,17,20,24,54,58,59)
P32211	1	(1 of 310,313,314,315,319,320,327)
P35436	1	(1 of 974,976,987,991,995,1001,1002,1004)
P40124	1	242
P41969	1	278
P42128	1	(1 of 515,516,517,520,528,531,532,534,535,538,541)
P42128	1	663
P42128	1	671

P42227	1	717
P43300	1	(1 of 370,372,373,376,378,385)
P43300	1	384
P43352	1	(1 of 309,310,313,316)
P45481	1	(1 of 316,317,319,320,325,329,330,336,341,344)
P45481	1	2360
P45481	1	147
P46660	1	(1 of 46,50,51)
P46660	1	72
P46660	1	440
P46660	1	55
P46935	1	(1 of 370,371,375,376,377,380,381)
P47708	1	346
P47941	1	(1 of 195,197,212,213,214,218,221,222,232,233)
P48318	1	(1 of 3,4,5,7,10,11,12,20,21,26,27,30,39)
P48432	1	(1 of 252,253,259)
P48432	1	248
P48432	1	258
P48678	1	644
P49442	1	394
P50516	1	257
P50516	1	260
P51141	1	(1 of 389,390,391,392,393,395,396,397,410)
P51141	1	383
P52963	1	(1 of 620,629)
P53783	1	332
P54728	3	(3 of 235,247,248,250,253,262,263,264,266,267,268,269,270,271)
P54728	2	(2 of 81,82,87,88,91,92,93,95,97,100,101,102,114,120,121,122,125,126,130,131,132,134,135,143,155,159,160,166, 167,171,172)
P55194	1	(1 of 491,492,496,503,509,510,514)
P55194	1	519
P56546	1	414
P56671	1	(1 of 141,155,162,168,169,170,178)
P58389	1	322
P58871	1	260
P58929	1	404
P59111	1	(1 of 1089,1090,1091)
P59114	1	(1 of 135,137,138,140,143,144,146,150,152)
P59326	1	(1 of 284,289,291,319)
P59326	1	196
P59326	1	198
P59764	2	(2 of 1651,1652,1653,1654,1656,1657,1660,1664,1667,1670,1672,1673,1682,1684,1685,1686,1687,1689,1690,1691 ,1693,1695,1699,1700,1701,1704,1705)

P59764	1	1806
P59823	1	(1 of 567,575,585,587,590,595,596,597,601)
P60469	1	(1 of 1188,1191,1193)
P60469	1	639
P60469	1	519
P60879	1	115
P60904	1	(1 of 167,169,177,179,181,182,185,188,191,194)
P62484	1	297
P62500	1	444
P62908	1	242
P63248	1	(1 of 59,60,61,64,74,76)
P63248	1	29
P63250	1	(1 of 16,17,18,19,20,22)
P70121	2	(2 of 217,224,226,227,228,232,234,235,236,237,238)
P70232	1	(1 of 823,824)
P70257	1	(1 of 452,453,454,455,463,466,468,471,472,475,476)
P70257	1	272
P70257	1	470
P70326	1	352
P70326	1	345
P70326	1	348
P70365	1	(1 of 642,644)
P70365	1	401
P70365	1	643
P70392	1	(1 of 760,762,763,764,765,766,767,769,770,771,772,774,778,783,788)
P70670	1	240
P81122	1	(1 of 924,933,936,937,938,939,942,944,945,948,949,952,954,957,958,959,961)
P81122	1	(1 of 1137,1138,1140,1142,1143,1144,1145,1146,1148,1151,1153,1158)
P83510	1	(1 of 914,915,917,922,930,931,932)
P83510	1	577
P83510	1	539
P83741	2	(2 of 1806,1808,1817,1818,1820,1821,1822,1823,1825)
P83741	3	(3 of 1655,1658,1661,1662,1663,1665,1669,1671,1674,1680,1681,1683,1687,1688,1689,1694)
P83741	1	(1 of 2281,2291,2292,2297,2298,2301,2304,2306,2307,2312)
P83741	1	(1 of 2365,2367,2372,2377)
P83741	1	(1 of 1270,1271,1274,1280,1281,1282,1290,1292,1294,1295,1297,1303)
P83741	1	(1 of 1229,1230,1239,1240,1241,1243,1248)
P83741	1	1860
P83741	1	2376
P83741	1	1801
P83741	1	1803
P83741	1	1841
P83741	1	1843

P83741	1	1844
P83741	1	1845
P83741	1	1945
P97300	1	230
P97379	1	235
P97379	1	245
P97460	1	(1 of 447,458,462,465,469,470,472,476)
P97765	1	(1 of 229,244,245)
P97772	1	(1 of 1159,1162,1164,1165,1168,1169,1172,1174,1178,1183,1186)
P97789	1	(1 of 1660,1664,1668,1669,1670,1671,1672,1679,1680,1684,1686,1692)
P97855	1	(1 of 260,266,268)
P99027	1	(1 of 64,74,79,86)
Q00422	1	(1 of 254,264,275,280,282,283)
Q01705	1	900
Q02248	1	(1 of 102,111,112,120)
Q02248	1	23
Q02614	1	233
Q03717	1	576
Q05186	1	49
Q05512	1	(1 of 408,409,418,419,421,423)
Q05512	1	(1 of 502,504,508)
Q08274	1	(1 of 453,457,461,465,467,468)
Q08874	1	(1 of 93,95,101,104,105,108,110)
Q08890	1	284
Q09XV5	1	(1 of 168,169,171,173,184,185,186,194)
Q09XV5	1	2524
Q0KL02	1	(1 of 2355,2356,2359,2360)
Q0P5V2	1	(1 of 352,356,358,360,365,371)
Q0VGT3	1	(1 of 251,252,254,255,256,257,258,260,262,265,266,278,281,282)
Q0VGT3	1	(1 of 417,421,422,423,425,426,427,433,436)
Q0VGT3	1	(1 of 349,350,351)
Q0VGT3	1	(1 of 687,691,692,697,699,707,708,709)
Q0VGT3	1	301
Q0VGY8	1	(1 of 1673,1674,1675,1676,1677,1678,1680,1681,1682,1683,1684,1686)
Q0VGY8	1	(1 of 1554,1555,1561)
Q0VGY8	1	(1 of 288,299,300,302)
Q148V7	1	169
Q148V7	1	468
Q148V7	1	469
Q149F3	1	(1 of 69,71,78,83,90,92,93,97)
Q14AX6	2	(2 of 588,589,590,592,593,595,597,604)
Q14AX6	1	1359
Q14BB9	1	(1 of 151,152,154,155,160,164)

Q14BB9	1	(1 of 107,123,124,125)
Q14BI1	1	319
Q14CH0	1	616
Q1HKZ5	1	566
Q1HKZ5	1	559
Q2M3X8	1	337
Q2NL51	2	(2 of 448,454,457,458,459,463,464,468,472,479,482,483,485,488,489,490)
Q2PFD7	1	245
Q2WF71	1	(1 of 669,676,677,681)
Q3TBU7	1	193
Q3TN34	1	(1 of 428,431,437,444,445)
Q3TN34	1	456
Q3TN34	1	489
Q3TN34	1	522
Q3TN85	1	(1 of 123,125,128,129,130,131,132,133,136,138,140,143,144,146,147)
Q3TN85	1	(1 of 92,94,100,101,109,112,117,118)
Q3U0V1	1	96
Q3U0V1	1	192
Q3U1N2	2	(2 of 117,138,142,144,146,147,151)
Q3U3C9	1	213
Q3U3E2	1	205
Q3UCQ1	1	(1 of 539,540,543,547,549)
Q3UDC3	1	(1 of 415,416)
Q3UH45	1	401
Q3UH60	1	222
Q3UH68	1	(1 of 950,951,952,953)
Q3UH68	1	(1 of 510,511,515,518,521,523,525)
Q3UH68	1	(1 of 500,502,505,506)
Q3UHC0	3	(3 of 754,755,756,757,761,763,764,766,767,768,769,770,771)
Q3UHC0	1	(1 of 1443,1444,1446,1447,1451,1453,1456,1458)
Q3UHC0	1	(1 of 1602,1603,1604,1607,1608,1609,1612)
Q3UHC1	1	(1 of 651,656,662,664,666,668)
Q3UHD9	1	(1 of 79,80,81,82,85,94,99)
Q3UHD9	1	(1 of 270,274,281,284,288,297,298,300,302,303,304,314)
Q3UHF7	1	(1 of 1308,1320)
Q3UHF7	1	(1 of 1163,1164,1167,1168)
Q3UHF7	1	(1 of 1501,1502,1503,1505,1506,1508,1510,1511,1512,1517,1519)
Q3UHF7	1	(1 of 1293,1294,1296,1298)
Q3UHF7	1	(1 of 2013,2014)
Q3UHF7	1	(1 of 2141,2148)
Q3UHF7	1	(1 of 2366,2367)
Q3UHF7	1	416
Q3UHF7	1	1056

Q3UHF7	1	420
Q3UHF7	1	548
Q3UHF7	1	1316
Q3UHF7	1	392
Q3UHF7	1	339
Q3UHF7	1	916
Q3UHF7	1	2005
Q3UHF7	1	2004
Q3UHF7	1	1271
Q3UHF7	1	251
Q3UHG7	1	20
Q3UHJ0	1	(1 of 729,732,740,746,747,749,751,754)
Q3UHJ0	1	(1 of 679,680,685,688,691,692,702)
Q3UHJ0	1	(1 of 441,445,448,450,455,460)
Q3UHJ0	1	416
Q3UHJ0	1	578
Q3UHJ0	1	360
Q3UHJ0	1	648
Q3UHJ0	1	572
Q3UHJ0	1	638
Q3UHK8	1	(1 of 1614,1621,1623,1626,1627,1628)
Q3UHK8	1	(1 of 1592,1594,1595,1596,1597,1600,1601,1604,1605,1606,1609,1610)
Q3UHK8	1	1622
Q3UHL1	1	(1 of 446,449,452,453)
Q3UHL1	1	(1 of 470,480,481,487,493,494)
Q3UHL1	1	457
Q3UHL1	1	459
Q3UHT7	1	(1 of 43,45,51,58,59,65,72,73,74)
Q3UHT7	1	381
Q3UHT7	1	7
Q3UNH4	1	(1 of 315,316,321,323)
Q3UNH4	1	(1 of 780,786)
Q3UNH4	1	(1 of 263,267,268,270,275,276,284,295,297,299,300)
Q3UNH4	1	607
Q3UNH4	1	343
Q3UPH1	1	(1 of 162,170,174,176,177)
Q3UPH1	1	189
Q3UPH1	1	157
Q3UQN2	1	(1 of 487,491,492,494,495,499)
Q3URQ4	1	(1 of 10,18,27,31,33,34,35,39)
Q3UVX5	1	(1 of 1065,1069,1073,1077,1078,1087,1091,1092)
Q3UVX5	1	(1 of 1046,1047,1048,1049,1052)
Q3UVX5	1	1058

Q3UZB0	1	106
Q3UZG4	1	100
Q3ZB59	1	326
Q499E5	1	907
Q4ACU6	2	(2 of 1364,1365,1366,1372,1373,1374,1375,1377,1378,1380,1381,1383,1384,1386,1387,1389,1393,1395,1397,1398,1404)
Q4ACU6	1	(1 of 1320,1321,1331,1332,1335,1338,1342,1343,1351,1355,1362)
Q4ACU6	1	(1 of 818,831,836,838)
Q4FE56	1	2551
Q4JIM5	1	(1 of 614,615,618,619,621)
Q4JIM5	1	(1 of 860,872,874,876)
Q4VAA2	1	(1 of 167,178,180,182,189)
Q501J7	1	(1 of 192,193,194,195,197,198,199,201,202,205,206,209,212)
Q501J7	1	190
Q501J7	1	231
Q52KI8	1	885
Q571G4	1	(1 of 106,109,111)
Q571G4	1	261
Q571G4	1	238
Q571K4	1	408
Q59J78	1	(1 of 143,147,148,149)
Q5DTX6	1	(1 of 59,60,63,67,69)
Q5F2E7	1	(1 of 369,373,374,376,378,379,381,382,383,384,385,386,389,391,393,394,395)
Q5F2E7	1	(1 of 407,409,410,412,414,422,425,429,436,437,441,443,446,447,449,451,457,460)
Q5F2E7	1	380
Q5FWH2	1	459
Q5HZI2	1	(1 of 55,58,69,70,71,77)
Q5QNQ6	1	140
Q5RJH6	1	(1 of 948,949)
Q5SFM8	1	(1 of 465,466,471,472,474,475,477,483,495,497,498,499)
Q5SFM8	1	546
Q5SPL2	1	472
Q5SPX8	1	(1 of 479,483,486,489,501)
Q5SQX6	1	1251
Q5SQX6	1	1252
Q5SRX1	1	(1 of 188,191,193,194,199,201,202,209,211,215,218)
Q5SRX1	1	177
Q5SRX1	1	187
Q5SSM3	1	(1 of 661,663,671,674,676,678,681,682,684,689,695,698,702,705,711,713,716,717,718)
Q5SUE8	1	199
Q5SUH7	1	(1 of 265,268,270,271,272,273)
Q5SUH7	1	622
Q5SVL6	1	516

Q5SWZ5	1	(1 of 178,179,180,181,184,185,187,188,189,190,193,199,200)
Q5SX19	1	(1 of 178,181)
Q5SXC4	1	(1 of 108,110,111,123,124)
Q5SXC4	1	117
Q5SXC4	1	118
Q5XJV5	1	(1 of 1714,1715,1719,1724,1725,1726,1733)
Q5XJV5	1	(1 of 1777,1780,1782,1783,1787,1788,1792,1795,1796,1799,1803,1805,1808,1809)
Q5XJV5	1	1646
Q5XJV5	1	1551
Q60598	1	345
Q60737	1	(1 of 344,347,348,353,356,357,360,362,370)
Q60737	1	378
Q60829	1	42
Q60865	1	(1 of 418,428,434,435,436,437,441,443,450,453)
Q60865	1	(1 of 468,470,473,476,477,479,480,481,486,495,496)
Q60902	1	(1 of 850,851,852,853,859,860)
Q60987	1	(1 of 432,433,434,435,436,441,442,447)
Q61001	1	(1 of 960,961,963,966,969,977,978,984)
Q61001	1	(1 of 2862,2867,2887,2890)
Q61001	1	(1 of 2396,2397)
Q61001	1	(1 of 2422,2427)
Q61097	2	(2 of 429,430,431,434,435,436,437,438,439,440,442,443,449,450,451,454,455,457,458,463)
Q61140	1	(1 of 81,88,101,104,109,115,123,125)
Q61191	2	(2 of 427,441,446,453,457,458,459,460,466,470,471,473,476)
Q61191	2	(2 of 726,727,733,734,737,738,739)
Q61191	1	(1 of 1055,1058,1061,1062)
Q61191	1	(1 of 666,669,674,678)
Q61191	2	(1 of 612,619,620,622,623,627,628,629,634)&(2 of 612,619,620,622,623,627,628,629)
Q61191	1	(1 of 586,587)
Q61191	1	(1 of 1494,1495,1497,1499,1500,1506,1516)
Q61191	1	771
Q61191	1	515
Q61191	1	518
Q61191	1	775
Q61191	1	779
Q61191	1	651
Q61191	1	652
Q61191	1	787
Q61191	1	405
Q61191	1	800
Q61191	1	806
Q61191	1	808
Q61191	1	563

Q61191	1	694
Q61191	1	831
Q61191	1	703
Q61191	1	579
Q61191	1	1224
Q61191	1	588
Q61191	1	1238
Q61191	1	1241
Q61191	1	603
Q61191	1	861
Q61191	1	1246
Q61191	1	480
Q61191	1	490
Q61191	1	495
Q61191	1	1139
Q61191	1	1148
Q61191	1	638
Q61315	1	(1 of 859,864,865,870,871,872)
Q61315	1	(1 of 2708,2711,2713,2717,2722)
Q61315	1	923
Q61548	1	(1 of 600,605,606,608,613,621,625,627)
Q61548	1	(1 of 305,306,312,313)
Q61548	1	(1 of 321,324,325,333,335,341,342)
Q61548	1	624
Q61548	1	309
Q61548	1	310
Q61548	1	303
Q61644	1	(1 of 334,335,336)
Q61644	1	329
Q61818	1	(1 of 1714,1716,1717,1718,1723,1724,1726,1728,1729,1731)
Q61827	1	134
Q62073	1	421
Q62073	1	383
Q62261	1	(1 of 2327,2330,2331,2334,2336,2337,2339,2340)
Q62261	1	2323
Q62277	1	(1 of 268,284,308,309,311)
Q62311	1	(1 of 480,481,483,485)
Q62311	1	(1 of 586,587,589,590,594,595,600,602)
Q62417	1	(1 of 105,109,111,118,125,126,127,131,133,139,140,143,144,148,149,150,155)
Q62417	1	1200
Q62417	1	1199
Q62418	1	(1 of 279,280)
Q62418	1	282

Q62418	1	314
Q62418	1	278
Q62419	1	284
Q62440	1	(1 of 282,284,287,288,290,291,293,294,295,296)
Q62441	1	(1 of 292,295,298,299,300,301,302,304,305)
Q62441	1	330
Q62448	1	505
Q62504	1	(1 of 2879,2883,2893,2895,2896,2899,2903)
Q62504	1	(1 of 3114,3119,3120,3127)
Q62504	1	2520
Q62523	1	(1 of 294,295,297,298,300,305,307)
Q62523	1	170
Q62523	1	237
Q63943	1	(1 of 133,134,145,149,152,153,157,160,161,162,165,167,170,171,172,174)
Q64092	1	(1 of 545,550,551,553,557)
Q640Q5	1	(1 of 231,235,237)
Q640R3	1	(1 of 333,334,335,343,345)
Q64213	1	(1 of 331,332,333,337,338)
Q64213	1	328
Q64213	1	315
Q64213	1	38
Q64213	1	31
Q64332	1	(1 of 422,426,432,433,438,440,446,447)
Q64332	1	(1 of 480,483,486,487,488,489,490,491,492,493,494,495,496,497,498,499,508,509,510,515,516,517,518,520)
Q64332	1	98
Q64332	1	44
Q64332	1	77
Q64332	1	50
Q64332	1	24
Q64332	1	95
Q64336	1	647
Q64700	1	(1 of 656,658,659,661,662)
Q68ED7	2	(2 of 411,413,416,417,421,423,429,436,437)
Q68FE6	2	(2 of 618,620,622,623,625,629,630,632,634,636,637,639,641,643,644,646,647,650,651,652)&(1 of 613,615,616,618,620,622,623,625,629,630,632,634,636,637,639,641,643,644,646,647,650,651,652,653,655)
Q68FE6	1	(1 of 661,662,664,665,673,674,675,676,679,680,681,683,685,687,688,694,695,696,697,700,701,705,711,715,719)
Q68FF6	1	570
Q68FG2	1	2354
Q68FG2	1	2101
Q68FG2	1	2134
Q68FG2	1	2359
Q68FH0	1	(1 of 238,239,242,246,248,250,252,258,261,262,263,264)
Q68FH0	1	(1 of 75,77,80,81,82,83,84)

Q68FH0	1	(1 of 197,202)
Q68FH0	1	225
Q68FH0	1	226
Q68FH0	1	1087
Q69ZA1	2	(2 of 1278,1285,1286,1287,1288,1289,1291)
Q69ZI1	1	512
Q69ZI1	1	524
Q69ZI1	1	527
Q69ZR2	1	(1 of 1481,1482,1485,1490,1492,1493,1497,1498,1500,1503)
Q69ZR2	1	1359
Q69ZS8	1	(1 of 41,49,55,56,58,63,67,71)
Q69ZW3	1	764
Q69ZX8	1	(1 of 418,419)
Q69ZX8	1	(1 of 276,277,279,280,282,286,287,290)
Q69ZX8	1	423
Q69ZX8	1	580
Q69ZX8	1	534
Q69ZX8	1	383
Q6A037	1	(1 of 560,571,573)
Q6A058	1	328
Q6A058	1	93
Q6A058	1	366
Q6A070	1	(1 of 1120,1123,1124,1126,1131,1132,1135,1138,1144,1149)
Q6A070	1	(1 of 1354,1356)
Q6A0A2	1	632
Q6A0A2	1	51
Q6AXB7	1	(1 of 325,336,337,340,343)
Q6DFV5	1	1668
Q6DID3	1	(1 of 734,739,741,745,749,750,761)
Q6KCD5	1	(1 of 1433,1437)
Q6KCD5	1	160
Q6NS60	1	387
Q6NSW3	1	(1 of 1244,1256,1263)
Q6NSW3	1	405
Q6NXI6	1	(1 of 432,438,441,442,452,453,457,459,461)
Q6NXI6	1	(1 of 992,995,996,998,999,1009,1010)
Q6NXI6	1	(1 of 547,549,551,559,560,564,566,573,576,577,579,580,581,583,586,587,588,590)
Q6NXI6	1	616
Q6NXI6	1	417
Q6NXI6	1	418
Q6NXJ0	1	531
Q6NZN0	1	696
Q6P9N8	1	(1 of 680,683,686,688,689,693,698,699,701,702,703,704,706,710,714)

Q6P9N8	1	895
Q6P9N8	1	902
Q6P9N8	1	798
Q6P9Q6	1	(1 of 306,310,315,317,319,325)
Q6PAJ1	1	150
Q6PAL7	1	(1 of 1574,1588,1590,1592,1593)
Q6PAL7	1	(1 of 1070,1071,1073,1076,1079,1080,1081,1082,1083,1084,1088)
Q6PB44	1	(1 of 818,827,828)
Q6PB44	1	(1 of 836,837,844,845,861,868,875)
Q6PB44	1	1552
Q6PB44	1	881
Q6PB75	1	420
Q6PCX9	1	695
Q6PD26	1	372
Q6PD28	1	(1 of 9,10,12,13,15,16,20)
Q6PD31	1	(1 of 444,445,449,452)
Q6PD31	1	(1 of 827,828,830,832,835,837)
Q6PDK2	2	(2 of 2738,2740,2741)
Q6PDK2	1	2359
Q6PDX6	1	53
Q6PFD5	1	(1 of 750,753,757,766)
Q6PFD5	1	(1 of 553,555,558,559,560,562,566,568)
Q6PFD5	1	579
Q6PFD5	1	587
Q6PFD5	1	578
Q6PFD9	1	(1 of 223,224,230,231,234,235,236,238,242,243,244,245,246,248,251)
Q6PIJ4	1	(1 of 1138,1143,1146,1147,1148,1151,1154,1158)
Q6PIJ4	1	(1 of 1025,1027,1030,1031,1036,1037)
Q6PIJ4	1	1064
Q6PIJ4	1	838
Q6PIJ4	1	1172
Q6PIJ4	1	1270
Q6QI06	1	(1 of 1216,1218,1221,1223,1224,1225,1226,1229,1230,1232,1233,1234,1236)
Q6ZPG2	1	328
Q6ZPJ0	1	174
Q6ZPJ0	1	175
Q6ZQ08	1	(1 of 1043,1044,1045,1046)
Q6ZQ08	1	1040
Q6ZQ08	1	1041
Q6ZQ08	1	1050
Q6ZQ08	1	1037
Q6ZQ29	1	(1 of 430,443,455,456,457,458,459,460)
Q6ZQH8	1	1528

Q6ZQH8	1	1524
Q7M739	1	1672
Q7TMY8	1	(1 of 2910,2917,2918,2922,2923,2925,2926,2927,2928)
Q7TMY8	1	(1 of 3246,3247,3248)
Q7TMY8	1	(1 of 2619,2632,2633,2635,2636,2640,2642,2643,2646,2649)
Q7TMY8	1	(1 of 3794,3795,3797,3798,3801,3803,3804)
Q7TN29	1	197
Q7TNC6	1	1013
Q7TPB0	1	(1 of 560,562,563,564,565,567,568,570,571)
Q7TPB0	1	379
Q7TPS5	1	(1 of 249,250,259,260,262)
Q7TQ95	1	(1 of 411,418,421,424)
Q7TQD2	1	(1 of 15,19)
Q7TQD2	1	154
Q7TQD2	1	158
Q7TQH0	1	(1 of 681,682,683,684,686,687)
Q7TQH0	1	(1 of 419,421,422,424,428,432,436,437)
Q7TQH0	1	(1 of 266,267,270,271,273,274,276)
Q7TQH0	2	(2 of 456,463,465,473,477,478,480,484,485,486,494,496,499)
Q7TQH0; A0A0U1RPL0	1	(1 of 463,465,473,477,478,480,484,485,486)
Q7TQH0; A0A0U1RPL0	1	(1 of 681,682)
Q7TQH0; A0A0U1RPL0	1	683
Q7TQH0; A0A0U1RPL0	1	686
Q7TSI3	1	(1 of 691,692,694,695,698,700,701,707,709,711,714,721,726)
Q7TSJ2	1	(1 of 79,86)
Q7TSJ2	1	(1 of 34,37,58)
Q7TSJ2	1	(1 of 774,776,778,779)
Q7TSJ2	1	705
Q7TSJ2	1	386
Q7TSJ2	1	294
Q7TSJ2	1	425
Q7TSJ2	1	110
Q7TSJ2	1	340
Q7TSJ2	1	182
Q7TSJ2	1	246
Q7TT18	1	(1 of 1022,1025,1026,1027,1028,1030,1031,1032,1036)
Q7TT18	2	(2 of 740,746,749,753,755,756,758,761,762,763,767,768)
Q7TT50	1	(1 of 984,986,988,991,992,993)
Q80TE4	1	1533
Q80TE4	1	1079
Q80TE7	1	(1 of 1357,1363,1371,1372,1375)

Q80TE7	1	(1 of 864,865,867,868,869)
Q80TI1	1	(1 of 1146,1153,1156)
Q80TR1	1	(1 of 1439,1448,1464,1465)
Q80TZ3	1	(1 of 605,623,627,628,629,631,632,639)
Q80TZ3	1	593
Q80TZ3	1	588
Q80TZ3	1	733
Q80TZ3	1	591
Q80TZ9	1	(1 of 1223,1229,1230,1242)
Q80U23	1	24
Q80U40	1	681
Q80U40	1	682
Q80U40	1	683
Q80U56	1	620
Q80U72	1	(1 of 936,939,943,948,949,951,955,959,961,962)
Q80U78	1	(1 of 798,800,801,803,804,807,809,810,811,814,815,816)
Q80U78	1	212
Q80U93	1	(1 of 1566,1567,1569,1573,1574,1580,1586)
Q80U93	1	(1 of 612,614,618,621,626,627,628,629)
Q80U93	1	(1 of 430,431,433,437,439,440,452,454,455,461,465,466,467,472,476,478,481,485,486)
Q80U93	1	(1 of 1257,1263,1272,1279,1282,1285,1286,1289,1290,1291,1293,1296,1300,1303,1304,1305)
Q80U93	1	(1 of 1109,1115,1116,1118,1120,1121)
Q80U93	1	(1 of 1204,1206,1209,1210,1211,1213)
Q80U93	1	(1 of 1505,1506,1518,1520,1521,1524,1526,1527,1529,1536,1537,1540,1543,1544)
Q80U93	1	(1 of 1336,1337,1342,1345,1347)
Q80U93	1	513
Q80U93	1	1314
Q80U93	1	1091
Q80U93	1	1316
Q80U93	1	1576
Q80U93	1	652
Q80U93	1	1557
Q80U93	1	504
Q80U93	1	506
Q80U93	1	507
Q80UE4	1	(1 of 708,716,718,719,721,723,724,725,726,727,728,731)
Q80UE4	1	713
Q80UG5	1	182
Q80UY2	1	(1 of 258,260,261,262,264,265,266,268,271,273,276,279,282,289,294)
Q80VC9	1	(1 of 946,947,952,958,962,963)
Q80VJ2	1	(1 of 66,67,78,79)
Q80VP1	1	(1 of 469,472,485,488,493,497)
Q80VP1	1	(1 of 500,506,511,514,516,526,528)

Q80VP1	1	416
Q80WT5	1	865
Q80X50	1	(1 of 665,667,669,670,671,672,675,679,684,687,688,693,694,695,697,700,702,708,709,710,711,714,715,718,719,723,725,726,727,728,729,730)
Q80X50	1	(1 of 388,400,402,404,405,406,407,408,409,414,415,416,418,420)
Q80X50	1	(1 of 480,481,482,487,490,491,495,496,497)
Q80X50	1	297
Q80X50	1	473
Q80X50	1	879
Q80X50	1	464
Q80X50	1	625
Q80X50	1	466
Q80X50	1	345
Q80X80	1	450
Q80X80	1	420
Q80X80	1	447
Q80XI3	1	(1 of 176,177,179,186,192,198,201,207,208,211,214)
Q80XI3	1	(1 of 314,316,317,319,322,325,327,330)
Q80XI3	1	265
Q80XK6	1	(1 of 239,240,244,245,250)
Q80XP9	1	(1 of 566,567,568,571,578,580,581,582,585,589,590,593,594,595,596)
Q80XP9	1	(1 of 1373,1377,1392,1394,1395,1399,1400,1402,1403,1406)
Q80YA3	1	(1 of 415,416,418,421,424,427,435,437,439,440,441,442,445,447,451,453,458)
Q80YA3	1	360
Q80YA9	1	(1 of 731,732,733,735,736,738,740,741)
Q80YA9	1	328
Q80YA9	1	329
Q80YA9	1	750
Q80YF9	1	(1 of 1039,1042,1045,1048,1051,1054,1055)
Q80YR4	1	(1 of 560,563,564,568,569,575,578,579)
Q80ZX0	1	(1 of 111,118,122,129,131,133,135,136,138,142,143)
Q80ZX0	1	299
Q811P8	1	(1 of 1433,1434,1439,1440,1441,1442,1446,1450,1451,1453,1465)
Q811P8	1	920
Q811P8	1	1027
Q811P8	1	1918
Q8BFU3	1	(1 of 612,613,614,619)
Q8BFU3	1	132
Q8BFW7	1	(1 of 179,181,195,199,210,212,213,215,216,217,218)
Q8BFW7	1	11
Q8BG40	1	461
Q8BG75	1	328
Q8BG75	1	329

Q8BG87	1	(1 of 495,496,497,503,506)
Q8BG95	1	542
Q8BGD5	1	794
Q8BGZ2	1	97
Q8BH48	1	150
Q8BH93	1	(1 of 2,6,15,16,23,25)
Q8BHL3	2	(2 of 66,67,69,70,72,73,75,76,78,79,80,81,86,90)
Q8BHL3	1	120
Q8BHL3	1	162
Q8BHL3	1	43
Q8BHL3	1	44
Q8BHR8	1	(1 of 171,176,177,178,179)
Q8BHR8	1	288
Q8BHR8	1	289
Q8BI84	1	1720
Q8BI84	1	1718
Q8BJ05	1	(1 of 251,252,255)
Q8BJ05	1	(1 of 369,370,373)
Q8BJ05	1	360
Q8BJ42	1	584
Q8BJ42	1	811
Q8BJ42	1	594
Q8BJ42	1	595
Q8BJ42	1	633
Q8BJH1	1	184
Q8BJH1	1	194
Q8BJH1	1	237
Q8BJM5	2	(2 of 141,146,151,154)
Q8BJM5	1	371
Q8BJM5	1	374
Q8BJY1	1	(1 of 486,497,498)
Q8BKP1	1	103
Q8BLK9	1	(1 of 567,576,577,580,581,583,585)
Q8BMB0	1	(1 of 226,228,231,232,234,235,237,238,239)
Q8BMB0	1	(1 of 498,499,500,502,505)
Q8BMB0	1	(1 of 1039,1047,1050,1051,1053)
Q8BMB0	1	192
Q8BMB0	1	200
Q8BMB0	1	521
Q8BMB0	1	1069
Q8BMB0	1	247
Q8BMC3	1	(1 of 17,18)
Q8BNA6	1	4090

Q8BNW9	2	(2 of 395,397,399)
Q8BNW9	1	400
Q8BPN8	1	(1 of 1943,1947,1952,1955,1956,1957,1962,1967)
Q8BPN8	1	1941
Q8BPN8	1	949
Q8BRM2	1	(1 of 80,82,87,90,92,93,94,95)
Q8BRT1	1	(1 of 475,476,477,480,481,483,484)
Q8BRT1	1	352
Q8BSS9	1	(1 of 702,703,705,707,709,711,712,715,716,717,720,723,724)
Q8BSS9	1	552
Q8BSS9	1	547
Q8BSS9	1	1254
Q8BT14	1	(1 of 550,551,555,557,558,560,568,569,572,573)
Q8BT14	1	331
Q8BT14	1	316
Q8BTI8	1	2200
Q8BTI8	1	2205
Q8BTI8	1	2199
Q8BTJ4	1	281
Q8BTJ4	1	261
Q8BU11	1	(1 of 405,406,407,409,413,420)
Q8BU25	1	267
Q8BUV3	1	(1 of 222,226,227,230,231,232,233,236)
Q8BUV3	1	250
Q8BUV3	1	260
Q8BW96	1	352
Q8BWT5	1	(1 of 134,135,136,137,138,139,141,142,143,144,145)
Q8BWW4	1	(1 of 569,578,579,581,583,586,590,592,595,596)
Q8BX02	1	421
Q8BXL9	2	(2 of 162,169,170,175,176,177,178,179,180,181,182,183,186,187,188,189)
Q8BYI9	1	(1 of 580,583,586,587,588,591,592)
Q8BYK6	1	(1 of 362,370,372,383,385,387,388)
Q8BYK6	1	(1 of 207,210,213,214,215,218,219,222,229,230,236,237)
Q8BYK6	1	201
Q8BYK6	1	205
Q8BYK6	1	167
Q8C0C0	1	(1 of 150,155,159,166,168,172,173,180)
Q8C0I4	1	(1 of 751,752,755,757)
Q8C0I4	1	(1 of 150,151)
Q8C0Q2	1	730
Q8C0Q2	1	581
Q8C0T5	1	(1 of 1578,1579)
Q8C0T5	1	(1 of 1430,1432,1433,1438,1440,1441,1442,1443,1444,1445,1446,1447)

Q8C0T5	1	1402
Q8C0T5	1	1135
Q8C0T5	1	1400
Q8C0T5	1	1114
Q8C0T5	1	1403
Q8C0T5	1	1404
Q8C120	1	(1 of 589,593,595,600,601,604,606,609,617,619,621)
Q8C180	1	(1 of 326,327,328,329,330,331,333,339)
Q8C2Q3	1	280
Q8C2Q3	1	244
Q8C2Q3	1	254
Q8C2Q3	1	231
Q8C3W1	1	(1 of 249,252,254,268)
Q8C483	1	(1 of 530,534)
Q8C5L3	2	(2 of 99,101,104,108,111,113,114,118,120,123,126,128)
Q8C5L3	1	155
Q8C729	1	440
Q8C729	1	318
Q8C790	1	298
Q8C8T7	1	591
Q8C9B9	2	(2 of 1273,1274,1279,1280,1281,1282,1284,1287,1288,1292,1293,1294,1296,1299,1302,1303)
Q8CAF4	1	(1 of 732,734,737,740,741,743,744,745,746,747,752,757,759,761,763,764,765)
Q8CAQ8	2	(2 of 182,184,185,190,191,192)
Q8CAQ8	1	180
Q8CAQ8	1	181
Q8CC35	1	(1 of 863,864,869,875,879,882,884,886,887,890,893,895)
Q8CC35	1	448
Q8CC35	1	551
Q8CC35	1	393
Q8CC35	1	397
Q8CC35	1	752
Q8CC35	1	753
Q8CC35	1	506
Q8CC35	1	507
Q8CCN5	1	806
Q8CDG3	1	1072
Q8CDG3	1	1075
Q8CDJ3	1	(1 of 448,454,456,458,459,462,467,468,469,475,476,480,482,483)
Q8CF89	1	393
Q8CF89	1	394
Q8CFI0	1	482
Q8CFN5	1	(1 of 140,146,150,151,154,158,162,163,176)
Q8CFN5	1	(1 of 266,269,271)

Q8CG79	1	339
Q8CGA2	1	146
Q8CGI1	1	(1 of 719,723,730,731,732,735,737,741,744)
Q8CGI1	1	709
Q8CGY8	1	(1 of 3,4,11,12,15)
Q8CGY8	1	393
Q8CGZ0	1	(1 of 378,382,383,397,398)
Q8CGZ0	1	403
Q8CH77	1	(1 of 617,619,621,625,627,628,630,632)
Q8CH77	1	543
Q8CHC4	1	(1 of 963,965,967)
Q8CHC4	1	1288
Q8CHC4	1	1081
Q8CHC4	1	1341
Q8CHH5	1	(1 of 577,582,584)
Q8CHH5	1	(1 of 594,596,597,599,601,604)
Q8CHI8	1	(1 of 2532,2534,2535,2538,2545)
Q8CHI8	1	(1 of 695,698,699,700,701,702,703,704,709,711,716)
Q8CHI8	1	(1 of 2594,2595,2596)
Q8CHI8	1	(1 of 2932,2936,2937,2940)
Q8CHI8	1	2624
Q8CHI8	1	2607
Q8CHP6	1	(1 of 651,653,656,659,671,672)
Q8CHP6	1	238
Q8CHS8	1	(1 of 171,172,178,180,181,182,183,184,185,187)
Q8CHS8	1	174
Q8CHU3	1	(1 of 369,375,380)
Q8CHU3	1	358
Q8CHU3	1	359
Q8CI08	2	(2 of 480,484,486,488,491,492,495,497,498,499,500,509,515,516,520,522,524)
Q8CI51	1	115
Q8CI51	1	110
Q8CIQ7	1	(1 of 1723,1725,1728,1731,1732,1733,1736,1738,1739,1740,1741,1743,1744,1745,1747,1750,1754,1755,1758,1759,1760)
Q8JZP2	1	487
Q8JZS0	1	(1 of 5,7,8,11,16,18,24)
Q8K004	1	402
Q8K021	1	(1 of 2,6,22,24,27)
Q8K021	1	(1 of 312,315,322,323,326,327)
Q8K021	1	67
Q8K021	1	59
Q8K099	1	(1 of 604,605,608)
Q8K0H5	1	(1 of 2,4,6,14,19,28,35,36,37,41)

Q8K0L9	1	(1 of 461,464,465,472,473)
Q8K0L9	1	480
Q8K0L9	1	449
Q8K0L9	1	268
Q8K0L9	1	436
Q8K0L9	1	444
Q8K0T0	1	275
Q8K0T0	1	278
Q8K0U4	1	(1 of 656,661,662,663)
Q8K0U4	1	20
Q8K0V4	1	(1 of 425,426,428,429,434,439,441,442,443,446,447,449,450,456,457,465,466,467)
Q8K1M6	1	(1 of 544,550,558)
Q8K1S4	1	(1 of 465,469,470,472,473,480)
Q8K212	2	(1 of 65,66,67,68,69,70,71,72,73)&(2 of 56,57,58,72,73)&(1 of 67,68,69,70,71,72,73,80)
Q8K212	1	(1 of 758,760,761,768,772,774,777,778,779,782,783,784,787)
Q8K212	1	64
Q8K212	1	59
Q8K310	1	33
Q8K382	1	(1 of 991,993,1002,1003,1004)
Q8K3X4	1	(1 of 265,285,287,289,290,293,294,295,296,297,298)
Q8K3X4	1	(1 of 149,159,162,163,164)
Q8K3Z9	1	(1 of 582,586,587,588,595,600)
Q8K3Z9	1	(1 of 604,606,613,621,622,623,624,626)
Q8K3Z9	3	(3 of 711,713,715,719,720,721,722,725,726,728,729,730,731,735,738,739,740,742)
Q8K3Z9	1	(1 of 649,650,658,660,664,665,667,668,670)
Q8K3Z9	1	661
Q8K3Z9	1	653
Q8K4I3	1	(1 of 558,559,560,561,562,564,565,567,568,570,571,572)
Q8K4Q0	1	(1 of 696,700,704,706)
Q8K558	1	(1 of 244,247,250,253,255,256,261,262,269)
Q8R001	1	(1 of 207,208,211,215,216,218,221,222)
Q8R191	1	(1 of 175,178,182,187,200,205,207,210,214,216,219,220,221)
Q8R1Q8	1	(1 of 412,414,415,419,421,427)
Q8R3B7	1	360
Q8R3E3	1	(1 of 389,390,391,394,395,400)
Q8R3L8	1	(1 of 410,411,412,413,419,420)
Q8R3V5	1	312
Q8R3V5	1	293
Q8R4S0	1	(1 of 47,51,52)
Q8R550	1	580
Q8R5H6	1	(1 of 293,295,298,299,301,310)
Q8VBX6	1	(1 of 342,345,346,347,351,353,354,355,356,357,358,359,360)
Q8VCF0	1	(1 of 373,374,379,383,384)

Q8VCF0	1	330
Q8VCF0	1	307
Q8VCF0	1	222
Q8VD37	1	(1 of 503,504,505,506,508,509,510,512,514,517,518,520,523,524)
Q8VD37	1	423
Q8VD37	1	420
Q8VD37	1	255
Q8VD65	1	(1 of 878,879)
Q8VD65	1	909
Q8VDQ8	1	366
Q8VDZ4	1	386
Q8VE52	1	(1 of 438,457,461,462,463)
Q8VHG2	1	755
Q8VHG2	1	196
Q8VHR5	1	(1 of 288,289,290)
Q8VHR5	1	585
Q8VHR5	1	298
Q8VHR5	1	495
Q8VHW2	1	(1 of 374,377)
Q8VHW2	1	379
Q8VI33	1	(1 of 202,206,207,208,217,221)
Q91VX2	1	(1 of 386,392,393,399,401,405,406,414,419,422)
Q91VX2	1	1020
Q91VX2	1	469
Q91W39	1	(1 of 401,404,405,410,416,418,420,426,427)
Q91W39	1	521
Q91W39	1	524
Q91WJ0	1	445
Q91WJ0	1	439
Q91X45	1	(1 of 216,218,221,223,224,225,226,228,235,236,242,247,255)
Q91X51	1	(1 of 216,220,223,224,225,228,244,245,251)
Q91X58	1	(1 of 157,158,159,160,163,165)
Q91X58	1	150
Q91X58	1	167
Q91XV3	1	(1 of 160,169)
Q91XV3	1	192
Q91XV3	1	217
Q91XV3	1	187
Q91XV3	1	173
Q91YD9	1	293
Q91YE8	1	(1 of 783,784,785,794,797,798)
Q91YS8	1	(1 of 360,369,370)
Q91Z31	1	(1 of 154,158,161,164,166,167,169,171,174,178)

Q91Z67	1	990
Q91Z69	1	981
Q91ZZ3	1	58
Q91ZZ3	1	53
Q91ZZ3	1	71
Q922J3	1	(1 of 144,146,149,154,157,158,159,162,164,171,173,174)
Q922J3	1	150
Q922Y1	1	192
Q924A2	1	(1 of 1851,1852,1855,1866)
Q924A2	1	(1 of 1465,1468,1472,1473,1489,1491)
Q924A2	2	(2 of 1872,1877,1878,1880,1887,1890,1895,1896)
Q924A2	1	(1 of 1029,1033,1034)
Q924A2	1	1907
Q924A2	1	2044
Q924S8	1	(1 of 162,165,166)
Q925J9	1	(1 of 1261,1265,1267,1269,1271,1272,1273,1274,1276,1277,1278,1280,1281,1283,1284,1285,1291,1292)
Q99JX3	1	(1 of 410,411,413,417,418,421)
Q99JX3	1	(1 of 366,371,379,380,383,389,390,398,403,404)
Q99JX3	1	426
Q99K90	1	456
Q99KP6	1	(1 of 133,148,149,152,169)
Q99LD8	1	261
Q99LD8	1	167
Q99LI5	1	(1 of 861,862,864,867,870,874,877,881,882)
Q99LI8	1	300
Q99LI8	1	295
Q99P69	1	24
Q99P72	1	(1 of 686,687,690,694,697)
Q99P72	1	(1 of 7,8,11,12,13,16)
Q99P72	1	(1 of 200,202,203,210,215,218,221,223,226,227,229)
Q99P72	1	(1 of 165,167,171,179,185,186)
Q99P72	1	113
Q99P72	1	509
Q99P72	1	510
Q9CPR8	1	279
Q9CQ25	1	(1 of 89,94,98,100,101,102,103,104,106)
Q9CQU0	1	134
Q9CQV4	1	(1 of 435,436,440,453,462,463)
Q9CR95	2	(2 of 218,225,233,238,239,240,246,247,248,256,257,259,260,261,270)
Q9CR95	1	(1 of 179,181,185)
Q9CR95	1	202
Q9CR95	1	162
Q9CRB6	1	114

Q9CS74	1	640
Q9CWK8	1	(1 of 93,94,97,101,104,106,107)
Q9CX80	1	184
Q9CX80	1	188
Q9CYZ8	1	360
Q9CZ62	1	473
Q9CZW6	1	357
Q9D032	1	(1 of 374,381,383,385,387)
Q9D2H6	1	(1 of 357,359,364,370,374,377,378,379,380,382,385)
Q9D415	1	(1 of 616,631,636,642,643,644,645,646,649,651,652)
Q9D415	1	535
Q9D4H9	1	(1 of 132,134,136,140,144,145,148,149,154,155,157,160,161,162,163,164,165,166,171)
Q9D7N9	1	161
Q9D824	1	204
Q9D824	1	229
Q9DAM7	1	72
Q9DAM7	1	73
Q9DAM7	1	76
Q9DAM7	1	69
Q9DAU1	1	(1 of 155,156)
Q9DBF1	1	(1 of 520,521,523,527,528,529)
Q9DBG5	1	(1 of 69,71,72)
Q9DBG5	1	128
Q9DBG5	1	76
Q9DBN4	1	(1 of 70,76,78,79,83,85,88,90,91)
Q9DBN4	1	(1 of 171,174,175,177,178,179,183)
Q9DBR7	1	(1 of 631,645,646,647,648,650,651,652)
Q9DBR7	1	(1 of 571,572,573)
Q9DBR7	1	(1 of 374,379,381,385,386,387,388,396,399,401,402,406,408,409)
Q9DBR7	1	577
Q9DBR7	1	585
Q9DBR7	1	589
Q9DBR7	1	656
Q9DBR7	1	566
Q9DBR7	1	759
Q9DBR7	1	570
Q9DBR7	1	637
Q9DBR7	1	575
Q9DC07	1	(1 of 61,63,64,68)
Q9DC07	1	113
Q9DC28	1	(1 of 337,344,347,349,350,352,355,356)
Q9DC28	1	382
Q9DCH4	1	24

Q9DCP9	1	(1 of 9,12,26,36,43)
Q9DCS9	1	(1 of 17,21,24,25,31,34)
Q9DCT8	1	(1 of 74,82,88)
Q9EP53	1	1071
Q9EPN1	2	(2 of 1792,1796,1797,1801,1805,1809,1811,1812,1813,1814,1822)
Q9EPN1	1	(1 of 1487,1488,1491,1492,1500,1502,1505,1507)
Q9EPN1	1	(1 of 1202,1203,1204,1208,1209,1211)
Q9EPN1	1	(1 of 997,999,1001,1004,1006,1011,1012,1014)
Q9EPN1	1	1637
Q9EQC8	1	228
Q9EQF6	1	520
Q9EQT6	1	(1 of 90,101,104,105,108,113,118,120)
Q9EQZ7	1	1528
Q9ERQ3	1	468
Q9ERU9	1	(1 of 2317,2320,2328,2329,2330,2335,2336,2337,2338,2339,2341,2342)
Q9ERU9	1	(1 of 1719,1725,1731)
Q9ERU9	1	(1 of 1304,1306,1307,1308,1313)
Q9ERU9	1	1138
Q9ES97	1	(1 of 342,343)
Q9ES97	1	385
Q9ES97	1	8
Q9ES97	1	377
Q9ES97	1	14
Q9ES97	1	206
Q9ES97	1	146
Q9ES97	1	18
Q9ES97	1	345
Q9ES97	1	61
Q9ES97	1	446
Q9ESC8	1	85
Q9ESJ4	1	(1 of 196,200,203,204,206,207,209,210,212,213,214,215,218,221,223,224,226,231,233,235)
Q9ESJ4	1	249
Q9ET43	1	241
Q9ET54	1	(1 of 763,767,769,770,771,773,774,775,776,779,782,784)
Q9JHC9	1	(1 of 372,374,375,376,380)
Q9JI44	1	(1 of 415,418,422,424,426,433)
Q9JI46	1	(1 of 153,158,159,161,162,163,165)
Q9JIL5	1	(1 of 844,850,851)
Q9JIL5	1	825
Q9JKD3	1	(1 of 221,224,226,230,232)
Q9JKR6	1	(1 of 598,607,612)
Q9JKR6	1	933
Q9JKV1	1	221

Q9JKV1	1	220
Q9JKV1	1	213
Q9JKV1	1	223
Q9JL04	1	373
Q9JL04	1	263
Q9JL60	1	442
Q9JLV1	1	(1 of 160,162,163,170)
Q9JLV1	1	(1 of 372,373,380,382,386,390)
Q9JM52	1	(1 of 545,546,554,557,559,565,567)
Q9JM52	1	601
Q9JMD0	2	(2 of 273,279,282,283,284,285,286,288,289,291,293,295,297,298)
Q9QWH1	1	(1 of 10,11)
Q9QXD8	1	(1 of 105,112,113,114,120,123)
Q9QXE7	1	(1 of 120,122,123,124,127,128)
Q9QXS6	1	(1 of 331,333,336,337,338,339,340,341,342,343,344)
Q9QY01	1	(1 of 749,750,751,754,755,756,757,760,763,765)
Q9QY01	1	613
Q9QY76	1	144
Q9QYB5	1	(1 of 402,409,411,414,419,423)
Q9QYB5	1	(1 of 2,3,5,6,11,12,17)
Q9QYB8	1	(1 of 396,403,405)
Q9QYB8	1	(1 of 629,632,636,656,662)
Q9QYB8	1	533
Q9QYC0	1	(1 of 480,481,482,483,494)
Q9QYC0	1	(1 of 408,415,417,420,423,427,429,431)
Q9QYC0	1	(1 of 558,559)
Q9QYC0	1	11
Q9QYC0	1	557
Q9QYC0	1	17
Q9QYC0	1	540
Q9QYC0	1	542
Q9QYE6	1	158
Q9QYG0	1	370
Q9QYH6	1	(1 of 19,23,29,37,42,43,46,50,55,58,59,63)
Q9QYX7	1	(1 of 3052,3057)&(1 of 3057,3060)
Q9QYX7	1	(1 of 2697,2702,2707,2710,2711,2714,2720)
Q9QYX7	1	(1 of 2326,2327,2328,2332,2361,2362,2367)
Q9QYX7	1	(1 of 2922,2924,2926)
Q9QYX7	1	(1 of 2279,2280)
Q9QYX7	2	(1 of 702,703,705,709,711,712,716,717,723,724)&(2 of 702,703,716,717)
Q9QYX7	1	(1 of 3651,3661,3662,3664,3666,3667,3669,3670,3673,3675)
Q9QYX7	1	(1 of 2394,2398)
Q9QYX7	1	(1 of 2012,2015,2016,2020,2021,2029,2030)

Q9QYX7	2	(2 of 2727,2729,2731,2732,2735,2736,2738,2740,2749,2750,2755,2756,2757)
Q9QYX7	1	(1 of 4580,4583,4584,4587,4588,4589,4592,4598,4600,4602)
Q9QYX7	1	(1 of 3443,3444,3449,3454,3457,3462)
Q9QYX7	1	(1 of 3763,3765)
Q9QYX7	1	(1 of 1954,1957,1966,1967,1968,1974,1982,1985,1986,1987,1988)
Q9QYX7	1	(1 of 4016,4020,4028,4029,4030)
Q9QYX7	1	(1 of 2068,2072,2073,2082,2085)
Q9QYX7	1	(1 of 745,746,748,752,755,757,761)
Q9QYX7	1	(1 of 4149,4150,4151,4152,4153,4154,4159,4160)
Q9QYX7	1	(1 of 4265,4268,4269,4273,4275)
Q9QYX7	1	(1 of 4830,4831,4835)
Q9QYX7	1	(1 of 3947,3948,3951,3952,3955,3956,3958,3961,3970,3971)
Q9QYX7	1	(1 of 2191,2199,2206,2208,2210,2213,2222,2224,2225,2230)
Q9QYX7	1	2050
Q9QYX7	1	2948
Q9QYX7	1	518
Q9QYX7	1	2315
Q9QYX7	1	2960
Q9QYX7	1	2961
Q9QYX7	1	2836
Q9QYX7	1	661
Q9QYX7	1	2839
Q9QYX7	1	2456
Q9QYX7	1	2455
Q9QYX7	1	2969
Q9QYX7	1	2971
Q9QYX7	1	2972
Q9QYX7	1	2717
Q9QYX7	1	3991
Q9QYX7	1	2968
Q9QYX7	1	2845
Q9QYX7	1	2843
Q9QYX7	1	1826
Q9QYX7	1	2978
Q9QYX7	1	2722
Q9QYX7	1	2983
Q9QYX7	1	2472
Q9QYX7	1	4137
Q9QYX7	1	2476
Q9QYX7	1	2988
Q9QYX7	1	3630
Q9QYX7	1	2481
Q9QYX7	1	2993

Q9QYX7	1	4146
Q9QYX7	1	3895
Q9QYX7	1	3770
Q9QYX7	1	2491
Q9QYX7	1	3903
Q9QYX7	1	3904
Q9QYX7	1	2881
Q9QYX7	1	2626
Q9QYX7	1	707
Q9QYX7	1	2889
Q9QYX7	1	2890
Q9QYX7	1	2382
Q9QYX7	1	3920
Q9QYX7	1	3921
Q9QYX7	1	2386
Q9QYX7	1	2517
Q9QYX7	1	856
Q9QYX7	1	4313
Q9QYX7	1	2268
Q9QYX7	1	733
Q9QYX7	1	864
Q9QYX7	1	2789
Q9QYX7	1	2664
Q9QYX7	1	2793
Q9QYX7	1	3436
Q9QYX7	1	3053
Q9QYX7	1	2669
Q9QYX7	1	3058
Q9QYX7	1	2291
Q9QYX7	1	4212
Q9QYX7	1	502
Q9QYX7	1	3065
Q9QYX7	1	2686
Q9QYY0	1	(1 of 365,367,369,371,372,382,384)
Q9QYY0	1	(1 of 274,276,277,278,286,289,291,293,298)
Q9QYY0	1	322
Q9QYY0	1	412
Q9QZ04	1	(1 of 824,825,827,831,832)
Q9QZN4	1	261
Q9QZS8	1	(1 of 391,400,403,406,408,410,411,415,416,418)
Q9R0K7	1	1179
Q9R190	1	(1 of 52,53,54,57)
Q9R1E0	1	(1 of 644,645)

Q9R1E0	1	646
Q9R1L5	1	(1 of 1145,1146,1149,1155,1156,1158,1159,1160,1163,1164,1165,1168,1171,1172,1174)
Q9WTQ5	1	861
Q9WTS4	2	(2 of 1505,1509,1513)
Q9WTS4	1	(1 of 225,228,236,237,238,241,247,252,258)
Q9WTS4	1	685
Q9WU42	1	(1 of 1778,1781,1782,1783,1784,1785,1796,1799,1800,1805,1806)
Q9WU42	1	1944
Q9WU42	1	2089
Q9WU42	1	1532
Q9WU42	1	1844
Q9WUM3	1	421
Q9WUU8	1	(1 of 70,73,76,77,80,83,91,95)
Q9WUU8	1	(1 of 103,105,108,109,110,112,114,115,118,126)
Q9WUU8	1	104
Q9WV18	1	(1 of 436,438,441,442)
Q9WV30	1	(1 of 674,676,677,680,684,688,693,696,700,701,709,713)
Q9WV60	1	(1 of 389,395,398,400)
Q9WV69	1	(1 of 90,91,92,96,103)
Q9WV69	1	(1 of 123,124,133,134,138)
Q9WV69	1	16
Q9WV69	1	18
Q9WV69	1	285
Q9WV69	1	110
Q9WV92	1	(1 of 580,584,585,586,588,591)
Q9WV92	1	(1 of 850,852,853,855,856)&(1 of 856,857)
Q9WV92	1	814
Q9WV92	1	847
Q9WV92	1	822
Q9WV92	1	470
Q9WV92	1	858
Q9WV92	1	859
Q9WV92	1	798
Q9WVG6	1	7
Q9WVG6	1	15
Q9WVI9	1	(1 of 362,364,365,367,368,371,374)
Q9WVJ0	1	(1 of 933,941,943)
Q9WVJ0	1	1046
Q9Z0F7	1	67
Q9Z0F7	1	54
Q9Z0P4	1	(1 of 103,108)
Q9Z0P4	1	(1 of 273,283,284,298,313)
Q9Z0R4	1	(1 of 884,887,890,892,894,895,897)

Q9Z0R4	1	718
Q9Z0U1	1	451
Q9Z0U1	1	999
Q9Z1R2	1	(1 of 448,451,465,474,477,488,498,501)
Q9Z1R2	1	(1 of 189,194,200,203,206,208,213,215,216,221)
Q9Z1R2	1	(1 of 92,96,99,100,102,104,106,108,117)
Q9Z2A0	1	(1 of 31,33,37,38,43,46)
Q9Z2C4	2	(2 of 647,649,650,651)
Q9Z2C4	1	667
Q9Z2D6	1	434
Q9Z2Y3	1	(1 of 242,248,249,256)
S4R180	1	(1 of 11,19,22,23,27,28,32,39)
S4R1C4	1	1120
S4R1M9	1	221
S4R2F3	1	(1 of 2754,2755,2759,2767,2769,2771,2773,2775,2778,2783)
S4R2F3	1	(1 of 3710,3714,3720,3733)
S4R2F3	1	(1 of 2183,2186,2192,2193,2195)
S4R2F3	1	(1 of 2818,2822,2823,2831,2832,2833,2835,2836)
S4R2F3	1	(1 of 2320,2322,2324,2327,2331)
S4R2F3	1	3787
S4R2F3	1	3212
S4R2F3	1	3213
S4R2F3	1	2959
S4R2F3	1	817
S4R2J9	1	(1 of 2419,2426,2427,2429,2432,2436,2438)
S4R2J9	1	(1 of 2161,2171)
S4R2J9	1	(1 of 2179,2183,2184,2185,2187,2188,2192,2193,2195,2197)
S4R2J9	1	(1 of 2136,2138,2141,2142,2144,2145,2146,2150,2153)
S4R2J9	1	(1 of 2714,2716,2717,2721,2723,2728)
S4R2J9	1	(1 of 374,375,376,385)
S4R2J9	1	(1 of 202,203,206,207)
S4R2J9	1	2280
S4R2J9	1	2635
S4R2J9	1	876
S4R2J9	1	1931
S4R2J9	1	880
S4R2K9	2	(1 of 1676,1679,1681,1683,1689,1690)&(2 of 1683,1689,1690)
S4R2K9	2	(2 of 1623,1624,1627,1628,1631)
S4R2K9	1	(1 of 1538,1541,1543,1544,1546)
S4R2K9	1	(1 of 1694,1697,1698,1700,1701)
S4R2K9	2	(2 of 1661,1664,1665,1667,1671,1672)
S4R2K9	1	(1 of 1506,1508,1509,1513)
S4R2K9	1	(1 of 1648,1651,1654,1655,1656)

S4R2K9	1	(1 of 2127,2129,2133,2136,2137,2153,2155)
S4R2K9	1	(1 of 1603,1605,1608,1617,1618,1620,1621)
S4R2K9	2	(2 of 1550,1551,1555,1556,1557,1558,1559)
S4R2K9	1	(1 of 1779,1782,1786,1790)
S4R2K9	2	(2 of 1745,1746,1748,1752,1753,1756,1759,1761)
S4R2K9	1	(1 of 2165,2169,2170,2176,2183)
S4R2K9	1	(1 of 1520,1522,1524,1525,1526,1528,1530,1532,1534)
S4R2K9	2	(2 of 1767,1768,1769,1770,1775)
S4R2K9	1	(1 of 1857,1859,1860,1862)
S4R2K9	1	(1 of 1562,1564,1568)
S4R2K9	1	(1 of 1636,1637,1639,1641,1645)
S4R2K9	1	(1 of 1488,1491,1492,1494,1500,1501)
V9GWT6	1	(1 of 105,109,110,115,116,120,122,134,137,138,142)
V9GWW6	1	(1 of 325,331,334,336,337,339,341)
V9GWW6	1	621
V9GXD9	1	(1 of 464,466,470,472,480,481)
V9GXD9	1	(1 of 635,637,638,645,649,654,655)
V9GXD9	1	627
V9GXJ1	1	(1 of 130,132,135,137,138,139,143)
V9GXX3	1	90

Appendix 5.5. O-GlcNAc Sites and Regions Identified in the Mouse Liver.

See also **Fig. 5.5**.

Protein	Min Sites	Site ID Constraints
A0A087WNL7	1	(1 of 2684,2687,2688,2689,2690,2691,2693,2694,2695)
A0A087WPF5	1	(1 of 151,152,153,154,157,159)
A0A087WPF5	1	161
A0A087WQI5	1	68
A0A0A0MQE8	1	(1 of 1893,1894,1895,1898,1899,1900,1902,1906,1910)
A0A0A0MQE8	1	(1 of 347,351,354,358,359,360)
A0A0A0MQM6	1	163
A0A0A6YWC8	1	34
A0A0G2JDK2	1	290
A0A0G2JDK2	1	71
A0A0G2JDW6	1	91
A0A0G2JG52	1	(1 of 1203,1205,1207,1208,1211,1213,1214,1215,1217,1218,1219,1222,1223,1225,1227,1228)
A0A0N4SUU0	1	120
A0A0N4SUU0	1	307
A0A0R4IZZ6	1	852
A0A0R4J060	1	(1 of 592,593,601,608,612,618,619,623,625,627,629,630,632,637,638)
A0A0R4J060	1	(1 of 802,806,807,813,815,817,819,825,828,832,839)
A0A0R4J060	1	(1 of 274,278,279,280,287,288,290)
A0A0R4J060	1	320
A0A0R4J092	1	115
A0A0R4J092	1	91
A0A0R4J0B2	1	529
A0A0R4J0I1	1	(1 of 268,272)
A0A0R4J0I1	1	187
A0A0R4J112	1	(1 of 194,195,197,204,210,216,219,225,226,229,232)
A0A0R4J131	1	138
A0A0R4J135	1	(1 of 402,403,404,407)
A0A0R4J138	1	(1 of 165,173,178,187,191)
A0A0R4J2B5	1	348
A0A0U1RPL0	1	432
A0A140LHN0	1	31
A0A1B0GR85	1	1085
A0A1B0GRV3	1	(1 of 106,108,110,113,115,116,117,119,121,125,134)
A0A1B0GRV3	1	248
A0A1B0GRV3	1	236

A0A1D5RLD8	1	208
A0A1L1STC6	1	8305
A0A1L1STC6	1	1956
A0A1L1SUT5	1	(1 of 89,90,91,95)
A0A1N9PTV1	1	(1 of 233,240,242,244,245,246)
A0A1W2P7C1	1	290
A0A1X7SB71	1	273
A0A1Y7VNM3	1	167
A0A286YDL1	1	(1 of 960,963,964)
A0A2I3BPN6	1	486
A0A2R8VHH9	1	203
A0A338P689	1	(1 of 310,315,331,332)
A0A338P6K9	1	(1 of 162,163,166,169)
A0A338P6K9	1	(1 of 19,22)
A0A338P6K9	1	45
A0A338P6K9	1	63
A0A338P6U8	1	1637
A0A3B2W837	1	95
A0A494B968	1	33
A0A5F8MQ25	1	(1 of 865,866,876,879,881,886,890)
A2A484	1	(1 of 755,756,757,758,763,767,771)
A2AC24	1	140
A2ADS6	1	(1 of 335,338,341,351)
A2AGT5	1	(1 of 1899,1900,1901,1904,1910,1914,1916,1917,1918,1920,1921,1925,1933)
A2AH22	1	441
A2AKB9	2	(2 of 314,318)
A2AKB9	1	364
A2AMI6	1	(1 of 187,188,190,196,202,208,211,217,218,221,224)
A2AQ25	1	(1 of 1893,1894,1895,1896,1897,1898,1899,1902,1905,1907,1908)
A2AS44	1	226
A2AS70	1	(1 of 262,265,267,268,274,276,278,281)
A2AS70	1	(1 of 413,416,418,419,421,423,424,425,428,432,434,435,436,437)
A2ASS6	1	(1 of 24801,24803,24807,24808,24810,24812,24816)
A2ASS6	1	(1 of 32261,32264)
A2ASS6	2	(2 of 299,301,305,307)
A2ASS6	1	(1 of 20562,20573)
A2AUY4	1	(1 of 3,9,10,13,14,15,16,18,19,20,21,24,27,30)
A2AVJ7	1	(1 of 103,110,119,123)
A2AVJ7	1	111
A2AWI9	1	(1 of 263,267,268,272,276,277,278,279,281,282,283,286,292,314,316)
A2AWL7	1	(1 of 1654,1655,1658,1659,1660,1664,1666)
A2BH40	1	(1 of 697,699,703,706,710)
A2BH40	1	(1 of 1391,1395,1411,1415,1423,1433,1439,1441,1444)

A2BH40	1	256
A2RSY1	1	(1 of 699,700,701,702,707,709,710,711,713,716,717,718,720,726,729)
A2RSY1	1	(1 of 538,539)
A2RSY1	1	(1 of 786,790,795,796,798,799,800)
A2RSY1	1	859
A2RSY1	1	534
A6H619	1	(1 of 1359,1363,1364,1365,1366,1368,1369,1376)
A9C497	1	(1 of 170,173)
A9Z1V5	1	382
B1AUC0	1	(1 of 456,460,461,462,463,469,471,472)
B2RRI2	1	125
B2RUJ2	1	(1 of 1125,1131,1132,1136,1140)
B2RUJ2	1	1068
B2RUQ2	1	(1 of 361,364,366,367,369)
B2RUQ2	1	(1 of 1618,1621,1624)
B2RXQ9	1	367
B9EKS2	2	(2 of 410,415,421,426,427,429,430,431,433,434)
B9EKS2	1	(1 of 652,655)&(1 of 655,658)
B9EKS2	1	661
D3YUC9	1	11
D3YUL8	2	(2 of 745,746,749,757)
D3YUL8	1	184
D3YUL8	1	742
D3Z197	1	(1 of 265,266,269,270,272,273,274)
D3Z2E7	1	(1 of 415,417)
D3Z2E7	1	(1 of 883,887)
D3Z2E7	1	408
D3Z2E7	1	434
D3Z2E7	1	392
D3Z3D5	1	74
D3Z3F8	1	478
D3Z3U7	1	328
D3Z3U7	1	327
D3Z5U3	1	89
D3Z7I3	1	(1 of 280,281,282,283,285)
D6RI42	1	313
D6RIL1	1	(1 of 283,286,287)
E9PUF4	1	(1 of 645,647,648,655,657,658,665,666,667,668,671)
E9PUL9	1	(1 of 539,541,543,545)
E9PVA6	1	(1 of 551,555)
E9PVA6	1	556
E9PYH6	1	(1 of 256,258,259,264,267,268,271,274,275)
E9PYH6	1	282

E9PYK3	1	(1 of 1229,1239,1241,1242,1249)
E9PYK3	1	1749
E9PZD2	1	384
E9PZD2	1	395
E9PZD2	1	373
E9PZD2	1	406
E9PZD2	1	439
E9PZD2	1	253
E9Q030	1	(1 of 178,179,180,183,186,190)
E9Q1M6	1	(1 of 1630,1631,1634,1635)
E9Q1M6	2	(2 of 1485,1509,1511,1512,1513,1514,1515,1519,1521,1522,1523,1524,1526)
E9Q1M6	1	(1 of 1783,1784)
E9Q1M6	1	1800
E9Q1M6	1	1801
E9Q1M6	1	2091
E9Q1M6	1	2096
E9Q1M6	1	1780
E9Q1M6	1	1816
E9Q1P8	1	(1 of 359,364,365,366,367)
E9Q1S3	1	183
E9Q2B2	1	(1 of 1002,1003)
E9Q2B2	1	(1 of 989,990)
E9Q2B2	1	993
E9Q2B2	1	1986
E9Q2B2	1	2027
E9Q2B2	1	2189
E9Q2B2	1	14
E9Q2B2	1	51
E9Q2B2	1	1429
E9Q2I4	1	(1 of 53,57,58,59,65,75,80)
E9Q3C1	1	395
E9Q3E2	1	(1 of 393,397)
E9Q3G8	1	(1 of 766,767)
E9Q3G8	1	(1 of 620,626,628,629,630,634,639,640,642,643,644,651)
E9Q3G8	1	(1 of 554,557,559,561,562,563,565,568,569,570,575,579,580,581)
E9Q3G8	1	(1 of 1158,1165,1167,1169)
E9Q3G8	1	(1 of 532,533,546,548)
E9Q3G8	1	513
E9Q3G8	1	514
E9Q3G8	1	899
E9Q3G8	1	517
E9Q3G8	1	909
E9Q3G8	1	1168

E9Q3G8	1	1044
E9Q3G8	1	1046
E9Q3G8	1	925
E9Q3G8	1	542
E9Q3G8	1	927
E9Q3G8	1	934
E9Q3G8	1	705
E9Q3G8	1	200
E9Q3G8	1	1102
E9Q3G8	1	1006
E9Q3G8	1	882
E9Q3G8	1	627
E9Q3G8	1	759
E9Q3W4	1	(1 of 2452,2456,2457,2461,2462)
E9Q5Z1	1	(1 of 6,7,10,13)
E9Q605	1	686
E9Q616	1	5376
E9Q6A7	1	(1 of 1595,1598,1601,1602,1604,1605,1606,1609,1611)
E9Q6A7	2	(2 of 1943,1944,1945,1946,1951,1952,1953,1954,1956)
E9Q7D5	1	(1 of 496,498,499,500,504,506)
E9Q7E2	1	656
E9Q7M2	1	(1 of 113,121,128,130,131,135,136,138,140,145,147,148)
E9Q7W0	1	(1 of 450,451,455,458,460,462,467,470,471,473,474,475,477,478,479,480,482,485)
E9Q804	1	(1 of 2068,2070,2075,2076,2085,2090,2091,2092,2093,2094,2096,2097,2098,2101,2102,2109,2121,2125)
E9Q804	1	(1 of 1671,1673,1678,1679,1681,1683,1684,1686)
E9Q804	1	(1 of 1945,1949,1950,1952,1956,1959,1961,1962,1963,1965,1966,1967,1969,1970,1971,1973,1978,1979,1980,1983,1985,1986,1988)
E9Q804	2	(2 of 2000,2001,2004,2005,2006,2007,2009,2010,2011,2013,2016,2017,2020,2023,2028)
E9Q804	1	1996
E9Q804	1	2381
E9Q804	1	1839
E9Q804	1	2192
E9Q804	1	2036
E9Q804	1	152
E9Q804	1	154
E9Q804	1	1820
E9Q804	1	1821
E9Q9B1	1	(1 of 3,7,9,11,14,15,16,17,18,19,20,22,23,25,27,29,30,32)
E9Q9M8	1	(1 of 443,444,446,449,450,453,457,458,461,463,466,467,468,471)
E9QA68	2	(2 of 111,115,116,117,119,120,123,125,127,128,129,131,132,134,135,136,137,139)
E9QAN9	1	(1 of 458,459,460,461,464,467,469)
E9QAN9	1	451
E9QAT4	1	(1 of 1087,1094,1099,1103,1106,1110,1112,1119,1122,1125,1136,1137,1139,1141,1142,1143,1145,1146)

E9QAT4	1	68
E9QAT4	1	69
E9QAT4	1	70
E9QAT4	1	2028
E9QAT4	1	2011
E9QAT4	1	127
E9QL43	1	238
E9QLT6	1	608
E9QLT6	1	592
E9QLT6	1	547
E9QML5	1	1370
E9QMU3	1	(1 of 452,453)
E9QPR4	1	(1 of 1986,1987,1988,1992)
E9QQ33	1	(1 of 523,525,526,531)
E9QQ33	1	511
F2Z3U3	1	(1 of 763,767,775,777,789,793,795,796)
F6S4K9	1	(1 of 297,300,302)
F6S4K9	1	286
F6S4K9	1	103
F6SPQ1	1	(1 of 177,181,182,192)
F6SPQ1	1	153
F6TB64	1	823
F6VJC5	1	(1 of 115,116,117,118,119,120,121,123,128,136,142,143,144,146,147,157,159,165,169)
F6VJC5	1	(1 of 72,73)
F6VJC5	1	58
F6VJC5	1	100
F6VJC5	1	71
F6WV21	1	854
F6Y6L6	1	132
F6Y6L6	1	127
F6YTG0	1	22
F6YTL8	1	(1 of 222,225,228,229,232,240,245)
F6YTL8	1	(1 of 1037,1047)
F6Z9A1	1	(1 of 72,77,78,79)
F6Z9T5	1	110
F6ZBY9	1	(1 of 292,295,298,299,300,301,302,304,305)
F6ZBY9	1	330
F6ZDS4	1	(1 of 1730,1731,1732,1736,1742)
F6ZDS4	1	1746
F8VPJ6	1	439
F8VPM9	1	(1 of 1565,1566,1583)
F8VPM9	1	1706
F8VPM9	1	1771

F8VPM9	1	2647
F8VPZ9	1	(1 of 707,712,713,719,723,727,739,742)
F8VPZ9	1	(1 of 1217,1225,1226)
F8VPZ9	1	(1 of 431,432,433,435,445)
F8VQJ3	1	(1 of 1216,1223)
F8VQJ3	1	(1 of 1201,1205,1206)
F8VQJ3	1	1380
F8WHT3	1	1984
F8WHT3	1	1803
F8WHT3	1	1798
F8WI14	1	(1 of 532,536,544)
F8WI14	1	(1 of 436,446)
F8WJ05	1	591
G3UX48	1	(1 of 42,43,46,47,53,59,61,64)
G3UZX7	1	(1 of 494,501,503)
G3X8T2	1	413
G3X928	1	(1 of 142,145,149,150,151,155,158,159,166)
G3X928	1	607
G3X972	1	(1 of 65,66,81,82,96,97,98)
G3X972	1	72
G3X9Z4	1	(1 of 169,174,175,178,181,182,184,186,187)
H3BJL2	1	(1 of 779,780)
H3BLE4	1	(1 of 138,140,149)
H9KV15	1	1092
H9KV15	1	262
H9KV15	1	1614
H9KV15	1	250
H9KV15	1	251
I7HIP8	1	(1 of 404,408,409,412,413,417,418)
J3QNT7	1	(1 of 395,403,404,406,407,409)
J3QNT7	1	167
J3QQ16	1	1846
J3QQ16	1	113
J3QQ16	1	1950
K3W4L3	1	237
K3W4L3	1	82
K3W4L3	1	459
K3W4L3	1	213
K4DI63	1	36
O08755	1	(1 of 440,450,452,454,455,456,457,458,459,460,461,463)
O08785	1	707
O08785	1	446
O08789	1	(1 of 157,158)

O09000	1	853
O09117	1	259
O09159	1	369
O09173	1	438
O35126	1	(1 of 353,357,365,366,367)
O35516	1	175
O35738	1	(1 of 91,92,94,97,98,99,102,104,106,108,109,111,112,113,114,115,116,117,118,119,120,121)
O35984	1	323
O55042	1	(1 of 44,53,54)
O55042	1	72
O55111	1	939
O55111	1	1060
O70305	1	(1 of 778,779,780,781,783,789)
O70305	1	(1 of 174,175,182,186,187,200,201,202)
O70305	1	(1 of 635,636,641,643,644,647)
O70305	1	745
O70305	1	189
O70305	1	727
O70318	1	(1 of 886,888,891,902,907,910,912,913,915,917,918,919,920,921,922,925)
O70400	1	128
O70400	1	135
O88531	1	199
O88532	1	(1 of 148,149,157)
O88532	1	(1 of 102,111,114,116,121)
O88532	1	195
O88532	1	423
O88532	1	135
O88532	1	136
O88532	1	202
O88532	1	167
O88532	1	300
O88532	1	180
O88569	1	199
O88587	1	(1 of 260,261,265)
O88935	1	(1 of 510,512,518,520,523,526)
O89017	1	(1 of 79,84)
O89017	1	95
P05784	1	(1 of 7,8,9,11,12)
P05784	1	32
P05784	1	31
P06537	1	43
P07724	1	(1 of 89,92)
P07758	1	(1 of 90,92,103,105,106)

P08113	1	(1 of 245,246,248)
P08113	1	64
P0C090	1	(1 of 789,792,793,794,799,801,803,806,810)
P0C090	1	(1 of 754,755)
P0C090	1	(1 of 552,555,560,561,565,569,573)
P0C090	1	592
P0C090	1	907
P0C7T6	1	(1 of 29,30,31,33,34,37,39,40,43,46)
P0C7T6	1	22
P0DOV2	1	137
P0DOV2	1	130
P10605	2	(2 of 199,204)
P10605	1	(1 of 210,216,218,228,229,231,233,235)
P11276	1	1008
P11276	1	432
P11679	1	489
P11679	1	482
P11679	1	34
P11725	1	81
P14602	1	178
P14602	1	63
P14869	1	286
P16951	1	(1 of 287,289,292,296,302,303,304,305,307,310,314,315,318,321,322)
P16951	1	272
P20029	1	638
P22361	1	(1 of 325,327,328,335,336,337,343,345,352,354,359,360,363,364)
P22361	1	(1 of 285,303,304,309,310,311,313,315)
P24369	1	117
P24527	1	(1 of 156,158,162)
P27612	1	(1 of 481,482,485,487,490,495)
P28665	1	1144
P29341	1	485
P33215	1	(1 of 325,329,330,331,332,338)
P40124	1	(1 of 217,221,224,227,242,243,244,245,247,250,252)
P42128	1	(1 of 691,699,701,702,705,710,717)
P42128	1	(1 of 663,671,675,676,677,678,679,681,682,683)
P42128	1	563
P42128	1	541
P42227	1	(1 of 714,716,717,719,721,727)
P43883	1	(1 of 23,24,25,30,31,35,36)
P43883	1	107
P43883	1	59
P45481	1	(1 of 316,317,319,320,325,329,330,336,341,344)

P45481	1	2360
P45481	1	147
P47941	1	(1 of 195,197,212,213,214,218,221,222,232,233)
P48678	1	611
P48678	1	644
P48678	1	613
P49429	1	(1 of 226,230,235)
P49442	1	394
P50247	1	2
P51141	1	(1 of 379,380,383,384,387)
P54254	1	(1 of 357,364,365,366,368,376,377)
P54254	1	81
P54254	1	23
P54728	1	(1 of 235,247,248,250,253,262,263,264,266,267,268,269,270,271)
P54728	1	(1 of 81,82,87,88,91,92,93,95,97,100,101,102,114,120,121,122,125,126,130,131,132,134,135,143,155,159,160,166,167,171,172)
P58462	1	476
P58462	1	446
P58871	1	298
P58871	1	260
P58929	1	404
P59326	1	196
P59326	1	198
P59759	1	(1 of 838,839,851,855,858)
P59759	1	245
P59759	1	214
P59759	1	207
P59764	1	1796
P59764	1	1806
P62806	1	(1 of 81,83)
P62908	1	242
P62960	1	(1 of 2,3,7,19,23,27,28,30,34,41,42)
P70121	1	(1 of 163,168,172,173,174,177,179)
P70121	1	(1 of 224,226,227)
P70121	1	(1 of 245,248,249,252,254,265,268,273)
P70121	1	235
P70121	1	228
P70121	1	238
P70257	1	(1 of 452,453,454)
P70257	1	272
P70257	1	470
P70665	1	357
P70665	1	429

P70699	1	925
P70699	1	142
P81269	1	(1 of 181,182,184,186,187,191,195,196,199,202,204,205)
P82343	1	(1 of 419,420,424,425,429)
P83741	1	(1 of 1801,1803,1806,1808,1817,1818,1820,1821,1822,1823,1825,1829)
P83741	1	(1 of 2376,2377)
P83741	1	(1 of 1270,1271,1274,1280,1281,1282,1290,1292,1294,1295,1297,1303)
P83741	1	(1 of 1841,1843)
P83741	1	1860
P83741	1	1230
P83741	1	1844
P83741	1	1945
P83741	1	2365
P97364	1	448
P97366	1	(1 of 37,39,41,43,47,51,53,55,58,59,60,61,62,63,64,66,67,69,71,73,74,76)
P97379	1	235
P97855	1	266
P99027	1	74
Q00422	1	264
Q00422	1	275
Q02614	1	233
Q02614	1	244
Q02614	1	241
Q02614	1	239
Q02780	1	(1 of 383,387,389,390,395,396,407)
Q02780	3	(3 of 479,483,484,485,486,492,494,495,497,499,500,502,503,504)
Q02780	1	(1 of 352,355,356,358,360,362,363,364,367,370,378)
Q02780	1	293
Q03265	1	(1 of 419,423)
Q06890	1	329
Q07797	1	71
Q07968	1	548
Q08122	1	(1 of 328,331,332,333,334)
Q08122	1	289
Q08874	1	(1 of 93,95,101,104,105,108,110)
Q09XV5	1	2524
Q14AX6	1	588
Q14AX6	1	589
Q2PFD7	1	(1 of 240,245,246,247,248,251)
Q2PFD7	1	(1 of 633,638)
Q3TJD7	1	(1 of 190,191,196,203,204,209,214,215,217,219,220)
Q3TN85	1	(1 of 123,125,128,129,130,131,132,133,136,138,140,143,144,146,147)
Q3TN85	1	(1 of 101,109,112)

Q3TN85	1	118
Q3TRM4	1	(1 of 1348,1350,1351)
Q3TZR9	1	(1 of 444,451,452,455,459)
Q3U0V1	1	192
Q3U0V1	1	96
Q3U1C4	1	(1 of 36,38,39,41)
Q3U2P1	1	(1 of 15,24,26,28,31,38,41,45,46,47,52,57)
Q3U2P1	1	(1 of 236,239,247,248,254,255,260,272)
Q3U3C9	1	125
Q3UCQ1	1	(1 of 539,540,543,547,549)
Q3UFM6	1	(1 of 434,441,443,444,445,450,452)
Q3UH06	1	(1 of 988,991,993,995,1001)
Q3UH06	1	1000
Q3UH06	1	1099
Q3UHC0	1	(1 of 1602,1603,1604,1607,1608,1609,1612)
Q3UHC0	1	(1 of 754,755,756,757,761,763,764,766,767,768,769,770,771,776,779,784)
Q3UHF7	1	(1 of 404,406,412,416)
Q3UHF7	1	(1 of 1308,1316,1320)
Q3UHJ0	1	416
Q3UHJ0	1	360
Q3UHK8	1	1251
Q3UHK8	1	1606
Q3UHK8	1	1621
Q3UHK8	1	1622
Q3UHK8	1	1623
Q3UMF0	1	(1 of 912,913,915,917,933)
Q3UMF0	1	(1 of 714,717,718,721,723,727,728,730,734,738)
Q3UMF0	1	963
Q3UMF0	1	868
Q3UMF0	1	869
Q3UMF0	1	1014
Q3UMF0	1	863
Q3UPF5	1	(1 of 467,468,469,477,483,487)
Q3UPF5	1	(1 of 557,558,559,562,564,567,570)
Q3UPH1	1	162
Q3UPH1	1	157
Q3UQN2	1	(1 of 477,487,491,492,494,495,499)
Q3UQN2	1	(1 of 507,508,509,510,512,513,514,516,518,522,524,528)
Q3URQ4	1	(1 of 10,18,27,31,33,34,35,39)
Q3UYJ1	1	(1 of 136,137,140,141,144,145)
Q3UYJ1	1	212
Q3UYJ1	1	149
Q3UYJ1	1	6

Q4FE56	1	2551
Q4G0F8	1	(1 of 862,864,865,868,869,870,871)
Q4VAA2	1	178
Q501J7	2	(1 of 192,199,201,202)&(1 of 199,201,202,205,206)&(1 of 205,206,209,212)
Q501J7	1	(1 of 296,297,298,301,307,309,310)
Q501J7	1	(1 of 244,245)
Q501J7	1	194
Q501J7	1	195
Q501J7	1	231
Q501J7	1	186
Q501J7	1	190
Q52KG4	1	(1 of 262,263,266)
Q52KI8	1	(1 of 461,463)
Q52KI8	1	(1 of 879,882,885)
Q52KI8	1	892
Q571G4	1	(1 of 106,109,111)
Q571G4	1	(1 of 284,286,288,290,295,296,299,300,301,303)
Q571G4	1	261
Q571G4	1	238
Q571K4	1	408
Q571K4	1	412
Q59J78	1	148
Q5EBG8	1	(1 of 181,190,193)
Q5F2E7	1	(1 of 381,382,383,384,385,386)
Q5F2E7	1	(1 of 407,409,410,412,414,422,425,429,436,437,441,443,446,447,449,451,457,460)
Q5F2E7	1	379
Q5F2E7	1	380
Q5F4T0	1	(1 of 1382,1383,1384,1386)
Q5FWH2	1	459
Q5SFM8	1	(1 of 465,466,471,472,474,475,477,483,495,497,498,499)
Q5SFM8	1	546
Q5SQA7	1	(1 of 29,31,34,35,37,38,40,41,42,43)
Q5SRX1	1	(1 of 187,188,191,193,194,199,201,202,209,211,215,218)
Q5SXC4	1	(1 of 126,127,130,131,137,138,140,141,142,143,144,146,149,150,151,153,154,155,156,162)
Q5SXC4	1	(1 of 108,110,111,117,118,123,124)
Q5U5Q9	1	(1 of 417,418,423,426,427,429,434,435)
Q5YD48	1	(1 of 526,533,534,537,539,540,542)
Q5YD48	1	557
Q5YD48	1	566
Q60737	1	(1 of 344,347,348,353,356,357,360,362,370,378)
Q60775	1	470
Q60865	1	(1 of 418,428,434,435,436,437,441,443,450,453)
Q60865	1	(1 of 468,470,473,476,477,479,480,481,486,495,496)

Q60953	1	(1 of 404,409,416,417,421,422,423,424)
Q61033	1	(1 of 157,158,159,163,165,166,167,171)
Q61147	1	139
Q61191	2	(2 of 427,441,446,453,457,458,459,460,466,470,471,473,476)
Q61191	1	(1 of 784,787)
Q61191	1	(1 of 702,703)
Q61191	1	(1 of 583,586,587,588)
Q61191	2	(2 of 612,619,620,622,623,627,628,629,634)
Q61191	1	(1 of 1243,1245,1247)
Q61191	1	515
Q61191	1	771
Q61191	1	517
Q61191	1	518
Q61191	1	779
Q61191	1	651
Q61191	1	652
Q61191	1	405
Q61191	1	669
Q61191	1	801
Q61191	1	806
Q61191	1	808
Q61191	1	685
Q61191	1	562
Q61191	1	563
Q61191	1	694
Q61191	1	831
Q61191	1	579
Q61191	1	592
Q61191	1	1235
Q61191	1	1238
Q61191	1	1495
Q61191	1	1241
Q61191	1	603
Q61191	1	861
Q61191	1	1246
Q61191	1	480
Q61191	1	490
Q61191	1	495
Q61191	1	1138
Q61191	1	1139
Q61191	1	1148
Q61471	1	(1 of 171,172,176,178,179,181,185)
Q61646	1	(1 of 150,152,154)

Q61666	1	547
Q61827	1	(1 of 142,146,147,148,149,153,156)
Q61827	1	134
Q62009	1	603
Q62073	1	383
Q62261	1	2322
Q62261	1	2323
Q62311	1	(1 of 356,358,360)
Q62311	1	(1 of 480,481,483,485,490,492,494)
Q62311	1	586
Q62311	1	594
Q62311	1	590
Q62318	1	(1 of 4,8,12,15,18,21,23,26,30)
Q62452	2	(2 of 333,335,338)
Q62452	1	71
Q62504	3	(3 of 347,350,351)
Q62504	1	(1 of 2879,2883,2893,2895,2896,2899,2903)
Q62504	1	(1 of 2523,2527,2528,2529,2530,2531)
Q62504	1	2520
Q62504	1	2786
Q62523	1	(1 of 170,171,180)
Q62523	1	305
Q62523	1	237
Q63880	1	313
Q63886	1	91
Q64092	1	(1 of 545,550,551,553,557)
Q64213	1	(1 of 331,332,333)
Q64213	1	(1 of 111,114)
Q64213	1	328
Q64213	1	337
Q67FY2	1	(1 of 931,933,935,939,943,944,946)
Q68ED7	1	(1 of 411,413,416,417,421,423,429,436,437)
Q68FG2	1	(1 of 2133,2134,2138,2144,2146,2148,2149)
Q68FG2	1	2354
Q68FG2	1	2101
Q68FG2	1	2359
Q69ZA1	1	(1 of 1340,1341,1343,1349,1350,1355,1356,1357)
Q69ZA1	1	(1 of 1278,1285,1286,1287,1288,1289,1291)
Q69ZK6	1	(1 of 1855,1857,1861,1862,1863,1867,1869,1874,1875)
Q69ZK6	1	1250
Q69ZR2	1	(1 of 1359,1361,1362)
Q69ZR2	1	(1 of 1481,1482,1485,1490,1492,1493,1497,1498,1500,1503)
Q69ZR2	1	1355

Q69ZR2	1	1574
Q69ZR2	1	1575
Q6A065	1	(1 of 1315,1317,1318,1319,1321,1324,1325,1326,1328,1329,1332,1333,1336,1340)
Q6A0A2	1	632
Q6A0A2	1	51
Q6DFZ1	1	1781
Q6DID3	1	(1 of 734,739,741,745,749,750,761)
Q6KCD5	1	160
Q6KCD5	1	161
Q6NS59	1	749
Q6NXI6	1	(1 of 432,438,441,442,452,453,457,459,461)
Q6NXI6	1	(1 of 622,623)
Q6NXI6	1	417
Q6NXI6	1	418
Q6NXI6	1	616
Q6NXI6	1	1010
Q6NXI6	1	573
Q6NZN0	1	696
Q6P2K6	1	(1 of 46,49,54)
Q6P2K6	1	774
Q6P6L0	1	1106
Q6PAL7	1	1593
Q6PB44	1	(1 of 880,881,882,885,891,892,894)
Q6PB44	1	(1 of 1540,1552,1553,1557)
Q6PB75	1	(1 of 415,419,420,424)
Q6PD26	1	372
Q6PDI6	1	(1 of 536,550,551,552,553,555,556,567,569,570)
Q6PDK2	1	2359
Q6PFD9	1	(1 of 223,224,230,231,234,235,236,238,242,243,244,245,246,248,251)
Q6PFD9	1	(1 of 1080,1081,1082,1085,1092,1095,1098)
Q6PFD9	1	1033
Q6PIJ4	1	(1 of 1073,1076,1077,1084)
Q6PIJ4	1	(1 of 1030,1031)
Q6PIJ4	1	(1 of 809,814,817)
Q6PIJ4	1	(1 of 1113,1118,1120,1123,1124,1125,1127,1130,1136)
Q6PIJ4	1	1027
Q6PIJ4	1	1284
Q6PIJ4	1	838
Q6PIJ4	1	1064
Q6PIJ4	1	1170
Q6PIJ4	1	1138
Q6PIJ4	1	1270
Q6PR54	1	(1 of 1180,1183,1184,1185,1186,1187,1189,1190,1193,1194,1195,1196,1198,1201,1203,1205,1210,1211)

Q6XBJ3	1	(1 of 207,213)
Q6XBJ3	1	92
Q6XLQ8	1	133
Q6ZPG2	1	328
Q6ZPJ0	1	(1 of 169,173,178,179,182,183)
Q6ZPJ0	1	(1 of 157,158,159,160,161,164,165,167)
Q6ZPJ0	1	174
Q6ZPJ0	1	175
Q6ZQ08	1	1037
Q6ZQ08	1	1040
Q6ZQ08	1	1041
Q6ZQ08	1	1042
Q6ZQ08	1	1050
Q6ZQH8	1	1524
Q6ZQH8	1	1526
Q78PY7	1	333
Q7M6Y3	2	(1 of 359,362,363,364,370)&(1 of 370,378)&(1 of 378,379,381,382,383,385,386)
Q7M6Y3	1	565
Q7M6Y3	1	356
Q7M6Y3	1	453
Q7SIG6	1	(1 of 759,765,771,773,776,777,779,783,784,785,786)
Q7TMY8	1	(1 of 2910,2917,2918,2922,2923,2925,2926,2927,2928)
Q7TMY8	1	(1 of 2619,2632,2633,2635,2636,2640,2642,2643,2646,2649)
Q7TN29	1	197
Q7TQH0	1	(1 of 419,421,422,424,428,432,436,437)
Q7TQH0	1	(1 of 682,683)
Q7TQH0	1	(1 of 266,267,270,271,273,274,276)
Q7TQH0	1	(1 of 456,463,465,473,477,478,480,484,485,486,494,496,499)
Q7TQH0	1	681
Q7TQH0	1	686
Q7TQH0	1	687
Q7TSI3	1	(1 of 691,692,694,695,698,700,701,707,709,711,714,721,726)
Q7TT18	1	(1 of 753,755)
Q7TT18	1	(1 of 893,894,895,896,902,903,911,914,919)
Q7TT18	1	(1 of 758,761,762)
Q7TT18	1	1028
Q7TT18	1	1030
Q7TT18	1	1032
Q7TT18	1	749
Q7TT18	1	948
Q7TT18	1	955
Q80TG1	1	(1 of 759,760,761,762,764,765,766,768,769,770,772,777,778,779)
Q80TZ9	1	1230

Q80U72	1	936
Q80U78	1	(1 of 798,800,801,803,804,807,809,810,811,814,815,816)
Q80U93	1	(1 of 1559,1560,1562)
Q80U93	1	(1 of 645,646,648,651,652,655,656)
Q80U93	1	(1 of 1899,1900,1907,1908,1913,1914,1920)
Q80U93	1	(1 of 1569,1573,1576)
Q80U93	1	(1 of 585,589,590,595,596,597,598,599,601,606,607,608)
Q80U93	1	(1 of 1505,1506,1518,1520,1521,1524,1526,1527,1529,1536,1537,1540,1543,1544)
Q80U93	1	1152
Q80U93	1	513
Q80U93	1	1314
Q80U93	1	1091
Q80U93	1	516
Q80U93	1	1060
Q80U93	1	1574
Q80U93	1	1337
Q80U93	1	683
Q80U93	1	1167
Q80U93	1	1362
Q80U93	1	627
Q80U93	1	626
Q80U93	1	1557
Q80U93	1	504
Q80U93	1	1049
Q80U93	1	634
Q80U93	1	507
Q80VJ2	1	79
Q80VP1	1	(1 of 411,415,416,418,419,420)
Q80VP1	1	(1 of 500,506,511,514,516,526,528)
Q80WC3	1	283
Q80WC7	1	(1 of 186,188)
Q80WC7	1	(1 of 451,457,458,463,465,466,470,474,475)
Q80WC7	1	193
Q80X50	1	(1 of 449,464,465,466,474,478)
Q80X50	1	(1 of 665,667,669,670,671,672,675,679,684,687,688,693,694,695,697,700,702,708,709,710,711,714,715,718,719,723,725,726,727,728,729,730)
Q80X50	1	(1 of 642,643,647,651,652,654,659,661)
Q80X50	1	(1 of 388,400,402,404,405,406,407,408,409,414,415,416,418,420)
Q80X50	1	(1 of 280,282,285,286,295,297)
Q80X50	1	(1 of 311,313,314,319,320,325,329,337,339)
Q80X50	1	345
Q80X50	1	473
Q80X81	1	12

Q80Y98	1	478
Q80YA3	1	360
Q80YR4	1	(1 of 693,708,715,716,720,721,723,728,730,731,732,733,734,735,736,737,738,739)
Q80YR4	1	(1 of 560,563,564,568,569,575,578,579)
Q80Z38	1	1292
Q811P8	1	(1 of 1007,1010,1012,1016,1027,1028,1030)
Q811P8	1	(1 of 409,413)
Q8BFR4	1	(1 of 356,357)
Q8BFR4	1	(1 of 267,270,272,273)
Q8BFW7	1	(1 of 25,26,28,33,35,37,38)
Q8BFW7	1	11
Q8BFW7	1	212
Q8BFW7	1	195
Q8BG87	1	(1 of 495,496,497,503,506)
Q8BGD9	1	(1 of 340,348,350,351,352,354,355)
Q8BGD9	1	495
Q8BGS1	1	(1 of 385,386,387,398)
Q8BHL3	1	(1 of 32,43,44,46,47)
Q8BI72	1	315
Q8BI72	1	460
Q8BI84	1	633
Q8BI84	1	253
Q8BJ05	1	(1 of 369,370,373)
Q8BJ05	1	255
Q8BJM5	1	374
Q8BJM5	1	375
Q8BKI2	1	(1 of 1503,1504,1506,1508,1509,1512,1513,1516,1523,1525,1528,1530,1534,1535,1536)
Q8BL65	1	(1 of 278,279,280,282,285,289,290,291,292,294,296)
Q8BL65	1	363
Q8BL65	1	381
Q8BMB0	1	(1 of 226,228,231,232,234,235,237,238,239)
Q8BMB0	1	(1 of 465,466,468,470)
Q8BMB0	1	192
Q8BMB0	1	200
Q8BMB0	1	521
Q8BMB0	1	1069
Q8BMB0	1	499
Q8BMB0	1	1047
Q8BMB0	1	247
Q8BT14	1	316
Q8BTI8	1	(1 of 2254,2262,2264,2266,2268,2271,2277,2278,2279)
Q8BTI8	1	2245
Q8BTI8	1	2188

Q8BTI8	1	2414
Q8BTI8	1	2426
Q8BTI8	1	2205
Q8BTJ4	1	281
Q8BTJ4	1	261
Q8BU11	1	406
Q8BUV3	1	260
Q8BWW4	1	578
Q8BX02	1	346
Q8BYK6	1	(1 of 219,222)
Q8BYK6	1	201
Q8BYK6	1	205
Q8BYK6	1	229
Q8BYK6	1	167
Q8BYR2	1	(1 of 473,475,478,481,483,484,486,489)
Q8BZH4	1	(1 of 358,359,360)
Q8BZH4	1	(1 of 251,252,254,255,256,257,258,260,262,265,266,278,281,282)
Q8BZH4	1	297
Q8BZH4	1	426
Q8BZH4	1	431
Q8C052	1	(1 of 694,701,704,705,707,709,712,714,716,724,730,732)
Q8C0C0	1	(1 of 264,265)
Q8C0C0	1	159
Q8C0Q2	1	(1 of 227,236,239)
Q8C0Q2	1	730
Q8C0Q2	1	581
Q8C180	1	(1 of 326,327,328,329,330,331,333,339)
Q8C2Q3	1	256
Q8C2Q3	1	521
Q8C2Q3	1	244
Q8C2Q3	1	280
Q8C2Q3	1	254
Q8C5L3	1	(1 of 99,101,104,108,111)
Q8C5L3	1	(1 of 118,120,123)
Q8C5L3	1	128
Q8C5L3	1	114
Q8C5R2	1	390
Q8CBF3	1	(1 of 931,934,938,939,944,947,948,957)
Q8CDG3	1	1072
Q8CDG3	1	1075
Q8CDG3	1	1076
Q8CF89	1	393
Q8CFE4	1	(1 of 759,760,765)

Q8CFE4	1	(1 of 720,722,728,729,731,732,734,736,737)
Q8CFE4	1	(1 of 622,630,631,632,635)
Q8CFE4	1	741
Q8CG79	1	339
Q8CGA2	1	312
Q8CGA2	1	313
Q8CGA2	1	146
Q8CGA2	1	311
Q8CGB6	1	(1 of 899,901,902,905,908,909,913,914,915)
Q8CGB6	1	1008
Q8CGI1	1	(1 of 47,49,50,54)
Q8CGI1	1	709
Q8CGN4	1	(1 of 588,589,592,593,595,604,605,606)
Q8CGZ0	1	(1 of 363,373,378,382,383,397,398,402,403)
Q8CHC4	1	(1 of 1075,1080,1081,1084,1088)
Q8CHC4	1	1341
Q8CHI8	1	(1 of 695,698,699)
Q8CHI8	1	(1 of 1205,1208)
Q8CHI8	1	(1 of 2592,2594,2595,2596,2599)
Q8CHI8	1	2624
Q8CHI8	1	709
Q8CHI8	1	2662
Q8CHI8	1	2535
Q8CHI8	1	2607
Q8CHP6	1	(1 of 108,109,110,112,114,116,119,120,122,124,125,128,130)
Q8CHP6	1	238
Q8CHS8	1	174
Q8CHY6	1	(1 of 61,62,67,69)
Q8CHY6	1	(1 of 201,202,205,206,207,208)
Q8CHY6	1	(1 of 582,585,586,589,594,596)
Q8CHY6	1	178
Q8CHY6	1	621
Q8CHY6	1	179
Q8CHY6	1	325
Q8CI08	1	(1 of 480,484,486,488,491,492,495,497,498,499,500,509,515,516,520,522,524)
Q8CI51	1	(1 of 118,119,120,121)
Q8CI51	1	(1 of 308,309,313,318,319,322,325,327,332,335,336,339)
Q8CI51	1	115
Q8CI51	1	110
Q8CI51	1	111
Q8K0E8	1	(1 of 368,378)
Q8K0L9	1	(1 of 492,494,495,497,502,506,513,514,519)
Q8K0L9	1	480

Q8K0L9	1	449
Q8K0L9	1	268
Q8K0L9	1	465
Q8K0L9	1	436
Q8K0L9	1	473
Q8K0L9	1	447
Q8K1N2	1	(1 of 546,549,550,551)
Q8K212	1	(1 of 52,53,54,55,56,57,58,59,64,65,66,67,68,69,70,71,72,73,80,82)
Q8K2K6	1	291
Q8K2K6	1	362
Q8K2K6	1	300
Q8K2K6	1	302
Q8K2K6	1	367
Q8K3X4	1	(1 of 265,285,287,289,290,293,294,295,296,297,298)
Q8K3X4	1	(1 of 195,198,199,200,203,204,207)
Q8K3X4	1	159
Q8K3Z9	1	(1 of 713,715,719,720,721,722,725,726,728,729,730,731,735,738,739,740,742)
Q8K3Z9	1	(1 of 582,586,587,588,595,600)
Q8K3Z9	1	711
Q8K3Z9	1	653
Q8K3Z9	1	661
Q8K3Z9	1	631
Q8K3Z9	1	665
Q8K558	1	(1 of 244,247,250,253,255,256,261,262,269)
Q8QZR3	1	(1 of 272,277,282,284)
Q8QZR3	1	83
Q8R084	1	98
Q8R0X2	1	126
Q8R0X2	1	111
Q8R1S4	1	(1 of 319,320,322,323,326,330,336)
Q8R1S4	1	580
Q8R242	1	285
Q8R3B7	1	360
Q8R3E3	1	(1 of 389,390,391,394,395,400)
Q8R3L8	1	411
Q8R4I1	1	(1 of 689,690,696,697,698,699,700,701,702,703,704,705,706,707,708,710,713)
Q8R4R6	1	(1 of 295,296,297,303)
Q8R4Y4	1	1532
Q8VC97	1	(1 of 378,391,392)
Q8VCF0	1	(1 of 278,280)
Q8VCF0	1	(1 of 309,310)
Q8VCF0	1	(1 of 235,239,242,244,247,250,251,253,254,255,256,257,259)
Q8VCF0	1	330

Q8VCF0	1	298
Q8VCF0	1	273
Q8VCF0	1	370
Q8VCF0	1	307
Q8VCF0	1	373
Q8VCF0	1	215
Q8VCF0	1	315
Q8VCF0	1	222
Q8VCF0	1	319
Q8VDM6	1	730
Q8VEB4	1	288
Q8VFP9	1	(1 of 279,282,291)
Q8VHR5	1	(1 of 489,490)
Q8VHR5	1	(1 of 288,289,290,298,303,304,305,306)
Q8VHR5	1	585
Q8VHR5	1	498
Q8VHR5	1	495
Q8VI33	1	(1 of 206,207,208,217,221)
Q8VI33	1	202
Q8VIJ6	1	644
Q91VX2	1	(1 of 877,881)
Q91VX2	1	(1 of 386,392,393,399,401,405,406,414,419,422)
Q91VX2	1	(1 of 652,655,658,659,660,661)
Q91VX2	1	(1 of 631,632,634,638,642)
Q91VX2	1	1108
Q91VX2	1	469
Q91VX2	1	1018
Q91VX2	1	1020
Q91VX2	1	1117
Q91W39	1	(1 of 520,521)
Q91W39	1	(1 of 401,404,405,410,416,418,420,426,427)
Q91W39	1	524
Q91WT8	1	490
Q91WT8	1	523
Q91WT8	1	508
Q91X51	1	(1 of 216,220,223,224,225,228,244,245,251)
Q91XD6	1	137
Q91XT4	1	804
Q91XT4	1	78
Q91YD3	1	399
Q91Z96	1	(1 of 375,376,379,380,381,384,387,388,390)
Q922J3	1	(1 of 144,146,149,150,154,157,158,159,162,164,171,173,174)
Q922Y1	1	192

Q924A2	1	1785
Q924A2	1	1034
Q924A2	1	772
Q924A2	1	2044
Q925J9	1	(1 of 996,998,1000)
Q925J9	1	(1 of 1261,1265,1267,1269,1271,1272,1273,1274,1276,1277,1278,1280,1281,1283,1284,1285,1291,1292)
Q99JX3	1	(1 of 432,435,443,448,451)
Q99JX3	1	425
Q99JX3	1	426
Q99JX3	1	417
Q99K90	1	456
Q99KG3	1	(1 of 510,514,515,518,519,521,523,525,527,530)
Q99KN9	1	(1 of 316,319,320)
Q99KN9	1	328
Q99KN9	1	630
Q99KP6	1	(1 of 133,148,149,152,169)
Q99LI5	1	(1 of 861,862,864,867,870,874,877,881,882)
Q99LI5	1	889
Q99LI8	1	(1 of 299,300,306,309,310,314,315)
Q99LI8	1	295
Q99MZ3	1	522
Q99NG0	2	(2 of 1072,1073,1074,1083,1084,1085)
Q99PP2	1	(1 of 1353,1358,1359,1362,1366,1367,1368,1369,1371)
Q9CS72	1	(1 of 1127,1128,1129,1131,1133,1136,1137,1138,1139,1140)
Q9CS74	1	640
Q9CWK8	1	(1 of 93,94,97,101,104,106,107)
Q9CX80	1	(1 of 180,187,188)
Q9CZN7	2	(2 of 184,186,187,192)
Q9D1J3	1	186
Q9D1J3	1	115
Q9D1M0	1	315
Q9D2H6	1	(1 of 357,359,364,370,374,377,378,379,380,382,385)
Q9D2H6	1	(1 of 186,187,188,189,190,191,195)
Q9D4H9	1	(1 of 132,134,136,140,144,145,148,149,154,155,157,160,161,162,163,164,165,166,171)
Q9D787	1	(1 of 493,499,500,501,502,504,506)
Q9D7N9	1	161
Q9D824	1	229
Q9D824	1	228
Q9D824	1	204
Q9D824	1	205
Q9DB43	1	165
Q9DBF1	1	(1 of 476,487,488)
Q9DBG5	1	(1 of 126,127)

Q9DBG5	1	(1 of 152,158,165)
Q9DBG5	1	128
Q9DBG5	1	72
Q9DBG5	1	76
Q9DBR7	1	(1 of 625,628,631)
Q9DBR7	1	(1 of 645,646,647,648,650)
Q9DBR7	1	(1 of 399,401,402)
Q9DBR7	1	(1 of 564,566,569,570,572,573,575,577,578)
Q9DBR7	1	379
Q9DBR7	1	381
Q9DBR7	1	571
Q9DBR7	1	637
Q9DC28	1	382
Q9DCS9	1	25
Q9DCT8	1	(1 of 74,82,88)
Q9EQC8	1	228
Q9ERG0	1	(1 of 324,325,326,329,334,341,344)
Q9ERU9	1	(1 of 2317,2320,2328,2329,2330,2335,2336,2337,2338,2339,2341,2342)
Q9ERU9	1	(1 of 1304,1306,1307,1308,1313)
Q9ERU9	1	(1 of 1038,1044,1046,1047,1056,1057,1060,1062,1064,1070,1071,1081,1087,1091,1093)
Q9ERU9	1	1138
Q9ET54	1	(1 of 767,769,770,771,773,774,775,776)
Q9ET54	1	763
Q9JHC9	1	(1 of 499,502,507)
Q9JHC9	1	(1 of 372,374,375)
Q9JHC9	1	380
Q9JHE7	1	(1 of 107,111,112,114,118)
Q9JI46	1	(1 of 153,158,159,161,162,163,165)
Q9JKR6	1	(1 of 580,582,583,589,590,591,598,607,612,633,634,639)
Q9JKR6	1	(1 of 513,517,518)
Q9JKR6	1	933
Q9JKV1	1	221
Q9JKV1	1	220
Q9JKV1	1	213
Q9JL19	1	(1 of 1742,1748,1752,1753,1754,1762)
Q9JL19	1	(1 of 1234,1235,1238)
Q9JL19	1	(1 of 1712,1713,1717,1722,1723,1724,1731,1738,1739)
Q9JL19	1	1243
Q9JL19	1	1644
Q9JLV1	1	(1 of 162,163)
Q9JLV1	1	320
Q9JLV1	1	170
Q9JLV1	1	372

Q9JLV1	1	183
Q9JLV1	1	188
Q9QXD8	1	(1 of 105,112,113,114,120,123)
Q9QXE0	1	(1 of 71,77)
Q9QXE7	1	123
Q9QY76	1	144
Q9QYC0	1	542
Q9QYE6	1	158
Q9QYG0	1	370
Q9QYS9	1	(1 of 211,217,221)
Q9QYY0	1	322
Q9QZM0	3	(2 of 104,113,114,117,118,119,122,123,124,125,126,127,128,129,130,131,139,140,141)&(3 of 113,114,117,118,119,122,123,124,125,126,127,128,129,130,131)
Q9QZM0	1	138
Q9R013	1	(1 of 358,362)
Q9R013	1	(1 of 105,109)
Q9R0N4	1	469
Q9R1E0	1	(1 of 644,645,646,648,651)
Q9WTN3	1	250
Q9WU42	1	(1 of 1778,1781,1782,1783,1784,1785,1796,1799,1800,1805,1806)
Q9WU42	1	1843
Q9WU42	1	1532
Q9WU42	1	1844
Q9WU42	1	1531
Q9WUM3	1	421
Q9WUU8	1	(1 of 103,104,105,108,109,110,112,114,115,118,126)
Q9WUU9	1	18
Q9WV30	1	(1 of 674,676,677,680,684,688,693,696,700,701,709,713)
Q9WV54	1	(1 of 254,259,260,261)
Q9WV69	1	(1 of 105,113,114)
Q9WV69	1	(1 of 284,285)
Q9WV69	1	(1 of 10,11,14,16,17,18)
Q9WV69	1	110
Q9WVJ3	1	396
Q9Z0M5	1	321
Q9Z0M5	1	153
Q9Z0R6	1	217
Q9Z0U1	1	(1 of 441,442,446,451,454)
Q9Z0U1	1	999
Q9Z103	1	412
Q9Z1A1	1	(1 of 122,132,133,134,140,151,153,154)
Q9Z1A1	1	373
Q9Z2D6	1	441

Q9Z2D6	1	434
S4R2A9	1	(1 of 90,91,92,101,114,118)
S4R2A9	1	499
S4R2A9	1	500
S4R2A9	1	542
S4R2A9	1	543
S4R2J9	1	(1 of 2280,2281,2282,2283,2284)
S4R2J9	1	(1 of 202,203,206,207)
S4R2J9	1	2146
S4R2J9	1	2630
S4R2J9	1	1931
S4R2J9	1	2188
S4R2J9	1	2635
S4R2J9	1	880
S4R2J9	1	2193
S4R2J9	1	2419
S4R2J9	1	2138
S4R2J9	1	2171
V9GXJ1	1	(1 of 130,132,135,137,138,139,143)
V9GXT3	1	(1 of 1452,1454,1461,1463,1465,1468,1469,1471,1472,1474,1475,1477,1479)
V9GXT3	1	1223
Z4YJT3	1	273

Appendix 5.6. Python and R Code for All Analyses.

All code was run in Jupyter notebook (v7.12). Also see **5.9. Experimental Methods**.

A5.6.1. Pre-Processing of Proteome Discoverer Output.

```
#import python packages
import re
import sys
import pandas as pd
import networkx as nx
import itertools as it
from collections import namedtuple
import numpy as np
import matplotlib
import matplotlib.pyplot as plt
from IPython.display import display
from functools import reduce
import seaborn as sns; sns.set()
from io import StringIO
from matplotlib_venn import venn2_unweighted #the unweighted is if you want to make circles that are the same size
from matplotlib_venn import venn2 #also import the normal one

#set up R environment and import R packages
import rpy2
import rpy2.ipython
%load_ext rpy2.ipython

#require R packages
%R require(limma)
%R require(ibb)

#magic function to show plots inline
%matplotlib inline
#import the proteins files from each of the 293T, brain, and liver PD searches

#list the filenames
fname0 = './293T_Interactome_Full/293T_Interactome_Repeat_Full_100-(2)_Proteins.txt'
fname1 = './293T_Interactome_SwissProt/293T_Interactome_Repeat_SwissProt_100-(3)_Proteins.txt'
fname2 = './Brain_Interactome_Full/Brain_Interactome_Full-(1)_Proteins.txt'
fname3 = './Brain_Interactome_SwissProt/Brain_Interactome_SwissProt-(2)_Proteins.txt'
fname4 = './Liver_Interactome_Full/Liver_Interactome_Full-(1)_Proteins.txt'
fname5 = './Liver_Interactome_SwissProt/Liver_Interactome_SwissProt-(1)_Proteins.txt'
fname6 = './LiverBrain_Interactome_Full/LiverBrain_Interactome_Full_Proteins.txt'
fname7 = './LiverBrain_Interactome_SwissProt/LiverBrain_Interactome_SwissProt_Proteins.txt'
fnames = [fname0, fname1, fname2, fname3, fname4, fname5, fname6, fname7] #concatenate into a single list

#import all of the files into dfs

#make lists for for loop
list_exp = ['293TF', '293TSP', 'BrainF', 'BrainSP', 'LiverF', 'LiverSP', 'LiverBrainF', 'LiverBrainSP']

#define all the dfs in a for loop
for i in range(8):
    locals()['df{}'.format(list_exp[i])] = pd.read_csv(fnames[i], sep='\t')


#set only these columns to keep
cols_to_keep = ['Accession', 'Description', 'Abundance Ratios log2 by Bio Rep SampleTrial 1  ControlTrial 1',
                'Abundance Ratios log2 by Bio Rep SampleTrial 2  ControlTrial 2',
                'Abundance Ratios log2 by Bio Rep SampleTrial 3  ControlTrial 3']

cols_to_keep2 = ['Accession', 'Description', 'Abundance Ratio log2 F1 Medium  F1 Light',
                 'Abundance Ratio log2 F2 Medium  F2 Light', 'Abundance Ratio log2 F3 Medium  F3 Light',
                 'Abundance Ratio log2 F4 Medium  F4 Light', 'Abundance Ratio log2 F5 Medium  F5 Light',
                 'Abundance Ratio log2 F6 Medium  F6 Light']

#make a list for these new dfs
list_df = ['293Full', '293SwissProt', 'BrainFull', 'BrainSwissProt', 'LiverFull', 'LiverSwissProt', 'LiverBrainFull',
           'LiverBrainSwissProt']

#use a for loop to get the relevant info from the first 6 dfs (also remove contaminant proteins)
#also get gene symbols from fasta lines and make all caps
#remove all IgGs and only keep proteins identified with 'High' confidence

for i in range(6):
    locals()['df{}'.format(list_df[i])] = \
    locals()['df{}'.format(list_exp[i])][locals()['df{}'.format(list_exp[i])].Contaminant == False]
    locals()['df{}'.format(list_df[i])] = \
    locals()['df{}'.format(list_exp[i])][locals()['df{}'.format(list_exp[i])]['Protein FDR Confidence Combined'] == 'High']
    locals()['df{}'.format(list_df[i])] = locals()['df{}'.format(list_df[i])][~locals()['df{}'.format(list_df[i])].\
                                          Description.str.contains('contaminant')]
    locals()['df{}'.format(list_df[i])] = locals()['df{}'.format(list_df[i])][~locals()['df{}'.format(list_df[i])].\
```

```
                                                Description.str.contains('Immunoglobulin')]
    locals()['df{}'.format(list_df[i])] = locals()['df{}'.format(list_df[i])][~locals()['df{}'.format(list_df[i])].\
                                                Description.str.contains('Ig ')]
    locals()['df{}'.format(list_df[i])] = locals()['df{}'.format(list_df[i])][cols_to_keep]
    locals()['df{}'.format(list_df[i])]['Gene'] = \
    locals()['df{}'.format(list_df[i])]['Description'].str.extract('GN=(.*) PE=')
    locals()['df{}'.format(list_df[i])].Gene = locals()['df{}'.format(list_df[i])].Gene.str.upper()

#do the same for the remaining 2 (liver and brain combined)
for i in range(6,8):
    locals()['df{}'.format(list_df[i])] = \
    locals()['df{}'.format(list_exp[i])][locals()['df{}'.format(list_exp[i])].Contaminant == False]
    locals()['df{}'.format(list_df[i])] = \
    locals()['df{}'.format(list_exp[i])][locals()['df{}'.format(list_exp[i])]['Protein FDR Confidence Combined'] == 'High']
    locals()['df{}'.format(list_df[i])] = locals()['df{}'.format(list_df[i])][~locals()['df{}'.format(list_df[i])].\
                                                Description.str.contains('contaminant')]
    locals()['df{}'.format(list_df[i])] = locals()['df{}'.format(list_df[i])][~locals()['df{}'.format(list_df[i])].\
                                                Description.str.contains('Immunoglobulin')]
    locals()['df{}'.format(list_df[i])] = locals()['df{}'.format(list_df[i])][~locals()['df{}'.format(list_df[i])].\
                                                Description.str.contains('Ig ')]
    locals()['df{}'.format(list_df[i])] = locals()['df{}'.format(list_df[i])][cols_to_keep2]
    locals()['df{}'.format(list_df[i])]['Gene'] = \
    locals()['df{}'.format(list_df[i])]['Description'].str.extract('GN=(.*) PE=')
    locals()['df{}'.format(list_df[i])].Gene = locals()['df{}'.format(list_df[i])].Gene.str.upper()
#now we need to count the heavy and ligth PSMs for each of the trials and add to the df

#make new dfs for the PSMs file as before
f0 = './293T_Interactome_Full/293T_Interactome_Repeat_Full_100-(2)_PSMs.txt'
f1 = './293T_Interactome_SwissProt/293T_Interactome_Repeat_SwissProt_100-(3)_PSMs.txt'
f2 = './Brain_Interactome_Full/Brain_Interactome_Full-(1)_PSMs.txt'
f3 = './Brain_Interactome_SwissProt/Brain_Interactome_SwissProt-(2)_PSMs.txt'
f4 = './Liver_Interactome_Full/Liver_Interactome_Full-(1)_PSMs.txt'
f5 = './Liver_Interactome_SwissProt/Liver_Interactome_SwissProt-(1)_PSMs.txt'
f6 = './LiverBrain_Interactome_Full/LiverBrain_Interactome_Full_PSMs.txt'
f7 = './LiverBrain_Interactome_SwissProt/LiverBrain_Interactome_SwissProt_PSMs.txt'
fnames_psm = [f0, f1, f2, f3, f4, f5, f6, f7]
list_exp2 = ['PSM293TF', 'PSM293TSP', 'PSMBrainF', 'PSMBrainSP', 'PSMLiverF', 'PSMLiverSP', 'PSMLiverBrainF',
         'PSMLiverBrainSP']
for i in range(8):
    locals()['df{}'.format(list_exp2[i])] = pd.read_csv(fnames_psm[i], sep='\t')

#for the 293T files group the samples from the same trial but different runs together
dfPSM293TF.loc[dfPSM293TF['File ID'] == 'F7', 'File ID'] = 'F1'
dfPSM293TF.loc[dfPSM293TF['File ID'] == 'F8', 'File ID'] = 'F1'
dfPSM293TF.loc[dfPSM293TF['File ID'] == 'F9', 'File ID'] = 'F2'
dfPSM293TF.loc[dfPSM293TF['File ID'] == 'F10', 'File ID'] = 'F2'
dfPSM293TF.loc[dfPSM293TF['File ID'] == 'F11', 'File ID'] = 'F3'
dfPSM293TF.loc[dfPSM293TF['File ID'] == 'F12', 'File ID'] = 'F3'
dfPSM293TSP.loc[dfPSM293TSP['File ID'] == 'F7', 'File ID'] = 'F1'
dfPSM293TSP.loc[dfPSM293TSP['File ID'] == 'F8', 'File ID'] = 'F1'
dfPSM293TSP.loc[dfPSM293TSP['File ID'] == 'F9', 'File ID'] = 'F2'
dfPSM293TSP.loc[dfPSM293TSP['File ID'] == 'F10', 'File ID'] = 'F2'
dfPSM293TSP.loc[dfPSM293TSP['File ID'] == 'F11', 'File ID'] = 'F3'
dfPSM293TSP.loc[dfPSM293TSP['File ID'] == 'F12', 'File ID'] = 'F3'

#name dfs
list_df2 = ['m293Full', 'm293SP', 'mBranFull', 'mBrainSP', 'mLiverFull', 'mLiverSP', 'mLiverBrainFull', 'mLiverBrainSP']

#now use a for loop to count up the PSMS for each protein, file, and byonic node
#then split the dfs by node and rename the counts column
#merge the dfs with H and L counts
#first do this for all the individual ones (since there are additional nodes in the LiverBrain combined file)
for i in range(6):
    locals()['dfpsm{}'.format(i)] = \
    locals()['df{}'.format(list_exp2[i])].groupby(
        ['Identifying Node No', 'Master Protein Accessions', 'File ID']).size().reset_index(name='Counts')
    dfs = [locals()['df{}'.format(list_df[i])]]
    for j in range(3):
        locals()['dfH{}psm{}'.format(j+1, i)] = \
        locals()['dfpsm{}'.format(i)][(locals()['dfpsm{}'.format(i)]['Identifying Node No'] == 2) & \
                                      (locals()['dfpsm{}'.format(i)]['File ID'] == ('F' + str(j+1)))]
        locals()['dfL{}psm{}'.format(j+1, i)] = \
        locals()['dfpsm{}'.format(i)][(locals()['dfpsm{}'.format(i)]['Identifying Node No'] == 7) & \
                                      (locals()['dfpsm{}'.format(i)]['File ID'] == ('F' + str(j+1)))]
        locals()['dfH{}psm{}'.format(j+1, i)].rename(columns={'Counts':'H{}Counts'.format(j+1),
                                            'Master Protein Accessions':'Accession'}, inplace=True)
        locals()['dfL{}psm{}'.format(j+1, i)].rename(columns={'Counts':'L{}Counts'.format(j+1),
                                            'Master Protein Accessions':'Accession'}, inplace=True)
        dfs.append(locals()['dfL{}psm{}'.format(j+1, i)])
        dfs.append(locals()['dfH{}psm{}'.format(j+1, i)])
    locals()['df{}'.format(list_df2[i])] = reduce(lambda left,right: pd.merge(left, right, on='Accession', how='left'),
                                      dfs).fillna(0)
    locals()['df{}'.format(list_df2[i])] = \
    locals()['df{}'.format(list_df2[i])].loc[:, ~locals()['df{}'.format(list_df2[i])].columns.str.contains('_')]

#now repeat the above for the combined
for i in range(6,8):
    locals()['dfpsm{}'.format(i)] = \
    locals()['df{}'.format(list_exp2[i])].groupby(
        ['Identifying Node No', 'Master Protein Accessions', 'File ID']).size().reset_index(name='Counts')
    dfs2 = [locals()['df{}'.format(list_df[i])]]
    for j in range(3):
        locals()['dfLiverH{}psm{}'.format(j+1, i)] = \
```

```
        locals()['dfpsm{}'.format(i)][(locals()['dfpsm{}'.format(i)]['Identifying Node No'] == 2) & \
                                      (locals()['dfpsm{}'.format(i)]['File ID'] == ('F' + str(j+4)))]
        locals()['dfLiverL{}psm{}'.format(j+1, i)] = \
        locals()['dfpsm{}'.format(i)][(locals()['dfpsm{}'.format(i)]['Identifying Node No'] == 7) & \
                                      (locals()['dfpsm{}'.format(i)]['File ID'] == ('F' + str(j+4)))]
        locals()['dfLiverH{}psm{}'.format(j+1, i)].rename(columns={'Counts':'H{}CountsHep'.format(j+1),
                                                'Master Protein Accessions':'Accession'}, inplace=True)
        locals()['dfLiverL{}psm{}'.format(j+1, i)].rename(columns={'Counts':'L{}CountsHep'.format(j+1),
                                                'Master Protein Accessions':'Accession'}, inplace=True)
        dfs2.append(locals()['dfLiverL{}psm{}'.format(j+1, i)])
        dfs2.append(locals()['dfLiverH{}psm{}'.format(j+1, i)])
    for k in range(3,6):
        locals()['dfBrainH{}psm{}'.format(k-2, i)] = \
        locals()['dfpsm{}'.format(i)][(locals()['dfpsm{}'.format(i)]['Identifying Node No'] == 11) & \
                                      (locals()['dfpsm{}'.format(i)]['File ID'] == ('F' + str(k-2)))]
        locals()['dfBrainL{}psm{}'.format(k-2, i)] = \
        locals()['dfpsm{}'.format(i)][(locals()['dfpsm{}'.format(i)]['Identifying Node No'] == 10) & \
                                      (locals()['dfpsm{}'.format(i)]['File ID'] == ('F' + str(k-2)))]
        locals()['dfBrainH{}psm{}'.format(k-2, i)].rename(columns={'Counts':'H{}CountsBrain'.format(k-2),
                                                'Master Protein Accessions':'Accession'}, inplace=True)
        locals()['dfBrainL{}psm{}'.format(k-2, i)].rename(columns={'Counts':'L{}CountsBrain'.format(k-2),
                                                'Master Protein Accessions':'Accession'}, inplace=True)
        dfs2.append(locals()['dfBrainL{}psm{}'.format(k-2, i)])
        dfs2.append(locals()['dfBrainH{}psm{}'.format(k-2, i)])
    locals()['df{}'.format(list_df2[i])] = reduce(lambda left,right: pd.merge(left, right, on='Accession', how='left'),
                                          dfs2).fillna(0)
    locals()['df{}'.format(list_df2[i])] = \
    locals()['df{}'.format(list_df2[i])].loc[:, ~locals()['df{}'.format(list_df2[i])].columns.str.contains('_')]


#make separate dfs for import into R (reading into R directly from pandas can be problematic) and export to txt

list_df3 = ['293Fsc', '293SPsc', 'BrainFsc', 'BrainSPsc', 'LiverFsc', 'LiverSPsc', 'LiverBrainFsc', 'LiverBrainSPsc']
list_df4 = ['293Fr', '293SPr', 'BrainFr', 'BrainSPr', 'LiverFr', 'LiverSPr', 'LiverBrainFr', 'LiverBrainSPr']

#first for the individual ones
for i in range(6):
    locals()['df{}'.format(list_df3[i])] = locals()['df{}'.format(list_df2[i])].iloc[:,-6:]
    locals()['df{}'.format(list_df3[i])].to_csv('df{}.txt'.format(list_df3[i]), sep='\t')
    locals()['df{}'.format(list_df4[i])] = locals()['df{}'.format(list_df2[i])].iloc[:,2:5]
    locals()['df{}'.format(list_df4[i])].to_csv('df{}.txt'.format(list_df4[i]), sep='\t')

#then for the combined ones
#first, split into separate dfs for liver and brain

list_split = ['Hep', 'Brain'] #using Hep so can search for 'L' and 'H' to find H/L counts in ibb script

#first output the spectral counts
for i in range(6,8):
    for j in list_split:
        locals()['df{}_{}'.format(list_df3[i], j)] = \
        locals()['df{}'.format(list_df2[i])].iloc[:,locals()['df{}'.format(list_df2[i])].columns.str.contains(
            '{}'.format(j))]
        locals()['df{}_{}'.format(list_df3[i], j)].to_csv('df{}_{}.txt'.format(list_df3[i], j), sep='\t')

#now output the ratios
for i in range(6,8):
    locals()['df{}_Liver'.format(list_df4[i])] = \
    locals()['df{}'.format(list_df2[i])].iloc[:, (
        locals()['df{}'.format(list_df2[i])].columns.str.contains('F4') |
        locals()['df{}'.format(list_df2[i])].columns.str.contains('F5') |
        locals()['df{}'.format(list_df2[i])].columns.str.contains('F6'))]
    locals()['df{}_Brain'.format(list_df4[i])] = \
    locals()['df{}'.format(list_df2[i])].iloc[:, (
        locals()['df{}'.format(list_df2[i])].columns.str.contains('F1') |
        locals()['df{}'.format(list_df2[i])].columns.str.contains('F2') |
        locals()['df{}'.format(list_df2[i])].columns.str.contains('F3'))]
    locals()['df{}_Liver'.format(list_df4[i])].to_csv('df{}_Liver.txt'.format(list_df4[i]), sep='\t')
    locals()['df{}_Brain'.format(list_df4[i])].to_csv('df{}_Brain.txt'.format(list_df4[i]), sep='\t')

%%R

#now we can calculate the p-values from limma in R
#limma is well-documented by bioconductor
#do not need to re-run this cell with the rest of the notebook after saving output

library(limma) #load the package

#read in the files
df1 = read.table("df293Fr.txt",sep="\t",header=TRUE,row.names=1)
df2 = read.table("df293SPr.txt",sep="\t",header=TRUE,row.names=1)
df3 = read.table("dfBrainFr.txt",sep="\t",header=TRUE,row.names=1)
df4 = read.table("dfBrainSPr.txt",sep="\t",header=TRUE,row.names=1)
df5 = read.table("dfLiverFr.txt",sep="\t",header=TRUE,row.names=1)
df6 = read.table("dfLiverSPr.txt",sep="\t",header=TRUE,row.names=1)
df7 = read.table("dfLiverBrainFr_Liver.txt",sep="\t",header=TRUE,row.names=1)
df8 = read.table("dfLiverBrainSPr_Liver.txt",sep="\t",header=TRUE,row.names=1)
df9 = read.table("dfLiverBrainFr_Brain.txt",sep="\t",header=TRUE,row.names=1)
df10 = read.table("dfLiverBrainSPr_Brain.txt",sep="\t",header=TRUE,row.names=1)

#perform limma
f1 = eBayes(lmFit(df1))
f2 = eBayes(lmFit(df2))
```

```
f3 = eBayes(lmFit(df3))
f4 = eBayes(lmFit(df4))
f5 = eBayes(lmFit(df5))
f6 = eBayes(lmFit(df6))
f7 = eBayes(lmFit(df7))
f8 = eBayes(lmFit(df8))
f9 = eBayes(lmFit(df9))
f10 = eBayes(lmFit(df10))

#write the tables
write.table(topTable(f1,n=Inf,confint=.95),"limmaOut_df293F.txt",sep="\t")
write.table(topTable(f2,n=Inf,confint=.95),"limmaOut_df293SP.txt",sep="\t")
write.table(topTable(f3,n=Inf,confint=.95),"limmaOut_dfBrainF.txt",sep="\t")
write.table(topTable(f4,n=Inf,confint=.95),"limmaOut_dfBrainSP.txt",sep="\t")
write.table(topTable(f5,n=Inf,confint=.95),"limmaOut_dfLiverF.txt",sep="\t")
write.table(topTable(f6,n=Inf,confint=.95),"limmaOut_dfLiverSP.txt",sep="\t")
write.table(topTable(f7,n=Inf,confint=.95),"limmaOut_dfLiverBrainF_Liver.txt",sep="\t")
write.table(topTable(f8,n=Inf,confint=.95),"limmaOut_dfLiverBrainSP_Liver.txt",sep="\t")
write.table(topTable(f9,n=Inf,confint=.95),"limmaOut_dfLiverBrainF_Brain.txt",sep="\t")
write.table(topTable(f10,n=Inf,confint=.95),"limmaOut_dfLiverBrainSP_Brain.txt",sep="\t")
%%R

#calculate the p-values from the ibb test in R
#this is an unsupported package
#see the documentation here: http://oncoproteomics.nl/statistical-analysis-of-count-data/
#do not need to re-run this cell with the rest of the notebook after saving output (it takes several hours)

library(ibb) #load the package

#read in the tables
df1 = read.table("df293Fsc.txt", header = TRUE, row.names = 1, sep="\t")
df2 = read.table("df293SPsc.txt", header = TRUE, row.names = 1, sep="\t")
df3 = read.table("dfBrainFsc.txt", header = TRUE, row.names = 1, sep="\t")
df4 = read.table("dfBrainSPsc.txt", header = TRUE, row.names = 1, sep="\t")
df5 = read.table("dfLiverFsc.txt", header = TRUE, row.names = 1, sep="\t")
df6 = read.table("dfLiverSPsc.txt", header = TRUE, row.names = 1, sep="\t")
df7 = read.table("dfLiverBrainFsc_Hep.txt", header = TRUE, row.names = 1, sep="\t")
df8 = read.table("dfLiverBrainSPsc_Hep.txt", header = TRUE, row.names = 1, sep="\t")
df9 = read.table("dfLiverBrainFsc_Brain.txt", header = TRUE, row.names = 1, sep="\t")
df10 = read.table("dfLiverBrainSPsc_Brain.txt", header = TRUE, row.names = 1, sep="\t")

#vector of group indicators, light and heavy are each replicated three times as alternating L and H
#i.e. this sets the groups as alternating just like in the file
g1 = rep(c("L","H"),3)
g2 = rep(c("L","H"),3)
g3 = rep(c("L","H"),3)
g4 = rep(c("L","H"),3)
g5 = rep(c("L","H"),3)
g6 = rep(c("L","H"),3)
g7 = rep(c("L","H"),3)
g8 = rep(c("L","H"),3)
g9 = rep(c("L","H"),3)
g10 = rep(c("L","H"),3)

#make a matrix by counting all the rows in each column
tx1 = colSums(df1)
tx2 = colSums(df2)
tx3 = colSums(df3)
tx4 = colSums(df4)
tx5 = colSums(df5)
tx6 = colSums(df6)
tx7 = colSums(df7)
tx8 = colSums(df8)
tx9 = colSums(df9)
tx10 = colSums(df10)

#now set the matrix of total sample counts as the average of both L and H rows (6 total columns)
#this is the total sample counts for each condition to be used by the ibb test
tx1 = c((tx1[1]+tx1[2])/2,(tx1[1]+tx1[2])/2,(tx1[3]+tx1[4])/2,(tx1[3]+tx1[4])/2,(tx1[5]+tx1[6])/2,(tx1[5]+tx1[6])/2)
tx2 = c((tx2[1]+tx2[2])/2,(tx2[1]+tx2[2])/2,(tx2[3]+tx2[4])/2,(tx2[3]+tx2[4])/2,(tx2[5]+tx2[6])/2,(tx2[5]+tx2[6])/2)
tx3 = c((tx3[1]+tx3[2])/2,(tx3[1]+tx3[2])/2,(tx3[3]+tx3[4])/2,(tx3[3]+tx3[4])/2,(tx3[5]+tx3[6])/2,(tx3[5]+tx3[6])/2)
tx4 = c((tx4[1]+tx4[2])/2,(tx4[1]+tx4[2])/2,(tx4[3]+tx4[4])/2,(tx4[3]+tx4[4])/2,(tx4[5]+tx4[6])/2,(tx4[5]+tx4[6])/2)
tx5 = c((tx5[1]+tx5[2])/2,(tx5[1]+tx5[2])/2,(tx5[3]+tx5[4])/2,(tx5[3]+tx5[4])/2,(tx5[5]+tx5[6])/2,(tx5[5]+tx5[6])/2)
tx6 = c((tx6[1]+tx6[2])/2,(tx6[1]+tx6[2])/2,(tx6[3]+tx6[4])/2,(tx6[3]+tx6[4])/2,(tx6[5]+tx6[6])/2,(tx6[5]+tx6[6])/2)
tx7 = c((tx7[1]+tx7[2])/2,(tx7[1]+tx7[2])/2,(tx7[3]+tx7[4])/2,(tx7[3]+tx7[4])/2,(tx7[5]+tx7[6])/2,(tx7[5]+tx7[6])/2)
tx8 = c((tx8[1]+tx8[2])/2,(tx8[1]+tx8[2])/2,(tx8[3]+tx8[4])/2,(tx8[3]+tx8[4])/2,(tx8[5]+tx8[6])/2,(tx8[5]+tx8[6])/2)
tx9 = c((tx9[1]+tx9[2])/2,(tx9[1]+tx9[2])/2,(tx9[3]+tx9[4])/2,(tx9[3]+tx9[4])/2,(tx9[5]+tx9[6])/2,(tx9[5]+tx9[6])/2)
tx10 = c((tx10[1]+tx10[2])/2,(tx10[1]+tx10[2])/2,(tx10[3]+tx10[4])/2,(tx10[3]+tx10[4])/2,(tx10[5]+tx10[6])/2,
        (tx10[5]+tx10[6])/2)


#run the ibb test with 8 threads, one sample t-test that there are less spectral counts in the L
# see also, http://oncoproteomics.nl/statistical-analysis-of-count-data/
# Note that this calculation takes a long time
out1 = ibb.test(df1, tx1, g1, alternative = "less", n.threads=8)
out2 = ibb.test(df2, tx2, g2, alternative = "less", n.threads=8)
out3 = ibb.test(df3, tx3, g3, alternative = "less", n.threads=8)
out4 = ibb.test(df4, tx4, g4, alternative = "less", n.threads=8)
out5 = ibb.test(df5, tx5, g5, alternative = "less", n.threads=8)
out6 = ibb.test(df6, tx6, g6, alternative = "less", n.threads=8)
out7 = ibb.test(df7, tx7, g7, alternative = "less", n.threads=8)
out8 = ibb.test(df8, tx8, g8, alternative = "less", n.threads=8)
out9 = ibb.test(df9, tx9, g9, alternative = "less", n.threads=8)
```

```
out10 = ibb.test(df10, tx10, g10, alternative = "less", n.threads=8)

#write this to a table
write.table(cbind(df1,out1$fc,out1$p.value,p.adjust(out1$p.value,"BH")),"ibbOut_293F.txt",sep="\t",row.names=TRUE)
write.table(cbind(df2,out2$fc,out2$p.value,p.adjust(out2$p.value,"BH")),"ibbOut_293SP.txt",sep="\t",row.names=TRUE)
write.table(cbind(df3,out3$fc,out3$p.value,p.adjust(out3$p.value,"BH")),"ibbOut_BrainF.txt",sep="\t",row.names=TRUE)
write.table(cbind(df4,out4$fc,out4$p.value,p.adjust(out4$p.value,"BH")),"ibbOut_BrainSP.txt",sep="\t",row.names=TRUE)
write.table(cbind(df5,out5$fc,out5$p.value,p.adjust(out5$p.value,"BH")),"ibbOut_LiverF.txt",sep="\t",row.names=TRUE)
write.table(cbind(df6,out6$fc,out6$p.value,p.adjust(out6$p.value,"BH")),"ibbOut_LiverSP.txt",sep="\t",row.names=TRUE)
write.table(cbind(df7,out7$fc,out7$p.value,p.adjust(out7$p.value,"BH")),"ibbOut_LiverBrainF_Hep.txt",sep="\t",row.names=TRUE)
write.table(cbind(df8,out8$fc,out8$p.value,p.adjust(out8$p.value,"BH")),
          "ibbOut_LiverBrainSP_Hep.txt",sep="\t",row.names=TRUE)
write.table(cbind(df9,out9$fc,out9$p.value,p.adjust(out9$p.value,"BH")),
          "ibbOut_LiverBrainF_Brain.txt",sep="\t",row.names=TRUE)
write.table(cbind(df10,out10$fc,out10$p.value,p.adjust(out10$p.value,"BH")),
          "ibbOut_LiverBrainSP_Brain.txt",sep="\t",row.names=TRUE)
#now I will import the results of the limma and ibb analysis and reform the data frames with the p values

#list the fnames
fname_list = ['293F', '293SP', 'BrainF', 'BrainSP', 'LiverF', 'LiverSP', 'LiverBrainF', 'LiverBrainSP']
final_df_list = ['293TFull', '293TSP', 'BrainFull', 'BrainSP', 'LiverFull', 'LiverSP', 'LiverBrainFull', 'LiverBrainSP']
list_split2 = ['Liver', 'Brain']

#use a for loop to import all the dfs, then only keep the index and the last column, finally merge everything and keep only
   # relevant columns (and rename)
#first for the first 6
for i in range(6):
   locals()['df_limma_{}'.format(fname_list[i])] = pd.read_csv('limmaOut_df{}.txt'.format(fname_list[i]), sep='\t')
   locals()['df_ibb_{}'.format(fname_list[i])] = pd.read_csv('ibbOut_{}.txt'.format(fname_list[i]), sep='\t')
   locals()['dflimmap_{}'.format(fname_list[i])] = locals()['df_limma_{}'.format(fname_list[i])].iloc[:,[0,-2,-1]]
   locals()['dflimmap_{}'.format(fname_list[i])].columns = ['limmaFC', 'limmapVal', 'limmaB']
   locals()['dfibbp_{}'.format(fname_list[i])] = locals()['df_ibb_{}'.format(fname_list[i])].iloc[:,[6,-1]]
   locals()['dfibbp_{}'.format(fname_list[i])].columns = ['ibbFC', 'ibbpVal']
   locals()['df_{}'.format(final_df_list[i])] = \
   locals()['df{}'.format(list_df2[i])].merge(
      locals()['dflimmap_{}'.format(fname_list[i])].merge(
         locals()['dfibbp_{}'.format(fname_list[i])], how='left', left_index=True, right_index=True), how='left',
      left_index=True, right_index=True)
   locals()['df_{}'.format(final_df_list[i])] = \
   locals()['df_{}'.format(final_df_list[i])][['Accession', 'Description', 'Gene', 'limmaFC', 'limmapVal', 'limmaB',
                                       'ibbFC', 'ibbpVal']]

#now repeat for the combined liver/brain
for i in range(6,8):
   for j in range(2):
      locals()['df_limma{}_{}'.format(fname_list[i], list_split2[j])] = \
      pd.read_csv('limmaOut_df{}_{}.txt'.format(fname_list[i], list_split2[j]), sep='\t')
      locals()['df_ibb{}_{}'.format(fname_list[i], list_split[j])] = \
      pd.read_csv('ibbOut_{}_{}.txt'.format(fname_list[i], list_split[j]), sep='\t')
      locals()['dflimmap_{}_{}'.format(fname_list[i], list_split2[j])] = \
      locals()['df_limma{}_{}'.format(fname_list[i], list_split2[j])].iloc[:,[0,-2,-1]]
      locals()['dflimmap_{}_{}'.format(fname_list[i], list_split2[j])].columns = \
      ['limmaFC{}'.format(list_split2[j]), 'limmapVal{}'.format(list_split2[j]), 'limmaB{}'.format(list_split2[j])]
      locals()['dfibbp{}_{}'.format(fname_list[i], list_split[j])] = \
      locals()['df_ibb{}_{}'.format(fname_list[i], list_split[j])].iloc[:,[-3,-1]]
      locals()['dfibbp{}_{}'.format(fname_list[i], list_split[j])].columns = \
      ['ibbFC{}'.format(list_split[j]), 'ibbpVal{}'.format(list_split[j])]

for i in range(6,8):
   locals()['df_{}'.format(final_df_list[i])] = \
   reduce(lambda left,right: pd.merge(
      left, right, left_index=True, right_index=True, how='left'),
        [locals()['df{}'.format(list_df2[i])], locals()['dflimmap_{}_Liver'.format(fname_list[i])],
         locals()['dflimmap_{}_Brain'.format(fname_list[i])], locals()['dfibbp{}_Hep'.format(fname_list[i])],
         locals()['dfibbp{}_Brain'.format(fname_list[i])]])
   locals()['df_{}'.format(final_df_list[i])] = \
   locals()['df_{}'.format(final_df_list[i])][['Accession', 'Description', 'Gene', 'limmaFCLiver', 'limmaFCBrain',
                                       'limmapValLiver', 'limmapValBrain', 'limmaBLiver', 'limmaBBrain',
                                       'ibbFCHep', 'ibbFCBrain', 'ibbpValHep', 'ibbpValBrain']]
#now we will sort the data frame to keep only significant interactors
#will take things with a pvalue < 0.5 in either the limma or ibb test
#will also remove things with a negative fc (or positive in the ibb test)
#will also keep things that have a pvalue <0.05 for either test for either the liver or brain

#list final dfs
list_final_df = ['293TF', '293TSwiss', 'BrainF', 'BrainSwiss', 'LiverF', 'LiverSwiss', 'LiverBrainF', 'LiverBrainSwiss']

for i in range(6):
   locals()['df_{}'.format(list_final_df[i])] = \
   locals()['df_{}'.format(final_df_list[i])][((locals()['df_{}'.format(final_df_list[i])].limmaFC > 0) |
                                       (locals()['df_{}'.format(final_df_list[i])].ibbFC < 0))
                                       & ((locals()['df_{}'.format(final_df_list[i])].limmapVal < 0.05) |
                                         (locals()['df_{}'.format(final_df_list[i])].ibbpVal < 0.05))]

for i in range(6,8):
   for j in range(2):
      locals()['df_{}_{}'.format(list_final_df[i], list_split2[j])] = \
      locals()['df_{}'.format(final_df_list[i])][
         ((locals()['df_{}'.format(final_df_list[i])]['limmaFC{}'.format(list_split2[j])] > 0) |
          (locals()['df_{}'.format(final_df_list[i])]['ibbFC{}'.format(list_split[j])] < 0)) &
         ((locals()['df_{}'.format(final_df_list[i])]['limmapVal{}'.format(list_split2[j])] < 0.05) |
           (locals()['df_{}'.format(final_df_list[i])]['ibbpVal{}'.format(list_split[j])] < 0.05))]
#now count up the number of interactors for each condition and export a list of genes for network analysis
```

```
#also export the whole dataframe as a csv

#drop all rows with 0 for gene name (uncharacterized proteins etc...) and export gene lists to csvs

#start with the first 6 individual ones
for i in range(6):
    locals()['df_{}'.format(list_final_df[i])] = \
    locals()['df_{}'.format(list_final_df[i])][locals()['df_{}'.format(list_final_df[i])].Gene != 0]
    locals()['df_{}'.format(list_final_df[i])]['Gene'].to_csv('Interactors{}.csv'.format(list_final_df[i]),
                                                              index=False, header=True)
    locals()['df_{}'.format(list_final_df[i])].to_csv(
        './20B25_Analyzed_PD_Output/Interactors{}.csv'.format(list_final_df[i]), index=False, header=True)

#then do the liver/brain combined
for i in range(6,8):
    for j in range(2):
        locals()['df_{}_{}'.format(list_final_df[i], list_split2[j])] = \
        locals()['df_{}_{}'.format(list_final_df[i], list_split2[j])][
            locals()['df_{}_{}'.format(list_final_df[i], list_split2[j])].Gene != 0]
        locals()['df_{}_{}'.format(list_final_df[i], list_split2[j])]['Gene'].to_csv(
            'Interactors{}{}.csv'.format(list_final_df[i], list_split2[j]), index=False, header=True)
        locals()['df_{}_{}'.format(list_final_df[i], list_split2[j])].to_csv(
            './20B25_Analyzed_PD_Output/Interactors{}_{}.csv'.format(list_final_df[i], list_split2[j]),
            index=False, header=True)

#now output the number of interactors in each condition, make a df export it to csv, and display it here

df_num_ints = pd.DataFrame(np.empty((8,1)))

for i in range(6):
    df_num_ints.iloc[i] = len(locals()['df_{}'.format(list_final_df[i])])
    df_num_ints.columns = ['Interactors']
    df_num_ints.rename(index={i:list_final_df[i]}, inplace=True)

#also calculate the combined number of interactors
df_num_ints.iloc[6] = len(set((list(df_LiverBrainF_Liver.Accession) + list(df_LiverBrainF_Brain.Accession))))
df_num_ints.iloc[7] = len(set((list(df_LiverBrainSwiss_Liver.Accession) + list(df_LiverBrainSwiss_Brain.Accession))))
df_num_ints.rename(index={6:'LiverBrainF', 7:'LiverBrainSwiss'}, inplace=True)

df_num_ints.Interactors = df_num_ints.Interactors.astype(int)

df_num_ints.to_csv('NumberInteractors.csv')
df_num_ints

#count up the number of substrates and display here
#also export gene lists as with interactors

#first import the files
#list the filenames
fnameg0 = './293T_Glycomics_Full/293T_Glycomics_Full_Proteins.txt'
fnameg1 = './293T_Glycomics_SwissProt/293T_Glycomics_SwissProt_Proteins.txt'
fnameg2 = './Brain_Glycomics_Full/Brain_Glycomics_Full_Proteins.txt'
fnameg3 = './Brain_Glycomics_SwissProt/Brain_Glycomics_SwissProt_Proteins.txt'
fnameg4 = './Liver_Glycomics_Full/Liver_Glycomics_Full_Proteins.txt'
fnameg5 = './Liver_Glycomics_SwissProt/Liver_Glycomics_SwissProt_Proteins.txt'
fnameg6 = './LiverBrain_Glycomics_Full/LiverBrain_Glycomics_Full_Proteins.txt'
fnameg7 = './LiverBrain_Glycomics_SwissProt/LiverBrain_Glycomics_SwissProt_Proteins.txt'
fnamesg = [fnameg0, fnameg1, fnameg2, fnameg3, fnameg4, fnameg5, fnameg6, fnameg7] #concatenate into a single list

#import all of the files into dfs

#make lists for for loop
list_expg = ['293TFg', '293TSPg', 'BrainFg', 'BrainSPg', 'LiverFg', 'LiverSPg', 'LiverBrainFg', 'LiverBrainSPg']

#define all the dfs in a for loop
for i in range(8):
    locals()['df{}'.format(list_expg[i])] = pd.read_csv(fnamesg[i], sep='\t')


#set only these columns to keep
cols_to_keepg = ['Accession', 'Description', 'Modifications']

#make a list for these new dfs
list_dfg = ['293Fullg', '293SwissProtg', 'BrainFullg', 'BrainSwissProtg', 'LiverFullg', 'LiverSwissProtg', 'LiverBrainFullg',
        'LiverBrainSwissProtg']

#use a for loop to get the relevant info from all 8 dfs (also remove contaminant proteins)
#also get gene symbols from fasta lines and make all caps
#remove all non-glycosylated proteins
#export list of substrate and sorted output

for i in range(8):
    locals()['df{}'.format(list_dfg[i])] = locals()['df{}'.format(list_expg[i])][locals()['df{}'.format(list_expg[i])].\
                                                  Contaminant == False]
    locals()['df{}'.format(list_dfg[i])] = locals()['df{}'.format(list_dfg[i])][~locals()['df{}'.format(list_dfg[i])].\
                                                  Description.str.contains('contaminant')]
    locals()['df{}'.format(list_dfg[i])].Modifications.fillna(' ', inplace=True)
    locals()['df{}'.format(list_dfg[i])] = locals()['df{}'.format(list_dfg[i])][locals()['df{}'.format(list_dfg[i])].\
                                                  Modifications.str.contains('GlcNAc')]
    locals()['df{}'.format(list_dfg[i])] = locals()['df{}'.format(list_dfg[i])][cols_to_keepg]
    locals()['df{}'.format(list_dfg[i])]['Gene'] = \
    locals()['df{}'.format(list_dfg[i])]['Description'].str.extract('GN=(.*) PE=')
    locals()['df{}'.format(list_dfg[i])].Gene = locals()['df{}'.format(list_dfg[i])].Gene.str.upper()
```

```
for i in list_dfg:
    locals()['df{}'.format(i)] = locals()['df{}'.format(i)][locals()['df{}'.format(i)].Gene != 0]
    locals()['df{}'.format(i)] = locals()['df{}'.format(i)][locals()['df{}'.format(i)].Gene != np.nan]
    locals()['df{}'.format(i)]['Gene'].to_csv('Substrates{}.csv'.format(i.replace(r'g', '')), index=False, header=True)
    locals()['df{}'.format(i)].to_csv(
        './20B25_Analyzed_PD_Output/Substrates{}.csv'.format(i.replace(r'g', '')), index=False, header=True)

#now output the number of interactors in each condition, make a df export it to csv, and display it here

df_num_subs = pd.DataFrame(np.empty((8,1)))

for i in range(8):
    df_num_subs.iloc[i] = len(locals()['df{}'.format(list_dfg[i])])
    df_num_subs.columns = ['Substrates']
    df_num_subs.Substrates = df_num_subs.Substrates.astype(int)
    df_num_subs.rename(index={i:list_dfg[i].replace(r'g', '')}, inplace=True) #remove g from index names as well this time

df_num_subs.to_csv('NumberSubstrates.csv')
df_num_subs

#make new dfs with the relevant informaton for making Venn diagrams for the substrates

#pick the relevant columns for the liver or the brain
columnsLiver = ['Found in File in F1', 'Found in File in F2', 'Found in File in F3', 'Found in File in F4']
columnsBrain = ['Found in File in F5', 'Found in File in F6', 'Found in File in F7', 'Found in File in F8']


#check whether a protein was found in any of the files for the liver and make a new True/False column 'Liver'
#then do the same thing for the brain

#first make lists to make setting up a for loop easier
list_venn = ['Liver', 'Brain']
list_venn1 = ['F', 'SP']

for i in range(2):
    for j in range(2):
        locals()['dfLiverBrain{}g'.format(list_venn1[i])]['{}'.format(list_venn[j])] =\
        locals()['dfLiverBrain{}g'.format(list_venn1[i])][locals()['columns{}'.format(
            list_venn[j])]].ne('Not Found').any(axis=1)

#now merge these back onto the processed df and make sets out of the unprot

#mae a list to facilitate the for loop
list_venn2 = ['Full', 'SwissProt']

for i in range(2):
    locals()['df_venn{}'.format(list_venn2[i])] = \
    locals()['dfLiverBrain{}g'.format(list_venn2[i])].merge(locals()['dfLiverBrain{}g'.format(list_venn1[i])], how='left',
                                          on='Accession')
    for j in list_venn:
        locals()['set_subs{}{}'.format(j, list_venn1[i])] = \
        set(locals()['df_venn{}'.format(list_venn2[i])][locals()['df_venn{}'.format(
            list_venn2[i])]['{}'.format(j)] == True].Accession)
#make new dfs with the relevant informaton for making Venn diagrams for the interactors

#make a list for the following for loop
list_venni = ['F', 'Swiss']

for i in list_venni:
    for j in list_split2:
        locals()['set_ints{}_{}'.format(i, j)] = set(locals()['df_LiverBrain{}_{}'.format(i, j)].Accession)
#now make the venn diagrams for the substrates and output to svg

#Full proteome
plt.figure(figsize=(7,7))
fig = venn2([set_subsBrainF, set_subsLiverF], ('Brain', 'Liver'), normalize_to=1000)
fig.get_patch_by_id('10').set_color('#5b7992')
fig.get_patch_by_id('01').set_color('#aaaaaa')
fig.get_patch_by_id('10').set_edgecolor('none')
fig.get_patch_by_id('01').set_edgecolor('none')
fig.get_patch_by_id('10').set_alpha(0.75)
fig.get_patch_by_id('01').set_alpha(0.5)
fig.get_patch_by_id('11').set_color('#027FF0')
fig.get_patch_by_id('11').set_edgecolor('none')
fig.get_patch_by_id('11').set_alpha(0.5)

#set the font size
for text in fig.set_labels: #need to call named object 'fig' from above, font size is set numerically
    text.set_fontsize(36) #this is the label names
for text in fig.subset_labels:
    text.set_fontsize(28) #this will change the numbers

plt.savefig('SubstrateOverlap_Full.svg') #save figure

#SwissProt
plt.figure(figsize=(7,7))
fig = venn2([set_subsBrainSP, set_subsLiverSP], ('Brain', 'Liver'), normalize_to=1000)
fig.get_patch_by_id('10').set_color('#5b7992')
fig.get_patch_by_id('01').set_color('#aaaaaa')
fig.get_patch_by_id('10').set_edgecolor('none')
fig.get_patch_by_id('01').set_edgecolor('none')
fig.get_patch_by_id('10').set_alpha(0.75)
```

```
fig.get_patch_by_id('01').set_alpha(0.5)
fig.get_patch_by_id('11').set_color('#027FF0')
fig.get_patch_by_id('11').set_edgecolor('none')
fig.get_patch_by_id('11').set_alpha(0.5)

#set the font size
for text in fig.set_labels: #need to call named object 'fig' from above, font size is set numerically
    text.set_fontsize(36) #this is the label names
for text in fig.subset_labels:
    text.set_fontsize(28) #this will change the numbers

plt.savefig('SubstrateOverlap_SwissProt.svg') #save figure

plt.show() #show the plot

#now make the venn diagrams for the interactors and output to svg

#Full proteome
plt.figure(figsize=(7,7))
fig = venn2([set_intsF_Brain, set_intsF_Liver], ('Brain', 'Liver'), normalize_to=1000)
fig.get_patch_by_id('10').set_color('#5b7992')
fig.get_patch_by_id('01').set_color('#aaaaaa')
fig.get_patch_by_id('10').set_edgecolor('none')
fig.get_patch_by_id('01').set_edgecolor('none')
fig.get_patch_by_id('10').set_alpha(0.75)
fig.get_patch_by_id('01').set_alpha(0.5)
fig.get_patch_by_id('11').set_color('#027FF0')
fig.get_patch_by_id('11').set_edgecolor('none')
fig.get_patch_by_id('11').set_alpha(0.5)

#set the font size
for text in fig.set_labels: #need to call named object 'fig' from above, font size is set numerically
    text.set_fontsize(36) #this is the label names
for text in fig.subset_labels:
    text.set_fontsize(28) #this will change the numbers

plt.savefig('InteractorOverlap_Full.svg') #save figure

#SwissProt
plt.figure(figsize=(7,7))
fig = venn2([set_intsSwiss_Brain, set_intsSwiss_Liver], ('Brain', 'Liver'), normalize_to=1000)
fig.get_patch_by_id('10').set_color('#5b7992')
fig.get_patch_by_id('01').set_color('#aaaaaa')
fig.get_patch_by_id('10').set_edgecolor('none')
fig.get_patch_by_id('01').set_edgecolor('none')
fig.get_patch_by_id('10').set_alpha(0.75)
fig.get_patch_by_id('01').set_alpha(0.5)
fig.get_patch_by_id('11').set_color('#027FF0')
fig.get_patch_by_id('11').set_edgecolor('none')
fig.get_patch_by_id('11').set_alpha(0.5)

#set the font size
for text in fig.set_labels: #need to call named object 'fig' from above, font size is set numerically
    text.set_fontsize(36) #this is the label names
for text in fig.subset_labels:
    text.set_fontsize(28) #this will change the numbers

plt.savefig('InteractorOverlap_SwissProt.svg') #save figure

plt.show() #show the plot

#now make the Venn diagrams for the substrates in the separate searches

#makes sets of the brain and liver data for matplotlibvenn from the individual dfs
for i in range(2):
    for j in range(2):
        locals()['set_subs2{}{}'.format(list_venn[i], list_venn2[j])] = \
        set(locals()['df{}{}g'.format(list_venn[i], list_venn2[j])]['Accession'])

#now make the Venn diagrams as before
#Full proteome
plt.figure(figsize=(7,7))
fig = venn2([set_subs2BrainFull, set_subs2LiverFull], ('Brain', 'Liver'), normalize_to=1000)
fig.get_patch_by_id('10').set_color('#5b7992')
fig.get_patch_by_id('01').set_color('#aaaaaa')
fig.get_patch_by_id('10').set_edgecolor('none')
fig.get_patch_by_id('01').set_edgecolor('none')
fig.get_patch_by_id('10').set_alpha(0.75)
fig.get_patch_by_id('01').set_alpha(0.5)
fig.get_patch_by_id('11').set_color('#027FF0')
fig.get_patch_by_id('11').set_edgecolor('none')
fig.get_patch_by_id('11').set_alpha(0.5)

#set the font size
for text in fig.set_labels: #need to call named object 'fig' from above, font size is set numerically
    text.set_fontsize(36) #this is the label names
for text in fig.subset_labels:
    text.set_fontsize(28) #this will change the numbers

#SwissProt
plt.figure(figsize=(7,7))
fig = venn2([set_subs2BrainSwissProt, set_subs2LiverSwissProt], ('Brain', 'Liver'), normalize_to=1000)
fig.get_patch_by_id('10').set_color('#5b7992')
```

```
fig.get_patch_by_id('01').set_color('#aaaaaa')
fig.get_patch_by_id('10').set_edgecolor('none')
fig.get_patch_by_id('01').set_edgecolor('none')
fig.get_patch_by_id('10').set_alpha(0.75)
fig.get_patch_by_id('01').set_alpha(0.5)
fig.get_patch_by_id('11').set_color('#027FF0')
fig.get_patch_by_id('11').set_edgecolor('none')
fig.get_patch_by_id('11').set_alpha(0.5)

#set the font size
for text in fig.set_labels: #need to call named object 'fig' from above, font size is set numerically
    text.set_fontsize(36) #this is the label names
for text in fig.subset_labels:
    text.set_fontsize(28) #this will change the numbers

plt.show() #show the plot

#now make the Venn diagrams for the interactors in the separate searches

list_venn4 = ['F', 'Swiss']

#makes sets of the brain and liver data for matplotlibvenn from the individual dfs
for i in range(2):
    for j in range(2):
        locals()['set_ints2{}{}'.format(list_venn[i], list_venn2[j])] = \
        set(locals()['df_{}{}'.format(list_venn[i], list_venn4[j])]['Accession'])

#now make the Venn diagrams as before
#Full proteome
plt.figure(figsize=(7,7))
fig = venn2([set_ints2BrainFull, set_ints2LiverFull], ('Brain', 'Liver'), normalize_to=1000)
fig.get_patch_by_id('10').set_color('#5b7992')
fig.get_patch_by_id('01').set_color('#aaaaaa')
fig.get_patch_by_id('10').set_edgecolor('none')
fig.get_patch_by_id('01').set_edgecolor('none')
fig.get_patch_by_id('10').set_alpha(0.75)
fig.get_patch_by_id('01').set_alpha(0.5)
fig.get_patch_by_id('11').set_color('#027FF0')
fig.get_patch_by_id('11').set_edgecolor('none')
fig.get_patch_by_id('11').set_alpha(0.5)

#set the font size
for text in fig.set_labels: #need to call named object 'fig' from above, font size is set numerically
    text.set_fontsize(36) #this is the label names
for text in fig.subset_labels:
    text.set_fontsize(28) #this will change the numbers

#SwissProt
plt.figure(figsize=(7,7))
fig = venn2([set_ints2BrainSwissProt, set_ints2LiverSwissProt], ('Brain', 'Liver'), normalize_to=1000)
fig.get_patch_by_id('10').set_color('#5b7992')
fig.get_patch_by_id('01').set_color('#aaaaaa')
fig.get_patch_by_id('10').set_edgecolor('none')
fig.get_patch_by_id('01').set_edgecolor('none')
fig.get_patch_by_id('10').set_alpha(0.75)
fig.get_patch_by_id('01').set_alpha(0.5)
fig.get_patch_by_id('11').set_color('#027FF0')
fig.get_patch_by_id('11').set_edgecolor('none')
fig.get_patch_by_id('11').set_alpha(0.5)

#set the font size
for text in fig.set_labels: #need to call named object 'fig' from above, font size is set numerically
    text.set_fontsize(36) #this is the label names
for text in fig.subset_labels:
    text.set_fontsize(28) #this will change the numbers

plt.show() #show the plot

#now make the Venn diagram for the whole proteome

#import the data from Huttlin 2010 (I preprocessed this so there are just 2 columns of protein names)
#also see '19G30 Brain vs Liver Venn Diagrams Update'
df_proteome = pd.read_csv('Proteome_Brain_Liver.csv')
df_phosphoproteome = pd.read_csv('Phoshoproteome_Brain_Liver.csv')

#make listsfor processing both datasets
list_prot = ['', 'phospho']
list_prot2 = ['Brain', 'Liver']

#drop nans and make sets for each dataset
for i in list_prot:
    for j in list_prot2:
        locals()['df_{}proteome{}'.format(i, j)] = locals()['df_{}proteome'.format(i)]['{}'.format(j)]
        locals()['df_{}proteome{}'.format(i, j)].dropna(inplace='True)
        locals()['set_{}proteome_{}'.format(i, j)] = set(locals()['df_{}proteome{}'.format(i, j)])

#now make the venn diagrams for the entire proteome and phosphoproteome and output to svg

#Full proteome
plt.figure(figsize=(7,7))
fig = venn2([set_proteome_Brain, set_proteome_Liver], ('Brain', 'Liver'), normalize_to=1000)
fig.get_patch_by_id('10').set_color('#5b7992')
fig.get_patch_by_id('01').set_color('#aaaaaa')
```

```
fig.get_patch_by_id('10').set_edgecolor('none')
fig.get_patch_by_id('01').set_edgecolor('none')
fig.get_patch_by_id('10').set_alpha(0.75)
fig.get_patch_by_id('01').set_alpha(0.5)
fig.get_patch_by_id('11').set_color('#027FF0')
fig.get_patch_by_id('11').set_edgecolor('none')
fig.get_patch_by_id('11').set_alpha(0.5)

#set the font size
for text in fig.set_labels: #need to call named object 'fig' from above, font size is set numerically
    text.set_fontsize(36) #this is the label names
for text in fig.subset_labels:
    text.set_fontsize(28) #this will change the numbers

plt.savefig('ProteomeOverlap.svg') #save figure

#Phosphoproteome
plt.figure(figsize=(7,7))
fig = venn2([set_phosphoproteome_Brain, set_phosphoproteome_Liver], ('Brain', 'Liver'), normalize_to=1000)
fig.get_patch_by_id('10').set_color('#5b7992')
fig.get_patch_by_id('01').set_color('#aaaaaa')
fig.get_patch_by_id('10').set_edgecolor('none')
fig.get_patch_by_id('01').set_edgecolor('none')
fig.get_patch_by_id('10').set_alpha(0.75)
fig.get_patch_by_id('01').set_alpha(0.5)
fig.get_patch_by_id('11').set_color('#027FF0')
fig.get_patch_by_id('11').set_edgecolor('none')
fig.get_patch_by_id('11').set_alpha(0.5)

#set the font size
for text in fig.set_labels: #need to call named object 'fig' from above, font size is set numerically
    text.set_fontsize(36) #this is the label names
for text in fig.subset_labels:
    text.set_fontsize(28) #this will change the numbers

plt.savefig('PhosphoproteomeOverlap.svg') #save figure

plt.show() #show the plot
```

A5.6.2. Preprocesing of PPI Databases.

```
#import python packages
import pandas as pd
import numpy as np
from io import StringIO
import urllib.request, urllib.parse, urllib.error,urllib.request,urllib.error,urllib.parse
#first the BioGRID database
fname = 'BIOGRID-ORGANISM-Homo_sapiens-3.5.181.tab2.txt' #set the filename
dfbg = pd.read_csv(fname, sep='\t') #import as df

#rename interactor columns
dfbg.rename(columns={'Official Symbol Interactor A':'Interactor_A', 'Official Symbol Interactor B':'Interactor_B'},
          inplace=True)

#keep only physical interactions
dfbg = dfbg[dfbg['Experimental System Type'] == 'physical']

#keep only relevant columns
dfbg = dfbg[['Interactor_A', 'Interactor_B']]

#make all strings uppercase and drop nans
dfbg['Interactor_A'] = dfbg.Interactor_A.str.upper()
dfbg['Interactor_B'] = dfbg.Interactor_B.str.upper()
dfbg.dropna(inplace='True)

dfbg.to_csv('BioGRID.txt', sep='\t', index=False) #export to tab delimited
dfbg #inspect

#now with the IntAct database
fname1 = 'IntAct-human-human.txt' #set the filename
dfi = pd.read_csv(fname1, sep='\t') #import as df
dfi = dfi[['#ID(s) interactor A', 'ID(s) interactor B']] #keep only relevant columns
dfi.columns = ['Interactor_A', 'Interactor_B'] #rename the columns as before

#keep only PPIs by filtering for uniprot acessions only in both columns
dfi = dfi[dfi.Interactor_A.str.contains('uniprot')]
dfi = dfi[dfi.Interactor_B.str.contains('uniprot')]

#groupby duplicates in both interactor A and B and count the number of times they are repeated
#this also creates a new column ('Number') to track how many incidences of each pair there are
dfi_1 = dfi.groupby(['Interactor_A', 'Interactor_B']).size().reset_index(name="Number")

#make a new df with only interactions that have more than 1 entry in the database (multivalidated)
dfi_mv = dfi_1[dfi_1.Number >1]

dfi_1 #inspect the original
```

```
#now will map the uniprot ids to their gene names

#make a new df to prevent having to reimport the entire IntAct databse if the df needs to be reset for any reason
dfia = dfi_1.copy()

#first clean up the entries
dfia.reset_index(inplace=True, drop=True) #reset the index
dfia.drop(columns={'Number'}, inplace=True) #drop the number column

#strip the uniprot ids
dfia['Interactor_A'] = dfia['Interactor_A'].map(lambda x: x.lstrip('uniprotkb:'))
dfia['Interactor_B'] = dfia['Interactor_B'].map(lambda x: x.lstrip('uniprotkb:'))

#now remove the isoform identifiers
dfia['Interactor_A'] = dfia['Interactor_A'].map(lambda x: x.split('-', 1)[0])
dfia['Interactor_B'] = dfia['Interactor_B'].map(lambda x: x.split('-', 1)[0])

#now make a list of uniprot ids to map to gene names
dfmap = pd.DataFrame(pd.concat([dfia['Interactor_A'], dfia['Interactor_B']])) #concatenate the columns in a new df
dfmap.drop_duplicates(inplace=True) #drop duplicates
dfmap.columns = ['UniprotID'] #rename the column
uniprot_input = list(dfmap.UniprotID) #make this item into a list for uploading
#now query uniprot

#define variables
url = 'https://www.uniprot.org/uploadlists/'
user_agent = 'Mozilla/5.0 (Windows NT 10.0; Win64; x64)'

#make a dictionary for the requests
params = {
    "from":"ACC+ID",
    "to":"ACC",
    "format":"tab",
    "columns": "genes(PREFERRED)",
    "query":" ".join(uniprot_input)
}

#query uniprot
data = urllib.parse.urlencode(params, doseq=False)
data = data.encode('ascii')
headers = {"User-Agent": user_agent}
request = urllib.request.Request(url, data, headers)
response = urllib.request.urlopen(request)
with urllib.request.urlopen(request) as f:
   response = f.read().decode()

#make a dataframe from the output
df_res = pd.read_csv(StringIO(response), sep='\t') #use the stringIO package to parse the output instead of making a file
df_res #inspect

#make a dictionary from the uniprot output and rename the uniprot ids in the intact database
#do the same for the multivalidated dataset (uses the same dictionary since it is a subset)

#copy the multivalidated interactor database
dfimv = dfi_mv.copy()

#first rename the columns for convenience
df_res.rename(columns={df_res.columns[0]: "Gene", df_res.columns[1]: "UniprotID"}, inplace=True)

#set up the dictionary for mapping
di = df_res.set_index('UniprotID')['Gene'].to_dict()

#replace the uniprot ids with gene names in the intact database
dfia['Interactor_A'].replace(di, inplace=True)
dfia['Interactor_B'].replace(di, inplace=True)
dfimv['Interactor_A'].replace(di, inplace=True)
dfimv['Interactor_A'].replace(di, inplace=True)

#drop all nans
dfia.dropna(inplace=True)
dfimv.dropna(inplace=True)

#export the data to a txt as with the biogrid database
dfia.to_csv('IntAct.txt', sep='\t', index=False)
dfimv.to_csv('IntAct_Multivalidated.txt', sep='\t', index=False)
dfia #inspect
```

A5.6.3. Construction of PPI Networks.

```
#import python packages
import re
import pandas as pd
import numpy as np
import matplotlib
import matplotlib.pyplot as plt

#ignore future warning
```

```
import warnings
warnings.filterwarnings("ignore")

#magic function to show plots inline
%matplotlib inline
#load in BioGRID and IntAct databases (keeping naming consistent with Yao's script)

#first BioGRID
dfPPI = pd.read_csv('BioGRID.txt', sep='\t')

#then IntAct
dfPPI2 = pd.read_csv('IntAct.txt', sep='\t')
#read in the OGT interactors and substrates

#make a list for naming the binders and substrates lists
list_lists = ['293T', 'Brain', 'Liver', 'LiverBrain']

#make a list for the filenames
list_fnames = ['293TF', 'BrainF', 'LiverF', 'LiverBrainF']

#use a for loop to import all of them except the liver brain combined
for i in range(3):
    locals()['df_OGTInt{}'.format(list_fnames[i])] = pd.read_csv('Interactors{}.csv'.format(list_fnames[i]))

#import the liver brain combined by concatenating the liver and brain datasets and dropping duplicates
locals()['df_OGTInt{}'.format(list_fnames[3])] = \
pd.concat([pd.read_csv('Interactors{}Liver.csv'.format(list_fnames[3])),
           pd.read_csv('Interactors{}Brain.csv'.format(list_fnames[3]))], axis=0)
locals()['df_OGTInt{}'.format(list_fnames[3])].drop_duplicates(inplace=True)

#make a new df and set up the columns as self interactors
for i in range(4):
    locals()['df_binders{}'.format(list_fnames[i])] = locals()['df_OGTInt{}'.format(list_fnames[i])].copy()
    locals()['df_binders{}'.format(list_fnames[i])].columns = ['Interactor_A']
    locals()['df_binders{}'.format(list_fnames[i])]['Interactor_B'] = \
    locals()['df_binders{}'.format(list_fnames[i])]['Interactor_A']
    locals()['bind_list{}'.format(list_lists[i])] = \
    locals()['df_binders{}'.format(list_fnames[i])]['Interactor_A'].values.tolist()

#now read in the substrates as with the interactors

#make a list for the filenames
list_fnames2 = ['293Full', 'BrainFull', 'LiverFull', 'LiverBrainFull']

#import everything with a for loop
for i in list_fnames2:
    locals()['dfOGTSubs{}'.format(i)] = pd.read_csv('Substrates{}.csv'.format(i))

for i in range(4):
    locals()['df_subs{}'.format(list_fnames2[i])] = locals()['dfOGTSubs{}'.format(list_fnames2[i])].copy()
    locals()['df_subs{}'.format(list_fnames2[i])].columns = ['Interactor_A']
    locals()['df_subs{}'.format(list_fnames2[i])]['Interactor_B'] = \
    locals()['df_subs{}'.format(list_fnames2[i])]['Interactor_A']
    locals()['subs_list{}'.format(list_lists[i])] = \
    locals()['df_subs{}'.format(list_fnames2[i])]['Interactor_A'].values.tolist()
#filter the BioGRID database for interactions between ints and ints and ints and subs

#filter for proteins that matched either an OGT interactor or an OGT substrate
for i in list_lists:
    locals()['bindsub_list{}'.format(i)] = locals()['bind_list{}'.format(i)] + locals()['subs_list{}'.format(i)]

#find all the interactions from A to B in BioGRID that are from the bind list to the concatenated lists
for i in list_lists:
    locals()['dfPPIA{}'.format(i)] = dfPPI[dfPPI.Interactor_A.isin(locals()['bind_list{}'.format(i)]) &
                                           dfPPI.Interactor_B.isin(locals()['bindsub_list{}'.format(i)])]

#do the same for interactions from B to A
for i in list_lists:
    locals()['dfPPIB{}'.format(i)] = dfPPI[dfPPI.Interactor_B.isin(locals()['bind_list{}'.format(i)]) &
                                           dfPPI.Interactor_A.isin(locals()['bindsub_list{}'.format(i)])]

#swap the two columns in dfPPIB because the interactions are undirectional (we will define A to B)
for i in list_lists:
    locals()['colList{}'.format(i)] = list(locals()['dfPPIB{}'.format(i)])
    locals()['colList{}'.format(i)][0], locals()['colList{}'.format(i)][1] = \
    locals()['colList{}'.format(i)][1], locals()['colList{}'.format(i)][0]
    locals()['dfPPIB{}'.format(i)].columns = locals()['colList{}'.format(i)]

#put everything together in one dataframe and drop duplicates
for i in list_lists:
    locals()['dfPPI{}'.format(i)] = locals()['dfPPIA{}'.format(i)].append(locals()['dfPPIB{}'.format(i)])
    locals()['dfPPI{}'.format(i)].drop_duplicates(subset=['Interactor_A', 'Interactor_B'], inplace=True)
    locals()['dfPPI{}'.format(i)].reset_index(inplace=True, drop=True)
#filter against super-interactors

#sort the df by number of times a protein appears in the Interactor_A column and make a new df
for i in list_lists:
    locals()['interactCount{}'.format(i)] = \
    locals()['dfPPI{}'.format(i)].groupby(['Interactor_A']).count().reset_index().rename(
        columns={'Interactor_B':'TotalCount'})

#make a new df of interactors from OGT interactors in column A to substrates in column B and vice versa
#also switch the column names for B to A df as before
```

```
for i in list_lists:
    locals()['dfPPIC{}'.format(i)] = \
    locals()['dfPPI{}'.format(i)][
        locals()['dfPPI{}'.format(i)].Interactor_A.isin(locals()['bind_list{}'.format(i)]) &
        locals()['dfPPI{}'.format(i)].Interactor_B.isin(locals()['subs_list{}'.format(i)])]
    locals()['dfPPID{}'.format(i)] = \
    locals()['dfPPI{}'.format(i)][
        locals()['dfPPI{}'.format(i)].Interactor_B.isin(locals()['bind_list{}'.format(i)]) &
        locals()['dfPPI{}'.format(i)].Interactor_A.isin(locals()['subs_list{}'.format(i)])]
    locals()['colList2{}'.format(i)] = list(locals()['dfPPID{}'.format(i)])
    locals()['colList2{}'.format(i)][0], locals()['colList2{}'.format(i)][1] = \
    locals()['colList2{}'.format(i)][1], locals()['colList2{}'.format(i)][0]
    locals()['dfPPID{}'.format(i)].columns = locals()['colList2{}'.format(i)]

#make a new dataframe of tha concatenated two previous dataframes (also drop duplicates and reset index)
for i in list_lists:
    locals()['bindsub{}'.format(i)] = locals()['dfPPIC{}'.format(i)].append(locals()['dfPPID{}'.format(i)])
    locals()['bindsub{}'.format(i)].drop_duplicates(subset=['Interactor_A', 'Interactor_B'], inplace=True)
    locals()['bindsub{}'.format(i)].reset_index(drop=True, inplace=True)

#make a new df grouped by the number of instances as before
for i in list_lists:
    locals()['bindsub{}'.format(i)] = \
    locals()['bindsub{}'.format(i)].groupby(['Interactor_A']).count().reset_index().rename(
        columns={'Interactor_B':'SubsCount'})

# make two new dfs from binders in column A to binders in column B and vice versa
#switching the columns for this second df as before
for i in list_lists:
    locals()['dfPPIE{}'.format(i)] = \
    locals()['dfPPI{}'.format(i)][
        locals()['dfPPI{}'.format(i)].Interactor_A.isin(locals()['bind_list{}'.format(i)]) &
        locals()['dfPPI{}'.format(i)].Interactor_B.isin(locals()['bind_list{}'.format(i)])]
    locals()['dfPPIF{}'.format(i)] = \
    locals()['dfPPI{}'.format(i)][
        locals()['dfPPI{}'.format(i)].Interactor_B.isin(locals()['bind_list{}'.format(i)]) &
        locals()['dfPPI{}'.format(i)].Interactor_A.isin(locals()['bind_list{}'.format(i)])]
    locals()['colList3{}'.format(i)] = list(locals()['dfPPIF{}'.format(i)])
    locals()['colList3{}'.format(i)][0], locals()['colList3{}'.format(i)][1] = \
    locals()['colList3{}'.format(i)][1], locals()['colList3{}'.format(i)][0]
    locals()['dfPPIF{}'.format(i)].columns = locals()['colList3{}'.format(i)]

#make a new df grouped by number of counts for these new dfs as before
for i in list_lists:
    locals()['bindbind{}'.format(i)] = locals()['dfPPIE{}'.format(i)].append(locals()['dfPPIF{}'.format(i)])
    locals()['bindbind{}'.format(i)].drop_duplicates(subset=['Interactor_A', 'Interactor_B'], inplace=True)
    locals()['bindbind{}'.format(i)].reset_index(drop=True, inplace=True)
    locals()['bindbind{}'.format(i)] = \
    locals()['bindbind{}'.format(i)].groupby(['Interactor_A']).count().reset_index().rename(
        columns={'Interactor_B':'BinderCount'})

#add everything back into the interactCount df
for i in list_lists:
    locals()['interactCount{}'.format(i)] = \
    locals()['interactCount{}'.format(i)].merge(
        locals()['bindsub{}'.format(i)], how='left', left_on='Interactor_A', right_on='Interactor_A')
    locals()['interactCount{}'.format(i)] = \
    locals()['interactCount{}'.format(i)].merge(
        locals()['bindbind{}'.format(i)], how='left', left_on='Interactor_A', right_on='Interactor_A')
    locals()['interactCount{}'.format(i)].fillna(0, inplace=True)

#drop highly interacting proteins, sort the dataframe, and reset the index
for i in list_lists:
    locals()['interactCount{}'.format(i)] = \
    locals()['interactCount{}'.format(i)][
        ~(locals()['interactCount{}'.format(i)].Interactor_A.str.contains('RPL') |
          locals()['interactCount{}'.format(i)].Interactor_A.str.contains('RPS') |
          locals()['interactCount{}'.format(i)].Interactor_A.str.contains('OGT') |
          locals()['interactCount{}'.format(i)].Interactor_A.str.contains('HSP') |
          locals()['interactCount{}'.format(i)].Interactor_A.str.contains('HNRP'))]
    locals()['interactCount{}'.format(i)] = \
    locals()['interactCount{}'.format(i)].sort_values(
        ['TotalCount','SubsCount','BinderCount','Interactor_A'], ascending=[0,0,0,0])
    locals()['interactCount{}'.format(i)].reset_index(drop=True, inplace=True)

#remove things with too many interactions, total instances less than 30

#make a list of superinteractors to remove
for i in list_lists:
    locals()['filtered{}'.format(i)] = \
    locals()['interactCount{}'.format(i)][locals()['interactCount{}'.format(i)].TotalCount < 30]
    locals()['interactCount{}'.format(i)].reset_index(drop=True, inplace=True)
    locals()['filterlist{}'.format(i)] = locals()['filtered{}'.format(i)].Interactor_A.values.tolist()

#remove the super interactors from the PPI database
for i in list_lists:
    locals()['dfPPI{}'.format(i)] = \
    locals()['dfPPI{}'.format(i)][locals()['dfPPI{}'.format(i)].Interactor_A.isin(locals()['filterlist{}'.format(i)])]

#remove OGT and keratin from the network
for i in list_lists:
    locals()['dfPPI{}'.format(i)] = \
    locals()['dfPPI{}'.format(i)][~locals()['dfPPI{}'.format(i)].Interactor_A.str.contains('OGT')]
```

```
    locals()['dfPPI{}'.format(i)] = \
    locals()['dfPPI{}'.format(i)][~locals()['dfPPI{}'.format(i)].Interactor_B.str.contains('OGT')]
    locals()['dfPPI{}'.format(i)] = \
    locals()['dfPPI{}'.format(i)][~locals()['dfPPI{}'.format(i)].Interactor_A.str.contains('KRT')]
    locals()['dfPPI{}'.format(i)] = \
    locals()['dfPPI{}'.format(i)][~locals()['dfPPI{}'.format(i)].Interactor_B.str.contains('KRT')]

# Assuming OGT interactor/substrate named protA
# Adds in pseudo protA-protA self interactions so that protA will be displayed
# in cytoscape no matter if it has any interactions with any other OGT interactor/substrates.
for i in range(4):
    locals()['dfPPI{}'.format(list_lists[i])] = \
    locals()['dfPPI{}'.format(list_lists[i])].append(locals()['df_binders{}'.format(list_fnames[i])])
    locals()['dfPPI{}'.format(list_lists[i])] = \
    locals()['dfPPI{}'.format(list_lists[i])].append(locals()['df_subs{}'.format(list_fnames2[i])])
#now I will repeat the same thing for the IntAct database

#find all the interactions from A to B in IntAct that are from the bind list to the concatenated lists
for i in list_lists:
    locals()['dfPPI2A{}'.format(i)] = dfPPI2[dfPPI2.Interactor_A.isin(locals()['bind_list{}'.format(i)]) &
                                    dfPPI2.Interactor_B.isin(locals()['bindsub_list{}'.format(i)])]

#do the same for interactions from B to A
for i in list_lists:
    locals()['dfPPI2B{}'.format(i)] = dfPPI2[dfPPI2.Interactor_B.isin(locals()['bind_list{}'.format(i)]) &
                                    dfPPI2.Interactor_A.isin(locals()['bindsub_list{}'.format(i)])]

#swap the two columns in dfPPI2B because the interactions are undirectional (we will define A to B)
for i in list_lists:
    locals()['col2List{}'.format(i)] = list(locals()['dfPPI2B{}'.format(i)])
    locals()['col2List{}'.format(i)][0], locals()['col2List{}'.format(i)][1] = \
    locals()['colList{}'.format(i)][1], locals()['colList{}'.format(i)][0]
    locals()['dfPPI2B{}'.format(i)].columns = locals()['col2List{}'.format(i)]

#put everything together in one dataframe and drop duplicates
for i in list_lists:
    locals()['dfPPI2{}'.format(i)] = locals()['dfPPI2A{}'.format(i)].append(locals()['dfPPI2B{}'.format(i)])
    locals()['dfPPI2{}'.format(i)].drop_duplicates(subset=['Interactor_A', 'Interactor_B'], inplace=True)
    locals()['dfPPI2{}'.format(i)].reset_index(inplace=True, drop=True)

#filter against super-interactors

#sort the df by number of times a protein appears in the Interactor_A column and make a new df
for i in list_lists:
    locals()['interactCount2{}'.format(i)] = \
    locals()['dfPPI2{}'.format(i)].groupby(['Interactor_A']).count().reset_index().rename(
        columns={'Interactor_B':'TotalCount'})

#make a new df of interactors from OGT interactors in column A to substrates in column B and vice versa
#also switch the column names for B to A df as before
for i in list_lists:
    locals()['dfPPI2C{}'.format(i)] = \
    locals()['dfPPI2{}'.format(i)][locals()['dfPPI2{}'.format(i)].Interactor_A.isin(locals()['bind_list{}'.format(i)]) &
                                locals()['dfPPI2{}'.format(i)].Interactor_B.isin(locals()['subs_list{}'.format(i)])]
    locals()['dfPPI2D{}'.format(i)] = \
    locals()['dfPPI2{}'.format(i)][locals()['dfPPI2{}'.format(i)].Interactor_B.isin(locals()['bind_list{}'.format(i)]) &
                                locals()['dfPPI2{}'.format(i)].Interactor_A.isin(locals()['subs_list{}'.format(i)])]
    locals()['col2List2{}'.format(i)] = list(locals()['dfPPI2D{}'.format(i)])
    locals()['col2List2{}'.format(i)][0], locals()['col2List2{}'.format(i)][1] = \
    locals()['col2List2{}'.format(i)][1], locals()['col2List2{}'.format(i)][0]
    locals()['dfPPI2D{}'.format(i)].columns = locals()['col2List2{}'.format(i)]

#make a new dataframe of tha concatenated two previous dataframes (also drop duplicates and reset index)
for i in list_lists:
    locals()['bindsub2{}'.format(i)] = locals()['dfPPI2C{}'.format(i)].append(locals()['dfPPI2D{}'.format(i)])
    locals()['bindsub2{}'.format(i)].drop_duplicates(subset=['Interactor_A', 'Interactor_B'], inplace=True)
    locals()['bindsub2{}'.format(i)].reset_index(drop=True, inplace=True)

#make a new df grouped by the number of instances as before
for i in list_lists:
    locals()['bindsub2{}'.format(i)] = \
    locals()['bindsub2{}'.format(i)].groupby(['Interactor_A']).count().reset_index().rename(
        columns={'Interactor_B':'SubsCount'})

# make two new dfs from binders in column A to binders in column B and vice versa
#switching the columns for this second df as before
for i in list_lists:
    locals()['dfPPI2E{}'.format(i)] = \
    locals()['dfPPI2{}'.format(i)][locals()['dfPPI2{}'.format(i)].Interactor_A.isin(locals()['bind_list{}'.format(i)]) &
                                locals()['dfPPI2{}'.format(i)].Interactor_B.isin(locals()['bind_list{}'.format(i)])]
    locals()['dfPPI2F{}'.format(i)] = \
    locals()['dfPPI2{}'.format(i)][locals()['dfPPI2{}'.format(i)].Interactor_B.isin(locals()['bind_list{}'.format(i)]) &
                                locals()['dfPPI2{}'.format(i)].Interactor_A.isin(locals()['bind_list{}'.format(i)])]
    locals()['col2List3{}'.format(i)] = list(locals()['dfPPI2F{}'.format(i)])
    locals()['col2List3{}'.format(i)][0], locals()['col2List3{}'.format(i)][1] = \
    locals()['col2List3{}'.format(i)][1], locals()['col2List3{}'.format(i)][0]
    locals()['dfPPI2F{}'.format(i)].columns = locals()['col2List3{}'.format(i)]

#make a new df grouped by number of counts for these new dfs as before
for i in list_lists:
    locals()['bindbind2{}'.format(i)] = locals()['dfPPI2E{}'.format(i)].append(locals()['dfPPI2F{}'.format(i)])
    locals()['bindbind2{}'.format(i)].drop_duplicates(subset=['Interactor_A', 'Interactor_B'], inplace=True)
    locals()['bindbind2{}'.format(i)].reset_index(drop=True, inplace=True)
```

```
    locals()['bindbind2{}'.format(i)] = \
    locals()['bindbind2{}'.format(i)].groupby(['Interactor_A']).count().reset_index().rename(
        columns={'Interactor_B':'BinderCount'})

#add everything back into the interactCount2 df
for i in list_lists:
    locals()['interactCount2{}'.format(i)] = \
    locals()['interactCount2{}'.format(i)].merge(
        locals()['bindsub2{}'.format(i)], how='left', left_on='Interactor_A', right_on='Interactor_A')
    locals()['interactCount2{}'.format(i)] = \
    locals()['interactCount2{}'.format(i)].merge(
        locals()['bindbind2{}'.format(i)], how='left', left_on='Interactor_A', right_on='Interactor_A')
    locals()['interactCount2{}'.format(i)].fillna(0, inplace=True)

#drop highly interacting proteins, sort the dataframe, and reset the index
for i in list_lists:
    locals()['interactCount2{}'.format(i)] = \
    locals()['interactCount2{}'.format(i)][
        ~(locals()['interactCount2{}'.format(i)].Interactor_A.str.contains('RPL') |
          locals()['interactCount2{}'.format(i)].Interactor_A.str.contains('RPS') |
          locals()['interactCount2{}'.format(i)].Interactor_A.str.contains('OGT') |
          locals()['interactCount2{}'.format(i)].Interactor_A.str.contains('HSP') |
          locals()['interactCount2{}'.format(i)].Interactor_A.str.contains('HNRP'))]
    locals()['interactCount2{}'.format(i)] = \
    locals()['interactCount2{}'.format(i)].sort_values(
        ['TotalCount','SubsCount','BinderCount','Interactor_A'], ascending=[0,0,0,0])
    locals()['interactCount2{}'.format(i)].reset_index(drop=True, inplace=True)

#remove things with too many interactions, total instances less than 30

#make a list of superinteractors to remove
for i in list_lists:
    locals()['filtered{}'.format(i)] = \
    locals()['interactCount{}'.format(i)][locals()['interactCount{}'.format(i)].TotalCount < 30]
    locals()['interactCount{}'.format(i)].reset_index(drop=True, inplace=True)
    locals()['filterlist{}'.format(i)] = locals()['filtered{}'.format(i)].Interactor_A.values.tolist()

#remove the super interactors from the PPI database
for i in list_lists:
    locals()['dfPPI2{}'.format(i)] = \
    locals()['dfPPI2{}'.format(i)][locals()['dfPPI2{}'.format(i)].Interactor_A.isin(locals()['filterlist{}'.format(i)])]

#remove OGT and keratin from the network
for i in list_lists:
    locals()['dfPPI2{}'.format(i)] = \
    locals()['dfPPI2{}'.format(i)][~locals()['dfPPI2{}'.format(i)].Interactor_A.str.contains('OGT')]
    locals()['dfPPI2{}'.format(i)] = \
    locals()['dfPPI2{}'.format(i)][~locals()['dfPPI2{}'.format(i)].Interactor_B.str.contains('OGT')]
    locals()['dfPPI2{}'.format(i)] = \
    locals()['dfPPI2{}'.format(i)][~locals()['dfPPI2{}'.format(i)].Interactor_A.str.contains('KRT')]
    locals()['dfPPI2{}'.format(i)] = \
    locals()['dfPPI2{}'.format(i)][~locals()['dfPPI2{}'.format(i)].Interactor_B.str.contains('KRT')]

# Assuming OGT interactor/substrate named protA
# Adds in pseudo protA-protA self interactions so that protA will be displayed
# in cytoscape no matter it has interaction to any other OGT interactor/substrates.
for i in range(4):
    locals()['dfPPI2{}'.format(list_lists[i])] = \
    locals()['dfPPI2{}'.format(list_lists[i])].append(locals()['df_binders{}'.format(list_fnames[i])])
    locals()['dfPPI2{}'.format(list_lists[i])] = \
    locals()['dfPPI2{}'.format(list_lists[i])].append(locals()['df_subs{}'.format(list_fnames2[i])])
#now merge the results from the two databases and export
#also export the interactor and substrate lists with an additional column containing 1s for cytoscape
#also export two additional columns, 'liver' and 'brain,' if the interactor or substrate is present in the liver or brain,
    #respectively

#combine the BioGRID and IntAct results and drop duplicates
for i in list_lists:
    locals()['df_combined{}'.format(i)] = \
    pd.concat([locals()['dfPPI{}'.format(i)], locals()['dfPPI2{}'.format(i)]], ignore_index=True)
    locals()['df_combined{}'.format(i)].drop_duplicates(inplace=True)
    locals()['df_combined{}'.format(i)].to_csv('PPINetwork{}F_ForCytoscape.csv'.format(i), index=False)

#add in the column of 1s to the ints and subs and export to csv for cytoscape for the first three
for i in range(3):
    locals()['df_OGTInt{}'.format(list_fnames[i])]['OGT_Interactor'] = 1
    locals()['dfOGTSubs{}'.format(list_fnames2[i])]['OGT_Substrate'] = 1
    locals()['df_OGTInt{}'.format(list_fnames[i])].to_csv('OGTInts{}F_ForCytoscape.csv'.format(list_lists[i]), index=False)
    locals()['dfOGTSubs{}'.format(list_fnames2[i])].to_csv('OGTSubs{}F_ForCytoscape.csv'.format(list_lists[i]), index=False)

#now do the same for the combined dataset but also add in columns for whether it is in the liver or brain

#import the output from the previous script for the interactors, make a new column for brain or liver, and merge it with the
    #gene list (convert all 1s to ints as well)
df_ints_brain = pd.read_csv('./20B25_Analyzed_PD_Output/InteractorsLiverBrainF_Brain.csv')
df_ints_brain['BrainInt'] = 1
df_ints_liver = pd.read_csv('./20B25_Analyzed_PD_Output/InteractorsLiverBrainF_Liver.csv')
df_ints_liver['LiverInt'] = 1
dfm_OGTIntLiverBrain = df_OGTIntLiverBrainF.merge(df_ints_brain, how='left', on='Gene')
dfm_OGTIntLiverBrain = dfm_OGTIntLiverBrain.merge(df_ints_liver, how='left', on='Gene')
dfm_OGTIntLiverBrain = dfm_OGTIntLiverBrain[['Gene', 'LiverInt', 'BrainInt']]
dfm_OGTIntLiverBrain['OGT_Interactor'] = 1
dfm_OGTIntLiverBrain[['LiverInt', 'BrainInt']] = dfm_OGTIntLiverBrain[['LiverInt', 'BrainInt']].astype('Int64')
```

```
dfm_OGTIntLiverBrain.to_csv('OGTIntsLiverBrainF_ForCytoscape.csv', index=False)

#for the substrates map the genes back to the uniprot ids and then use the original PD output 'found in' columns to make a
    #liver and brain column

#import the PD output
df_PD = pd.read_csv('./LiverBrain_Glycomics_Full/LiverBrain_Glycomics_Full_Proteins.txt', sep='\t')

#pick the relevant columns for the liver or the brain
columnsLiver = ['Found in File in F1', 'Found in File in F2', 'Found in File in F3', 'Found in File in F4']
columnsBrain = ['Found in File in F5', 'Found in File in F6', 'Found in File in F7', 'Found in File in F8']

#make a new column with True or False for whether it is found in any of the files
df_PD['LiverSub'] = df_PD[columnsLiver].ne('Not Found').any(axis=1)
df_PD['BrainSub'] = df_PD[columnsBrain].ne('Not Found').any(axis=1)

#slice out the relevant columns
df_PD2 = df_PD[['Accession', 'LiverSub', 'BrainSub']]

#replace true false with 1 or nan
df_PD2.LiverSub[df_PD2.LiverSub == False] = np.nan
df_PD2.BrainSub[df_PD2.BrainSub == False] = np.nan

#import output from previous script of the processed substrates, merge with the df above, drop irrelevant columns, and add
    #in a column of 1s (OGT_Substrate); also convert all 1s to ints
df_out_subs = pd.read_csv('./20B25_Analyzed_PD_Output/SubstratesLiverBrainFull.csv')
df_out_subs2 = df_out_subs.merge(df_PD2, how='left', on='Accession')
df_subs_out = df_out_subs2[['Gene', 'LiverSub', 'BrainSub']]
df_subs_out['OGT_Substrate'] = 1
df_subs_out[['LiverSub', 'BrainSub']] = df_subs_out[['LiverSub', 'BrainSub']].astype('Int64')
df_subs_out.to_csv('OGTSubsLiverBrainF_ForCytoscape.csv', index=False)

#the indeivudal networks can now be loaded into cytoscape and visualized
```

A5.6.4. Sites and Regions Analysis.

This script was run twice, first, with the data from searched against the full proteins, and second, with the data searched against the Swiss-Prot proteome. The analysis has 5 parts:

1. Processing of the 293T, brain, and liver datasets separately. This will serve to calculate the total number of sites in each of the tissues.
2. Processing with the multiple experiments sites and regions script to keep the ETD and EThcD runs separate and then calculating the overlap between them for 293T cells, brain, and liver.
3. Filtering the input data by activation type and running the sites and regions separately for the 293T cells, brain, and liver. This will allow us to calculate both the total and stratified (i.e. regions vs sites with xx localization probability) number of sites and regions found by each activation method.
4. Using the multiple experiments sites and regions script on the brain/liver combined search to calculate the site/region level overlap between the two tissues.

5. Finally, using the multiple experiments sites and regions script for the BAP1 KO quantitative glycomics samples. Raw files are separated to compare top speed to top N before averaging the top speeed/top N for the analysis. Then, limma is used to find the significantly changing sites and normalize the rations to their protein expression

```
#import python packages
import re
import sys
import pandas as pd
import networkx as nx
import itertools as it
from collections import namedtuple
import numpy as np
import matplotlib
import matplotlib.pyplot as plt
from IPython.display import display
from functools import reduce
import seaborn as sns; sns.set()
from io import StringIO
from matplotlib_venn import venn2_unweighted #the unweighted is if you want to make circles that are the same size
from matplotlib_venn import venn2 #also import the normal one
import pandas as pd
import numpy as np
from io import StringIO
import urllib.request, urllib.parse, urllib.error,urllib.request,urllib.error,urllib.parse

#set up R environment and import R packages
import rpy2
import rpy2.ipython
%load_ext rpy2.ipython

#require R packages
%R require(limma)
%R require(ibb)

#magic function to show plots inline
%matplotlib inline

#ignore warnings
import warnings
warnings.filterwarnings("ignore")
#Import the necessary files (I am only using the full proteome searches)

#list the filenames
fname0 = './293T_Glycomics_Full/293T_Glycomics_Full_PSMs.txt'
fname1 = './Brain_Glycomics_Full/Brain_Glycomics_Full_PSMs.txt'
fname2 = './Liver_Glycomics_Full/Liver_Glycomics_Full_PSMs.txt'
fname3 = './LiverBrain_Glycomics_Full/LiverBrain_Glycomics_Full_PSMs.txt'
fnameq = './BAP1KO_Glycomics_Full/BAP1KO_Glycomics_Full_PSMs.txt'
fnamep = './BAP1KO_ProteinExpression_Full/BAP1KO_ProteinExpression_Full_Proteins.txt' #protein expression
list_fnames = [fname0, fname1, fname2, fname3, fnameq]
#Preprocess the data for the sites and regions script, starting with the individual runs
#Partially based on preprocessPD.py from Mike Sweredoski 1/24/2020

SITE_NAME = "GlcNAc502" #define the mod name

#make a list for naming the dfs
list_dfs = ['293T', 'Brain', 'Liver', 'LiverBrain', 'Quant']

#set up a for loop for completing the operations on all dfs
for i in range(4):
    locals()['df{}'.format(list_dfs[i])] = pd.read_csv(list_fnames[i], sep='\t').rename(columns={
        "Spectrum File":"RawFile","Master Protein Accessions":"Protein","First Scan":"ScanNumber",
        "Activation Type":"Fragmentation"})
    locals()['df{}'.format(list_dfs[i])]['Fragmentation'] = \
    locals()['df{}'.format(list_dfs[i])]['Fragmentation'].map(lambda x: x.split(' ', 1)[0])
    locals()['df{}'.format(list_dfs[i])].Modifications.dropna(inplace=True)
    locals()['df{}'.format(list_dfs[i])]["NumMods"] = locals()['df{}'.format(list_dfs[i])]["Modifications"].apply(
        lambda s: s.count(SITE_NAME))
    locals()['df{}'.format(list_dfs[i])] = \
    locals()['df{}'.format(list_dfs[i])][locals()['df{}'.format(list_dfs[i])]["NumMods"]>0]
    locals()['df{}'.format(list_dfs[i])]["Probabilities"] = \
    locals()['df{}'.format(list_dfs[i])]["ptmRS %s Site Probabilities"%SITE_NAME].apply(
        lambda s: ";".join([str(round(float(v.split()[-1])/100, 3)) for v in s.split("; ")]))
    locals()['df{}'.format(list_dfs[i])]["Positions"] = \
    locals()['df{}'.format(list_dfs[i])].apply(lambda x: ";".join(
        [str(int(v.split("(")[1].split(")")[0])-1+x["Position in Protein"]) for v in x[
            "ptmRS %s Site Probabilities"%SITE_NAME].split("; ")]),axis=1)

#repeat for the BAP1 KO run (different SITE_NAME)
Q_SITE_NAME = "GlcNAc731"
```

```
i=4
locals()['df{}'.format(list_dfs[i])] = pd.read_csv(list_fnames[i], sep='\t').rename(columns={
    "Spectrum File":"RawFile","Master Protein Accessions":"Protein","First Scan":"ScanNumber",
    "Activation Type":"Fragmentation"})
locals()['df{}'.format(list_dfs[i])]['Fragmentation'] = \
locals()['df{}'.format(list_dfs[i])]['Fragmentation'].map(lambda x: x.split(' ', 1)[0])
locals()['df{}'.format(list_dfs[i])].Modifications.dropna(inplace=True)
locals()['df{}'.format(list_dfs[i])]["NumMods"] = locals()['df{}'.format(list_dfs[i])]["Modifications"].apply(
    lambda s: s.count(Q_SITE_NAME))
locals()['df{}'.format(list_dfs[i])] = \
locals()['df{}'.format(list_dfs[i])][locals()['df{}'.format(list_dfs[i])]["NumMods"]>0]
locals()['df{}'.format(list_dfs[i])]["Probabilities"] = \
locals()['df{}'.format(list_dfs[i])]["ptmRS %s Site Probabilities"%Q_SITE_NAME].apply(
    lambda s: ";".join([str(round(float(v.split()[-1])/100, 3)) for v in s.split("; ")]))
locals()['df{}'.format(list_dfs[i])]["Positions"] = \
locals()['df{}'.format(list_dfs[i])].apply(lambda x: ";".join(
    [str(int(v.split("(")[1].split(")")[0])-1+x["Position in Protein"]) for v in x[
        "ptmRS %s Site Probabilities"%Q_SITE_NAME].split("; ")]),axis=1)

#choose columns to keep
cols_to_keep = ["RawFile","Fragmentation","ScanNumber","Protein","Positions","Probabilities","NumMods"]

for i in range(5):
    locals()['df{}_table'.format(list_dfs[i])] = locals()['df{}'.format(list_dfs[i])][cols_to_keep]
```

Part 1

```
### Set All HCD Localization Probabilities Equal Across S/Ts ###

#PD/ptmRS cannot handle glycan NLs, so the localization probabilities for HCD are patently wrong
#Because the glycan is almost always lost, I will set the localization probability to equal for all S/Ts
#This seems to be a reasonable assumption after manually curating dozens of sepctra

#write a for loop to perform this for all dfs
for i in list_dfs:
    #count the number of S/Ts
    locals()['df{}_table'.format(i)]['NumSites'] = locals()['df{}_table'.format(i)].Probabilities.str.count(';') + 1
    #calculate the probability at each site based on the number of S/Ts (round to 3 decimals as in PD)
    locals()['df{}_table'.format(i)]['Prob'] = round(1/locals()['df{}_table'.format(i)].NumSites, 3)
    #define a function to make a repeating list of probability values based on the number of S/Ts
    def repeat(row):
        return [row.Prob]*row.NumSites
    #apply this function to each df
    locals()['df{}_table'.format(i)]['ProbList'] = locals()['df{}_table'.format(i)].apply(repeat, axis=1)
    #transform the list into a semi-colon separated string for the sites and regions script
    locals()['df{}_table'.format(i)]['ProbListFinal'] = locals()['df{}_table'.format(i)].ProbList.apply(
        lambda s: ';'.join(map(str, s)))
    #replace the probability values for HCD
    locals()['df{}_table'.format(i)].loc[locals()['df{}_table'.format(i)].Fragmentation == 'HCD', 'Probabilities'] = \
    locals()['df{}_table'.format(i)].ProbListFinal
    #remake the original table with the columns required for the sites and regions script
    locals()['df{}_tableF'.format(i)] = locals()['df{}_table'.format(i)][cols_to_keep]
    #export final tables to tsv files
    locals()['df{}_tableF'.format(i)].to_csv(
        './20D15_SitesAndRegions/{}_Preprocessed.txt'.format(i), sep='\t', index=False)
%%capture
#supresses the output of the cell

#run the sites and regions script for each experiment
%run -i SitesAndRegions.py 20D15_SitesAndRegions/293T_Preprocessed.txt 20D15_SitesAndRegions/maxparcon_293T.txt \
20D15_SitesAndRegions/bestms2_293T.txt
%run -i SitesAndRegions.py 20D15_SitesAndRegions/Brain_Preprocessed.txt 20D15_SitesAndRegions/maxparcon_Brain.txt \
20D15_SitesAndRegions/bestms2_Brain.txt
%run -i SitesAndRegions.py 20D15_SitesAndRegions/Liver_Preprocessed.txt 20D15_SitesAndRegions/maxparcon_Liver.txt \
20D15_SitesAndRegions/bestms2_Liver.txt
%run -i SitesAndRegions.py 20D15_SitesAndRegions/LiverBrain_Preprocessed.txt \
20D15_SitesAndRegions/maxparcon_LiverBrain.txt 20D15_SitesAndRegions/bestms2_LiverBrain.txt
%run -i SitesAndRegions.py 20D15_SitesAndRegions/Quant_Preprocessed.txt 20D15_SitesAndRegions/maxparcon_BAP1KO.txt \
20D15_SitesAndRegions/bestms2_BAP1KO.txt
#import the sites and regions output into dfs and count the number of sites for each

list_dfs2 = ['293T', 'Brain', 'Liver', 'LiverBrain', 'BAP1KO']

for i in list_dfs2:
    locals()['dfallsites_{}'.format(i)] = pd.read_csv('./20D15_SitesAndRegions/bestms2_{}.txt'.format(i), sep='\t')
    locals()['dfregions_{}'.format(i)] = pd.read_csv('./20D15_SitesAndRegions/maxparcon_{}.txt'.format(i), sep='\t')
    #remove sites/regions that match to two master proteins
    #this seems to happen sometimes when there is real evidence of two isoforms
    #all cases checked were already explained by other data, so they can be reasonably ignored
    locals()['dfregions_{}'.format(i)] = locals()['dfregions_{}'.format(i)][
        ~locals()['dfregions_{}'.format(i)].Protein.str.contains(';')]
    locals()['dfallsites_{}'.format(i)] = locals()['dfallsites_{}'.format(i)][
        ~locals()['dfallsites_{}'.format(i)].Protein.str.contains(';')]

#initialize an empty df
df_numsites = pd.DataFrame(np.empty((5,5)))

#calculate the number of sites, localized sites, and regions
for i in range (5):
    #set the column and index names
    df_numsites.columns = [['Total Number of Sites', 'Localized Sites', 'Unlocalized Sites', 'Regions',
                            'Percent Localized']]
    df_numsites.rename(index={i:list_dfs2[i]}, inplace=True)
    #count the total number of sites
```

```
    df_numsites.loc[list_dfs2[i], 'Total Number of Sites'] = \
    locals()['dfregions_{}'.format(list_dfs2[i])]['Min Sites'].sum()
    #count the number of localized sites
    df_numsites.loc[list_dfs2[i], 'Localized Sites'] = len(
        locals()['dfregions_{}'.format(list_dfs2[i])][
            locals()['dfregions_{}'.format(list_dfs2[i])]['Site ID Constraints'].str.contains('of') == False])
    df_numsites.loc[list_dfs2[i], 'Unlocalized Sites'] = locals()['dfregions_{}'.format(list_dfs2[i])][
        locals()['dfregions_{}'.format(list_dfs2[i])][
            'Site ID Constraints'].str.contains('of') == True]['Min Sites'].sum()
    df_numsites.loc[list_dfs2[i], 'Regions'] = len(
        locals()['dfregions_{}'.format(list_dfs2[i])][
            locals()['dfregions_{}'.format(list_dfs2[i])]['Site ID Constraints'].str.contains('of') == True])
    df_numsites.loc[list_dfs2[i], 'Percent Localized'] = \
    (df_numsites.loc[list_dfs2[i], 'Localized Sites'].to_numpy() / df_numsites.loc[
        list_dfs2[i], 'Total Number of Sites'].to_numpy())*100

df_numsites = df_numsites.astype(int) #convert to ints
df_numsites.to_csv('TotalSitesAndRegionsAll.csv') #export
df_numsites #inspect
#make a pie chart of the sites and regions (with the sites stratified by localization probability)

#add to the max parsimonious site constraints file whether each region is a site or a region
for i in list_dfs2:
    locals()['dfregions_{}'.format(i)].loc[
        locals()['dfregions_{}'.format(i)]['Site ID Constraints'].str.contains('of'), 'Type'] = 'Region'
    locals()['dfregions_{}'.format(i)].loc[
        ~locals()['dfregions_{}'.format(i)]['Site ID Constraints'].str.contains('of'), 'Type'] = 'Site'

#merge with best ms2 for sites file
for i in list_dfs2:
    locals()['dfmerge_{}'.format(i)] = locals()['dfallsites_{}'.format(i)].merge(
        locals()['dfregions_{}'.format(i)], how='left', on='Region ID')
    #now fill the bins with values for the pie chart
    locals()['regions_{}'.format(i)] = locals()['dfregions_{}'.format(i)][
        locals()['dfregions_{}'.format(i)].Type == 'Region']['Min Sites'].sum()
    locals()['bin975_{}'.format(i)] = len(
        locals()['dfmerge_{}'.format(i)][(locals()['dfmerge_{}'.format(i)].Type == 'Site') &
                                         (locals()['dfmerge_{}'.format(i)]['Best Probability'] < 0.975)])
    locals()['bin99_{}'.format(i)] = len(
        locals()['dfmerge_{}'.format(i)][(locals()['dfmerge_{}'.format(i)].Type == 'Site') &
                                         ((locals()['dfmerge_{}'.format(i)]['Best Probability'] >= 0.975) &
                                          (locals()['dfmerge_{}'.format(i)]['Best Probability'] < 0.99))])
    locals()['bin991_{}'.format(i)] = len(
        locals()['dfmerge_{}'.format(i)][(locals()['dfmerge_{}'.format(i)].Type == 'Site') &
                                         ((locals()['dfmerge_{}'.format(i)]['Best Probability'] >= 0.99) &
                                          (locals()['dfmerge_{}'.format(i)]['Best Probability'] < 1))])
    locals()['bin1_{}'.format(i)] = len(
        locals()['dfmerge_{}'.format(i)][(locals()['dfmerge_{}'.format(i)].Type == 'Site') &
                                         (locals()['dfmerge_{}'.format(i)]['Best Probability'] == 1)])
#make the pie charts
for i in list_dfs2:
    locals()['list_values_{}'.format(i)] = [locals()['regions_{}'.format(i)], locals()['bin975_{}'.format(i)],
                                            locals()['bin99_{}'.format(i)], locals()['bin991_{}'.format (i)],
                                            locals()['bin1_{}'.format(i)]]

sns.set_context('paper')

#make a list of labels and colors to use
list_labels = ['Unlocalized', '<97.5%', '97.5-99%', '99-100%', '100%']
colors = ["#cbcdcd", "#f39b9f", "#9aacd7", "#be9ec7", "#b3e0a7"]
explode = (0.1, 0, 0, 0, 0) #to have the regions pop out separately

###293T###
plt.figure()
plt.title('293T')
p, tx, nums = plt.pie(list_values_293T, labels=list_labels, colors=colors, autopct="", explode=explode, startangle=90)
for i, a in enumerate(nums):
    a.set_text('{}'.format(list_values_293T[i]))
local_prob_293T = str(round(dfmerge_293T[dfmerge_293T.Type == 'Site']['Best Probability'].mean()*100, 1)) + '%'
plt.gcf().text(0.9, 0.5, local_prob_293T, fontsize=12)
plt.savefig('./20D15_SitesAndRegions/293T_PieChart.svg')
plt.show()

###Brain###
plt.figure()
plt.title('Brain')
p, tx, nums = plt.pie(list_values_Brain, labels=list_labels, colors=colors, autopct="", explode=explode, startangle=90)
for i, a in enumerate(nums):
    a.set_text('{}'.format(list_values_Brain[i]))
local_prob_Brain = str(round(dfmerge_Brain[dfmerge_Brain.Type == 'Site']['Best Probability'].mean()*100, 1)) + '%'
plt.gcf().text(0.9, 0.5, local_prob_Brain, fontsize=12)
plt.savefig('./20D15_SitesAndRegions/Brain_PieChart.svg')
plt.show()

###Liver###
plt.figure()
plt.title('Liver')
p, tx, nums = plt.pie(list_values_Liver, labels=list_labels, colors=colors, autopct="", explode=explode, startangle=90)
for i, a in enumerate(nums):
    a.set_text('{}'.format(list_values_Liver[i]))
local_prob_Liver = str(round(dfmerge_Liver[dfmerge_Liver.Type == 'Site']['Best Probability'].mean()*100, 1)) + '%'
plt.gcf().text(0.9, 0.5, local_prob_Liver, fontsize=12)
plt.savefig('./20D15_SitesAndRegions/Liver_PieChart.svg')
```

```
plt.show()

###LiverBrain###
plt.figure()
plt.title('LiverBrain')
p, tx, nums = plt.pie(list_values_LiverBrain, labels=list_labels, colors=colors, autopct="", explode=explode,
                      startangle=90)
for i, a in enumerate(nums):
    a.set_text('{}'.format(list_values_LiverBrain[i]))
local_prob_LiverBrain = str(round(
    dfmerge_LiverBrain[dfmerge_LiverBrain.Type == 'Site']['Best Probability'].mean()*100, 1)) + '%'
plt.gcf().text(0.9, 0.5, local_prob_LiverBrain, fontsize=12)
plt.savefig('./20D15_SitesAndRegions/LiverBrain_PieChart.svg')
plt.show()

###BAP1 KO###
plt.figure()
plt.title('BAP1 KO')
p, tx, nums = plt.pie(list_values_BAP1KO, labels=list_labels, colors=colors, autopct="", explode=explode, startangle=90)
for i, a in enumerate(nums):
    a.set_text('{}'.format(list_values_BAP1KO[i]))
local_prob_BAP1KO = str(round(dfmerge_BAP1KO[dfmerge_BAP1KO.Type == 'Site']['Best Probability'].mean()*100, 1)) + '%'
plt.gcf().text(0.9, 0.5, local_prob_BAP1KO, fontsize=12)
plt.savefig('./20D15_SitesAndRegions/BAP1KO_PieChart.svg')
plt.show()
```

Part 2

```
#Copy the dfs to new dfs for part 2
#Make a new 'Experiment' column based on the raw file and export for the sites and regions multi-experiment script

for i in list_dfs[0:4]:
    locals()['df{}_tableF_2'.format(i)] = locals()['df{}_tableF'.format(i)].copy()
    locals()['df{}_tableF_2'.format(i)].loc[
        locals()['df{}_tableF_2'.format(i)].RawFile.str.contains('ETD'), 'Experiment'] = 'ETD'
    locals()['df{}_tableF_2'.format(i)].loc[
        locals()['df{}_tableF_2'.format(i)].RawFile.str.contains('EThcD'), 'Experiment'] = 'EThcD'
    locals()['df{}_tableF_2'.format(i)].to_csv(
        './20D15_SitesAndRegions/{}_Preprocessed_2.txt'.format(i), sep='\t', index=False)
%%capture
#supresses the output of the cell

#run the sites and regions script for each experiment
%run -i SitesAndRegionsMultiExperiment.py 20D15_SitesAndRegions/293T_Preprocessed_2.txt \
20D15_SitesAndRegions/maxparcon_293T_2.txt 20D15_SitesAndRegions/bestms2_293T_2.txt
%run -i SitesAndRegionsMultiExperiment.py 20D15_SitesAndRegions/Brain_Preprocessed_2.txt \
20D15_SitesAndRegions/maxparcon_Brain_2.txt 20D15_SitesAndRegions/bestms2_Brain_2.txt
%run -i SitesAndRegionsMultiExperiment.py 20D15_SitesAndRegions/Liver_Preprocessed_2.txt \
20D15_SitesAndRegions/maxparcon_Liver_2.txt 20D15_SitesAndRegions/bestms2_Liver_2.txt
%run -i SitesAndRegionsMultiExperiment.py 20D15_SitesAndRegions/LiverBrain_Preprocessed_2.txt \
20D15_SitesAndRegions/maxparcon_LiverBrain_2.txt 20D15_SitesAndRegions/bestms2_LiverBrain_2.txt
#reimport the output
for i in list_dfs2[0:4]:
    locals()['dfallsites2_{}'.format(i)] = pd.read_csv('./20D15_SitesAndRegions/bestms2_{}_2.txt'.format(i), sep='\t')
    locals()['dfregions2_{}'.format(i)] = pd.read_csv('./20D15_SitesAndRegions/maxparcon_{}_2.txt'.format(i), sep='\t')
    #remove sites/regions that match to two master proteins
    #this seems to happen sometimes when there is real evidence of two isoforms
    #all cases checked were already explained by other data, so they can be reasonably ignored
    locals()['dfregions2_{}'.format(i)] = locals()['dfregions2_{}'.format(i)][
        ~locals()['dfregions2_{}'.format(i)].Protein.str.contains(';')]
    locals()['dfallsites2_{}'.format(i)] = locals()['dfallsites2_{}'.format(i)][
        ~locals()['dfallsites2_{}'.format(i)].Protein.str.contains(';')]

#add to the max parsimonious site constraints file whether each region is a site or a region
for i in list_dfs2[0:4]:
    locals()['dfregions2_{}'.format(i)].loc[
        locals()['dfregions2_{}'.format(i)]['Site ID Constraints'].str.contains('of'), 'Type'] = 'Region'
    locals()['dfregions2_{}'.format(i)].loc[
        ~locals()['dfregions2_{}'.format(i)]['Site ID Constraints'].str.contains('of'), 'Type'] = 'Site'

#merge the two dfs together and count up how many sites are found in the ETD vs EThcD runs
for i in list_dfs2[0:4]:
    locals()['dfmerge2_{}'.format(i)] = locals()['dfallsites2_{}'.format(i)].merge(
        locals()['dfregions2_{}'.format(i)], how='left', on='Region ID')
    #define a function to make a new column stating which experiment each region id belongs to and apply it to merged df
    def experiment(x):
        if x.Experiment.eq('ETD').all():
            return 'ETD'
        elif x.Experiment.eq('EThcD').all():
            return 'EThcD'
        else:
            return 'Both'
    locals()['df2_exp_{}'.format(i)] = locals()['dfmerge2_{}'.format(i)].groupby(['Region ID']).apply(experiment)
    #make a new column in the regions df with the experiments each region was found in
    locals()['dfregions2_{}'.format(i)]['Experiment'] = locals()['df2_exp_{}'.format(i)]
    locals()['series2_{}'.format(i)] = locals()['dfregions2_{}'.format(i)].groupby('Experiment')['Min Sites'].sum()
#Make Venn diagrams of the overlapping sites

for i in list_dfs[0:4]:
    plt.figure(figsize=(7,7))
    fig = venn2([locals()['series2_{}'.format(i)][1], locals()['series2_{}'.format(i)][2],
                 locals()['series2_{}'.format(i)][0]], ('ETD', 'EThcD'))
    plt.title('{}'.format(i), fontsize=42)
    fig.get_patch_by_id('10').set_color('#5b7992')
```

```
    fig.get_patch_by_id('01').set_color('#aaaaaa')
    fig.get_patch_by_id('10').set_edgecolor('none')
    fig.get_patch_by_id('01').set_edgecolor('none')
    fig.get_patch_by_id('10').set_alpha(0.75)
    fig.get_patch_by_id('01').set_alpha(0.5)
    fig.get_patch_by_id('11').set_color('#027FF0')
    fig.get_patch_by_id('11').set_edgecolor('none')
    fig.get_patch_by_id('11').set_alpha(0.5)
    for text in fig.set_labels: #need to call named object 'fig' from above, font size is set numerically
        text.set_fontsize(36) #this is the label names
    for text in fig.subset_labels:
        text.set_fontsize(28) #this will change the numbers
    plt.savefig('./20D15_SitesAndRegions/{}_ET(hc)D_TrialOverlap.svg'.format(i))
    plt.show()
```

Part 3

```
#Copy the dfs to new dfs for part 2
#Separate and export the data from the different fragmentation types separately

list_frag = ['HCD', 'ETD', 'EThcD']

for i in list_dfs:
    locals()['df{}_tableF_3'.format(i)] = locals()['df{}_tableF'.format(i)].copy()
    for j in list_frag:
        locals()['df{}_tableF_3_{}'.format(i,j)] = locals()['df{}_tableF_3'.format(i)][
            locals()['df{}_tableF_3'.format(i)].Fragmentation == j]
        locals()['df{}_tableF_3_{}'.format(i,j)].to_csv(
            './20D15_SitesAndRegions/{}_{}_Preprocessed_3.txt'.format(i,j), sep='\t', index=False)
    locals()['df{}_tableF_3'.format(i)]['NumST'] = locals()['df{}_tableF_3'.format(i)].Probabilities.str.count(';') + 1
%%capture
#supresses the output of the cell

#run the sites and regions script for each experiment
%run -i SitesAndRegions.py 20D15_SitesAndRegions/293T_ETD_Preprocessed_3.txt \
20D15_SitesAndRegions/maxparcon_293T_ETD_3.txt 20D15_SitesAndRegions/bestms2_293T_ETD_3.txt
%run -i SitesAndRegions.py 20D15_SitesAndRegions/293T_EThcD_Preprocessed_3.txt \
20D15_SitesAndRegions/maxparcon_293T_EThcD_3.txt 20D15_SitesAndRegions/bestms2_293T_EThcD_3.txt
%run -i SitesAndRegions.py 20D15_SitesAndRegions/293T_HCD_Preprocessed_3.txt \
20D15_SitesAndRegions/maxparcon_293T_HCD_3.txt 20D15_SitesAndRegions/bestms2_293T_HCD_3.txt

%run -i SitesAndRegions.py 20D15_SitesAndRegions/Brain_ETD_Preprocessed_3.txt \
20D15_SitesAndRegions/maxparcon_Brain_ETD_3.txt 20D15_SitesAndRegions/bestms2_Brain_ETD_3.txt
%run -i SitesAndRegions.py 20D15_SitesAndRegions/Brain_EThcD_Preprocessed_3.txt \
20D15_SitesAndRegions/maxparcon_Brain_EThcD_3.txt 20D15_SitesAndRegions/bestms2_Brain_EThcD_3.txt
%run -i SitesAndRegions.py 20D15_SitesAndRegions/Brain_HCD_Preprocessed_3.txt \
20D15_SitesAndRegions/maxparcon_Brain_HCD_3.txt 20D15_SitesAndRegions/bestms2_Brain_HCD_3.txt

%run -i SitesAndRegions.py 20D15_SitesAndRegions/Liver_ETD_Preprocessed_3.txt \
20D15_SitesAndRegions/maxparcon_Liver_ETD_3.txt 20D15_SitesAndRegions/bestms2_Liver_ETD_3.txt
%run -i SitesAndRegions.py 20D15_SitesAndRegions/Liver_EThcD_Preprocessed_3.txt \
20D15_SitesAndRegions/maxparcon_Liver_EThcD_3.txt 20D15_SitesAndRegions/bestms2_Liver_EThcD_3.txt
%run -i SitesAndRegions.py 20D15_SitesAndRegions/Liver_HCD_Preprocessed_3.txt \
20D15_SitesAndRegions/maxparcon_Liver_HCD_3.txt 20D15_SitesAndRegions/bestms2_Liver_HCD_3.txt

%run -i SitesAndRegions.py 20D15_SitesAndRegions/LiverBrain_ETD_Preprocessed_3.txt \
20D15_SitesAndRegions/maxparcon_LiverBrain_ETD_3.txt 20D15_SitesAndRegions/bestms2_LiverBrain_ETD_3.txt
%run -i SitesAndRegions.py 20D15_SitesAndRegions/LiverBrain_EThcD_Preprocessed_3.txt \
20D15_SitesAndRegions/maxparcon_LiverBrain_EThcD_3.txt 20D15_SitesAndRegions/bestms2_LiverBrain_EThcD_3.txt
%run -i SitesAndRegions.py 20D15_SitesAndRegions/LiverBrain_HCD_Preprocessed_3.txt \
20D15_SitesAndRegions/maxparcon_LiverBrain_HCD_3.txt 20D15_SitesAndRegions/bestms2_LiverBrain_HCD_3.txt

%run -i SitesAndRegions.py 20D15_SitesAndRegions/Quant_ETD_Preprocessed_3.txt \
20D15_SitesAndRegions/maxparcon_BAP1KO_ETD_3.txt 20D15_SitesAndRegions/bestms2_BAP1KO_ETD_3.txt
%run -i SitesAndRegions.py 20D15_SitesAndRegions/Quant_EThcD_Preprocessed_3.txt \
20D15_SitesAndRegions/maxparcon_BAP1KO_EThcD_3.txt 20D15_SitesAndRegions/bestms2_BAP1KO_EThcD_3.txt
%run -i SitesAndRegions.py 20D15_SitesAndRegions/Quant_HCD_Preprocessed_3.txt \
20D15_SitesAndRegions/maxparcon_BAP1KO_HCD_3.txt 20D15_SitesAndRegions/bestms2_BAP1KO_HCD_3.txt
#reimport the output and process as before also adding back in whether each is a site or a region
#also match the raw file/scan number back to the preprocessed df which has the number of S/Ts

#rename dfQuant_tableF_3 to dfBAP1KO... to make the scipt match
dfBAP1KO_tableF_3 = dfQuant_tableF_3

for i in list_dfs2:
    for j in list_frag:
        locals()['dfallsites3_{}_{}'.format(i,j)] = pd.read_csv(
            './20D15_SitesAndRegions/bestms2_{}_{}_3.txt'.format(i, j), sep='\t')
        locals()['dfregions3_{}_{}'.format(i,j)] = pd.read_csv(
            './20D15_SitesAndRegions/maxparcon_{}_{}_3.txt'.format(i, j), sep='\t')
        locals()['dfallsites3_{}_{}'.format(i,j)] = locals()['dfallsites3_{}_{}'.format(i,j)][
            ~locals()['dfallsites3_{}_{}'.format(i,j)].Protein.str.contains(';')]
        locals()['dfregions3_{}_{}'.format(i,j)] = locals()['dfregions3_{}_{}'.format(i,j)][
            ~locals()['dfregions3_{}_{}'.format(i,j)].Protein.str.contains(';')]
        locals()['dfregions3_{}_{}'.format(i,j)].loc[
            locals()['dfregions3_{}_{}'.format(i,j)]['Site ID Constraints'].str.contains('of'), 'Type'] = 'Region'
        locals()['dfregions3_{}_{}'.format(i,j)].loc[
            ~locals()['dfregions3_{}_{}'.format(i,j)]['Site ID Constraints'].str.contains('of'), 'Type'] = 'Site'
        locals()['dfmerge3_{}_{}'.format(i,j)] = locals()['dfallsites3_{}_{}'.format(i,j)].merge(
            locals()['dfregions3_{}_{}'.format(i,j)], how='left', on='Region ID')
        locals()['dfmerge3_{}_{}'.format(i,j)].rename(
            columns={'Best Raw File':'RawFile', 'Best Scan Number':'ScanNumber'}, inplace=True)
        locals()['dfmerge3_{}_{}'.format(i,j)] = locals()['dfmerge3_{}_{}'.format(i,j)].merge(
            locals()['df{}_tableF_3'.format(i)], how='left', on=['RawFile', 'ScanNumber'])
```

```
        locals()['dfmerge3_{}_{}'.format(i,j)].drop(
            columns={'Protein_y', 'Fragmentation', 'Protein', 'Positions', 'Probabilities', 'NumMods'}, inplace=True)
        locals()['dfmerge3_{}_{}'.format(i,j)].rename(columns={'Protein_x':'Protein'}, inplace=True)
#output the numbers of sites and regions in each df (see above for making dfs)
for i in range(5):
    locals()['df_numsites3_{}'.format(list_dfs2[i])] = pd.DataFrame(np.empty((3,7)))
    for j in range(3):
        locals()['df_numsites3_{}'.format(list_dfs2[i])].columns = ['Total Number of Sites', 'Localized Sites',
                                                    'Average Localization Probability', 'Single ST',
                                                    'Unlocalized Sites', 'Regions', 'Percent Localized']
        locals()['dftemp3_{}_{}'.format(list_dfs2[i], list_frag[j])] = \
        locals()['dfmerge3_{}_{}'.format(list_dfs2[i], list_frag[j])][['Region ID', 'NumST']]
        locals()['dftemp3_{}_{}'.format(list_dfs2[i], list_frag[j])].drop_duplicates(inplace=True)
        locals()['dfregions3_{}_{}'.format(list_dfs2[i],list_frag[j])] = \
        locals()['dfregions3_{}_{}'.format(list_dfs2[i],list_frag[j])].merge(
            locals()['dftemp3_{}_{}'.format(list_dfs2[i], list_frag[j])], how='left', on='Region ID')
        locals()['df_numsites3_{}'.format(list_dfs2[i])].rename(index={j:list_frag[j]}, inplace=True)
        locals()['df_numsites3_{}'.format(list_dfs2[i])].loc[list_frag[j], 'Total Number of Sites'] = \
        locals()['dfregions3_{}_{}'.format(list_dfs2[i],list_frag[j])]['Min Sites'].sum()
        locals()['df_numsites3_{}'.format(list_dfs2[i])].loc[list_frag[j], 'Localized Sites'] = len(
            locals()['dfregions3_{}_{}'.format(list_dfs2[i],list_frag[j])][
                (locals()['dfregions3_{}_{}'.format(list_dfs2[i],list_frag[j])].Type == 'Site') & \
                (locals()['dfregions3_{}_{}'.format(list_dfs2[i],list_frag[j])].NumST != 1)])
        locals()['df_numsites3_{}'.format(list_dfs2[i])].loc[list_frag[j], 'Average Localization Probability'] = \
        (locals()['dfmerge3_{}_{}'.format(list_dfs2[i], list_frag[j])][
            (locals()['dfmerge3_{}_{}'.format(list_dfs2[i], list_frag[j])].Type == 'Site') & \
            (locals()['dfmerge3_{}_{}'.format(list_dfs2[i], list_frag[j])].NumST != 1)]['Best Probability'].mean())*100
        locals()['df_numsites3_{}'.format(list_dfs2[i])].loc[list_frag[j], 'Single ST'] = len(
            locals()['dfregions3_{}_{}'.format(list_dfs2[i],list_frag[j])][
                locals()['dfregions3_{}_{}'.format(list_dfs2[i],list_frag[j])].NumST == 1])
        locals()['df_numsites3_{}'.format(list_dfs2[i])].loc[list_frag[j], 'Unlocalized Sites'] = \
        locals()['dfregions3_{}_{}'.format(list_dfs2[i],list_frag[j])][
            locals()['dfregions3_{}_{}'.format(list_dfs2[i],list_frag[j])].Type == 'Region']['Min Sites'].sum()
        locals()['df_numsites3_{}'.format(list_dfs2[i])].loc[list_frag[j], 'Regions'] = len(
            locals()['dfregions3_{}_{}'.format(list_dfs2[i],list_frag[j])][
                locals()['dfregions3_{}_{}'.format(list_dfs2[i],list_frag[j])].Type == 'Region'])
        locals()['df_numsites3_{}'.format(list_dfs2[i])].loc[list_frag[j], 'Percent Localized'] = \
        (locals()['df_numsites3_{}'.format(list_dfs2[i])].loc[list_frag[j], 'Localized Sites'] / \
        locals()['df_numsites3_{}'.format(list_dfs2[i])].loc[list_frag[j], 'Total Number of Sites'])*100
        locals()['df_numsites3_{}'.format(list_dfs2[i])] = locals()['df_numsites3_{}'.format(list_dfs2[i])].astype({
            'Total Number of Sites':int, 'Localized Sites':int, 'Single ST':int, 'Unlocalized Sites':int, 'Regions':int})
#output the previous info to csv  files
for i in list_dfs2:
    locals()['df_numsites3_{}'.format(i)].to_csv('SitesAndRegionsByFrag_{}.csv'.format(i))

display(df_numsites3_293T)
display(df_numsites3_Brain)
display(df_numsites3_Liver)
display(df_numsites3_LiverBrain)
display(df_numsites3_BAP1KO)
#Now I will calculate the overlap between ETD and EThcD localized sites only, first make sets of the sites

#make a new list for just ETD and EThcD
list_frag2 = ['ETD', 'EThcD']

#concatentate the protein and position ot make a unique site identifier
#make sets out of these unique site identifiers for each sample
for i in list_dfs2:
    for j in list_frag2:
        locals()['dfmerge3_{}_{}'.format(i,j)]['Site'] = \
        locals()['dfmerge3_{}_{}'.format(i,j)].Protein.str.cat(
            locals()['dfmerge3_{}_{}'.format(i,j)].Position.astype(str), sep='@')
        locals()['set3_{}_{}'.format(i,j)] = set(
            locals()['dfmerge3_{}_{}'.format(i,j)][(locals()['dfmerge3_{}_{}'.format(i,j)].Type == 'Site') & \
                                    (locals()['dfmerge3_{}_{}'.format(i,j)].NumST != 1)].Site)
#Now make the Venn diagrams

for i in list_dfs2:
    plt.figure(figsize=(7,7))
    fig = venn2([locals()['set3_{}_ETD'.format(i)], locals()['set3_{}_EThcD'.format(i)]], ('ETD', 'EThcD'))
    plt.title('{}'.format(i), fontsize=42)
    fig.get_patch_by_id('10').set_color('#5b7992')
    fig.get_patch_by_id('01').set_color('#aaaaaa')
    fig.get_patch_by_id('10').set_edgecolor('none')
    fig.get_patch_by_id('01').set_edgecolor('none')
    fig.get_patch_by_id('10').set_alpha(0.75)
    fig.get_patch_by_id('01').set_alpha(0.5)
    fig.get_patch_by_id('11').set_color('#027FF0')
    fig.get_patch_by_id('11').set_edgecolor('none')
    fig.get_patch_by_id('11').set_alpha(0.5)
    for text in fig.set_labels: #need to call named object 'fig' from above, font size is set numerically
        text.set_fontsize(36) #this is the label names
    for text in fig.subset_labels:
        text.set_fontsize(28) #this will change the numbers
    plt.savefig('./20D15_SitesAndRegions/{}_ET(hc)D_SiteOverlap.svg'.format(i))
    plt.show()
#Now I will make the stacked bar graphs

#set the context for searborn (and remove graph boarders)
sns.set_style('ticks')
sns.set_context('poster')
sns.set_context(rc = {'patch.linewidth': 0.0})
```

```
#make a for loop to make the graphs for all samples
for i in list_dfs2:
    plt.figure()
    g1 = sns.barplot(x = locals()['df_numsites3_{}'.format(i)].index,
                     y = locals()['df_numsites3_{}'.format(i)]['Total Number of Sites'].values, color='#5b7992')
    g2 = sns.barplot(x = locals()['df_numsites3_{}'.format(i)].index,
                     y = (locals()['df_numsites3_{}'.format(i)]['Unlocalized Sites'].values + \
                          locals()['df_numsites3_{}'.format(i)]['Localized Sites'].values), color='#67b2f6ff')
    g3 = sns.barplot(x = locals()['df_numsites3_{}'.format(i)].index,
                     y = locals()['df_numsites3_{}'.format(i)]['Unlocalized Sites'].values, color='#d4d4d4')
    for j in range(3):
        g3.text(j, (locals()['df_numsites3_{}'.format(i)]['Total Number of Sites'][j] + \
                    locals()['df_numsites3_{}'.format(i)]['Total Number of Sites'].max()*0.05),
                int(locals()['df_numsites3_{}'.format(i)]['Total Number of Sites'][j]), color='black', ha='center')
    sns.despine()
    plt.savefig('./20D15_SitesAndRegions/{}_StackedBar.svg'.format(i))
```

Part 4

```
#Using the final table from part three I will make a separate column for 'Experiment' based on the raw file

#copy the df from part 3 into a new df
dfLiverBrain_tableF_4 = dfLiverBrain_tableF_3.copy()

#add a new experiment column based on the raw file and export for SitesAndRegions script
dfLiverBrain_tableF_4.loc[dfLiverBrain_tableF_4.RawFile.str.contains('Brain'), 'Experiment'] = 'Brain'
dfLiverBrain_tableF_4.loc[dfLiverBrain_tableF_4.RawFile.str.contains('Liver'), 'Experiment'] = 'Liver'
dfLiverBrain_tableF_4.to_csv('./20D15_SitesAndRegions/SiteOverlap_LiverBrain_Preprocessed_4.txt', sep='\t', index=False)
%%capture
#supresses the output of the cell

#run the sites and regions script
%run -i SitesAndRegionsMultiExperiment.py 20D15_SitesAndRegions/SiteOverlap_LiverBrain_Preprocessed_4.txt \
20D15_SitesAndRegions/maxparcon_LiverBrainOverlap_4.txt 20D15_SitesAndRegions/bestms2_LiverBrainOverlap_4.txt
#Import the output and process as before
dfallsites4 = pd.read_csv('./20D15_SitesAndRegions/bestms2_LiverBrainOverlap_4.txt', sep='\t')
dfregions4 = pd.read_csv('./20D15_SitesAndRegions/maxparcon_LiverBrainOverlap_4.txt', sep='\t')
dfallsites4 = dfallsites4[~dfallsites4.Protein.str.contains(';')]
dfregions4 = dfregions4[~dfregions4.Protein.str.contains(';')]

dfregions4.loc[dfregions4['Site ID Constraints'].str.contains('of'), 'Type'] = 'Region'
dfregions4.loc[~dfregions4['Site ID Constraints'].str.contains('of'), 'Type'] = 'Site'

dfmerge4 = dfallsites4.merge(dfregions4, how='left', on='Region ID')

def experimentO(x):
    if x.Experiment.eq('Brain').all():
        return 'Brain'
    elif x.Experiment.eq('Liver').all():
        return 'Liver'
    else:
        return 'Both'
df4_exp = dfmerge4.groupby(['Region ID']).apply(experimentO)
dfregions4['Experiment'] = df4_exp

series4_sites = dfregions4[dfregions4.Type == 'Site'].groupby('Experiment')['Min Sites'].sum()
series4_sr = dfregions4.groupby('Experiment')['Min Sites'].sum()
#Make the Venn diagrams

###Sites Only###
plt.figure(figsize=(7,7))
fig = venn2([series4_sites[1], series4_sites[2], series4_sites[0]], ('Brain', 'Liver'))
plt.title('Sites Overlap', fontsize=42)
fig.get_patch_by_id('10').set_color('#5b7992')
fig.get_patch_by_id('01').set_color('#aaaaaa')
fig.get_patch_by_id('10').set_edgecolor('none')
fig.get_patch_by_id('01').set_edgecolor('none')
fig.get_patch_by_id('10').set_alpha(0.75)
fig.get_patch_by_id('01').set_alpha(0.5)
fig.get_patch_by_id('11').set_color('#027FF0')
fig.get_patch_by_id('11').set_edgecolor('none')
fig.get_patch_by_id('11').set_alpha(0.5)
for text in fig.set_labels: #need to call named object 'fig' from above, font size is set numerically
    text.set_fontsize(36) #this is the label names
for text in fig.subset_labels:
    text.set_fontsize(28) #this will change the numbers
plt.savefig('./20D15_SitesAndRegions/LiverBrain_SiteOverlap_4.svg')
plt.show()

###Sites and Regions###
plt.figure(figsize=(7,7))
fig = venn2([series4_sr[1], series4_sr[2], series4_sr[0]], ('Brain', 'Liver'))
plt.title('Sites and Regions Overlap', fontsize=42)
fig.get_patch_by_id('10').set_color('#5b7992')
fig.get_patch_by_id('01').set_color('#aaaaaa')
fig.get_patch_by_id('10').set_edgecolor('none')
fig.get_patch_by_id('01').set_edgecolor('none')
fig.get_patch_by_id('10').set_alpha(0.75)
fig.get_patch_by_id('01').set_alpha(0.5)
fig.get_patch_by_id('11').set_color('#027FF0')
fig.get_patch_by_id('11').set_edgecolor('none')
fig.get_patch_by_id('11').set_alpha(0.5)
for text in fig.set_labels: #need to call named object 'fig' from above, font size is set numerically
    text.set_fontsize(36) #this is the label names
```

```
for text in fig.subset_labels:
    text.set_fontsize(28) #this will change the numbers
plt.savefig('./20D15_SitesAndRegions/LiverBrain_SiteRegionOverlap_4.svg')
plt.show()
#I will also re-calculate the sites and regions for the brain and liver based on this combined dataset

#Note, use this with caution, since the sites are counted as a site if they are a site in either of the two datasets
#(although this is probably mostly alright, it is perfectly reasonable that the sites localized in the brain are not
    #the same as some of the sites that were unlocalized in the liver)

#initialize an empty df
df_numsites4 = pd.DataFrame(np.empty((2,5)))

#make a list for iterating over liver and brain
list_lb = ['Brain', 'Liver']

#make a for loop to go through liver and brain
for i in range(2):
    df_numsites4.columns = ['Total Number of Sites', 'Localized Sites', 'Unlocalized Sites', 'Regions',
                            'Percent Localized']
    df_numsites4.rename(index={i:list_lb[i]}, inplace=True)
    df_numsites4.loc[list_lb[i], 'Total Number of Sites'] = dfregions4[
        (dfregions4.Experiment == '{}'.format(list_lb[i])) | (dfregions4.Experiment == 'Both')]['Min Sites'].sum()
    df_numsites4.loc[list_lb[i], 'Localized Sites'] = dfregions4[
        ((dfregions4.Experiment == '{}'.format(list_lb[i])) | (dfregions4.Experiment == 'Both')) & \
        (dfregions4.Type == 'Site')]['Min Sites'].sum()
    df_numsites4.loc[list_lb[i], 'Unlocalized Sites'] = dfregions4[
        ((dfregions4.Experiment == '{}'.format(list_lb[i])) | (dfregions4.Experiment == 'Both')) & \
        (dfregions4.Type == 'Region')]['Min Sites'].sum()
    df_numsites4.loc[list_lb[i], 'Regions'] = len(
        dfregions4[((dfregions4.Experiment == '{}'.format(list_lb[i])) | (dfregions4.Experiment == 'Both')) & \
                (dfregions4.Type == 'Region')])

df_numsites4['Percent Localized'] = (df_numsites4['Localized Sites'] / df_numsites4['Total Number of Sites'])*100
df_numsites4 = df_numsites4.astype({'Total Number of Sites':int, 'Localized Sites':int, 'Unlocalized Sites':int,
                                    'Regions':int})
df_numsites4.to_csv('SitesAndRegionsByTissue_LiverBrain.csv')
df_numsites4
```

Part 5

```
#Using the final table from part three I will make a separate column for 'Experiment' based on the raw file as in part 4

#copy the df from part 3 into a new df
dfQuant_tableF_5 = dfQuant_tableF_3.copy()

#make a list of experiment types
list_mstype = ['TopN', 'TopSpeed']

#add a new experiment column based on the raw file and export for SitesAndRegions script
for i in range(3):
    for j in list_mstype:
        dfQuant_tableF_5.loc[(dfQuant_tableF_5.RawFile.str.contains('_{}_'.format(i+1)) & \
                              dfQuant_tableF_5.RawFile.str.contains(
            '{}'.format(j))), 'Experiment'] = '{}{}'.format(j,i+1)

dfQuant_tableF_5.to_csv('./20D15_SitesAndRegions/Quant_Preprocessed_ByRawFile_5.txt', sep='\t', index=False)
%%capture
#supresses the output of the cell

#run the sites and regions script
%run -i SitesAndRegionsMultiExperiment.py 20D15_SitesAndRegions/Quant_Preprocessed_ByRawFile_5.txt \
20D15_SitesAndRegions/maxparcon_BAP1KO_ByRawFile_5.txt 20D15_SitesAndRegions/bestms2_BAP1KO_ByRawFile_5.txt
#Import the output and process as before
dfallsites5 = pd.read_csv('./20D15_SitesAndRegions/bestms2_BAP1KO_ByRawFile_5.txt', sep='\t')
dfregions5 = pd.read_csv('./20D15_SitesAndRegions/maxparcon_BAP1KO_ByRawFile_5.txt', sep='\t')
dfallsites5 = dfallsites5[~dfallsites5.Protein.str.contains(';')]
dfregions5 = dfregions5[~dfregions5.Protein.str.contains(';')]

dfregions5.loc[dfregions5['Site ID Constraints'].str.contains('of'), 'Type'] = 'Region'
dfregions5.loc[~dfregions5['Site ID Constraints'].str.contains('of'), 'Type'] = 'Site'

dfmerge5 = dfallsites5.merge(dfregions5, how='left', on='Region ID')

#clean up this df
dfmerge5.rename(columns={'Protein_x': 'Protein'}, inplace=True)
dfmerge5.drop(columns={'Protein_y'}, inplace=True)

#add whether sites/regions were found in top n, top speed, or both to the regions df
def experimentR(x):
    if x.Experiment.str.contains('TopSpeed').all():
        return 'TopSpeed'
    elif x.Experiment.str.contains('TopN').all():
        return 'TopN'
    else:
        return 'Both'
df5_exp = dfmerge5.groupby(['Region ID']).apply(experimentR)
dfregions5['Experiment'] = df5_exp
#Make a Venn diagram of the overlap between top speed and top n

#make series for the Venn diagrams
series5_sites = dfregions5[dfregions5.Type == 'Site'].groupby('Experiment')['Min Sites'].sum()
series5_sr = dfregions5.groupby('Experiment')['Min Sites'].sum()
```

```
###Sites Only###
plt.figure(figsize=(7,7))
fig = venn2([series5_sites[1], series5_sites[2], series5_sites[0]], ('Top N', 'Top Speed'))
plt.title('Sites Overlap', fontsize=42)
fig.get_patch_by_id('10').set_color('#5b7992')
fig.get_patch_by_id('01').set_color('#aaaaaa')
fig.get_patch_by_id('10').set_edgecolor('none')
fig.get_patch_by_id('01').set_edgecolor('none')
fig.get_patch_by_id('10').set_alpha(0.75)
fig.get_patch_by_id('01').set_alpha(0.5)
fig.get_patch_by_id('11').set_color('#027FF0')
fig.get_patch_by_id('11').set_edgecolor('none')
fig.get_patch_by_id('11').set_alpha(0.5)
for text in fig.set_labels: #need to call named object 'fig' from above, font size is set numerically
    text.set_fontsize(36) #this is the label names
for text in fig.subset_labels:
    text.set_fontsize(28) #this will change the numbers
plt.savefig('./20D15_SitesAndRegions/BAP1KO_MethodOverlapSites_5.svg')
plt.show()

###Sites and Regions###
plt.figure(figsize=(7,7))
fig = venn2([series5_sr[1], series5_sr[2], series5_sr[0]], ('Top N', 'Top Speed'))
plt.title('Sites and Regions Overlap', fontsize=42)
fig.get_patch_by_id('10').set_color('#5b7992')
fig.get_patch_by_id('01').set_color('#aaaaaa')
fig.get_patch_by_id('10').set_edgecolor('none')
fig.get_patch_by_id('01').set_edgecolor('none')
fig.get_patch_by_id('10').set_alpha(0.75)
fig.get_patch_by_id('01').set_alpha(0.5)
fig.get_patch_by_id('11').set_color('#027FF0')
fig.get_patch_by_id('11').set_edgecolor('none')
fig.get_patch_by_id('11').set_alpha(0.5)
for text in fig.set_labels: #need to call named object 'fig' from above, font size is set numerically
    text.set_fontsize(36) #this is the label names
for text in fig.subset_labels:
    text.set_fontsize(28) #this will change the numbers
plt.savefig('./20D15_SitesAndRegions/BAP1KO_MethodOverlapSitesRegions_5.svg')
plt.show()
#Pull in the MS3 data from the psms file

#reimport the psms file
df5_psm = pd.read_csv(fnameq, sep='\t')

#pull out just the relevant information
df5_psm = df5_psm[['Spectrum File', 'First Scan', 'Abundance 127N', 'Abundance 129C', 'Abundance 130N']]

#rename the columns to facilitate merging
df5_psm.rename(columns={'Spectrum File':'Best Raw File', 'First Scan':'Best Scan Number'}, inplace=True)

#now merge this with the sites and regions data frame on raw file and scan number
df5_quant = dfmerge5.merge(df5_psm, how='left', on=['Best Raw File', 'Best Scan Number'])

#normalize the abundances based on the summed abundance for each channel/raw file
for i in set(df5_quant['Best Raw File']):

    #127N
    df5_quant.loc[df5_quant['Best Raw File'] == i, 'Norm-127N'] = \
    df5_quant.loc[df5_quant['Best Raw File'] == i, 'Abundance 127N'] / df5_quant.loc[
        df5_quant['Best Raw File'] == i, 'Abundance 127N'].sum()

    #129C
    df5_quant.loc[df5_quant['Best Raw File'] == i, 'Norm-129C'] = \
    df5_quant.loc[df5_quant['Best Raw File'] == i, 'Abundance 129C'] / df5_quant.loc[
        df5_quant['Best Raw File'] == i, 'Abundance 129C'].sum()

    #130N
    df5_quant.loc[df5_quant['Best Raw File'] == i, 'Norm-130N'] = \
    df5_quant.loc[df5_quant['Best Raw File'] == i, 'Abundance 130N'] / df5_quant.loc[
        df5_quant['Best Raw File'] == i, 'Abundance 130N'].sum()

#take the ratios based on the experiment
df5_quant.loc[df5_quant.Experiment.str.contains('1'), 'Ratio'] = \
df5_quant.loc[df5_quant.Experiment.str.contains('1'), 'Norm-130N'] / df5_quant.loc[
    df5_quant.Experiment.str.contains('1'), 'Norm-127N']

df5_quant.loc[df5_quant.Experiment.str.contains('2'), 'Ratio'] = \
df5_quant.loc[df5_quant.Experiment.str.contains('2'), 'Norm-129C'] / df5_quant.loc[
    df5_quant.Experiment.str.contains('2'), 'Norm-127N']

df5_quant.loc[df5_quant.Experiment.str.contains('3'), 'Ratio'] = \
df5_quant.loc[df5_quant.Experiment.str.contains('3'), 'Norm-130N'] / df5_quant.loc[
    df5_quant.Experiment.str.contains('3'), 'Norm-127N']

#make a new trial column based on the experiment (to facilitate averaging top speed and top n)
for i in range(3):
    df5_quant.loc[df5_quant.Experiment.str.contains('{}'.format(i+1)), 'Trial'] = 'Trial{}'.format(i+1)

#average the ratios of top speed and top n trials and merge this into the regions df
dfratios5 = dfregions5.merge(
    df5_quant.groupby(['Region ID', 'Trial']).Ratio.mean().unstack().reset_index(), how='left', on='Region ID')

#set this up for the limma script and output to txt
```

```
dflimma5 = dfratios5[['Trial1', 'Trial2', 'Trial3']]
dflimma5 = np.log2(dflimma5)
dflimma5.to_csv('BAP1KO_SitesRegions_Ratios_Limma.txt', sep='\t')
%%R

#calculate the p-values for changing sites with limma in R

library(limma) #load the package
df1 = read.table("BAP1KO_SitesRegions_Ratios_Limma.txt",sep="\t",header=TRUE,row.names=1) #read in the file
f1 = eBayes(lmFit(df1)) #perform limma
write.table(topTable(f1,n=Inf,confint=.95),"BAP1KO_limmaOut.txt",sep="\t") #write table
#Import the limma results and integrate them into the ratios table

df5_limmaout = pd.read_csv('BAP1KO_limmaOut.txt', sep='\t')
df5_limmaout.rename(columns={'adj.P.Val':'P-Val'}, inplace=True)
dfratiosF5 = dfratios5.iloc[:, 0:6]
dfratiosF5[['logFC', 'P-Val', 'B']] = df5_limmaout[['logFC', 'P-Val', 'B']]

#add in a new column for the gene name (duplicate protein column) and prepare the list for querying uniport
dfratiosF5.insert(1, 'Gene', dfratiosF5.Protein)
uniprot_input = list(dfratiosF5.Protein)

#Output the number of unique proteins
print('The number of unique proteins is:')
len(dfratiosF5.drop_duplicates('Protein'))
#Query uniprot to get list of gene names

#define variables
url = 'https://www.uniprot.org/uploadlists/'
user_agent = 'Mozilla/5.0 (Windows NT 10.0; Win64; x64)'

#make a dictionary for the requests
params = {
    "from":"ACC+ID",
    "to":"ACC",
    "format":"tab",
    "columns": "genes(PREFERRED)",
    "query":" ".join(uniprot_input)
}

#query uniprot
data = urllib.parse.urlencode(params, doseq=False)
data = data.encode('ascii')
headers = {"User-Agent": user_agent}
request = urllib.request.Request(url, data, headers)
response = urllib.request.urlopen(request)
with urllib.request.urlopen(request) as f:
   response = f.read().decode()

#make a dataframe from the output
df_res = pd.read_csv(StringIO(response), sep='\t')
df_res #inspect
#Add the gene names to the ratios table from above based on the uniprot output
#Then, normalize the ratios based on the protein expression ratios

#rename the uniprot output columns
df_res.rename(columns={df_res.columns[0]: "Gene", df_res.columns[1]: "UniprotID"}, inplace=True)

#set up the dictionary for mapping
di = df_res.set_index('UniprotID')['Gene'].to_dict()

#replace the gene name column in the ratios df with the gene name based on the above dictionary
dfratiosF5['Gene'].replace(di, inplace=True)

#import the PD output for protein expression and get the gene name for merging with ratios df
dfproteins = pd.read_csv(fnamep, sep='\t')
dfproteins = dfproteins[['Description', 'Abundance Ratio log2 BAP1 KO  Control']]
dfproteins['Gene'] = dfproteins.Description.str.extract('GN=(.*) PE=')
dfproteins.rename(columns={'Abundance Ratio log2 BAP1 KO  Control':'logFC Protein'}, inplace=True)
dfproteins = dfproteins.groupby('Gene', as_index=False).mean()

#merge with ratios file (validating that there are not duplicate gene names in the proteins file)
dfratiosproteins5 = dfratiosF5.merge(dfproteins, how='left', on='Gene', validate='m:1')

#export this as a txt file
dfratiosproteins5.to_csv('BAP1KO_SitesRegions_Ratios.csv', index=False)
#Now I will correct the sites and regions ratios for changes in protein expression and re-run limma

dflimmaC5 = dflimma5.copy() #make a copy of the original ratios table

#define log protein expression value to subtract
logPE = dfratiosproteins5['logFC Protein'].fillna(0)

dflimmaC5[['Trial1', 'Trial2', 'Trial3']] = \
dflimmaC5[['Trial1', 'Trial2', 'Trial3']] - [logPE, logPE, logPE]

#export for running the limma script
dflimmaC5.to_csv('BAP1KO_SitesRegions_RatiosCorrected_Limma.txt', sep='\t')
%%R

#calculate the p-values for changing sites with limma in R

library(limma) #load the package
```

```
df1 = read.table("BAP1KO_SitesRegions_RatiosCorrected_Limma.txt",sep="\t",header=TRUE,row.names=1) #read in the file
f1 = eBayes(lmFit(df1)) #perform limma
write.table(topTable(f1,n=Inf,confint=.95),"BAP1KO_limmaOut_Corrected.txt",sep="\t") #write table
#Read the limma output back in, clean up, and export a new df with the final ratios
#Also export a df with just Gene, Protein, and Site ID Constraints of significantly changing sites for cytoscape

#import and clean up limma output
df5_limmaoutC = pd.read_csv('BAP1KO_limmaOut_Corrected.txt', sep='\t')
df5_limmaoutC.rename(columns={'adj.P.Val':'P-Val_Corrected', 'B':'B_Corrected', 'logFC':'logFC_Corrected'},
                     inplace=True)

#make a copy of the previous final ratios df and add the protein expression corrected columns in
dfcorrectedratios5 = dfratiosproteins5.copy()
dfcorrectedratios5[['logFC_Corrected', 'P-Val_Corrected', 'B_Corrected']] = df5_limmaoutC[['logFC_Corrected',
                                                                                          'P-Val_Corrected',
                                                                                          'B_Corrected']]

#export final list of ratios
dfcorrectedratios5.to_csv('BAP1KO_SitesRegions_Ratios_Corrected.csv', index=False)

#export table for cytoscape

#get relevant columns
dfsrRatios_ForCytoscape = dfcorrectedratios5[['Gene', 'Protein', 'Site ID Constraints', 'logFC_Corrected',
                                              'P-Val_Corrected', 'logFC Protein']]

#add column for whether protein expression is corrected for
dfsrRatios_ForCytoscape.loc[dfsrRatios_ForCytoscape['logFC Protein'].isnull(),
                            'Corrected for Protein Expression'] = 'No'
dfsrRatios_ForCytoscape.loc[~dfsrRatios_ForCytoscape['logFC Protein'].isnull(),
                            'Corrected for Protein Expression'] = 'Yes'

#drop log FC protein column, add an additional column for cytoscape splicing, and combine rows with the same gene
dfsrRatios_ForCytoscape.drop(columns={'logFC Protein'}, inplace=True)
dfsrRatios_ForCytoscape.loc[dfcorrectedratios5['P-Val_Corrected'] < 0.05, 'Significantly Changing Site'] = 1

#concatentate sites/regions together with their position and fold change in a new column
dfsrRatios_ForCytoscape['Sites_Regions'] = (dfsrRatios_ForCytoscape['Protein'] + '@' +
                                            dfsrRatios_ForCytoscape['Site ID Constraints'] + ' (FC: ' +
                                            dfsrRatios_ForCytoscape['logFC_Corrected'].round(2).astype(str) +')')

#calculate the average fold change per gene and save in a separate df
dfavgFC = dfsrRatios_ForCytoscape.groupby(['Gene'])['logFC_Corrected'].mean().reset_index()
dfavgFC.rename(columns={'logFC_Corrected':'AvgLogFC'}, inplace=True)

#store the concatenated sites/regions for each gene as a separate df
dfsrconcat = dfsrRatios_ForCytoscape.groupby(['Gene'])['Sites_Regions'].apply('; '.join).reset_index()
dfsrconcat.rename(columns={'Sites_Regions':'O-GlcNAc Sites and Regions'}, inplace=True)

#store the concatenated significant sites/regions for each gene as a separate df
dfsigsrconcat = dfsrRatios_ForCytoscape[dfsrRatios_ForCytoscape['Significantly Changing Site'] == 1].groupby(
    ['Gene'])['Sites_Regions'].apply('; '.join).reset_index()
dfsigsrconcat.rename(columns={'Sites_Regions':'Significant Sites and Regions'}, inplace=True)

#combine everything together in the same df
dfsrRatios_ForCytoscape = dfsrRatios_ForCytoscape.merge(dfavgFC, how='left', on='Gene')
dfsrRatios_ForCytoscape = dfsrRatios_ForCytoscape.merge(dfsrconcat, how='left', on='Gene')
dfsrRatios_ForCytoscape = dfsrRatios_ForCytoscape.merge(dfsigsrconcat, how='left', on='Gene')

#export for loading into cytoscape
dfsrRatios_ForCytoscape[['Gene', 'AvgLogFC', 'Corrected for Protein Expression', 'O-GlcNAc Sites and Regions',
                         'Significant Sites and Regions']].to_csv('BAP1KO_SitesRegions_ForCytoscape.csv', index=False)
```

A5.6.5. Sites and Regions Programs.

A5.6.5.1. Code for SitesAndRegions.py.

```
# ASSUME INPUT TABLE HAS THE FOLLOWING COLUMNS EXACTLY NAMED: "RawFile", "Protein", "ScanNumber", "NumMods", "Positions" (semicolon separated), "Probabilities"
(semicolon separated)

### USAGE: python SitesAndRegionsGeneric.py Input_SiteAndRegionsTable_Filename Output_MaxParSiteConstraints Output_BestMS2forSites
### NOTE: rounding for probability threshold needs to be adjusted for the rounding of MS data anlysis program, e.g. in ProtomeDiscoverer 2/3 is 3 decimals (0.667)
import re
import sys
import networkx as nx
import itertools as it
import pandas as pd
```

```
from collections import namedtuple

# Define number of decimals to round probabilities
roundto = 3 # For ProteomeDiscoverer

YES = "YES"
MAYBE = "MAYBE"
NO = "NO"

psmTable = pd.read_table(sys.argv[1])

requiredCols = ["RawFile","ScanNumber","Protein","Positions","Probabilities","NumMods"]
for c in requiredCols:
	assert c in psmTable.columns, "Missing %s in input table"%c

regionID = 0
fhMaxPar = open(sys.argv[2],'w')
fhMaxPar.write("Protein\tRegion ID\tMin Sites\tSite ID Constraints\n")
fhBestSiteMS2 = open(sys.argv[3],'w')
fhBestSiteMS2.write("Protein\tPosition\tBest Probability\tBest Raw File\tBest Scan Number\tRegion ID\n")


BestObservation = namedtuple("BestObservation",["RawFile","ScanNumber","Probability"])
MaybeGroup = namedtuple("MaybeGroup",["NumMods","Positions"])

# For each protein
for prot,protPSMs in psmTable.groupby("Protein"):
	print("Working on protein %s"%prot)
	bestScanTable = {} # key: protein position, value: tuple(raw file,scan number, probability)
	yesPositions = set() # set of accepted positions
	maybeGroups = set() # set of maybe groups, where each group is tuple(nMods,set(positions))

	### CLASSIFY EACH POSITION AS YES, NO, or MAYBE WITHIN EACH PSM
	for psm in protPSMs.itertuples():
		# Split probabilities and positions into lists
		siteProbs = list(map(float,psm.Probabilities.split(";")))
		siteLocs = list(map(int,psm.Positions.split(";")))

		# Check that number of probabilities and positions is the same
		assert len(siteProbs)==len(siteLocs), "Number of probabilities does not equal number of positions for PSM: %s"%str(psm)

		# Sort sites by highest probability to lowest
		siteProbs,siteLocs = list(zip(*sorted(zip(siteProbs,siteLocs),reverse=True)))

		# Determine which sites are YES (probability > nMods/(1+nMods), rounded [see above]), MAYBE (not YES, but needed to explain spectra), or NO (otherwise)
		minYesProb = round(psm.NumMods/(1.+psm.NumMods), roundto)
		siteCats = []
		for i in range(len(siteProbs)):
			if siteProbs[i] > minYesProb: # Site probability is greater than required threshold, must include
				siteCats.append(YES)
			elif ( (i == 0) or ((siteProbs[i] == siteProbs[i-1]) and (siteCats[-1]==MAYBE)) or (sum(siteProbs[:i]) < (psm.NumMods-minYesProb)) ): # Either highest probability site doesn't pass threshold OR site has same probability of previous site that was also a MAYBE, OR need more sites to explain number of observed modifications
				siteCats.append(MAYBE)
			else:
				siteCats.append(NO)

		maybeList = [] # LIST OF MAYBE SITES POSITIONS
		nYes = 0
		for siteProb,siteLoc,siteCat in zip(siteProbs,siteLocs,siteCats):

			if siteCat == YES:
				# IF ALREADY YES, BUT WORSE PROBABILITY, UPDATE WITH BETTER EXAMPLE
				if siteLoc in yesPositions:
					if bestScanTable[siteLoc].Probability < siteProb:
						bestScanTable[siteLoc] = BestObservation(psm.RawFile,psm.ScanNumber,siteProb)
				# NOT PREVIOUS YES, SO SET BEST PROB AND ADD TO YES SET
				else:
					bestScanTable[siteLoc] = BestObservation(psm.RawFile,psm.ScanNumber,siteProb)
					yesPositions.add(siteLoc)
				nYes += 1
			if siteCat == MAYBE:
				maybeList.append(siteLoc)
				if (not siteLoc in bestScanTable) or ((not siteLoc in yesPositions) and (bestScanTable[siteLoc].Probability < siteProb)):
					bestScanTable[siteLoc] = BestObservation(psm.RawFile,psm.ScanNumber,siteProb)
		if len(maybeList)>0:
			maybeGroups.add(MaybeGroup(psm.NumMods-nYes,frozenset(maybeList)))

	### REMOVE KNOWN YES SITES FROM MAYBE GROUPS
	changed = True
	while changed:
		changed = False
		_maybeGroups = set()
		for mgCount,mgPositions in maybeGroups: # for each maybe group, remove YES positions and decrease count
			prevYesPositions = mgPositions & yesPositions  # find sites that are classified as YES for other PSMs
			if len(prevYesPositions) > 0: # if some maybe group sites are YES in other PSMs, update the group
				changed = True
				# update required count and remove from set
				_mgCount = mgCount - len(prevYesPositions)
				_mgPositions = mgPositions - yesPositions
				if _mgCount > 0: # if there are still maybe positions left..
					assert _mgCount <= len(_mgPositions), "Not enough remaining sites to cover required mods"
					if _mgCount == len(_mgPositions): # if exactly enough sites to cover required mods, make them all YES, should RARELY happen
```

```
                                                print("Converted MAYBE to YES via process of elmination for %s"%prot)
                                                yesPositions.update(_mgPositions)
                                        else:
                                                _maybeGroups.add(MaybeGroup(_mgCount,_mgPositions))
                                else: # no change to group, put back in new set
                                        _maybeGroups.add(MaybeGroup(mgCount,mgPositions))
                maybeGroups = _maybeGroups # replace old set of groups with updated set

        ### REMOVE ALL "SUBSET" GROUPS (another group has >= set of positions or >= required mods)
        maybeGroups = list(maybeGroups)
        subsetIndices = set()
        for i in range(len(maybeGroups)):
                for j in range(len(maybeGroups)):
                        if i != j:
                                if maybeGroups[i].NumMods >= maybeGroups[j].NumMods and maybeGroups[i].Positions.issuperset(maybeGroups[j].Positions):
                                        subsetIndices.add(j)
        _maybeGroups = []
        for i in range(len(maybeGroups)):
                if not i in subsetIndices:
                        _maybeGroups.append(maybeGroups[i])
        maybeGroups = _maybeGroups

        ### IDENTIFY REGIONS
        while len(maybeGroups) > 0:
                # SEED ALGORITHM WITH FIRST MAYBE GROUP
                regionGroups = [maybeGroups.pop(0)]
                regionPositions = set(regionGroups[0].Positions)
                changed = True
                while changed: # iterate while you keep adding new maybe groups
                        changed = False
                        for i in reversed(list(range(len(maybeGroups)))): # iterate through remaining groups
                                if not regionPositions.isdisjoint(maybeGroups[i].Positions): # if there is some overlap, add to region
                                        regionGroups.append(maybeGroups.pop(i))
                                        regionPositions.update(regionGroups[-1].Positions)
                                        changed = True

                # FIND MIN NUMBER OF SITES TO SATISTFY ALL GROUPS IN REGION
                satisfiedGroups = False
                minNumSites = 0
                while not satisfiedGroups: # TRY SUCESSIVELY LARGER NUMBER OF SITES
                        minNumSites += 1
                        for testSites in it.combinations(regionPositions,minNumSites): # TRY EACH COMBINATION OF POTENTIAL SITES
                                satisfiedGroups = True
                                testSet = set(testSites)
                                for mgCount,mgPositions in regionGroups: # TEST IF EACH MAYBE GROUP IS SATISFIED
                                        if len(mgPositions&testSet) < mgCount: # IF THE TEST SET DOESN"T EXPLAIN THE GROUP, FLAG AS NOT
SATISFIED
                                                satisfiedGroups = False
                                                break
                                if satisfiedGroups:
                                        break
                        if satisfiedGroups:
                                break
                maybeGroupStrs = []
                for mgCount,mgPositions in regionGroups:
                        maybeGroupStrs.append("(%d of %s)"%(mgCount,",".join(map(str,sorted(mgPositions)))))
                fhMaxPar.write("%s\t%d\t%d\t%s\n"%(prot,regionID,minNumSites,"&".join(maybeGroupStrs)))
                for sitePos in regionPositions:

        fhBestSiteMS2.write("%s\t%d\t%f\t%s\t%d\t%d\n"%(prot,sitePos,bestScanTable[sitePos].Probability,bestScanTable[sitePos].RawFile,bestScanTable[sitePos].ScanNumber,region
ID))
                regionID += 1

        ### OUTPUT YES SITES FROM PROTEIN
        for sitePos in yesPositions:
                fhMaxPar.write("%s\t%d\t%d\t%d\n"%(prot,regionID,1,sitePos))

        fhBestSiteMS2.write("%s\t%d\t%f\t%s\t%d\t%d\n"%(prot,sitePos,bestScanTable[sitePos].Probability,bestScanTable[sitePos].RawFile,bestScanTable[sitePos].ScanNumber,region
ID))
                regionID += 1

fhMaxPar.close()
fhBestSiteMS2.close()
```

A5.6.5.2. Code for SitesAndRegionsMultiExperiment.py.

```
### ASSUME INPUT TABLE HAS THE FOLLOWING COLUMNS EXACTLY NAMED: "RawFile", "Experiment", "Protein", "ScanNumber", "NumMods", "Positions" (semicolon
separated), "Probabilities" (semicolon separated)

### USAGE: python SitesAndRegionsGeneric.py Input_SiteAndRegionsTable_Filename Output_MaxParSiteConstraints Output_BestMS2forSites
### NOTE: rounding for probability threshold needs to be adjusted for the rounding of MS data anlysis program, e.g. in ProtomeDiscoverer 2/3 is 3 decimals (0.667)


import re
```

```
import sys
import networkx as nx
import itertools as it
import pandas as pd
from collections import namedtuple

# Define number of decimals to round probabilities
roundto = 3 # For ProteomeDiscoverer

YES = "YES"
MAYBE = "MAYBE"
NO = "NO"

psmTable = pd.read_table(sys.argv[1])

requiredCols = ["RawFile","ScanNumber","Experiment","Protein","Positions","Probabilities","NumMods"]
for c in requiredCols:
	assert c in psmTable.columns, "Missing %s in input table"%c

regionID = 0
fhMaxPar = open(sys.argv[2],'w')
fhMaxPar.write("Protein\tRegion ID\tMin Sites\tSite ID Constraints\n")
fhBestSiteMS2 = open(sys.argv[3],'w')
fhBestSiteMS2.write("Protein\tPosition\tExperiment\tBest Probability\tBest Raw File\tBest Scan Number\tRegion ID\n")


BestObservation = namedtuple("BestObservation",["RawFile","ScanNumber","Probability"])
MaybeGroup = namedtuple("MaybeGroup",["NumMods","Positions"])


# For each protein
for prot,protPSMs in psmTable.groupby("Protein"):
	print("Working on protein %s"%prot)
	bestScanTable = {} # key: protein position, value: tuple(raw file,scan number, probability)
	yesPositions = set() # set of accepted positions
	maybeGroups = set() # set of maybe groups, where each group is tuple(nMods,set(positions))

	### CLASSIFY EACH POSITION AS YES, NO, or MAYBE WITHIN EACH PSM
	for psm in protPSMs.itertuples():
		# Split probabilities and positions into lists
		siteProbs = list(map(float,psm.Probabilities.split(";")))
		siteLocs = list(map(int,psm.Positions.split(";")))

		# Check that number of probabilities and positions is the same
		assert len(siteProbs)==len(siteLocs), "Number of probabilities does not equal number of positions for PSM: %s"%str(psm)

		# Sort sites by highest probability to lowest
		siteProbs,siteLocs = list(zip(*sorted(zip(siteProbs,siteLocs),reverse=True)))

		# Determine which sites are YES (probability > nMods/(1+nMods), rounded [see above]), MAYBE (not YES, but needed to explain spectra), or NO
(otherwise)
		minYesProb = round(psm.NumMods/(1.+psm.NumMods), roundto)
		siteCats = []
		for i in range(len(siteProbs)):
			if siteProbs[i] > minYesProb: # Site probability is greater than required threshold, must include
				siteCats.append(YES)
			elif ( (i == 0) or ((siteProbs[i] == siteProbs[i-1]) and (siteCats[-1]==MAYBE)) or (sum(siteProbs[:i]) < (psm.NumMods-minYesProb)) ):
# Either highest probability site doesn't pass threshold OR site has same probability of previous site that was also a MAYBE, OR need more sites to explain number of observed modifications
				siteCats.append(MAYBE)
			else:
				siteCats.append(NO)

		maybeList = [] # LIST OF MAYBE SITES POSITIONS
		nYes = 0
		for siteProb,siteLoc,siteCat in zip(siteProbs,siteLocs,siteCats):
			if siteCat == YES:
				yesPositions.add(siteLoc)
				nYes += 1
			if siteCat == MAYBE:
				maybeList.append(siteLoc)

			if not siteLoc in bestScanTable:
				bestScanTable[siteLoc] = {}
			if not psm.Experiment in bestScanTable[siteLoc]:
				bestScanTable[siteLoc][psm.Experiment] = BestObservation(psm.RawFile,psm.ScanNumber,siteProb)
			else:
				if bestScanTable[siteLoc][psm.Experiment].Probability < siteProb:
					bestScanTable[siteLoc][psm.Experiment] =
BestObservation(psm.RawFile,psm.ScanNumber,siteProb)

		if len(maybeList)>0:
			maybeGroups.add(MaybeGroup(psm.NumMods-nYes,frozenset(maybeList)))

	### REMOVE KNOWN YES SITES FROM MAYBE GROUPS
	changed = True
	while changed:
		changed = False
		_maybeGroups = set()
		for mgCount,mgPositions in maybeGroups: # for each maybe group, remove YES positions and decrease count
			prevYesPositions = mgPositions & yesPositions  # find sites that are classified as YES for other PSMs
			if len(prevYesPositions) > 0: # if some maybe group sites are YES in other PSMs, update the group
				changed = True
				# update required count and remove from set
```

```
                                                _mgCount = mgCount - len(prevYesPositions)
                                                _mgPositions = mgPositions - yesPositions
                                                if _mgCount > 0: # if there are still maybe positions left..
                                                        assert _mgCount <= len(_mgPositions), "Not enough remaining sites to cover required mods"
                                                        if _mgCount == len(_mgPositions): # if exactly enough sites to cover required mods, make them
all YES, should RARELY happen
                                                                print("Converted MAYBE to YES via process of elmination for %s"%prot)
                                                                yesPositions.update(_mgPositions)
                                                        else:
                                                                _maybeGroups.add(MaybeGroup(_mgCount,_mgPositions))
                                        else: # no change to group, put back in new set
                                                _maybeGroups.add(MaybeGroup(mgCount,mgPositions))
                                maybeGroups = _maybeGroups # replace old set of groups with updated set

                ### REMOVE ALL "SUBSET" GROUPS (another group has >= set of positions or >= required mods)
                maybeGroups = list(maybeGroups)
                subsetIndices = set()
                for i in range(len(maybeGroups)):
                        for j in range(len(maybeGroups)):
                                if i != j:
                                        if maybeGroups[i].NumMods >= maybeGroups[j].NumMods and
maybeGroups[i].Positions.issuperset(maybeGroups[j].Positions):
                                                subsetIndices.add(j)
                _maybeGroups = []
                for i in range(len(maybeGroups)):
                        if not i in subsetIndices:
                                _maybeGroups.append(maybeGroups[i])
                maybeGroups = _maybeGroups

                ### IDENTIFY REGIONS
                while len(maybeGroups) > 0:
                        # SEED ALGORITHM WITH FIRST MAYBE GROUP
                        regionGroups = [maybeGroups.pop(0)]
                        regionPositions = set(regionGroups[0].Positions)
                        changed = True
                        while changed: # iterate while you keep adding new maybe groups
                                changed = False
                                for i in reversed(list(range(len(maybeGroups)))): # iterate through remaining groups
                                        if not regionPositions.isdisjoint(maybeGroups[i].Positions): # if there is some overlap, add to region
                                                regionGroups.append(maybeGroups.pop(i))
                                                regionPositions.update(regionGroups[-1].Positions)
                                                changed = True

                        # FIND MIN NUMBER OF SITES TO SATISTFY ALL GROUPS IN REGION
                        satisfiedGroups = False
                        minNumSites = 0
                        while not satisfiedGroups: # TRY SUCESSIVELY LARGER NUMBER OF SITES
                                minNumSites += 1
                                for testSites in it.combinations(regionPositions,minNumSites): # TRY EACH COMBINATION OF POTENTIAL SITES
                                        satisfiedGroups = True
                                        testSet = set(testSites)
                                        for mgCount,mgPositions in regionGroups: # TEST IF EACH MAYBE GROUP IS SATISFIED
                                                if len(mgPositions&testSet) < mgCount: # IF THE TEST SET DOESN"T EXPLAIN THE
GROUP, FLAG AS NOT SATISFIED
                                                        satisfiedGroups = False
                                                        break
                                        if satisfiedGroups:
                                                break
                                if satisfiedGroups:
                                        break
                        maybeGroupStrs = []
                        for mgCount,mgPositions in regionGroups:
                                maybeGroupStrs.append("(%d of %s)"%(mgCount,",".join(map(str,sorted(mgPositions)))))
                        fhMaxPar.write("%s\t%d\t%d\t%s\n"%(prot,regionID,minNumSites,"&".join(maybeGroupStrs)))
                        for sitePos in regionPositions:
                                for eName in bestScanTable[sitePos]:

                fhBestSiteMS2.write("%s\t%d\t%s\t%f\t%s\t%d\t%d\n"%(prot,sitePos,eName,bestScanTable[sitePos][eName].Probability,bestScanTable[sitePos][eName].RawFile,bestScanT
able[sitePos][eName].ScanNumber,regionID))
                        regionID += 1

                ### OUTPUT YES SITES FROM PROTEIN
                for sitePos in yesPositions:
                        fhMaxPar.write("%s\t%d\t%d\t%d\n"%(prot,regionID,1,sitePos))
                        for eName in bestScanTable[sitePos]:

                fhBestSiteMS2.write("%s\t%d\t%s\t%f\t%s\t%d\t%d\n"%(prot,sitePos,eName,bestScanTable[sitePos][eName].Probability,bestScanTable[sitePos][eName].RawFile,bestScanT
able[sitePos][eName].ScanNumber,regionID))
                        regionID += 1

fhMaxPar.close()
fhBestSiteMS2.close()
```

A5.6.6. 293T Interactor Volcano Plot.

```
#import python packages
import re
```

```
import sys
import pandas as pd
import networkx as nx
import itertools as it
from collections import namedtuple
import numpy as np
import matplotlib
import matplotlib.pyplot as plt
from IPython.display import display
from functools import reduce
import seaborn as sns; sns.set()
from io import StringIO
from matplotlib_venn import venn2, venn2_unweighted, venn3_unweighted, venn2_circles, venn3_circles

#set up R environment and import R packages
import rpy2
import rpy2.ipython
%load_ext rpy2.ipython

#require R packages
%R require(limma)
%R require(ibb)

#magic function to show plots inline
%matplotlib inline

#ignore warnings
import warnings
warnings.filterwarnings('ignore')

#read in the interactors and PPI databases

df = pd.read_csv('./20D21_Full_Interactomics_Dataset/AllProteinsInteracomtics293TF.csv')
dfintact = pd.read_csv('IntAct.txt', sep='\t') #using the full rather than the multivalidated db
dfbiogrid = pd.read_csv('BioGRID.txt', sep='\t')

#remove entries from the interactomics dataset where the fold change of either ibb or limma was less/greater (respectively)
    #than 0; these are clearly crapome proteins

df = df[(df.limmaFC > 0) | (df.ibbFC < 0)]

#select only the OGT interactors from the PPI databases
dfbap1_intact = set(list(dfintact.loc[dfintact.Interactor_A == 'OGT', 'Interactor_B']) + list(
    dfintact.loc[dfintact.Interactor_B == 'OGT', 'Interactor_A']))
dfbap1_biogrid = set(list(dfbiogrid.loc[dfbiogrid.Interactor_A == 'OGT', 'Interactor_B']) + list(
    dfbiogrid.loc[dfbiogrid.Interactor_B == 'OGT', 'Interactor_A']))
#add an additional column specifying if a gene is a known interactor and if it is significant
df['Known Interactor'] = df.Gene.isin((dfbap1_intact | dfbap1_biogrid))
df['Significant'] = (df.limmapVal < 0.05) | (df.ibbpVal < 0.05)

#set OGT as a known interactor
df.loc[df.Gene == 'OGT', 'Known Interactor'] = True

#keep only relevant columns
dfgraph = df[['Gene', 'limmapVal', 'ibbpVal', 'Known Interactor', 'Significant']]

#take the negative log of both pvalues
dfgraph[['limmapVal', 'ibbpVal']] = -np.log10(dfgraph[['limmapVal', 'ibbpVal']])
dfgraph.rename(columns={'limmapVal':'-Log(P-Value), SILAC Ratio', 'ibbpVal':'-Log(P-Value), Spectral Counts'}, inplace=True)

#count the number of unknown interactors found
print('The number of unknown interactors is:')
len(dfgraph[(dfgraph.Significant == True) & (dfgraph['Known Interactor'] == False)])

#make the graph

plt.figure(figsize=(7,7))
sns.set_context('poster')
sns.set_style('ticks')

#plot 4 scatter plots on top each other to highlight the known/unknown and significant/insignificant interactors
g1 = sns.scatterplot(
    x='-Log(P-Value), SILAC Ratio', y='-Log(P-Value), Spectral Counts',
    data=dfgraph[(dfgraph.Significant == False) & (dfgraph['Known Interactor'] == False)],
    facecolor='none', edgecolor='black', marker="o", legend=False, alpha=0.75)

g2 = sns.scatterplot(
    x='-Log(P-Value), SILAC Ratio', y='-Log(P-Value), Spectral Counts',
    data=dfgraph[(dfgraph.Significant == True) & (dfgraph['Known Interactor'] == False)],
    facecolor='none', edgecolor='blue', marker="o", legend=False, alpha=0.75)

g3 = sns.scatterplot(
    x='-Log(P-Value), SILAC Ratio', y='-Log(P-Value), Spectral Counts',
    data=dfgraph[(dfgraph.Significant == False) & (dfgraph['Known Interactor'] == True)],
    facecolor='red', edgecolor='none', marker="o", legend=False, alpha=0.75)

g4 = sns.scatterplot(
    x='-Log(P-Value), SILAC Ratio', y='-Log(P-Value), Spectral Counts',
    data=dfgraph[(dfgraph.Significant == True) & (dfgraph['Known Interactor'] == True)],
    facecolor='red', edgecolor='none', marker="o", legend=False, alpha=0.75)

#define points to label
ptl = ['HCFC1', 'BAP1', 'TET2', 'DDB1', 'BUB3', 'WNK1', 'TRAK1', 'OGT', 'QSER1', 'EIF4G3', 'TET1', 'DDX3X', 'ELMSAN1',
```

```
    'RBM4']

#plot them as text objects
for i in ptl:
    g4.text((dfgraph['-Log(P-Value), SILAC Ratio'][dfgraph.Gene == i].max() + 0.1),
            (dfgraph['-Log(P-Value), Spectral Counts'][dfgraph.Gene == i].max() - 0.08),
            i, color='black', fontsize=12, weight='bold')

#add in HIVEP1 and others on the far right
g4.text((dfgraph['-Log(P-Value), SILAC Ratio'][dfgraph.Gene == 'HIVEP1'].min() + 0.1),
            (dfgraph['-Log(P-Value), Spectral Counts'][dfgraph.Gene == 'HIVEP1'].max() - 0.08),
            'HIVEP1', color='black', fontsize=12, weight='bold')

g4.text((dfgraph['-Log(P-Value), SILAC Ratio'][dfgraph.Gene == 'GTSE1'].max() - .59),
            (dfgraph['-Log(P-Value), Spectral Counts'][dfgraph.Gene == 'GTSE1'].max() - 0.08),
            'GTSE1', color='black', fontsize=12, weight='bold', ha='left')

g4.text((dfgraph['-Log(P-Value), SILAC Ratio'][dfgraph.Gene == 'KDM1B'].max() - .625),
            (dfgraph['-Log(P-Value), Spectral Counts'][dfgraph.Gene == 'KDM1B'].max() - 0.08),
            'KDM1B', color='black', fontsize=12, weight='bold', ha='left')

#export as svg
plt.savefig('InteractorVolcanoPlot.svg')
```

A5.6.7. Querying the Uniprot Knowledgebase.

```
#import required packages
import re
import sys
import pandas as pd
import networkx as nx
import itertools as it
from collections import namedtuple
import numpy as np
import matplotlib
import matplotlib.pyplot as plt
from IPython.display import display
from functools import reduce
import seaborn as sns; sns.set()
from io import StringIO
from matplotlib_venn import venn2_unweighted #the unweighted is if you want to make circles that are the same size
from matplotlib_venn import venn2 #also import the normal one
import pandas as pd
import numpy as np
from io import StringIO
import urllib.request, urllib.parse, urllib.error,urllib.request,urllib.error,urllib.parse
from Bio import SeqIO

#magic function to show plots inline
%matplotlib inline

#ignore warnings
import warnings
warnings.filterwarnings("ignore")
#Import the sites and regions final output and the final substrates and ints lists

#make lists to import the filenames
list_sr = ['293T', 'Liver', 'Brain']
list_ints = ['293TF', '293TSwiss', 'BrainF', 'BrainSwiss', 'LiverF', 'LiverSwiss']
list_subs = ['293Full', '293SwissProt', 'BrainFull', 'BrainSwissProt', 'LiverFull', 'LiverSwissProt']

#import the sites and regions from the full proteome
for i in list_sr:
    locals()['dfsrFull{}'.format(i)] = pd.read_csv('./20D15_SitesAndRegions/maxparcon_{}.txt'.format(i), sep='\t')

#and for the SwissProt proteome
for i in list_sr:
    locals()['dfsrSwiss{}'.format(i)] = pd.read_csv('./20D22_SitesAndRegions_SwissProt/maxparcon_{}.txt'.format(i), sep='\t')

#import the interactors
for i in list_ints:
    locals()['dfints{}'.format(i)] = pd.read_csv(
        './20B25_Analyzed_PD_Output/Interactors{}.csv'.format(i))[['Accession', 'Gene']]

#import the substrates
for i in list_subs:
    locals()['dfsubs{}'.format(i)] = pd.read_csv(
        './20B25_Analyzed_PD_Output/Substrates{}.csv'.format(i))[['Accession', 'Modifications', 'Gene']]
#Set up variables and query uniprot with a for loop (starting with full sites and regions)

url = "https://www.uniprot.org/uploadlists/"
user_agent = 'Mozilla/5.0 (Windows NT 10.0; Win64; x64)'

#make a for loop for all three tissues
for i in list_sr:
    output = set(locals()['dfsrFull{}'.format(i)].Protein) #define 'output for setting the params'
```

```
    #set values to query uniprot for
    params = {
        "from":"ACC+ID",
        "to":"ACC",
        "format":"tab",
        "columns": "id,entry name,protein names(recommended name),reviewed,keywords,comment(FUNCTION),comment(PATHWAY),"
        "go(biological process),go(molecular function),go(cellular component),comment(SUBCELLULAR LOCATION),comment(PTM),"
        "feature(MODIFIED RESIDUE),feature(GLYCOSYLATION),comment(DOMAIN),feature(DOMAIN EXTENT),feature(COILED COIL),"
        "feature(COMPOSITIONAL BIAS),feature(MOTIF),feature(REGION),feature(REPEAT),feature(ZINC FINGER)",
        "query":" ".join(list(output))}

    #query uniprot
    data = urllib.parse.urlencode(params)
    data = data.encode('ascii')
    headers = {"User-Agent": user_agent}
    request = urllib.request.Request(url, data, headers)
    with urllib.request.urlopen(request) as f:
      response = f.read().decode()

    #read the response into a df, drop the last column (repeat of input list), and export to csv
    locals()['dfres_srFull{}'.format(i)] = pd.read_csv(StringIO(response), sep='\t')
    locals()['dfres_srFull{}'.format(i)].drop(locals()['dfres_srFull{}'.format(i)].columns[-1], axis=1, inplace=True)
    locals()['dfres_srFull{}'.format(i)].to_csv('./20D22_UniprotOutput/RawOutput_srFull{}.csv'.format(i))
#Repeat for SwissProt sites and regions

#make a for loop for all three tissues
for i in list_sr:
    output = set(locals()['dfsrSwiss{}'.format(i)].Protein) #define 'output for setting the params'

    #set values to query uniprot for
    params = {
        "from":"ACC+ID",
        "to":"ACC",
        "format":"tab",
        "columns": "id,entry name,protein names(recommended name),reviewed,keywords,comment(FUNCTION),comment(PATHWAY),"
        "go(biological process),go(molecular function),go(cellular component),comment(SUBCELLULAR LOCATION),comment(PTM),"
        "feature(MODIFIED RESIDUE),feature(GLYCOSYLATION),comment(DOMAIN),feature(DOMAIN EXTENT),feature(COILED COIL),"
        "feature(COMPOSITIONAL BIAS),feature(MOTIF),feature(REGION),feature(REPEAT),feature(ZINC FINGER)",
        "query":" ".join(list(output))}

    #query uniprot
    data = urllib.parse.urlencode(params)
    data = data.encode('ascii')
    headers = {"User-Agent": user_agent}
    request = urllib.request.Request(url, data, headers)
    with urllib.request.urlopen(request) as f:
      response = f.read().decode()

    #read the response into a df, drop the last column (repeat of input list), and export to csv
    locals()['dfres_srSwiss{}'.format(i)] = pd.read_csv(StringIO(response), sep='\t')
    locals()['dfres_srSwiss{}'.format(i)].drop(locals()['dfres_srSwiss{}'.format(i)].columns[-1], axis=1, inplace=True)
    locals()['dfres_srSwiss{}'.format(i)].to_csv('./20D22_UniprotOutput/RawOutput_srSwiss{}.csv'.format(i))
#Now run for the interactors

#make a for loop for all three tissues
for i in list_ints:
    output = set(locals()['dfints{}'.format(i)].Accession) #define 'output for setting the params'

    #set values to query uniprot for
    params = {
        "from":"ACC+ID",
        "to":"ACC",
        "format":"tab",
        "columns": "id,entry name,protein names(recommended name),reviewed,keywords,comment(FUNCTION),comment(PATHWAY),"
        "go(biological process),go(molecular function),go(cellular component),comment(SUBCELLULAR LOCATION),comment(PTM),"
        "feature(MODIFIED RESIDUE),feature(GLYCOSYLATION),comment(DOMAIN),feature(DOMAIN EXTENT),feature(COILED COIL),"
        "feature(COMPOSITIONAL BIAS),feature(MOTIF),feature(REGION),feature(REPEAT),feature(ZINC FINGER)",
        "query":" ".join(list(output))}

    #query uniprot
    data = urllib.parse.urlencode(params)
    data = data.encode('ascii')
    headers = {"User-Agent": user_agent}
    request = urllib.request.Request(url, data, headers)
    with urllib.request.urlopen(request) as f:
      response = f.read().decode()

    #read the response into a df, drop the last column (repeat of input list), and export to csv
    locals()['dfres_ints{}'.format(i)] = pd.read_csv(StringIO(response), sep='\t')
    locals()['dfres_ints{}'.format(i)].drop(locals()['dfres_ints{}'.format(i)].columns[-1], axis=1, inplace=True)
    locals()['dfres_ints{}'.format(i)].to_csv('./20D22_UniprotOutput/RawOutput_ints{}.csv'.format(i))
#Finally run for the substrates

#make a for loop for all three tissues
for i in list_subs:
    output = set(locals()['dfsubs{}'.format(i)].Accession) #define 'output for setting the params'

    #set values to query uniprot for
    params = {
        "from":"ACC+ID",
        "to":"ACC",
        "format":"tab",
        "columns": "id,entry name,protein names(recommended name),reviewed,keywords,comment(FUNCTION),comment(PATHWAY),"
```

```
    "go(biological process),go(molecular function),go(cellular component),comment(SUBCELLULAR LOCATION),comment(PTM),"
    "feature(MODIFIED RESIDUE),feature(GLYCOSYLATION),comment(DOMAIN),feature(DOMAIN EXTENT),feature(COILED COIL),"
    "feature(COMPOSITIONAL BIAS),feature(MOTIF),feature(REGION),feature(REPEAT),feature(ZINC FINGER)",
    "query":" ".join(list(output))}

#query uniprot
data = urllib.parse.urlencode(params)
data = data.encode('ascii')
headers = {"User-Agent": user_agent}
request = urllib.request.Request(url, data, headers)
with urllib.request.urlopen(request) as f:
  response = f.read().decode()

#read the response into a df, drop the last column (repeat of input list), and export to csv
locals()['dfres_subs{}'.format(i)] = pd.read_csv(StringIO(response), sep='\t')
locals()['dfres_subs{}'.format(i)].drop(locals()['dfres_subs{}'.format(i)].columns[-1], axis=1, inplace=True)
locals()['dfres_subs{}'.format(i)].to_csv('./20D22_UniprotOutput/RawOutput_subs{}.csv'.format(i))
```

A5.6.8. Domains and PTMs Bioinformatics Analysis.

```
#import required packages
import re
import sys
import pandas as pd
import networkx as nx
import itertools as it
from collections import namedtuple
import numpy as np
import matplotlib
import matplotlib.pyplot as plt
from IPython.display import display
from functools import reduce
import seaborn as sns; sns.set()
from io import StringIO
from matplotlib_venn import venn2_unweighted #the unweighted is if you want to make circles that are the same size
from matplotlib_venn import venn2 #also import the normal one
import pandas as pd
import numpy as np
from io import StringIO
import urllib.request, urllib.parse, urllib.error,urllib.request,urllib.error,urllib.parse
from Bio import SeqIO
import math
import operator

#magic function to show plots inline
%matplotlib inline

#ignore warnings
import warnings
warnings.filterwarnings("ignore")
#Import the outputs from the uniprot

#folder location uniprot output
ufolder = './20D22_UniprotOutput/'
folderout = './20D23_BioinformaticsAnalyses/'
srfolder = './20D15_SitesAndRegions/'
srfolderswiss = './20D22_SitesAndRegions_SwissProt/'

#define lists for for loop
list_type_sr = ['Full', 'Swiss']
list_exp1 = ['293T', 'Brain', 'Liver']
list_exp2 = ['293', 'Brain', 'Liver']
list_type_subs = ['Full', 'SwissProt']
list_types_ints = ['F', 'Swiss']

#import the sr data
for i in list_exp1:
    for j in list_type_sr:
        locals()['df_sr{}{}'.format(i,j)] = pd.read_csv('%sRawOutput_sr{}{}.csv'.format(j,i)%(ufolder), index_col=0)

#import the interactors data
for i in list_exp1:
    for j in list_types_ints:
        locals()['df_ints{}{}'.format(i,j)] = pd.read_csv('%sRawOutput_ints{}{}.csv'.format(i,j)%(ufolder), index_col=0)

#import the substrates data
for i in list_exp2:
    for j in list_type_subs:
        locals()['df_subs{}{}'.format(i,j)] = pd.read_csv('%sRawOutput_subs{}{}.csv'.format(i,j)%(ufolder), index_col=0)
#Now I will reformat the uniprot data so that is easier to work with

#first for the sites and regions
#find the start and end of every decsription as well as start and end of the domain in aa numbers
#extract the string in between for each of the above
#make a list of lists for the domain start, end, and the domain names for each protein
#drop the extra column this makes in the original dataframe
```

```
#make a list of the columns to tidy (domain will be separate because it has a different column name structure)
list_t = ['Motif', 'Region', 'Repeat']

for i in list_exp1:
    for j in list_type_sr:
        #start with domain
        locals()['df_sr{}{}'.format(i,j)]['DomainList'] = locals()[
            'df_sr{}{}'.format(i,j)]['Domain [FT]'].str.extractall('note="(.*?)"').unstack().apply(
            lambda x: '@Unique@Joiner@'.join(x.dropna()), axis=1).str.split('@Unique@Joiner@')
        locals()['df_sr{}{}'.format(i,j)]['DomainStart'] = locals()[
            'df_sr{}{}'.format(i,j)]['Domain [FT]'].str.extractall('DOMAIN\s(.*?)(?=\.|;)').unstack().apply(
            lambda x: ','.join(x.dropna()), axis=1).str.split(',').apply(lambda x: [int(i) for i in x])
        locals()['df_sr{}{}'.format(i,j)]['DomainEnd'] = locals()[
            'df_sr{}{}'.format(i,j)]['Domain [FT]'].str.extractall('\.\.(.*?);').unstack().apply(
            lambda x: ','.join(x.dropna()), axis=1).str.split(',').apply(lambda x: [int(i) for i in x])

        #then do motif, region, and repeat
        for k in list_t:
            locals()['df_sr{}{}'.format(i,j)]['{}List'.format(k)] = locals()[
                'df_sr{}{}'.format(i,j)]['{}'.format(k)].str.extractall('note="(.*?)"').unstack().apply(
                lambda x: '@Unique@Joiner@'.join(x.dropna()), axis=1).str.split('@Unique@Joiner@')
            locals()['df_sr{}{}'.format(i,j)]['{}Start'.format(k)] = locals()[
                'df_sr{}{}'.format(i,j)]['{}'.format(k)].str.extractall(
                '{}\s(.*?)(?=\.|;)'.format(str.upper(k))).unstack().apply(
                lambda x: ','.join(x.dropna()), axis=1).str.split(',').apply(lambda x: [int(i) for i in x])
            locals()['df_sr{}{}'.format(i,j)]['{}End'.format(k)] = locals()[
                'df_sr{}{}'.format(i,j)]['{}'.format(k)].str.extractall('\.\.(.*?);').unstack().apply(
                lambda x: ','.join(x.dropna()), axis=1).str.split(',').apply(lambda x: [int(i) for i in x])
#Make the same columns for the subs and ints tables

#ints
for i in list_exp1:
    for j in list_types_ints:
        #start with domain
        locals()['df_ints{}{}'.format(i,j)]['DomainList'] = locals()[
            'df_ints{}{}'.format(i,j)]['Domain [FT]'].str.extractall('note="(.*?)"').unstack().apply(
            lambda x: '@Unique@Joiner@'.join(x.dropna()), axis=1).str.split('@Unique@Joiner@')
        locals()['df_ints{}{}'.format(i,j)]['DomainStart'] = locals()[
            'df_ints{}{}'.format(i,j)]['Domain [FT]'].str.extractall('DOMAIN\s(.*?)(?=\.|;)').unstack().apply(
            lambda x: ','.join(x.dropna()), axis=1).str.split(',').apply(lambda x: [int(i) for i in x])
        locals()['df_ints{}{}'.format(i,j)]['DomainEnd'] = locals()[
            'df_ints{}{}'.format(i,j)]['Domain [FT]'].str.extractall('\.\.(.*?);').unstack().apply(
            lambda x: ','.join(x.dropna()), axis=1).str.split(',').apply(lambda x: [int(i) for i in x])

        #then do motif, region, and repeat
        for k in list_t:
            locals()['df_ints{}{}'.format(i,j)]['{}List'.format(k)] = locals()[
                'df_ints{}{}'.format(i,j)]['{}'.format(k)].str.extractall('note="(.*?)"').unstack().apply(
                lambda x: '@Unique@Joiner@'.join(x.dropna()), axis=1).str.split('@Unique@Joiner@')
            locals()['df_ints{}{}'.format(i,j)]['{}Start'.format(k)] = locals()[
                'df_ints{}{}'.format(i,j)]['{}'.format(k)].str.extractall(
                '{}\s(.*?)(?=\.|;)'.format(str.upper(k))).unstack().apply(
                lambda x: ','.join(x.dropna()), axis=1).str.split(',').apply(lambda x: [int(i) for i in x])
            locals()['df_ints{}{}'.format(i,j)]['{}End'.format(k)] = locals()[
                'df_ints{}{}'.format(i,j)]['{}'.format(k)].str.extractall('\.\.(.*?);').unstack().apply(
                lambda x: ','.join(x.dropna()), axis=1).str.split(',').apply(lambda x: [int(i) for i in x])

#subs
for i in list_exp2:
    for j in list_type_subs:
        #start with domain
        locals()['df_subs{}{}'.format(i,j)]['DomainList'] = locals()[
            'df_subs{}{}'.format(i,j)]['Domain [FT]'].str.extractall('note="(.*?)"').unstack().apply(
            lambda x: '@Unique@Joiner@'.join(x.dropna()), axis=1).str.split('@Unique@Joiner@')
        locals()['df_subs{}{}'.format(i,j)]['DomainStart'] = locals()[
            'df_subs{}{}'.format(i,j)]['Domain [FT]'].str.extractall('DOMAIN\s(.*?)(?=\.|;)').unstack().apply(
            lambda x: ','.join(x.dropna()), axis=1).str.split(',').apply(lambda x: [int(i) for i in x])
        locals()['df_subs{}{}'.format(i,j)]['DomainEnd'] = locals()[
            'df_subs{}{}'.format(i,j)]['Domain [FT]'].str.extractall('\.\.(.*?);').unstack().apply(
            lambda x: ','.join(x.dropna()), axis=1).str.split(',').apply(lambda x: [int(i) for i in x])

        #then do motif, region, and repeat
        for k in list_t:
            locals()['df_subs{}{}'.format(i,j)]['{}List'.format(k)] = locals()[
                'df_subs{}{}'.format(i,j)]['{}'.format(k)].str.extractall('note="(.*?)"').unstack().apply(
                lambda x: '@Unique@Joiner@'.join(x.dropna()), axis=1).str.split('@Unique@Joiner@')
            locals()['df_subs{}{}'.format(i,j)]['{}Start'.format(k)] = locals()[
                'df_subs{}{}'.format(i,j)]['{}'.format(k)].str.extractall(
                '{}\s(.*?)(?=\.|;)'.format(str.upper(k))).unstack().apply(
                lambda x: ','.join(x.dropna()), axis=1).str.split(',').apply(lambda x: [int(i) for i in x])
            locals()['df_subs{}{}'.format(i,j)]['{}End'.format(k)] = locals()[
                'df_subs{}{}'.format(i,j)]['{}'.format(k)].str.extractall('\.\.(.*?);').unstack().apply(
                lambda x: ','.join(x.dropna()), axis=1).str.split(',').apply(lambda x: [int(i) for i in x])
#Test whether there are any lists of unequal length for the start and end positions of interests
    #These will be fixed in the original uniprot output files (some regions etc... only have one amino acid)
        #Single amino acid regions etc will be duplicated to give the same start and end position in the df
            #Thus, there will be both a start and end position for every region, etc... and matching will be more
            #straightforward

#list the types of features
list_topsi = ['Domain', 'Motif', 'Region', 'Repeat']

#first check sites and regions
```

```
for i in list_exp1:
    for j in list_type_sr:
        for k in list_topsi:
            locals()['test{}{}{}'.format(i,j,k)] = locals()['df_sr{}{}'.format(i,j)].dropna(subset=['{}Start'.format(k)])
            display('{}{}{}'.format(i,j,k), len(
                locals()['test{}{}{}'.format(i,j,k)][
                    locals()['test{}{}{}'.format(i,j,k)]['{}Start'.format(k)].str.len() != \
                    locals()['test{}{}{}'.format(i,j,k)]['{}End'.format(k)].str.len()]))

#now the ints
for i in list_exp1:
    for j in list_types_ints:
        for k in list_topsi:
            locals()['test{}{}{}'.format(i,j,k)] = locals()['df_ints{}{}'.format(i,j)].dropna(subset=['{}Start'.format(k)])
            display('{}{}{}'.format(i,j,k), len(
                locals()['test{}{}{}'.format(i,j,k)][
                    locals()['test{}{}{}'.format(i,j,k)]['{}Start'.format(k)].str.len() != \
                    locals()['test{}{}{}'.format(i,j,k)]['{}End'.format(k)].str.len()]))
#finally the subs
for i in list_exp2:
    for j in list_type_subs:
        for k in list_topsi:
            locals()['test{}{}{}'.format(i,j,k)] = locals()['df_subs{}{}'.format(i,j)].dropna(subset=['{}Start'.format(k)])
            display('{}{}{}'.format(i,j,k), len(
                locals()['test{}{}{}'.format(i,j,k)][
                    locals()['test{}{}{}'.format(i,j,k)]['{}Start'.format(k)].str.len() != \
                    locals()['test{}{}{}'.format(i,j,k)]['{}End'.format(k)].str.len()]))

# Prepare tables of top domains in the subs and ints for the different tissues (using the full and SwissProt protome)

#first the ints
for j in list_topsi:
    for i in list_exp1:
        for k in range(2):
            locals()['dfintstop{}{}{}'.format(j,i,list_types_ints[k])] = locals()[
                'df_ints{}{}'.format(i,list_types_ints[k])]['{}List'.format(j)].explode().value_counts().rename(
                '{}{}Counts'.format(i,list_type_sr[k])).reset_index().rename(
                columns={'index':'{}{}{}'.format(i,list_type_sr[k],j)})

for i in list_topsi:
    locals()['dfintslist{}'.format(i)] = []
    locals()['dfintslist{}'.format(i)].extend(
        value for name, value in locals().items() if name.startswith('dfintstop{}'.format(i)))
    pd.concat(locals()['dfintslist{}'.format(i)], axis=1).to_csv(
        '%sInteractors_Top{}s.csv'.format(i)%(folderout), index=False)

#then the subs
for j in list_topsi:
    for i in list_exp2:
        for k in range(2):
            locals()['dfsubstop{}{}{}'.format(j,i,list_type_subs[k])] = locals()[
                'df_subs{}{}'.format(i,list_type_subs[k])]['{}List'.format(j)].explode().value_counts().rename(
                '{}{}Counts'.format(i,list_type_sr[k])).reset_index().rename(
                columns={'index':'{}{}{}'.format(i,list_type_sr[k],j)})

for i in list_topsi:
    locals()['dfsubslist{}'.format(i)] = []
    locals()['dfsubslist{}'.format(i)].extend(
        value for name, value in locals().items() if name.startswith('dfsubstop{}'.format(i)))
    pd.concat(locals()['dfsubslist{}'.format(i)], axis=1).to_csv(
        '%sSubstrates_Top{}s.csv'.format(i)%(folderout), index=False)
#Output the integrated tables for both substrates and interactors

#add the gene names (from the PD output file)

#name the folder
folderpd = './20B25_Analyzed_PD_Output/'

#ints
for i in list_exp1:
    for j in list_types_ints:
        locals()['dfintsgenes{}{}'.format(i,j)] = pd.read_csv('%sInteractors{}{}.csv'.format(i,j)%(folderpd))
        locals()['df_ints{}{}'.format(i,j)] = locals()['df_ints{}{}'.format(i,j)].merge(
            locals()['dfintsgenes{}{}'.format(i,j)][['Accession', 'Gene']], how='left', left_on='Entry',
            right_on='Accession').drop(columns={'Accession'})
        cols = ([locals()['df_ints{}{}'.format(i,j)].columns[0]] +
                [locals()['df_ints{}{}'.format(i,j)].columns[-1]] +
                list(locals()['df_ints{}{}'.format(i,j)].columns[1:-1]))
        locals()['df_ints{}{}'.format(i,j)] = locals()['df_ints{}{}'.format(i,j)][cols]

#subs
for i in list_exp2:
    for j in list_type_subs:
        locals()['dfsubsgenes{}{}'.format(i,j)] = pd.read_csv('%sSubstrates{}{}.csv'.format(i,j)%(folderpd))
        locals()['df_subs{}{}'.format(i,j)] = locals()['df_subs{}{}'.format(i,j)].merge(
            locals()['dfsubsgenes{}{}'.format(i,j)][['Accession', 'Gene']], how='left', left_on='Entry',
            right_on='Accession').drop(columns={'Accession'})
        cols = ([locals()['df_subs{}{}'.format(i,j)].columns[0]] +
                [locals()['df_subs{}{}'.format(i,j)].columns[-1]] +
                list(locals()['df_subs{}{}'.format(i,j)].columns[1:-1]))
        locals()['df_subs{}{}'.format(i,j)] = locals()['df_subs{}{}'.format(i,j)][cols]

#putput the ints
```

```
for i in list_exp1:
    for j in range(2):
        locals()['df_ints{}{}'.format(i, list_types_ints[j])].to_csv(
            '%sIntegratedInteractorsTable{}{}.csv'.format(i, list_type_sr[j])%(folderout), index=False)

#output the subs
for i in range(3):
    for j in range(2):
        locals()['df_subs{}{}'.format(list_exp2[i], list_type_subs[j])].to_csv(
            '%sIntegratedSubstratesTable{}{}.csv'.format(list_exp1[i], list_type_sr[j])%(folderout), index=False)
#Now check if a localized site is in a domain/motif/region/repeat

#first load in the regions outputs into dfs (I will do both Swiss Prot and the full proteome)

#make a list of folder names
list_sr_proteome = [srfolder, srfolderswiss]

#import the regions into dfs (remove lines with more than one protein as before)
#make an additional column to indicate whether the line is a site or region
#merge the data with the uniprot output
for i in range(3):
    for j in range(2):
        locals()['dfregions_{}{}'.format(list_exp1[i], list_type_sr[j])] = pd.read_csv(
            '%smaxparcon_{}.txt'.format(list_exp1[i])%(list_sr_proteome[j]), sep='\t')
        locals()['dfregions_{}{}'.format(list_exp1[i], list_type_sr[j])] = \
        locals()['dfregions_{}{}'.format(list_exp1[i], list_type_sr[j])][
            ~locals()['dfregions_{}{}'.format(list_exp1[i], list_type_sr[j])].Protein.str.contains(';')]
        locals()['dfregions_{}{}'.format(list_exp1[i], list_type_sr[j])].loc[
            locals()['dfregions_{}{}'.format(list_exp1[i], list_type_sr[j])]['Site ID Constraints'].str.contains('of'),
            'Type'] = 'Region'
        locals()['dfregions_{}{}'.format(list_exp1[i], list_type_sr[j])].loc[
            ~locals()['dfregions_{}{}'.format(list_exp1[i], list_type_sr[j])]['Site ID Constraints'].str.contains('of'),
            'Type'] = 'Site'
        locals()['dfmerged_{}{}'.format(list_exp1[i], list_type_sr[j])] = locals()['dfregions_{}{}'.format(
            list_exp1[i], list_type_sr[j])].merge(locals()['df_sr{}{}'.format(
            list_exp1[i], list_type_sr[j])], how='left', left_on='Protein', right_on='Entry')
        locals()['dfmerged_{}{}'.format(list_exp1[i], list_type_sr[j])].drop(columns={'Entry'}, inplace=True)
#Find sites that are within the bounds of domains/motifs/regions/repeats

#define a function for finding sites that exist w/in features in the dfs
def sitecheck(df, Name, Column1, Column2, SiteColumn):
    return [df[Name][i] for i in range(len(df[Name])) if (
        (df[Column1][i] <= df[SiteColumn]) & (df[Column2][i] >= df[SiteColumn]))]

#make a for loops to iterate over all dfs and all types
#return the empty lists back into NaNs
for i in list_exp1:
    for j in list_type_sr:
        locals()['dfsitemerged_{}{}'.format(i,j)] = locals()['dfmerged_{}{}'.format(i,j)][locals()[
            'dfmerged_{}{}'.format(i,j)].Type == 'Site']
        locals()['dfsitemerged_{}{}'.format(i,j)]['Site ID Constraints'] = \
        locals()['dfsitemerged_{}{}'.format(i,j)]['Site ID Constraints'].astype(int)
        globals()['dfsitemerged_{}{}'.format(i,j)] = globals()['dfsitemerged_{}{}'.format(i,j)].fillna(
            {column: {ind: [] for ind in globals()['dfsitemerged_{}{}'.format(i,j)].index}
             for column in globals()['dfsitemerged_{}{}'.format(i,j)].columns})
        for k in list_topsi:
            locals()['dfsitemerged_{}{}'.format(i,j)]['SitesIn{}s'.format(k)] = \
            locals()['dfsitemerged_{}{}'.format(i,j)].apply(
                sitecheck, args=('{}List'.format(k), '{}Start'.format(k), '{}End'.format(k), 'Site ID Constraints'),
                axis=1)
        dfmaptemp = locals()['dfsitemerged_{}{}'.format(i,j)].applymap(lambda x: x == [])
        locals()['dfsitemerged_{}{}'.format(i,j)] = locals()['dfsitemerged_{}{}'.format(i,j)][dfmaptemp == False]
#Count the number of sites across all features for SwissProt and Full

#initialize empty lists, append them with the sum of all counts over each feature, and finally sum and display
for i in list_exp1:
    for j in list_type_sr:
        locals()['featurecount{}{}'.format(i,j)] = []
        for k in list_topsi:
            locals()['featurecount{}{}'.format(i, j)].append(locals()['dfsitemerged_{}{}'.format(i,j)][
                'SitesIn{}s'.format(k)].explode().value_counts().sum())
        display('{}{}'.format(i,j), sum(locals()['featurecount{}{}'.format(i,j)]))

#Now export the results for the top features for all sites in each tissue (from both the full and SwissProt proteome)

#Based on the above, the liver/brain have many more annotated features in the full proteome while 293Ts have more
    # annotated features in the SwissProt proteome (this is in line with the human SwissProt proteome being significantly
    # more complete than the mouse SwissProt proteome)

#export each feature as its own table as before
for i in list_exp1:
    for j in list_topsi:
        for k in list_type_sr:
            locals()['dfsitestop{}{}{}'.format(j,i,k)] = locals()['dfsitemerged_{}{}'.format(i,k)][
                'SitesIn{}s'.format(j)].explode().value_counts().rename('{}{}Counts'.format(i,k)).reset_index().rename(
                columns={'index':'{}{}{}'.format(i,k,j)})

for i in list_topsi:
    locals()['dfsiteslist{}'.format(i)] = []
    locals()['dfsiteslist{}'.format(i)].extend(
        value for name, value in locals().items() if name.startswith('dfsitestop{}'.format(i)))
    pd.concat(locals()['dfsiteslist{}'.format(i)], axis=1).to_csv(
        '%sSites_Top{}s.csv'.format(i)%(folderout), index=False)
```

Integrating with PhosphoSitePlus Database

```
#Define the folder name where the PhosphoSitePlus db was downloaded
folderpsp = './20D28_PhosphoSitePlus/'

#import the PTM datasets

#make a list of the PTMs and other dbs to import
list_dbs = ['Acetylation', 'Methylation', 'O-GalNAc', 'O-GlcNAc', 'Phosphorylation', 'Sumoylation', 'Ubiquitination',
        'Disease-associated', 'Regulatory']

#import the dfs in a for loop and remove the dash from dfs containing it
for i in list_dbs:
    locals()['df_{}_Sites'.format(i)] = pd.read_csv('%s{}_site_dataset.txt'.format(i)%(folderpsp), sep='\t', header=2)

df_OGlcNAc_Sites = locals()['df_O-GlcNAc_Sites']
df_OGalNAc_Sites = locals()['df_O-GalNAc_Sites']
df_Disease_Sites = locals()['df_Disease-associated_Sites']

#import the PTMVar dataset
df_PTMVar_Sites = pd.read_csv('%sPTMVar.txt'%(folderpsp), sep='\t', header=6)
#Extract the relevant columns from the datasets

#make a new list of df names
list_dbs2 = ['Acetylation', 'Methylation', 'OGalNAc', 'OGlcNAc', 'Phosphorylation', 'Sumoylation', 'Ubiquitination',
        'Disease', 'Regulatory', 'PTMVar']

#take the columns of interest and split the modification residue into the site number only
#rename the MOD_RSD column to the name of the modification
for i in list_dbs2[0:7]:
    locals()['df_{}_Sites'.format(i)] = locals()['df_{}_Sites'.format(i)][['ACC_ID', 'MOD_RSD', 'ORGANISM', 'DOMAIN']]

#now extract from the other three datasets (also add a column to the disease and regulatory dfs to define mod type)
df_Disease_Sites = df_Disease_Sites[['DISEASE', 'ALTERATION', 'ACC_ID', 'ORGANISM', 'MOD_RSD', 'DOMAIN', 'NOTES']]
df_Disease_Sites.rename(columns={'NOTES':'NotesDisease'}, inplace=True)
df_Disease_Sites['ModTypeDisease'] = df_Disease_Sites.MOD_RSD.map(lambda x: x.split('-')[1])

df_Regulatory_Sites = df_Regulatory_Sites[['ACC_ID', 'ORGANISM', 'MOD_RSD', 'ON_FUNCTION', 'ON_PROCESS', 'DOMAIN',
                        'ON_PROT_INTERACT', 'ON_OTHER_INTERACT', 'NOTES']]
df_Regulatory_Sites.rename(columns={'NOTES':'NotesRegulatory'}, inplace=True)
df_Regulatory_Sites['ModTypeRegulatory'] = df_Regulatory_Sites.MOD_RSD.map(lambda x: x.split('-')[1])

df_PTMVar_Sites = df_PTMVar_Sites[['FTID', 'dbSNP', 'MUT_RSD#', 'VAR_TYPE', 'DISEASE(s)', 'ACC_ID', 'MOD_RSD',
                    'RSD_CONSERVATION', 'MOD_TYPE']]
df_PTMVar_Sites.rename(columns={'MOD_RSD':'OtherClosePTMs', 'ACC_ID':'Protein', 'MOD_Type':'ModTypePTMVar',
                    'MUT_RSD#':'PTMVarSite'}, inplace=True)

for i in list_dbs2[0:9]:
    locals()['df_{}_Sites'.format(i)].MOD_RSD = locals()['df_{}_Sites'.format(i)].MOD_RSD.str.extract('[A-Za-z](.*?)-')
    locals()['df_{}_Sites'.format(i)].rename(
        columns={'MOD_RSD':'{}Site'.format(i), 'ACC_ID':'Protein', 'DOMAIN':'{}Domain'.format(i)}, inplace=True)
#Move the protein to the first column for the PTMVar and Disease dfs to facilitate grouping below

cols_disease = list(df_Disease_Sites.columns)
cols_disease = [cols_disease[2]] + cols_disease[0:2] + cols_disease[3:]
df_Disease_Sites = df_Disease_Sites[cols_disease]

cols_ptm = list(df_PTMVar_Sites.columns)
cols_ptm = [cols_ptm[5]] + cols_ptm[0:5] + cols_ptm[6:]
df_PTMVar_Sites = df_PTMVar_Sites[cols_ptm]
#Now merge these cleaned dfs with the respective regions df from above

#first merge the site merged dfs back to the full region dfs
for i in list_exp1:
    for j in list_type_sr:
        locals()['dfmergedF_{}{}'.format(i,j)] = locals()['dfmerged_{}{}'.format(i,j)].merge(
            locals()['dfsitemerged_{}{}'.format(i,j)], how='left', on='Region ID', suffixes=('','_y'))
        locals()['dfmergedF_{}{}'.format(i,j)].drop(
            locals()['dfmergedF_{}{}'.format(i,j)].filter(regex='_y$').columns.tolist(), axis=1, inplace=True)

#set up the PTMVar df for merging with the human sites dfs
temp3 = df_PTMVar_Sites
temp3 = temp3.astype(str)
temp3.replace({'-':np.nan,'nan':np.nan}, inplace=True)
temp4 = temp3.groupby('Protein').agg(lambda x: '@Unique@Identifier@'.join(x.fillna(''))).reset_index()
for l in temp4.columns[1::]:
    temp4[l] = temp4[l].str.split('@Unique@Identifier@')
temp4.PTMVarSite = temp4.PTMVarSite.apply(lambda x: [int(i) for i in x])

#group each of the database lists by protein (start with human for the 293T cells)
for i in list_type_sr:
    locals()['dfsites_293T_{}'.format(i)] = locals()['dfmergedF_293T{}'.format(i)]
    for j in list_dbs2[0:9]:
        temp = locals()['df_{}_Sites'.format(j)][locals()['df_{}_Sites'.format(j)].ORGANISM == 'human']
        temp.drop(columns={'ORGANISM'}, inplace=True)
        temp2 = temp.groupby('Protein').agg(lambda x: '@Unique@Identifier@'.join(x.fillna(''))).reset_index()
        for k in temp2.columns[1::]:
            temp2[k] = temp2[k].str.split('@Unique@Identifier@')
        temp2['{}Site'.format(j)] = temp2['{}Site'.format(j)].apply(lambda x: [int(i) for i in x])
        locals()['dfsites_293T_{}'.format(i)] = locals()['dfsites_293T_{}'.format(i)].merge(
            temp2, how='left', on='Protein')
    locals()['dfsites_293T_{}'.format(i)] = locals()['dfsites_293T_{}'.format(i)].merge(temp4, how='left', on='Protein')
```

```
#Repeat for the liver and brain with the mouse entries (excluding O-GalNAc which has no mouse sites)
for i in list_exp1[1::]:
    for j in list_type_sr:
        locals()['dfsites_{}_{}'.format(i,j)] = locals()['dfmergedF_{}{}'.format(i,j)]
        for k in (list_dbs2[0:2] + list_dbs2[3:9]):
            mtemp = locals()['df_{}_Sites'.format(k)][locals()['df_{}_Sites'.format(k)].ORGANISM == 'mouse']
            mtemp.drop(columns={'ORGANISM'}, inplace=True)
            mtemp2 = mtemp.groupby('Protein').agg(lambda x: '@Unique@Identifier@'.join(x.fillna(''))).reset_index()
            for l in mtemp2.columns[1::]:
                mtemp2[l] = mtemp2[l].str.split('@Unique@Identifier@')
            mtemp2['{}Site'.format(k)] = mtemp2['{}Site'.format(k)].apply(lambda x: [int(i) for i in x])
            locals()['dfsites_{}_{}'.format(i,j)] = locals()['dfsites_{}_{}'.format(i,j)].merge(
                mtemp2, how='left', on='Protein')
#Find sites that overlap with or are w/in 10aa of ptms

#define functions to parse the data

#first ptms
def sitecheckptm10aa(df, PTM, Domain, SiteColumn):
    return [[df[PTM][i], df[Domain][i]] for i in range(len(df[PTM])) if (
        ((df[PTM][i] - 10) <= df[SiteColumn]) & ((df[PTM][i] + 10) >= df[SiteColumn]))]
def sitecheckptmSame(df, PTM, Domain, SiteColumn):
    return [[df[PTM][i], df[Domain][i]] for i in range(len(df[PTM])) if (df[PTM][i] == df[SiteColumn])]

#then regulatory sites
def sitecheckRegulatorySame(df, PTM, Domain, SiteColumn):
    return [[df[PTM][i], df[Domain][i], df['ModTypeRegulatory'][i], df['ON_FUNCTION'][i], df['ON_PROCESS'][i],
             df['ON_PROT_INTERACT'][i], df['ON_OTHER_INTERACT'][i], df['NotesRegulatory'][i]] for i in range(
        len(df[PTM])) if (df[PTM][i] == df[SiteColumn])]
def sitecheckRegulatory10aa(df, PTM, Domain, SiteColumn):
    return [[df[PTM][i], df[Domain][i], df['ModTypeRegulatory'][i], df['ON_FUNCTION'][i], df['ON_PROCESS'][i],
             df['ON_PROT_INTERACT'][i], df['ON_OTHER_INTERACT'][i], df['NotesRegulatory'][i]] for i in range(
        len(df[PTM])) if (((df[PTM][i] - 10) <= df[SiteColumn]) & ((df[PTM][i] + 10) >= df[SiteColumn]))]

#then disease sites
def sitecheckDiseaseSame(df, PTM, Domain, SiteColumn):
    return [[df[PTM][i], df[Domain][i], df['ModTypeDisease'][i], df['DISEASE'][i], df['ALTERATION'][i],
             df['NotesDisease'][i]] for i in range(len(df[PTM])) if (df[PTM][i] == df[SiteColumn])]
def sitecheckDisease10aa(df, PTM, Domain, SiteColumn):
    return [[df[PTM][i], df[Domain][i], df['ModTypeDisease'][i], df['DISEASE'][i], df['ALTERATION'][i],
             df['NotesDisease'][i]] for i in range(len(df[PTM])) if
            (((df[PTM][i] - 10) <= df[SiteColumn]) & ((df[PTM][i] + 10) >= df[SiteColumn]))]

#finally PTMVar sites
def sitecheckPTMVarSame(df, PTM, SiteColumn):
    return [[df[PTM][i], df['MOD_TYPE'][i], df['FTID'][i], df['dbSNP'][i], df['VAR_TYPE'][i], df['DISEASE(s)'][i],
            df['OtherClosePTMs'][i], df['RSD_CONSERVATION'][i]] for i in range(len(df[PTM])) if
            (df[PTM][i] == df[SiteColumn])]
def sitecheckPTMVar10aa(df, PTM, SiteColumn):
    return [[df[PTM][i], df['MOD_TYPE'][i], df['FTID'][i], df['dbSNP'][i], df['VAR_TYPE'][i], df['DISEASE(s)'][i],
            df['OtherClosePTMs'][i], df['RSD_CONSERVATION'][i]] for i in range(len(df[PTM])) if
            (((df[PTM][i] - 10) <= df[SiteColumn]) & ((df[PTM][i] + 10) >= df[SiteColumn]))]

#make a list to call the above functions
list_func = ['10aa', 'Same']

#first do the ptms for 293Ts
for i in list_type_sr:
    for j in list_dbs2[0:7]:
        temp = locals()['dfsites_293T_{}'.format(i)][locals()['dfsites_293T_{}'.format(i)].Type == 'Site']
        temp.dropna(subset=['{}Site'.format(j)], inplace=True)
        temp['Site ID Constraints'] = temp['Site ID Constraints'].astype(int)
        for k in list_func:
            temp['{}{}Info'.format(j,k)] = temp.apply(
                locals()['sitecheckptm{}'.format(k)], args=(
                    '{}Site'.format(j), '{}Domain'.format(j), 'Site ID Constraints'), axis=1)
            temp.loc[temp['{}{}Info'.format(j,k)].map(lambda x: len(x)) > 0, '{}{}'.format(j,k)] = 'Yes'
            locals()['dfsites_293T_{}'.format(i)][['{}{}Info'.format(j,k), '{}{}'.format(j,k)]] = temp[[
                '{}{}Info'.format(j,k), '{}{}'.format(j,k)]]

#then do the PTMs for the Brain and Liver
for i in list_exp1[1:3]:
    for j in list_type_sr:
        for k in list_dbs2[0:2] + list_dbs2[3:7]:
            temp = locals()['dfsites_{}_{}'.format(i,j)][locals()['dfsites_{}_{}'.format(i,j)].Type == 'Site']
            temp.dropna(subset=['{}Site'.format(k)], inplace=True)
            temp['Site ID Constraints'] = temp['Site ID Constraints'].astype(int)
            for l in list_func:
                temp['{}{}Info'.format(k,l)] = temp.apply(
                    locals()['sitecheckptm{}'.format(l)], args=(
                        '{}Site'.format(k), '{}Domain'.format(k), 'Site ID Constraints'), axis=1)
                temp.loc[temp['{}{}Info'.format(k,l)].map(lambda x: len(x)) > 0, '{}{}'.format(k,l)] = 'Yes'
                locals()['dfsites_{}_{}'.format(i,j)][['{}{}Info'.format(k,l), '{}{}'.format(k,l)]] = temp[[
                    '{}{}Info'.format(k,l), '{}{}'.format(k,l)]]

#finally do disease and regulatory sites for 293Ts, brian, and liver and PTMVar sites for 293Ts (only human data)

#293Ts disease and regulatory
for i in list_type_sr:
    for j in list_dbs2[7:9]:
        temp = locals()['dfsites_293T_{}'.format(i)][locals()['dfsites_293T_{}'.format(i)].Type == 'Site']
        temp.dropna(subset=['{}Site'.format(j)], inplace=True)
        temp['Site ID Constraints'] = temp['Site ID Constraints'].astype(int)
```

```
        for k in list_func:
            temp['{}{}Info'.format(j,k)] = temp.apply(
                locals()['sitecheck{}{}'.format(j,k)], args=(
                    '{}Site'.format(j), '{}Domain'.format(j), 'Site ID Constraints'), axis=1)
            temp.loc[temp['{}{}Info'.format(j,k)].map(lambda x: len(x)) > 0, '{}{}'.format(j,k)] = 'Yes'
            locals()['dfsites_293T_{}'.format(i)][['{}{}Info'.format(j,k), '{}{}'.format(j,k)]] = temp[[
                '{}{}Info'.format(j,k), '{}{}'.format(j,k)]]

#brain and liver disease and regulatory
for i in list_exp1[1:3]:
    for j in list_type_sr:
        for k in list_dbs2[7:9]:
            temp = locals()['dfsites_{}_{}'.format(i,j)][locals()['dfsites_{}_{}'.format(i,j)].Type == 'Site']
            temp.dropna(subset=['{}Site'.format(k)], inplace=True)
            temp['Site ID Constraints'] = temp['Site ID Constraints'].astype(int)
            for l in list_func:
                temp['{}{}Info'.format(k,l)] = temp.apply(
                    locals()['sitecheck{}{}'.format(k,l)], args=(
                        '{}Site'.format(k), '{}Domain'.format(k), 'Site ID Constraints'), axis=1)
                temp.loc[temp['{}{}Info'.format(k,l)].map(lambda x: len(x)) > 0, '{}{}'.format(k,l)] = 'Yes'
                locals()['dfsites_{}_{}'.format(i,j)][['{}{}Info'.format(k,l), '{}{}'.format(k,l)]] = temp[[
                    '{}{}Info'.format(k,l), '{}{}'.format(k,l)]]

#293Ts PTMVar sites
for i in list_type_sr:
    for j in list_dbs2[9:10]:
        temp = locals()['dfsites_293T_{}'.format(i)][locals()['dfsites_293T_{}'.format(i)].Type == 'Site']
        temp.dropna(subset=['{}Site'.format(j)], inplace='True)
        temp['Site ID Constraints'] = temp['Site ID Constraints'].astype(int)
        for k in list_func:
            temp['{}{}Info'.format(j,k)] = temp.apply(
                locals()['sitecheck{}{}'.format(j,k)], args=('{}Site'.format(j), 'Site ID Constraints'), axis=1)
            temp.loc[temp['{}{}Info'.format(j,k)].map(lambda x: len(x)) > 0, '{}{}'.format(j,k)] = 'Yes'
            locals()['dfsites_293T_{}'.format(i)][['{}{}Info'.format(j,k), '{}{}'.format(j,k)]] = temp[[
                '{}{}Info'.format(j,k), '{}{}'.format(j,k)]]
#Export these to save the full tables
for i in list_exp1:
    for j in list_type_sr:
        locals()['dfsites_{}_{}'.format(i,j)].to_csv(
            '%sIntegratedRegionsTable{}{}.csv'.format(i,j)%(folderout), index=False)
#Export the top domains, disease, etc... from each sample

#list of info to count up in regulatory sites
list_reg = ['Function', 'Process', 'ProtInteraction', 'OtherInteraction']

#293T samples
for i in list_exp1[0:1]:
    for j in list_type_sr:
        for k in list_func:
            for l in (list_dbs2[0:2] + list_dbs2[3:7]):
                locals()['dfptmstop{}{}{}{}'.format(i,j,k,l)] = locals()[
                    'dfsites_{}_{}'.format(i,j)]['{}{}Info'.format(l,k)][
                    locals()['dfsites_{}_{}'.format(i,j)]['{}{}Info'.format(l,k)].notnull()].apply(
                    lambda x: [e[1] for e in x]).explode().value_counts().rename(
                    '{}{}Counts'.format(l,k)).reset_index().rename(columns={'index':'{}{}Domains'.format(l,k)})
            for l in list_dbs2[7:8]:
                locals()['dfptmstop{}{}{}{}'.format(i,j,k,l)] = locals()[
                    'dfsites_{}_{}'.format(i,j)]['{}{}Info'.format(l,k)][
                    locals()['dfsites_{}_{}'.format(i,j)]['{}{}Info'.format(l,k)].notnull()].apply(
                    lambda x: [e[3] for e in x]).explode().value_counts().rename(
                    '{}{}Counts'.format(l,k)).reset_index().rename(columns={'index':'{}{}'.format(l,k)})
            for l in list_dbs2[9:10]:
                locals()['dfptmstop{}{}{}{}'.format(i,j,k,l)] = locals()[
                    'dfsites_{}_{}'.format(i,j)]['{}{}Info'.format(l,k)][
                    locals()['dfsites_{}_{}'.format(i,j)]['{}{}Info'.format(l,k)].notnull()].apply(
                    lambda x: [e[5] for e in x]).explode().value_counts().rename(
                    '{}{}Counts'.format(l,k)).reset_index().rename(columns={'index':'{}{}'.format(l,k)})
            for l in list_dbs2[8:9]:
                for m in range(4):
                    locals()['dfptmstop{}{}{}{}{}'.format(i,j,k,l,list_reg[m])] = locals()[
                        'dfsites_{}_{}'.format(i,j)]['{}{}Info'.format(l,k)][
                        locals()['dfsites_{}_{}'.format(i,j)]['{}{}Info'.format(l,k)].notnull()].apply(
                        lambda x: [e[m+3] for e in x]).explode().value_counts().rename(
                        '{}{}{}Counts'.format(l,list_reg[m],k)).reset_index().rename(
                        columns={'index':'{}{}{}'.format(l,list_reg[m],k)})

#mouse samples
for i in list_exp1[1:3]:
    for j in list_type_sr:
        for k in list_func:
            for l in (list_dbs2[0:2] + list_dbs2[3:7]):
                locals()['dfptmstop{}{}{}{}'.format(i,j,k,l)] = locals()[
                    'dfsites_{}_{}'.format(i,j)]['{}{}Info'.format(l,k)][
                    locals()['dfsites_{}_{}'.format(i,j)]['{}{}Info'.format(l,k)].notnull()].apply(
                    lambda x: [e[1] for e in x]).explode().value_counts().rename(
                    '{}{}Counts'.format(l,k)).reset_index().rename(columns={'index':'{}{}Domains'.format(l,k)})
            for l in list_dbs2[7:8]:
                locals()['dfptmstop{}{}{}{}'.format(i,j,k,l)] = locals()[
                    'dfsites_{}_{}'.format(i,j)]['{}{}Info'.format(l,k)][
                    locals()['dfsites_{}_{}'.format(i,j)]['{}{}Info'.format(l,k)].notnull()].apply(
                    lambda x: [e[3] for e in x]).explode().value_counts().rename(
                    '{}{}Counts'.format(l,k)).reset_index().rename(columns={'index':'{}{}'.format(l,k)})
            for l in list_dbs2[8:9]:
```

```
            for m in range(4):
                locals()['dfptmstop{}{}{}{}{}'.format(i,j,k,l,list_reg[m])] = locals()[
                    'dfsites_{}_{}'.format(i,j)]['{}{}Info'.format(l,k)][
                    locals()['dfsites_{}_{}'.format(i,j)]['{}{}Info'.format(l,k)].notnull()].apply(
                    lambda x: [e[m+3] for e in x]).explode().value_counts().rename(
                    '{}{}{}Counts'.format(l,list_reg[m],k)).reset_index().rename(
                    columns={'index':'{}{}{}'.format(l,list_reg[m],k)})

for i in list_exp1:
    for j in list_type_sr:
        locals()['dfptmslist{}{}'.format(i,j)] = []
        locals()['dfptmslist{}{}'.format(i,j)].extend(
            value for name, value in locals().items() if name.startswith('dfptmstop{}{}'.format(i,j)))
        pd.concat(locals()['dfptmslist{}{}'.format(i,j)], axis=1).to_csv(
            '%sPTMs_TopInfo_{}{}Sites.csv'.format(i,j)%(folderout), index=False)
#Export a count of the number of sites that are also, or within 10aa of, PTM/regulatory, etc... sites

#construct series out of the df length data and concatentate them together for export as above

#first for 293T cells
for i in list_exp1[0:1]:
    for j in list_type_sr:
        for k in list_func:
            for l in list_dbs2:
                locals()['series{}{}{}{}'.format(i,j,k,l)] = pd.Series(
                    [len(locals()['dfsites_{}_{}'.format(i,j)][
                        locals()['dfsites_{}_{}'.format(i,j)]['{}{}'.format(l,k)] == 'Yes']),
                    len(locals()['dfsites_{}_{}'.format(i,j)][
                        locals()['dfsites_{}_{}'.format(i,j)].Type == 'Site'])], name='{}{}'.format(l,k),
                    index=['Number','Total Sites'])

#for liver and brain
for i in list_exp1[1:3]:
    for j in list_type_sr:
        for k in list_func:
            for l in (list_dbs2[0:2] + list_dbs2[3:9]):
                locals()['series{}{}{}{}'.format(i,j,k,l)] = pd.Series(
                    [len(locals()['dfsites_{}_{}'.format(i,j)][
                        locals()['dfsites_{}_{}'.format(i,j)]['{}{}'.format(l,k)] == 'Yes']),
                    len(locals()['dfsites_{}_{}'.format(i,j)][
                        locals()['dfsites_{}_{}'.format(i,j)].Type == 'Site'])], name='{}{}'.format(l,k),
                    index=['Number','Total Sites'])

#export
for i in list_exp1:
    for j in list_type_sr:
        locals()['serieslist{}{}'.format(i,j)] = []
        locals()['serieslist{}{}'.format(i,j)].extend(
            value for name, value in locals().items() if name.startswith('series{}{}'.format(i,j)))
        pd.concat(locals()['serieslist{}{}'.format(i,j)], axis=1).to_csv(
            '%sSiteOverlapCount_{}{}.csv'.format(i,j)%(folderout), index=True)
#Prepare substrates and interactors tables for importing into cytoscape

#I will integrate the sites and regions tables into the substrates table so the sites are visible in cytoscape

#list columns to join
joincols293T = ['Protein', 'Site ID Constraints']
joincolsmouse = ['Protein', 'Site ID Constraints']
for i in list_dbs2:
    for j in list_func:
        joincols293T.append('{}{}'.format(i,j))
for i in (list_dbs2[0:2] + list_dbs2[3:9]):
    for j in list_func:
        joincolsmouse.append('{}{}'.format(i,j))
for i in list_topsi:
    joincols293T.append('SitesIn{}s'.format(i))
    joincolsmouse.append('SitesIn{}s'.format(i))

#list cols to join from integrated regions table (sites in features)
colsfeatures = ['Protein', 'Region ID', 'Min Sites', 'Site ID Constraints', 'SitesInDomains', 'SitesInMotifs',
            'SitesInRegions', 'SitesInRepeats']

#merge the original regions list with the substrates table and the sites in features column from the full regions table
#also merge with the relevant PTM information from the integrated sites in PTMs table
#finally group everything by gene/protien for output to cytoscape

#first 293Ts
for i in range(1):
    for j in range(2):
        locals()['dfcyto_{}{}'.format(list_exp1[i],list_type_sr[j])] = \
        locals()['dfregions_{}{}'.format(list_exp1[i],list_type_sr[j])].merge(
            locals()['df_subs{}{}'.format(list_exp2[i],list_type_subs[j])], how='left', left_on='Protein',
            right_on='Entry').merge(locals()['dfsites_{}_{}'.format(list_exp1[i], list_type_sr[j])][colsfeatures],
                                    how='left', on=['Protein', 'Region ID', 'Min Sites', 'Site ID Constraints'])
        locals()['dfcyto_{}{}'.format(list_exp1[i],list_type_sr[j])] = \
        locals()['dfcyto_{}{}'.format(list_exp1[i],list_type_sr[j])].merge(
            locals()['dfsites_{}_{}'.format(list_exp1[i],list_type_sr[j])][joincols293T], how='left',
            on=['Protein', 'Site ID Constraints'], suffixes=('','_y'))
        locals()['dfcyto_{}{}'.format(list_exp1[i],list_type_sr[j])].drop(
            list(locals()['dfcyto_{}{}'.format(list_exp1[i],list_type_sr[j])].filter(regex='_y')), axis=1, inplace=True)
        locals()['dfcytoF_{}{}'.format(list_exp1[i],list_type_sr[j])] = \
        locals()['dfcyto_{}{}'.format(list_exp1[i],list_type_sr[j])].sort_values(
            by=['Gene', 'Status']).drop_duplicates(subset='Gene', keep='first').dropna(subset=['Gene'])
```

```
        locals()['dfcyto_{}{}'.format(list_exp1[i],list_type_sr[j])]['Site ID Constraints'] = \
        (locals()['dfcyto_{}{}'.format(list_exp1[i],list_type_sr[j])]['Protein'] + '@' +
         locals()['dfcyto_{}{}'.format(list_exp1[i],list_type_sr[j])]['Site ID Constraints'])
        temp = locals()['dfcyto_{}{}'.format(list_exp1[i],list_type_sr[j])].groupby(
            'Gene')[joincols293T[1:]].agg(lambda x: x.fillna('').astype(str).str.cat(sep='; ')).reset_index()
        for k in joincols293T[1:]:
            locals()['dfcytoF_{}{}'.format(list_exp1[i],list_type_sr[j])][k] = temp[k].values

#then for mouse samples
for i in range(1,3):
    for j in range(2):
        locals()['dfcyto_{}{}'.format(list_exp1[i],list_type_sr[j])] = \
        locals()['dfregions_{}{}'.format(list_exp1[i],list_type_sr[j])].merge(
            locals()['df_subs{}{}'.format(list_exp2[i],list_type_subs[j])], how='left', left_on='Protein',
            right_on='Entry').merge(locals()['dfsites_{}_{}'.format(list_exp1[i], list_type_sr[j])][colsfeatures],
                                    how='left', on=['Protein', 'Region ID', 'Min Sites', 'Site ID Constraints'])
        locals()['dfcyto_{}{}'.format(list_exp1[i],list_type_sr[j])] = \
        locals()['dfcyto_{}{}'.format(list_exp1[i],list_type_sr[j])].merge(
            locals()['dfsites_{}_{}'.format(list_exp1[i],list_type_sr[j])][joincolsmouse], how='left',
            on=['Protein', 'Site ID Constraints'], suffixes=('','_y'))
        locals()['dfcyto_{}{}'.format(list_exp1[i],list_type_sr[j])].drop(
            list(locals()['dfcyto_{}{}'.format(list_exp1[i],list_type_sr[j])].filter(regex='_y')), axis=1, inplace=True)
        locals()['dfcytoF_{}{}'.format(list_exp1[i],list_type_sr[j])] = \
        locals()['dfcyto_{}{}'.format(list_exp1[i],list_type_sr[j])].sort_values(
            by=['Gene', 'Status']).drop_duplicates(subset='Gene', keep='first').dropna(subset=['Gene'])
        locals()['dfcyto_{}{}'.format(list_exp1[i],list_type_sr[j])]['Site ID Constraints'] = \
        (locals()['dfcyto_{}{}'.format(list_exp1[i],list_type_sr[j])]['Protein'] + '@' +
         locals()['dfcyto_{}{}'.format(list_exp1[i],list_type_sr[j])]['Site ID Constraints'])
        temp = locals()['dfcyto_{}{}'.format(list_exp1[i],list_type_sr[j])].groupby(
            'Gene')[joincolsmouse[1:]].agg(lambda x: x.fillna('').astype(str).str.cat(sep='; ')).reset_index()
        for k in joincolsmouse[1:]:
            locals()['dfcytoF_{}{}'.format(list_exp1[i],list_type_sr[j])][k] = temp[k].values

#export these new substrate tables
for i in list_exp1:
    for j in list_type_sr:
        locals()['dfcytoF_{}{}'.format(i,j)].drop(['Protein', 'Region ID', 'Min Sites', 'Type'], axis=1).to_csv(
            '%sCytoscape_IntegratedSubstratesTable{}{}.csv'.format(i, j)%(folderout), index=False)

#finally filter the interactors table by unique genes and export
for i in list_exp1:
    for j in range(2):
        locals()['df_ints{}{}'.format(i, list_types_ints[j])].sort_values(by=['Gene', 'Status']).drop_duplicates(
            subset='Gene', keep='first').dropna(subset=['Gene']).to_csv(
            '%sCytoscape_IntegratedInteractorsTable{}{}.csv'.format(i, list_type_sr[j])%(folderout), index=False)
```

A5.6.9. Export Sites for Motif and Enrichment Analysis.

```
#import required packages
import re
import sys
import networkx as nx
import itertools as it
import pandas as pd
import numpy as np
from io import StringIO
from Bio import SeqIO
from IPython.display import display

#ignore warnings
import warnings
warnings.filterwarnings("ignore")
#Import all of the sites and regions files and take only sites from each

#name the folders
srfolder = './20D15_SitesAndRegions/'
srfolderswiss = './20D22_SitesAndRegions_SwissProt/'
folderout = './20D29_SitesWith10aa/'

#make lists for importing the data
list_sr_proteome = [srfolder, srfolderswiss]
list_type_sr = ['Full', 'Swiss']
list_exp1 = ['293T', 'BAP1KO', 'Brain', 'Liver']

#import the regions into dfs with a for loop (remove lines with more than one protein as before)
#make an additional column to indicate whether the line is a site or region
#keep only the sites in a new df, rename the column to 'Site', and drop the 'Type' column
for i in range(4):
    for j in range(2):
        locals()['dfregions_{}{}'.format(list_exp1[i], list_type_sr[j])] = pd.read_csv(
            '%smaxparcon_{}.txt'.format(list_exp1[i])%(list_sr_proteome[j]), sep='\t')
        locals()['dfregions_{}{}'.format(list_exp1[i], list_type_sr[j])] = \
        locals()['dfregions_{}{}'.format(list_exp1[i], list_type_sr[j])][
            ~locals()['dfregions_{}{}'.format(list_exp1[i], list_type_sr[j])].Protein.str.contains(';')]
        locals()['dfregions_{}{}'.format(list_exp1[i], list_type_sr[j])].loc[
```

```
        locals()['dfregions_{}{}'.format(list_exp1[i], list_type_sr[j])]['Site ID Constraints'].str.contains('of'),
        'Type'] = 'Region'
    locals()['dfregions_{}{}'.format(list_exp1[i], list_type_sr[j])].loc[
        ~locals()['dfregions_{}{}'.format(list_exp1[i], list_type_sr[j])]['Site ID Constraints'].str.contains('of'),
        'Type'] = 'Site'
    locals()['dfsites_{}{}'.format(list_exp1[i], list_type_sr[j])] = \
    locals()['dfregions_{}{}'.format(list_exp1[i], list_type_sr[j])][
        locals()['dfregions_{}{}'.format(list_exp1[i], list_type_sr[j])].Type == 'Site']
    locals()['dfsites_{}{}'.format(list_exp1[i], list_type_sr[j])].rename(
        columns={'Site ID Constraints':'Site'}, inplace=True)
    locals()['dfsites_{}{}'.format(list_exp1[i], list_type_sr[j])].drop(columns={'Type'}, inplace=True)
#Import the fasta files and use them to extract the 10 flanking amino acids

#define a list for importing fasta files
list_fasta = ['Uniprot', 'SwissProt']

#make a for loop for importing human databases
for i in list_fasta:
    locals()['seqDict_Human_{}'.format(i)] = {}
    p = SeqIO.parse('%s20A25_{}_Human.fasta'.format(i)%(folderout), 'fasta')
    for r in p:
        locals()['seqDict_Human_{}'.format(i)][r.id.split("|")[1]] = str(r.seq)

#repeat for the mouse databases
for i in list_fasta:
    locals()['seqDict_Mouse_{}'.format(i)] = {}
    p = SeqIO.parse('%s20A21_{}_Mouse.fasta'.format(i)%(folderout), 'fasta')
    for r in p:
        locals()['seqDict_Mouse_{}'.format(i)][r.id.split("|")[1]] = str(r.seq)

#add the sequences to the sites dfs as a new column
#first for 293Ts
for i in list_exp1[0:2]:
    for j in range(2):
        locals()['dfsites_{}{}'.format(i,list_type_sr[j])]['FASTA Sequence'] = \
        locals()['dfsites_{}{}'.format(i,list_type_sr[j])]['Protein'].map(
            locals()['seqDict_Human_{}'.format(list_fasta[j])])

#then for the brain and liver
for i in list_exp1[2:4]:
    for j in range(2):
        locals()['dfsites_{}{}'.format(i,list_type_sr[j])]['FASTA Sequence'] = \
        locals()['dfsites_{}{}'.format(i,list_type_sr[j])]['Protein'].map(
            locals()['seqDict_Mouse_{}'.format(list_fasta[j])])

#pad the fasta sequence on both ends with underscores and pull out the relevant info:
    #GlcNAc Site, 10 aa before, 10 aa after, and centered sequence
for i in list_exp1:
    for j in list_type_sr:
        locals()['dfsites_{}{}'.format(i,j)]['FASTA Sequence'] = ('__________' +
                                                locals()['dfsites_{}{}'.format(i,j)]['FASTA Sequence'] +
                                                '__________')
        locals()['dfsites_{}{}'.format(i,j)]['Length'] = locals()['dfsites_{}{}'.format(i,j)].apply(
            lambda x: len(x['FASTA Sequence']), axis=1)
        locals()['dfsites_{}{}'.format(i,j)].Site = locals()['dfsites_{}{}'.format(i,j)].Site.astype(int)
        locals()['dfsites_{}{}'.format(i,j)]['GlcNAc AA'] = locals()['dfsites_{}{}'.format(i,j)].apply(
            lambda x: x['FASTA Sequence'][x.Site + 9], axis=1)
        locals()['dfsites_{}{}'.format(i,j)]['10 AA Before'] = locals()['dfsites_{}{}'.format(i,j)].apply(
            lambda x: x['FASTA Sequence'][(x.Site - 1):(x.Site + 9)], axis=1)
        locals()['dfsites_{}{}'.format(i,j)]['10 AA After'] = locals()['dfsites_{}{}'.format(i,j)].apply(
            lambda x: x['FASTA Sequence'][(x.Site + 10):(x.Site + 20)], axis=1)
        locals()['dfsites_{}{}'.format(i,j)]['Centered Sequence'] = \
        (locals()['dfsites_{}{}'.format(i,j)]['10 AA Before'] + locals()['dfsites_{}{}'.format(i,j)]['GlcNAc AA'] +
        locals()['dfsites_{}{}'.format(i,j)]['10 AA After'])
#Check to make sure none of the sites are out of sequence space and all of the sites are S/T

for i in list_exp1:
    for j in list_type_sr:
        display('{}{}:'.format(i,j), len(locals()['dfsites_{}{}'.format(i,j)][
            (locals()['dfsites_{}{}'.format(i,j)]['GlcNAc AA'] != 'S') &
            (locals()['dfsites_{}{}'.format(i,j)]['GlcNAc AA'] != 'T')]), len(
            locals()['dfsites_{}{}'.format(i,j)][locals()['dfsites_{}{}'.format(i,j)].Length <
                                    locals()['dfsites_{}{}'.format(i,j)].Site.astype(int)]))

#Export the relevant information as a csv file for Matt (he will do the seqeunce and motif analysis)
for i in list_exp1:
    for j in list_type_sr:
        locals()['dfsites_{}{}'.format(i,j)][['Protein', 'Site', 'GlcNAc AA', '10 AA Before', '10 AA After',
                                    'Centered Sequence']].to_csv(
                                        '%sGlcNAcCenteredSequence{}{}.csv'.format(i,j)%(folderout),
                                        index=False)
```

A5.6.10. Calculating Adapter Protein Rank.

```
#import packages
import re
```

```
import pandas as pd
import numpy as np
import matplotlib
import matplotlib.pyplot as plt

#ignore warnings
import warnings
warnings.filterwarnings("ignore")
#Load in the networks for all tissues

#set up lists for importing
list_exp = ['293T', 'Brain', 'Liver', 'LiverBrain']

#first import the PPIs
for i in list_exp:
    locals()['df{}'.format(i)] = pd.read_csv('PPINetwork{}F_ForCytoscape.csv'.format(i))

#import the substrates and interacor lists and merge them into the above df
for i in list_exp:
    locals()['dfsubs{}'.format(i)] = pd.read_csv('OGTSubs{}F_ForCytoscape.csv'.format(i))
    locals()['dfints{}'.format(i)] = pd.read_csv('OGTInts{}F_ForCytoscape.csv'.format(i))
    locals()['df{}'.format(i)] = locals()['df{}'.format(i)].merge(
        locals()['dfints{}'.format(i)], how='left', left_on='Interactor_B', right_on='Gene').drop('Gene', axis=1)
    locals()['df{}'.format(i)] = locals()['df{}'.format(i)].merge(
        locals()['dfsubs{}'.format(i)], how='left', left_on='Interactor_B', right_on='Gene').drop('Gene', axis=1)
#Now calculate a score for each pair

#Interactions with substrates (regardless of if those substrates are also interactors) are given one point
#Interactors with interactors that are not substrates are given -0.5 points
def score(df):
    if df.OGT_Substrate == 1:
        return 1
    else:
        return -0.5

#calculate the score for each df and drop all of the instances of self interactions in the table
#group the df by interactor a to make an adapter rank df
for i in list_exp:
    locals()['df{}'.format(i)]['Score'] = locals()['df{}'.format(i)].apply(score, axis=1)
    locals()['df{}'.format(i)] = locals()['df{}'.format(i)][locals()[
        'df{}'.format(i)].Interactor_A != locals()['df{}'.format(i)].Interactor_B]
    locals()['dfar_{}'.format(i)] = locals()['df{}'.format(i)].groupby(
        'Interactor_A').Score.sum().reset_index().sort_values(by=['Score'], ascending=False)
#Remove genes that are only substrates to make the final adapter ranking list

#first merge the df with the interactor list and then drop all nan from the interactor column (and drop added columns)
for i in list_exp:
    locals()['dfarF_{}'.format(i)] = locals()['dfar_{}'.format(i)].merge(
        locals()['dfints{}'.format(i)], how='left', left_on='Interactor_A', right_on='Gene').dropna(
        subset=['OGT_Interactor']).drop(['OGT_Interactor', 'Gene'], axis=1)
#Export the final adapter rank lists
for i in list_exp:
    locals()['dfarF_{}'.format(i)].to_csv('AdapterRankList_{}.csv'.format(i), index=False)
```

A5.6.11. Generating Clustermaps after Enrichment Analysis.

```
#import python packages
import re
import sys
import pandas as pd
import networkx as nx
import itertools as it
from collections import namedtuple
import numpy as np
import scipy
from scipy.cluster.hierarchy import dendrogram, set_link_color_palette
from fastcluster import linkage
from matplotlib.colors import rgb2hex, colorConverter
from collections import defaultdict
import matplotlib
import matplotlib.pyplot as plt
from matplotlib.colors import LogNorm, PowerNorm, BoundaryNorm, ListedColormap
from IPython.display import display
from functools import reduce
import seaborn as sns; sns.set()
from io import StringIO
from matplotlib_venn import venn2_unweighted #the unweighted is if you want to make circles that are the same size
from matplotlib_venn import venn2 #also import the normal one
import pandas as pd
import numpy as np
from io import StringIO
from pylab import *
from numpy import *
from matplotlib.colors import LinearSegmentedColormap

#magic function to show plots inline
```

```
%matplotlib inline

#ignore warnings
import warnings
warnings.filterwarnings("ignore")
#Import the gProfiler output into dataframes
#There are two files, one for the 293T cells and one with the combined liver and brain data

#define the folders
folder = './20C31 Cytoscape Networks/'
folderout = './20E03_GO_ResultsAndClustermaps/'

dfgprof293T = pd.read_csv('%s293T_GO_Analysis.csv'%(folder), header=17)
dfgprofLiverBrain = pd.read_csv('%sLiverBrain_Separate_GO_Analysis.csv'%(folder), header=17)
#Extract and separate all of the data into separate dfs

#first, remake the dfs keeping only the relevant columns (p-values)

#define a function for extracting out the relevant columns
def colfilter(df):
    return pd.concat([df[['source', 'term_name']], df.filter(regex='adjusted_p_value__')], axis=1)

#extract out the columns for each df
df293T = colfilter(dfgprof293T)
dfLiverBrain = colfilter(dfgprofLiverBrain)

#now make seperate dfs for each group

#list group (they are the same for both dfs)
list_go = df293T.source.drop_duplicates().to_list()
list_gof = [s.replace('GO:', '') for s in list_go] #remove the colons to name the dfs

#make the new dfs
for i in range(11):
    locals()['df293T{}'.format(list_gof[i])] = df293T[df293T.source == list_go[i]]
    locals()['dfLiverBrain{}'.format(list_gof[i])] = dfLiverBrain[dfLiverBrain.source == list_go[i]]

#format the tables for seaborn clustermap (drop source column and move term name to index)

#list the experiments
list_exp = ['293T', 'LiverBrain']

#reformat all tables and rename the columns
for i in list_exp:
    for j in list_gof:
        locals()['df{}{}'.format(i,j)] = locals()['df{}{}'.format(i,j)].set_index(
            locals()['df{}{}'.format(i,j)].term_name).drop(columns={'source', 'term_name'})
        locals()['df{}{}'.format(i,j)].columns  = \
        locals()['df{}{}'.format(i,j)].columns.str.lstrip('adjusted_p_value__')
        locals()['df{}{}'.format(i,j)].columns = locals()['df{}{}'.format(i,j)].columns.str.replace('_', ' ')
        locals()['df{}{}'.format(i,j)].index.name = 'Term'
#In the LiverBrain df, make an additional column for which column has the highest significance for a given term
    # (separately for the liver and brain)
    # This can be used to color code the network clusters on the clustermaps to see unique ones

#define functions to easily create the new column
def liverclusterterms(row):
    if (row.filter(regex='Liver') < 0.01).any():
        return row.filter(regex='Liver').index[(row.filter(regex='Liver') == row.filter(regex='Liver').min())][0]

def brainclusterterms(row):
    if (row.filter(regex='Brain') < 0.01).any():
        return row.filter(regex='Brain').index[(row.filter(regex='Brain') == row.filter(regex='Brain').min())][0]

#aplly the functions to all of the dfs
for i in list_exp[1:]:
    for j in list_gof:
        locals()['dfmap{}{}'.format(i,j)] = locals()['df{}{}'.format(i,j)].iloc[:,6:]
        locals()['dfmap{}{}'.format(i,j)]['BrainCluster'] = locals()['dfmap{}{}'.format(i,j)].apply(
            brainclusterterms, axis=1)
        locals()['dfmap{}{}'.format(i,j)]['LiverCluster'] = locals()['dfmap{}{}'.format(i,j)].apply(
            liverclusterterms, axis=1)
#For just the liver and brain biological processes calculate the percent overlap of each cluster with all BP GO terms
    # that were significant in the other organ

#split into liver and brain dfs
dfBrain = dfLiverBrainBP.filter(regex='Brain')
dfLiver = dfLiverBrainBP.filter(regex='Liver')

#drop rows that have no columns less than 0.01
dfBrain = dfBrain[dfBrain < 0.01].dropna(how='all')
dfLiver = dfLiver[dfLiver < 0.01].dropna(how='all')

#initialize an empty list for liver and brain clusters to facilitate visualizing the data
brainoverlap = []
liveroverlap = []

#first do the brain storing the values in a list
for i in range(11):
    overlap = set(dfBrain[dfBrain['Cluster{} Brain'.format(i+1)] < 0.01].index) & set(dfLiver.index)
    brainoverlap.append(np.float64(len(overlap)) /
                        np.float64(len(set(dfBrain[dfBrain['Cluster{} Brain'.format(i+1)] < 0.01].index))))
```

```
#then to the liver
for i in range(14):
    overlap = set(dfLiver[dfLiver['Cluster{} Liver'.format(i+1)] < 0.01].index) & set(dfBrain.index)
    liveroverlap.append(np.float64(len(overlap)) /
                        np.float64(len(set(dfLiver[dfLiver['Cluster{} Liver'.format(i+1)] < 0.01].index))))

dfoverlap = pd.DataFrame(data={'Brain':pd.Series(brainoverlap), 'Liver':pd.Series(liveroverlap)})
dfoverlap.index.rename('Cluster', inplace=True)
dfoverlap
```

Overall, can see that there is a pretty high degree of overlap between individual clusters and significant terms in the opposite tissue. However, the clusters are quite large and contain many terms (with a small number of genes). It is unlikely that the major functions of these clusters are as similar (i.e. the terms with many genes or with the most genes are likely quite different).

```
#Now I will make colored labels for the network clusters to show next to the heat map (just for the liver vs brain)
#This will be done all at once, but they can easily be remade with each individual heatmap if necessary

#list GO terms from the liver and brain cluster column (see above)
#set up a color palette based on the number of columns in each
#set up a dictionary to map GO terms to colors (based on which cluster it is most significant in, again, see above)
#map each go term to one of the colors
#finally combine the row colors into a df for labeling on the clustermap
for i in list_gof:
    locals()['labels{}1'.format(i)] = locals()['dfmapLiverBrain{}'.format(i)]['BrainCluster']
    locals()['labels{}2'.format(i)] = locals()['dfmapLiverBrain{}'.format(i)]['LiverCluster']
    locals()['color_pal{}1'.format(i)] = sns.color_palette("Paired", len(locals()['labels{}1'.format(i)].unique()))
    locals()['color_pal{}2'.format(i)] = sns.color_palette("Paired_r", len(locals()['labels{}2'.format(i)].unique()))
    locals()['lut{}1'.format(i)] = dict(zip(locals()['labels{}1'.format(i)].unique(),
                                locals()['color_pal{}1'.format(i)]))
    locals()['lut{}2'.format(i)] = dict(zip(locals()['labels{}2'.format(i)].unique(),
                                locals()['color_pal{}2'.format(i)]))
    locals()['lut{}1'.format(i)][None] = (1, 1, 1)
    locals()['lut{}2'.format(i)][None] = (1, 1, 1)
    locals()['row_colors{}1'.format(i)] = locals()['labels{}1'.format(i)].map(locals()['lut{}1'.format(i)])
    locals()['row_colors{}2'.format(i)] = locals()['labels{}2'.format(i)].map(locals()['lut{}2'.format(i)])
    locals()['row_colorsdf{}'.format(i)] = pd.DataFrame(
        locals()['row_colors{}1'.format(i)].rename('Brain')).join(locals()['row_colors{}2'.format(i)].rename('Liver'))
#Repeat the above for the 293T data (making colored labels etc...)

#define functions to easily create the new column
def terms293T(row):
    if (row < 0.01).any():
        return row.index[row == row.min()][0]

#aplly the functions to all of the dfs
for i in list_exp[0:1]:
    for j in list_gof:
        locals()['dfmap{}{}'.format(i,j)] = locals()['df{}{}'.format(i,j)].iloc[:,3:]
        locals()['dfmap{}{}'.format(i,j)]['Cluster'] = locals()['dfmap{}{}'.format(i,j)].apply(
            terms293T, axis=1)

for i in list_gof:
    locals()['labels293T{}'.format(i)] = locals()['dfmap293T{}'.format(i)]['Cluster']
    locals()['color_pal293T{}'.format(i)] = sns.color_palette("Paired", len(locals()['labels293T{}'.format(i)].unique()))
    locals()['lut293T{}'.format(i)] = dict(zip(locals()['labels293T{}'.format(i)].unique(),
                                locals()['color_pal293T{}'.format(i)]))
    locals()['lut293T{}'.format(i)][None] = (1, 1, 1)
    locals()['row_colors293T{}'.format(i)] = locals()['labels293T{}'.format(i)].map(locals()['lut293T{}'.format(i)])
    locals()['row_colors293Tdf{}'.format(i)] = pd.DataFrame(locals()['row_colors293T{}'.format(i)])
#Now visualize the colormap for the liver/brain combined dataset

#set the levels for a non-linear colormap by make a list of evenly spaced exponents
levels = [10**(-(x+1)) for x in reversed(range(20))]

#use BoundaryNorm to make an artificial log color scale
log_norm = BoundaryNorm(levels, ncolors=250)

#set legend font size
plt.rcParams['legend.title_fontsize'] = 22

#make the font bigger
sns.set(font_scale=2)

#make the clustermap (rasterize the image to avoid rendering the rectangles)
g = sns.clustermap(dfLiverBrainBP.iloc[:,0:6], figsize=(15,10), cmap='Blues_r', col_cluster=False, yticklabels=False,
                   row_colors=row_colorsdfBP, norm=log_norm, linewidths=0, cbar_pos=(0.235,0.845, 0.05, 0.2),
                   rasterized=True)

#create and ax object and format the color bar
ax = g.ax_heatmap
cbar = ax.collections[0].colorbar
cbar.set_ticks([0.05, 1e-5, 1e-10, 1e-15, 5e-20])
cbar.set_ticklabels(['>1e-2', 1e-5, 1e-10, 1e-15, '<1e-20'])
cbar.ax.tick_params(labelsize=15)
cbar.set_label('p-value', labelpad=15)
cbar.solids.set_edgecolor("face")

#set x and y labels
ax.set_ylabel('')
ax.set_xticklabels(['All\nBrain', 'All\nLiver', 'Substrates\nBrain', 'Substrates\nLiver', 'Interactors\nBrain',
                    'Interactors\nLiver'])
plt.setp(g.ax_heatmap.xaxis.get_majorticklabels(), rotation=0)
cbar.ax.yaxis.set_label_position('left')
```

```
#make a legend to identify the clusters

#first clear the 'Brain/Liver' from the cluster names
x = labelsBP1.unique()
y = labelsBP2.unique()

for i in range(len(x)):
    if x[i] != None:
        x[i] = re.sub(' Brain', '', x[i])
    else:
        x[i] = x[i]

for i in range(len(y)):
    if y[i] != None:
        y[i] = re.sub(' Liver', '', y[i])
    else:
        y[i] = y[i]

for i in range(len(x)):
    g.ax_col_dendrogram.bar(0, 0, color=lutBP1[labelsBP1.unique()[i]], label=x[i], linewidth=0)
for i in range(len(y)):
    g.ax_row_dendrogram.bar(0, 0, color=lutBP2[labelsBP2.unique()[i]], label=y[i], linewidth=0)

l1 = g.ax_col_dendrogram.legend(loc="center", title='Brain', ncol=5, bbox_to_anchor=(0.65, 1),
                                bbox_transform=gcf().transFigure, prop={'size':15})
l2 = g.ax_row_dendrogram.legend(loc="center", title='Liver', ncol=5, bbox_to_anchor=(0.65, 0.89),
                                bbox_transform=gcf().transFigure, prop={'size':15})


#make the dendrogram smaller
row = g.ax_row_dendrogram.get_position()
g.ax_row_dendrogram.set_position([row.x0+0.145, row.y0, row.width*0.25, row.height])
g.savefig('{}{}LiverBrain_Clustermap_BP.svg'.format(folder,folderout), dpi=2000)

#Now make the cluster specific maps for the brain and liver

###Brain

#make a new df that only contains clusters with significant functions, drop go terms that are not signficant
#replace nan values with those from the original df (clustermap cannot take nans)
dfBrainCM = dfLiverBrainBP.iloc[:,np.r_[6:8, 9:13, 14]]
dfBrainCM = dfBrainCM[dfBrainCM < 0.01].dropna(how='all')
dfBrainCM[dfBrainCM.isnull()] = dfLiverBrainBP.iloc[:,np.r_[6:8, 9:13, 14]]

#set the levels for a non-linear colormap by make a list of evenly spaced exponents
levels = [10**(-(x+1)) for x in reversed(range(10))]

#use BoundaryNorm to make an artificial log color scale
log_norm = BoundaryNorm(levels, ncolors=250)

#make the font bigger
sns.set(font_scale=2.2)

row_colors=row_colorsBP1[dfBrainCM.index].rename('Cluster')

#make the clustermap
g = sns.clustermap(dfBrainCM, figsize=(7,7), cmap='Blues_r', col_cluster=False, rasterized=True,
                   yticklabels=False, row_colors=row_colors, norm=log_norm, linewidths=0, method='ward',
                   cbar_pos=(0.4, 0.22, 0.3, 0.05), cbar_kws={'orientation':'horizontal'})

#create and ax object and format the color bar
ax = g.ax_heatmap
cbar = ax.collections[0].colorbar
cbar.set_ticks([0.05, 5e-6, 5e-10])
cbar.set_ticklabels(['>1e-2', 1e-5, '<1e-10'])
cbar.ax.tick_params(labelsize=12)
cbar.set_label('p-value', fontsize=16, labelpad=7)
cbar.solids.set_edgecolor("face")
cbar.ax.xaxis.set_ticks_position('bottom')
cbar.ax.xaxis.set_label_position('top')

#set x and y labels
ax.set_ylabel('')
ax.set_xticklabels(['1', '2', '4', '5', '6', '7', '9'])
plt.setp(g.ax_heatmap.xaxis.get_majorticklabels(), rotation=0)



#make the dendrogram smaller
row = g.ax_row_dendrogram.get_position()
g.ax_row_dendrogram.set_position([row.x0+0.145, row.y0, row.width*0.25, row.height])
plt.savefig('{}{}Brain_IndividualClusters_BP.svg'.format(folder,folderout), dpi=2000)

#Now make the cluster specific maps for the brain and liver

###Liver

#make a new df that only contains clusters with significant functions, drop go terms that are not signficant
#replace nan values with those from the original df (clustermap cannot take nans)
dfLiverCM = dfLiverBrainBP.iloc[:,np.r_[17:22, 24:28]]
dfLiverCM = dfLiverCM[dfLiverCM < 0.01].dropna(how='all')
dfLiverCM[dfLiverCM.isnull()] = dfLiverBrainBP.iloc[:,np.r_[17:22, 24:28]]
```

```
#set the levels for a non-linear colormap by make a list of evenly spaced exponents
levels = [10**(-(x+1)) for x in reversed(range(10))]

#use BoundaryNorm to make an artificial log color scale
log_norm = BoundaryNorm(levels, ncolors=250)

#make the font bigger
sns.set(font_scale=2.2)

row_colors=row_colorsBP2[dfLiverCM.index].rename('Cluster')

#make the clustermap
g = sns.clustermap(dfLiverCM, figsize=(7,7), cmap='Blues_r', col_cluster=False, rasterized=True,
                   yticklabels=False, row_colors=row_colors, norm=log_norm, linewidths=0, method='ward',
                   cbar_pos=(0.4, 0.22, 0.3, 0.05), cbar_kws={'orientation':'horizontal'})

#create and ax object and format the color bar
ax = g.ax_heatmap
cbar = ax.collections[0].colorbar
cbar.set_ticks([0.05, 5e-6, 5e-10])
cbar.set_ticklabels(['>1e-2', 1e-5, '<1e-10'])
cbar.ax.tick_params(labelsize=12)
cbar.set_label('p-value', fontsize=16, labelpad=7)
cbar.solids.set_edgecolor("face")
cbar.ax.xaxis.set_ticks_position('bottom')
cbar.ax.xaxis.set_label_position('top')

#set x and y labels
ax.set_ylabel('')
ax.set_xticklabels(['1', '2', '3', '4', '5', '8', '9', '10', '11'])
plt.setp(g.ax_heatmap.xaxis.get_majorticklabels(), rotation=0)



#make the dendrogram smaller
row = g.ax_row_dendrogram.get_position()
g.ax_row_dendrogram.set_position([row.x0+0.145, row.y0, row.width*0.25, row.height])
plt.savefig('{}{}Liver_IndividualClusters_BP.svg'.format(folder,folderout), dpi=2000)

#Make the cluster specific cluster map for the 293T cells

#make a new df that only contains clusters with significant functions, drop go terms that are not signficant
#replace nan values with those from the original df (clustermap cannot take nans)
df293TCM = df293TBP.iloc[:,3:8]
df293TCM = df293TCM[df293TCM < 0.01].dropna(how='all')
df293TCM[df293TCM.isnull()] = df293TBP.iloc[:,3:8]

#set the levels for a non-linear colormap by make a list of evenly spaced exponents
levels = [10**(-(x+1)) for x in reversed(range(20))]

#use BoundaryNorm to make an artificial log color scale
log_norm = BoundaryNorm(levels, ncolors=250)

#make the font bigger
sns.set(font_scale=1.75)

row_colors=row_colors293TBP[df293TCM.index]

#make the clustermap
g = sns.clustermap(df293TBP.iloc[:,0:8], figsize=(7,5), cmap='Blues_r', col_cluster=False, rasterized='True,
                   yticklabels=False, row_colors=row_colors, norm=log_norm, linewidths=0, method='ward',
                   cbar_pos=(0.4, 0.15, 0.3, 0.05), cbar_kws={'orientation':'horizontal'})

#create and ax object and format the color bar
ax = g.ax_heatmap
cbar = ax.collections[0].colorbar
cbar.set_ticks([0.05, 5e-11, 5e-20])
cbar.set_ticklabels(['>1e-2', 1e-10, '<1e-20'])
cbar.ax.tick_params(labelsize=12)
cbar.set_label('p-value', fontsize=16, labelpad=7)
cbar.solids.set_edgecolor("face")
cbar.ax.xaxis.set_ticks_position('bottom')
cbar.ax.xaxis.set_label_position('top')

#set x and y labels
ax.set_ylabel('')
ax.set_xticklabels(['All', 'Subs', 'Ints', '1', '2', '3', '4', '5'])
plt.setp(g.ax_heatmap.xaxis.get_majorticklabels(), rotation=0)



#make the dendrogram smaller
row = g.ax_row_dendrogram.get_position()
g.ax_row_dendrogram.set_position([row.x0+0.145, row.y0, row.width*0.25, row.height])
plt.savefig('{}{}293T_IndividualClusters_BP.svg'.format(folder,folderout), dpi=2000)

#Now, output the clustermaps for the remaining processes for 293T cells

#make a list for the titles and for the functions to plot
list_titles = ['GO Molecular Function', 'GO Cellular Component', 'KEGG Pathways', 'Reactome Pathways', 'WikiPathways',
               'TRANSFAC Database', 'miRTarBase miRNA Interactions', 'Human Protein Atlas', 'CORUM Complexes',
               'Human Phenotype Ontology']
list_gop = list_gof[0:1] + list_gof[2:]
```

```
#make the plots
for i in list_gop:
    #make a new df that only contains clusters with significant functions, drop go terms that are not signficant
    #replace nan values with those from the original df (clustermap cannot take nans)
    #reset the indices for all dfs because there are colons in some
    plt.figure()
    locals()['df293TCM{}'.format(i)] = locals()['df293T{}'.format(i)].iloc[:,3:8]
    locals()['df293TCM{}'.format(i)] = locals()['df293TCM{}'.format(i)].reset_index(drop=True)
    locals()['df293TCM{}'.format(i)] = \
    locals()['df293TCM{}'.format(i)][locals()['df293TCM{}'.format(i)] < 0.01].dropna(how='all')
    locals()['df293TCM{}'.format(i)][locals()['df293TCM{}'.format(i)].isnull()] = \
    locals()['df293T{}'.format(i)].iloc[:,3:8].reset_index(drop=True)

    #set the levels for a non-linear colormap by make a list of evenly spaced exponents
    levels = [10**(-(x+1)) for x in reversed(range(10))]

    #use BoundaryNorm to make an artificial log color scale
    log_norm = BoundaryNorm(levels, ncolors=250)

    #make the font bigger
    sns.set(font_scale=1.75)

    locals()['row_colors{}'.format(i)]=locals()['row_colors293T{}'.format(i)].reset_index(
        drop=True)[locals()['df293TCM{}'.format(i)].index]

    #make the clustermap
    g = sns.clustermap(locals()['df293T{}'.format(i)].iloc[:,0:8].reset_index(drop=True), figsize=(7,5), cmap='Blues_r',
                       col_cluster=False, rasterized=True, yticklabels=False,
                       row_colors=locals()['row_colors{}'.format(i)], norm=log_norm, linewidths=0, method='ward',
                       cbar_pos=(0.4, 0.15, 0.3, 0.05), cbar_kws={'orientation':'horizontal'})

    #set titles
    g.ax_heatmap.set_title(list_titles[list_gop.index(i)], ha='center')

    #create and ax object and format the color bar
    ax = g.ax_heatmap
    cbar = ax.collections[0].colorbar
    cbar.set_ticks([0.05, 5e-6, 5e-10])
    cbar.set_ticklabels(['>1e-2', 1e-5, '<1e-10'])
    cbar.ax.tick_params(labelsize=12)
    cbar.set_label('p-value', fontsize=16, labelpad=7)
    cbar.solids.set_edgecolor("face")
    cbar.ax.xaxis.set_ticks_position('bottom')
    cbar.ax.xaxis.set_label_position('top')

    #set x and y labels
    ax.set_ylabel('')
    ax.set_xticklabels(['All', 'Subs', 'Ints', '1', '2', '3', '4', '5'])
    plt.setp(g.ax_heatmap.xaxis.get_majorticklabels(), rotation=0)

    #make the dendrogram smaller
    row = g.ax_row_dendrogram.get_position()
    g.ax_row_dendrogram.set_position([row.x0+0.145, row.y0, row.width*0.25, row.height])
    plt.savefig('{}{}293T_Clustermap_{}.svg'.format(folder,folderout,i), dpi=2000)

#Make the plots for each database with the brain and liver samples

#set the levels for a non-linear colormap by make a list of evenly spaced exponents
levels = [10**(-(x+1)) for x in reversed(range(10))]

#use BoundaryNorm to make an artificial log color scale
log_norm = BoundaryNorm(levels, ncolors=250)

#set legend font size
plt.rcParams['legend.title_fontsize'] = 22

#make a list for the titles and for the functions to plot (remove HPA)
list_titlesm = ['GO Molecular Function', 'GO Cellular Component', 'KEGG Pathways', 'Reactome Pathways', 'WikiPathways',
          'TRANSFAC Database', 'miRTarBase miRNA Interactions', 'CORUM Complexes', 'Human Phenotype Ontology']
list_gopm = list_gof[0:1] + list_gof[2:8] + list_gof[9:11]

#make the font bigger
sns.set(font_scale=2)


for i in list_gopm:
    #make the clustermap (rasterize the image to avoid rendering the rectangles)
    plt.figure()
    g = sns.clustermap(locals()['dfLiverBrain{}'.format(i)].iloc[:,0:6].reset_index(drop=True), figsize=(15,10),
                       cmap='Blues_r', col_cluster=False, yticklabels=False,
                       row_colors=locals()['row_colorsdf{}'.format(i)].reset_index(drop=True),
                       norm=log_norm, linewidths=0, cbar_pos=(0.235,0.845, 0.05, 0.2), rasterized=True)

    #create and ax object and format the color bar
    ax = g.ax_heatmap
    cbar = ax.collections[0].colorbar
    cbar.set_ticks([0.05, 5e-6, 5e-10])
    cbar.set_ticklabels(['>1e-2', 1e-5, '<1e-10'])
    cbar.ax.tick_params(labelsize=15)
    cbar.set_label('p-value', labelpad=15)
    cbar.solids.set_edgecolor("face")
```

```
    #set x and y labels
    ax.set_ylabel('')
    ax.set_xticklabels(['All\nBrain', 'All\nLiver', 'Substrates\nBrain', 'Substrates\nLiver', 'Interactors\nBrain',
                        'Interactors\nLiver'])
    plt.setp(g.ax_heatmap.xaxis.get_majorticklabels(), rotation=0)
    cbar.ax.yaxis.set_label_position('left')

    #make a legend to identify the clusters

    #first clear the 'Brain/Liver' from the cluster names
    x = locals()['labels{}1'.format(i)].unique()
    y = locals()['labels{}2'.format(i)].unique()

    for j in range(len(x)):
        if x[j] != None:
            x[j] = re.sub(' Brain', '', x[j])
        else:
            x[j] = x[j]

    for j in range(len(y)):
        if y[j] != None:
            y[j] = re.sub(' Liver', '', y[j])
        else:
            y[j] = y[j]

    for j in range(len(x)):
        g.ax_col_dendrogram.bar(0, 0, color=locals()['lut{}1'.format(i)][locals()['labels{}1'.format(i)].unique()[j]],
                                label=x[j], linewidth=0)
    for j in range(len(y)):
        g.ax_row_dendrogram.bar(0, 0, color=locals()['lut{}2'.format(i)][locals()['labels{}2'.format(i)].unique()[j]],
                                label=y[j], linewidth=0)

    l1 = g.ax_col_dendrogram.legend(loc="center", title='Brain', ncol=5, bbox_to_anchor=(0.65, 1),
                                    bbox_transform=gcf().transFigure, prop={'size':15})
    l2 = g.ax_row_dendrogram.legend(loc="center", title='Liver', ncol=5, bbox_to_anchor=(0.65, 0.89),
                                    bbox_transform=gcf().transFigure, prop={'size':15})

    #set titles
    g.ax_heatmap.set_title(list_titlesm[list_gopm.index(i)], ha='center', pad=175)

    #make the dendrogram smaller
    row = g.ax_row_dendrogram.get_position()
    g.ax_row_dendrogram.set_position([row.x0+0.145, row.y0, row.width*0.25, row.height])
    g.savefig('LiverBrain_Clustermap_{}.svg'.format(i), dpi=2000)
#Export the cleaned dataframes to csv
for i in list_exp:
    for j in list_gof:
        locals()['df{}{}'.format(i,j)].to_csv('{}{}{}_GoTable_{}.csv'.format(folder,folderout,i,j))
```

Chapter 6

Improving MS Technologies for the Detection and Site-Mapping of O-GlcNAcylated Peptides

Presented in part as:

Thompson, J. W., Sweredoski, M. J., Griffin, M. E., Lomenick, B., Moradian, A., Garbis, S. D., Hsieh-Wilson, L. C. Development of a novel mass spectrometry decision tree for O-GlcNAc site mapping. American Society of Mass Spectrometry 2020 Annual Conference. June 1, 2020.

6.1. Abstract.

The dynamic, inducible PTM of proteins with O-GlcNAc is an important regulator of diverse cellular processes. However, its study has lagged behind that of other PTMs, such as phosphorylation, due to unique difficulties in detecting and mapping O-GlcNAcylation sites. We previously developed (**Chapter 5**) a novel MS-based O-GlcNAcomics workflow for the high-throughput detection of O-GlcNAcylation events across the proteome. There, we noticed that while both ETD and EThcD fragmentation were effective methods for sequencing O-GlcNAcylated peptides, each method identified non-overlapping sets of O-GlcNAc peptides and sites. To our knowledge, systematic efforts to understand how O-GlcNAcylated peptides are optimally fragmented and identified using MS have not been undertaken. Herein, we report the first studies into the fragmentation of O-GlcNAc peptides by an array of ETD fragmentation methods, enabled by the development of our robust, streamlined chemoenzymatic labeling and enrichment workflow developed for O-GlcNAc peptides (**Chapter 5**). We find that fragmentation efficiency of O-GlcNAcylated peptides by different methods depends heavily on their charge density. For instance, at high charge densities (low *m/z*), ETD significantly outperforms EThcD, while the opposite is true at lower charge densities. In fact, ETD is essentially ineffective over 1,000 *m/z*. Finally, ETD reaction time has little effect on fragmentation efficiency, with charge-dependent time constants as low as 0.5τ having a minimal impact on the number of peptides or O-GlcNAc sites identified. Taken together, these insights allowed the development of a novel, online MS decision tree to fragment O-GlcNAcylated peptides by either ETD or EThcD based on their *m/z*, significantly improving identification, site mapping, and instrument efficiency over ETD or EThcD methods alone. We believe that this new decision tree approach will greatly facilitate the

mapping and identification of O-GlcNAc sites across diverse sample types and treatments, a critical endeavor for understanding the role O-GlcNAc in cellular function and disease.

6.2. Introduction.

O-GlcNAc site mapping by MS has been actively investigated for almost three decades (reviewed in **Chapters 2 and 4**). However, given the lability of the modification to standard MS fragmentation, it was not until the advent of ETD-based fragmentation methods that localizing native O-GlcNAc sites to specific serine and threonine residues became reliable and robust.[1] ETD relies on the transfer of electrons from a negatively charged reagent gas to peptide cations subsequently causing non-ergodic fragmentation along the peptide backbone, and thus generally leaves intact side chain modifications such as O-GlcANc and phosphorylation.[2] However, while leaving PTMs intact, ETD often suffers from poor fragmentation efficiency along on the peptide backbone presumably because peptide fragments tend to remain non-covalently associated after electron transfer and fragmentation.[3] This lack of fragmentation efficiency has been largely addressed with the advent of new supplemental activation (SA) methods such as ETD with CID SA (ETciD)[3] and, more recently, EThcD.[4] Yet, these methods often add significant time the instrument duty cycle resulting in a decrease in the overall number of peptides identifications.[5,6] Furthermore, the use of ETD with SA for PTM analysis is only beginning to be explored.[4,7-9]

To better understand how O-GlcNAcylated peptides behave under various ETD fragmentation parameters, we first systematically subjected a synthetic, O-GlcNAcylated peptide to different ETD fragmentation parameters, including differing SA, ETD anion reagent and peptide cation amounts, and ETD reaction times. Then we used the information gathered therein to design a series of parameters to test in O-GlcNAcylated peptides enriched from 293T lysates using our chemoenzymatic labeling method (**Chapter 5**). We found not only that relationships between charge density and ETD fragmentation efficiency for unmodified peptides held for O-GlcNAcylated peptides,[6] but also, surprisingly, that SA was actually detrimental to fragmentation efficiency of peptides with a higher charge density. Finally, we found little difference in the fragmentation efficiency of O-GlcNAcylated peptides with a wide variety of ETD reaction times, although noting that set ETD reaction times of 100 or 200 ms (previously suggested as optimal for the fragmentation of glycosylated peptides[8]) underperformed charge dependent ETD reaction times with a set time constant, τ.[10] The aforementioned observation suggests that the increased

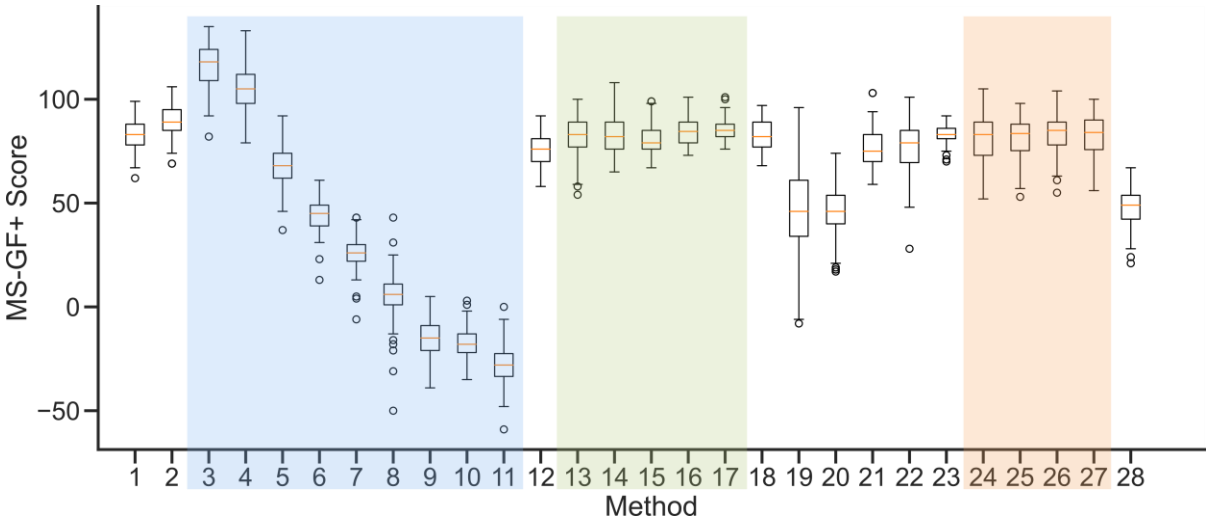

Fig. 6.1. Distribution of MS-GF+ Score for the Different ETD Fragmentation Reaction Conditions Outlined in Table 6.1.
Note the decreasing score with increasing SA and relatively constant scores varying peptide cation and ETD anion reagent amounts. In general longer ETD reaction times reduce fragmentation efficiency (18-20).

instrument cycle time inherent to ETD-MS analyses could be drastically reduced by decreasing ETD reaction time. Overall, these observations facilitated the development of a novel MS decision tree where O-GlcNAcylated peptides <625 *m/z* are fragmented by ETD and >625 *m/z* by EThcD, thus maximizing instrument efficiency and number of O-GlcNAcylated peptides identified in a single MS run.

6.3. Optimization of ETD Fragmentation Parameters on Synthetic O-GlcNAc Peptides.

To first understand how O-GlcNAcylated peptides behaved under various ETD fragmentation conditions in the Orbitrap Fusion Tribrid (Thermo Fisher Scientific), the synthetic O-GlcNAc peptide, TAT[S(O-ß-GlcNAc)]SPASTPLSPM[R(13C6; 15N4)] (Peptide 11), was resuspended in 50:50 methanol:0.2% formic acid and directly injected into the instrument. We identified a clear peak at 572.9498 *m/z*, corresponding to the triply charged cation of the above peptide. This peak was then isolated and subjected to the ETD fragmentation reactions outlined in **Table 6.1**. Foremost, we sought to understand how ETD fragmentation efficiency various with increasing SA (as to our knowledge this has yet to be systematically explored). We also wanted to understand how increasing the peptide cation and anion gas amounts effected fragmentation

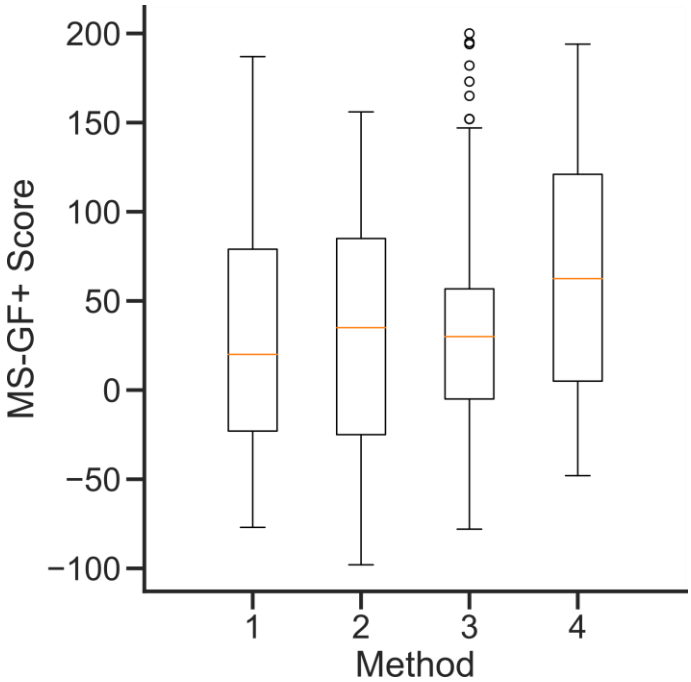

Fig. 6.2. Distribution of All Peptide MS-GF+ Scores for Methods 1-4 in Table 6.3.

(under various set ETD reaction times). Specifically, as the ETD reaction follows pseudo-first order kinetics, we wanted to ascertain whether we could increase fragmentation efficiency or decrease reaction time by increasing the precursor (i.e. peptide and ETD reagent gas) concentrations.[10,11]

Each method was run for 1 min to generate multiple spectra which were subsequently searched using MS-GF+.[12] Score distributions for each method are plotted in **Fig. 6.1**. Here, we find a clear trend towards decreasing fragmentation efficiency with increasing SA energies (EThcD). We also find that varying the amounts of peptide cation or ETD anion reagent do not strongly affect the fragmentation efficiency, at least under the conditions and with the single peptide investigated here. Others have found an optimal ETD anion reagent amount around 4e5, the current default instrument settings.[10] However, the data herein suggest that longer ETD reaction times are likely detrimental to, or at least not beneficial to, peptide fragmentation and identification, in contrast to what has previously been suggested by others. [8] Thus, significant

Method Number	ETD Reaction Time	SA	Pep AGC	ETD AGC	Max IT	Detector
1	100	20	5.E+04	1.E+06	1000	Orbitrap
2	CD	15	1.E+05	Default	120	Orbitrap
3	100	0	5.E+04	1.E+06	1000	Orbitrap
4	100	10	5.E+04	1.E+06	1000	Orbitrap
5	100	30	5.E+04	1.E+06	1000	Orbitrap
6	100	40	5.E+04	1.E+06	1000	Orbitrap
7	100	50	5.E+04	1.E+06	1000	Orbitrap
8	100	60	5.E+04	1.E+06	1000	Orbitrap
9	100	70	5.E+04	1.E+06	1000	Orbitrap
10	100	80	5.E+04	1.E+06	1000	Orbitrap
11	100	90	5.E+04	1.E+06	1000	Orbitrap
12	CD	20	5.E+04	Default	1000	Orbitrap
13	100	20	5.E+04	1.E+06	1000	Orbitrap
14	100	20	1.E+05	2.E+06	1000	Orbitrap
15	100	20	2.E+05	4.E+06	1000	Orbitrap
16	100	20	5.E+05	1.E+07	1000	Orbitrap
17	100	20	1.E+06	2.E+07	1000	Orbitrap
18	CD	20	2.E+05	Default	1000	Orbitrap
19	200	20	5.E+04	1.E+06	1000	Orbitrap
20	100	30	1.E+04	1.E+05	1000	Ion Trap
21	75	20	5.E+04	1.E+06	1000	Orbitrap
22	150	20	5.E+04	1.E+06	1000	Orbitrap
23	CD	20	1.E+06	Default	1000	Orbitrap
24	100	20	5.E+04	2.E+05	1000	Orbitrap
25	100	20	5.E+04	5.E+06	1000	Orbitrap
26	100	20	5.E+04	5.E+05	1000	Orbitrap
27	100	20	5.E+04	2.E+06	1000	Orbitrap
28	CD	20	1.E+04	Default	1000	Ion Trap

Table 6.1. Direct Injection ETD Fragmentation Reaction Parameters.
Peptide 11 was subjected to these 28 ETD fragmentation reactions. The blue highlighted cells represent increasing SA, the green highlighted cells represent increasing ETD anion regent and peptide cations at a fixed ratio of the two, and the orange highlighted cells represent increasing ETD anion reagent with fixed peptide cation amounts, in all cases with all other parameters fixed. CD: charge-dependent ETD reaction time (instrument default), AGC: automatic gain control, IT: injection time.

instrument cycle time could be saved by employing charge-dependent (CD), e.g. ~42 ms for a doubly charged peptide, or faster ETD reaction times versus a fixed 100 ms reaction time.

We next sought to apply the insights gained from the experiments with Peptide 11 to a mixture of 18 synthetic O-GlcNAcylated peptides (**Table 6.2**). The individual peptides were reconstituted in 0.2% formic acid at equal volumes to partially simulate the dynamic range present in shotgun proteomics experiments. We designed four online LC-MS methods for head-to-head comparison (**Table 6.3**), focusing on varying ETD reaction time and the two most promising SA energies. Again, after LC-MS analysis, we analyzed the data using MS-GF+ and extracted the scores for all spectra (**Fig. 6.2**). Here we again find similar fragmentation efficiencies across varying ETD reaction times (methods 1-3), including almost no difference even with reaction

Peptide	Sequence	MW
1	[R(13C6; 15N4)]PHFPQF[S(O-ß-GlcNAc)]YSASGTA	1866.65
2	DGA[T(O-ß-GlcNAc)]MKTF[C(CAM)]GTPEYLAPEVLEDNDYG[R(13C6; 15N4)]	3264.23
3	DGATMKTF[C(CAM)]G[T(O-ß-GlcNAc)]PEYLAPEVLEDNDYG[R(13C6; 15N4)]	3264.23
4	SGSP[S(O-ß-GlcNAc)]DNSGAEEMEVSLA[K(13C6; 15N2)]	2106.15
5	SGSPSDN[S(O-ß-GlcNAc)]GAEEMEVSLA[K(13C6; 15N2)]	2106.15
6	G[S(O-ß-GlcNAc)]APPGPVPEGSI[R(13C6; 15N4)]	1534.32
7	TAT[S(O-ß-GlcNAc)]SPASTPLSPM[R(13C6; 15N4)]	1717.57
8	T[C(CAM)]PVQLWV[S(O-ß-GlcNAc)]ATPPAGS[R(13C6; 15N4)]	2040.96
9	AQPPSSAA[S(O-ß-GlcNAc)][R(13C6; 15N4)]	1184.89
10	QV[T(O-ß-GlcNAc)]ITGSAASISLAQYLINA[R(13C6; 15N4)]	2391.32
11	QVTI[T(O-ß-GlcNAc)]GSAASISLAQYLINA[R(13C6; 15N4)]	2391.32
12	AIPV[S(O-ß-GlcNAc)]REE[K(13C6; 15N2)]	1239.31
13	KKFELLP[T(O-ß-GlcNAc)]PPLSPSR[R(13C6; 15N4)]	2080.09
14	YSPT[S(O-ß-GlcNAc)]PS[K(13C6; 15N2)]	1077.08
15	QTTAPA[T(O-ß-GlcNAc)]MSTAASGTTMGVEQA[K(13C6; 15N2)]	2451.63
16	ATPATEESTVPA[T(O-ß-GlcNAc)]QSSALPAA[K(13C6; 15N2)]	2339.46
17	[S(O-ß-GlcNAc)]EASSSPPVVTSSSHS[R(13C6; 15N4)]	1915.63
18	SEASSSPPVV[T(O-ß-GlcNAc)]SSSHS[R(13C6; 15N4)]	1915.6

Table 6.2. 18 Synthetic Peptides Used for ETD Optimization Experiments.

Method	SA	ETD Reaction Time	Peptide AGC	ETD AGC	Max IT	Other
1	0%	CD	5.00E+04	1.00E+06	1000 ms	
2	0%	100 ms	5.00E+04	1.00E+06	1000 ms	
3	0%	10 ms	5.00E+04	1.00E+06	1000 ms	No ETD on doubly charged ions
4	20%	CD	5.00E+04	1.00E+06	1000 ms	

Table 6.3. ETD Fragmentation Methods for LC-MS Analysis of Synthetic Peptide Mixture. See **Table 6.1.** for abbreviations.

times as short as 10 ms. However, in this case, we also see that EThcD SA provides a small improvement to the overall score in contrast to the results with the single peptide. Given that the single peptide used for the previous analysis was triply charged and most of the peptides in this experiment were doubly charged, we then decided to break the scoring down further by peptide charge density. Previously, Coon and colleagues have shown that ETD fragmentation becomes highly favorable for peptides with lower length/charge (higher charge density).[6,13] We indeed find a similar trend for O-GlcNAcylated peptides in this experiment (**Figs. 6.3a and 6.3b**). However, surprisingly, we find that SA is actually detrimental to the fragmentation of peptides at with higher charge densities (e.g. see left of **Fig. 6.3b**), a phenomenon that, to our knowledge, has not previously been described. There is also a clear drop-off for ETD spectra above a residue/charge of ~10. Finally, again, there is almost no difference between the MS-GF+ scores of peptides subjected to ETD reaction times as low as 10 ms, regardless of their length to charge. Overall, we observe a clear trend of increasing peptide fragmentation efficiency and MS-GF+ score at higher charge densities with the opposite being true at lower charge densities, providing the first systematic description of optimal ETD fragmentation parameters for O-GlcNAcylated peptides.

6.4. Expanding Optimized ETD Fragmentation Parameters to Shotgun O-GlcNAcomics Experiments.

We hypothesized that the previous observation that ETD and EThcD fragmentation resulted in non-overlapping O-GlcNAc site identifications (**Chapter 5**) may be due to different fragmentation efficiencies of O-GlcNAcylated peptides by each method depending on their charge density. In fact, plotting *m/z* versus the Byonic score for all O-GlcNAcylated peptides identified in 293T cells in the aforementioned experiment reveals a strikingly similar trend to that seen with the O-GlcNAcylated peptide mixture (**Fig. 6.4a**). Plotting the Byonic delta mod score (**Fig. 6.4.b**), a measure of how well localized the O-GlcNAc site is, further confirms that ETD is better able to map O-GlcNAc sites at lower *m/z* and vice versa for EThcD. Finally, visualizing the *m/z* of all PSMs reveals strikingly different characteristics for those identified by ETD compared to those identified by EThcD (**Fig. 6.4c**). Repeating this process for the BAP1 KO dataset, where every O-GlcNAcylated precursor was fragmented sequentially by ETD and EThcD, confirms this trend holds in spite of stochastic differences between samples and MS runs (**Fig. 6.5a-c**). We can also see that unique O-GlcNAcylated peptides identified by either method are also highly skewed towards those with low versus high *m/z* for ETD and EThcD, respectively (**Fig. 6.5d**). Moreover, this confirms that the same trend holds for both the Orbitrap and Ion Trap mass analyzers.

To better understand how SA affects O-GlcNAcylated peptide fragmentation, we again enriched O-GlcNAcylated proteins from HEK 293T cell lysate using our previously described chemoenzymatic labeling and enrichment workflow (**Chapter 5**). Importantly, this workflow adds an additional primary amine to O-GlcNAcylated peptides which is protonated under the conditions

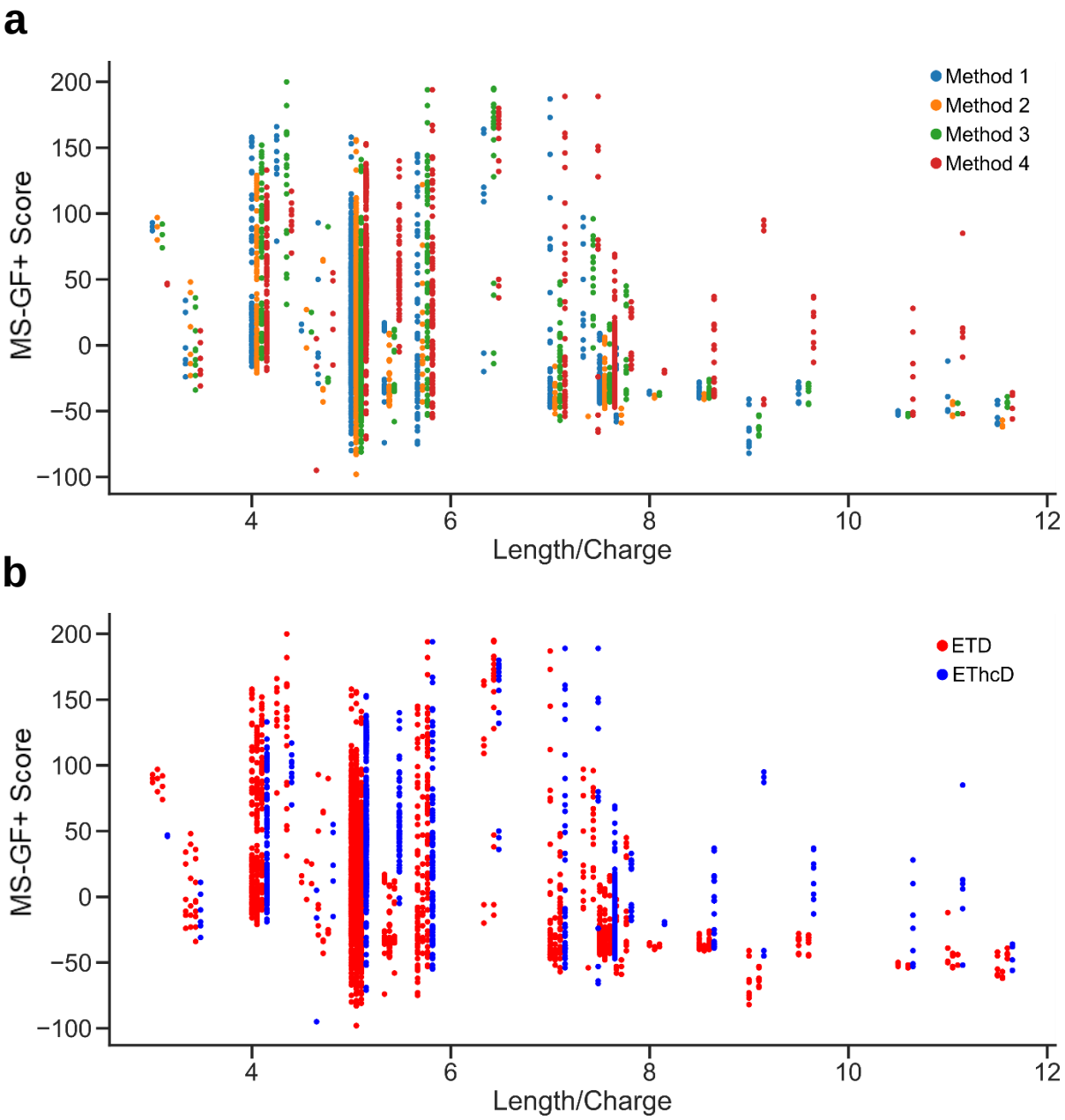

Fig. 6.3. MS-GF+ Scores versus Charge Density for All Identified Spectra in Methods 1-4. The MS-GF+ score for each spectra is plotted against its length/charge for each method individually **(a)** and ETD methods versus EThcD methods **(b)**. Note the clear benefit of ETD at lower length/charge and vice versa at higher length/charge as well as the slight benefit of CD or 10 ms reaction times (methods 1 and 3 respectively) over a 100 ms reaction time (method 2), although there is overall a minimal difference.

used for LC-MS. Thus, O-GlcNAcylated peptides enriched in this manner have significantly increased charge density, which is highly favorable for ETD fragmentation both as shown above

for O-GlcNAcylated peptides and as previously described for unmodified peptides.[14] After enrichment, O-GlcNAcylated peptides were subjected to our 300.1 *m/z* product-ion-triggered ETD/EThcD LC-MS. However, in this case, after observation of the 300.1 *m/z* product ion, precursors were fragmented sequentially by ETD or EThcD with 10, 20, or 30% SA. As a result, the fragmentation of every precursor by each of the above methods can be directly compared,

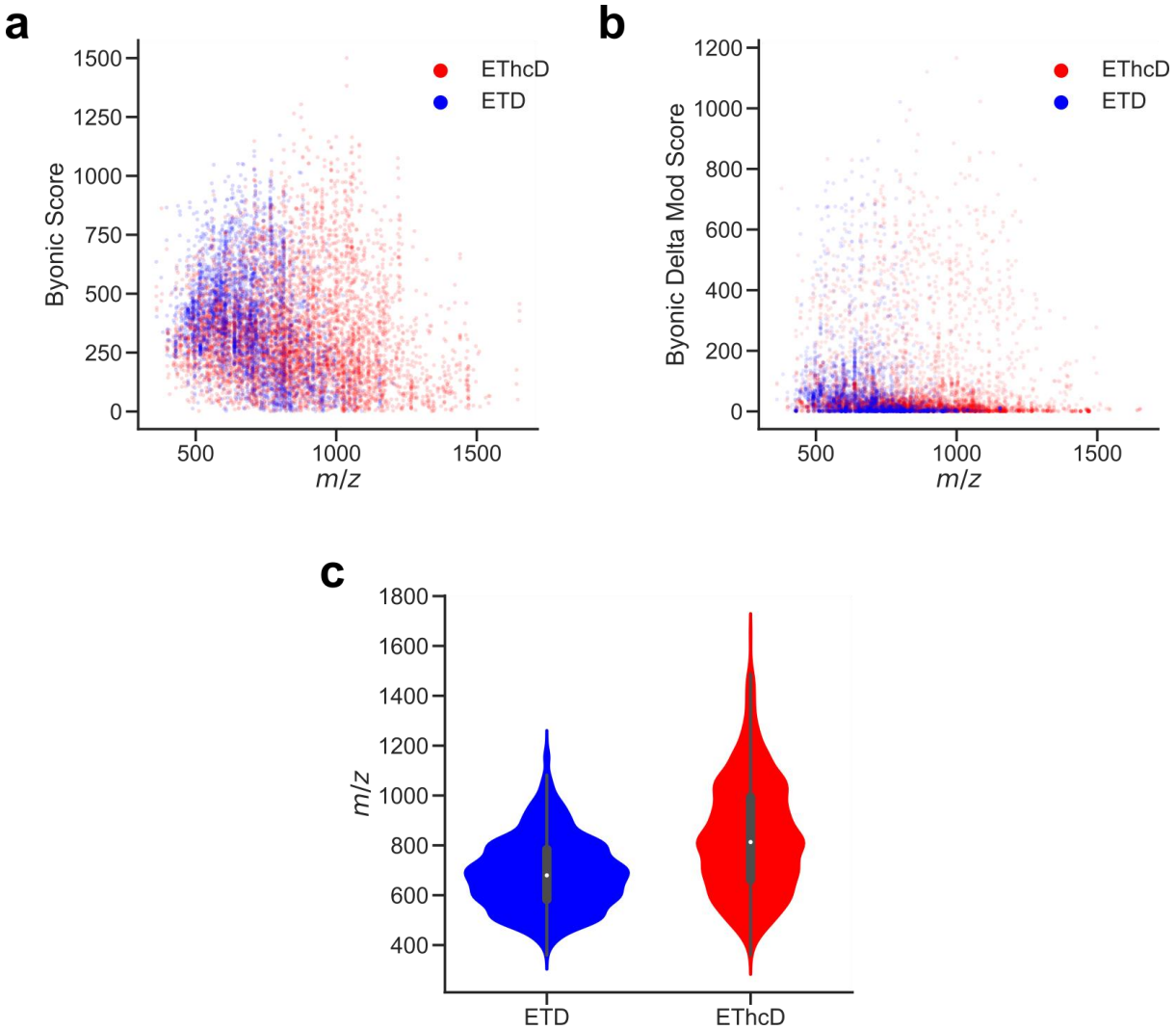

Fig. 6.4. ETD and EThcD Differentially Fragment Peptides Proteome-Wide.
There is a clear trend in fragmentation efficiency with ETD showing higher scores **(a)** and delta mod scores **(b)** at lower *m/z* and vice versa for EThcD. Interestingly, ETD is essentially ineffective for peptides above 1,000 *m/z*. There is also a clear difference in the *m/z* distributions of all peptides identified by ETD or EThcD **(c)** with ETD, again, showing a preference for lower *m/z* peptides. These data are from the 293T O-GlcNAcome defined in **Chapter 4**; all spectra were acquired in the Orbitrap and ETD/EThcD spectra were acquired across separate, duplicate runs.

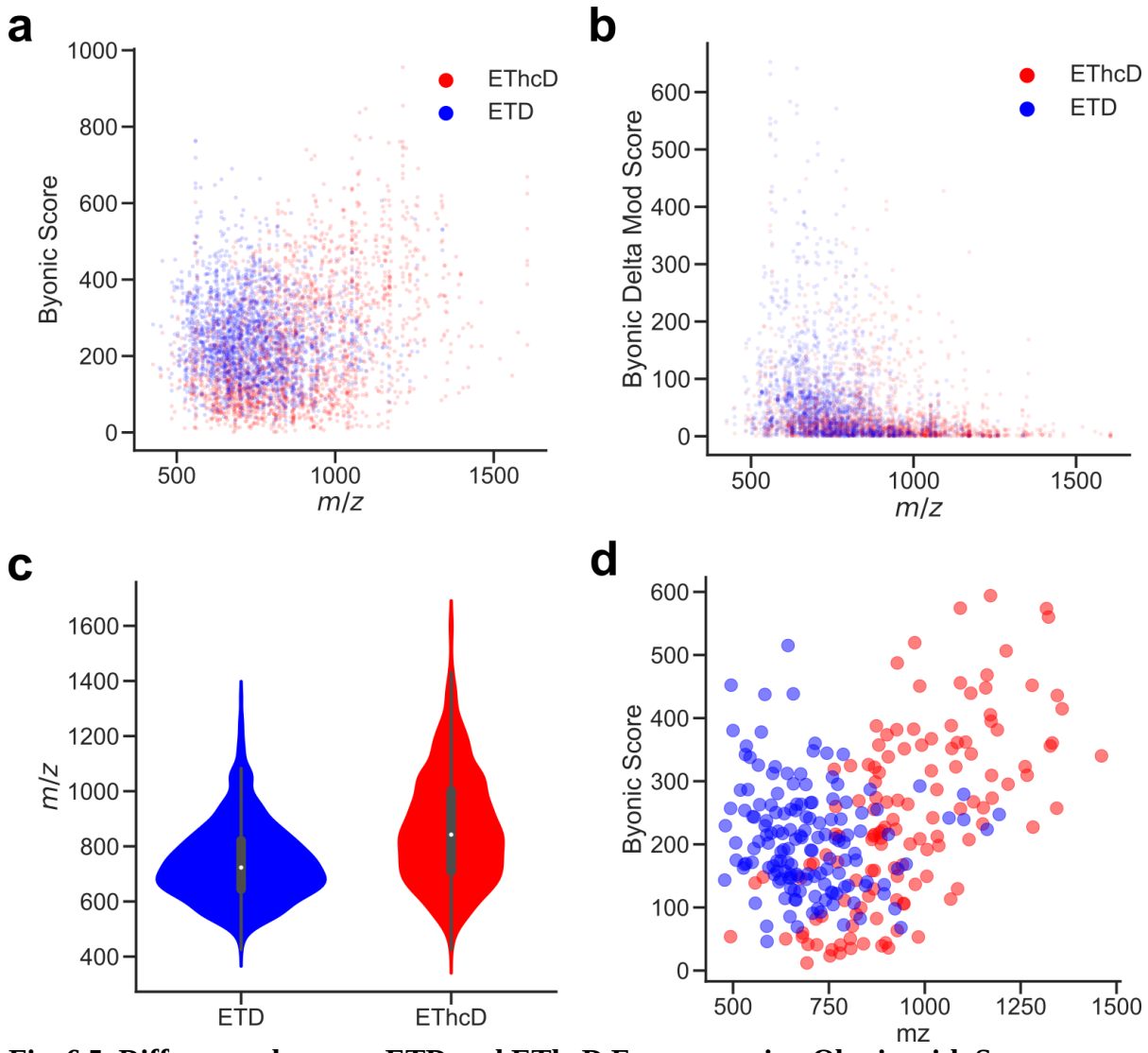

Fig. 6.5. Differences between ETD and EThcD Fragmentation Obtain with Spectra Acquired in the Same Run.
(a-c) As in **Fig. 6.4. (d)** There is also a marked difference in *m/z* for the peptides uniquely identified by either ETD or EThcD, highlighting the importance of using both methods for complete coverage of the O-GlcNAcome. These data are from the BAP1 KO quantitative O-GlcNAcome defined in **Chapter 4**. ETD and EThcD spectra were acquired together in the Ion Trap across n=3 biological replicates of BAP1 KO and control 293T cells (6 samples in total).

avoiding the stochastic differences between runs inherent to MS. As expected, we replicate the clear trend of ETD outperforming EThcD at lower *m/z* and vice versa at higher *m/z* (**Fig. 6.6a**). However, we do see significantly more peptides identified by EThcD at higher *m/z*, with no peptides over 1000 *m/z* identified by ETD as before (**Fig 6.6a-b**). Furthermore, plotting MaxQuant

score versus length/charge (**Fig. 6.6c**), we see essentially the same trend, which validates *m/z* as an appropriate substitute for length/charge in this case. Importantly, unlike length/charge, *m/z* is an actionable parameter in instrument method design; thus, in contrast to previous reports,[6] it may be possible to use *m/z* to reliably sort peptides for fragmentation by ETD or EThcD.

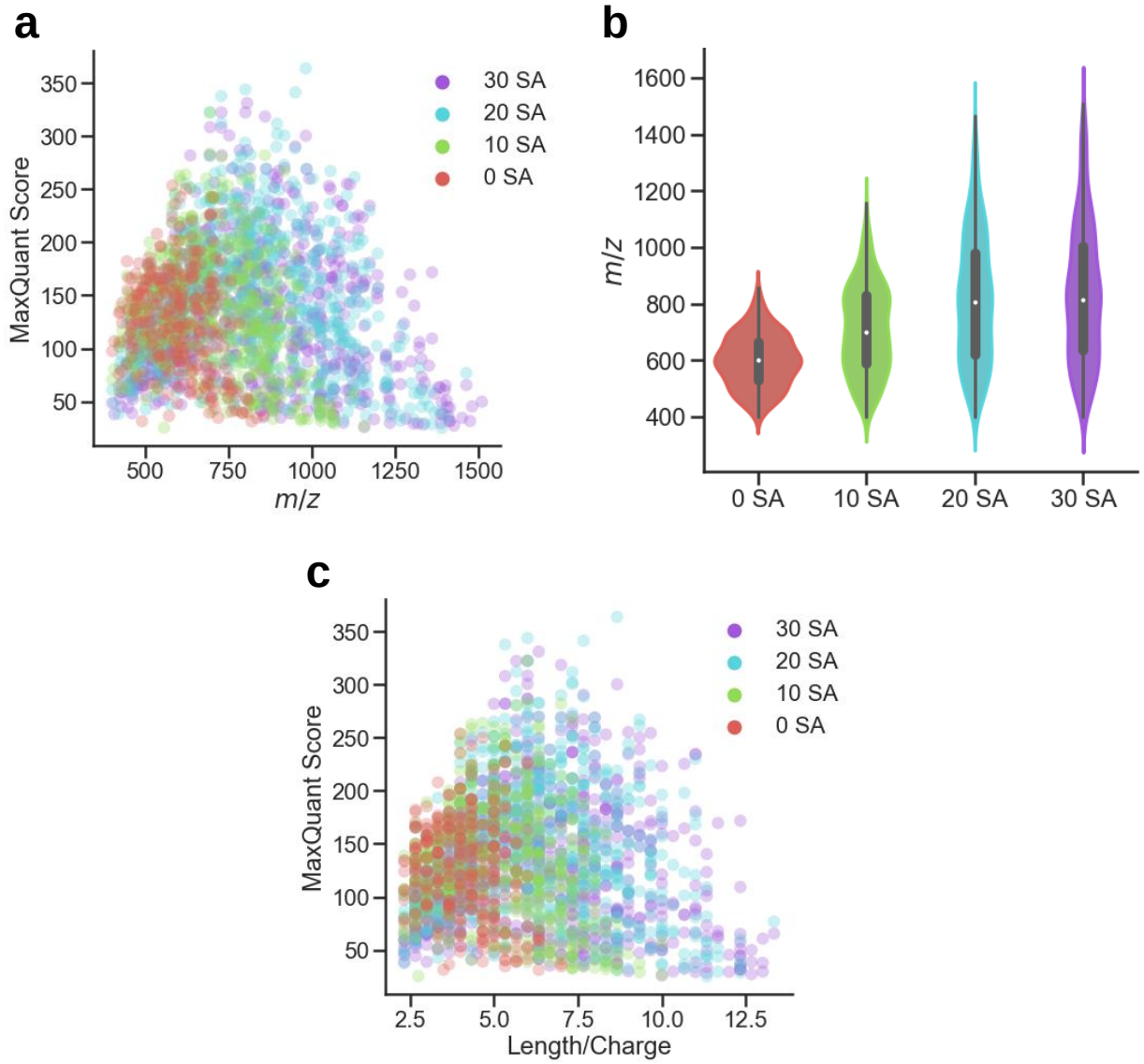

Fig. 6.6. Systematic Optimization of EThcD SA Reveals Preferences (Dis)Advantages of SA in Different *m/z* Regimes.
(a) MaxQuant score versus *m/z* of every PSM identified by each fragmentation method. **(b)** Violin plots of the *m/z* of all peptides identified by each method shows clear differences in the peptide populations identified. **(c)** Plotting MaxQuant score versus length/charge gives a similar trend suggesting that *m/z* can likely be used interchangeably with length/charge. SA: supplemental activation (%).

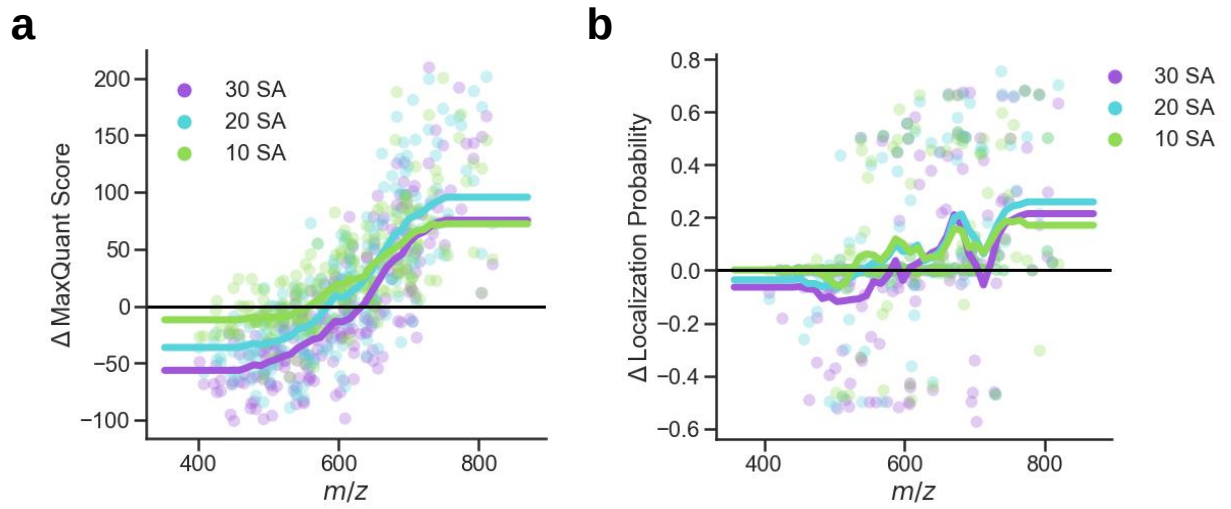

Fig. 6.7. ETD Outperforms EThcD at Lower *m/z* Values and Vice Versa at Higher *m/z* Values.
(a) Difference in MaxQuant score (Δ MaxQuant Score) between EThcD with 10, 20, or 30% SA and ETD only for peptides identified by all 4 methods. **(b)** Difference in localization probability (Δ Localization Probability) as in **(a)**. Lines represent the result of K-Nearest Neighbors (50) regression on each SA subset. In both cases, there is a clear advantage of ETD at lower *m/z* values and of EThcD with 20% SA at higher *m/z* values. SA: supplemental activation (%).

Next, we plotted the difference in MaxQuant score between each of the three SA conditions and ETD alone using only peptides that were identified by all four methods. We then used K-Nearest Neighbors regression to estimate the trend in score difference between EThcD and ETD (**Fig. 6.7a**). Here, we see clear evidence that ETD fragmentation gives higher scores for peptides with lower *m/z* values, regardless of precursor charge. Furthermore, as *m/z* increases, there is also a clear advantage of 20% SA over 10 and 30%, indicating that this is likely the optimal SA for fragmenting O-GlcNAcylated peptides with higher *m/z*; in fact, there is minimal difference between 20 and 30% SA out to 1,500 *m/z* (**Fig. 6.6a**). We also performed the same analysis using the difference in O-GlcNAc localization probability (**Fig. 6.7b**). Again, we see the same trend of ETD outperforming EThcD at lower *m/z* values and EThcD with 20% SA outperforming the other methods at higher *m/z* values suggesting that peptide fragmentation (which correlates highly with overall score) as well as O-GlcNAc site mapping (localization probability) would be optimized by

a combination of ETD and EThcD with 20% SA. To our knowledge, this is the first such evidence of its kind; in fact it has been previously suggested that SA is universally beneficial for fragmenting unmodified peptides.[3]

Having established a clear trend in O-GlcNAcylated peptide fragmentation with both ETD and EThcD, we also assessed (1) whether these trends held for ETciD and (2) if there were any

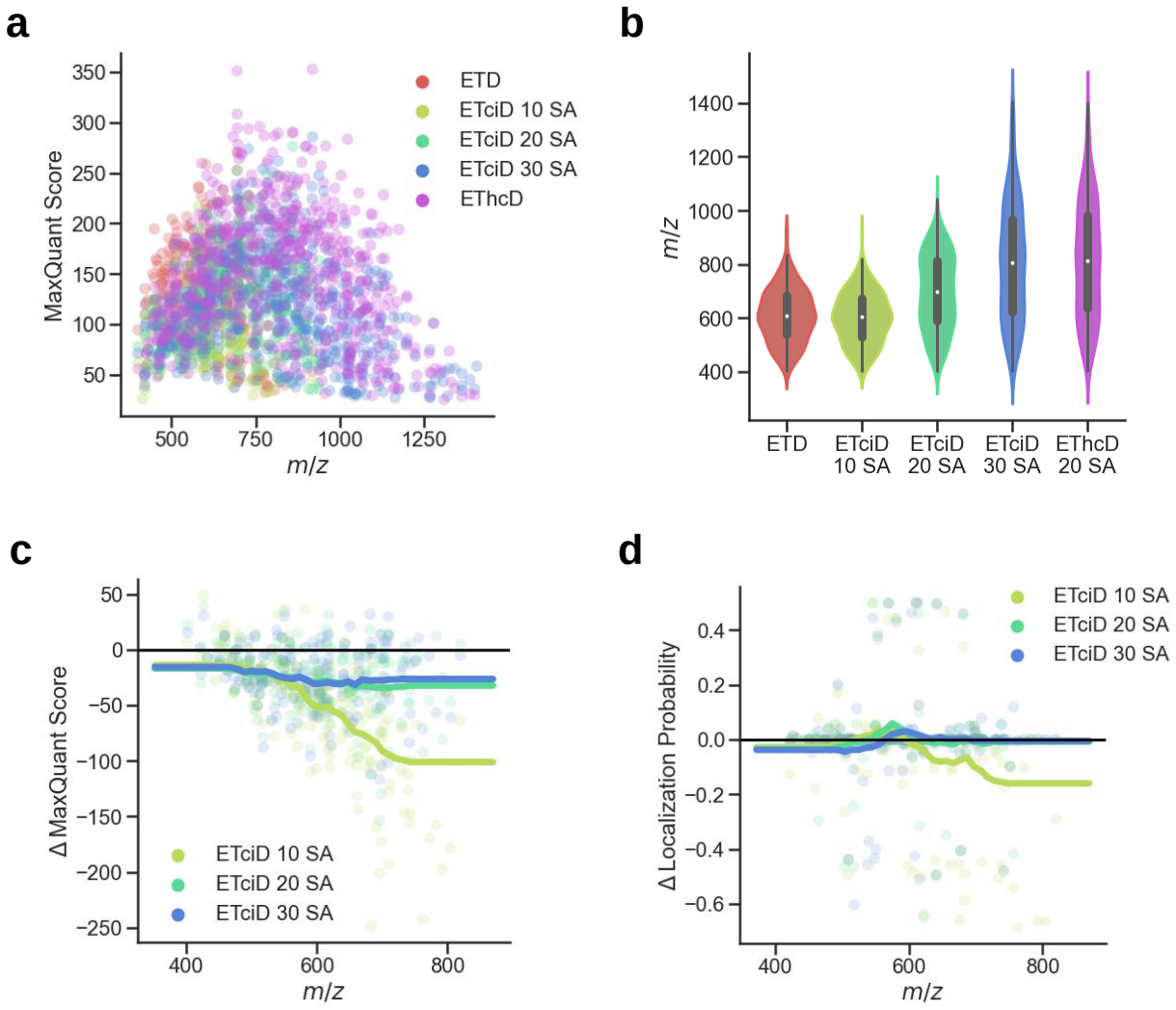

Fig. 6.8. Systematic Comparison of ETD/EThcD with ETciD.
(a-b) As in Fig. **6.6a-b**. EThcD is with 20% SA. **(c)** Difference in MaxQuant score (Δ MaxQuant Score) between ETciD with 10, 20, or 30% SA and EThcD only for peptides identified by all 5 methods (i.e. including ETD without SA). **(d)** Difference in localization probability (Δ Localization Probability) as in **(c)**. Lines represent the result of K-Nearest Neighbors (50) regression on each SA subset. There is a slight advantage of EThcD over ETciD for MaxQuant score and a negligible difference in localization probability. SA: supplemental activation (%).

advantages of CID versus HCD SA. Specifically, we created an MS method that fragments each precursor using ETD; EThcD (20% SA); and ETciD with 10, 20, and 30% SA. Again, we compared MaxQuant score versus *m/z* for all identified PSMs and saw the same clear trend in ETD and ETciD fragmentation as was observed for EThcD fragmentation (**Fig. 6.8a-b**). Interestingly, ETciD with 20% activation failed to identify any peptides greater than approximately 1,100 *m/z* while ETciD with 30% SA was roughly comparable to EThcD with 20% SA (**Fig. 6.8b**). We then plotted the difference in MaxQuant score (**Fig. 6.8c**) and localization probability (**Fig. 6.8d**) of ETciD with 10, 20, and 30% SA compared to EThcD with 20% SA. We did not compare the difference in MaxQuant score or localization probability directly with ETD given the same observed trend of ETD outperforming ETciD at lower *m/z* values as seen with EThcD. Overall, we find a slight underperformance of ETciD compared to EThcD for fragmentation (score) and essentially negligible differences for site mapping (localization probability) of O-GlcNAcylated peptides. However, if ETciD is employed, our data suggest that 30% SA is optimal.

Taking the above data together, we hypothesized that 625 *m/z* may be an optimal decision boundary between ETD and EThcD fragmentation. With this in mind, we next tested whether different ETD reaction times could also affect fragmentation and site mapping. Importantly, the shorter instrument cycle times that would result by decreasing ETD reaction time (generally the most time intensive element of an MS workflow) would allow for additional peptides to be analyzed within a single MS experiment. In turn, these shorter instrument cycle times may increase the number of O-GlcNAcylated peptide identifications in large-scale proteomics experiments.[10] Moreover, due to the predominance of doubly-charged peptides in traditional proteomics experiments, efforts to optimize ETD reaction times for more highly charged peptides have been limited.[3,10] To address this shortcoming, we set up two LC-MS/MS runs using the same 300.1 *m/z*

HCD product-ion triggered ETD/EThcD method described previously: (1) O-GlcNAcylated peptides less than 625 *m/z* were fragmented by ETD without supplemental activation, and (2) O-GlcNAcylated peptides greater than 625 *m/z* were fragmented with EThcD (20% SA). In both cases, every precursor was subjected to 3 set ETD reaction times corresponding to an ETD reaction

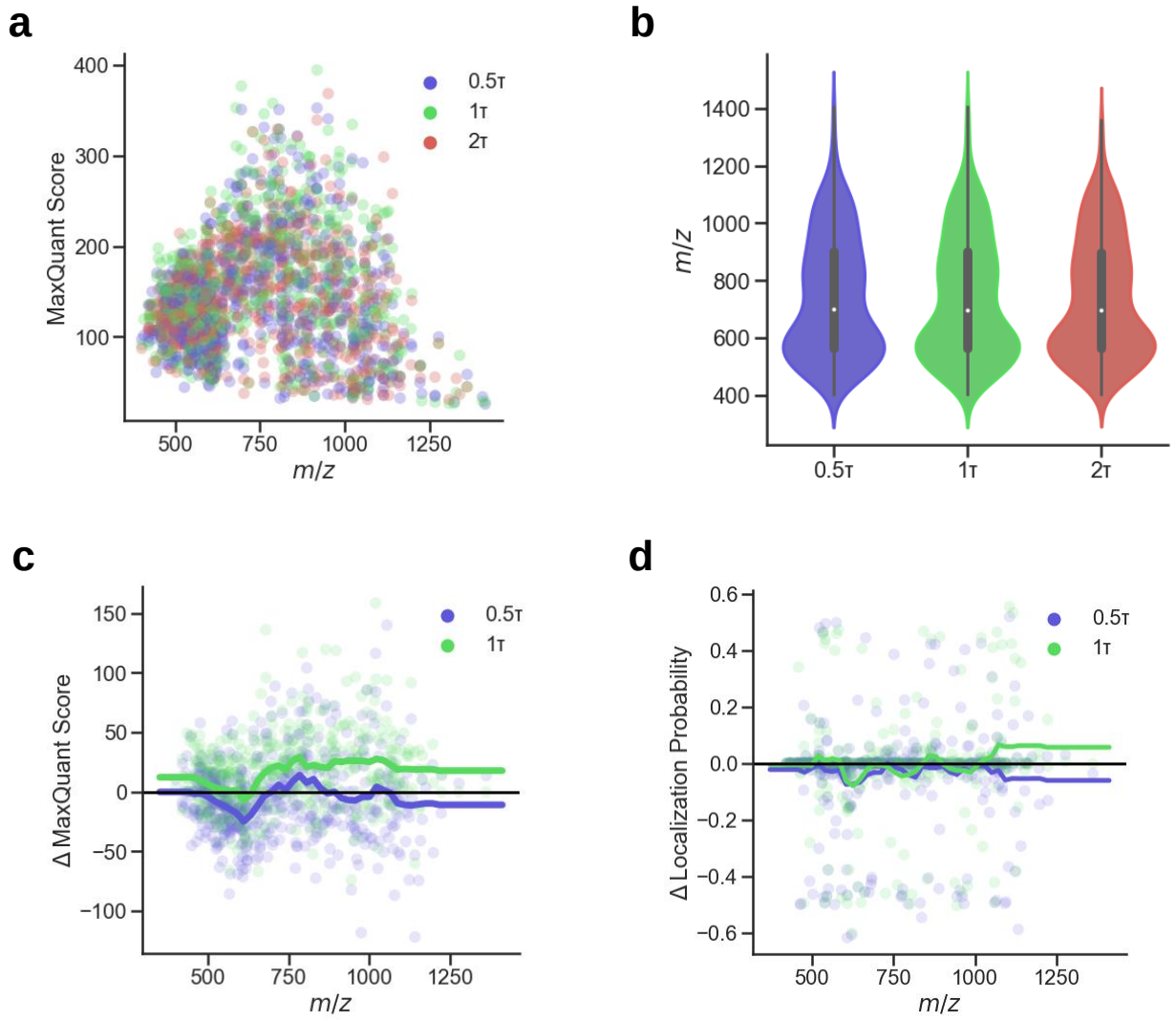

Fig. 6.9. Systematic Comparison of ETD Reaction Time Constants for O-GlcNAcylated Peptide Fragmentation and Site Mapping.
(a-b) As in Fig. 6.6a-b. (c) Difference in MaxQuant score (Δ MaxQuant Score) between an ETD reaction time constant of 0.5 or 1τ and the instrument default of 2τ. **(d)** Difference in localization probability (Δ Localization Probability) as in **(c)**. Lines represent the result of K-Nearest Neighbors (50) regression on each reaction time constant subset. There is perhaps a slight advantage of using a time constant of 1τ for fragmentation and site mapping of peptides at higher *m/z* values.

time constant of 2 (instrument default charge depended ETD reaction time parameters), 1, and 0.5τ.[10] For simplicity, only triply charged peptides were fragmented and analyzed, which corresponds to an ETD reaction time of 42.75, 21.38, and 10.69 ms for time constants of 2, 1, and 0.5τ respectively. Plotting MaxQuant score versus *m/z* for all PSMs (**Fig. 6.9a**), we do not see any clear relationship between *m/z* and score at different reaction times. In fact, the *m/z* distribution of peptides identified using all 3 reaction times are essentially the same (**Fig. 6.9b**). Finally, we plotted the difference in MaxQuant score (**Fig. 6.9c**) and localization probability (**Fig. 6.9d**) of 0.5 and 1, versus 2τ, only for peptides identified by all 3 methods. As before, we estimated the trend in score and localization probability difference using K-Nearest Neighbors (50) regression. We do not see any clear advantages of faster ETD reaction times versus the instrument default of 2τ, although there might be a slight advantage for both score and localization probability of using an ETD reaction time constant of 1τ at higher *m/z* values.

Finally, to see if EThcD SA might affect how the ETD reaction time constant relates to fragmentation and localization probability, we also repeated the experiment where every peptide is fragmented by ETD and EThcD with 10, 20, and 30% SA twice more using and ETD reaction time constants of 0.5 and 1τ for 3-6+ peptides (the original experiment was done with an ETD reaction time constant of 2τ) (**Fig. 6.10**). However, we did not observe any clear differences in either the trends of score or localization probability versus *m/z* or in how the different time constants affect score or localization probability with different EThcD SA. Overall, the above data suggest that, at the very least, there are minimal differences with drastically reduced ETD reaction

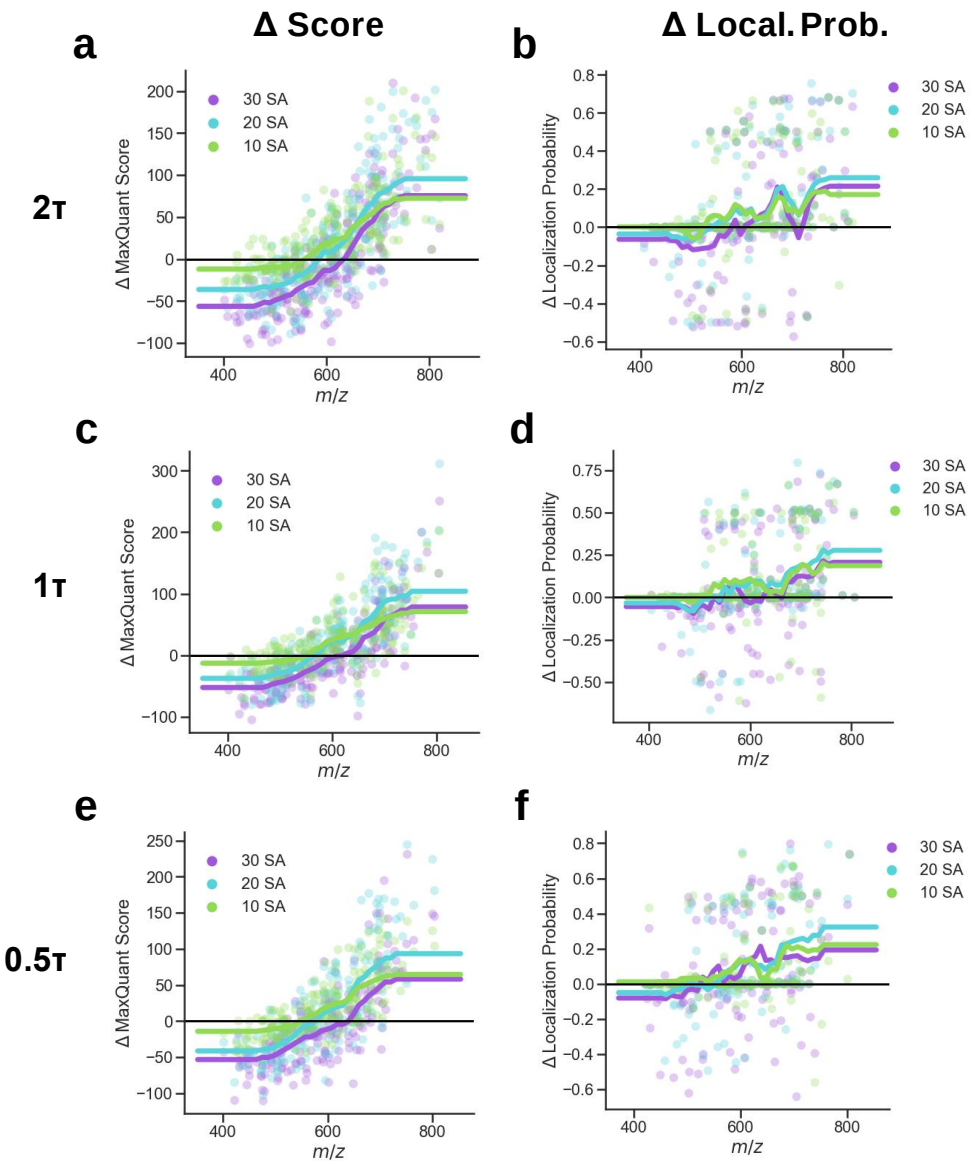

Fig. 6.10. Relationship between Score and Localization Probability and Peptide m/z for all ETD Reaction Time Constants.
(a, c, and e) Difference in MaxQuant score (Δ MaxQuant Score) between EThcD with 10, 20, or 30% SA and ETD only for peptides identified by all 4 methods for ETD reaction time constants 2, 1, and 0.5τ. **(b, d, and f)** Difference in localization probability (Δ Localization Probability) as in **(a, c, and e)**, respectively.

time constants. This finding has the potential to lead to the development of MS methods with significantly reduced instrument cycle time. In our case particularly, the slight advantage of shorter ETD reaction times for the *m/z* regimes where EThcD is would be employed might help to offset the inherently longer cycle time of this method.

Using the above insights, we at last constructed an online LC-MS/MS decision tree that uses our previously developed HCD product ion trigger to fragment O-GlcNAcylated peptides less than 625 *m/z* by ETD and greater than 625 *m/z* by EThcD. We used this method to profile O-GlcNAcylated peptides enriched from 293T cells as previously described and found a relatively even distribution of scores across all *m/z* values (**Fig. 6.11**), highlighting our ability to capture the advantages of ETD and EThcD in a single run. The same sample of O-GlcNAcylated peptides was also subjected to our previous HCD product ion-triggered EThcD method (which slightly outperformed ETD alone). In both cases, we analyzed the data using Proteome Discoverer using the same parameters as used previously in **Chapter 5** to avoid any biases or artefacts that may arise from different search engines followed by the application of our sites and regions script as described in **Chapter 5**. Overall, we found essentially the same number of sites using each method (1,264 versus 1,268 for the decision tree and EThcD only methods, respectively). However, both methods acquired HCD spectra for all peptides which generally outperforms ETD and EThcD for raw identifications despite being essentially unable to localize O-GlcNAc sites to specific S/T residues (**see Chapter 5**).

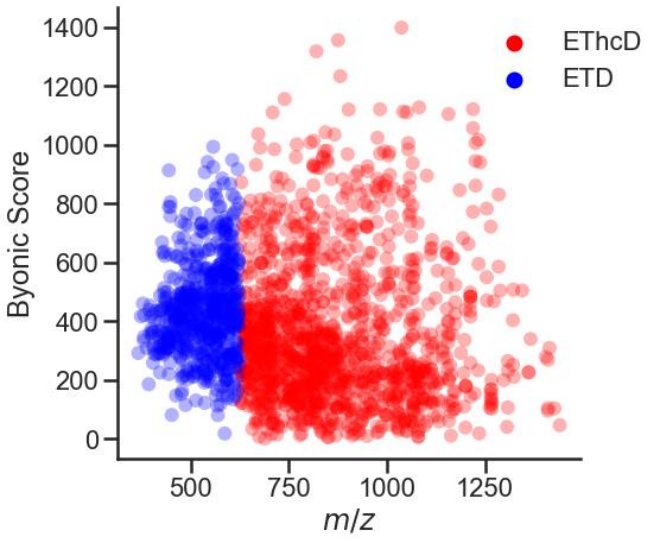

Fig. 6.11. O-GlcNAcylated Peptide Fragmentation by MS Decision Tree Results in an Even Distribution of Scores Across all m/z Values.
MaxQuant score versus *m/z* is plotted for every identified PSM.

We repeated the sites and regions analysis after separating the PSMs by fragmentation method and compared only ETD/EThcD to EThcD. Here, we found 1,251 O-GlcNAc sites using the decision

tree compared to 1,177 found by EThcD alone, an increase of 6.3%. Notably, we also found that the percentage of sites that were localized was markedly higher for ETD spectra in this dataset 71.5% versus 53.3% in the previous experiment (**Chapter 5**). This likely represents a large number of ETD spectra that are acquired for peptides not likely to fragment well by ETD alone, again underlining the significant savings in cycle time that this new decision tree method may bring. Finally, it is worth noting that the ThermoFisher instrument control software for the Orbitrap Fusion Tribrid (used for initial optimization experiments and those in **Chapter 5**) and Orbitrap Fusion Lumos (used for the direct comparison between the EThcD and decision tree methods) is not capable of implementing a true decision tree workflow. Herein, precursors are first sorted by *m/z* before being fragmented in order of decreasing intensity. Ideally, the intensity sort would happen first to avoid spending the additional time fragmenting low abundance precursors (whose resulting spectra are less likely to be matched) in the first *m/z* bin before moving to the second *m/z* bin. In the future, this method is likely to benefit greatly from modified instrument control software that is capable of sorting by intensity and subsequently fragmenting each precursor by ETD or EThcD depending on its *m/z*. Currently, our decision tree method is implemented by first performing fragmentation on the precursors less than 625 *m/z* first given the smaller bin size (overall we select precursors from 350 – 1800 *m/z*) and faster cycle time of ETD compared with EThcD.

6.5. High pH Reversed-Phase Fractionation to Expand O-GlcNAc Proteome Depth.

After the significant improvement in and optimization of fragmentation parameters for O-GlcNAcylated peptides, we next sought to apply these new methods along with advanced offline fractionation techniques for deep O-GlcNAc proteome profiling. To our knowledge, fractionation

of O-GlcNAcylated peptides has not been previously performed, although fractionation on native peptides prior to O-GlcNAcomics experiments have been shown to increase O-GlcNAc proteome depth.[15,16] We focused on high pH reversed-phase (HpHRP) given its recent explosion in success for in phosphoproteomics analyses.[17,18] Specifically, because the amount of O-GlcNAcylated peptides that we are able to obtain from this workflow is relatively small, we were particularly focused on whether fractionation was appropriate for these samples. Thus, to first determine if HpHRP fractionation could increase the depth in our O-GlcNAcomics experiments, we subjected a portion of the same samples prepared to test the decision tree against EThcD fragmentation alone (**Section 6.4**) to offline HpHRP fractionation using the method outlined by Olsen and coworkers.[17] 1 minute fractions were collected for 64 minutes and concatenated into 8 fractions for each sample. These 8 fractions were then subjected to LC-MS/MS analysis using our previously optimized decision tree method or our HCD product ion triggered EThcD method as before. Notably, this comparison will also shed light on how savings in instrument cycle time versus the complimentary fragmentation efficiencies of ETD and EThcD contribute to the improvements previously observed with the decision tree. In fractionated samples, there is a much lower demand for instrument cycle time.

In the combined fractionated samples from the decision tree, we found 1,594 O-GlcNAc sites compared to 1,448 with EThcD alone (including HCD spectra). This confirms a modest increase in O-GlcNAcome depth could be achieved by HpHRP fractionation. However, given the relatively small amount of material used in this analysis, it is likely that these benefits would be significantly amplified by the use of more material. In fact, injecting 2.5 times as much material (only possible for two out of the eight fractions) yielded about 50% more O-GlcNAc site identifications. Moreover, we see a 10.1% increase in total identified sites and regions using the

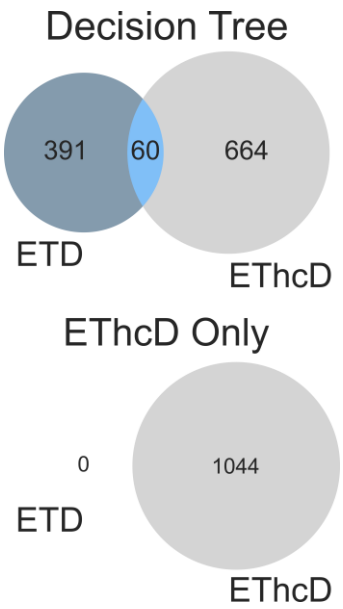

Fig. 6.12. Non-Redundant, Localized O-GlcNAc Sites Identified by the Decision Tree and EThcD Only Methods for HpHRP Fractionated Samples.

decision tree (even including HCD spectra). As before, we also separated the PSMs by fragmentation type and repeated the sites and regions analysis on only the ETD/EThcD and EThcD spectra. Here, we identified 1,555 versus 1,358 sites with ETD/EThcD and EThcD alone, respectively. This represents a more dramatic 14.5% increase the total number of sites identified using the decision tree to perform ETD or EThcD depending on precursor *m/z*. Furthermore, comparing only localized, non-overlapping sites (**Fig. 6.12**), we found 1,115 compared to 1,044 with the decision tree versus EThcD alone, representing a 6.8% increase in localized sites. Interestingly, the further advantage of the decision tree in fractionated samples highly suggests that savings in instrument cycle time contribute less to the increase in identification in comparison to the advantage of ETD over EThcD for both fragmentation and site localization at lower *m/z* values. Finally, the additional sites identified using the decision tree are highly orthogonal to those identified using EThcD alone as they were mapped to 728 unique protein groups versus 662, respectively, an increase of 10.0%. In total, fractionation also increased the number of proteins identified by 22.6 and 10.7% for the decision tree and EThCD runs, respectively, again indicating the utility of HpHRP fractionation for significantly increasing the O-GlcNAc proteome depth.

6.6. Conclusion.

In summary, the experiments performed in this chapter represent the first systematic investigation into the fragmentation and MS analysis of O-GlcNAcylated peptides. Importantly,

we developed a novel MS-based decision tree for fragmenting O-GlcNAcylated peptides during online LC-MS/MS by either ETD or EThcD depending on their *m/z*. This method, after HpHRP fractionation, increased the number of sites identified by ETD/EThcD by 10.1% compared to EThcD alone. This increase in identified O-GlcNAc sites also translated to a 10.0% increase in the number of O-GlcNAcylated proteins identified, underlining the fact that there are different subsets of O-GlcNAcylated peptides that are identified by ETD versus EThcD. Overall, the power of our method to probe both of these subsets in a single MS run will greatly facilitate the mapping and identification of O-GlcNAc sites across diverse samples and treatments while maximizing instrument efficiency.

6.7. Experimental Methods.

6.7.1. Preparation and Direct Injection of Synthetic O-GlcNAc Peptide 11.

Peptides in **Table 6.2** were obtained from ThermoFisher Scientific (custom synthesis) in 50:50 acetonitrile:0.1% trifluoroacetic acid (TFA). For direct injection experiments, approximately 1 mg of peptide 11 was dried by vacuum centrifugation and resuspended in 500 μL of 50:50 methanol:0.2% formic acid. This solution was then loaded into a syringe and injected into an Orbitrap Fusion Tribrid instrument at 100 nL/min. After manually inspecting both MS1 spectra and MS2 spectra (after fragmentation by HCD, ETD, and EThcD) to confirm the expected product ions, we targeted the triply charged precursor ion at 572.9498 *m/z* for analysis by the 28 methods in **Table 6.1** Each method was run for 1 min to acquire multiple spectra of the peptide. MS1 acquisition parameters were as described below.

Peptide	MW	Concentration (mg/mL)
1	1866.65	25
2	3264.23	10
3	3264.23	10
4	2106.15	17
5	2106.15	34
6	1534.32	13
7	1717.57	4
8	2040.96	3.75
9	1184.89	13.5
10	2391.32	5.75
11	2391.32	25.25
12	1239.31	2
13	2080.09	1.75
14	1077.08	2.25
15	2451.63	12.75
16	2339.46	13.5
17	1915.63	26
18	1915.6	5.75

Table 6.4. Concentrations of Synthetic Peptides 1-18.

6.7.2. Preparation and MS Analysis of Synthetic Peptide Mixture.

Approximately 50 µL of each peptide were combined and dried by vacuum centrifugation (for concentrations see **Table 6.4**). The peptide mixture was then reconstituted in 10 µL 0.2% formic acid with bath sonication. These samples were subjected to LC-MS/MS analysis on a nanoflow LC system, EASY-nLC II, (ThermoFisher Scientific) coupled to an Orbitrap Fusion Tribrid mass spectrometer (ThermoFisher Scientific) equipped with a Nanospray Flex ion source. For the EASY-nLC II system, solvent A consisted of 97.8% H2O, 2% ACN, and 0.2% formic acid and solvent B consisted of 19.8% H2O, 80% ACN, and 0.2% formic acid. 0.5 µL of the reconstituted mixture was then loaded onto a 16-cm analytical HPLC column (50 µm ID) packed in-house with ReproSil-Pur C18AQ 3 µm resin (120 Å pore size, Dr. Maisch, Ammerbuch, Germany) and separated using a 30 min gradient at a flow rate of 220 nL/min. The column was heated to 60 °C. The gradient was as follows: 2-30% Solvent B (30 min), 30-100% B (1 min), and 100% B (9 min). MS1 spectra were acquired at 120,000 resolution with a scan range from 350-1800 *m/z*; AGC was set to accumulate 50,000 ions, with a maximum injection time of 50 ms. Top speed (3 s cycle time) data-dependent MS2 analysis was then performed in which features were filtered for monoisotopic peaks with a charge state of 2-7 and a minimum intensity of 25,000, with dynamic exclusion set

to exclude features after 1 time for 5 seconds with a 10 ppm mass tolerance and exclude isotopes turned on. HCD fragmentation was performed for every method with normalized collision energy of 28 after quadrupole isolation of features using an isolation window of 1.6 *m/z*, an AGC target of 1e5, and a maximum injection time of 100 ms. MS2 scans were then acquired at 30K resolution in Centroid mode with the scan range set to automatic. ETD fragmentation was performed as outlined in **Table 6.3**.

6.7.3. Cell Culture.

The parental HEK-293T cell line was obtained from American Type Culture Collection (Manassas, VA). Cells were cultured in DMEM supplemented with high glucose, GlutaMAX, 10% fetal bovine serum (PBS), and 1x penicillin–streptomycin (P/S) (complete DMEM).

6.7.4. Chemoenzymatic Labeling and Enrichment of O-GlcNAcylated Peptides from 293T Cell Lysate.

HEK-293T lysate (5 mg) was diluted with 1% SDS, 20 mM HEPES pH 7.6 to 2.5 mg/mL. Samples were reduced using 10 mM TCEP-HCl pH 7.6 for 10 min at RT and alkylated with 30 mM iodoacetamide for 30 min at RT protected from light. Four volumes (~10 mL) of -20 °C acetone was added, and the sample was vortexed and incubated at -20 °C for 2 h. The precipitated protein was pelleted by centrifugation at 5,000 x g for 10 min at 4 °C. Acetone was removed, and the pellet was allowed to air dry. Dried protein was then redissolved at 5 mg/mL with 1 mL of 1% SDS, 20 mM HEPES pH 7.9 using probe sonication. Samples were then diluted with 2 mL of 2.5x GalT labeling buffer (50 mM HEPES pH 7.9, 125 mM NaCl, 5% IGEPAL CA-630), 1.2 mL of ddH2O, and 275 µL of 100 mM MnCl2. The mixture was chilled on ice for 5 min, and then 250

μL of 0.1 mM UDP-GalNAz, 250 μL of 2 mg/mL Y289L GalT, and 25 μL of 500 kU/mL PNGase F (New England Biolabs) were added with gentle mixing after each addition. The sample was rotated end-over-end overnight at 4 °C. The following day, 10 μL of 10 kU/mL calf intestinal phosphatase was added to the sample with incubation for 3 h at 37 °C. Samples were then acetone precipitated as described above. The protein pellet was redissolved at 5 mg/mL in 1 mL of 1% SDS, 20 mM HEPES pH 7.6. The solution was diluted with 2.85 mL of ddH2O and 0.15 mL of 200 mM HEPES pH 7.6. In a separate tube, a 5x CuAAC mix was prepared by sequential addition of 785 μL of ddH2O, 10 μL of 50 mM biotin-Dmpt-alkyne in DMSO, 5 μL of 100 mM BTTAA (Click Chemistry Tools, Scottsdale, AZ) in DMSO, 100 μL of 50 mM CuSO4 (freshly prepared), and 100 μL of 100 mM sodium ascorbate (freshly prepared). The 5x mix was then added directly to the protein sample and mixed end-over-end for 1 h at RT followed by acetone precipitation. The protein was resuspended at 5 mg/mL in 1 mL of 5% sodium deoxycholate, 50 mM HEPES pH 7.6, 10 mM EDTA to chelate residual Cu2+ and diluted with 4 mL of 50 mM HEPES pH 7.6. Then, 10 μL of 1 M CaCl2 and 100 μg Pierce trypsin protease (1:50 w/w) was added, and the sample was rotated end-over-end overnight at 37 °C. Two 15-mL 10 kDa MWCO Amicon concentrator tubes were rinsed with 2 x 5 mL of 50% MeOH and 2 x 5 mL of ddH2O by centrifugation at 4,000 x g for 5 min. Tryptic solutions were then centrifuged in the rinsed concentrator tubes at 4,000 x g for 20 min. The remaining residue was rinsed 2 x 2.5 mL of H2O by centrifugation, and the flowthrough fractions were combined. The sample was diluted two-fold with ddH2O. In a separate tube, 100 μL of a 50% slurry of high capacity Neutravidin agarose (ThermoFisher Scientific) was washed 2 x 5 min with 0.5 mL of 50% MeOH and 2 x 5 min with 0.5 mL of ddH2O. The agarose resin was then added to the sample and rotated end-over-end for 1 h at RT. The resin was pelleted by centrifugation at 500 x g for 5 min and then transferred to a 900 μL spin filter (ThermoFisher

Scientific) pre-rinsed twice with 50% MeOH and 50% ddH2O. Beads were washed 5 min each with the following solutions: 5 x 0.5 mL of 20 mM HEPES pH 7.6, 5 x 0.5 mL of 2 M NaCl, 3 x 0.5 mL of ddH2O, 3 x 0.5 mL of 50% MeOH, 2 x 0.5 mL of ddH2O. Captured peptides were eluted in twice with 0.5 mL of 2% v/v NH2OH with end-over-end rotation for 1 h at RT. Elution fractions were combined and concentrated to dryness with vacuum centrifugation. The eluted peptides were redissolved in 20 µL of 0.2% formic acid and desalted with a C18 ZipTip pipette tip.

6.7.5. HpHRP Fractionation of O-GlcNAcylated Peptides.

O-GlcNAcylated peptides enriched from 20 mg of 293T lysate were resuspended in 40 µL of 0.2% formic acid, and 10 µL was removed for direct MS analysis as described below. The remaining 30 µL was diluted to 100 µL with 100 mM ammonium hydroxide before fractionating on an Agilent (Santa Clara, CA) 1200 series HPLC system. Peptides were separated at a flow rate of 200 nL/min on an XBridge BEH C18 2.1 x 100mm (5µm) column (Waters, Milford, MA). Buffer A consisted of 10 mM ammonium hydroxide and buffer B consisted of 90:10 acetonitrile:10 mM ammonium hydroxide. The gradient was as follows: 1% Solvent B (4 min), 1-30% B (50 min), 30-60% B (4 min), 60-70% B (2 min), and 70-90% B (5 min). 64 1 min fractions were collected into 96 deep-well plates, and every eighth fraction was mixed. Concatenated fractions were then acidified to 1% formic acid and 0.1% TFA and partially dried by vacuum centrifugation to remove acetonitrile. Fractions were then desalted using an Oasis HLB µElution plate (Waters Milford, MA) following the manufacturer's instructions. Desalted samples were then partially dried by vacuum centrifugation to remove acetonitrile reconstituted to 27 µL in 0.1% formic acid for MS analysis.

6.7.6. LC-MS/MS Analysis of O-GlcNAcylated Peptides from 293T Cell Lysates.

Chemoenzymatically labeled and enriched samples for initial decision tree optimization experiments were analyzed on a nanoflow LC system, EASY-nLC 1000 (ThermoFisher Scientific), coupled to an Orbitrap Fusion Tribrid mass spectrometer (ThermoFisher Scientific) equipped with a Nanospray Flex ion source. O-GlcNAcylated peptides enriched from 5 mg of 293T lysate were resuspended in 10 μL of 0.2% formic acid, and 2 μL was directly loaded onto a PicoFrit column (New Objective, Woburn, MA) packed in house with ReproSil-Pur C18AQ 1.9 μm resin (120 Å pore size, Dr. Maisch, Ammerbuch, Germany). The 20 cm x 50 μm ID column was heated to 60 °C. The peptides were separated with a 120-min gradient at a flow rate of 220 nL/min. The gradient was as follows: 2-6% Solvent B (7.5 min), 6-25% B (82.5 min), and 25-40% B (30 min) and to 100% B (9 min). Solvent A and B were the same as described above. Full spectra were acquired over *m/z* 350-1800 in the Orbitrap (120 K resolution at 200 *m/z*); automatic gain control (AGC) was set to accumulate 50,000 ions, with a maximum injection time of 50 ms. Data-dependent MS2 analysis was then performed in which features were filtered for monoisotopic peaks with a charge state of 3-8 and a minimum intensity of 25,000, with dynamic exclusion set to exclude features after 1 time for 15 seconds with a 10 ppm mass tolerance and exclude isotopes turned on using a top-speed approach (cycle time of 5 s). Multiple fragmentation methods were used as described in the text. In all cases, an HCD product ion triggered method was employed. The normalized collision energy was optimized at 28% for high collision dissociation (HCD) fragmentation. The intensity threshold for fragmentation was set to 25,000. HCD fragmentation spectra was collected in Orbitrap operating at 30K resolution at 200 *m/z*. For triggered ETD and EThcD methods, fragmentation was performed for precursor ions whose HCD spectra contained a fragment of mass 300.1303 *m/z* (15 ppm tolerance). AGC was set to 50,000 with a maximum

injection time set at 500 ms and the spectra were acquired in the Orbitrap operating at 30K resolution. ETD reaction times were set as described in the text above.

Chemoenzymatically labeled and enriched samples for the decision tree versus EThcD comparison (with and without fractionation) were analyzed on a nanoflow LC system, EASY-nLC 1000 (ThermoFisher Scientific), coupled to an Orbitrap Fusion Lumos mass spectrometer equipped with a Nanospray Flex ion source. O-GlcNAcylated peptides enriched from 20 mg of 293T lysate were resuspended in 40 μL of 0.2% formic acid and 4 μL was directly used for analysis before fractionation. Fractionated samples were prepared as described above, and 4 μL was used for analysis. In both cases, the samples were loaded onto a 360x75μm column/tip packed in house with ReproSil-Pur C18AQ 1.9 μm resin (120 Å pore size, Dr. Maisch, Ammerbuch, Germany) at 1μL/min at 600 bar constant pressure for 15 μL. The column was heated to 60 °C. The peptides were separated with a 135-min gradient at a flow rate of 300 nL/min. Solvent A consisted of 99.9% water and 0.1% formic acid and Solvent B consisted of 80% acetonitrile, 19.9% water, and 0.1% formic acid. The gradient was as follows: 2-32% Solvent B (120 min), 32-63% B (10 min), 63-100%B (2 min), and 100% B (3 min) Full spectra were acquired over *m/z* 350-1800 in the Orbitrap (120 K resolution at 200 *m/z*); automatic gain control (AGC) was set to accumulate 50,000 ions, with a maximum injection time of 50 ms. Data-dependent MS2 analysis was performed using a top-speed approach (cycle time of 5 s) as described above for HCD product ion triggered EThcD analyses. For the decision tree analyses, the HCD scans were performed separately for precursors 350 – 625 *m/z* and 625 – 1800 *m/z*. The presence of the 300.1 *m/z* product ion was then used to trigger ETD (350 – 625 *m/z*) or EThcD (625 – 1800 *m/z*) using charge dependent ETD reaction times (with the instrument default 2τ time constant).

6.7.7. Data Analysis.

All raw files were searched using Proteome Discoverer 2.4.0.305 (ThermoFisher Scientific) with the Byonic (Protein Metrics, Cupertino, CA) search node v3.7.4. Peak lists were searched against the mouse UniProtKB databases (Mus musculus, retrieved January 21, 2020) supplemented with database of frequently observed contaminants (245 sequences). The following parameters were set: MS1 tolerance of 5 ppm, MS2 tolerance of 10 ppm, minimum peptide length of 6 amino acid, a maximum of three missed cleavages, carbamidomethylation of cysteine residues was set as a fixed modification, acetylation of the protein N-terminus and oxidation of methionine (common2) were set as a variable modifications, and the tagged O-GlcNAc was set as a variable modification (common 2). Data was filtered to a 1% false discovery rate on PSMs using the Percolator algorithm in Proteome Discoverer. Localization of O-GlcNAc sites was performed using the ptmRS node. For HCD spectra, equal localization probabilities were assigned to every serine/threonine due to neutral loss of the glycan.

Subsequent data analysis was performed using the Python language (Python Software Foundation. Python Language Reference, version 3.7.3. Available at http://www.python.org) with all Anaconda packages installed (Anaconda Software Distribution, version 4.8.3. Available at https://anaconda.com). K-Nearest Neighbors regression was performed using the Scikit-learn Python package (v0.22.1).[19] Sites and regions analysis is described in **Chapter 5**.

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Chapter 7

Systems-Level Analysis of the O-GlcNAcome in db/db Mouse Livers Reveals Widespread Remodeling of Protein and O-GlcNAcylation Networks

This project was a collaboration, running title:

Quantitative Functional Glycoproteomics Reveals Widespread Changes in the db/db Mouse Liver.

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7.1. Abstract.

O-GlcNAcylation is a widespread PTM of intracellular serine and threonine residues that is finely regulated in response to stimuli. However, methods to understand this regulation, especially in the context of disease, have lagged behind other PTMs due to unique difficulties in identifying, site mapping, and quantifying changes in O-GlcNAcylation across different stimuli or disease states. Herein, we present a new, integrated workflow for quantitative O-GlcNAcomics that builds isotopic encoding into our previously established chemoenzymatic labeling and enrichment workflow (**Chapter 5**). We then use this strategy along with our state-of-art MS decision tree and HpHRP fractionation techniques (**Chapter 6**) to profile changes in O-GlcNAcylation in the livers of a mouse model of NAFLD, metabolic syndrome, and T2DM. Next, using advanced proteomics techniques to simultaneously profile protein expression to reveal relative O-GlcNAc site occupancy changes in diseased versus healthy livers. Finally, we integrate this information with previously identified liver OGT interactors (**Appendix 5.3**) to build a dynamic PPI network (dynamic NOTISE analysis) to better understand the regulation of O-GlcNAcylation in the diseased liver. Overall, we identified 1,315 and 1,217 O-GlcNAc sites in WT and db/db livers (1,639 unique sites), improving our coverage of the mouse liver O-GlcNAcome by almost 50%. Interestingly, there were 131 upregulated and 237 *downregulated* O-GlcNAc regions (on 107 and 168 proteins, respectively), significantly challenging the theory that there is universal upregulation of O-GlcNAcylation in the context of hyperglycemia and metabolic disease. Lastly, we quantified 4,586 proteins, 2,654 of which were differentially expressed, suggesting a previously unrecognized widespread remodeling of the proteome in response to liver disease. Taken together, the rich datasets provided herein offer unprecedented insight into the dynamic O-GlcNAcylation networks in metabolic diseases of the liver.

7.2. Introduction.

T2DM is a worldwide epidemic that is estimated to affect almost 10% of the global population aged 20-79.[1] Although there have been a number of new therapies developed in the last 20 years, we still lack any treatments that can reverse or cure the disease, and the number of people affected by this devastating disease only continues to rise. Furthermore, T2DM can severely detract from quality of life and is associated with a host of complications, including kidney failure, nerve damage, blindness, and increased risk for cardiovascular events, that together are responsible for upwards of 750 billion dollars in associated healthcare costs.[1] The closely associated conditions, metabolic syndrome and NAFLD, often co-occur with T2DM and are characterized by derangements in lipid metabolism, obesity, and hypertension (metabolic syndrome) or abnormal accumulation of fat (>5% of hepatocytes) in the liver (NAFLD).[2,3] Combined, they are estimated to affect almost 2 billion people worldwide.[2,3] Despite the enormous burden of these disease on patients and society and an increasing, worldwide biomedical research effort, we still do not have a mechanistic understanding of their pathogenesis. In fact, one of the most interesting conundrums is why NAFLD is so closely associated with insulin resistance and T2DM; in theory, insulin resistance should cause decreased liver lipogenesis and, indeed, specific KO of the IR in the mouse liver results in markedly increased liver lipolysis and an overall decrease in liver weight.[4-6] In contrast, perhaps the most common mouse model of T2DM, metabolic disease, and NAFLD, leptin receptor KO (which results in marked hyperphagia, obesity, and over recapitulates most of the features of metabolic syndrome and T2DM) mice (db/db mice) demonstrate profound accumulation of fat in the liver.

Recently, dysregulated O-GlcNAcylation in response to hyperglycemia has emerged as a potential resolution to the paradox of how liver lipogenesis accelerates in the context of insulin

resistance. O-GlcNAcylation is a ubiquitous PTM of signaling molecules and transcription factors in the liver, and in many instances, modification of proteins involved with lipogenesis and lipid metabolism results in a shift toward increased and de novo lipogenesis (discussed in detail in **Chapter 1**).[7] However, methods to characterize O-GlcNAcylation in the context of fatty liver have been limited to studies of single proteins, and, to date, there has been no systematic account of how O-GlcNAcylation changes across the liver proteome in NAFLD/T2DM. Thus, such questions as whether increased O-GlcNAcylation is a general feature in diabetic livers and whether other pathways could be affected remain completely unexplored. These questions have remained unanswered largely because of a lack of robust tools for profiling dynamic changes in O-GlcNAcylation at the systems-level.

Herein, we develop a new quantitative O-GlcNAcomics technique that builds on the advances in chemoenzymatic labeling and MS methods in **Chapters 5** and **6**, respectively, to assay changing O-GlcNAcylation across the proteome in db/db versus WT mouse livers. An important feature of this workflow is the isotopic encoding of sample information in a novel cleavable biotin linker used for the labeling and enrichment of O-GlcNAcylated proteins. Like our previous biotin-Dmpt-alkyne linker (**Chapter 5**), this linker allows for the quantitative labeling, enrichment, and gentle, hydroxylamine-mediated elution of O-GlcNAcylated proteins while still leaving the final peptides with an additional positive charge important for ETD fragmentation. However, unlike the quantitative O-GlcNAcomics strategy employed with biotin-Dmpt-alkyne, this linker (1) allows for labeling and combination of samples before enrichment and digestion, significantly decreasing intersample variability, and (2) does not require expensive TMT reagents which can reach tens of thousands of dollars when labeling large amounts of protein or many conditions. Using these new chemical and mass spectrometric methods, we identify 1,315 and 1,217 O-GlcNAc sites in WT

and db/db livers, respectively, a total of 1,639 unique sites. Importantly, we were also able to obtain quantitative information on 919 of these sites, representing the most extensive dynamic O-GlcNAcome ever reported in the context of disease. Moreover, we identified 368 differentially expressed O-GlcNAcylated regions, significantly updating our understanding of aberrant O-GlcNAcylation in diabetic livers. Additionally, to account for changes in protein expression, we also performed quantitative proteomics on these same samples and were able to identify changes in the relative O-GlcNAc site occupancy in 275 O-GlcNAcylated regions across 192 proteins. We also quantified 4,856 proteins, of which a staggering 2,654 were differentially expressed. This represents the most extensive dataset of differential protein expression in metabolic disease and suggests that there is widespread proteomic remodeling in fatty livers. Finally, we expand our previous NOTISE approach to integrate dynamic protein expression information and identify diverse cellular networks engaged by OGT in the diabetic liver. Interestingly, we find that there is a greater preponderance of downregulated O-GlcNAcylation sites and a slight inverse correlation between putative adapter protein expression and O-GlcNAcylation levels on target proteins. Overall, the data and insights provided by these first studies of dynamic O-GlcNAcylation in db/db mouse livers will undoubtedly stimulate new research into the role of O-GlcNAcylation in liver function and disease for years to come.

7.3. Development of Biotin-Dmpt-Val0/6-Alkyne.

A key aspect of our chemoenzymatic enrichment protocol is the identification of a suitable, isotopically encoded biotin-alkyne linker for PTM functionalization. A number of cleavable linkers have been reported recently; however, many suffer disadvantages, ranging from relatively large residual fragments, incomplete cleavage, or sensitivity to acidic conditions used in peptide

purification.[8-10] In **Chapter 5**, we described the chemical optimization of our first-generation biotin-Dde-alkyne linker by replacement of the Dde group with the Dmpt group, which affords the higher stability necessary to survive standard trypsin digestion conditions. To quantify site-specific changes in protein O-GlcNAcylation, we sought to modify our linker with an isotopic tag. Previously, the addition of light and heavy amino acids such as valine or phenylalanine to encode each sample has been used successfully for numerous approaches including activity-based protein profiling and enrichment of azide- or alkyne-labeled proteins.[11,12] Here, we report a simple modification of biotin-Dmpt-alkyne to incorporate light and heavy isotopes of valine (+6; $^{13}C_5$, ^{15}N) to produce the pair of isotopically labeled, chemically cleavable biotin-Dmpt-Val0-alkyne **1** and biotin-Dmpt-Val6-alkyne **2** (**Fig. 7.1)**. Importantly, these modifications to the original linker scaffold minimally increase the residual mass left after cleavage and preserve the presence of a primary amine after cleavage (which adds an additional positive charge to peptides during the acidic conditions of LC-MS).

After preparation of this linker, we assessed its ability to quantitatively capture O-GlcNAc peptides while preserving information about sample abundance. Towards this end we labeled O-GlcNAcylated peptides from 293T cell lysate with either biotin-Dmpt-Val0-alkyne or biotin-Dmpt-Val6-alkyne. We then mixed portions of these samples together at defined ratios (1:5, 1:2, 1:1, 2:1, and 5:1 Val6:Val0) and performed the streptavidin enrichment and digestion as described in **Chapter 5**. We subject a small about of this sample to HCD-MS analysis to determine if the

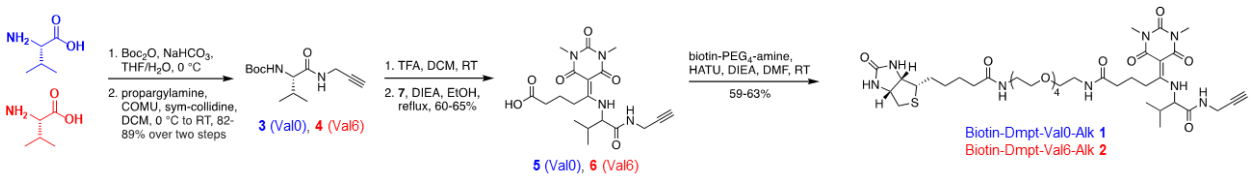

Fig. 7.1. Synthesis of Biotin-Dmpt-Val0/6-Alkyne.

valine 0/6 linker produced the same triggering diagnostic ions. Importantly, we clearly observed the same 300.1 *m/z* fragment representing cleavage of both the peptide bond between GalNAc and valine and the glycosidic bond between GalNAc and GlcNAc (see also **Fig. 5.11**). Interestingly, we also observed additional fragments at 399.2 and 405.2 *m/z* which represent the linker after cleavage of the glycosidic bond, but not the peptide bond. Nevertheless, we decided to move forward with using the same 300.1 *m/z* tag diagnostic ion to ensure consistent triggering between the two tags. Thus, we were able to use the same MS decision tree workflow from **Chapter 6** to map 559 and 441 O-GlcNAc sites from the Val0 and Val6 tags, respectively. As noted in **Chapter 6**, we again noticed a higher overall percentage of localized sites compared to previous experiments, with over 78 percent mapped to a single S/T for both tags.

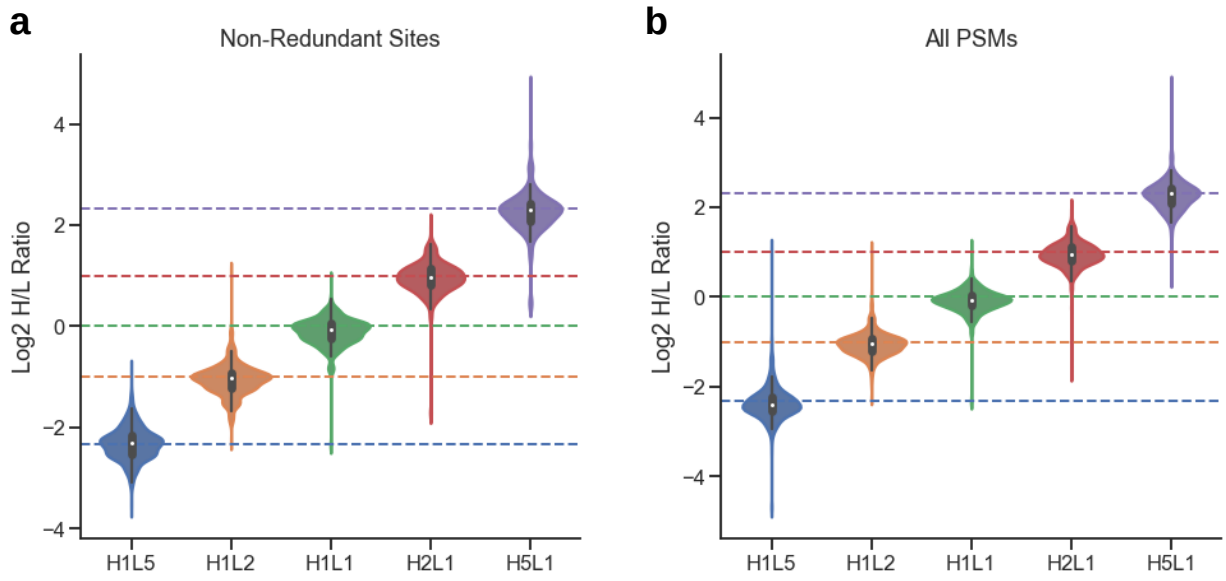

Fig. 7.2. Labeling with Biotin-Dmpt-Val0/6-Alkyne Labeling Yields Expected Ratios in a H:L Mixing Experiment.
O-GlcNAcylated peptides from 293T cell lysate were labeled with either the Val0 or Val6 linker and mixed at the indicated ratios by weight. The calculated ratios for all non-redundant GlcNAc sites are plotted in **(a)**. The ratios for all identified O-GlcNAcylated PSMs are plotted in **(b)**. H: Val6, L: Val0.

To calculate ratios for the different experiments, we used an innovative strategy to take advantage of the advanced PTM identification and localization, feature mapping, and label-free quantification abilities of MaxQuant[13] to match sites with quantified isotope patterns. Briefly, we searched the data twice, once without quantification to identify the O-GlcNAcylation sites (site-mapping search), and a second time looking for a +/- 6 Da isotope pattern across all features (quantification search). Children MS/MS scans from quantified features were then matched between the site identification and quantification runs using an in-house script. However, because we are inherently unable to ensure the same S/T was O-GlcNAcylated in both H/L peptides with this method, we performed the quantification at the region (O-GlcNAcylated peptide) level by removing all localization probability information before using our sites and regions script (**Chapter 5**) to enumerate non-redundant O-GlcNAcylation sites. In total, we quantified 284 O-GlcNAc regions. Excitingly, their mean calculated ratios corresponded almost exactly their expected ratio based on how they were mixed (**Fig. 7.2a**). We also plotted the ratios of all O-GlcNAc PSMs with matching isotope patterns (**Fig. 7.2b**) and similarly found that the ratios are consistent and as expected across a large ratio space. In summary, the characterization of biotin-Dmpt-Val0/6-alkyne supports its use as a powerful new tool for quantitative O-GlcNAcomics.

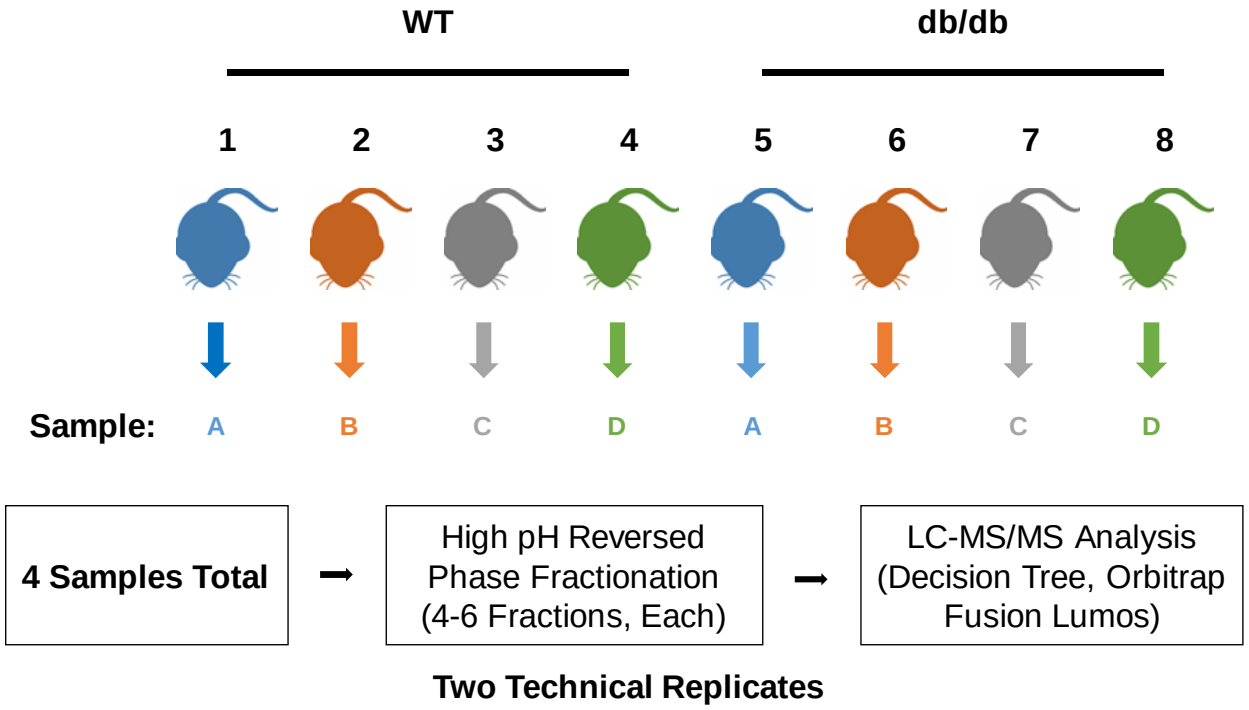

Fig. 7.3. Workflow for LC-MS/MS Analysis of O-GlcNAcylated Peptides Purified from db/db and WT Mouse Livers.
4 pairs of WT and db/db mice were selected at random, and peptides from each were labeled with the Val0 or Val6 linker, respectively, before combing 5 mg from each condition into pairs A-D for enrichment, digestion, fractionation, and LC-MS/MS analysis.

7.4. O-GlcNAc Site Mapping in db/db and WT Mouse Livers.

Having validated our new linker, we next applied it to understand differential O-GlcNAcylation in the livers of db/db versus WT mice. We harvested livers from 8 week old WT and db/db mice and subjected lysate prepared from a single lobe to enrichment with biotin-Dmpt-Val0-alkyne (WT) or biotin-Dmpt-Val6-alkyne (db/db). After labeling, protein mass was normalized and 5 mg from each condition (n=4) were combined before streptavidin capture, linker cleavage and trypsin digestion. O-GlcNAcylated peptides were then subjected to HpHRP fractionation, concatenated into 4-6 fractions, and subjected to LC-MS/MS analysis using the decision tree method on an Orbitrap Fusion Lumos. A second labeling and enrichment replicate

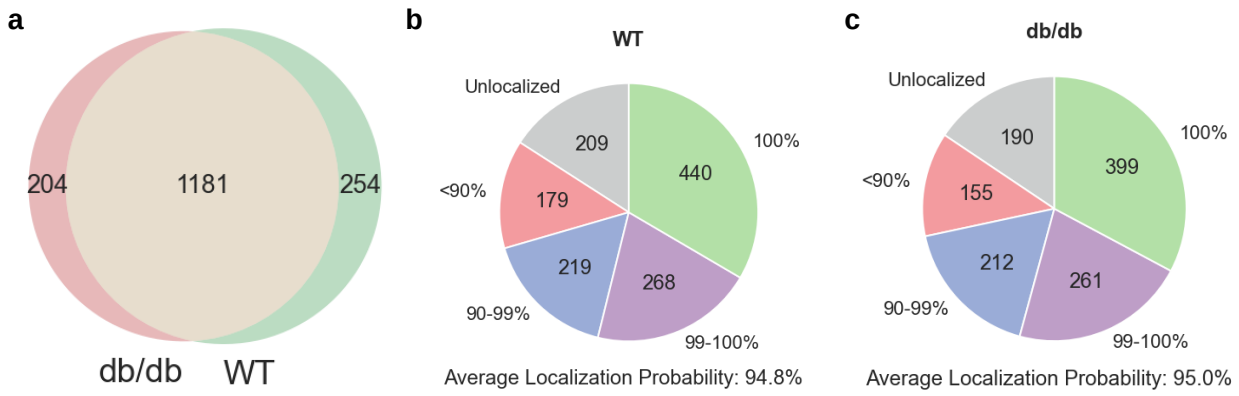

Fig. 7.4. O-GlcNAc Site Mapping in db/db and WT Mouse Livers.
(a) Overlap in sites identified in db/db/ and WT mouse livers. **(b-c)** Pie charts of localization probability of all sites identified in WT and db/db mouse livers, respectively.

was also prepared and subjected to microscale HpHRP fractionation[14] given the relatively small sample amounts. The overall workflow is outlined in **Fig. 7.3**. The data from these two experiments were then searched together in MaxQuant using the previously outlined strategy. In total, we identified 1,315 sites labeled with the Val0 tag (WT) and 1,217 sites labeled with the Val6 tag (db/db) (**Appendix 7.1**). Even without isotope pattern matching between the two tags, there was a high degree of overlap in sites identified by the two samples, with 1,181 sites shared between the two samples, 204 unique to db/db mouse livers, and 254 unique to WT mouse livers for a total of 1,639 unique sites (**Fig. 7.4a**), suggesting that there are not massive shifts in the liver O-GlcNAcome in response to metabolic derangement. As in the ratio tests described previously, the sites were extremely well localized, with 84% mapped to a single S/T in both samples with an average localization probability of 94.8 and 95.0% in WT and db/db livers, respectively (**Figs. 7.4b** and **7.4c**) Altogether, this rich dataset is a significant update to our understanding of O-GlcNAcylation in the mouse liver, elucidating and mapping > 60% more O-GlcNAc sites than were identified in **Chapter 5**.

7.5. Quantitative Comparison of db/db and WT Liver Proteomes.

Because of the significant liver pathology associated with leptin receptor KO, we also performed quantitative protein expression profiling to better understand if changes in O-GlcNAcylation were the result of changes in protein expression versus changes in OGT/OGA activity at individual sites. Towards this end, we performed TMT labeling on 100 μg of peptides from the same liver lysates used for O-GlcNAcomics. These peptides were also subjected to HpHRP fractionation, concatenated into 16 fractions, and subjected to LC-MS/MS analysis (**Fig. 7.5**). Overall, we quantified 4,586 proteins in all 8 samples. Notably, there was a high correlation between log2 TMT intensities and sample of origin, demonstrating that intersample variation far

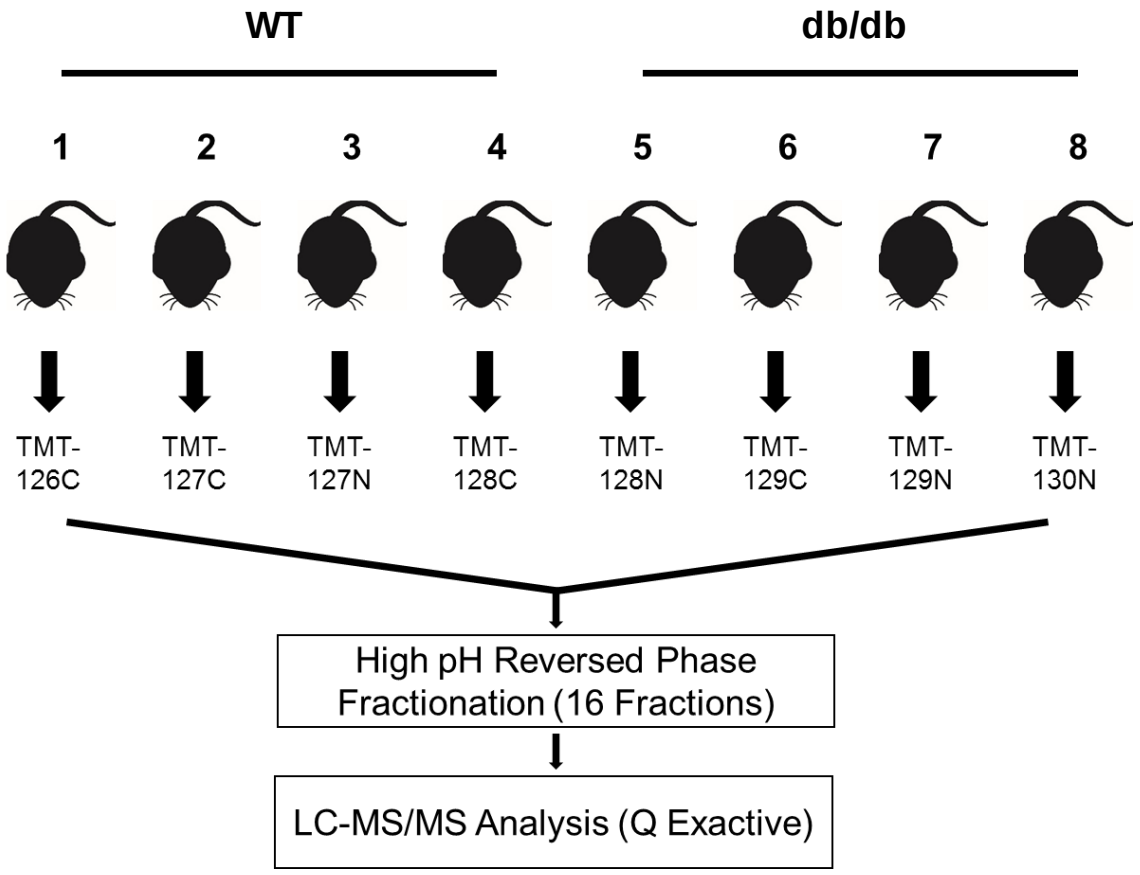

Fig. 7.5. Workflow for Quantitative Proteomics in db/db vs WT Mouse Livers.
Peptides from liver lysate used for quantitative O-GlcNAcomics (**Fig. 7.3**) were also TMT labeled and used to correct for changes in protein expression between the two conditions.

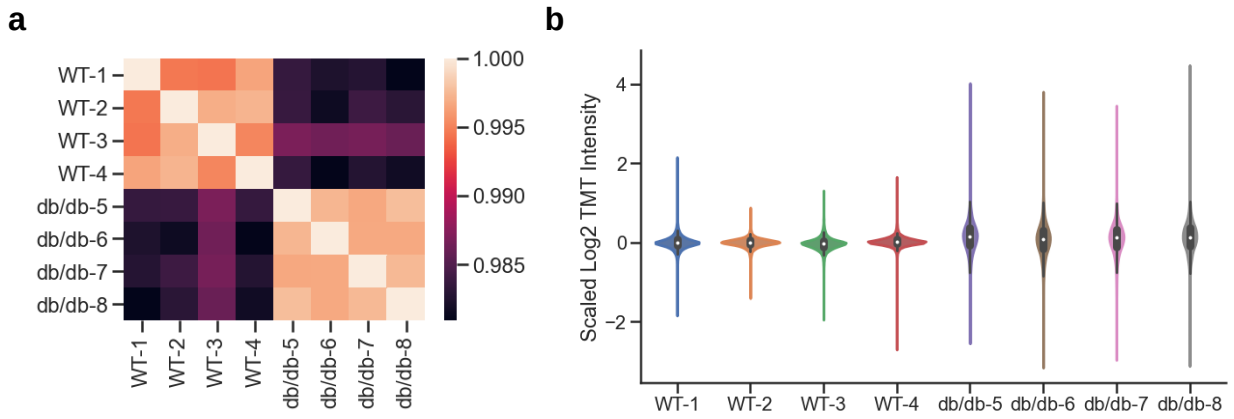

Fig. 7.6. Protein Expression in db/db and WT Mouse Livers.
(a) Heatmap of Pearson's correlation coefficiencts calculated between the log2 TMT intensities of all samples. **(b)** Violin plot of the scaled (by WT median) log2 TMT intensities of all samples.

outstrips intrasample variation (**Fig. 7.6a**). Interestingly, there was also significantly greater range in the db/db TMT intensities, suggesting that multiple proteins are highly differentially expressed in response to fatty liver (**Fig. 7.6b**). We then identified differentially expressed proteins in db/db versus WT samples using the limma-moderated t-test.[15] Strikingly, we identified 2,654 differentially expressed proteins, with greater than twice as many (1,880) upregulated than downregulated (774), suggesting a previously unrecognized and massive reorganization of the liver proteome in db/db mice (**Fig. 7.7a**). Hierarchical clustering analysis also grouped WT and db/db mice together, confirmed the relatively minimal intrasample variation, and demonstrated multiple co-regulated groups of up and downregulated proteins (**Fig. 7.7b**). The differentially expressed proteins were also involved in multiple pathways with top hits in MetaCore and Ingenuity Pathway Analysis focusing on expected pathways like lipid and bile acid metabolism as well as relatively less expected ones, ranging from mRNA splicing to cytoskeletal dynamics and FAK1 signaling (**Appendix 7.1**). Interestingly, we also found that both OGT and, to a much greater extent, OGA expression were upregulated in db/db livers (**Fig 7.7c**). This suggests cells are likely actively responding to global changes in O-GlcNAcylation as a result of metabolic derangement.

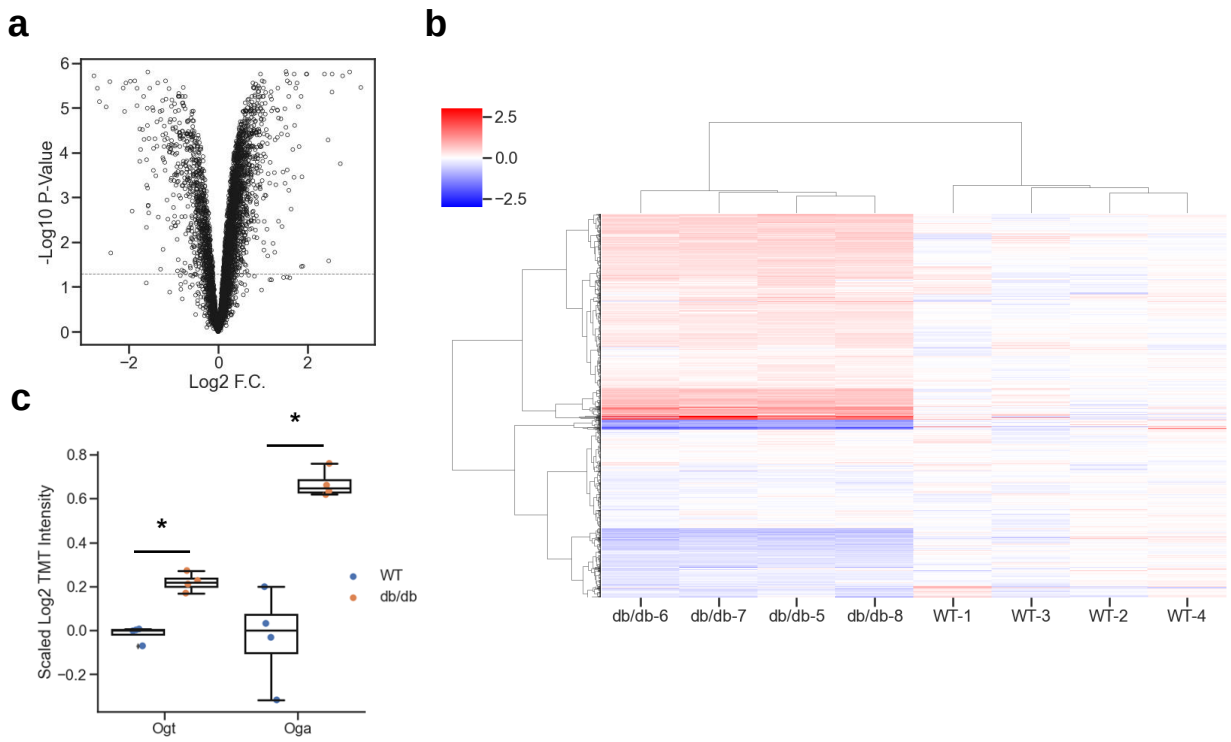

Fig. 7.7. Differentially Expressed Proteins in db/db Mouse Livers.
(a) Volcano plot of the log2 fold change in expression vs the –log10 limma-moderated p-values. **(b)** Hierarchical clustering of scaled (to WT median) log2 TMT intensities shows clustering by condition and differential protein expression. **(c)** Expression levels of OGT and OGA are upregulated in db/db livers. *p < 5e-4 by limma-moderated t-test, corrected for multiple comparisons using the Benjamini-Hochberg method.

Finally, we calculated protein expression ratios for mouse pairs A-D (**Fig. 7.3**) to use for calculated relative O-GlcNAc site occupancy ratios. Altogether, our quantitative proteomics analysis updates our understanding of differential protein expression in db/db mice by more than a factor of two, which will undoubtedly inform future mechanistic studies of liver pathology in T2DM.

7.6. Quantitative O-GlcNAcomics in db/db versus WT Mouse Livers.

With the protein expression and O-GlcNAcomics datasets in hand, we next set out to quantify differences in relative O-GlcNAcylation in peptide regions between db/db and WT mice. As described for the quantification during the linker validation, we removed all localization

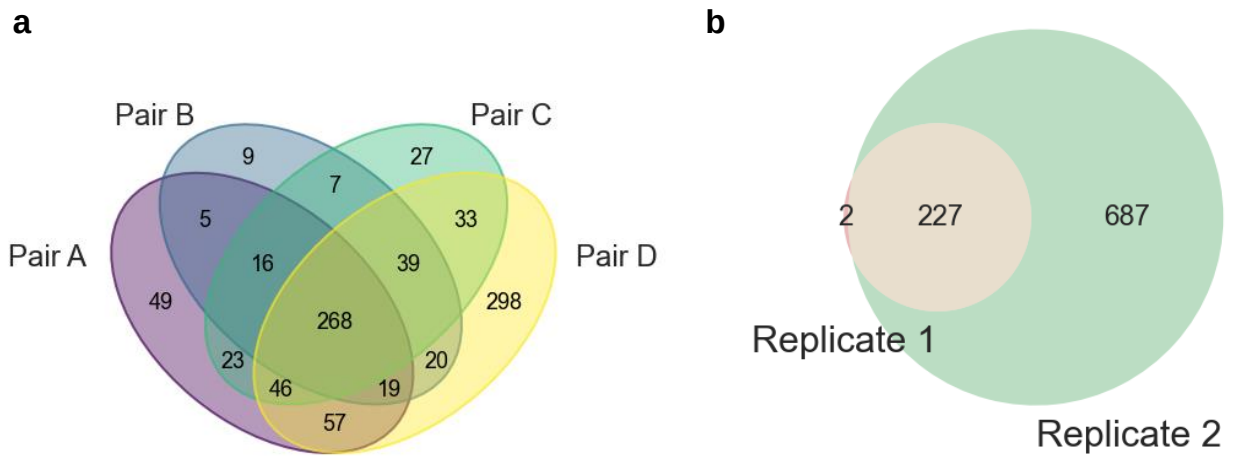

Fig. 7.8. Overlap between Biological and Technical Quantitative O-GlcNAcomics Replicates
Venn diagrams of inter-mouse **(a)** and inter-replicate **(b)** overlap.

probability information before resubmitting the PSMs to our sites and regions script and matching the regions back to quantified isotope patterns from the quantification run. As a result, our quantification is performed at the region level (for cases with more than 1 S/T this essentially corresponds to the peptide level). Excitingly, we were able to quantify 916 regions (with 919 total sites) on 594 proteins (**Appendix 7.2**), slightly shy of our previous O-GlcNAcomics experiment in 293T cells, which have a significantly larger O-GlcNAcome than the mouse liver (**Chapter 5**). Notably, there was a high degree of overlap between peptides quantified in both biological and technical replicates (**Fig. 7.8a-b**) Correcting for changes in protein expression, we were able to quantify 597 regions (598 sites) on 536 proteins. Thus, along with the data presented in **Chapter 5**, we present the two largest protein-expression corrected O-GlcNAcomics datasets ever reported. Importantly, correcting for protein expression markedly increased the number of O-GlcNAc regions found to be differentially regulated, highlighting the importance of performing protein expression normalization for quantitative O-GlcNAcomics experiments (**Fig. 7.8a**) We also found 131 (96) upregulated regions on 107 (77) proteins and 237 (179) downregulated regions on 168 (115) proteins (corrected for protein expression) (**Fig. 7.8b**). Interestingly, we found O-

GlcNAcylation was upregulated on 4/5 members of the perilipin (Plin) family of proteins, which sequester lipid droplets from metabolism by lipases.[16] Recently, it was reported that Plin1 O-GlcNAcylation opposes phosphorylation, which is necessary for lipid droplet breakdown.[17] Therefore, our results likely highlight a previously unrecognized role for Plin O-GlcNAcylation in fatty liver disease and strong evidence that O-GlcNAcylation may be playing a role in the paradoxical development of fatty liver in the context of insulin resistance. Specifically, increased perilipin O-GlcNAcylation (due to hyperglycemia induced flux through the HBP or modulation of other signaling mechanisms) may be preventing the breakdown of hepatocyte lipid droplets (the

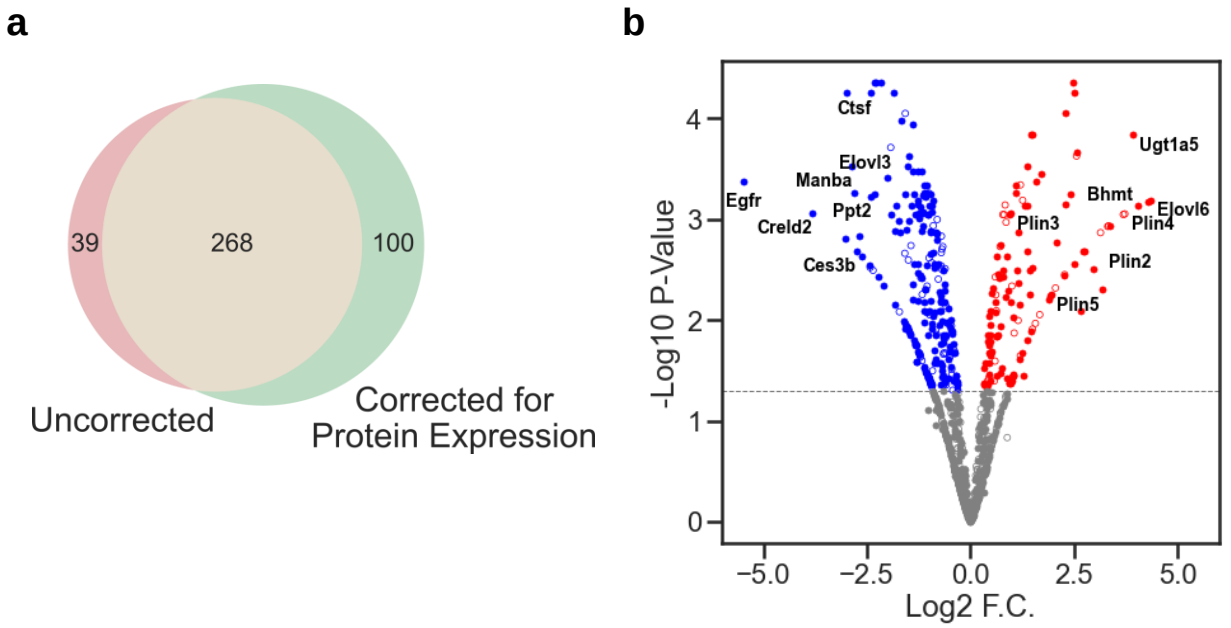

Fig. 7.9. Protien Expression Corrected O-GlcNAcomics in db/db versus WT Livers.
(a) Correction for protein expression results in the identification of significantly more differentially O-GlcNAcylated regions as well as eliminates many sites that likely suggest only differential protein expression rather than O-GlcNAcylation. **(b)** Volcano plot of all quantified O-GlcNAcylated regions. Note the expression of multiple members of the Plin family as well as the opposed upregulation and downregulation of Elov6 and 3, respectively. Other selected, highly differentially expressed genes involved in metabolism, autophagy, transcriptional regulation, and detoxification. Ugta5: UDP-glucuronosyltransferase 1-5; Bhmt: betaine--homocysteine S-methyltransferase 1, Ctsf: cathespin F, Ppt2: lysosomal thioesterase PPT2, Manba: beta-mannosidase, Ces3b: carboxylesterase 3B, Creld2: protein disulfide isomerase Creld2, Egfr: epidermal growth factor receptor.

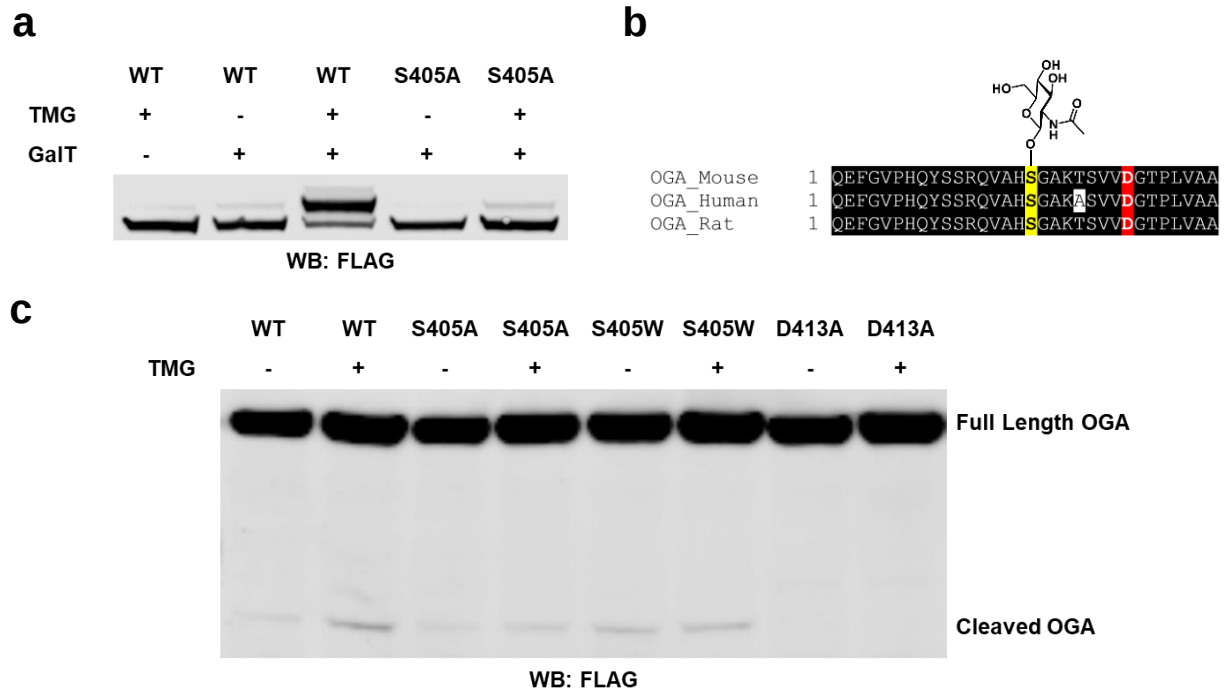

Fig. 7.10. S405 Is a Major Regulatory O-GlcNAcylation Site on OGA.
(a) Chemoenzymatic labeling of O-GlcNAcylation WT and S405A mutant OGT reveals an almost complete absence of OGA activity responsive OGA O-GlcNAcylation in the absence of S405. **(b)** S405 is highly conserved and close to the known capase-3 cleavage site at D413. **(c)** O-GlcNAcylation at S405 increases the caspase-3 mediated cleavage of OGA.

main pathological feature of NAFLD) and significantly contributing to the buildup of intracellular lipids even in the context of insulin resistance.

We also find two members of the elongation of very long chain fatty acid protein (Elovl) family, with Elovl6 having the highest upregulation of O-GlcNAcylation of any protein while Elovl3 had close to the lowest. Both Elovl3 and Elovl6 catalyze the rate limiting step in the long-chain fatty acid elongation cycle but are known to have different substrate specificities.[18,19] Interestingly, Elovl6 KO mice have a profound resistance to the development of hyperinsulinemia and other features of T2DM, suggesting that this enzyme plays a major role in metabolic homeostasis.[20] Relatively less is known about Elvol3, previously generated KO mice were only shown to have a sparse hair coat, defects in coat water repulsion, and increased trans-epidermal

water loss.[21] Nevertheless, this represents an interesting conundrum, that, taken with the striking Elvol6 KO mouse phenotype, is ripe for further investigation. Finally, we found that OGA O-GlcNAcylation at S405, a site originally identified more than 10 years ago as being differentially O-GlcNAcylated in the brain in response to PUGNAc,[22] was significantly downregulated in db/db mouse livers. To see (1) if this represents the major site of O-GlcNAc on OGA and (2) if this site is also dynamic to OGA inhibition in liver tissue, we overexpressed FLAG-tagged WT or S405A mutant OGA in HepG2 cells. After lysis, chemoenzymatic labeling with high MW PEG, and WB as described in **Chapter 2**, we noted an almost complete loss of O-GlcNAcylation on the S405A mutant (**Fig. 7.9a**). Moreover, inhibition of OGA activity with TMG markedly increased O-GlcNAcylation at this site, suggesting that it is indeed responsive to OGA activity in hepatocytes. A recent report also found that O-GlcNAcylation at this site severely reduced protein half-life without directly affecting stability.[23] Notably, this site highly conserved and close to the known caspase-3 cleavage site at D413 (**Fig. 7.9b**).[24] To test if O-GlcNAcylation may be protecting OGA from caspase-3 mediated cleavage, we expressed 4 flag-tagged OGA constructs, WT, S405A, S405W, and D413A, in HepG2 cells before treating with activating anti-Fas antibody to induce apoptosis. Consistent with the suggestion that O-GlcNAcylation at S405 might regulate OGA stability, we find that TMG treatment increases the cleavage of OGA, a phenomena that can be almost entirely prevented by mutation of that site to alanine (**Fig. 7.9c**). Furthermore, the S405W O-GlcNAc mimetic[25] showed increased baseline cleavage that was not further increased by TMG stimulation. Taken together, these multiple lines of evidence suggest that OGA expression, activity, and stability may be simultaneously upregulated in db/db livers, something that is also consistent with the preponderance of downregulated O-GlcNAc sites. This would represent the

first in vivo evidence of homeostatic regulatory mechanisms for O-GlcNAc in the context of disease.

In addition to the specific examples highlighted above, GO term analysis of proteins with upregulated O-GlcNAcylation revealed a strong enrichment for proteins involved in catabolism/metabolism and glucuronidation, phase II conjugation of compounds, and drug metabolism pathways. Proteins with downregulated O-GlcNAcylation were enriched for an array of biological processes, including regulation of gene expression, nucleic acid and protein biosynthesis, and various metabolic processes. There was also a strong enrichment for proteins involved in lysosomal and protein processing in the ER pathways. Overall, this data provides significant insight into the major regulatory functions of O-GlcNAcylation in response to

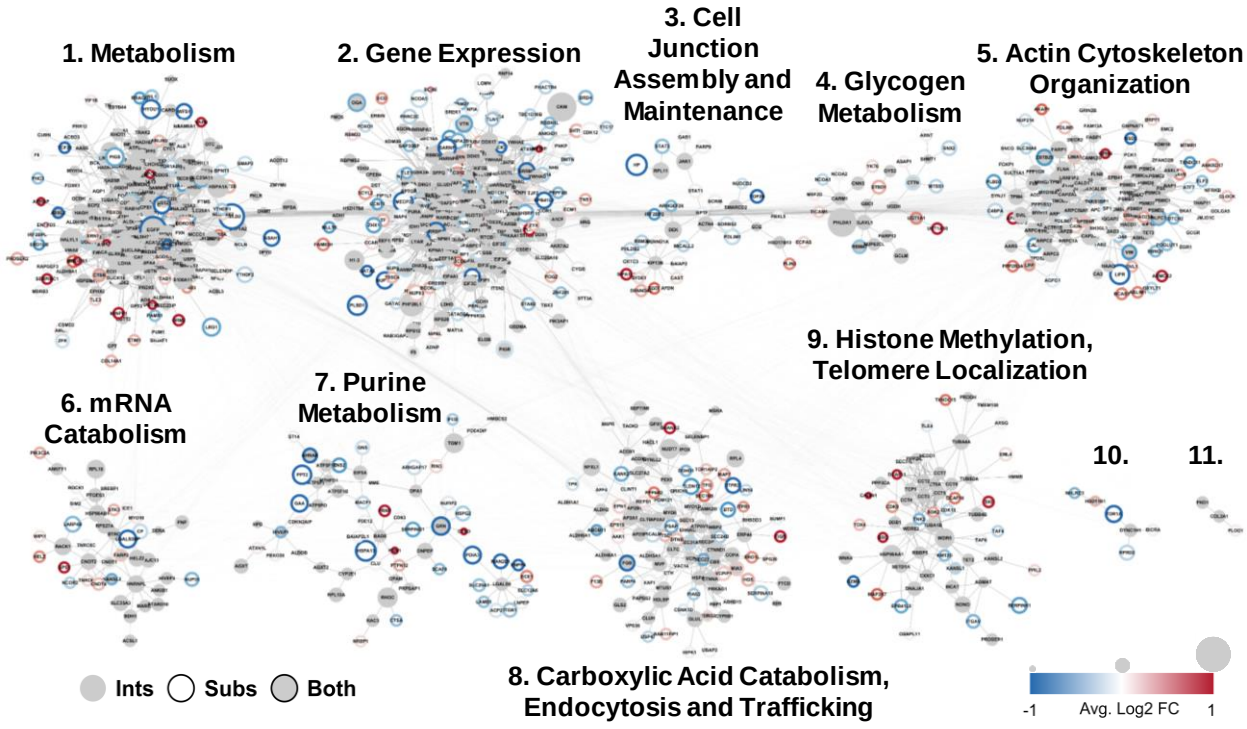

Fig. 7.11. Dynamic NOTISE Analysis in db/db and WT Mouse Livers.
Dynamic NOTISE analysis reveals widespread changes in O-GlcNAcylation and protein expression across every O-GlcNAc functional community in db/db mice. Protein expression is represented by node size and O-GlcNAcylation by node border color.

metabolic disease. We also provide the first systems-level evidence that O-GlcNAcylation is finely controlled in the context of hyperglycemia, with increased OGA activity and other regulatory mechanisms resulting in the downregulation of hundreds of O-GlcNAcylation sites rather than the universal upregulation (presumably in response to increased HBP flux) that has been previously suggested.[26]

7.7. Dynamic NOTISE Analysis Reveals O-GlcNAcylation and Protein Expression Changes across the OGT Substrate Interactor PPI Network.

To gain a deeper understanding about how db/db affects OGT substrate interactor networks in metabolic disease, we expanded our previously developed NOTISE analysis (**Chapter 5**) to integrate the quantitative information about protein expression and O-GlcNAcylation provided above. Again, PPI network generation, GLay community clustering, and ClueGO-guided[27] annotation based on biological process GO terms resulted in 11 functionally distinct communities (**Fig. 7.10**). These communities were enriched for proteins involved in (1) metabolism, (2) gene expression, (3) cell junction assembly and maintenance, (4) glycogen metabolism, (5) actin cytoskeleton organization, (6) mRNA catabolism, (7) metabolism, (8) carboxylic acid catabolism and endocytosis/trafficking, and (9) histone methylation and telomere localization. Although many of these communities are similar, e.g. various facets of metabolism, histone modification, and actin cytoskeletal organization, we also see new communities involved in cell junction assembly and maintenance and glycogen metabolism which may represent, at least in part, the differential engagement of OGT substrate interactor networks in db/db mouse livers.

Interestingly, we see widespread changes across every functional community in both O-GlcNAcylation and protein expression. Communities 1 and 7 showed a particularly large

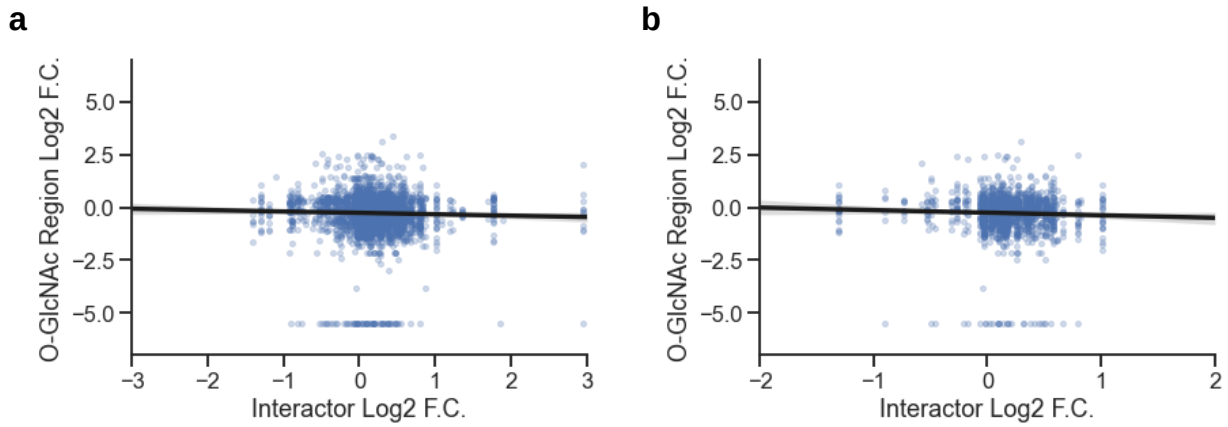

Fig. 7.12. Correlation between OGT Interactor Protein Expression and Secondary Interactor O-GlcNAcylation.
(a) There is a slight negative correlation (Spearman's ρ: -0.0756, p-value: 6.55e-6) between the protein expression of OGT interacting proteins and the O-GlcNAcylation on associated secondary interactors. **(b)** This trend is preserved for interactors with an adaptor rank > 2 (Spearman's ρ: -0.0515, p-value: 0.031).

proportion of differential protein and O-GlcNAcylation expression, respectively, confirming for the first time at the systems level that O-GlcNAcylation is involved with multiple metabolic networks in response to T2DM/NAFLD. As we observed with the KO of putative adapter protein BAP1 in **Chapter 5**, we also observed both upregulation and downregulation of O-GlcNAcylation in substrates connected to putative adaptor proteins, further suggesting that OGT interacting proteins may be able to both facilitate and block O-GlcNAcylation of their interactors. To gain more insight into how OGT interactor expression affected the O-GlcNAcylation of OGT interactor interactors, we plotted the change in interactor expression of all interacting proteins relative to the O-GlcNAcylation of the proteins that those interactors interact with. Surprisingly, we found a small but significant negative correlation (**Fig. 7.11a**), suggesting that increased expression of OGT interactors might block rather than facilitate O-GlcNAcylation of secondary interactors. To try and differentiate whether this correlation was a result of other signaling mechanisms outside of OGT-protein interactions, we also repeated our adaptor rank analysis to score putative OGT

adaptor proteins. Plotting only OGT interactors with an adaptor rank score of two (meaning that they interact with at least two more OGT substrates than other interactors), the weak but significant negative correlation is preserved (**Fig. 7.11b**). This analysis advances the idea that OGT-protein interactions may do more to block O-GlcNAcylation of secondary interactors than promote it (as the adaptor protein hypothesis originally envisioned).

Finally, in addition to our adaptor rank program, quantitative NOTISE allows us to look for putative OGT adaptor/blocker proteins by searching for the interactors and their connect substrates that are (anti-)correlated. With stringent cutoffs for protein and O-GlcNAcylation fold change, as well as only accepting O-GlcNAcylation fold change that was corrected for protein expression, we identified multiple potential OGT adaptor/blocker-target pairs with a preponderance of the latter (i.e. increased expression leading to decreased O-GlcNAcylation of target proteins) (**Appendix 7.4**). Specifically, we identified a new putative targeting interaction between myb-binding protein 1A and basigin, which are known members of a PPI network that was recently implicated in the regulation of metabolism, autophagy, and of mammalian target of rapamycin (mTOR) signaling.[28] We also found that increased WDR5 expression results in the downregulation of multiple sites on HCFC1 suggesting that, like with BAP1 KO in **Chapter 5**, HCFC1 O-GlcNAcylation may be blocked by OGT-adaptor or adaptor-HCFC1 binding. However, we readily admit that specific adaptor/blocker protein pairs identified by this analysis require future validation given the likely remodeling of signaling networks in db/db livers. However, as new tools for disrupting specific PPIs are becoming increasingly available,[29] dynamic NOTISE is likely to serve an important role in identifying which PPIs to target in any given context. In summary, the powerful updates to our NOTISE analysis outlined herein significantly enhance our ability to study changes in O-GlcNAcylation in response to disease or stimuli, identify the major

O-GlcNAcylation site and protein players involved in specific functional cellular networks, and provide a new framework for understanding OGT regulation.

7.8. Conclusion.

We have integrated advanced tools in chemistry and MS to provide the first insights into how liver O-GlcNAcylation changes in response to metabolic disease. First, we combined novel MS tools (**Chapter 6**) with a new isotopically defined biotin-Dmpt-alkyne linker in the development of an expedient and robust workflow for quantitative O-GlcNAcomics. Importantly, in contrast to other techniques, which rely on metabolic labeling[9] or use expensive TMT reagents,[30] this workflow allows for near quantitative enrichment of O-GlcNAcylated proteins at a significantly reduced cost. Furthermore, it is highly efficient for mapping O-GlcNAc sites to specific S/T, and we were able to localize nearly 80% of sites in db/db and WT mouse livers. Next, we applied this workflow to understand how O-GlcNAcylation changes in response to metabolic disease, the first large-scale simultaneous protein and PTM analysis to date in this context. Here, we identified thousands of differentially expressed proteins involved in multiple pathways ranging from metabolism to RNA splicing. We also identified hundreds of differentially O-GlcNAcylated proteins with a significant percentage of up and downregulated sites on proteins intimately involved in metabolism/catabolism of nucleic acids, proteins, carbohydrates, and toxins. Finally, we synthesize these datasets in a new dynamic NOTISE workflow that reveals key OGT substrates and interactors that are differentially expressed or O-GlcNAcylated in diabetic livers. This analysis also sheds new light on the role of OGT adaptor proteins in regulating OGT, suggesting that, in addition to targeting, OGT interactors are perhaps more likely to block O-GlcNAcylation of their interactors. We then use our innovative networking approach to identify putative adaptor/blocker

pairs for further study. In total, the data gathered, processed, and synthesized herein represent an unprecedented and significant step towards a deeper mechanistic understanding of OGT (dys)regulation in the context of metabolic disease.

7.9. Experimental Methods.

7.9.1. Chemicals and Reagents.

All chemicals were purchased from Sigma-Aldrich (St. Louis, MO), and all cell culture materials were purchased from ThermoFisher Scientific (Waltham, MA) unless otherwise noted. All primers were purchased from Integrated DNA Technologies (Coralville, IA), and all molecular biology supplies were purchased from New England Biolabs (NEB, Ipswich, MA) unless otherwise indicated.

7.9.2. Synthesis of Biotin-Dmpt-Val0/6-Alkyne.

7.9.2.1. N-(tert-butoxycarbonyl)-N'-propargyl-L-valinamide (Boc-Val0-Alk, 3).

Valine (200 mg, 1.71 mmol) and NaHCO3 (287 mg, 2 eq) were suspended in 3 mL H2O and cooled to 0 °C. Boc2O (410 mg, 1.1 eq) was dissolved in 3 mL THF and added dropwise to the mixture. The reaction was stirred at 0 °C for 1 h and then allowed to warm to RT overnight. The reaction was diluted with H2O and extracted twice with EtOAc. Organic layers were combined and extracted twice with sat. NaHCO3. Aqueous layers were combined, acidified to pH 2 with ice-cold 1 N HCl, and extracted thrice with EtOAc. Organic layers were combined, dried over MgSO4, and concentrated. The resulting oil was then redissolved in 10 mL dry CH2Cl2 under

Ar. To the solution was added sym-collidine (451 μL, 2 eq) and propargylamine (164 μL, 1.5 eq). The mixture was cooled to 0 °C, and COMU (1.10 g, 1.5 eq) was added slowly over 15 min. The reaction was stirred at 0 °C for 1 h and then allowed to warm to RT overnight. The solution was then diluted with EtOAc and extracted twice with dilute HCl (pH 2), twice with sat. NaHCO¬3, and twice with brine. The organic layer was dried over MgSO4 and concentrated. The product was further purified by flash silica column chromatography (2:1 hexanes/EtOAc) to yield a white solid (355 mg, 82% over two steps). 1H NMR (400 MHz, CDCl3): δ 6.68 (bs, 1H, NH), 5.18 (bs, 1H, NH), 4.13-3.90 (m, 3H, NCH2, Val-CαH), 2.20 (td, J = 2.6, 1.4 Hz, 1H, ≡CH), 2.10 (bs, 1H, Val-CH), 1.43 (s, 9H, Boc-CH3), 0.94 (dd, J = 14.1, 6.8 Hz, 6H, Val-CH3). 13C NMR (100 MHz, CDCl3) δ 171.72, 171.69, 156.09, 80.13, 79.44, 71.66, 59.93, 31.12, 29.11, 28.64, 28.46, 19.36, 18.11. ESI-HRMS (*m/z*): [M+H]+ calc'd for C13H22N2O3: 255.1703, found: 255.1700.

7.9.2.2. N-(tert-butoxycarbonyl)-N'-propargyl-L-valinamide-13C5,15N (Boc-Val6-Alk, 4).

Synthesized as described above (89% yield over two steps). 1H NMR (400 MHz, CDCl3): δ 7.18 (bs, 1H, NH), 5.50 (d, J = 9.0 Hz, 0.5H, 15NH), 5.27 (d, J = 9.0 Hz, 0.5H, 15NH), 4.23-3.74 (m, 3H, NCH2, Val-13CαH), 2.17 (m, 1.5H, Val-13CH, ≡CH), 1.87 (bs, 0.5H, Val-13CH), 1.40 (s, 9H, Boc-CH3), 1.07 (dp, J = 9.7, 4.8 Hz, 3H, Val-13CH3), 0.76 (dp, J = 10.3, 4.9 Hz, 3H, Val-13CH3). 13C NMR (100 MHz, CDCl3) δ 172.19, 171.93, 171.67, 156.24, 155.99, 79.90, 79.54, 79.52, 71.43, 62.33, 61.89, 61.45, 60.27, 60.15, 59.92, 59.80, 59.74, 59.62, 59.39, 59.27, 31.82, 31.47, 31.31, 31.12, 30.96, 30.77, 28.94, 28.44, 19.58, 19.41, 19.23, 19.07, 18.44, 18.09, 17.65, 17.29. ESI-HRMS (*m/z*): [M+H]+ calc'd for C813C5H22N15NO3: 261.1841, found: 261.1823.

7.9.2.3. 5-(4-carboxy-1-(N-propargyl-L-valinamido)butylidine)-1,3-dimethylpyrimidine-2,4,6-trione (GA-Dmpt-Val0-Alk, 5).

Boc-Val0-Alk **3** (75.0 mg, 0.295 mmol) was dissolved in 4 mL 3:1 TFA/CH_2Cl_2 and stirred for 3 h at RT. The mixture was then concentrated and co-concentrated three times with EtOH to remove all residual TFA. The residue was then redissolved in 5 mL EtOH, and GA-Dmpt **4** (104 mg, 1.3 eq) and DIEA (154 µL, 3 eq) were added. The reaction was refluxed for 3 h and then concentrated. The residue was redissolved in EtOAc and extracted with 1 M $KHSO_4$ and brine. The organic layer was dried over Na_2SO_4, filtered, and concentrated. The compound was then purified by flash silica column chromatography (9:1 CH_2Cl_2/MeOH + 0.02% acetic acid) to afford a white solid (78.1 mg, 65% over two steps).^{1}H NMR (400 MHz, MeOD-d_4): δ 4.43 (d, J = 6.1 Hz, 1H, Val-C$_\alpha$*H*), 4.01 (qd, J = 17.5, 2.6 Hz, 2H, NCH_2), 3.27 (s, 6H, NCH_3), 3.17 – 3.03 (m, 2H, CH_2), 2.62 (t, J = 2.5 Hz, 1H, ≡C*H*), 2.49 (t, J = 7.0 Hz, 2H, CH_2), 2.27 (h, J = 6.7, 1H, Val-C*H*), 1.80 (ddt, J = 14.0, 11.7, 7.1 Hz, 2H, CH_2), 1.06 (dd, J = 6.8, 5.4 Hz, 6H, Val-CH_3). ^{13}C NMR (101 MHz, MeOD-d_4): δ 177.84, 177.06, 171.50, 152.86, 91.08, 80.12, 72.51, 63.57, 34.36, 33.42, 30.42, 29.55, 28.17, 24.09, 19.36, 18.27. ESI-HRMS (*m/z*): $[M+Na]^+$ calc'd for $C_{19}H_{26}N_4O_6$: 429.1750, found: 429.1738.

7.9.2.4. 5-(4-carboxy-1-(N-propargyl-L-valinamido)butylidine)-1,3-dimethylpyrimidine-2,4,6-trione-13C5,15N (GA-Dmpt-Val6-Alk, 6).

Synthesized as described above (60% yield over two steps). ^{1}H NMR (400 MHz, MeOD-d_4): δ 13.11 (d, J = 8.4 Hz, 0.2H, ^{15}N*H*), 12.89 (d, J = 8.4 Hz, 0.2H, ^{15}N*H*), 4.60 (s, 0.5H, Val-^{13}C$_\alpha$*H*), 4.25 (s, 0.5H, Val-^{13}C$_\alpha$*H*), 4.01 (qdd, J = 17.5, 3.6, 2.5 Hz, 2H, NCH_2), 3.28 (s, 6H, NCH_3), 3.16 – 3.04 (m, 2H, CH_2), 2.62 (t, J = 2.5 Hz, 1H, ≡C*H*), 2.49 (t, J = 7.0 Hz, 2H, CH_2), 2.44 (bs,

0.5H, Val-^{13}C*H*), 2.11 (bs, 0.5H, Val-^{13}C*H*), 1.91 – 1.73 (m, 2H, C*H*$_2$), 1.22 (h, *J* = 5.0 Hz, 3H, Val-^{13}C*H*$_3$), 0.91 (h, *J* = 5.0 Hz, 3H, Val-^{13}C*H*$_3$). ^{13}C NMR (101 MHz, MeOD-*d*$_4$): δ 171.50 (d, *J* = 52.4 Hz), 152.86, 91.09, 80.12, 72.51, 63.54 (ddd, *J* = 52.5, 33.6, 10.7 Hz), 34.35, 33.39 (q, *J* = 34.6 Hz), 30.42, 29.54, 28.16, 24.09, 19.35 (d, *J* = 35.2 Hz), 18.25 (d, *J* = 35.0 Hz). ESI-HRMS (*m/z*): $[M+Na]^+$ calc'd for $C_{14}{}^{13}C_5H_{26}N_3{}^{15}NO_6$: 435.1888, found: 435.1888.

7.9.2.5. 5-(4-(2-(2-(2-(2-(2-(N-biotinyl)aminoethoxy)ethoxy)ethoxy)ethylamino) carbonyl-1-(N-propargyl-L-valinamido)butylidine)-1,3-dimethylpyrimidine-2,4,6-trione (Biotin-Dmpt-Val0-Alk, 1).

GA-Dmpt-Val0-Alk **7** (50.0 mg, 0.123 mmol) was dissolved in 2 mL DMF. DIEA (42.9 µL, 2 eq) and HATU (56.1 mg, 1.2 eq) were then added sequentially. The reaction was stirred for 5 min at RT, after which biotin-PEG$_4$-amine (BroadPharm, 250 mg/mL in DMF, 250 µL, 1.1 eq) was added by syringe. The mixture was then stirred at RT for 1 h and then concentrated. The residue was redissolved in EtOAc and extracted with 1 M $KHSO_4$ and brine. The organic layer was dried over Na_2SO_4, filtered, and concentrated. The product was then purified by flash silica column chromatography (9:1 CH_2Cl_2/MeOH) to afford an off-white solid (43.2 mg, 41% yield). ^{1}H NMR (400 MHz, DMSO-*d*$_6$): δ 12.74 (d, *J* = 8.8 Hz, 1H, N*H*), 8.79 (t, *J* = 5.5 Hz, 1H, N*H*), 8.03 (t, *J* = 5.6 Hz, 1H, N*H*), 7.84 (t, *J* = 5.6 Hz, 1H, N*H*), 6.43 (s, 1H, N*H*), 6.37 (s, 1H, N*H*), 4.38 (dd, *J* = 8.9, 6.2 Hz, 1H, Val-C$_\alpha$*H*), 4.30 (dd, *J* = 7.8, 5.0 Hz, 1H, biotin-C*H*), 4.12 (ddd, *J* = 7.4, 4.5, 1.8 Hz, 1H, biotin-C*H*), 3.91 (qdd, *J* = 17.4, 5.4, 2.5 Hz, 2H, NC*H*$_2$), 3.53 – 3.47 (m, 11H, NC*H*$_3$, biotin-C*H*, OC*H*$_2$), 3.40 (dt, *J* = 12.3, 5.9 Hz, 4H, OC*H*$_2$), 3.28 – 3.04 (m, 12H, OC*H*$_2$, NC*H*$_2$), 3.03 – 2.90 (m, 2H, C*H*$_2$), 2.81 (dd, *J* = 12.4, 5.0 Hz, 1H, biotin-C*H*), 2.57 (d, *J* = 12.4 Hz, 1H, biotin-C*H*), 2.25 (t, *J* = 7.4 Hz, 2H, C*H*$_2$), 2.16 (h, *J* = 6.7 Hz, 1H, Val-C*H*), 2.06 (t, *J* = 7.4

Hz, 2H, biotin-CH_2), 1.86 (bs, 1H, ≡C*H*), 1.73 – 1.53 (m, 3H, CH_2, biotin-CH_2), 1.56 – 1.38 (m, 3H, biotin-CH_2), 1.35 – 1.20 (m, 2H, biotin-CH_2), 0.94 (d, *J* = 6.7 Hz, 6H, Val-CH_3). ^{13}C NMR (101 MHz, DMSO-d_6): δ 175.80, 172.13, 171.68, 168.77, 162.73, 150.57, 89.15, 80.49, 73.31, 69.80, 69.73, 69.58, 69.18, 69.11, 61.28, 61.05, 59.21, 55.46, 39.88, 38.59, 38.45, 35.11, 34.84, 31.55, 28.89, 28.22, 28.13, 28.06, 27.56, 25.29, 23.41, 18.69, 17.80. ESI-HRMS (*m/z*): $[M+Na]^+$ calc'd for $C_{39}H_{62}N_8O_{11}S$: 873.4156, found: 873.4185.

7.9.2.6. 5-(4-(2-(2-(2-(2-(2-(N-biotinyl)aminoethoxy)ethoxy)ethoxy)ethylamino) carbonyl-1-(N-propargyl-L-valinamido)butylidine)-1,3-dimethylpyrimidine-2,4,6-trione-13C5,15N (Biotin-Dmpt-Val6-Alk, 2).

Synthesized as described above (50% yield). ^{1}H NMR (400 MHz, DMSO-d_6): δ 12.85 (d, *J* = 8.5 Hz, 0.5H, ^{15}N*H*), 12.63 (d, *J* = 8.4 Hz, 0.5H, ^{15}N*H*), 8.82 (q, *J* = 5.2 Hz, 1H, N*H*), 8.04 (t, *J* = 5.5 Hz, 1H, N*H*), 7.85 (t, *J* = 5.6 Hz, 1H, N*H*), 6.44 (s, 1H, N*H*), 6.38 (s, 1H, N*H*), 4.57 (bs, 0.5H, Val-$^{13}C_\alpha$*H*), 4.30 (dd, *J* = 7.8, 5.0 Hz, 1H, biotin-C*H*), 4.22 (bs, 0.5H, Val-$^{13}C_\alpha$*H*), 4.16 – 4.08 (m, 1H, biotin-C*H*), 3.91 (qdt, *J* = 17.5, 5.6, 3.0 Hz, 2H, NCH_2), 3.56 – 3.44 (s, 11H, NCH_3, biotin-C*H*, OCH_2), 3.40 (dt, *J* = 12.3, 5.9 Hz, 4H, OCH_2), 3.28 – 3.04 (m, 12H, OCH_2, NCH_2), 3.02 – 2.91 (m, 2H, CH_2), 2.81 (dd, *J* = 12.4, 5.0 Hz, 1H, biotin-C*H*), 2.57 (d, *J* = 12.4 Hz, 1H, biotin-C*H*), 2.33 (bs, 0.5H, Val-^{13}C*H*), 2.25 (t, *J* = 7.4 Hz, 2H, CH_2), 2.06 (t, *J* = 7.4 Hz, 2H, biotin-CH_2), 1.99 (bs, 0.5H, Val-^{13}C*H*), 1.87 (bs, 1H, ≡C*H*), 1.74 – 1.53 (m, 3H, CH_2, biotin-CH_2), 1.56 – 1.39 (m, 3H, biotin-CH_2), 1.38 – 1.19 (m, 2H, biotin-CH_2), 1.09 (t, *J* = 5.3 Hz, Val-^{13}CH_3), 0.78 (t, *J* = 5.2 Hz, Val-^{13}CH_3). ^{13}C NMR (101 MHz, DMSO-d_6): δ 175.85, 175.71, 172.15, 171.71, 168.79 (d, *J* = 52.1 Hz), 162.76, 150.57, 89.14, 80.50, 73.29, 69.81, 69.74, 69.59, 69.19, 69.11, 61.23 (ddd, *J* = 52.3, 33.9, 10.5 Hz), 59.23, 55.46, 39.89, 38.59, 38.46, 35.11, 34.88, 31.55 (q, *J* =

34.7 Hz), 28.91, 28.23, 28.12, 28.07, 27.56, 25.30, 23.45, 18.67 (d, *J* = 34.8 Hz), 17.82 (d, *J* = 35.1 Hz). ESI-HRMS (*m/z*): $[M+Na]^+$ calc'd for $C_{34}{}^{13}C_5H_{62}N_7{}^{15}NO_{11}S$: 879.4295, found: 879.4297.

7.9.3. Cell Culture.

The parental HEK-293T and HepG2 cell lines were obtained from American Type Culture Collection (Manassas, VA). Both cell lines were cultured in DMEM supplemented with high glucose, GlutaMAX, 10% fetal bovine serum (PBS), and 1x penicillin–streptomycin (P/S) (complete DMEM). HepG2 cells were maintained on plates coated with 0.1% (w/v) collagen (C8919, Sigma-Aldrich).

7.9.4. Chemoenzymatic Labeling and Enrichment of O-GlcNAcylated Proteins from 293T Cells.

Protein lysate (5 mg) was diluted with 1% SDS, 20 mM HEPES pH 7.6 to 2.5 mg/mL. Samples were reduced using 10 mM TCEP-HCl pH 7.6 for 10 min at RT and alkylated with 30 mM iodoacetamide for 30 min at RT protected from light. Four volumes (~10 mL) of -20 °C acetone was added, and the sample was vortexed and incubated at -20 °C for 2 h. The precipitated protein was pelleted by centrifugation at 5,000 x g for 10 min at 4 °C. Acetone was removed, and the pellet was allowed to air dry. Dried protein was then redissolved at 5 mg/mL with 1 mL of 1% SDS, 20 mM HEPES pH 7.9 using probe sonication. Samples were then diluted with 2 mL of 2.5x GalT labeling buffer (50 mM HEPES pH 7.9, 125 mM NaCl, 5% IGEPAL CA-630), 1.2 mL of ddH2O, and 275 µL of 100 mM MnCl2. The mixture was chilled on ice for 5 min, and then 250 µL of 0.1 mM UDP-GalNAz, 250 µL of 2 mg/mL Y289L GalT, and 25 µL of 500 kU/mL PNGase F (New England Biolabs) were added with gentle mixing after each addition. Sample was rotated end-over-end overnight at 4 °C. The following day, 10 µL of 10 kU/mL calf intestinal phosphatase

was added to the sample with incubation for 3 h at 37 °C. Samples were then acetone precipitated as described above. The protein pellet was redissolved at 5 mg/mL in 1 mL of 1% SDS, 20 mM HEPES pH 7.6. The solution was diluted with 2.85 mL of ddH2O and 0.15 mL of 200 mM HEPES pH 7.6. In a separate tube, a 5x CuAAC mix was prepared by sequential addition of 785 µL of ddH2O, 10 µL of 50 mM biotin-Dmpt-Val0/6-alkyne in DMSO, 5 µL of 100 mM BTTAA (Click Chemistry Tools, Scottsdale, AZ) in DMSO, 100 µL of 50 mM CuSO4 (freshly prepared), and 100 µL of 100 mM sodium ascorbate (freshly prepared). The 5x mix was then added directly to the protein sample and mixed end-over-end for 1 h at RT followed by acetone precipitation. The protein, mixed in equal (w/w) proportions as described in the next was resuspended at 5 mg/mL in 2 mL of 5% sodium deoxycholate, 50 mM HEPES pH 7.6, 10 mM EDTA to chelate residual Cu2+ and diluted with 8 mL of 50 mM HEPES pH 7.6. Then, 20 µL of 1 M CaCl2 and 200 µg Pierce trypsin protease (1:50 w/w) was added, and the sample was rotated end-over-end overnight at 37 °C. Two 15-mL 10 kDa MWCO Amicon concentrator tubes were rinsed with 2 x 5 mL of 50% MeOH and 2 x 5 mL of ddH2O by centrifugation at 4,000 x g for 5 min. Tryptic solutions were then centrifuged in the rinsed concentrator tubes at 4,000 x g for 20 min. The remaining residue was rinsed 2 x 2.5 mL of H2O by centrifugation, and the flowthrough fractions were combined. The sample was diluted two-fold with ddH2O. In a separate tube, 250 µL of a 50% slurry of high capacity Neutravidin agarose (ThermoFisher Scientific) was washed 2 x 5 min with 0.5 mL of 50% MeOH and 2 x 5 min with 0.5 mL of ddH2O. The agarose resin was then added to the sample and rotated end-over-end for 1 h at RT. The resin was pelleted by centrifugation at 500 x g for 5 min and then transferred to a 900 µL spin filter (ThermoFisher Scientific) pre-rinsed twice with 50% MeOH and 50% ddH2O. Beads were washed 5 min each with the following solutions: 5 x 0.5 mL of 20 mM HEPES pH 7.6, 5 x 0.5 mL of 2 M NaCl, 3 x 0.5 mL of ddH2O, 3 x 0.5 mL of

50% MeOH, 2 x 0.5 mL of ddH2O. Captured peptides were eluted in twice with 0.5 mL of 2% v/v NH2OH with end-over-end rotation for 1 h at RT. Elution fractions were combined and concentrated to dryness with vacuum centrifugation. The eluted peptides were redissolved in 20 μL of 0.2% formic acid and desalted with a C18 ZipTip pipette tip.

7.9.5. Liver Lysate Preparation.

WT (C57BLKS/J, #000662) and db/db (BKS.Cg-Dock7^{m} +/+ Lepr^{db}/J, # 000642) mouse livers (n=4 each) harvested from 8 week old mice were ordered from The Jackson Laboratory (Bar Harbor, ME) and immediately transferred to LN_2 upon receipt. A single lobe from each liver was used for analysis. Each lobe was first washed with ice cold PBS, pH 7.4 and rapidly lysed in 2% sodium deoxycholate (SDC) in 100 mM Triethylammonium bicarbonate buffer (TEAB) pH 8.5 containing Roche cOmplete protease inhibitor cocktail and 0.1 mM TMG using a dounce homogenizer. The resulting lysate was then centrifuged at 21,130 x g to pellet debris and the oily supernatant removed before transferring to a new tube. Protein concentration was determined by BCA assay.

7.9.6. Chemoenzymatic Labeling and Enrichment of O-GlcNAcylated Proteins from Mouse Livers.

Liver protein lysate (5 mg) was diluted to 2 mg/ml in 1% SDS in 20 mM HEPES before being subjected to chemoenzymatic labeling as described above, with the WT liver lysate being labeled with biotin-Dmpt-Val0 alkyne and db/db liver lysate being labeled with biotin-Dmpt-Val6-alkyne.

7.9.7. Preparation of Peptides for Quantitative Proteomics.

A 100 μg aliquot was removed from each liver lobe lysate prepared as described above and diluted to 0.5% SDC concentration in ice cold H_2O containing protease inhibitors and 0.1 mg/ml TMG as described ablve. 0.25 U/μL of benzonase nuclease (Santa Cruz Biotechnology, Dallas, TX) was then added and the samples were left to rotate end-over-end for 30 minutes at 4 °C. 2 μg of Pierce MS Grade Trypsin Protease (ThermoFisher Scientific) (1:50 w/w enzyme:protein) was then added, and the samples were then left to digest for 20 hours at 37 °C. The following day, detergent was removed by acid precipitation (final concentration 5% formic acid) and phase transfer as previously described.[31] Peptides were then dried by vacuum centrifugation, reconsitituted in 100 μL of 100 mM TEAB and labeled with the TMT10plex Isobaric Labeling Kit (ThermoFisher Scientific) per the manufacturer's instructions. After labeling, peptides from all groups were combined and dried in a vacuum centrifuge.

7.9.8. HpHRP Fractionation of Peptides.

Both O-GlcNAcylated peptides (half of each sample was fractionated) and those for quantitative proteomics were reconstituted in 100 μL of 10 mM ammonium hydroxide and fractionated on an Agilent (Santa Clara, CA) 1200 series HPLC system. Peptides were separated at a flow rate of 200 nL/min on an XBridge BEH C18 2.1 x 100mm (5μm) column (Waters, Milford, MA). Buffer A consisted of 10 mM ammonium hydroxide and buffer B consisted of 90:10 acetonitrile:10 mM ammonium hydroxide. The gradient was as follows: 1% Solvent B (4 min), 1-30% B (50 min), 30-60% B (4 min), 60-70% B (2 min), and 70-90% B (5 min). 64 1 min fractions were collected into 96 deep-well plates. For quantitative proteomics fractions were concatenated into 16 fractions; for O-GlcNAcomics samples were concatenated into either 4 or 6 fractions.

Concatenated fractions were then acidified to 1% formic acid and 0.1% TFA and partially dried by vacuum centrifugation to remove acetonitrile. Fractions were then desalted using an Oasis HLB μElution plate (Waters Milford, MA) following the manufacturer's instructions. Desalted samples were then partially dried by vacuum centrifugation to remove acetonitrile reconstituted to 10 μL in 0.1% formic acid for MS analysis.

7.9.9. Microscale HpHRP Fractionation of O-GlcNAcylated Peptides.

For the second enrichment replicate, two of the liver pairs were subjected to microscale HpHPR fractionation using spin columns as previously described.[14] Briefly, spin columns were prepared by adding Jupiter C18 slurry (5 μm, Phenomenex, Torrance, CA) to fritted spin columns (ThermoFisher Scientific). Peptides, reconstituted in 100 μL of 10 mM ammonium hydroxide, were loaded onto the column, washed three times with 100 μL 10 mM ammonium hydroxide, and eluted with 7 fractions of 100 μL portions of 5%, 10%, 15%, 20%, 25%, 30%, and 90% acetonitrile in 100 mM NH4HCO3 pH 8.0. Each fraction was then dried by vacuum centrifugation and resuspended in 10 μL of 0.1% formic acid for MS analysis.

7.9.10. MS Analysis for Protein Expression Profiling.

2 μL of each fraction was loaded onto a 360x100 μm precolumn prior (2cm Monitor C18, Waters) to separation on a 360x75μm column/tip (9cm BEH 1.7 μm, Waters) at 1μL/min at 600 bar constant pressure for 15 μL. The column was heated to 60 °C. The peptides were separated with a 180 min gradient at a flow rate of 250 nL/min. Solvent A consisted of 99.9% water and 0.1% formic acid and Solvent B consisted of 80% acetonitrile, 19.9% water, and 0.1% formic acid. The gradient was as follows: 2% Solvent B (10 min), 2-25% B (120 min), 25-40% B (30 min), 40-

95% B (2 min), and 95% B (18 min). Full spectra were acquired over *m/z* 350-1500 in the Orbitrap (70 K resolution at 200 *m/z*); automatic gain control (AGC) was set to accumulate 1,000,000 ions, with a maximum injection time of 100 ms. Data-dependent MS2 analysis was performed as described previously[32] using a top 12 approach with HCD fragmentation with 32% normalized collision energy at 35 K resolution, an intensity threshold of 100,000 ions, a max injection time of 120 ms, and an isolation window of 1.2 *m/z*.

7.9.11. MS Analysis for O-GlcNAcomics Samples.

7.9.11.1. Valine Linker Optimization Experiments.

Samples enriched using the biotin-Dmpt-Val0/6-alkyne linker were analyzed on a nanoflow LC system, EASY-nLC 1000 (ThermoFisher Scientific), coupled to an Orbitrap Fusion Tribrid mass spectrometer (ThermoFisher Scientific) equipped with a Nanospray Flex ion source. O-GlcNAcylated peptides enriched from each of the ratio pairs (2.5 mg total for each pair) were resuspended in 5 µL of 0.2% formic acid and 2 µL was directly loaded onto a PicoFrit column (New Objective, Woburn, MA) packed in house with ReproSil-Pur C18AQ 1.9 µm resin (120 Å pore size, Dr. Maisch, Ammerbuch, Germany). The 20 cm x 50 µm ID column was heated to 60 °C. The peptides were separated with a 120-min gradient at a flow rate of 220 nL/min. The gradient was as follows: 2-6% Solvent B (7.5 min), 6-25% B (82.5 min), and 25-40% B (30 min) and to 100% B (9 min). Solvent A and B were the same as described above. Full spectra were acquired over *m/z* 350-1800 in the Orbitrap (120 K resolution at 200 *m/z*); automatic gain control (AGC) was set to accumulate 50,000 ions, with a maximum injection time of 50 ms. Data-dependent MS2 analysis was then performed in which features were filtered for monoisotopic peaks with a charge

state of 3-8 and a minimum intensity of 25,000, with dynamic exclusion set to exclude features after 1 time for 15 seconds with a 10 ppm mass tolerance and exclude isotopes turned on using a top-speed approach (cycle time of 5 s). The HCD product ion triggered method decision tree method described in **Chapter 6** was employed. Briefly, the normalized collision energy was optimized at 28% for high collision dissociation (HCD) fragmentation. The intensity threshold for fragmentation was set to 25,000. HCD fragmentation spectra was collected in Orbitrap operating at 30K resolution at 200 *m/z* separately for precursors 350 – 625 *m/z* and 625 – 1800 *m/z*. The presence of the 300.1 *m/z* product ion was then used to trigger ETD (350 – 625 *m/z*) or EThcD (625 – 1800 *m/z*) using charge dependent ETD reaction times (with the instrument default 2τ time constant). AGC was set to 50,000 with a maximum injection time set at 500 ms and the spectra were acquired in the Orbitrap operating at 30K resolution. CD ETD reaction times were used.

7.9.11.2. Mouse Liver Experiments.

Chemoenzymatically labeled and enriched samples were analyzed on a nanoflow LC system, EASY-nLC 1000 (ThermoFisher Scientific), coupled to an Orbitrap Fusion Lumos mass spectrometer equipped with a Nanospray Flex ion source. 4 μL of the unfractionated or 4 μL of each O-GlcANc peptide fraction was used for analysis. In both cases the samples were loaded onto a 360x75μm column/tip packed in house with ReproSil-Pur C18AQ 1.9 μm resin (120 Å pore size, Dr. Maisch, Ammerbuch, Germany) at 1μL/min at 600 bar constant pressure for 15 μL. The column was heated to 60 °C. The peptides were separated with a 135-min gradient at a flow rate of 300 nL/min. Solvent A consisted of 99.9% water and 0.1% formic acid and Solvent B consisted of 80% acetonitrile, 19.9% water, and 0.1% formic acid. The gradient was as follows: 2-32% Solvent B (120 min), 32-63% B (10 min), 63-100%B (2 min), and 100% B (3 min) Full spectra

were acquired over *m/z* 350-1800 in the Orbitrap (120 K resolution at 200 *m/z*); automatic gain control (AGC) was set to accumulate 50,000 ions, with a maximum injection time of 50 ms. Data-dependent MS2 analysis was performed using a top-speed approach (cycle time of 5 s) as described above for HCD product ion triggered EThcD analyses. For the decision tree analyses, the HCD scans were performed separately for precursors 350 – 625 *m/z* and 625 – 1800 *m/z*. The presence of the 300.1 *m/z* product ion was then used to trigger ETD (350 – 625 *m/z*) or EThcD (625 – 1800 *m/z*) using CD ETD reaction times.

7.9.12. Data Analysis.

7.9.12.1. Quantitative Proteomics Data Analysis.

Raw files were searched using MaxQuant version 1.6.14 against the mouse UniProt database downloaded on May 20, 2020 as well as a contaminant database (245 sequences). All fractions were searched together with the match between runs and dependent peptides option checked. MS2 reporter ion quantification was employed with TMT-labeled (**Fig. 7.5**) K and N-termini were specified. A co-isolation threshold of 25% (maximum) was set for quantification. The enzyme digestion parameters were set to trypsin with up to three missed cleavages. N-terminal acetylation, methionine oxidations, and phosphorylation (STY) were included as variable modifications in the search. Carbamidomethylation of cysteine was specified as a fixed modification. A 1% false discovery rate threshold was specified at the peptide and protein level. All other parameters were left as specified in the default configuration. Ratios from proteins only identified by modified peptides were excluded. Protein expression ratios were then calculated as outlined in **A7.5.2**.

7.9.12.2. Quantitative O-GlcNAcomics Data Analysis.

All raw files were searched using MaxQuant version 1.6.1.0 against the mouse UniProt database downloaded on May 20, 2020. Two searches were performed. Unless otherwise mentioned, parameters were left at their default values.

The first (quantification search) was performed with the enzyme digestion parameters were set to trypsin with 0 missed cleavages. No variable modifications were specified. Carbamidomethylation of cysteine was specified as a fixed modification. A 1% false discovery rate threshold was specified at the peptide and protein level. Standard type quantification with a multiplicity of 2 was selected with no light labels, and a +6 (15C5, 15N1) heavy label on the pyrrolysine. A maximum of 5 labeled amino acids was specified. The match between runs (including matching of unidentified features), dependent peptides, and re-quantify options were checked. Importantly, O-GlcNAcylated peptides should not be matched in this search, but rather isotope pairs are quantified and reported in the allPeptides file.

The second search (site mapping search) was performed with the enzyme digestion parameters were set to trypsin with 3 missed cleavages. N-terminal acetylation, methionine oxidations, and Val0/6 labeled GlcNAc (+601.27076 and + 607.28456, respectively) were included as variable modifications in the search. Carbamidomethylation of cysteine was specified as a fixed modification. A 1% false discovery rate threshold was specified at the peptide and protein level with a minimum score and delta score threshold for modified peptides set to 25 and 3, respectively.[33]This search identifies the O-GlcNAcylated peptides and their sites.

MS/MS scans were then registered between the two searches to match O-GlcNAcylated peptides identified in the first search to quantified isotope patterns identified in the second search as described in **A7.5.1** and **A7.5.3**.

7.9.12.3. General and Statistics.

All data analysis was performed using the Python language (Python Software Foundation. Python Language Reference, version 3.7.3. Available at http://www.python.org) with all Anaconda packages installed (Anaconda Software Distribution, version 4.8.3. Available at https://anaconda.com). For the limma moderated t-test[91] (package, limma v3.42.2the R language (R Development Core Team, version 3.6.1. Available at https://www.R-project.org) was employed using the rpy2 (Laurent Gautier, v2.9.4) python package. Multiple hypothesis testing correction was performed with either the Benjamini-Hochberg method. A p-value of less than 0.05 was considered significant. The PPI networks were constructed as outlined in **A5.6.3**. Code for all analyses and figures is in **Appendix 7.5**.

7.9.13. Construction of OGA Mutants.

Myc-DDK-tagged OGA (NM_023799) was purchased from Origene (Rockville, MD). All point mutations were produced using the Q5 Site-Directed Mutagenesis Kit (NEB) according to the manufacturer's protocols. All primers were designed with the NEBaseChanger software. The final plasmids were purified using ZymoPURE II Plasmid Kit (Zymo Research, Irvine, CA), sequenced (Laragen, Culver City, CA), and resolved by 1% agarose gel electrophoresis to ensure fidelity. Plasmids were transfected into HepG2 cells using (1 μg per well of a 12-well plate) Lipofectamine 3000 (ThermoFisher Scientific) according to the manufacturer's protocols.

7.9.14. Western Blotting.

Samples were diluted with 4x SDS-PAGE buffer (200 mM Tris-HCl pH 6.8, 400 mM DTT, 8% SDS, 0.4% bromophenol blue, 40% glycerol), resolved on a NuPAGE 4-12% Bis-Tris protein gel (ThermoFisher Scientific), and transferred to Immobilion-FL PVDF membrane (MilliporeSigma, Burlington, MA). Blots were blocked for 1 h at RT with LiCor Odyssey Blocking Buffer (927-50003, LI-COR Biosciences, Lincoln NE) before probing overnight at 4 °C with FLAG (1:5000, F3165, Sigma-Aldrich) antibody. Blots were rinsed three times with TBST and then probed with the appropriate secondary antibodies in blocking buffer: anti-mouse AlexaFluor 680 conjugate (A21057, ThermoFisher), or anti-mouse IgG DyLight 800 (A11357, ThermoFisher). Blots were washed 3 x 5 min with TBST and then imaged using an Odyssey Infrared Imaging System (LI-COR Biosciences). Images were processed using ImageStudio v5.2 (LI-COR Biosciences).

7.9.15. Chemoenzymatic Labeling with High MW PEG.

HepG2 cells expressing WT or mutant OGA were lysed in 2% SDS in HEPES pH 7.9 containing Roche cOmplete protease inhibitor cocktail and 0.1 mM TMG. 150 μg of lysate from each condition was then subjected to chemoenzymatic labeling as previously described.[34] Briefly, lysate containing 150 μg of protein was diluted to 200 μL in water, and proteins were precipitated by the addition of 3 volumes of methanol, 1 volume of chloroform, and 2.25 volumes of water followed by centrifugation at 21,130 x g for 5 minutes to reveal a disc-like protein pellet at the aqueous-organic interface. The aqueous layer was removed and pellet washed three times with 2.25 volumes of methanol. Protein pellets were then resolubilized with 40 μL dissolution buffer (20 mM HEPES, 1% SDS, pH 7.9). Water (49 μL), 5.5 mM MnCl (11 μL), and 80 μL 2.5x GalT

labeling buffer (50 mM HEPES, 125 mM NaCl, 5% IGEPAL CA-630, pH 7.9) were added and the solution was vortexed gently before adding 10 μL Y289L GalT (1 mg/mL), and 10 μL of UDP-GalNAz (0.5 mM in 10 mM HEPES, pH 7.9). The reaction was then left to rotate end-over-end at 4 °C overnight. The following day, IAA was added to 12.5 mM final concentration to alkylate free cysteine residues, and the samples left to rotate end-over-end in the dark for 45 minutes. Proteins were then precipitated as before and redissolved in 180 μL of 1% SDS in TBS.[35] 20 μL of 10 mM DBCO-mPEG (A118, Click Chemistry Tools, Scottsdale, Arizona) was then added to the samples before vortexing briefly and incubating at 95 °C for 5 min. Proteins were then precipitated as described, except they were washed 5 times with 3 volumes of methanol. Pellets were then redissolved by boiling in 90 μL of 1 % SDS in TBS before analysis by WB as described above.

7.10. References.

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Appendix 7.1. O-GlcNAcylation Sites and Regions Identified in db/db and WT Mouse Livers.

A7.1.1. GlcNAc Sites Identified with the Val0 Tag in WT Mouse Livers.

Protein	Min Sites	Site ID Constraints
A0A087WNV1	1	(1 of 267,269,270,272)
A0A087WNV1	1	260
A0A087WNV1	1	262
A0A087WNV1	1	327
A0A087WNV1	1	251
A0A087WNV1	1	319
A0A087WP65	1	90
A0A087WQ86	1	2161
A0A087WQH5	1	579
A0A087WQN7	1	1328
A0A087WQN7	1	1332
A0A087WRQ4	1	50
A0A087WRU0	1	953
A0A0A0MQ73	1	(1 of 2362,2366)
A0A0A0MQ73	1	2359
A0A0A0MQ98	1	1431
A0A0A0MQ98	1	1492
A0A0A0MQ98	1	2047
A0A0A0MQB4	1	360
A0A0A0MQJ4	1	(1 of 211,214,217,218,219)
A0A0A0MQJ4	1	(1 of 165,166,168,170,171,172)&(1 of 172,174)
A0A0A0MQJ4	1	163
A0A0A0MQJ4	1	167
A0A0A0MQJ4	1	204
A0A0A0MQJ4	1	175
A0A0A0MQJ4	1	159
A0A0A6YVU8	1	(1 of 217,219)
A0A0A6YVU8	1	213
A0A0A6YVU8	1	220
A0A0A6YVU8	1	221
A0A0A6YVZ3	1	(1 of 130,131,133,134)&(1 of 129,130,131,133)
A0A0A6YVZ3	1	(1 of 120,122,123,124,126)
A0A0A6YWM5	1	600
A0A0A6YXS8	1	65
A0A0B4J1G5	1	(1 of 283,285,286)

A0A0G2JDK2	1	290
A0A0G2JDK2	1	291
A0A0G2JDK2	1	71
A0A0G2JDL6	1	75
A0A0G2JDL6	1	76
A0A0G2JDV2	1	663
A0A0G2JEI9	1	85
A0A0G2JF07	1	104
A0A0G2JF07	1	108
A0A0G2JFW6	1	(1 of 912,913)
A0A0G2JFW6	1	359
A0A0G2JFW6	1	525
A0A0G2JFW6	1	334
A0A0G2JFW6	1	533
A0A0G2JFW6	1	409
A0A0G2JFW6	1	346
A0A0G2JFW6	1	540
A0A0G2JFW6	1	927
A0A0G2JGL7	1	(1 of 19,21)
A0A0G2JGT1	1	(1 of 146,148,154,155,157)
A0A0J9YU61	1	(1 of 440,441)
A0A0J9YU61	1	706
A0A0J9YU61	1	446
A0A0J9YUF9	1	(1 of 145,148)
A0A0J9YUF9	1	151
A0A0J9YV30	1	116
A0A0N4SUS4	1	1064
A0A0N4SUV0	1	274
A0A0N4SV80	1	1369
A0A0N4SV80	1	1370
A0A0R4J032	1	(1 of 275,278)
A0A0R4J079	1	(1 of 317,318)
A0A0R4J0D3	1	637
A0A0R4J0I1	1	184
A0A0R4J0I9	1	(1 of 726,732)
A0A0R4J0I9	1	3784
A0A0R4J0I9	1	4363
A0A0R4J0I9	1	3788
A0A0R4J0I9	1	4078
A0A0R4J0I9	1	4367
A0A0R4J0I9	1	2130
A0A0R4J0I9	1	2617
A0A0R4J0M5	1	201
A0A0R4J0M9	1	1072
A0A0R4J0M9	1	1075

A0A0R4J0X5	1	(1 of 90,92)
A0A0R4J0X5	1	103
A0A0R4J131	1	138
A0A0R4J1H6	1	167
A0A0R4J1T3	1	(1 of 547,551)
A0A0R4J2B5	1	348
A0A0U1RNH9	1	251
A0A0U1RQB6	1	138
A0A0U1RQB6	1	147
A0A140LHQ8	1	(1 of 343,344)
A0A140LHQ8	1	(1 of 327,328)
A0A140LHQ8	1	337
A0A140LHQ8	1	444
A0A140LHQ8	1	181
A0A140LHR4	1	120
A0A140LHR4	1	116
A0A140LIZ8	1	142
A0A140T8T5	1	70
A0A1B0GR76	1	(1 of 1435,1437)
A0A1B0GR76	1	1204
A0A1B0GR78	1	170
A0A1B0GR78	1	172
A0A1B0GR85	1	(1 of 1083,1084)
A0A1B0GR85	1	1085
A0A1B0GRB5	1	551
A0A1B0GRJ0	1	1020
A0A1B0GRV3	1	248
A0A1B0GSG3	1	270
A0A1B0GSN3	1	(1 of 20,21)
A0A1B0GSY0	1	(1 of 525,526)
A0A1B0GSY0	1	523
A0A1B0GT43	1	108
A0A1C7ZMY3	1	1071
A0A1D5RLU0	1	(1 of 107,108)
A0A1D5RML9	1	510
A0A1I7Q4G8	1	(1 of 179,181)
A0A1I7Q4G8	1	(1 of 182,184,185)
A0A1I7Q4G8	1	(1 of 67,69)
A0A1I7Q4G8	1	(1 of 61,62)
A0A1I7Q4G8	1	328
A0A1I7Q4G8	1	178
A0A1I7Q4G8	1	206
A0A1I7Q4G8	1	606
A0A1L1SUN4	1	4
A0A1L1SUR6	1	531

A0A1L1SV73	1	(1 of 87,88)
A0A1N9M4K1	1	285
A0A1N9M4K1	1	357
A0A1N9M4K1	1	286
A0A1N9PTV1	1	246
A0A1W2P7D7	1	152
A0A1W2P7D7	1	153
A0A1W2P7G2	1	103
A0A1W2P7I2	1	(1 of 183,185)
A0A1W2P7I2	1	128
A0A1W2P7Q7	1	134
A0A1Y7VJM4	1	123
A0A1Y7VJM4	1	141
A0A1Y7VK55	1	297
A0A1Y7VLT3	1	82
A0A1Y7VMI0	1	185
A0A1Y7VMT6	1	(1 of 19,20)
A0A1Y7VP49	1	79
A0A2I3BPN6	1	486
A0A2I3BQ92	1	67
A0A2I3BQE0	1	(1 of 327,328,329,331,334)
A0A2I3BQE1	1	143
A0A2I3BRS9	1	23
A0A2R8VHH9	1	203
A0A2R8VHQ0	1	1000
A0A2R8VHQ0	1	891
A0A2R8VHW4	1	161
A0A338P6J9	1	72
A0A338P6J9	1	74
A0A338P6J9	1	75
A0A338P6J9	1	79
A0A338P6J9	1	85
A0A338P6K9	1	163
A0A338P6K9	1	1067
A0A338P6K9	1	45
A0A338P6K9	1	303
A0A338P6K9	1	63
A0A338P771	2	(2 of 358,359,361,362,363)
A0A3B2W7J8	1	785
A0A3B2WBH9	1	(1 of 994,999)
A0A3B2WBH9	1	451
A0A3B2WCD8	1	96
A0A3B2WCD8	1	145
A0A3B2WCD8	1	192
A0A3Q4L2X0	1	(1 of 2,3)

A0A3Q4L2X0	1	6
A0A494B962	1	37
A0A494B968	1	33
A0A494B9T4	1	(1 of 36,37,42,43,46,47)
A0A494BAF3	1	378
A0A494BB11	1	262
A0A571BEI2	1	487
A0A571BFA7	1	(1 of 949,950,951,952,954)
A0A5F8MPU2	1	668
A0A5F8MPU2	1	805
A0A5F8MPU2	1	807
A0A5F8MPY2	1	64
A0A5F8MPY2	1	74
A0A5F8MPY2	1	79
A0JNY3	1	296
A0JNY3	1	301
A2A5Y4	1	(1 of 822,823,824,825)
A2A5Y4	1	832
A2AC24	1	145
A2AC24	1	140
A2ADB1	1	(1 of 2486,2487,2489)
A2ADB1	1	2496
A2ADB1	1	2499
A2ADB1	1	2504
A2ADB1	1	2505
A2ADB1	1	2762
A2AEW0	1	(1 of 510,515,516,518,522)
A2AFQ0	1	(1 of 2620,2633,2634,2636,2637,2641,2643,2644,2647,2650)
A2AFQ0	1	3796
A2AFQ0	1	2924
A2AGG1	1	244
A2AGJ9	1	55
A2AH22	1	(1 of 441,442)
A2AKB9	1	(1 of 356,357,358,361,362,363)&(1 of 354,355,356,357)
A2AKB9	1	364
A2AKB9	1	365
A2AKI5	1	(1 of 829,835)
A2AKJ2	1	33
A2AKJ2	1	34
A2AMY5	1	(1 of 657,658)
A2AMY5	1	(1 of 1028,1030)
A2AMY5	1	641
A2AMY5	1	1001
A2AMY5	1	1107
A2AMY5	1	468

A2AMY5	1	660
A2AMY5	1	1019
A2AP93	1	(1 of 378,382,383)
A2APL5	1	206
A2APT9	1	295
A2AQE9	1	174
A2AQE9	1	167
A2AQW6	1	10
A2ATI9	1	406
A2ATI9	1	397
A2ATI9	1	398
A2ATI9	1	405
A2ATR8	1	245
A2AVJ7	1	111
A2AVP4	1	(1 of 768,769)
A2AVP4	1	895
A2AVR3	1	82
A2AWN8	1	225
A2AWN8	1	223
A2CEK6	1	170
A2RSY1	1	539
A2RSY1	1	534
A6H619	1	1365
A9C497	1	(1 of 170,173)
B1AR09	1	(1 of 399,400,402,403,404,405)&(1 of 398,399)
B1ARU1	1	1680
B1ATR2	1	158
B1ATR2	1	174
B1ATR2	1	175
B1AWT4	1	64
B1AZ15	1	(1 of 819,824,826,827,830)
B1AZ15	1	836
B1AZ15	1	685
B1AZ46	1	512
B1AZA8	1	145
B1B0C7	1	847
B2RQE8	1	709
B2RQG2	1	(1 of 1509,1511,1512,1513)
B2RRC9	1	(1 of 1474,1476)
B2RRC9	1	1309
B2RUJ2	1	1068
B2RUQ2	1	349
B2RUQ2	1	367
B2RXC8	1	462
B7ZC18	1	(1 of 688,690)

B7ZC18	1	691
B7ZC23	1	(1 of 146,147)
B7ZC23	1	140
B7ZC94	1	(1 of 816,817,818,819,820,821)&(1 of 814,816,817)
B7ZN55	1	(1 of 594,596)
B7ZNH7	1	140
B7ZNJ1	1	(1 of 435,436)
B7ZNJ1	1	1000
B7ZNJ1	1	524
B7ZNJ1	1	1008
B7ZNJ1	1	432
B7ZNJ1	1	530
B8JJB2	1	89
B9EJX2	1	(1 of 831,833)
B9EJX2	1	832
C0HKG6	1	218
C0HKG6	1	82
D3YU17	1	430
D3YUC9	1	2
D3YUV1	1	542
D3YUW8	1	(1 of 335,336)
D3YUW8	1	(1 of 253,254)
D3YUW8	1	149
D3YUW8	1	263
D3YVM4	1	169
D3YVM4	1	172
D3YWA4	1	75
D3YXZ5	1	454
D3YY42	1	19
D3YYR9	1	65
D3YYR9	1	55
D3YYY8	1	252
D3YZ00	1	272
D3Z069	1	581
D3Z0Y0	1	185
D3Z0Y0	1	186
D3Z216	1	456
D3Z2E7	1	392
D3Z2E7	1	434
D3Z2L1	1	205
D3Z2T4	1	(1 of 154,155,156)
D3Z2T4	1	146
D3Z3F1	1	(1 of 258,259)
D3Z3F1	1	260
D3Z3F1	1	237

D3Z3F1	1	190
D3Z3F1	1	189
D3Z3F8	1	474
D3Z3F8	1	478
D3Z3Q3	1	698
D3Z3Q3	1	699
D3Z3U7	1	328
D3Z3U7	1	324
D3Z5G4	1	195
D3Z5G4	1	135
D3Z5G4	1	136
D3Z5G4	1	202
D3Z5G4	1	148
D3Z5G4	1	149
D3Z5G4	1	157
D3Z5I1	1	(1 of 467,468,469,477,483)
D3Z5I1	1	(1 of 557,558,559,562,564)
D3Z5I1	1	489
D3Z5I1	1	487
D3Z5I1	1	551
D3Z5I1	1	567
D3Z5I9	1	(1 of 739,740)
D3Z5I9	1	738
D3Z5X0	1	(1 of 41,42)
D3Z656	1	1360
D3Z656	1	1121
D3Z656	1	1374
D3Z665	1	175
D3Z6W7	1	384
D6RDD4	1	58
D6REF0	1	65
D6RGN2	1	60
D6RGR1	1	115
D6RGR1	1	91
D6RHA2	1	(1 of 408,409)
D6RHA2	1	413
D6RJL6	1	40
D6RJL6	1	17
D6RJL6	1	22
E0CXE3	1	673
E0CY18	1	167
E0CY18	1	150
E0CY18	1	159
E0CYH7	1	1055
E0CYN0	1	11

E0CYQ2	1	121
E0CZ61	1	(1 of 38,39,44,49)
E9PUF4	1	667
E9PUM5	1	665
E9PV38	1	478
E9PV38	1	102
E9PV69	1	126
E9PV80	1	895
E9PVA8	1	22
E9PVC6	1	21
E9PVC6	1	1015
E9PWM3	1	595
E9PWW2	1	208
E9PWX8	1	1973
E9PYK3	1	1750
E9PYL2	1	(1 of 652,653)
E9PYX7	1	561
E9PZ00	1	210
E9PZ00	1	330
E9PZ00	1	454
E9PZ00	1	79
E9PZD2	1	384
E9PZD2	1	373
E9PZD2	1	406
E9PZD2	1	439
E9Q113	1	126
E9Q150	1	608
E9Q150	1	613
E9Q1P8	1	(1 of 364,365,366,367)
E9Q1S3	1	183
E9Q284	1	(1 of 7,9)
E9Q286	1	1564
E9Q2M4	1	(1 of 442,443,444)
E9Q2M5	1	624
E9Q2T3	1	320
E9Q3G8	1	(1 of 557,559,561,562,563)&(1 of 554,557,559,561)
E9Q3G8	1	(1 of 1056,1057)
E9Q3G8	1	(1 of 1048,1050,1053)
E9Q3G8	1	705
E9Q3G8	1	200
E9Q3G8	1	1067
E9Q3G8	1	1101
E9Q3G8	1	1102
E9Q3G8	1	1168
E9Q3G8	1	1169

E9Q3G8	1	1044
E9Q3G8	1	1046
E9Q3G8	1	569
E9Q3G8	1	699
E9Q3G8	1	925
E9Q3G8	1	926
E9Q3G8	1	927
E9Q449	1	1346
E9Q481	1	787
E9Q4Q2	1	(1 of 331,332,333,337)
E9Q4Q2	1	328
E9Q5G1	1	(1 of 485,486)
E9Q5Q0	1	(1 of 146,147,150,151,153,154,156)
E9Q5Q0	1	(1 of 564,566)
E9Q5Q0	1	561
E9Q5Q0	1	563
E9Q5Q0	1	567
E9Q616	1	5376
E9Q616	1	787
E9Q616	1	5166
E9Q638	1	(1 of 383,384,386)
E9Q640	1	696
E9Q6A7	1	1635
E9Q6A7	1	1624
E9Q6A7	1	1628
E9Q6A7	1	1629
E9Q6A7	1	1598
E9Q6B8	1	287
E9Q6E2	1	(1 of 345,346)
E9Q6T8	1	697
E9Q6T8	1	126
E9Q6T8	1	127
E9Q7B0	1	112
E9Q7R8	1	14
E9Q8A6	1	45
E9Q8A6	1	43
E9Q8A6	1	53
E9Q8H9	1	(1 of 764,765)
E9Q8H9	1	1024
E9Q8H9	1	993
E9Q8H9	1	1027
E9Q8H9	1	1188
E9Q8H9	1	735
E9QA62	1	(1 of 213,214)
E9QA62	1	206

E9QAF9	1	1666
E9QAN9	1	451
E9QAT4	1	(1 of 130,131,138)
E9QAT4	1	68
E9QAT4	1	69
E9QAT4	1	70
E9QAT4	1	60
E9QAT4	1	127
E9QJU8	1	345
E9QJU8	1	334
E9QKG6	1	(1 of 1421,1423)
E9QKG6	1	1436
E9QL13	1	280
E9QL13	1	244
E9QL13	1	254
E9QLA5	1	(1 of 359,362,364,370,371,372,375,376,377,379,380)
E9QLQ9	1	(1 of 2314,2315)
E9QMU3	1	(1 of 452,453)
E9QMU3	1	(1 of 456,457,463)
E9QN70	1	1091
E9QNG1	1	217
F2Z4B7	1	426
F6QJV5	1	90
F6RDR0	1	70
F6S4K9	1	103
F6S5I0	1	(1 of 25,26,27,28,31,32,34,35,36,37,40)
F6TS96	1	279
F6UTU1	1	(1 of 93,94)
F6V513	1	144
F6V8M6	1	213
F6V8M6	1	141
F6V8M6	1	127
F6VV02	1	36
F6VV02	1	21
F6W4D3	1	228
F6WV21	1	(1 of 822,823,831,832,833,836,837,839)
F6WV21	1	1173
F6Y6L6	1	132
F6YC79	1	(1 of 426,428,432)
F6YIN5	1	(1 of 169,175,176,177)
F6YIN5	1	163
F6YIN5	1	164
F6YT69	1	(1 of 82,85)
F6YT69	1	79
F6YUG5	1	9

F6Z4B2	1	(1 of 932,934)
F6Z4B2	1	(1 of 373,375)
F6Z4B2	1	192
F6Z4B2	1	615
F6Z4B2	1	846
F6Z4B2	1	568
F6Z4B2	1	927
F6Z9A1	1	77
F6Z9A1	1	78
F6Z9E6	1	212
F6Z9T5	1	110
F6ZBY9	1	321
F7AYW2	1	(1 of 1037,1040)
F7AYW2	1	1226
F7AYW2	1	1045
F7BXV7	1	6
F7CDR2	1	(1 of 104,105,106)
F7CDR2	1	101
F7CIP8	1	(1 of 141,142)
F7CIP8	1	32
F7CIP8	1	137
F7CIP8	1	108
F7CIP8	1	105
F7DE17	1	(1 of 588,590,594,597)
F7DE17	1	(1 of 276,279,282,283,287,288,290)
F7DE17	1	291
F7DE17	1	133
F7DE17	1	135
F7DE17	1	586
F7DE17	1	124
F7DE17	1	125
F8VPM9	1	(1 of 1790,1791)
F8VPM9	1	1760
F8VPM9	1	1706
F8VPM9	1	1771
F8VPM9	1	1711
F8VPM9	1	2647
F8VPM9	1	1694
F8VPZ9	1	1225
F8VQJ3	1	1201
F8VQJ3	1	1223
F8WHP5	1	(1 of 707,710,711,715)
F8WHP5	1	697
F8WI14	1	536
F8WI14	1	532

F8WIE5	1	1569
F8WIN6	1	48
F8WIN6	1	250
F8WIN6	1	246
F8WJL9	1	(1 of 760,761)
F8WJL9	1	(1 of 115,116,119)
F8WJL9	1	121
F8WJL9	1	751
G3UWE3	1	602
G3UWE3	1	431
G3UXW9	1	(1 of 8,9,11,12,13,15,18)
G3UXW9	1	518
G3UY24	1	36
G3UYL7	1	415
G3UYV8	1	(1 of 46,47)
G3UZP7	1	202
G3UZP7	1	282
G3X8Q1	1	2073
G3X8R2	1	72
G3X8R2	1	59
G3X8T3	1	(1 of 344,346,347,350)
G3X8T3	1	157
G3X928	1	600
G3X928	1	185
G3X928	1	186
G3X928	1	607
G3X960	1	167
G3X973	1	897
G3X973	1	1538
G3X973	1	1012
G3X973	1	1532
G3X973	1	2046
G3X9D6	1	23
G3X9K4	1	825
G3X9T8	1	139
G3X9Z4	1	181
G5E8W7	1	208
H3BIX4	1	81
H3BK31	1	(1 of 224,226,227)
H3BK31	1	232
H3BK31	1	235
H3BKD4	1	948
H3BL34	1	296
H3BL34	1	297
H3BL34	1	276

H3BLE4	1	9
H3BLE4	1	107
H3BLE4	1	14
H7BWY5	1	311
H9KUY5	1	94
H9KUY5	1	95
H9KV01	1	1092
H9KV01	1	262
H9KV01	1	1614
H9KV01	1	251
H9KV01	1	250
H9KV01	1	283
H9KV01	1	1086
I7HIP8	1	(1 of 417,418)
I7HIP8	1	404
I7HIP8	1	413
I7HJQ9	1	658
I7HJQ9	1	669
J3QJX3	1	556
J3QMX8	1	(1 of 393,396)
J3QMX8	1	(1 of 380,381)
J3QMX8	1	379
J3QNY6	1	(1 of 782,784)
J3QP71	1	(1 of 20,23,25)
J3QP71	1	138
J3QP71	1	28
J3QPD5	1	4
J3QPR1	1	81
J3QPR1	1	26
J3QPR1	1	23
K4DI63	1	36
K4DI63	1	6
K4DI63	1	92
M0QWZ1	1	992
M0QWZ1	1	995
O08553	1	512
O08553	1	517
O08750	1	275
O09117	1	259
O09159	1	369
O35114	1	124
O35114	1	47
O35516	1	675
O35516	1	175
O35887	1	133

O35949	1	8
O35949	1	4
O55022	1	74
O55042	1	72
O55042	1	53
O55042	1	54
O55111	1	(1 of 1056,1059,1060,1063,1064,1069,1071,1072,1074)
O70400	1	128
O70400	1	248
O70400	1	123
O70400	1	135
O88531	1	199
O88569	1	199
O88783	1	777
O88783	1	1516
O88783	1	973
O88783	1	774
O88904	1	(1 of 992,998,1001,1004,1008,1009)
O88904	1	(1 of 158,159,160,161,163,164)
O88904	1	853
O88904	1	854
O89017	1	95
O89020	1	404
O89103	1	279
P01029	1	1388
P01029	1	1326
P01029	1	223
P01902	1	199
P04925	1	198
P07361	1	106
P07724	1	294
P08046	1	117
P08113	1	64
P08113	1	42
P08113	1	44
P08113	1	219
P08113	1	447
P08228	1	99
P08607	1	418
P08607	1	224
P08607	1	426
P08607	1	71
P09055	1	408
P09055	1	521
P09055	1	214

P0C7T6	1	(1 of 29,30,31,33,34,37)
P0C7T6	1	40
P0C7T6	1	22
P0C7T6	1	23
P0DOV2	1	(1 of 122,123,125)
P0DOV2	1	137
P0DOV2	1	130
P10605	1	(1 of 231,233)
P10605	1	39
P11032	1	171
P11438	1	(1 of 83,85)
P11438	1	80
P11679	1	489
P11679	1	482
P11881	1	2505
P16301	1	43
P16301	1	110
P23953	1	81
P24472	1	120
P24668	1	83
P26039	1	(1 of 2169,2170)
P27773	1	91
P28665	1	290
P28665	1	995
P28665	1	296
P28665	1	1144
P28665	1	1182
P29341	1	485
P29341	1	351
P29788	1	(1 of 97,98)
P29788	1	88
P29788	1	243
P33587	1	216
P33587	1	292
P35831	1	625
P42128	1	(1 of 515,516)
P42128	1	(1 of 535,538,541)
P42128	1	663
P42703	1	384
P42703	1	674
P42703	1	387
P43883	1	(1 of 121,122)
P43883	1	(1 of 101,102,107)
P46978	1	546
P46978	1	550

P48678	1	644
P48678	1	613
P49182	1	169
P49182	1	404
P54869	1	346
P54869	1	348
P56677	1	774
P58252	1	404
P58871	1	260
P58929	1	404
P62908	1	242
P70274	1	193
P70274	1	178
P70324	1	(1 of 395,396)
P70324	1	394
P70670	1	240
P70699	1	(1 of 915,919,925,928)
P70699	1	(1 of 149,151,153)
P70699	1	392
P70699	1	142
P70699	1	885
P70699	1	469
P70699	1	472
P83741	1	(1 of 2376,2377)
P83741	1	1860
P83741	1	1930
P83741	1	1836
P83741	1	1843
P83741	1	1844
P83741	1	1845
P83741	1	1945
P83741	1	2365
P97364	1	448
P97370	1	199
P97426	1	113
Q00547	1	548
Q00547	1	550
Q01339	1	164
Q01339	1	159
Q01705	1	900
Q02614	1	233
Q02614	1	241
Q02614	1	239
Q03311	1	372
Q05BG1	1	328

Q05BG1	1	313
Q06890	1	329
Q06890	1	291
Q07456	1	235
Q07456	1	229
Q07797	1	542
Q07797	1	71
Q07968	1	548
Q07968	1	543
Q14AX6	1	(1 of 1353,1354)
Q14AX6	1	(1 of 588,589,590,592,593,595,597,604)
Q14AX6	1	1359
Q14BJ1	1	2
Q14BJ1	1	4
Q14BJ1	1	6
Q3LFS7	1	72
Q3TBU7	1	193
Q3TC93	1	280
Q3TCN2	1	514
Q3TCN2	1	522
Q3TIU4	1	27
Q3TJI8	1	131
Q3TN85	1	132
Q3TVI8	1	453
Q3TYD4	1	(1 of 498,499)
Q3TZR9	1	444
Q3U7T5	1	50
Q3U7T5	1	55
Q3U9N4	1	385
Q3U9N4	1	278
Q3UEQ1	1	184
Q3UH06	1	(1 of 988,991,993,995)
Q3UH06	1	1000
Q3UH06	1	1001
Q3UHJ0	1	360
Q3UHJ0	1	354
Q3UI14	1	438
Q3UN10	1	(1 of 673,674,675)&(1 of 669,670,673)
Q3UR03	1	22
Q3UR91	1	664
Q3UR91	1	85
Q3UR91	1	589
Q3USK2	1	382
Q3UYJ1	1	124
Q3UYJ1	1	137

Q3UYJ1	1	212
Q4G0F8	1	(1 of 875,876)&(1 of 875,878,880,881,882,884)
Q4PZA2	1	632
Q52KG4	1	262
Q571K4	1	553
Q571K4	1	385
Q571K4	1	412
Q58FA4	1	609
Q59J78	1	148
Q5DTZ3	1	245
Q5DTZ3	1	207
Q5F2E7	1	(1 of 381,382,383)&(1 of 383,384,385,386,389,391,393,394,395)
Q5F2E7	1	369
Q5F2E7	1	380
Q5F2E7	1	373
Q5QGU6	1	196
Q5QGU6	1	198
Q5RIM6	1	(1 of 1501,1503)
Q5RIM6	1	(1 of 2,3,4)
Q5RIM6	1	(1 of 1275,1278)
Q5RIM6	1	2053
Q5RIM6	1	1901
Q5RIM6	1	14
Q5RIM6	1	1874
Q5RIM6	1	51
Q5RIM6	1	1878
Q5RIM6	1	1497
Q5RIM6	1	1918
Q5RJH6	1	578
Q5RJH6	1	575
Q5SFM8	1	546
Q5SFM8	1	539
Q5SQA7	1	34
Q5SUH7	1	(1 of 258,259)
Q5SUH7	1	320
Q5SUH7	1	457
Q5SUH7	1	299
Q5SXC4	1	118
Q5XJV5	1	(1 of 1650,1654)
Q5XJV5	1	1646
Q61001	1	928
Q61001	1	2049
Q61009	1	(1 of 332,333)
Q61009	1	326
Q61009	1	286

Q61029	1	275
Q61029	1	287
Q61084	1	110
Q61084	1	111
Q61169	1	(1 of 499,502,503,505,509,511,512,513,514,515,517,521)
Q61191	1	(1 of 1055,1058)
Q61191	1	(1 of 583,586)
Q61191	1	515
Q61191	1	771
Q61191	1	518
Q61191	1	775
Q61191	1	522
Q61191	1	779
Q61191	1	405
Q61191	1	801
Q61191	1	1061
Q61191	1	1062
Q61191	1	806
Q61191	1	808
Q61191	1	685
Q61191	1	563
Q61191	1	579
Q61191	1	1220
Q61191	1	1224
Q61191	1	588
Q61191	1	726
Q61191	1	1495
Q61191	1	1241
Q61191	1	1497
Q61191	1	858
Q61191	1	603
Q61191	1	861
Q61191	1	1246
Q61191	1	607
Q61191	1	480
Q61191	1	490
Q61191	1	1139
Q61191	1	1148
Q61471	1	(1 of 171,172)
Q61606	1	120
Q61646	1	150
Q61827	1	(1 of 133,134,135,138)
Q61827	1	153
Q62009	1	603
Q62086	1	256

Q62261	1	2322
Q62261	1	2323
Q62261	1	2316
Q62311	1	(1 of 589,590,594,595,600,602)
Q62311	1	481
Q62311	1	586
Q62313	1	112
Q62419	1	284
Q63880	1	313
Q63886	1	91
Q64511	1	1200
Q68FG2	1	2354
Q68FG2	1	2364
Q68FG2	1	2101
Q68FG2	1	2359
Q69ZA1	1	1286
Q69ZS0	1	840
Q6A058	1	366
Q6A0A2	1	632
Q6A0A2	1	51
Q6A0A9	1	504
Q6DFZ1	1	1858
Q6DFZ1	1	1781
Q6DID3	1	819
Q6KCD5	1	(1 of 1018,1020,1021)
Q6KCD5	1	(1 of 1678,1679)
Q6KCD5	1	1024
Q6KCD5	1	161
Q6P5E4	1	266
Q6P5E4	1	271
Q6P6J9	1	138
Q6P6J9	1	150
Q6PAL7	1	(1 of 800,801)
Q6PAL7	1	1080
Q6PAL7	1	1593
Q6PAL7	1	1574
Q6PD26	1	372
Q6PDI5	1	(1 of 1669,1670)
Q6PIJ4	1	(1 of 1076,1077)
Q6PIJ4	1	(1 of 1138,1143,1146,1147,1148)
Q6PIJ4	1	1027
Q6PIJ4	1	838
Q6PIJ4	1	1031
Q6PIJ4	1	1064
Q6PIJ4	1	1172

Q6PIJ4	1	1270
Q6PIJ4	1	1151
Q6XBJ3	1	(1 of 492,495,496,497,498,499,500,501,503)
Q6XLQ8	1	136
Q6XLQ8	1	133
Q78PY7	1	909
Q78T81	1	(1 of 186,187,188,190)
Q78T81	1	180
Q7M6Z4	1	248
Q7M6Z4	1	252
Q7M6Z4	1	254
Q7M739	1	1672
Q7M739	1	2055
Q7TN29	1	197
Q7TPN9	1	319
Q7TT18	1	1032
Q7TT50	1	(1 of 968,969,970)
Q80U72	1	948
Q80U78	1	(1 of 212,214,220,227,228,229,233)
Q80U78	1	800
Q80U93	1	(1 of 1357,1358)
Q80U93	1	(1 of 645,646)
Q80U93	1	513
Q80U93	1	1314
Q80U93	1	1316
Q80U93	1	1317
Q80U93	1	1574
Q80U93	1	635
Q80U93	1	652
Q80U93	1	1362
Q80U93	1	1204
Q80U93	1	1557
Q80U93	1	1109
Q80U93	1	504
Q80U93	1	1337
Q80U93	1	506
Q80U93	1	507
Q80UF7	1	314
Q80VP1	1	416
Q80X50	1	480
Q80X50	1	803
Q80X50	1	879
Q80X50	1	1009
Q80X50	1	799
Q80X71	1	186

Q80X81	1	12
Q80YR4	1	564
Q80YX8	1	65
Q8BFR4	1	272
Q8BFR4	1	270
Q8BFW7	1	312
Q8BFW7	1	11
Q8BFW7	1	212
Q8BG19	1	499
Q8BGD9	1	(1 of 497,498,500,504,506,507)
Q8BGD9	1	352
Q8BGD9	1	355
Q8BGD9	1	495
Q8BGQ4	1	655
Q8BGS1	1	(1 of 385,386,387,398)
Q8BH35	1	45
Q8BH80	1	144
Q8BHE4	1	161
Q8BHE4	1	162
Q8BHL3	1	(1 of 44,46,47)
Q8BHL3	1	43
Q8BI72	1	(1 of 304,305,306)
Q8BI72	1	326
Q8BI72	1	199
Q8BI72	1	328
Q8BI72	1	395
Q8BI72	1	315
Q8BI72	1	187
Q8BI72	1	317
Q8BI84	1	1729
Q8BI84	1	250
Q8BI84	1	633
Q8BI84	1	1754
Q8BI84	1	253
Q8BJ05	1	(1 of 369,370,373)
Q8BJ05	1	132
Q8BJ05	1	134
Q8BJ05	1	360
Q8BJ05	1	78
Q8BJ05	1	251
Q8BJ05	1	255
Q8BJ71	1	52
Q8BJ71	1	55
Q8BJS4	1	(1 of 651,652,654,655)
Q8BJS4	1	648

Q8BKI2	1	(1 of 1158,1159,1161)
Q8BMB0	1	(1 of 1072,1073)
Q8BMB0	1	(1 of 500,502,505)
Q8BMB0	1	192
Q8BMB0	1	200
Q8BMB0	1	521
Q8BMB0	1	1069
Q8BMB0	1	499
Q8BNV8	1	148
Q8BP97	1	382
Q8BS54	1	291
Q8BTI8	1	(1 of 2199,2200)
Q8BTI8	1	2245
Q8BTI8	1	2341
Q8BTI8	1	2122
Q8BTI8	1	2123
Q8BTI8	1	2188
Q8BTI8	1	2414
Q8BTI8	1	2205
Q8BTJ4	1	281
Q8BTJ4	1	261
Q8BU25	1	267
Q8BUN3	1	365
Q8BUN3	1	366
Q8BWS5	1	318
Q8BX02	1	346
Q8BX02	1	421
Q8BYB9	1	205
Q8BYK6	1	201
Q8BYK6	1	205
Q8BYK6	1	167
Q8BYU6	1	320
Q8BZX4	1	489
Q8C0C0	1	265
Q8C0C0	1	166
Q8C0C0	1	150
Q8C0C3	1	236
Q8C0I4	1	751
Q8C0Q2	1	733
Q8C0Q2	1	730
Q8C0Q2	1	236
Q8C0Q2	1	581
Q8C129	1	144
Q8C180	1	(1 of 327,328)
Q8C180	1	329

Q8C180	1	326
Q8C341	1	531
Q8C341	1	527
Q8C5R2	1	390
Q8C7E7	1	160
Q8C8Z9	1	(1 of 601,605)
Q8C8Z9	1	608
Q8CBB6	1	113
Q8CBB6	1	116
Q8CCH2	1	208
Q8CEC2	1	552
Q8CF89	1	393
Q8CFE4	1	640
Q8CFE4	1	741
Q8CFE4	1	630
Q8CG48	1	867
Q8CGM2	1	(1 of 3,4)
Q8CGN4	1	588
Q8CHH5	1	590
Q8CHI8	1	2624
Q8CHI8	1	2940
Q8CHI8	1	709
Q8CHS8	1	174
Q8CI51	1	120
Q8CI51	1	90
Q8CI51	1	115
Q8CI51	1	110
Q8JZZ0	1	54
Q8K099	1	(1 of 604,605,608)
Q8K0D5	1	76
Q8K0E8	1	378
Q8K0L9	1	(1 of 303,304)
Q8K0L9	1	480
Q8K0L9	1	449
Q8K0L9	1	451
Q8K0L9	1	485
Q8K0L9	1	263
Q8K0L9	1	268
Q8K0L9	1	16
Q8K0L9	1	436
Q8K0L9	1	309
Q8K0L9	1	439
Q8K0L9	1	444
Q8K0L9	1	447
Q8K154	1	440

Q8K2Q9	1	502
Q8K3X4	1	204
Q8K3Z9	1	664
Q8K3Z9	1	665
Q8K3Z9	1	653
Q8QZR3	1	272
Q8QZR3	1	277
Q8R066	1	182
Q8R080	1	(1 of 267,268)
Q8R084	1	98
Q8R0F3	1	140
Q8R121	1	280
Q8R242	1	285
Q8R3E3	1	395
Q8R3E3	1	391
Q8R4R6	1	(1 of 296,297)
Q8R4R6	1	55
Q8R4R6	1	316
Q8R4R6	1	53
Q8R4R6	1	295
Q8R4U0	1	1512
Q8R4U0	1	910
Q8VBZ3	1	297
Q8VC97	1	392
Q8VCF0	1	(1 of 309,310)
Q8VCF0	1	298
Q8VCF0	1	330
Q8VCF0	1	370
Q8VCF0	1	373
Q8VCF0	1	374
Q8VCF0	1	343
Q8VCF0	1	314
Q8VCF0	1	315
Q8VCF0	1	319
Q8VCI0	1	529
Q8VCI0	1	450
Q8VCI0	1	446
Q8VCU1	1	313
Q8VDZ4	1	386
Q8VHR5	1	(1 of 587,589,591)
Q8VHR5	1	(1 of 288,289,290)
Q8VHR5	1	(1 of 487,489,490)
Q8VHR5	1	585
Q8VHR5	1	498
Q8VHR5	1	526

Q8VHR5	1	495
Q91WH2	1	(1 of 309,312,315)
Q91WK2	1	14
Q91WU0	1	81
Q91X84	1	(1 of 320,322,326,327)
Q91X84	1	321
Q91XL1	1	316
Q91XT4	1	(1 of 64,66)
Q91XT4	1	68
Q91XT4	1	78
Q91YQ5	1	(1 of 386,391)
Q91YQ5	1	302
Q91YT7	1	202
Q91YZ8	1	615
Q921I1	1	514
Q921I1	1	515
Q921L6	1	308
Q922U1	1	176
Q99LI5	1	(1 of 861,862,864,867,870,874,877,881,882)
Q99LI5	1	889
Q99LI5	1	886
Q99LI5	1	775
Q99MZ3	1	618
Q9CQW1	1	172
Q9CR23	1	40
Q9CS74	1	640
Q9CWK8	1	(1 of 104,106,107)
Q9CX80	1	184
Q9CYA0	1	190
Q9D0J8	1	5
Q9D136	1	212
Q9D136	1	262
Q9D1M0	1	313
Q9D1M0	1	315
Q9D787	1	501
Q9D7N9	1	(1 of 203,205)
Q9D7N9	1	161
Q9D8C4	1	(1 of 269,273,282,283,285,286)
Q9D8N1	1	145
Q9D9M9	1	78
Q9DAC2	1	120
Q9DAC2	1	141
Q9DAC2	1	126
Q9DB77	1	(1 of 441)
Q9DB77	1	433

Q9DBG5	1	128
Q9DBG5	1	58
Q9DBG5	1	76
Q9DBG5	1	71
Q9DBG6	1	105
Q9DBG6	1	108
Q9DBG6	1	103
Q9DBJ3	1	251
Q9DBR7	1	(1 of 645,646,647,648,650,651,652,653,656,658)
Q9DBR7	1	637
Q9DBS5	1	(1 of 609,611,612,616)
Q9EP52	1	82
Q9EPU0	1	951
Q9EQQ9	1	405
Q9ER39	1	161
Q9ERG0	1	(1 of 324,325,326,329,334,341,344)
Q9ERG0	1	279
Q9ERU9	1	(1 of 2317,2320,2328,2329,2330)
Q9ERU9	1	2339
Q9ERU9	1	1457
Q9ERU9	1	1138
Q9ERU9	1	1592
Q9ERU9	1	1599
Q9ERZ6	1	396
Q9ESC8	1	85
Q9ESY9	1	107
Q9ET43	1	241
Q9JHP7	1	154
Q9JI95	1	21
Q9JKR6	1	(1 of 607,612)
Q9JKR6	1	513
Q9JKR6	1	933
Q9JKR6	1	598
Q9JKR6	1	871
Q9JL60	1	442
Q9JLV1	1	(1 of 380,382,386,390)
Q9JLV1	1	320
Q9JLV1	1	145
Q9JLV1	1	177
Q9JLV1	1	179
Q9JLV1	1	372
Q9JLV1	1	183
Q9JLV1	1	188
Q9QWV9	1	474
Q9QYC7	1	572

Q9QYC7	1	629
Q9QYE6	1	158
Q9QYG0	1	(1 of 330,332)
Q9QYG0	1	353
Q9QYG0	1	370
Q9QYG0	1	334
Q9QYG0	1	335
Q9QZN4	1	266
Q9QZN4	1	261
Q9QZS5	1	332
Q9R013	1	358
Q9R1E0	1	645
Q9WU60	1	1084
Q9WU60	1	413
Q9WUD0	1	141
Q9WUM3	1	421
Q9WUU7	1	188
Q9WUU7	1	183
Q9WV54	1	259
Q9WV69	1	18
Q9WV69	1	285
Q9WV69	1	110
Q9WVF5	1	(1 of 525,530)
Q9WVF5	1	350
Q9WVJ3	1	396
Q9Z0F7	1	27
Q9Z0K8	1	134
Q9Z103	1	412
Q9Z2D6	1	(1 of 440,441)
Q9Z2D6	1	434
Q9Z329	1	2458
S4R1I7	1	64
S4R294	1	(1 of 2138,2140,2143,2144)
S4R294	1	(1 of 2632,2633)
S4R294	1	(1 of 2282,2283)
S4R294	1	2148
S4R294	1	1929
S4R294	1	2284
S4R294	1	1933
S4R294	1	2637
S4R294	1	2127
S4R294	1	2285
S4R294	1	209
S4R294	1	882
S4R294	1	2644

S4R294	1	2645
S4R294	1	374
S4R294	1	2101
S4R294	1	2649
S4R294	1	1918
S4R2A9	1	495
S4R2A9	1	499
S4R2A9	1	500
S4R2A9	1	542
S4R2A9	1	927
V9GX34	1	432
V9GX34	1	439
V9GXT3	1	(1 of 1391,1392,1394,1396,1399,1400,1404)
V9GXT3	1	2186
V9GXT3	1	1054
V9GXT3	1	2183
Z4YL55	1	208
Z4YL55	1	205
Z4YN17	1	60

A7.1.2. GlcNAc Sites Identified with the Val6 Tag in db/db Mouse Livers.

Protein	Min Sites	Site ID Constraints
A0A087WNV1	1	(1 of 319,325)
A0A087WNV1	1	251
A0A087WNV1	1	260
A0A087WNV1	1	262
A0A087WNV1	1	327
A0A087WP65	1	90
A0A087WQ86	2	(2 of 153,154,155)
A0A087WQH5	1	579
A0A087WQN7	1	1664
A0A087WQN7	1	1332
A0A087WRU0	1	953
A0A0A0MQ73	1	(1 of 2362,2366)
A0A0A0MQ73	1	2359
A0A0A0MQ98	1	(1 of 1489,1490)
A0A0A0MQ98	1	1431
A0A0A0MQ98	1	1492
A0A0A0MQ98	1	2047
A0A0A0MQJ4	1	(1 of 211,214,217,218,219)
A0A0A0MQJ4	1	(1 of 166,167,168)
A0A0A0MQJ4	1	(1 of 170,171)
A0A0A0MQJ4	1	163
A0A0A0MQJ4	1	165
A0A0A0MQJ4	1	204
A0A0A0MQJ4	1	175
A0A0A0MQJ4	1	159
A0A0A6YVU8	1	211
A0A0A6YVU8	1	213
A0A0A6YVU8	1	217
A0A0A6YVU8	1	219
A0A0A6YVU8	1	220
A0A0A6YVU8	1	221
A0A0A6YXS8	1	65
A0A0A6YXS8	1	10
A0A0B4J1G5	1	(1 of 285,286,287)
A0A0G2JDK2	1	290
A0A0G2JDK2	1	71
A0A0G2JDL6	1	75
A0A0G2JDL6	1	76
A0A0G2JDV2	1	567

A0A0G2JDV2	1	575
A0A0G2JF07	1	104
A0A0G2JF07	1	108
A0A0G2JFD6	1	4
A0A0G2JFW6	1	(1 of 1003,1004)&(1 of 1004,1005)
A0A0G2JFW6	1	359
A0A0G2JFW6	1	334
A0A0G2JFW6	1	532
A0A0G2JFW6	1	533
A0A0G2JFW6	1	409
A0A0G2JFW6	1	346
A0A0G2JGT1	1	(1 of 146,148,154,155,157)
A0A0J9YU61	1	446
A0A0N4SUV0	1	274
A0A0N4SV80	1	1370
A0A0R4IZZ5	1	210
A0A0R4J079	1	318
A0A0R4J0D3	1	637
A0A0R4J0H0	1	786
A0A0R4J0I1	1	184
A0A0R4J0I9	1	(1 of 2617,2622,2623)
A0A0R4J0I9	1	3784
A0A0R4J0I9	1	4363
A0A0R4J0I9	1	3788
A0A0R4J0I9	1	4078
A0A0R4J0I9	1	2130
A0A0R4J0I9	1	2132
A0A0R4J0I9	1	726
A0A0R4J0M9	1	1072
A0A0R4J0M9	1	1075
A0A0R4J0M9	1	1076
A0A0R4J0X5	1	(1 of 90,92)
A0A0R4J0X5	1	103
A0A0R4J131	1	138
A0A0R4J187	1	319
A0A0R4J1H6	1	167
A0A0R4J2B5	1	348
A0A0U1RNM3	1	(1 of 107,113,114)
A0A0U1RQB6	1	138
A0A0U1RQB6	1	147
A0A0U1RQB6	1	143
A0A140LHQ8	1	(1 of 340,341,343,344)
A0A140LHQ8	1	337
A0A140LHQ8	1	442
A0A140LHQ8	1	181

A0A140LHQ8	1	327
A0A140LHR4	1	120
A0A140T8T5	1	70
A0A1B0GR78	1	170
A0A1B0GR78	1	172
A0A1B0GR85	1	(1 of 1083,1084)
A0A1B0GR85	1	1085
A0A1B0GRB5	1	551
A0A1B0GRJ0	1	1020
A0A1B0GRV3	1	248
A0A1B0GS41	1	(1 of 365,367)
A0A1B0GSG3	1	(1 of 269,270)
A0A1B0GSY0	1	523
A0A1B0GSY0	1	525
A0A1B0GT43	1	108
A0A1C7ZMY3	1	1065
A0A1C7ZMY3	1	1071
A0A1D5RLU0	1	(1 of 107,108)
A0A1I7Q4G8	1	(1 of 61,62,67,69)
A0A1I7Q4G8	1	328
A0A1I7Q4G8	1	315
A0A1I7Q4G8	1	206
A0A1I7Q4G8	1	606
A0A1L1SQN1	1	(1 of 196,197,199,200,201,207,208,210)
A0A1L1SRY4	1	312
A0A1L1SUR6	1	531
A0A1N9M4K1	1	285
A0A1N9M4K1	1	357
A0A1N9M4K1	1	286
A0A1N9PTV1	1	246
A0A1W2P7C1	1	611
A0A1W2P7D7	1	153
A0A1W2P7G2	1	103
A0A1W2P7I2	1	(1 of 183,185)
A0A1W2P7Q7	1	134
A0A1Y7VJM4	1	123
A0A1Y7VK55	1	297
A0A1Y7VMB1	1	7
A0A1Y7VMT6	1	(1 of 19,20)
A0A1Y7VP49	1	79
A0A286YCQ0	1	(1 of 269,271)
A0A2I3BPM1	1	64
A0A2I3BPN6	1	(1 of 490,491)
A0A2I3BPN6	1	486
A0A2I3BQ92	1	(1 of 64,65)

A0A2I3BQ92	1	67
A0A2I3BQE0	1	328
A0A2I3BQE1	1	143
A0A2R8VHH9	1	203
A0A2R8VHQ0	1	1000
A0A2R8VHQ0	1	891
A0A2R8VHW4	1	161
A0A2R8VKN7	1	102
A0A2R8W6T9	1	(1 of 171,173,174,175,178)
A0A338P6F2	1	13
A0A338P6J9	1	72
A0A338P6J9	1	74
A0A338P6J9	1	85
A0A338P6J9	1	79
A0A338P6K9	1	(1 of 162,163)
A0A338P6K9	1	45
A0A338P6K9	1	303
A0A338P7E6	1	83
A0A3B2W7J8	1	786
A0A3B2WBH9	1	(1 of 441,442)
A0A3B2WBH9	1	451
A0A3B2WBH9	1	999
A0A3B2WCD8	1	(1 of 194,196,201)
A0A3B2WCD8	1	96
A0A3B2WCD8	1	145
A0A3B2WCD8	1	192
A0A494B962	1	37
A0A494B968	1	(1 of 33,35,37,41)
A0A494BAF3	1	378
A0A494BB11	1	262
A0A571BDN3	1	659
A0A571BEC9	1	288
A0A571BEC9	1	321
A0A571BEC9	1	354
A0A571BEC9	1	585
A0A571BEC9	1	618
A0A571BEC9	1	1230
A0A571BEC9	1	181
A0A571BEC9	1	214
A0A571BEC9	1	189
A0A571BEC9	1	222
A0A571BEC9	1	255
A0A571BEI2	1	487
A0A571BFA7	1	950
A0A5F8MPD8	1	(1 of 856,857,859,861,864,866)

A0A5F8MPD8	1	(1 of 473,474,478,481)
A0A5F8MPS7	1	169
A0A5F8MPU2	1	805
A0A5F8MPU2	1	807
A0A5F8MPY2	1	64
A0A5F8MPY2	1	74
A0A5F8MPY2	1	86
A0A5K1VVQ1	1	8907
A0A5K1VVQ1	1	8149
A0A5K1VVQ1	1	8150
A0A5K1VVQ1	1	8911
A0JNY3	1	296
A0JNY3	1	300
A0JNY3	1	301
A0JNY3	1	286
A1L358	1	642
A2A5Y4	1	(1 of 822,823,824,825,827,828,829)
A2A5Y4	1	832
A2A953	1	(1 of 63,64)
A2AC24	1	140
A2ACM0	1	700
A2ADB1	1	(1 of 2486,2487,2489)
A2ADB1	1	2496
A2ADB1	1	2499
A2ADB1	1	2504
A2ADB1	1	2505
A2ADB1	1	2762
A2ADS8	1	(1 of 335,338,341,351)
A2AFQ0	1	(1 of 2923,2924)
A2AFQ0	1	3796
A2AGJ9	1	55
A2AKB9	1	(1 of 354,355)
A2AKB9	1	(1 of 356,357,358,361,362)
A2AKB9	1	363
A2AKB9	1	364
A2AKB9	1	365
A2AKI5	1	829
A2AKJ2	1	34
A2AMY5	1	(1 of 1028,1030)
A2AMY5	1	(1 of 1000,1001)
A2AMY5	1	641
A2AMY5	1	1107
A2AMY5	1	1019
A2AMY5	1	468
A2AP93	1	421

A2AP93	1	383
A2APL5	1	206
A2APT9	1	295
A2AQE9	1	174
A2AS44	1	226
A2ATI9	1	397
A2ATI9	1	406
A2ATR8	1	240
A2AVP4	1	(1 of 768,769)
A2AWN8	1	225
A2AWN8	1	223
A2RSY1	1	534
A6H619	1	551
A7TU71	1	1093
A8Y5E6	1	200
B1AR09	1	(1 of 398,399)
B1AR76	1	305
B1AR76	1	314
B1ARD8	1	772
B1ARD8	1	774
B1ARU1	1	1680
B1ATR2	1	(1 of 159,160,161,164,165,167)
B1ATR2	1	158
B1ATR2	1	173
B1ATR2	1	174
B1ATR2	1	175
B1AUF2	1	502
B1AYL1	1	853
B1AYL1	1	855
B1AZ15	1	(1 of 819,824,826,827,830)
B1AZ15	1	836
B1AZA8	1	145
B1B0C7	1	847
B2RQG2	1	(1 of 1509,1511,1512,1513)
B2RQG2	1	1765
B2RT14	1	116
B2RUJ2	1	(1 of 1013,1018)
B2RUJ2	1	1011
B2RUJ2	1	1068
B2RXC8	1	462
B2RXS4	1	146
B7ZC18	1	691
B7ZC94	1	(1 of 811,813,814,816,817,818,819,820,821)
B7ZCC2	1	179
B7ZN55	1	596

B7ZNH7	1	140
B7ZNJ1	1	(1 of 435,436)
B7ZNJ1	1	1000
B7ZNJ1	1	524
B7ZNJ1	1	1008
B7ZNJ1	1	432
B7ZNJ1	1	530
B8JJB2	1	89
C0HKG6	1	218
D3YU17	1	430
D3YUV1	1	542
D3YUW8	1	149
D3YUW8	1	254
D3YVM4	1	169
D3YWA4	1	72
D3YWA4	1	75
D3YXZ5	1	454
D3YY42	1	(1 of 33,34,35,38)
D3YY42	1	19
D3YYR9	1	55
D3YYY8	1	252
D3Z069	1	459
D3Z069	1	461
D3Z0Y0	1	185
D3Z216	1	456
D3Z2E7	1	392
D3Z2E7	1	434
D3Z2L1	1	205
D3Z3F1	1	(1 of 258,259,260,261,263,265,266,267,269)
D3Z3F1	1	237
D3Z3F1	1	190
D3Z3F1	1	189
D3Z3F8	1	474
D3Z3F8	1	478
D3Z3Q3	1	699
D3Z3U7	1	328
D3Z3U7	1	333
D3Z4C0	1	387
D3Z4Q7	1	54
D3Z4U8	1	506
D3Z5G4	1	195
D3Z5G4	1	135
D3Z5G4	1	202
D3Z5G4	1	148
D3Z5G4	1	149

D3Z5I1	1	(1 of 557,558,559,562,564)
D3Z5I1	1	551
D3Z5I1	1	567
D3Z5I6	1	15
D3Z5I9	1	(1 of 739,740)
D3Z5I9	1	738
D3Z656	1	1360
D3Z656	1	1121
D3Z656	1	1374
D3Z665	1	(1 of 188,195,196)
D3Z665	1	187
D3Z6S3	1	112
D3Z6S3	1	107
D3Z6W7	1	384
D3Z7R3	1	(1 of 92,93)
D6RDD4	1	58
D6RGR1	1	91
D6RHA2	1	413
D6RJL6	1	17
E0CXE3	1	673
E0CY18	1	167
E0CY18	1	150
E0CY18	1	159
E0CYH7	1	(1 of 1045,1047,1049,1050,1051,1054)
E0CYH7	1	1055
E0CYN0	1	3
E0CYN0	1	11
E0CYN0	1	13
E0CZ61	1	(1 of 44,49)
E0CZ61	1	39
E9PUF4	1	(1 of 665,666,667)
E9PV38	1	(1 of 91,92)
E9PV38	1	478
E9PV38	1	102
E9PV69	1	126
E9PVA8	1	22
E9PVC6	1	21
E9PVC6	1	1015
E9PWM3	1	595
E9PWW2	1	208
E9PWX8	1	1973
E9PXN7	1	73
E9PYK3	1	1212
E9PYL2	1	(1 of 652,653)
E9PYL2	1	1842

E9PYX7	1	(1 of 561,562)
E9PZ00	1	210
E9PZ00	1	330
E9PZ00	1	454
E9PZ00	1	79
E9PZD2	1	384
E9PZD2	1	373
E9PZD2	1	406
E9PZD2	1	439
E9Q113	1	126
E9Q150	1	608
E9Q150	1	613
E9Q1P8	1	(1 of 364,365,366,367)
E9Q1S3	1	183
E9Q2T3	1	320
E9Q3G8	1	(1 of 1056,1057)
E9Q3G8	1	(1 of 932,934,937)
E9Q3G8	1	(1 of 1048,1050,1053)
E9Q3G8	1	705
E9Q3G8	1	1067
E9Q3G8	1	1101
E9Q3G8	1	1102
E9Q3G8	1	561
E9Q3G8	1	1044
E9Q3G8	1	1046
E9Q3G8	1	926
E9Q3G8	1	927
E9Q449	1	1346
E9Q481	1	787
E9Q4Q2	1	328
E9Q5M6	1	1681
E9Q5M6	1	1686
E9Q5Q0	1	(1 of 146,147,150,151,153,154,156)
E9Q5Q0	1	561
E9Q5Q0	1	563
E9Q5Q0	1	566
E9Q5Q0	1	567
E9Q616	1	5376
E9Q640	1	696
E9Q6A7	1	(1 of 1609,1611)
E9Q6A7	1	1635
E9Q6A7	1	1624
E9Q6A7	1	1628
E9Q6A7	1	1629
E9Q6A7	1	1598

E9Q6E2	1	346
E9Q6R7	1	2210
E9Q7B0	1	112
E9Q7D5	1	496
E9Q7D5	1	500
E9Q7R8	1	14
E9Q8A6	1	53
E9Q8A6	1	43
E9Q8A6	1	45
E9Q8H9	1	735
E9Q9Q7	1	108
E9QAT4	1	(1 of 2010,2011)
E9QAT4	1	68
E9QAT4	1	69
E9QAT4	1	70
E9QAT4	1	422
E9QAT4	1	60
E9QAT4	1	127
E9QAU4	1	1399
E9QJU8	1	345
E9QJU8	1	334
E9QKG6	1	1436
E9QKG6	1	1942
E9QKT0	1	274
E9QL13	1	280
E9QL13	1	244
E9QL13	1	254
E9QLA5	1	(1 of 377,379,380)
E9QLQ9	1	(1 of 2314,2315)
E9QM14	1	276
E9QMU3	1	(1 of 452,453,456,457,463)
E9QN70	1	1091
E9QNG1	1	217
F2Z4B7	1	(1 of 195,197)
F2Z4B7	1	190
F6QJV5	1	90
F6RDR0	1	70
F6S4K9	1	103
F6S5I0	1	26
F6SSP6	1	463
F6TS96	1	236
F6TS96	1	279
F6UVB2	1	23
F6V513	1	144
F6V8M6	1	(1 of 208,212,213,214,215,216,217,220,221,223,224)

F6V8M6	1	(1 of 174,175,176,177)
F6V8M6	1	123
F6V8M6	1	141
F6V8M6	1	134
F6V8M6	1	127
F6VV02	1	(1 of 31,32,36,37)
F6VV02	1	21
F6W4D3	1	228
F6W6I1	1	64
F6WV21	1	(1 of 822,823)
F6XZS9	1	1074
F6XZS9	1	197
F6XZS9	1	189
F6Y6L6	1	132
F6Y6L6	1	127
F6YC79	1	432
F6YIN5	1	(1 of 175,176,177)
F6YIN5	1	163
F6YT69	1	82
F6YT69	1	79
F6YUG5	1	9
F6Z4B2	1	(1 of 565,567,568)
F6Z4B2	1	(1 of 614,615)
F6Z4B2	1	192
F6Z4B2	1	927
F6Z9A1	1	77
F6Z9E6	1	212
F6Z9E6	1	207
F6Z9T5	1	110
F6ZBY9	1	321
F7AYW2	1	(1 of 1037,1040)
F7AYW2	1	1045
F7CDR2	1	(1 of 99,100)
F7CDR2	1	101
F7CGP0	1	434
F7CIP8	1	32
F7CIP8	1	137
F7CIP8	1	105
F7DE17	1	291
F7DE17	1	133
F7DE17	1	586
F7DE17	1	124
F7DE17	1	125
F8VPM9	1	(1 of 1790,1791,1805,1807)
F8VPM9	1	1771

F8VPM9	1	2647
F8VQJ3	1	1223
F8WGL3	1	8
F8WH96	1	102
F8WHP5	1	697
F8WI14	1	532
F8WIE5	1	(1 of 1575,1577)
F8WIE5	1	1569
F8WIE5	1	1487
F8WIN6	1	250
F8WIN6	1	246
F8WJL9	1	121
F8WJL9	1	102
F8WJL9	1	751
G3UWE3	1	(1 of 453)
G3UWE3	1	448
G3UWE3	1	435
G3UWE3	1	431
G3UXW9	1	9
G3UXW9	1	11
G3UXW9	1	518
G3UY24	1	36
G3UZC7	1	681
G3UZC7	1	771
G3UZP7	1	202
G3UZP7	1	282
G3X8R2	1	72
G3X8T3	1	157
G3X928	1	600
G3X928	1	185
G3X928	1	186
G3X928	1	607
G3X960	1	167
G3X973	1	897
G3X973	1	1532
G3X973	1	2046
G3X9D6	1	23
G3X9K4	1	825
G3X9T8	1	139
G3X9T8	1	140
G3X9V4	1	944
G5E850	1	5
G5E874	1	1143
G5E8W7	1	208
H3BIX4	1	81

H3BIX4	1	165
H3BIZ9	1	241
H3BK31	1	217
H3BK31	1	235
H3BKD4	1	948
H3BL34	1	276
H3BL34	1	277
H3BLE4	1	(1 of 105,106,107,108,109,110,112)
H3BLE4	1	9
H3BLE4	1	149
H3BLE4	1	14
H3BLE9	1	33
H9KUY5	1	(1 of 93,94,95,96,97,98,99,100,101,102,103,104,105,106,107,108,109,110,111,112,113)
H9KV01	1	256
H9KV01	1	1092
H9KV01	1	1605
H9KV01	1	262
H9KV01	1	1614
H9KV01	1	250
H9KV01	1	1086
I7HIP8	1	417
I7HIP8	1	413
I7HJQ9	1	658
I7HJQ9	1	669
J3QJX3	1	556
J3QJX3	1	549
J3QMX8	1	(1 of 376,393,396)
J3QMX8	1	379
J3QP71	1	(1 of 138,139)
J3QP71	1	136
J3QP71	1	25
J3QP71	1	28
J3QPR1	1	81
J3QPR1	1	23
J3QPR1	1	87
K4DI63	1	36
K4DI63	1	92
L7N209	1	(1 of 290,291)
M0QWF0	1	213
M0QWZ1	1	992
M0QWZ1	1	995
O08553	1	512
O08553	1	517

O08715	1	(1 of 351,356)
O08715	1	371
O09117	1	259
O09159	1	369
O35114	1	124
O35490	1	389
O35516	1	(1 of 667,671)
O35516	1	675
O35516	1	175
O35887	1	133
O35945	1	497
O35949	1	(1 of 3,4,8)
O55042	1	72
O55042	1	44
O55042	1	53
O55042	1	54
O55111	1	912
O55111	1	1060
O70400	1	128
O70400	1	123
O70400	1	135
O88531	1	214
O88531	1	199
O88569	1	199
O88783	1	(1 of 774,776)
O88783	1	973
O88904	1	854
O89020	1	404
O89103	1	262
P01029	1	1388
P01029	1	223
P01902	1	199
P04925	1	198
P07361	1	106
P07724	1	294
P08113	1	64
P08113	1	447
P08226	1	134
P08228	1	99
P08607	1	426
P08607	1	71
P09055	1	408
P09055	1	209
P09055	1	214
P0C7T6	1	40

P0C7T6	1	22
P0C7T6	1	23
P0DOV2	1	(1 of 122,123)
P0DOV2	1	130
P10605	1	39
P11438	1	80
P11679	1	489
P11679	1	482
P11881	1	2505
P11881	1	2500
P12265	1	629
P16301	1	110
P23953	1	(1 of 271,276,277,278)
P23953	1	81
P25444	1	(1 of 285,292,293)
P26039	1	(1 of 2169,2170)
P27773	1	91
P28665	1	(1 of 995,999)
P28665	1	296
P28665	1	290
P28665	1	1144
P28665	1	1182
P29341	1	485
P29341	1	351
P29788	1	88
P29788	1	243
P33215	1	329
P33587	1	216
P33587	1	292
P35831	1	625
P35831	1	642
P42703	1	384
P43883	1	420
P43883	1	102
P43883	1	107
P43883	1	45
P43883	1	23
P43883	1	122
P43883	1	59
P43883	1	30
P48678	1	(1 of 633,637)
P48678	1	629
P48678	1	644
P48678	1	613
P49182	1	169

P49182	1	404
P50247	1	2
P51141	1	383
P52430	1	326
P52430	1	318
P52430	1	255
P58871	1	298
P58871	1	260
P58929	1	404
P62908	1	242
P63028	1	98
P70274	1	193
P70274	1	178
P70324	1	(1 of 395,396)
P70699	1	392
P70699	1	885
P70699	1	469
P70699	1	142
P83741	1	1860
P83741	1	2376
P83741	1	1836
P83741	1	1841
P83741	1	1843
P83741	1	1844
P83741	1	1845
P83741	1	1945
P83741	1	2365
P97364	1	448
P97370	1	199
P97426	1	113
Q01339	1	164
Q01339	1	159
Q01705	1	900
Q01705	1	822
Q02013	1	44
Q02614	1	233
Q02614	1	241
Q02614	1	239
Q03311	1	372
Q05BG1	1	313
Q06770	1	322
Q06770	1	319
Q06890	1	329
Q06890	1	291
Q07456	1	235

Q07456	1	229
Q07797	1	71
Q07968	1	548
Q07968	1	543
Q3TBU7	1	193
Q3TBU7	1	186
Q3TBU7	1	188
Q3TC93	1	280
Q3TCN2	1	522
Q3TJI8	1	131
Q3TN85	1	(1 of 123,125,128,129,130,131,132,133,136,138,140,143,144,146,147)
Q3TQC7	1	257
Q3TWZ5	1	308
Q3TZ89	1	979
Q3TZR9	1	444
Q3U332	1	(1 of 350,351)
Q3U7T5	1	50
Q3U7T5	1	55
Q3U9N4	1	385
Q3U9N4	1	278
Q3UEI1	1	328
Q3UEI1	1	4
Q3UEI1	1	6
Q3UEQ1	1	184
Q3UH06	1	(1 of 1097,1099,1100,1101,1103,1106,1108,1111,1112)
Q3UH06	1	(1 of 988,991)
Q3UH06	1	1000
Q3UHJ0	1	360
Q3UHJ0	1	354
Q3UI14	1	438
Q3UIA2	1	803
Q3UR91	1	85
Q3URQ4	1	(1 of 31,33,34,35)
Q3URQ4	1	(1 of 10,18,27)
Q3USK2	1	382
Q3UYJ1	1	212
Q3V117	1	453
Q3V1K7	1	151
Q4G0F8	1	(1 of 875,876)
Q4PZA2	1	(1 of 167,169,171)
Q4PZA2	1	(1 of 247,249)
Q4PZA2	1	632
Q4VBF8	1	1114
Q505F4	1	144
Q52KG4	1	262

Q571K4	1	(1 of 402,405,407,408)
Q571K4	1	412
Q59J78	1	148
Q5DTZ3	1	245
Q5DTZ3	1	207
Q5F2E7	2	(1 of 381,382,383,384,385,386,389,391,393,394,395)&(1 of 369,373,381,393,394,395)&(1 of 369,373,374)
Q5F2E7	1	376
Q5F2E7	1	380
Q5RIM6	1	(1 of 1561,1562)
Q5RIM6	1	(1 of 2,3,4)
Q5RIM6	1	1056
Q5RIM6	1	2053
Q5RIM6	1	1901
Q5RIM6	1	14
Q5RIM6	1	1874
Q5RIM6	1	51
Q5RIM6	1	1878
Q5RIM6	1	1494
Q5RIM6	1	1497
Q5RJH6	1	578
Q5RJH6	1	575
Q5SFM8	1	546
Q5SQA7	1	(1 of 31,34)
Q5SQA7	1	29
Q5SUH7	1	320
Q5SUH7	1	259
Q5SUH7	1	316
Q5XJV5	1	1646
Q61001	1	2049
Q61009	1	332
Q61029	1	275
Q61191	1	(1 of 583,586,587,588,592)
Q61191	1	(1 of 771,775)
Q61191	1	515
Q61191	1	518
Q61191	1	779
Q61191	1	405
Q61191	1	801
Q61191	1	1061
Q61191	1	806
Q61191	1	808
Q61191	1	685
Q61191	1	563
Q61191	1	579

Q61191	1	1220
Q61191	1	1224
Q61191	1	726
Q61191	1	1495
Q61191	1	858
Q61191	1	603
Q61191	1	1246
Q61191	1	480
Q61191	1	490
Q61191	1	495
Q61191	1	1139
Q61191	1	1148
Q61391	1	287
Q61471	1	(1 of 171,172)
Q61827	1	(1 of 133,134,135,138)
Q61827	1	153
Q62009	1	603
Q62086	1	256
Q62261	1	2323
Q62311	1	(1 of 480,481,483,485)
Q62311	1	(1 of 594,595,600,602)&(1 of 590,594,595)
Q62311	1	586
Q62419	1	284
Q63880	1	313
Q63886	1	91
Q68FG2	1	2354
Q68FG2	1	2101
Q68FG2	1	2359
Q69ZA1	1	1286
Q69ZL1	1	494
Q6A058	1	366
Q6A0A2	1	(1 of 46,50,51)
Q6A0A2	1	(1 of 620,622)
Q6A0A2	1	632
Q6A0A9	1	(1 of 504,505,506,508,509,511)
Q6DFV5	1	1668
Q6DFZ1	1	1781
Q6DID3	1	819
Q6KCD5	1	(1 of 1678,1679)
Q6KCD5	1	161
Q6P5E4	1	266
Q6P5E4	1	271
Q6P6J9	1	145
Q6P6J9	1	138
Q6P6J9	1	150

Q6P6J9	1	167
Q6PAL7	1	1593
Q6PB44	1	880
Q6PB44	1	881
Q6PD26	1	372
Q6PDI5	1	(1 of 1669,1670)
Q6PIJ4	1	1027
Q6PIJ4	1	838
Q6PIJ4	1	1031
Q6PIJ4	1	1064
Q6PIJ4	1	1172
Q6PIJ4	1	1077
Q6PIJ4	1	1270
Q6XLQ8	1	133
Q78PY7	1	909
Q7M739	1	1672
Q7M739	1	1649
Q7M739	1	2055
Q7TN29	1	197
Q7TPN9	1	319
Q7TQE2	1	206
Q7TT18	1	1032
Q7TT50	1	(1 of 968,969,970,972,976,979)
Q80U72	1	(1 of 936,939,943,948,949,951)
Q80U93	1	(1 of 1566,1567,1569,1573,1574,1576,1580,1586)
Q80U93	1	(1 of 645,646,648)
Q80U93	1	(1 of 1357,1358)
Q80U93	1	(1 of 1109,1115,1116,1118,1120,1121)
Q80U93	1	513
Q80U93	1	1314
Q80U93	1	1313
Q80U93	1	1316
Q80U93	1	635
Q80U93	1	652
Q80U93	1	494
Q80U93	1	1362
Q80U93	1	1557
Q80U93	1	502
Q80U93	1	504
Q80U93	1	1337
Q80U93	1	506
Q80U93	1	507
Q80UF7	1	314
Q80VP1	1	416
Q80WQ2	1	500

Q80X50	1	(1 of 480,481,482,487,490,491,495,496,497)
Q80X50	1	803
Q80X50	1	799
Q80X50	1	879
Q80X81	1	12
Q80YR4	1	(1 of 563,564,568,569)
Q80YW7	1	(1 of 342,344)
Q80YW7	1	346
Q810N5	1	2
Q810N9	1	(1 of 54,60)
Q8BFR4	1	272
Q8BFR4	1	267
Q8BFR4	1	270
Q8BFW7	1	312
Q8BFW7	1	11
Q8BFW7	1	212
Q8BG19	1	499
Q8BGD9	1	(1 of 504,506,507)
Q8BGD9	1	352
Q8BGD9	1	355
Q8BGD9	1	495
Q8BGQ4	1	650
Q8BGQ4	1	655
Q8BGS1	1	(1 of 385,386,387,398)
Q8BH35	1	45
Q8BH80	1	144
Q8BHL3	1	43
Q8BI72	1	(1 of 187,188,189,190)
Q8BI72	1	(1 of 318,319)
Q8BI72	1	199
Q8BI72	1	328
Q8BI72	1	395
Q8BI72	1	315
Q8BI72	1	317
Q8BI84	1	1729
Q8BI84	1	1766
Q8BI84	1	250
Q8BI84	1	633
Q8BI84	1	1754
Q8BI84	1	253
Q8BJ05	1	(1 of 132,133)
Q8BJ05	1	(1 of 77,78)
Q8BJ05	1	360
Q8BJ05	1	252
Q8BJ05	1	134

Q8BJ05	1	255
Q8BJ71	1	(1 of 51,52)
Q8BJ71	1	55
Q8BJS4	1	(1 of 651,652,654,655)
Q8BJS4	1	648
Q8BKI2	1	(1 of 1158,1159,1161)
Q8BKI2	1	310
Q8BM88	1	98
Q8BMB0	1	(1 of 1072,1073)
Q8BMB0	1	(1 of 196,200,202)
Q8BMB0	1	192
Q8BMB0	1	499
Q8BMB0	1	1069
Q8BMI0	1	806
Q8BNV8	1	148
Q8BP97	1	382
Q8BTI8	1	(1 of 2199,2200)
Q8BTI8	1	2341
Q8BTI8	1	2122
Q8BTI8	1	2123
Q8BTI8	1	2414
Q8BTI8	1	2205
Q8BTJ4	1	281
Q8BTJ4	1	261
Q8BU11	1	406
Q8BU25	1	267
Q8BUN3	1	365
Q8BUN3	1	366
Q8BVZ1	1	55
Q8BX02	1	346
Q8BX02	1	421
Q8BYK6	1	201
Q8BYK6	1	205
Q8BYK6	1	167
Q8BYU6	1	320
Q8C0C0	1	(1 of 594,597)
Q8C0C0	1	150
Q8C0C0	1	166
Q8C0C3	1	(1 of 238,239)
Q8C0C3	1	236
Q8C0Q2	1	730
Q8C0Q2	1	236
Q8C0Q2	1	733
Q8C180	1	(1 of 326,327,328)
Q8C180	1	329

Q8C341	1	527
Q8C5R2	1	390
Q8C6E0	1	193
Q8C7E7	1	192
Q8C7E7	1	160
Q8C8Z9	1	608
Q8CBB6	1	113
Q8CCH2	1	208
Q8CF89	1	393
Q8CFE4	1	622
Q8CFE4	1	741
Q8CFE4	1	630
Q8CG48	1	867
Q8CHI8	1	(1 of 2614,2617,2619,2620,2624,2626,2627,2628)
Q8CHI8	1	(1 of 2932,2936,2937,2940)
Q8CHI8	1	709
Q8CHS8	1	174
Q8CI51	1	110
Q8CI51	1	208
Q8CI51	1	115
Q8CI51	1	118
Q8CI51	1	120
Q8CI51	1	90
Q8JZK9	1	507
Q8JZZ0	1	54
Q8K099	1	(1 of 604,605,608)
Q8K0E8	1	378
Q8K0L9	1	(1 of 461,464,465,472,473)
Q8K0L9	1	480
Q8K0L9	1	449
Q8K0L9	1	451
Q8K0L9	1	485
Q8K0L9	1	263
Q8K0L9	1	268
Q8K0L9	1	436
Q8K0L9	1	309
Q8K0L9	1	447
Q8K2Q9	1	(1 of 492,493,494,496)
Q8K2Q9	1	502
Q8K382	1	1002
Q8K3X4	1	204
Q8K3Z9	1	(1 of 649,650,653)
Q8K3Z9	1	664
Q8K558	1	(1 of 253,255,256,261,262)
Q8QZR3	1	(1 of 277,282,284)

Q8QZR3	1	272
Q8R080	1	(1 of 267,268)
Q8R084	1	98
Q8R0F3	1	140
Q8R121	1	280
Q8R143	1	41
Q8R242	1	285
Q8R3E3	1	391
Q8R4R6	1	(1 of 295,296,297,303)
Q8R4R6	1	53
Q8R4R6	1	55
Q8R4U0	1	1512
Q8VBZ3	1	297
Q8VC34	1	9
Q8VC97	1	392
Q8VCF0	1	(1 of 255,256)
Q8VCF0	1	298
Q8VCF0	1	330
Q8VCF0	1	370
Q8VCF0	1	242
Q8VCF0	1	373
Q8VCF0	1	310
Q8VCF0	1	343
Q8VCF0	1	374
Q8VCF0	1	314
Q8VCF0	1	315
Q8VCI0	1	529
Q8VCI0	1	446
Q8VCN5	1	(1 of 54,55,60)
Q8VDZ4	1	386
Q8VHR5	1	(1 of 587,589,591)
Q8VHR5	1	585
Q91W29	2	(2 of 20,22,24)
Q91WK2	1	14
Q91WP0	1	643
Q91WU0	1	88
Q91WU0	1	81
Q91X84	1	(1 of 320,322,326,327)
Q91X84	1	321
Q91XD6	1	137
Q91XD6	1	133
Q91XL1	1	316
Q91XT4	1	(1 of 70,74)
Q91XT4	1	8
Q91XT4	1	66

Q91XT4	1	68
Q91XT4	1	78
Q91YQ5	1	(1 of 386,391)
Q91YQ5	1	302
Q91YT7	1	202
Q921H8	1	243
Q921I1	1	514
Q921I1	1	515
Q921L6	1	308
Q922U1	1	176
Q922U1	1	172
Q99K94	1	(1 of 704,708,710)
Q99LI5	1	(1 of 881,882)
Q99LI5	1	(1 of 774,775,776,780,781,782)
Q99LI5	1	889
Q99LI5	1	886
Q99LI5	1	239
Q99MZ3	1	618
Q9CQW1	1	172
Q9CQW1	1	149
Q9CS74	1	640
Q9CU24	1	316
Q9CWK8	1	(1 of 104,106,107)
Q9CYA0	1	190
Q9D0J8	1	5
Q9D136	1	212
Q9D136	1	262
Q9D1M0	1	315
Q9D787	1	501
Q9D7N9	1	161
Q9D8N1	1	(1 of 96,97)
Q9D8N1	1	145
Q9DAC2	1	120
Q9DAC2	1	141
Q9DAC2	1	126
Q9DBG5	1	(1 of 138,139,141,142)
Q9DBG5	1	128
Q9DBG5	1	130
Q9DBG5	1	71
Q9DBG5	1	72
Q9DBG5	1	137
Q9DBG5	1	76
Q9DBG5	1	83
Q9DBG5	1	58
Q9DBG5	1	126

Q9DBG5	1	127
Q9DBG6	1	105
Q9DBG6	1	108
Q9DBR7	1	(1 of 625,628,631,637,645,646,647,648,650,651,652,653,656,658)
Q9EP52	1	82
Q9EQQ9	1	405
Q9ER39	1	161
Q9ERG0	1	(1 of 326,329,334,341,344)&(1 of 325,326)
Q9ERG0	1	279
Q9ERL9	1	(1 of 108,109)
Q9ERU9	1	(1 of 2443,2444,2445,2447)
Q9ERU9	1	1731
Q9ERU9	1	2339
Q9ERU9	1	1134
Q9ERU9	1	1457
Q9ERU9	1	1138
Q9ERU9	1	1428
Q9ERU9	1	1141
Q9ERU9	1	1599
Q9ERZ6	1	396
Q9ESC8	1	689
Q9ESC8	1	85
Q9ESY9	1	107
Q9ET43	1	241
Q9JHP7	1	154
Q9JI95	1	21
Q9JKR6	1	513
Q9JKR6	1	933
Q9JKR6	1	598
Q9JKR6	1	871
Q9JL60	1	442
Q9JLB4	1	2552
Q9JLV1	1	(1 of 380,382,386)
Q9JLV1	1	(1 of 186,187)
Q9JLV1	1	(1 of 188,189)
Q9JLV1	1	(1 of 289,291)
Q9JLV1	1	320
Q9JLV1	1	163
Q9JLV1	1	179
Q9JLV1	1	373
Q9JLV1	1	183
Q9QWV9	1	474
Q9QYC7	1	572
Q9QYC7	1	629
Q9QYE6	1	(1 of 150,152,153)

Q9QYE6	1	158
Q9QYG0	1	353
Q9QYG0	1	370
Q9QYG0	1	334
Q9QYG0	1	335
Q9QZN4	1	261
Q9QZS5	1	332
Q9R013	1	358
Q9R182	1	117
Q9R1E0	1	645
Q9WU60	1	1084
Q9WUM3	1	421
Q9WUU7	1	188
Q9WV54	1	259
Q9WV69	1	18
Q9WV69	1	285
Q9WV69	1	110
Q9WVJ3	1	396
Q9Z0K8	1	149
Q9Z0K8	1	134
Q9Z103	1	412
Q9Z2D6	1	434
Q9Z2L6	1	238
Q9Z2V4	1	549
S4R1Q8	1	(1 of 318,319)
S4R1Q8	1	2154
S4R1Y6	1	(1 of 1507,1508,1512,1517)
S4R294	1	(1 of 2138,2140,2143)
S4R294	1	(1 of 2632,2633)
S4R294	1	(1 of 2101,2102)
S4R294	1	2148
S4R294	1	2283
S4R294	1	1933
S4R294	1	2637
S4R294	1	2285
S4R294	1	209
S4R294	1	882
S4R294	1	2644
S4R294	1	2645
S4R294	1	374
S4R294	1	1918
S4R2A9	1	499
S4R2A9	1	500
S4R2A9	1	542
S4R2A9	1	927

V9GWU5	1	82
V9GWU5	1	140
V9GWU5	1	142
V9GXT3	1	1054
V9GXT3	1	1391
Z4YL55	1	208
Z4YL55	1	205
Z4YN17	1	60

Appendix 7.2. Pathway Analysis of Differentially Expressed Proteins in db/db Mouse Livers.

A7.2.1. MetaCore Pathway Analysis.

#	Maps	Total	p-value	FDR	In Data	Network Objects from Active Data
1	Cytoskeleton remodeling_Regulation of actin cytoskeleton organization by the kinase effectors of Rho GTPases	58	1.967E-15	2.866E-12	32	BETA-PIX, Talin, RhoA, ROCK, Actomyosin, PAK, Rac1-related, Cdc42 subfamily, Vinculin, MSN (moesin), ERM proteins, F-Actin cytoskeleton, Spectrin, MRLC, PRK1, ARPC1B, RhoA-related, Myosin II, Cortactin, Caldesmon, CDC42, Actin cytoskeletal, Alpha-actinin, Filamin A, Alpha adducin, RhoC, PIP5KI, MyHC, MLCK, Paxillin, Rac1, RhoGDI alpha
2	CFTR folding and maturation (normal and CF)	24	1.418E-12	1.033E-09	18	OST complex, DNAJB6 (Hdj-1), PARP-1, GANAB, UGCGL1, Csp, Aha1, HSP40, Calnexin, HSP105, HSP90 alpha, Hdj-2, ERp29, Sti1, HSP70, BAG-3, HSP90 beta, p23 co-chaperone
3	FAK1 signaling in melanoma	42	2.343E-12	1.138E-09	24	Talin, RhoA, ITGB1, Vitronectin, RelA (p65 NF-kB subunit), B-Raf, ROCK2, PKC-alpha, ITGB3, alpha-V/beta-3 integrin, N-Ras, FAK1, MEK1/2, alpha-5/beta-1 integrin, Actin cytoskeletal, CRK, SOS, NF-kB, RhoC, ITGA5, Fibronectin, WASF2, Paxillin, Rac1
4	Regulation of metabolism_Bile acids regulation of glucose and lipid metabolism via FXR	41	1.048E-10	3.819E-08	22	VLDL, PPCKC, SREBP1 precursor, ACACA, ME1, SREBP1 (nuclear), SCD, ACACB, Insulin receptor, ANGPTL3, G6PT, HNF1-alpha, APOB, CYP7A1, APOE, APOC2, PLTP, AKT(PKB), FXR, FASN, HNF4-alpha, F16P
5	PXR-mediated direct regulation of xenobiotic metabolizing enzymes / Human version	42	1.955E-10	5.696E-08	22	CYP2C8, CYP27A1, ACLY, S14 protein, SR-BI, SULT2A1, CYP3A7, G6PT, CYP3A5, SLC21A2, ELOVL6, CYP7A1, CYP2A6, MRP3, CYP3A4, UGT1A4, ALAS1, CD36, MDR1, ABCC2, CYP2B6, UGT1A6
6	PXR-mediated direct regulation of xenobiotic metabolizing enzymes / Rodent version	39	2.568E-10	6.235E-08	21	CYP2C8, CYP27A1, ACLY, S14 protein, SR-BI, SULT2A1, CYP3A7, G6PT, CYP3A5, SLC21A2, ELOVL6, CYP7A1, MRP3, CYP3A4, UGT1A4, ALAS1, CD36, MDR1, ABCC2, CYP2B6, UGT1A6
7	Immune response_Antigen presentation by MHC class I, classical pathway	54	3.514E-10	7.314E-08	25	MHC Class I alpha chain, TAP1 (PSF1), PDIA3, Beta-2-microglobulin, Sec24, GANAB, UGCGL1, PSMB10, Endoplasmin, Calreticulin, PSMB2, TAP2 (PSF2), PSMB1, PSMB5, MHC class I, PSMB9, Calnexin, HSP90 alpha, Bleomycin hydrolase, Sec23, Tapasin, HSP70, BCAP31, TAP, Impas 1
8	Translation_Regulation of translation initiation	27	4.712E-10	8.582E-08	17	RACK1, eIF6 (ITGB4BP), eIF5B (IF-2), PABPC1, eIF3S8, RPS6, eIF1, eIF4A, eIF4E, eIF5, eIF3S7, eIF3S3, eIF4G1/3, PABPC4, PDK (PDPK1), p70 S6 kinase2, eIF1A
9	HSP70 and HSP40-dependent folding in Huntington's disease	25	1.092E-09	1.767E-07	16	Ubiquitin, PSMD1, DNAJB6 (Hdj-1), HSC70, ST13 (Hip), HSP27, HSP40, HSP90 alpha, Hdj-2, HSP90, Sti1, HSP70, SGTA, HSP90 beta, Cathepsin D, HSPA1A
10	Glucocorticoid-induced elevation of intraocular pressure as glaucoma risk factor	62	2.220E-09	3.043E-07	26	RhoA, ITGB1, ROCK, PI3K cat class IA, GCR Beta, GCR, PI3K cat class IA (p110-beta), ITGB3, Antileukoproteinase 1, alpha-V/beta-3 integrin, EGFR, SERPINA3 (ACT), FAK1, Syndecan-4, CDC42, Actin cytoskeletal, Alpha-actinin, GCR Alpha, Filamin A, CLIM1, Srp40, Fibronectin, MLCK, CD47, Rac1, RhoGDI alpha
11	Chemotaxis_SDF-1/ CXCR4-induced chemotaxis of immune cells	79	2.297E-09	3.043E-07	30	BETA-PIX, Talin, RhoA, RAP-1A, Pyk2(FAK2), ITGB1, PIPKI gamma, PI3K cat class IA, VCAM1, PAK, NCK1, PLC-beta, ICAM1, Vinculin, PKA-cat alpha, G-protein alpha-i family, F-Actin cytoskeleton,

						PAK2, FAK1, MEK1/2, CDC42, Fyn, CRK, AKT(PKB), Csk, SFK, CXCR4, Paxillin, Rac1, G-protein alpha-13
12	Cell adhesion_Classical cadherin-mediated cell adhesion	26	2.524E-09	3.064E-07	16	RAP-1A, F-Actin, Vinculin, BAIAP2, F-Actin cytoskeleton, VAV-2, Beta-catenin, Cortactin, CDC42, Actin cytoskeletal, Alpha-actinin, Plakoglobin, p120-catenin, WASF2, Alpha-catenin, Rac1
13	CAR-mediated direct regulation of xenobiotic metabolizing enzymes / Human version	40	3.822E-09	4.283E-07	20	GSTP1, PPCKC, CYP2A13, CYP1A2, CYP2C8, SULT2A1, CYP3A7, CYP3A5, AL1A1, CYP7A1, CYP2A6, MRP3, ACOX1, CYP3A4, NQO1, ALAS1, MDR1, ABCC2, CYP2B6, UGT1A6
14	Transport_RAN regulation pathway	18	4.472E-09	4.449E-07	13	Importin (karyopherin)-beta, CRM1, NTF2, NUP58, RanBP1, NUP153, NUP54, Importin (karyopherin)-alpha, RANBP3, RanGAP1, RanBP2, E2I, Ran
15	Inhibition of remyelination in multiple sclerosis: regulation of cytoskeleton proteins	44	4.580E-09	4.449E-07	21	Tubulin beta, RhoA, CDK5, Tubulin alpha, PCBP-1, ROCK2, PKC-alpha, alpha-V/beta-1 integrin, MRLC, FAK1, Myosin II, CDC42, Actin cytoskeletal, Fyn, MELC, hnRNP A2, Fibronectin, WASF2, Paxillin, Rac1, Tubulin (in microtubules)
16	CHDI_Correlations from Replication data_Cytoskeleton and adhesion module	64	5.016E-09	4.568E-07	26	Plasminogen, Talin, RhoA, RAP-1A, ROCK, ICAM1, Vinculin, alpha-V/beta-3 integrin, MRLC, FAK1, CrkL, CDC42, Actin cytoskeletal, Fyn, Alpha-actinin, Plasmin, AKT(PKB), MELC, Fibronectin, MyHC, Intersectin, ILK, CXCR4, Paxillin, Rac1, IP3 receptor
17	Cell adhesion_Histamine H1 receptor signaling in the interruption of cell barrier integrity	45	7.628E-09	6.538E-07	21	Talin, RhoA, Pyk2(FAK2), ROCK, PLC-beta, Vinculin, PKC-alpha, ZO-1, MRLC, FAK1, Myosin II, Beta-catenin, Actin cytoskeletal, Alpha-actinin, G-protein alpha-q/11, MELC, p120-catenin, Alpha-catenin, MLCK, Paxillin, IP3 receptor
18	Cytoskeleton remodeling_Regulation of actin cytoskeleton nucleation and polymerization by Rho GTPases	46	1.247E-08	1.009E-06	21	RhoA, DRF, Rac1-related, HDIA2, Cdc42 subfamily, DAAM1, BAIAP2, F-Actin cytoskeleton, RhoA-related, CDC42, Actin cytoskeletal, IQGAP1, WASF subunit, FHOD1, RhoC, PIP5KI, FNBP1, WASF2, CYFIP1, FNBP1L, Rac1
19	Blood coagulation_GPCRs in platelet aggregation	71	1.397E-08	1.072E-06	27	Talin, RhoA, RAP-1A, ROCK, VAMP3, G-protein alpha-s, alpha-IIb/beta-3 integrin, ITGA2B, PKC-alpha, PI3K cat class IA (p110-beta), ITGB3, RAP-1B, G-protein alpha-i family, MRLC, LARG, Myosin II, Actin cytoskeletal, G-protein alpha-q, MELC, Syntaxin 4, Fibrinogen (fibrin), SNAP-23, PLC-beta3, G-protein alpha-i2, PKA-cat (cAMP-dependent), IP3 receptor, G-protein alpha-13
20	Cytoskeleton remodeling_Fibronectin-binding integrins in cell motility	32	1.755E-08	1.279E-06	17	Talin, RhoA, ROCK, PI3K cat class IA, ITGAV, Vinculin, alpha-V/beta-3 integrin, FAK1, CDC42, alpha-5/beta-1 integrin, Actin cytoskeletal, Fyn, Alpha-actinin, ITGA5, Fibronectin, ILK, Rac1
21	Effect of H. pylori infection on gastric epithelial cells motility	43	1.868E-08	1.281E-06	20	ITGB1, Vinculin, PKC-alpha, Lyn, ZO-1, FAK1, CrkL, Beta-catenin, Cortactin, alpha-5/beta-1 integrin, Actin cytoskeletal, Alpha-actinin, CRK, Csk, p120-catenin, Actin, Alpha-catenin, Paxillin, Rac1, VIL2 (ezrin)
22	Chemotaxis_Lysophosphatidic acid signaling via GPCRs	129	1.935E-08	1.281E-06	39	RhoA, ROCK, cPKC (conventional), G-protein alpha-12 family, Caspase-7, PAK, AKT1, PLC-eta 1, PKC, PLC-beta, Vinculin, PI3K cat class IA (p110-beta), alpha-V/beta-3 integrin, EGFR, G-protein alpha-i family, H-Ras, F-Actin cytoskeleton, Caspase-3, LARG, PRK1, FAK1, CREB1, Beta-catenin, MEK1/2, Rho GTPase, CDC42, Actin cytoskeletal, CRK, AKT(PKB), G-protein alpha-q/11, PDK (PDPK1), PLC-beta3, CD36, Paxillin, Rac1, IP3 receptor, mTOR, E3KARP (NHERF2), G-protein gamma 12

23	CAR-mediated direct regulation of xenobiotic metabolizing enzymes / Rodent version	40	2.761E-08	1.687E-06	19	GSTP1, PPCKC, CYP2A13, CYP1A2, CYP2C8, SULT2A1, CYP3A7, CYP3A5, AL1A1, CYP7A1, MRP3, ACOX1, CYP3A4, NQO1, ALAS1, MDR1, ABCC2, CYP2B6, UGT1A6
24	Cell adhesion_Endothelial cell contacts by junctional mechanisms	26	2.779E-08	1.687E-06	15	RAP-1A, Plakophilin 4, Cingulin, AF-6, ZO-1, Desmoplakin, Beta-catenin, Actin cytoskeletal, Alpha-actinin, Plakoglobin, p120-catenin, Vimentin, Claudin-3, Alpha-catenin, ZO-2
25	LRRK2 in neurons in Parkinson's disease	33	3.219E-08	1.876E-06	17	Ubiquitin, NSF, AP-2 alpha subunits, MSN (moesin), AP2A1, Beta-adaptin 2, 14-3-3, MEK1/2, Actin cytoskeletal, Actin cytoplasmic 2, HSP90, PKA-cat (cAMP-dependent), ACTB, Rac1, eEF1A, Tubulin (in microtubules), VIL2 (ezrin)
26	Cytoskeleton remodeling_PDGF signaling via calcium and Rho GTPases	83	3.783E-08	2.120E-06	29	SLC31A1, Pyk2(FAK2), CDK5, AKT1, ARP2, PKC, NCK1, F-Actin, Vinculin, PKC-alpha, VAV-2, FAK1, Beta-catenin, Cortactin, EBP50, CDC42, Actin cytoskeletal, Fyn, IQGAP1, ATOX1, WASF subunit, Dynamin-2, PKA-cat (cAMP-dependent), WASF2, ARPC2, Paxillin, Rac1, IP3 receptor, E3KARP (NHERF2)
27	Cytoskeleton remodeling_Integrin outside-in signaling	49	4.916E-08	2.653E-06	21	Talin, MEK1(MAP2K1), Vitronectin, PIPKI gamma, Vinculin, alpha-V/beta-3 integrin, H-Ras, FAK1, Beta-catenin, alpha-5/beta-1 integrin, Actin cytoskeletal, Alpha-parvin, Alpha-actinin, SOS, Beta-parvin, Filamin A, AKT(PKB), Fibronectin, ILK, Paxillin, Rac1
28	Development_Thromboxane A2 signaling pathway	50	7.530E-08	3.918E-06	21	RhoA, EGF, cPKC (conventional), G-protein alpha-12 family, PI3K cat class IA, B-Raf, G-protein alpha-s, PKC, PLC-beta, EGFR, RAP-1B, G-protein alpha-i family, H-Ras, CREB1, Beta-catenin, MEK1/2, G-protein alpha-q, AKT(PKB), PKA-cat (cAMP-dependent), IP3 receptor, G-protein alpha-13
29	Transcription_Sirtuin6 regulation and functions	63	8.519E-08	4.280E-06	24	PPCKC, Ubiquitin, SREBP1 precursor, ACACA, RelA (p65 NF-kB subunit), PARP-1, HMGCS1, SREBP1 (nuclear), Histone H3, ICAM1, SCD, LDLR, AMPK beta subunit, G6PT, AMPK alpha subunit, ELOVL6, AMPK gamma subunit, KPYR, SMARCA5, HXK4, ACOX1, FASN, SREBP1 (Golgi membrane), CD36
30	Regulation of degradation of deltaF508-CFTR in CF	39	1.120E-07	5.345E-06	18	Ubiquitin, RNF5, SEC61 complex, USP19, UBE1, HSC70, Csp, Aha1, SUMO-2, HSP27, HSP105, UBE2J1, Hdj-2, HSP90, Sti1, HSP70, SAE1, E2I
31	Development_Signaling pathways in embryonic hepatocyte maturation	51	1.137E-07	5.345E-06	21	STAT3, ALDOB, APOA1, gp130, PI3K cat class IA, APOA2, CPSM, Transferrin, K-RAS, G6PT, HNF1-alpha, APOC3, APOB, TAT, Beta-catenin, APOC2, SOS, AKT(PKB), FXR, HNF4-alpha, p120-catenin
32	Cytoskeleton remodeling_Hyaluronic acid/ CD44 signaling pathways	43	1.182E-07	5.382E-06	19	RhoA, ROCK, PRK2, MSN (moesin), H-Ras, LARG, VAV-2, Cortactin, MEK1/2, CDC42, Actin cytoskeletal, Fyn, SOS, Dynamin-2, Actin, MLCK, Rac1, RhoGDI alpha, VIL2 (ezrin)
33	Development_VEGF signaling via VEGFR2 - generic cascades	93	1.710E-07	7.408E-06	30	MEK1(MAP2K1), RhoA, Pyk2(FAK2), PI3K cat class IA, PKC, NCK1, Vinculin, PKC-alpha, alpha-V/beta-3 integrin, HSP27, H-Ras, PAK2, MEK3(MAP2K3), eIF4E, eNOS, FAK1, CREB1, Beta-catenin, CDC42, Actin cytoskeletal, Fyn, SOS, AKT(PKB), HSP90, MNK1, PDK (PDPK1), MLCK, Paxillin, Rac1, IP3 receptor
34	Immune response_Antigen presentation by MHC class II	118	1.729E-07	7.408E-06	35	MHC class II alpha chain, Cathepsin L, RhoA, Cathepsin F, PI3K cat class IA, AKT1, FCGRT, Rab-7, HSC70, PKC, SPPL2a, AP complex 2 medium (mu) chain, PKC-alpha, MYO1E, Endoplasmin, CLEC10A, SWAP-70, Fc gamma RII beta, HSP90 alpha, CDC42, MANR, Legumain, HSP90, R-Ras, PDK (PDPK1), Dynamin-2, Cathepsin S, Cathepsin V, TAP, HSP90 beta, LRP1, Rac1, SPTBN2, mTOR, Tubulin (in microtubules)
35	Stem cells_Pancreatic cancer stem cells in tumor metastasis	40	1.811E-07	7.538E-06	18	RhoA, Pyk2(FAK2), ROCK, G-protein alpha-i family, F-Actin cytoskeleton, MRLC, LARG, FAK1, Myosin II, CDC42, Fyn, MELC, MyHC, MLCK, CXCR4, Rac1, IP3 receptor, G-protein alpha-13

36	Cell adhesion_Role of tetraspanins in the integrin-mediated cell adhesion	37	2.745E-07	1.111E-05	17	Talin, RhoA, ITGB1, ROCK, CD82, CD81, Vinculin, PKC-alpha, FAK1, CDC42, alpha-5/beta-1 integrin, Actin cytoskeletal, Filamin A, Fibronectin, Actin, Rac1, VIL2 (ezrin)
37	Translation_Regulation of EIF4F activity	54	3.626E-07	1.390E-05	21	MEK1(MAP2K1), EGF, PI3K cat class IA, eIF4G2, EGFR, H-Ras, eIF4A, MEK3(MAP2K3), eIF4E, eIF4B, eIF4H, CDC42, SOS, eIF4G1/3, AKT(PKB), MNK1, eIF4G1, PDK (PDPK1), p70 S6 kinase2, Rac1, mTOR
38	NRF2 regulation of oxidative stress response	54	3.626E-07	1.390E-05	21	GSTP1, Casein kinase II, alpha chains, Ubiquitin, Casein kinase II, beta chain (Phosvitin), MEK1(MAP2K1), Thioredoxin, Heme oxygenase 1, PI3K cat class IA, CRM1, PKC, GSTA1, GCL reg, DJ-1, Actin cytoskeletal, Fyn, GSTA2, AKT(PKB), GSTM3, PDK (PDPK1), NRF2, NQO1
39	Neurophysiological process_Receptor-mediated axon growth repulsion	46	4.308E-07	1.610E-05	19	RhoA, RAP-1A, ROCK, CDK5, B-Raf, ROCK2, EGFR, F-Actin cytoskeleton, GRB7, LARG, VAV-2, Cortactin, CDC42, Actin cytoskeletal, Fyn, CRMP2, Ephexin, Rac1, Tubulin (in microtubules)
40	Signal transduction_mTORC2 downstream signaling	68	4.516E-07	1.614E-05	24	PPCKC, RhoA, cPKC (conventional), ACACA, AKT1, SREBP1 (nuclear), PKC, PKC-alpha, SCD, Insulin receptor, IGF-2, G6PT, F-Actin cytoskeleton, Beta-catenin, CDC42, HXK4, Filamin A, AKT(PKB), FASN, p27KIP1, PKA-cat (cAMP-dependent), Paxillin, Rac1, mTOR
41	Development_Regulation of cytoskeleton proteins in oligodendrocyte differentiation and myelination	59	4.542E-07	1.614E-05	22	Tubulin beta, RhoA, CDK5, Tubulin alpha, PCBP-1, MAP4, ROCK2, CNP1, MRLC, TPPP (p24), FAK1, Myosin II, Cortactin, CDC42, Actin cytoskeletal, Fyn, MELC, hnRNP A2, WASF2, Paxillin, Rac1, Tubulin (in microtubules)
42	Cell adhesion_Endothelial cell contacts by non-junctional mechanisms	24	6.506E-07	2.257E-05	13	Vitronectin, alpha-V/beta-3 integrin, F-Actin cytoskeleton, Beta-catenin, alpha-5/beta-1 integrin, PECAM1, Alpha-actinin, alpha-1/beta-1 integrin, Plakoglobin, Fibronectin, p120-catenin, ESAM, Alpha-catenin
43	Cell adhesion_Integrin-mediated cell adhesion and migration	48	9.460E-07	3.205E-05	19	Talin, RhoA, ROCK, PIPKI gamma, Vinculin, MRLC, FAK1, alpha-5/beta-1 integrin, Actin cytoskeletal, Alpha-actinin, CRK, alpha-1/beta-1 integrin, MELC, Fibronectin, MyHC, MYLK1, MLCK, Paxillin, Rac1
44	Signal transduction_Angiotensin II signaling via Beta-arrestin	57	1.043E-06	3.453E-05	21	Casein kinase II, beta chain (Phosvitin), MEK1(MAP2K1), RhoA, ROCK, p70 S6 kinases, AP-2 alpha subunits, EGFR, SET, MRLC, eIF4E, Beta-adaptin 2, 14-3-3, ARF6, AKT(PKB), MNK1, Beta-arrestin1, Casein kinase II, alpha' chain (CSNK2A2), MYLK1, p27KIP1, MLCK, p23 co-chaperone
45	Transport_Clathrin-coated vesicle cycle	71	1.115E-06	3.611E-05	24	Rab-4, Syntaxin 7, GS15, NSF, Rab-7, SAR1, VAMP8, Epsin 1, Myosin I, Syntaxin 5, HIP1, VPS45A, PREB, Rab-8, BIN1 (Amphiphysin II), Coatomer, GOS-28, Actin cytoskeletal, Optineurin, EEA1, PICALM, Dynamin-2, Actin, VAMP2
46	Defective macrophage-mediated bacterial phagocytosis in COPD	25	1.208E-06	3.825E-05	13	MBL2, C6orf134, Tubulin alpha, SR-BI, MSR1, Calreticulin, CDC42, MANR, AKT(PKB), NRF2, LRP1, CD36, Tubulin (in microtubules)
47	Adiponectin in pathogenesis of type 2 diabetes	29	1.493E-06	4.627E-05	14	PPCKC, SREBP1 precursor, AdipoR2, ACACA, SREBP1 (nuclear), SCD, ACACB, Insulin receptor, G6PT, AMPK alpha subunit, CREB1, ACADM, ACOX1, FASN
48	Cytoskeleton remodeling_Role of PKA in cytoskeleton reorganisation	41	1.637E-06	4.970E-05	17	BETA-PIX, RhoA, ROCK, G-protein alpha-s, F-Actin cytoskeleton, CDC42, Actin cytoskeletal, LASP1, Alpha adducin, Beta adducin, MELC, PLC-beta3, PKA-cat (cAMP-dependent), MLCK, Paxillin, Rac1, IP3 receptor
49	Cytoskeleton remodeling_Substance P mediated membrane blebbing	16	2.278E-06	6.772E-05	10	RhoA, G-protein alpha-12 family, Tubulin alpha, ROCK2, Substance P receptor, MRLC, Myosin II, Dynamin, MLCK, Tubulin (in microtubules)

50	Translation_Insulin regulation of translation	42	2.447E-06	7.131E-05	17	MEK1(MAP2K1), eEF2, PI3K cat class IA, eIF2B5, RPS6, Insulin receptor, H-Ras, eIF4A, eIF4E, eIF4B, eIF4H, SOS, eIF4G1/3, AKT(PKB), PDK (PDPK1), p70 S6 kinase2, mTOR
51	Development_SDF-1 signaling in hematopoietic stem cell homing	38	2.597E-06	7.419E-05	16	RhoA, RAP-1A, Pyk2(FAK2), PI3K cat class IA, Lyn, H-Ras, FAK1, CrkL, MEK1/2, CDC42, CRK, PDK (PDPK1), G-protein alpha-i2, CXCR4, Paxillin, Rac1
52	Signal transduction_mTORC1 downstream signaling	60	2.741E-06	7.679E-05	21	STAT3, SC5D, PDK1, eEF2, p70 S6 kinases, SREBP1 (nuclear), G6PD, SCD, PDCD4, RPS6, eIF4A, eIF4E, eIF4B, CAD, HMGCS2, CBP80, p70 S6 kinase2, MVK, p27KIP1, UBF, PDIP46
53	Role of Tissue factor-induced Thrombin signaling in cancerogenesis	65	3.028E-06	8.323E-05	22	MEK1(MAP2K1), RhoA, ROCK, G-protein alpha-12 family, RelA (p65 NF-kB subunit), Fibrinogen alpha, PKC-alpha, EGFR, G-protein alpha-i family, MRLC, LARG, FAK1, Actin cytoskeletal, AKT(PKB), G-protein alpha-q/11, MELC, Fibrinogen (fibrin), PDK (PDPK1), PLC-beta3, MLCK, Paxillin, IP3 receptor
54	Mechanisms of drug resistance in SCLC	70	3.239E-06	8.741E-05	23	ITGB1, PI3K cat class IA, VCAM1, RelA (p65 NF-kB subunit), B-Raf, CD81, alpha-V/beta-1 integrin, RPS6, alpha-V/beta-3 integrin, tBid, Caspase-3, FAK1, alpha-5/beta-1 integrin, AKT(PKB), HSP70, PDK (PDPK1), Fibronectin, p70 S6 kinase2, c-Kit, HSPA1A, MDR1, mTOR, Bid
55	Glucagon-induced glucose upregulation in type 2 diabetes in liver	52	3.911E-06	1.020E-04	19	PPCKC, F261, G-protein alpha-s, PYGL, PLC-beta, PHK gamma (liver), G-protein alpha-i family, G6PT, Casein kinase II, PYC, CREB1, KPYR, PHK beta, G-protein alpha-q/11, PHK alpha (liver), HNF4-alpha, PLC-beta3, PKA-cat (cAMP-dependent), IP3 receptor
56	Cell adhesion_PLAU signaling	39	3.919E-06	1.020E-04	16	Casein kinase II, alpha chains, Plasminogen, Casein kinase II, beta chain (Phosvitin), MEK1(MAP2K1), Vitronectin, EGF, Nucleolin, gp130, PI3K cat class IA, EGFR, H-Ras, FAK1, Plasmin, SOS, AKT(PKB), ILK
57	Cell adhesion_Alpha-4 integrins in cell migration and adhesion	35	4.095E-06	1.047E-04	15	BETA-PIX, ITGB1, PI3K cat class IA, VCAM1, F-Actin cytoskeleton, FAK1, ARF6, CDC42, Actin cytoskeletal, CRK, Filamin A, Fibronectin, PKA-cat (cAMP-dependent), Paxillin, Rac1
58	Glutathione metabolism	71	4.257E-06	1.069E-04	23	GSTP1, GPX3, GSTM5, GSTK1, 5-oxoprolinase, GCTG, GSTT2, GSTA1, G6PD, GCL reg, GPX4, GSTM1, GSTM2, MAAI, GSTA2, MGST, GSTA5, GSTT1, GSTM3, GSHR, GSTM4, GSTA4, CD13
59	Immune response_IL-3 signaling via ERK and PI3K	102	4.942E-06	1.220E-04	29	Talin, RAP-1A, ITGB1, p70 S6 kinases, cPKC (conventional), PI3K cat class IA, B-Raf, FLII, Lyn, RPS6, H-Ras, 14-3-3 zeta/delta, FAK1, CREB1, CrkL, MEK1/2, CDC42, alpha-5/beta-1 integrin, SOS, AKT(PKB), R-Ras, A-Raf-1, PDK (PDPK1), p27KIP1, PKA-cat (cAMP-dependent), Paxillin, Rac1, IP3 receptor, mTOR
60	ErbB2-induced breast cancer cell invasion	67	5.340E-06	1.297E-04	22	EGF, PI3K cat class IA, PKC-alpha, Neuregulin 1, PDCD4, EGFR, H-Ras, MEK3(MAP2K3), VAV-2, FAK1, MEK1/2, CDC42, Actin cytoskeletal, SOS, NF-kB, AKT(PKB), PDK (PDPK1), p120-catenin, WASF2, SLK, Rac1, IP3 receptor
61	Development_SLIT-ROBO1 signaling	40	5.813E-06	1.388E-04	16	RhoA, ROCK, PI3K cat class IA, NCK1, FLII, F-Actin cytoskeleton, PAK2, ARF6, Myosin II, CDC42, Fyn, AKT(PKB), Endophilin A2, CXCR4, ACTB, Rac1
62	Development_Role of CNTF and LIF in regulation of oligodendrocyte development	28	6.152E-06	1.446E-04	13	STAT3, gp130, PI3K cat class IA, RelA (p65 NF-kB subunit), Annexin V, IMPA1, Caspase-3, CLIC4, 14-3-3, AKT(PKB), PDK (PDPK1), RhoGDI alpha, LIF receptor
63	Possible regulation of HSF-1/ chaperone pathway in Huntington's disease	21	7.484E-06	1.731E-04	11	PKC-alpha, SUMO-2, HSP27, HSP40, HSP90 alpha, HSP90, PLA2, HSP70, E2I, HSP90 beta, p23 co-chaperone

64	Immune response_Antigen presentation by MHC class I: cross-presentation	99	7.995E-06	1.820E-04	28	Cathepsin L, Rab-4A, SEC61 complex, HYOU1, FCGRT, Rab-7, VAMP8, MSR1, Endoplasmin, Calreticulin, MHC class I, ARF6, HSP105, HSP90 alpha, MANR, HSP60, HSP90, Syntaxin 4, HSP70, Rab8B, SNAP-23, Cathepsin S, Rab-35, TAP, LRP1, Cathepsin B, EHD1, HSPA1A
65	Transport_The role of AVP in regulation of Aquaporin 2 and renal water reabsorption	50	8.922E-06	2.000E-04	18	MYH9, RAP-1A, VAMP3, G-protein alpha-s, MRLC, CREB1, MRLC2, Myosin II, Actin cytoskeletal, Tropomyosin-1, Actin cytoplasmic 2, Syntaxin 4, MyHC, SNAP-23, PKA-cat (cAMP-dependent), VAMP2, MLCK, ACTB
66	Putative pathways of activation of monoclonal protein secretion in multiple myeloma	25	9.182E-06	2.027E-04	12	SSR-delta, DNAJB11, GRP78, DAD-1, ARMET, Kappa chain (Ig light chain), SRP-alpha, Cyclophilin B, IgJ, DnaJB9, DNAJC3, ERP5
67	Cigarette smoke-mediated regulation of NRF2-antioxidant pathway in airway epithelial cells	29	9.938E-06	2.161E-04	13	Heme oxygenase 1, ME1, GSTA1, G6PD, GCL reg, Pirin, DJ-1, TALDO, Catalase, NRF2, GSHR, NQO1, UGT1A4
68	Signal transduction_CXCR4 signaling via PI3K cascade	46	1.054E-05	2.258E-04	17	PPCKC, Ubiquitin, PI3K cat class IA, AKT1, RelA (p65 NF-kB subunit), PARP-1, DEPTOR, G-protein alpha-i family, G6PT, Caspase-3, eNOS, Beta-catenin, AKT(PKB), PDK (PDPK1), CXCR4, Rac1, mTOR
69	Epithelial cell anoikis in COPD	51	1.227E-05	2.590E-04	18	Talin, PI3K cat class IA, Vinculin, H-Ras, MEK3(MAP2K3), FAK1, MMP-12, MEK1/2, Actin cytoskeletal, Alpha-parvin, Alpha-actinin, BPAG1, SOS, Beta-parvin, AKT(PKB), PDK (PDPK1), ILK, Paxillin
70	Regulation of lipid metabolism_Insulin signaling: generic cascades	47	1.469E-05	3.058E-04	17	MEK1(MAP2K1), eEF2, PI3K cat class IA, ACLY, eIF2B5, RPS6, Insulin receptor, H-Ras, eIF4B, SOS, LIPS, AKT(PKB), PDHA (somatic), PDK (PDPK1), p70 S6 kinase2, PKA-cat (cAMP-dependent), mTOR
71	Role of CNTF and LIF in regulation of oligodendrocyte development in multiple sclerosis	30	1.563E-05	3.208E-04	13	STAT3, gp130, PI3K cat class IA, RelA (p65 NF-kB subunit), Annexin V, IMPA1, Caspase-3, CLIC4, 14-3-3, AKT(PKB), PDK (PDPK1), RhoGDI alpha, LIF receptor
72	HGF receptor (Met) and MSP receptor (RON) signaling pathways in SCLC	43	1.730E-05	3.500E-04	16	STAT3, Pyk2(FAK2), PI3K cat class IA, AKT1, PKR, MEK3(MAP2K3), FAK1, CREB1, CrkL, MEK1/2, Alpha adducin, AKT(PKB), PDK (PDPK1), Paxillin, mTOR, Gamma adducin
73	Cytoskeleton remodeling_FAK signaling	57	1.815E-05	3.622E-04	19	Talin, MEK1(MAP2K1), RhoA, RAP-1A, PI3K cat class IA, TRAF3, PLC-beta, H-Ras, RIPK1, FAK1, CDC42, CRK, SOS, AKT(PKB), G-protein alpha-q/11, Fibronectin, Paxillin, Rac1, IP3 receptor
74	Blood coagulation_GPIb-IX-V-dependent platelet activation	77	1.924E-05	3.737E-04	23	Talin, MEK1(MAP2K1), RAP-1A, Pyk2(FAK2), VAMP3, AKT1, alpha-IIb/beta-3 integrin, PKC-alpha, PI3K cat class IA (p110-beta), ITGB3, Lyn, RAP-1B, 14-3-3 zeta/delta, MEK3(MAP2K3), eNOS, Fyn, Alpha-actinin, Filamin A, Syntaxin 4, Fibrinogen (fibrin), SNAP-23, Actin, IP3 receptor
75	Apoptosis and survival_NGF/ TrkA PI3K-mediated signaling	77	1.924E-05	3.737E-04	23	RhoG, BETA-PIX, RhoA, RAP-1A, ROCK, PI3K cat class IA, AKT1, MSN (moesin), H-Ras, PAK2, MRLC, VAV-2, CREB1, Myosin II, CDC42, Actin cytoskeletal, SOS, AKT(PKB), PDK (PDPK1), ILK, Rac1, mTOR, Tubulin (in microtubules)
76	Translation _Regulation of EIF2 activity	39	1.993E-05	3.820E-04	15	Casein kinase II, alpha chains, Casein kinase II, beta chain (Phosvitin), MEK1(MAP2K1), EGF, PI3K cat class IA, eIF2B5, PKR, Insulin receptor, EGFR, H-Ras, Casein kinase I, SOS, eIF2S1, AKT(PKB), PDK (PDPK1)
77	Mechanisms of CAM-DR in multiple myeloma	35	2.230E-05	4.220E-04	14	STAT3, TOP2 beta, Talin, RhoA, ITGB1, ROCK, gp130, VCAM1, ICAM1, Vinculin, alpha-5/beta-1 integrin, HSP70, Fibronectin, p27KIP1

78	Cytoskeleton remodeling_ESR1 action on cytoskeleton remodeling and cell migration	23	2.285E-05	4.268E-04	11	RhoA, PI3K cat class IA, ROCK2, MSN (moesin), ERM proteins, F-Actin cytoskeleton, FAK1, EBP50, AKT(PKB), ILK, G-protein alpha-13
79	Cell adhesion_Integrin inside-out signaling	58	2.401E-05	4.428E-04	19	Talin, ITGB1, G-protein alpha-12 family, PIPKI gamma, PLC-beta, alpha-IIb/beta-3 integrin, ITGA2B, ITGB3, alpha-V/beta-3 integrin, G-protein alpha-i family, FAK1, alpha-5/beta-1 integrin, Actin cytoskeletal, alpha-1/beta-1 integrin, G-protein alpha-q/11, Fibrinogen (fibrin), Fibronectin, CXCR4, IP3 receptor
80	Immune response_Sublytic effects of membrane attack complex	68	2.511E-05	4.574E-04	21	RhoA, C8, AKT1, GRP78, PKC, HSP27, EGFR, Endoplasmin, G-protein alpha-i family, H-Ras, MEK3(MAP2K3), GRP75, MEK1/2, Actin cytoskeletal, C9, SOS, eIF2S1, AKT(PKB), MNK1, XAF1, IP3 receptor
81	Blood coagulation_GPVI-dependent platelet activation	54	3.001E-05	5.332E-04	18	Talin, RhoA, RAP-1A, VAMP3, alpha-IIb/beta-3 integrin, PKC-alpha, PI3K cat class IA (p110-beta), ITGB3, Lyn, RAP-1B, CDC42, Fyn, PECAM1, Syntaxin 4, Fibrinogen (fibrin), SNAP-23, Rac1, IP3 receptor
82	Role of ER stress in obesity and type 2 diabetes	54	3.001E-05	5.332E-04	18	SREBP1 precursor, AdipoR2, PI3K cat class IA, GRP78, HMGCS1, SREBP1 (nuclear), PKR, SCD, LDLR, Insulin receptor, G6PT, CREB1, PTP-1B, HXK4, eIF2S1, DnaJB9, FASN, SREBP1 (Golgi membrane)
83	Immune response_IL-6-induced acute-phase response in hepatocytes	36	3.252E-05	5.709E-04	14	STAT3, APCS, Heme oxygenase 1, gp130, SAA1, Fibrinogen alpha, SAA2, HP, CRP, G6PT, HNF1-alpha, Fibrinogen beta, Hemopexin, Fibrinogen gamma
84	Cytoskeleton remodeling_Reverse signaling by Ephrin-B	32	3.603E-05	6.176E-04	13	Tubulin alpha, F-Actin, G-protein alpha-i family, H-Ras, PINCH-2, FAK1, Beta-catenin, Actin cytoskeletal, SOS, ILK, CXCR4, Paxillin, Tubulin (in microtubules)
85	Signal transduction_ERK1/2 signaling pathway	32	3.603E-05	6.176E-04	13	MEK1(MAP2K1), RAP-1A, B-Raf, SOS2, K-RAS, PKC-alpha, cAMP-GEFII, N-Ras, H-Ras, MEK1/2, SOS, SOS1, A-Raf-1
86	Immune response_Lectin induced complement pathway	50	3.720E-05	6.230E-04	17	MBL2, C8, C4a, C1 inhibitor, C6, Factor I, C5a, C8alpha, C4b, Clusterin, C5, C8gamma, C8beta, C9, C5b, C4, MASP2
87	The role of PTEN and PI3K signaling in melanoma	50	3.720E-05	6.230E-04	17	STAT3, MCAM, PI3K cat class IA, AKT1, B-Raf, alpha-V/beta-3 integrin, N-Ras, Caspase-3, FAK1, Beta-catenin, alpha-5/beta-1 integrin, AKT(PKB), RhoC, PDK (PDPK1), Fibronectin, Rac1, mTOR
88	Signal transduction_MIF signaling pathway	60	4.100E-05	6.712E-04	19	Heme oxygenase 1, PI3K cat class IA, VCAM1, RelA (p65 NF-kB subunit), SPPL2a, ICAM1, Lyn, GCL reg, G-protein alpha-i family, MIF, MEK1/2, NF-kB, AKT(PKB), Beta-arrestin1, PDK (PDPK1), NRF2, SFK, NQO1, CXCR4
89	Triacylglycerol metabolism p.1	60	4.100E-05	6.712E-04	19	TPI1, AL1B1, ALD9A1, ACSL4, AKR1C4, AL3A2, ACSL5, AKR7A2, GPD1, ALDR, AKR1C1, AL7A1, GPAM, ALDX, PLCB, AK1BA, PLCC, GNPAT, PLCE
90	EGFR signaling in Prostate Cancer	46	4.564E-05	7.359E-04	16	STAT3, MEK1(MAP2K1), EGF, gp130, PI3K cat class IA, RelA (p65 NF-kB subunit), K-RAS, Neuregulin 1, EGFR, N-Ras, H-Ras, SOS, AKT(PKB), PDK (PDPK1), p27KIP1, mTOR
91	Oxidative stress_ROS-induced cellular signaling	108	4.633E-05	7.359E-04	28	GSTP1, Casein kinase II, alpha chains, ELAVL1 (HuR), Thioredoxin, Heme oxygenase 1, ACACA, RelA (p65 NF-kB subunit), SREBP1 (nuclear), PKC, IRP1, SCD, PKA-cat alpha, HSP27, DLC1 (Dynein LC8a), GRP75, AMPK alpha subunit, HDAC1, Pin1, NF-kB, SAE2, AKT(PKB), Catalase, FASN, NRF2, E2I, APEX, HSPA1A, mTOR
92	DeltaF508-CFTR traffic / ER-to-Golgi in CF	17	4.697E-05	7.359E-04	9	Ubiquitin, Sec24, PIST (CAL), SAR1, PREB, Coatomer, Sec31, EBP50, Sec23
93	wtCFTR traffic / ER-to-Golgi (normal)	17	4.697E-05	7.359E-04	9	Ubiquitin, Sec24, PIST (CAL), SAR1, PREB, Coatomer, Sec31, EBP50, Sec23

94	Development_The role of GDNF ligand family/ RET receptor in cell survival, growth and proliferation	92	5.036E-05	7.806E-04	25	STAT3, RhoA, RAP-1A, ITGB1, ROCK, PI3K cat class IA, B-Raf, NCK1, alpha-V/beta-3 integrin, N-Ras, H-Ras, F-Actin cytoskeleton, VAV-2, FAK1, CREB1, MEK1/2, CDC42, CRK, SOS, NF-kB, AKT(PKB), PDK (PDPK1), Paxillin, Rac1, IP3 receptor
95	Development_Positive regulation of STK3/4 (Hippo) pathway and negative regulation of YAP/TAZ function	71	5.147E-05	7.812E-04	21	RhoA, MOBKL1A, MALS-3, SCRIB, G-protein alpha-s, Cullin 2, PKA-cat alpha, AMPK beta subunit, Alpha-1 catenin, 14-3-3, AMPK alpha subunit, Casein kinase I epsilon, AMPK gamma subunit, Beta-catenin, EBP50, Actin cytoskeletal, PKA-cat (cAMP-dependent), Alpha-catenin, RhoGDI alpha, ZO-2, LIF receptor
96	Signal transduction_Adenosine A2B receptor signaling pathway	71	5.147E-05	7.812E-04	21	Cullin 1, Ubiquitin, PDK1, RAP-1A, PI3K cat class IA, B-Raf, G-protein alpha-s, PKC, PLC-beta, cAMP-GEFII, RAP-1B, eNOS, CREB1, MEK1/2, AKT(PKB), G-protein alpha-q/11, PDK (PDPK1), PKA-cat (cAMP-dependent), IP3 receptor, E3KARP (NHERF2), VIL2 (ezrin)
97	Development_c-Kit ligand signaling pathway during hemopoiesis	61	5.297E-05	7.880E-04	19	STAT3, Pyk2(FAK2), PI3K cat class IA, PKC-alpha, Lyn, H-Ras, CrkL, MEK1/2, Fyn, SOS, AKT(PKB), PDK (PDPK1), c-Kit, p27KIP1, CXCR4, Paxillin, Rac1, IP3 receptor, mTOR
98	Development_Role of PKR1 and ILK in cardiac progenitor cells	33	5.300E-05	7.880E-04	13	MEK1(MAP2K1), Pyk2(FAK2), ITGB1, PI3K cat class IA, PLC-beta, H-Ras, Beta-catenin, SOS, AKT(PKB), G-protein alpha-q/11, Fibronectin, c-Kit, ILK
99	Proteolysis_Putative SUMO-1 pathway	29	5.800E-05	8.536E-04	12	Ubiquitin, PML, GCR, SAE1/2, RanGAP1, NF-kB, SAE2, TOP2, SAE1, RanBP2, E2I, CBX4
100	Regulation of lipid metabolism_Regulation of lipid metabolism via LXR, NF-Y and SREBP	38	6.578E-05	9.584E-04	14	CYP51A1, SREBP1 precursor, Importin (karyopherin)-beta, ACACA, ACLY, SREBP1 (nuclear), SCD, LDLR, AMPK beta subunit, AMPK alpha subunit, CREB1, AMPK gamma subunit, FASN, SREBP1 (Golgi membrane)
101	CCR7 signaling pathways in dendritic cells in allergic contact dermatitis	57	6.769E-05	9.612E-04	18	MEK1(MAP2K1), RhoA, RAP-1A, Pyk2(FAK2), ROCK, ICAM1, G-protein alpha-i family, H-Ras, Myosin II, CDC42, Actin cytoskeletal, SOS, AKT(PKB), PDK (PDPK1), Fibronectin, Paxillin, Rac1, IP3 receptor
102	Signal transduction_Adenosine A1 receptor signaling pathway	62	6.795E-05	9.612E-04	19	STAT3, TTC1, PKC, PLC-beta, PKC-alpha, PI3K cat class IA (p110-beta), EGFR, G-protein alpha-i family, H-Ras, CREB1, MEK1/2, NF-kB, AKT(PKB), G-protein alpha-q/11, PDK (PDPK1), SFK, PLC-beta3, PKA-cat (cAMP-dependent), IP3 receptor
103	Regulation of CFTR activity (normal and CF)	62	6.795E-05	9.612E-04	19	Casein kinase II, alpha chains, Casein kinase II, beta chain (Phosvitin), RACK1, Annexin V, G-protein alpha-s, PP2A structural, AMPK beta subunit, G-protein alpha-i family, PDZK1, EBP50, PP2A regulatory, AMPK gamma1, Filamin A, PP2C, SNAP-23, PKA-cat (cAMP-dependent), E3KARP (NHERF2), Tubulin (in microtubules), VIL2 (ezrin)
104	G-protein signaling_RhoA regulation pathway	34	7.652E-05	1.062E-03	13	RhoA, RhoGDI beta, ROCK, G-protein alpha-12 family, LARG, PRK1, FAK1, Fyn, Ephexin, G-protein alpha-q/11, Rac1, RhoGDI alpha, VIL2 (ezrin)
105	G-protein signaling_G-Protein alpha-q signaling cascades	34	7.652E-05	1.062E-03	13	RhoA, Pyk2(FAK2), ROCK, PI3K cat class IA, PLC-beta, H-Ras, LARG, SOS, NF-kB, AKT(PKB), G-protein alpha-q/11, PDK (PDPK1), IP3 receptor
106	Regulation of lipid metabolism_Insulin regulation of fatty acid metabolism	89	8.079E-05	1.110E-03	24	MEK1(MAP2K1), SREBP1 precursor, INSIG2, ACACA, PI3K cat class IA, PDH, ACLY, SREBP1 (nuclear), ODP2, PDH alpha, ELOVL1, SCD, Insulin receptor, H-Ras, ELOVL6, HXK4, SOS, LIPS, AKT(PKB), PDHA (somatic), PDK (PDPK1), FASN, SREBP1 (Golgi membrane), PKA-cat (cAMP-dependent)
107	Signal transduction_Adenosine A3 receptor signaling pathway	48	8.230E-05	1.110E-03	16	STAT3, PI3K cat class IA, RelA (p65 NF-kB subunit), PKC, PLC-beta, G-protein alpha-i family, H-Ras, CREB1, MEK1/2, Rho GTPase, G-protein alpha-i3, AKT(PKB), G-protein alpha-q/11, PDK (PDPK1), G-protein alpha-i2, IP3 receptor
108	Development_Adiponectin signaling	48	8.230E-05	1.110E-03	16	STAT3, Casein kinase II, beta chain (Phosvitin), MEK1(MAP2K1), AdipoR2, gp130, PI3K cat class IA,

						PLC-beta, H-Ras, Caspase-3, eNOS, AMPK alpha subunit, SOS, AKT(PKB), HSP90, A-Raf-1, IP3 receptor
109	Development_Insulin, IGF-1 and TNF-alpha in brown adipocyte differentiation	53	8.608E-05	1.130E-03	17	G3P2, MEK1(MAP2K1), SREBP1 precursor, A-FABP, AKT1, SREBP1 (nuclear), COX II, SCD, PI3K cat class IA (p110-beta), Insulin receptor, CREB1, LIPS, AKT(PKB), FASN, p27KIP1, PKA-cat (cAMP-dependent), mTOR
110	Translation_Translation regulation by Alpha-1 adrenergic receptors	53	8.608E-05	1.130E-03	17	MEK1(MAP2K1), RhoA, Pyk2(FAK2), eEF2, PI3K cat class IA (p110-beta), H-Ras, eIF4A, VAV-2, eIF4E, PRK1, G-protein alpha-11, G-protein alpha-q, eIF4G1/3, SOS1, p70 S6 kinase2, IP3 receptor, mTOR
111	Cell cycle_Influence of Ras and Rho proteins on G1/S Transition	53	8.608E-05	1.130E-03	17	STAT3, MEK1(MAP2K1), RhoA, PI3K cat class IA, RelA (p65 NF-kB subunit), ROCK2, H-Ras, MRLC, FAK1, CDC42, alpha-5/beta-1 integrin, AKT(PKB), PDK (PDPK1), p27KIP1, MLCK, Rac1, CDK6
112	Blood coagulation_Blood coagulation	39	9.145E-05	1.190E-03	14	Plasminogen, HC II, Fibrinogen alpha, Alpha 1-antitrypsin, Protein C, Coagulation factor XIII A, SERPINF2, Fibrinogen beta, Coagulation factor XI, Fibrinogen gamma, Plasmin, CPB2, Plasma kallikrein, Fibrinogen (fibrin)
113	CAR signaling via cross-talk / Human Version	26	9.289E-05	1.198E-03	11	PPCKC, CYP2C8, SREBP1 (nuclear), GCR, ECHP, G6PT, CYP7A1, ACOX1, CYP3A4, HNF4-alpha, CYP2B6
114	Main pathways of Schwann cells transformation in neurofibromatosis type 1	80	1.154E-04	1.474E-03	22	MEK1(MAP2K1), ITGB1, EGF, PI3K cat class IA, K-RAS, Neuregulin 1, RPS6, EGFR, N-Ras, H-Ras, FAK1, Beta-catenin, MEK1/2, BRD4, CDC42, B-FABP, AKT(PKB), PDK (PDPK1), SOX9, CXCR4, IP3 receptor, mTOR
115	Activation of Cortisol production in major depressive disorder	40	1.254E-04	1.589E-03	14	RhoA, CYP11B1, ASAH, SREBP1 (nuclear), G-protein alpha-s, CYP11B2, FDX1, SF1, CREB1, MEK1/2, CYP17, CYP21A2, PKA-cat (cAMP-dependent), MDR1
116	SCAP/SREBP Transcriptional Control of Cholesterol and FA Biosynthesis	45	1.366E-04	1.686E-03	15	SREBP1 precursor, INSIG2, ACACA, ACLY, HMGCS1, SREBP1 (nuclear), ELOVL1, SCD, ELOVL6, HMGCS2, GPAM, FASN, SREBP1 (Golgi membrane), MVK, ACSA
117	Cell adhesion_Ephrin signaling	45	1.366E-04	1.686E-03	15	RhoA, RAP-1A, NCK1, G-protein alpha-i family, H-Ras, GRB7, VAV-2, FAK1, CDC42, Fyn, Ephexin, ADAM10, Intersectin, Paxillin, Rac1
118	Role of cell adhesion molecules in progression of pancreatic cancer	45	1.366E-04	1.686E-03	15	MEK1(MAP2K1), ITGB1, Caspase-7, K-RAS, alpha-V/beta-3 integrin, H-Ras, Caspase-3, FAK1, Beta-catenin, alpha-5/beta-1 integrin, SOS, Plakoglobin, ITGA5, Fibronectin, Alpha-catenin
119	Development_Role of IL-8 in angiogenesis	65	1.377E-04	1.686E-03	19	STAT3, Ubiquitin, MEK1(MAP2K1), RhoA, SREBP1 precursor, PI3K cat class IA, SREBP1 (nuclear), LDLR, EGFR, G-protein alpha-i family, FAK1, NF-kB, AKT(PKB), PDK (PDPK1), FASN, SREBP1 (Golgi membrane), Cathepsin B, Paxillin, Rac1
120	CAR signaling via cross-talk / Rodent version	27	1.400E-04	1.699E-03	11	PPCKC, CYP2C8, SREBP1 (nuclear), GCR, ECHP, G6PT, CYP7A1, ACOX1, CYP3A4, HNF4-alpha, CYP2B6
121	VEGF signaling in multiple myeloma	50	1.425E-04	1.716E-03	16	STAT3, MEK1(MAP2K1), Pyk2(FAK2), ITGB1, PI3K cat class IA, VCAM1, AKT1, ICAM1, PKC-alpha, H-Ras, alpha-5/beta-1 integrin, SOS, PDK (PDPK1), Fibronectin, MDR1, IP3 receptor
122	KLF6 and regulation of KLF6 alternative splicing in HCC	23	1.477E-04	1.749E-03	10	EGF, PI3K cat class IA, AKT1, PARP-1, SFRS1 (SF2), EGFR, H-Ras, Caspase-3, SOS, PDK (PDPK1)
123	G-protein signaling_Cross-talk between Ras-family GTPases	23	1.477E-04	1.749E-03	10	RhoA, RAP-1A, PI3K cat class IA, B-Raf, H-Ras, CDC42, RhoGAP5, AKT(PKB), PDK (PDPK1), Rac1
124	CHDI_Correlations from Discovery data_Causal network (positive)	36	1.515E-04	1.780E-03	13	STAT3, Talin, gp130, Vinculin, FAK1, CDC42, alpha-5/beta-1 integrin, Actin cytoskeletal, Actin, Intersectin, CD47, Paxillin, Rac1

125	Development_TGF-beta-dependent induction of EMT via RhoA, PI3K and ILK	46	1.806E-04	2.088E-03	15	RhoA, PI3K cat class IA, RelA (p65 NF-kB subunit), ZO-1, H-Ras, Beta-catenin, Caldesmon, Tropomyosin-1, AKT(PKB), PDK (PDPK1), Fibronectin, Vimentin, Actin, ILK, ACTB
126	Signal transduction_PTEN pathway	46	1.806E-04	2.088E-03	15	MEK1(MAP2K1), EGF, PI3K cat class IA, EGFR, H-Ras, Caspase-3, FAK1, Beta-catenin, alpha-5/beta-1 integrin, SOS, AKT(PKB), PDK (PDPK1), ILK, Paxillin, mTOR
127	Airway smooth muscle contraction in asthma	56	1.843E-04	2.106E-03	17	RhoA, ROCK, G-protein alpha-s, PLC-beta, PKC-alpha, G-protein alpha-i family, MRLC, LARG, Telokin, Ca-ATPase2, Myosin II, G-protein alpha-q/11, MELC, MyHC, PKA-cat (cAMP-dependent), MLCK, IP3 receptor
128	Anti-apoptotic action of ErbB2 in breast cancer	51	1.850E-04	2.106E-03	16	STAT3, EGF, AKT1, Neuregulin 1, EGFR, H-Ras, Caspase-3, VAV-2, MEK1/2, SOS, AKT(PKB), PDK (PDPK1), ITGA5, p27KIP1, Rac1, mTOR
129	Role of red blood cell adhesion to endothelium in vaso-occlusion in Sickle cell disease	37	2.084E-04	2.353E-03	13	RAP-1A, VCAM1, alpha-IIb/beta-3 integrin, alpha-V/beta-3 integrin, RAP-1B, G-protein alpha-i family, BCAM, MEK1/2, Fibronectin, PKA-cat (cAMP-dependent), CD47, CD147, CD36
130	Role of neuropeptides in pathogenesis of SCLC	67	2.138E-04	2.396E-03	19	Pyk2(FAK2), cPKC (conventional), G-protein alpha-12 family, PKC, Neprilysin, PLC-beta, PKC-alpha, PI3K cat class IA (p110-beta), EGFR, H-Ras, Substance P receptor, MEK1/2, Fyn, G-protein alpha-q, SOS, AKT(PKB), G-protein alpha-q/11, IP3 receptor, mTOR
131	Transport_HDL-mediated reverse cholesterol transport	42	2.270E-04	2.506E-03	14	APOA1, CES1, APOA2, SR-BI, Medium HDL, LCAT, Pre beta-1 HDL, Large alpha-1 HDL, Small HDL, APOE, PLTP, HDL, Nascent HDL, Large apoE-rich HDL
132	GLP-1 in inhibition of beta cell proliferation and function in type 2 diabetes	42	2.270E-04	2.506E-03	14	RAP-1A, AKT1, B-Raf, GLUT2, G-protein alpha-s, EGFR, IGF-2, CREB1, Beta-catenin, MEK1/2, HXK4, PDK (PDPK1), ADAM10, PKA-cat (cAMP-dependent)
133	Regulation of degradation of wtCFTR	20	2.323E-04	2.532E-03	9	Ubiquitin, RNF5, SEC61 complex, UBE1, HSC70, Csp, HSP105, UBE2J1, HSP90
134	Immune response_Fc gamma R-mediated phagocytosis in macrophages	47	2.363E-04	2.532E-03	15	RhoA, Pyk2(FAK2), PI3K cat class IA, Vinculin, PKC-alpha, Lyn, F-Actin cytoskeleton, ARF6, Myosin II, CDC42, Actin cytoskeletal, PIP5KI, Paxillin, Rac1, IP3 receptor
135	Chemotaxis_Lipoxin inhibitory action on Formyl-Met-Leu-Phe-induced neutrophil chemotaxis	47	2.363E-04	2.532E-03	15	RhoA, ROCK, ICAM1, Lyn, HSP27, G-protein alpha-i family, F-Actin cytoskeleton, MEK3(MAP2K3), CDC42, Actin cytoskeletal, Fibrinogen gamma, AKT(PKB), Fibrinogen (fibrin), PDK (PDPK1), Rac1
136	wtCFTR and deltaF508 traffic / Membrane expression (normal and CF)	47	2.363E-04	2.532E-03	15	Ubiquitin, Rab-4, RACK1, Annexin V, Calreticulin, EBP50, Filamin A, PIP5KI, SNAP-23, PKA-cat (cAMP-dependent), EHD1, Rac1, E3KARP (NHERF2), Tubulin (in microtubules), VIL2 (ezrin)
137	Deficient alpha-MSH signaling in melanoma	33	2.514E-04	2.635E-03	12	RhoA, PI3K cat class IA, B-Raf, PKA-cat alpha, N-Ras, CREB1, MEK1/2, AKT(PKB), PDK (PDPK1), PKA-cat (cAMP-dependent), SOX9, Rac1
138	IGF family, invasion and metastasis in colorectal cancer	33	2.514E-04	2.635E-03	12	RhoA, ITGB1, Vitronectin, PI3K cat class IA, ITGAV, IGF-2, Alpha-1 catenin, Beta-catenin, alpha-V/beta-6 integrin, alpha-1/beta-1 integrin, Fibronectin, Rac1
139	Apoptosis and survival_Granzyme B signaling	33	2.514E-04	2.635E-03	12	NUMA1, Caspase-7, PARP-1, Tubulin alpha, ROCK2, tBid, Caspase-3, Lamin B1, Lamin A/C, DFF40 (CAD), Smac/Diablo, Bid
140	Immune response_Role of integrins in NK cells cytotoxicity	38	2.825E-04	2.919E-03	13	MEK1(MAP2K1), RACK1, Pyk2(FAK2), HLA-E, VCAM1, ICAM1, Lyn, H-Ras, MEK3(MAP2K3), SOS, Fibronectin, Paxillin, Rac1

141	Cell adhesion_Tight junctions	38	2.825E-04	2.919E-03	13	ITGB1, Actomyosin, Cingulin, F-Actin, LYRIC, AF-6, ZO-1, Myosin II, ZO-3, CSDA, Claudin-3, Actin, ZO-2
142	Development_ACM2 and ACM4 activation of ERK	43	3.001E-04	2.970E-03	14	MEK1(MAP2K1), RAP-1A, Pyk2(FAK2), PLC-beta, PKC-alpha, EGFR, G-protein alpha-i family, H-Ras, CREB1, Caldesmon, Fyn, SOS, G-protein alpha-i2, IP3 receptor
143	ESR1 (membrane) 36 kDa isoform signaling in breast cancer	43	3.001E-04	2.970E-03	14	PI3K cat class IA, PLC-beta, PKC-alpha, EGFR, H-Ras, AL1A1, MEK1/2, G-protein alpha-q, SOS, AKT(PKB), HSP90, PDK (PDPK1), CXCR4, IP3 receptor
144	Apoptosis and survival_TNF-alpha-induced Caspase-8 signaling	43	3.001E-04	2.970E-03	14	Acid sphingomyelinase, Caspase-7, AKT1, PP2A structural, tBid, Caspase-3, RIPK1, HSP90 alpha, PP2A regulatory, AKT(PKB), HSP90, Cathepsin D, Cathepsin B, Bid
145	Immune response_Classical complement pathway	53	3.037E-04	2.970E-03	16	C8, C4a, C1 inhibitor, C6, CRP, Factor I, C5a, C8alpha, C4b, Clusterin, C5, C8gamma, C8beta, C9, C5b, C4
146	Chemotaxis_Inhibitory action of lipoxins on IL-8- and Leukotriene B4-induced neutrophil migration	53	3.037E-04	2.970E-03	16	Talin, Actomyosin, ICAM1, G-protein alpha-i family, MRLC, Myosin II, Actin cytoskeletal, Alpha-actinin, AKT(PKB), MELC, PDK (PDPK1), PIP5KI, MYLK1, Actin, MLCK, Rac1
147	Signal transduction_CXCR4 signaling via MAPKs cascades	53	3.037E-04	2.970E-03	16	Ubiquitin, MEK1(MAP2K1), RhoA, ROCK, PAK, RelA (p65 NF-kB subunit), K-RAS, N-Ras, G-protein alpha-i family, CREB1, Cortactin, MEK1/2, G-protein alpha-i2, CXCR4, Rac1, G-protein alpha-13
148	Immune response_Alternative complement pathway	53	3.037E-04	2.970E-03	16	Vitronectin, C8, CRIg, Factor B, C6, CRP, Factor I, C5a, Factor Bb, C8alpha, Clusterin, C5, Factor H, C9, C5b, Factor Ba
149	Proliferative action of Gastrin in gastric cancer	53	3.037E-04	2.970E-03	16	MEK1(MAP2K1), cPKC (conventional), PI3K cat class IA, PKC, PKC-alpha, EGFR, H-Ras, FAK1, CREB1, Beta-catenin, G-protein alpha-q, SOS, G-protein alpha-q/11, PDK (PDPK1), p70 S6 kinase2, IP3 receptor
150	Fenofibrate in treatment of type 2 diabetes and metabolic syndrome X	25	3.371E-04	3.275E-03	10	APOA1, APOA2, Fibrinogen alpha, SR-BI, Fibrinogen beta, APOC3, Fibrinogen gamma, ACOX1, Fibrinogen (fibrin), Acyl-CoA synthetase
151	DNA damage_Role of SUMO in p53 regulation	17	3.591E-04	3.465E-03	8	Ubiquitin, PML, SAE1/2, SAE2, AKT(PKB), SAE1, RanBP2, E2I
152	Proliferative action of Gastrin in pancreatic cancer	44	3.924E-04	3.723E-03	14	STAT3, MEK1(MAP2K1), RhoA, Pyk2(FAK2), PI3K cat class IA, PKC-alpha, H-Ras, LARG, FAK1, G-protein alpha-q, SOS, PDK (PDPK1), p70 S6 kinase2, IP3 receptor
153	Apoptosis and survival_FAS signaling cascades	44	3.924E-04	3.723E-03	14	NUMA1, Caspase-7, PARP-1, BRE, HSP27, tBid, PAK2, Caspase-3, RIPK1, Lamin A/C, DFF40 (CAD), Lamin B, Smac/Diablo, Bid
154	Transcription_CREB signaling pathway	49	3.935E-04	3.723E-03	15	MEK1(MAP2K1), cPKC (conventional), PI3K cat class IA, G-protein alpha-s, PKC-alpha, H-Ras, MEK3(MAP2K3), CDO1, CREB1, SOS, AKT(PKB), PDK (PDPK1), HPD, PKA-cat (cAMP-dependent), Rac1
155	Immune response_B cell antigen receptor (BCR) pathway	110	4.232E-04	3.978E-03	26	MEK1(MAP2K1), VCAM1, RelA (p65 NF-kB subunit), B-Raf, NCK1, K-RAS, ICAM1, Lyn, N-Ras, H-Ras, MEK3(MAP2K3), VAV-2, MEK1/2, CDC42, Actin cytoskeletal, NF-kB, BCAP, AKT(PKB), SOS1, PDK (PDPK1), Fibronectin, PIP5KI, Rac1, IP3 receptor, mTOR, CDK6
156	Signal transduction_mTORC2 upstream signaling	65	4.282E-04	3.999E-03	18	EGF, PI3K cat class IA, DEPTOR, RPS16, RPL5, RPL7, RPL26, RPS6, RPL23, Insulin receptor, EGFR, RPL23a, AKT(PKB), HSP70, PDK (PDPK1), HSP90 beta, Rac1, mTOR

157	Oxidative stress_Role of Sirtuin1 and PGC1-alpha in activation of antioxidant defense system	60	4.579E-04	4.250E-03	17	GSTP1, PRDX3, Thioredoxin, Heme oxygenase 1, GSTM5, PRDX5, GCL reg, MT-TRX, AMPK beta subunit, MSRA, AMPK alpha subunit, AMPK gamma subunit, PBEF, Catalase, NRF2, GSHR, NQO1
158	Role of growth factor receptors transactivation by Hyaluronic acid / CD44 signaling in tumor progression	35	4.711E-04	4.317E-03	12	PI3K cat class IA, AKT1, PKC-alpha, EGFR, H-Ras, LARG, VAV-2, FAK1, MEK1/2, MDR1, Rac1, RhoGDI alpha
159	Role of adhesion of SCLC cells in tumor progression	35	4.711E-04	4.317E-03	12	RhoA, ITGB1, VCAM1, CD81, ICAM1, alpha-V/beta-1 integrin, FAK1, CDC42, alpha-5/beta-1 integrin, Fibronectin, CXCR4, Rac1
160	Development_Fetal brown fat cell differentiation	55	4.831E-04	4.400E-03	16	MEK1(MAP2K1), SREBP1 precursor, PI3K cat class IA, SREBP1 (nuclear), G-protein alpha-s, Insulin receptor, IGF-2, H-Ras, CREB1, SOS, AKT(PKB), IGF-2 receptor, PDK (PDPK1), FASN, p70 S6 kinase2, PKA-cat (cAMP-dependent)
161	G-protein signaling_Ras family GTPases in kinase cascades	26	4.898E-04	4.405E-03	10	MEK1(MAP2K1), RAP-1A, B-Raf, K-RAS, N-Ras, H-Ras, MEK3(MAP2K3), CDC42, R-Ras, Rac1
162	Development_S1P2 and S1P3 receptors in cell proliferation and differentiation	26	4.898E-04	4.405E-03	10	MEK1(MAP2K1), RhoA, ROCK2, MYH11, H-Ras, Transgelin, G-protein alpha-q, Actin, G-protein alpha-i2, G-protein alpha-13
163	CHDI_Correlations from Replication data_Causal network (negative correlations)	40	4.996E-04	4.466E-03	13	Plasminogen, RhoA, PKC, alpha-V/beta-3 integrin, CREB1, Beta-catenin, CtBP, G-protein alpha-q, Plasmin, AKT(PKB), Fibronectin, LPP3, ILK
164	Role of alpha-6/beta-4 integrins in carcinoma progression	45	5.080E-04	4.513E-03	14	EGF, PI3K cat class IA, AKT1, PKC-alpha, Neuregulin 1, EGFR, eIF4E, Actin cytoskeletal, AKT(PKB), PDK (PDPK1), 14-3-3 theta, Rac1, IP3 receptor, mTOR
165	PXR signaling via cross-talk / Rodent version	22	5.509E-04	4.835E-03	9	PPCKC, CYP2C8, GCR, SULT2A1, G6PT, CREB1, CYP7A1, HNF4-alpha, CD36
166	PXR signaling via cross-talk / Human Version	22	5.509E-04	4.835E-03	9	PPCKC, CYP2C8, GCR, SULT2A1, G6PT, CREB1, CYP7A1, HNF4-alpha, CD36
167	Autocrine production of eosinophil pro-survival cytokines in asthma	31	5.786E-04	5.048E-03	11	ELAVL1 (HuR), PI3K cat class IA, AUF1, VCAM1, ICAM1, C5a, YB-1, Pin1, NF-kB, hnRNP C, Fibronectin
168	Blood coagulation_Platelet microparticle generation	72	5.822E-04	5.049E-03	19	ITGB1, cPKC (conventional), Talin-1, PKC, PLC-beta, alpha-IIb/beta-3 integrin, MSN (moesin), Caspase-3, SLC21A2, Alpha-fodrin, Actin cytoskeletal, G-protein alpha-q, PTP-1B, Filamin A, Fibrinogen (fibrin), Fibronectin, MyHC, MYLK1, IP3 receptor
169	Mitogenic action of ErbB2 in breast cancer	56	6.027E-04	5.196E-03	16	EGF, PI3K cat class IA, Neuregulin 1, EGFR, H-Ras, Beta-catenin, MEK1/2, SOS, NF-kB, AKT(PKB), Cullin 3, PDK (PDPK1), p70 S6 kinase2, p27KIP1, Rac1, mTOR
170	PI3K signaling in gastric cancer	51	6.327E-04	5.423E-03	15	ELAVL1 (HuR), EGF, PI3K cat class IA, RelA (p65 NF-kB subunit), Neuregulin 1, alpha-V/beta-3 integrin, HSP27, EGFR, FAK1, Beta-catenin, G-protein alpha-q, AKT(PKB), G-protein alpha-q/11, PDK (PDPK1), MDR1
171	Ligand-independent activation of Androgen receptor in Prostate Cancer	67	6.383E-04	5.435E-03	18	STAT3, MEK1(MAP2K1), EGF, PI3K cat class IA, B-Raf, K-RAS, NCOA3 (pCIP/SRC3), Neuregulin 1, EGFR, N-Ras, H-Ras, Beta-catenin, PP2A regulatory, HDAC1, SOS, AKT(PKB), PDK (PDPK1), DDX5
172	Development_G-protein-mediated regulation of MAPK-ERK signaling	46	6.512E-04	5.435E-03	14	MEK1(MAP2K1), RAP-1A, Pyk2(FAK2), G-protein alpha-12 family, B-Raf, G-protein alpha-s, PLC-beta, G-protein alpha-i family, H-Ras, SOS, G-protein alpha-q/11, R-Ras, PKA-cat (cAMP-dependent), IP3 receptor

173	High shear stress-induced platelet activation	46	6.512E-04	5.435E-03	14	Talin, alpha-IIb/beta-3 integrin, Vinculin, PI3K cat class IA (p110-beta), ITGB3, RAP-1B, G-protein alpha-i family, 14-3-3 zeta/delta, Actin cytoskeletal, Alpha-actinin, Filamin A, AKT(PKB), Fibrinogen (fibrin), Fibronectin
174	Transcription_Hypoxia- and receptor-mediated HIF-1 activation	46	6.512E-04	5.435E-03	14	STAT3, EGF, PI3K cat class IA, NCOA3 (pCIP/SRC3), Neuregulin 1, RPS6, EGFR, IGF-2, eIF4E, MEK1/2, AKT(PKB), MNK1, PDK (PDPK1), APEX
175	Immune response_Neurotensin-induced activation of IL-8 in colonocytes	41	6.528E-04	5.435E-03	13	MEK1(MAP2K1), Pyk2(FAK2), RelA (p65 NF-kB subunit), PKC-alpha, G-protein alpha-i family, H-Ras, G-protein alpha-11, CDC42, G-protein alpha-q, SOS, NF-kB, Rac1, IP3 receptor
176	Pancreatic cancer cell resistance to Tarceva (erlotinib)	27	6.956E-04	5.758E-03	10	EGF, PI3K cat class IA, Neuregulin 1, EGFR, Beta-catenin, Plakoglobin, AKT(PKB), PDK (PDPK1), Vimentin, mTOR
177	Regulation and signaling of HGF receptor (Met) and MSP receptor (RON) in lung cancer	73	7.006E-04	5.767E-03	19	STAT3, PI3K cat class IA, NCK1, K-RAS, PKC-alpha, H-Ras, MEK3(MAP2K3), FAK1, CREB1, CrkL, Beta-catenin, CDC42, SOS, Alpha adducin, AKT(PKB), PDK (PDPK1), Paxillin, Rac1, Gamma adducin
178	Leucine, isoleucine and valine metabolism.p.2	79	7.522E-04	6.157E-03	20	PCC, PCCB, HADHA, MCC, MCCA, MUTA, PCCA, HMGCL, MMSA, HCD2, HCDH, MCEE, GABT, AOX1, HMGCS2, HIBCH, SCOT, ACDSB, ACAT1, MCCC2
179	Putative pathways for stimulation of fat cell differentiation by Bisphenol A	32	7.877E-04	6.412E-03	11	SREBP1 precursor, A-FABP, PI3K cat class IA, GCR, SCD, GPD1, CREB1, Beta-catenin, AKT(PKB), PDK (PDPK1), FASN
180	Role of alpha-V/ beta-6 integrin in colorectal cancer	23	8.101E-04	6.557E-03	9	Plasminogen, PKC, ITGAV, Caspase-3, MEK1/2, alpha-V/beta-6 integrin, Plasmin, Fibronectin, ITGB6
181	G-protein signaling_Regulation of p38 and JNK signaling mediated by G-proteins	37	8.338E-04	6.704E-03	12	RhoA, Pyk2(FAK2), G-protein alpha-12 family, PLC-beta, G-protein alpha-i family, MEK3(MAP2K3), LARG, VAV-2, PRK1, CDC42, G-protein alpha-q/11, Rac1
182	Immune response_IL-6 signaling pathway via MEK/ERK and PI3K/AKT cascades	74	8.392E-04	6.704E-03	19	STAT3, gp130, PI3K cat class IA, Proepithelin, K-RAS, RPS6, N-Ras, H-Ras, eIF4E, CREB1, MEK1/2, SOS, AKT(PKB), MNK1, PDK (PDPK1), ADAM10, p27KIP1, IP3 receptor, mTOR
183	Chemoresistance pathways mediated by constitutive activation of PI3K pathway and BCL-2 in small cell lung cancer	42	8.437E-04	6.704E-03	13	PI3K cat class IA, Caspase-7, PARP-1, RPS6, Caspase-3, FAK1, alpha-5/beta-1 integrin, AKT(PKB), PDK (PDPK1), Fibronectin, p70 S6 kinase2, c-Kit, mTOR
184	Propionate metabolism p.2	63	8.467E-04	6.704E-03	17	ACACA, HADHA, SCS-G, BUP1, ACACB, ACAT2, HMGCL, MMSA, HCDH, GABT, ACADM, SUCLG2, HIBCH, SCOT, SUCLG1, ACAT1, ACSA
185	Effect of H. pylori infection on gastric epithelial cell proliferation	58	9.189E-04	7.237E-03	16	MEK1(MAP2K1), RAP-1A, B-Raf, Lyn, EGFR, H-Ras, CREB1, CrkL, CRK, HDAC1, SOS1, Csk, p27KIP1, Histone H4, Rac1, IP3 receptor
186	Putative pathways of activation of classical complement system in major depressive disorder	28	9.676E-04	7.580E-03	10	C6, C4B protein, C4b, C5, C1qa, C9, C5b, C4A protein, C1qb, C4
187	Neurophysiological process_Activity-dependent synaptic AMPA receptor removal	64	1.027E-03	7.960E-03	17	eEF2, NSF, cPKC (conventional), PIPKI gamma, PKC, PLC-beta, AP-2 alpha subunits, FMR1, AP complex 2 medium (mu) chain, PKC-alpha, Beta-adaptin 2, ARF6, Actin cytoskeletal, G-protein alpha-q, Dynamin-2, Clathrin light chain, IP3 receptor

188	Oxidative stress in adipocyte dysfunction in type 2 diabetes and metabolic syndrome X	64	1.027E-03	7.960E-03	17	PRDX3, Heme oxygenase 1, A-FABP, Small LDL, GPX3, PI3K cat class IA, RelA (p65 NF-kB subunit), G6PD, AL3A2, Insulin receptor, APOE, AKT(PKB), Catalase, PLA2, NRF2, GSTA4, CD36
189	G-protein signaling_Regulation of CDC42 activity	33	1.056E-03	8.140E-03	11	Rich1, RhoGDI beta, Caspase-3, CDGAP, RHG7, CDC42, Fyn, DOCK6, RhoGAP5, RhoGDI alpha, VIL2 (ezrin)
190	Apoptosis and survival_Anti-apoptotic action of Gastrin	43	1.079E-03	8.215E-03	13	MEK1(MAP2K1), RhoA, ROCK, PI3K cat class IA, PKC-alpha, FAK1, CDC42, G-protein alpha-q, AKT(PKB), G-protein alpha-q/11, PDK (PDPK1), Rac1, IP3 receptor
191	Development_S1P3 receptor signaling pathway	43	1.079E-03	8.215E-03	13	RhoA, PI3K cat class IA, PLC-beta, ROCK2, G-protein alpha-i family, eNOS, G-protein alpha-q, AKT(PKB), PDK (PDPK1), G-protein alpha-i2, Rac1, IP3 receptor, G-protein alpha-13
192	Signal transduction_Cyclic AMP signaling	38	1.088E-03	8.215E-03	12	RAP-1A, G-protein alpha-s, PKC, PHK alpha, PKC-alpha, cAMP-GEFII, G-protein alpha-i family, PHK gamma, KDELR, CREB1, LIPS, PKA-cat (cAMP-dependent)
193	Defective efferocytosis in COPD	38	1.088E-03	8.215E-03	12	MBL2, SP-A, Stabilin-2, alpha-V/beta-3 integrin, Calreticulin, ELMO1, FAK1, PECAM1, CRK, LRP1, CD36, Rac1
194	Neurophysiological process_Dynein-dynactin motor complex in axonal transport in neurons	54	1.217E-03	9.140E-03	15	Ubiquitin, Importin (karyopherin)-beta, CDK5, DYNLL, Rab-7, MAPRE3(EB3), DYNLT, Importin (karyopherin)-alpha, BPAG1, AKT(PKB), PAFAH alpha (LIS1), Vimentin, MAPRPE1(EB1), SPTBN2, Tubulin (in microtubules)
195	Development_Melanocyte development and pigmentation	49	1.301E-03	9.654E-03	14	MEK1(MAP2K1), RACK1, PI3K cat class IA, B-Raf, G-protein alpha-s, Galpha(s)-specific peptide GPCRs, H-Ras, CREB1, Beta-catenin, SOS, AKT(PKB), PDK (PDPK1), c-Kit, PKA-cat (cAMP-dependent)
196	Tissue Factor signaling in cancer via PAR1 and PAR2	49	1.301E-03	9.654E-03	14	MEK1(MAP2K1), Pyk2(FAK2), EGF, G-protein alpha-12 family, PI3K cat class IA, PKC-alpha, EGFR, H-Ras, SOS, AKT(PKB), G-protein alpha-q/11, Beta-arrestin1, IP3 receptor, mTOR
197	Immune response_IFN-alpha/beta signaling via PI3K and NF-kB pathways	94	1.305E-03	9.654E-03	22	STAT3, p70 S6 kinases, PI3K cat class IA, AKT1, RelA (p65 NF-kB subunit), IFIT1, PKC-alpha, PDCD4, RPS6, DHFR, eIF4A, eIF4E, IFNAR2, CREB1, eIF4B, MEK1/2, NF-kB, eIF4G1/3, AKT(PKB), MNK1, PDK (PDPK1), p27KIP1
198	Role of Neuregulin 1 and Thymosin beta-4 in myocardium regeneration after infarction	29	1.321E-03	9.721E-03	10	ITGB1, PI3K cat class IA, Neuregulin 1, alpha-5/beta-1 integrin, Alpha-parvin, AKT(PKB), Thymosin beta-4, ITGA5, Fibronectin, ILK
199	Role of XBP1 protein in multiple myeloma	20	1.340E-03	9.759E-03	8	DNAJB11, GRP78, PSMA7, PSMA5, DnaJB9, DNAJC3, PSMA6, ERP5
200	wtCFTR and deltaF508-CFTR traffic / Clathrin coated vesicles formation (normal and CF)	20	1.340E-03	9.759E-03	8	Epsin 1, Myosin I, HIP1, BIN1 (Amphiphysin II), Actin cytoskeletal, PICALM, Dynamin-2, Actin
201	Aberrant lipid trafficking and metabolism in age-related macular degeneration pathogenesis	60	1.366E-03	9.786E-03	16	APCS, Vitronectin, CYP27A1, CD36L2, SR-BI, CRP, LDLR, Caspase-3, Clusterin, APOB, LDL, APOE, EEA1, HDL, Cathepsin D, CD36
202	Transport_Macropinocytosis	12	1.383E-03	9.786E-03	6	SNX5, Rab-7, Actin cytoskeletal, EEA1, SNX1, Tubulin (in microtubules)
203	Transport_RAB1A regulation pathway	12	1.383E-03	9.786E-03	6	Golgin-84, Rab-1A, Coatomer, SNAPs, p115, Golgin-95
204	Apoptosis and survival_Caspase cascade	34	1.395E-03	9.786E-03	11	NUMA1, Caspase-7, PARP-1, tBid, Caspase-3, RIPK1, Lamin A/C, DFF40 (CAD), Lamin B, AKT(PKB), Bid

205	Development_S1P1 receptor signaling via beta-arrestin	34	1.395E-03	9.786E-03	11	MEK1(MAP2K1), p70 S6 kinases, G-protein alpha-i family, H-Ras, G-protein alpha-i3, SOS, Beta-arrestin1, Dynamin-2, p70 S6 kinase2, G-protein alpha-i2, mTOR
206	Development_PACAP signaling in neural cells	39	1.404E-03	9.786E-03	12	MEK1(MAP2K1), RAP-1A, cPKC (conventional), B-Raf, G-protein alpha-s, PLC-beta, cAMP-GEFII, Caspase-3, CREB1, G-protein alpha-q/11, PKA-cat (cAMP-dependent), IP3 receptor
207	Atorvastatin in treatment of type 2 diabetes and metabolic syndrome X	39	1.404E-03	9.786E-03	12	MEK1(MAP2K1), RhoA, APOA1, GPX3, OATP8, APOC3, APOE, PLTP, GSHR, PON1, CD36, Rac1
208	VLDL, LDL dyslipidemia in type 2 diabetes and metabolic syndrome X	39	1.404E-03	9.786E-03	12	Small LDL, Biglycan proteoglycan, SR-BI, MSR1, LDLR, VLDL1, Insulin receptor, APOC3, APOB, APOE, VLDL1 remnant, CD36
209	FGF2 signaling in melanoma	39	1.404E-03	9.786E-03	12	STAT3, RhoA, PI3K cat class IA, B-Raf, N-Ras, Perlecan, Syndecan-4, MEK1/2, CDC42, SOS, Fibronectin, Rac1
210	Immune response_Immunological synapse formation	55	1.492E-03	1.035E-02	15	Talin, RAP-1A, ITGB1, PI3K cat class IA, VCAM1, NCK1, ICAM1, Vinculin, PKC-alpha, MHC class I, CrkL, CDC42, Fyn, WASF2, Rac1
211	Regulation of lipid metabolism_Stimulation of Arachidonic acid production by ACM receptors	72	1.583E-03	1.090E-02	18	BETA-PIX, MEK1(MAP2K1), RhoA, Pyk2(FAK2), PKC, PKC-alpha, Monoglyceride lipase, MEK3(MAP2K3), G-protein alpha-11, ARF6, CDC42, G-protein alpha-q, G-protein alpha-i3, ADAM10, LPP3, Rac1, IP3 receptor, G-protein alpha-13
212	Development_IGF-1 receptor signaling	50	1.612E-03	1.090E-02	14	MEK1(MAP2K1), PI3K cat class IA, RPS6, IGF-2, H-Ras, 14-3-3 zeta/delta, eIF4E, CREB1, SOS, NF-kB, AKT(PKB), MNK1, PDK (PDPK1), p70 S6 kinase2
213	Pro-inflammatory action of Gastrin in gastric cancer	50	1.612E-03	1.090E-02	14	ELAVL1 (HuR), MEK1(MAP2K1), RhoA, PI3K cat class IA, RelA (p65 NF-kB subunit), EGFR, H-Ras, LARG, FAK1, CREB1, G-protein alpha-q, SOS, AKT(PKB), G-protein alpha-q/11
214	IGF-1 signaling in multiple myeloma	50	1.612E-03	1.090E-02	14	RhoA, ITGB1, PI3K cat class IA, H-Ras, FAK1, MEK1/2, CDC42, SOS, NF-kB, AKT(PKB), PDK (PDPK1), Fibronectin, Paxillin, mTOR
215	Development_Glucocorticoid receptor signaling	25	1.623E-03	1.090E-02	9	GCR Beta, GCR, FKBP4, GCR Alpha, NF-kB, HSP90, HSP70, E2I, p23 co-chaperone
216	Apoptosis and survival_Role of nuclear PI3K in NGF/ TrkA signaling	25	1.623E-03	1.090E-02	9	Nucleolin, PI3K cat class IA, AKT1, Ebp1, DFF40 (CAD), RPS3, AKT(PKB), PDK (PDPK1), Acinus
217	Cytoskeleton remodeling_Neurofilaments	25	1.623E-03	1.090E-02	9	Tubulin beta, Desmin, DCTN2, CDK5, Tubulin alpha, Actin cytoskeletal, BPAG1, Vimentin, Tubulin (in microtubules)
218	Development_EPO-induced MAPK pathway	45	1.716E-03	1.142E-02	13	MEK1(MAP2K1), RAP-1A, SOS2, K-RAS, PKC-alpha, Lyn, N-Ras, H-Ras, CrkL, SOS, c-Kit, Rac1, IP3 receptor
219	Mechanisms of resistance to EGFR inhibitors in lung cancer	45	1.716E-03	1.142E-02	13	MEK1(MAP2K1), PI3K cat class IA, K-RAS, EGFR, H-Ras, Beta-catenin, SOS, AKT(PKB), HSP90, PDK (PDPK1), Fibronectin, Vimentin, mTOR
220	Muscle contraction_S1P2 receptor-mediated smooth muscle contraction	30	1.773E-03	1.163E-02	10	RhoA, ROCK2, PKC-alpha, MRLC, G-protein alpha-q, PLC-beta3, G-protein alpha-i2, MLCK, IP3 receptor, G-protein alpha-13
221	Development_Osteopontin signaling in osteoclasts	30	1.773E-03	1.163E-02	10	RhoA, Pyk2(FAK2), ROCK2, MSN (moesin), alpha-V/beta-3 integrin, FAK1, CDC42, Actin cytoskeletal, PIP5KI, VIL2 (ezrin)
222	Cell adhesion_Gap junctions	30	1.773E-03	1.163E-02	10	Tubulin beta, Cingulin, Tubulin alpha, PKC, Connexin 26, ZO-1, ZO-3, Actin, ZO-2, Tubulin (in microtubules)
223	Platelet activation as a result of endothelial dysfunction after stenting	56	1.818E-03	1.172E-02	15	Plasminogen, RhoA, G-protein alpha-s, PKC, alpha-IIb/beta-3 integrin, G-protein alpha-i family, Actin cytoskeletal, G-protein alpha-q, PDE2A, Plasmin, Fibrinogen (fibrin), PLC-beta3, PKA-cat (cAMP-dependent), IP3 receptor, G-protein alpha-13

224	Muscle contraction_ACM regulation of smooth muscle contraction	56	1.818E-03	1.172E-02	15	BETA-PIX, RhoA, ROCK, PKC, MRLC, CDC42, G-protein alpha-q, G-protein alpha-i3, PDK (PDPK1), PLC-beta3, LPP3, MLCK, Rac1, IP3 receptor, G-protein alpha-13
225	Development_Regulation of telomere length and cellular immortalization	35	1.818E-03	1.172E-02	11	Dyskerin (NAP57), hnRNP A1, PI3K cat class IA, PKC-alpha, Ku70, AKT(PKB), HSP90, RPL22, PDK (PDPK1), hnRNP C, p23 co-chaperone
226	Role of Tissue factor in cancer independent of coagulation protease signaling	35	1.818E-03	1.172E-02	11	MEK1(MAP2K1), PKC-alpha, Lyn, H-Ras, FAK1, CDC42, Actin cytoskeletal, SOS, Filamin A, AKT(PKB), Rac1
227	Putative pathways of MHC class I-dependent postsynaptic long-term depression in major depressive disorder	21	1.940E-03	1.245E-02	8	MHC Class I alpha chain, TAP1 (PSF1), Beta-2-microglobulin, HLA-A, TAP2 (PSF2), MHC class I, PIRB, TAP
228	Role of GIP in pathogenesis of type 2 diabetes	46	2.136E-03	1.359E-02	13	Ubiquitin, RAP-1A, B-Raf, G-protein alpha-s, cAMP-GEFII, MEK3(MAP2K3), Caspase-3, AMPK alpha subunit, CREB1, MEK1/2, Kv1.4, AKT(PKB), PKA-cat (cAMP-dependent)
229	Development_Endothelin-1/EDNRA transactivation of EGFR	46	2.136E-03	1.359E-02	13	MEK1(MAP2K1), Pyk2(FAK2), PI3K cat class IA, PLC-beta, EGFR, H-Ras, SOS, AKT(PKB), G-protein alpha-q/11, PDK (PDPK1), p70 S6 kinase2, IP3 receptor, mTOR
230	Regulation of lipid metabolism_Insulin regulation of glycogen metabolism	57	2.200E-03	1.394E-02	15	MEK1(MAP2K1), PI3K cat class IA, PYGL, PHK alpha, PHK gamma (liver), Insulin receptor, G6PT, H-Ras, PHK gamma, HXK4, SOS, PHK beta, AKT(PKB), PDK (PDPK1), PKA-cat (cAMP-dependent)
231	Pioglitazone and Rosiglitazone in treatment of type 2 diabetes and metabolic syndrome X	26	2.224E-03	1.402E-02	9	PPCKC, A-FABP, GLUT2, SR-BI, Insulin receptor, GPD1, HXK4, SORBS1, CD36
232	Pro-tumoral TNF-alpha signaling in melanoma	41	2.262E-03	1.415E-02	12	ITGB1, RhoGDI beta, PI3K cat class IA, VCAM1, AKT1, Filamin-A (CTF), MHC class I, alpha-5/beta-1 integrin, NF-kB, AKT(PKB), PDK (PDPK1), Fibronectin
233	Transcription_Sin3 and NuRD in transcription regulation	41	2.262E-03	1.415E-02	12	Mi-2, Histone H3, SAP18, Mi-2 beta, HDAC1, NRB54, PSF, RBBP4 (RbAp48), p66alpha, MTA2, ARID4A, Histone H4
234	Prolactin/ ERK signaling in breast cancer	36	2.341E-03	1.427E-02	11	PI3K cat class IA, H-Ras, VAV-2, FAK1, GSTM1, MEK1/2, SOS, AKT(PKB), PDK (PDPK1), Paxillin, Rac1
235	Statin action on the PI3K/ Akt pathway in COPD	36	2.341E-03	1.427E-02	11	RhoA, ROCK, p70 S6 kinases, PI3K cat class IA, eNOS, AKT(PKB), HSP90, p70 S6 kinase2, p27KIP1, NIP3, mTOR
236	Propionate metabolism p.1	36	2.341E-03	1.427E-02	11	THEM2, PCC, PCCB, 3HIDH, MUTA, PCCA, MMSA, HCD2, HCDH, MCEE, ACSA
237	E-cadherin signaling and its regulation in gastric cancer	36	2.341E-03	1.427E-02	11	Ubiquitin, RhoA, EGF, EGFR, Beta-catenin, Alpha-actinin, IQGAP1, Plakoglobin, p120-catenin, Actin, Alpha-catenin
238	Role of IL-8 in melanoma	36	2.341E-03	1.427E-02	11	MEK1(MAP2K1), Vitronectin, RelA (p65 NF-kB subunit), B-Raf, ICAM1, alpha-V/beta-3 integrin, G-protein alpha-i family, Beta-catenin, NF-kB, AKT(PKB), PKA-cat (cAMP-dependent)
239	NETosis in SLE	31	2.341E-03	1.427E-02	10	PKC, Histone H3, HMGB1, Pin1, HP1 beta, Histone H2, Histone H2A, Histone H1.2, Histone H4, Histone H1
240	Transport_Macropinocytosis regulation by growth factors	63	2.370E-03	1.439E-02	16	EGF, K-RAS, BAIAP2, EGFR, AMPK beta subunit, H-Ras, VAV-2, AMPK alpha subunit, AMPK gamma subunit, CDC42, Actin cytoskeletal, SOS, AKT(PKB), CtBP1, WASF2, Rac1

241	Cell adhesion_Integrin inside-out signaling in T cells	52	2.421E-03	1.446E-02	14	Talin, RhoA, RAP-1A, ITGB1, VCAM1, ICAM1, Vinculin, PKA-cat alpha, G-protein alpha-i family, Csk, PIP5KI, PLC-beta3, CXCR4, Rac1
242	G-protein signaling_Proinsulin C-peptide signaling	52	2.421E-03	1.446E-02	14	MEK1(MAP2K1), PI3K cat class IA, ATP1A1, ATP1B1, PLC-beta, PKC-alpha, G-protein alpha-i family, H-Ras, eNOS, SOS, NF-kB, AKT(PKB), PDK (PDPK1), IP3 receptor
243	Development_Endothelin-1/EDNRA signaling	52	2.421E-03	1.446E-02	14	MEK1(MAP2K1), Pyk2(FAK2), PI3K cat class IA, G-protein alpha-s, G-protein alpha-i family, H-Ras, Beta-catenin, CDC42, SOS, AKT(PKB), G-protein alpha-q/11, PLC-beta3, Rac1, IP3 receptor
244	Signal transduction_Adenosine A2A receptor signaling pathway	52	2.421E-03	1.446E-02	14	RelA (p65 NF-kB subunit), G-protein alpha-s, ENPP1, H-Ras, eNOS, CREB1, ARF6, MEK1/2, SOS, AKT(PKB), SK4/IK1, SFK, Cathepsin K, PKA-cat (cAMP-dependent)
245	Chemotaxis_CXCR3-A signaling	69	2.496E-03	1.484E-02	17	RhoA, Vinculin, ZO-1, H-Ras, FAK1, CREB1, MEK1/2, CDC42, SOS, AKT(PKB), Beta-arrestin1, PDK (PDPK1), PLC-beta3, G-protein alpha-i2, Cathepsin B, Rac1, IP3 receptor
246	Fructose metabolism	81	2.635E-03	1.555E-02	19	ALDOB, F261, MANA, AMYP, ALDOA, F263, DHSO, HXK1, G6PT, KHK, GPI, ALDR, GALM, HXK4, AK1BA, AMYS, F16Q, PMM2, F16P
247	Development_PIP3 signaling in cardiac myocytes	47	2.636E-03	1.555E-02	13	G-protein alpha-12 family, PI3K cat class IA, RPS6, Insulin receptor, H-Ras, 14-3-3, CREB1, CDC42, PTP-1B, SOS, AKT(PKB), PDK (PDPK1), mTOR
248	EGF- and HGF-dependent stimulation of metastasis in gastric cancer	22	2.734E-03	1.593E-02	8	MEK1(MAP2K1), RhoA, EGF, EGFR, H-Ras, FAK1, SOS, Paxillin
249	Development_S1P4 receptor signaling pathway	22	2.734E-03	1.593E-02	8	MEK1(MAP2K1), RhoA, G-protein alpha-12 family, PLC-beta, G-protein alpha-i family, H-Ras, CDC42, IP3 receptor
250	Translation_Role of Retinoic acid signaling in the initiation of translation	22	2.734E-03	1.593E-02	8	CRM1, FMR1, RPS6, H-Ras, eIF4E, PUR-alpha, MEK1/2, mTOR
251	Apoptosis and survival_BAD phosphorylation	42	2.830E-03	1.636E-02	12	MEK1(MAP2K1), PI3K cat class IA, G-protein alpha-s, EGFR, H-Ras, 14-3-3, SOS, PP2C, AKT(PKB), PDK (PDPK1), p70 S6 kinase2, PKA-cat (cAMP-dependent)
252	Estradiol metabolism	42	2.830E-03	1.636E-02	12	CYP1A2, CYP2C8, UGT2B28, UGT1A10, SULT2A1, CYP3A5, SULT1E1, COMT, CYP3A4, SULT1A1, UGT2B17, UGT1A4
253	Down-regulation of mast cell functions through ITIM-containing inhibitory receptors in asthma	37	2.978E-03	1.700E-02	11	K-RAS, Lyn, alpha-V/beta-3 integrin, MHC class I, Fyn, PECAM1, SOS1, Csk, PIRB, c-Kit, CD47
254	G-protein signaling_RAC1 in cellular process	37	2.978E-03	1.700E-02	11	RhoA, NCK1, BAIAP2, F-Actin cytoskeleton, PAK2, CDC42, Actin cytoskeletal, POR1, PIP5KI, WASF2, Rac1
255	Attenuation of IFN type I signaling in melanoma cells	37	2.978E-03	1.700E-02	11	STAT3, TAP1 (PSF1), STAT2, HLA-A, TAP2 (PSF2), IFNAR2, MHC class I, PSMB9, Tapasin, TAP, Rac1
256	DeltaF508-CFTR traffic / Sorting endosome formation in CF	27	2.988E-03	1.700E-02	9	Ubiquitin, Hrs, NSF, Rab-7, VPS45A, EEA1, Vps25, TSG101, VAMP2
257	EML4/ALK fusion protein in nonsmoking-related lung cancer	32	3.047E-03	1.721E-02	10	STAT3, MEK1(MAP2K1), PI3K cat class IA, B-Raf, K-RAS, EGFR, H-Ras, EML4, NF-kB, AKT(PKB)
258	Epithelial cell apoptosis in COPD	32	3.047E-03	1.721E-02	10	Heme oxygenase 1, PSMA1, PSMB6, GCL reg, DJ-1, NF-kB, AKT(PKB), NRF2, NQO1, NIP3

259	Neuroendocrine transdifferentiation in Prostate Cancer	48	3.229E-03	1.809E-02	13	STAT3, MEK1(MAP2K1), EGFR, H-Ras, CREB1, Beta-catenin, PTP-1B, SOS, AKT(PKB), PDK (PDPK1), AMACR, PKA-cat (cAMP-dependent), mTOR
260	Neurophysiological process_ACM regulation of nerve impulse	48	3.229E-03	1.809E-02	13	RhoA, cPKC (conventional), PKC, PLC-beta, ROCK2, PKC-alpha, G-protein alpha-i family, G-protein alpha-11, G-protein alpha-q, G-protein alpha-q/11, G-protein alpha-i2, PKA-cat (cAMP-dependent), IP3 receptor
261	Development_Role of proteases in hematopoietic stem cell mobilization	18	3.252E-03	1.815E-02	7	VCAM1, alpha-5/beta-1 integrin, DPP4, Fibronectin, c-Kit, Cathepsin K, CXCR4
262	Neurophysiological process_Constitutive and regulated NMDA receptor trafficking	65	3.333E-03	1.853E-02	16	Casein kinase II, alpha chains, RACK1, Pyk2(FAK2), cPKC (conventional), CDK5, G-protein alpha-s, PKC, PLC-beta, CASK, G-protein alpha-i family, MALS, Fyn, G-protein alpha-q, PKA-cat (cAMP-dependent), VAMP2, IP3 receptor
263	Development_EGFR signaling pathway	71	3.444E-03	1.908E-02	17	STAT3, MEK1(MAP2K1), EGF, PI3K cat class IA, Caspase-7, PARP-1, NCK1, PKC-alpha, EGFR, H-Ras, FAK1, SOS, NF-kB, AKT(PKB), PDK (PDPK1), ILK, Rac1
264	Nicotine signaling in dopaminergic neurons, Pt. 2 - axon terminal	43	3.508E-03	1.929E-02	12	Plasminogen, CDK5, G-protein alpha-s, PLC-beta, G-protein alpha-i family, CREB1, Casein kinase I epsilon, G-protein alpha-q, Plasmin, PKA-cat (cAMP-dependent), VAMP2, IP3 receptor
265	Regulation of metabolism_Role of Adiponectin in regulation of metabolism	43	3.508E-03	1.929E-02	12	PPCKC, SREBP1 precursor, AdipoR2, ACACA, Raptor, Insulin receptor, G6PT, AMPK alpha subunit, CREB1, ACADM, ACOX1, mTOR
266	ERBB family and HGF signaling in gastric cancer	54	3.538E-03	1.938E-02	14	STAT3, EGF, PI3K cat class IA, Neuregulin 1, EGFR, H-Ras, GRB7, MEK3(MAP2K3), Beta-catenin, MEK1/2, SOS, AKT(PKB), PDK (PDPK1), p27KIP1
267	Cell adhesion_Role of CDK5 in cell adhesion	10	3.588E-03	1.958E-02	5	Talin, ITGB1, CDK5, Beta-catenin, Alpha-catenin
268	G-protein signaling_G-Protein alpha-12 signaling pathway	38	3.749E-03	1.996E-02	11	MEK1(MAP2K1), RhoA, RAP-1A, ROCK, G-protein alpha-12 family, PI3K cat class IA, LARG, CDC42, R-Ras, PKA-cat (cAMP-dependent), Rac1
269	wtCFTR and deltaF508-CFTR traffic / Generic schema (normal and CF)	38	3.749E-03	1.996E-02	11	Ubiquitin, Rab-4, Hrs, PIST (CAL), Rab-7, VAMP8, Coatomer, EBP50, Vps25, TSG101, VAMP2
270	Impaired macrophage phagocytic function in asthma	38	3.749E-03	1.996E-02	11	GSTP1, RhoA, ROCK, SP-A, GCL reg, Calreticulin, GSTM1, GSTT1, NRF2, LRP1, Rac1
271	HDL dyslipidemia in type 2 diabetes and metabolic syndrome X	38	3.749E-03	1.996E-02	11	Small LDL, APOA1, LCAT, Pre beta-1 HDL, Large alpha-1 HDL, Small HDL, APOE, PLTP, HDL, Nascent HDL, PON1
272	Transcription_ChREBP regulation pathway	23	3.760E-03	1.996E-02	8	G-protein alpha-s, AMPK beta subunit, G-protein alpha-i family, AMPK alpha subunit, AMPK gamma subunit, KPYR, PKA-cat (cAMP-dependent), Acyl-CoA synthetase
273	Role of stellate cells in progression of pancreatic cancer	60	3.767E-03	1.996E-02	15	MEK1(MAP2K1), PI3K cat class IA, RelA (p65 NF-kB subunit), alpha-V/beta-3 integrin, EGFR, H-Ras, FAK1, Galectin-1, alpha-5/beta-1 integrin, SOS, AKT(PKB), Fibrinogen (fibrin), PDK (PDPK1), Fibronectin, NF-kB p65/p65
274	Immune response_LTBR1 signaling	60	3.767E-03	1.996E-02	15	RAP-1A, PI3K cat class IA, AUF1, CRM1, PKC, PLC-beta, G-protein alpha-i family, H-Ras, eNOS, MEK1/2, AKT(PKB), G-protein alpha-q/11, PDK (PDPK1), Rac1, IP3 receptor
275	Oxidative stress_ROS-mediated MAPK activation via canonical pathways	60	3.767E-03	1.996E-02	15	GSTP1, Pyk2(FAK2), EGFR, H-Ras, MEK3(MAP2K3), RIPK1, MEK1/2, CDC42, Fyn, CRK, SOS, SFK, Rac1, IP3 receptor, CaMK II delta

276	SDF-1 axis in endothelial progenitor cell recruitment in healing myocardial infarction	33	3.913E-03	2.044E-02	10	Heme oxygenase 1, ICAM1, RPS6, eNOS, AKT(PKB), PDK (PDPK1), ILK, CXCR4, Rac1, mTOR
277	Development_EGFR signaling via small GTPases	33	3.913E-03	2.044E-02	10	EGF, PI3K cat class IA, K-RAS, EGFR, N-Ras, H-Ras, VAV-2, MEK1/2, SOS, Rac1
278	Development_Activation of astroglial cells proliferation by ACM3	33	3.913E-03	2.044E-02	10	RhoA, PI3K cat class IA, eIF4E, ARF6, G-protein alpha-q, AKT(PKB), PDK (PDPK1), IP3 receptor, mTOR, G-protein alpha-13
279	Development_EGF-induced proliferation of Type C cells in SVZ of adult brain	33	3.913E-03	2.044E-02	10	MEK1(MAP2K1), EGF, PI3K cat class IA, EGFR, H-Ras, Fyn, SOS, AKT(PKB), PDK (PDPK1), p27KIP1
280	Rho-dependent regulation of normal and asthmatic smooth muscle contraction	28	3.944E-03	2.052E-02	9	RACK1, RhoA, ROCK, PKC, PLC-beta, G-protein alpha-i family, MRLC, Myosin II, G-protein alpha-q/11
281	Signal transduction_Angiotensin II/ AGTR1 signaling via RhoA and JNK	78	4.063E-03	2.107E-02	18	RhoA, Pyk2(FAK2), ROCK, G-protein alpha-12 family, NCK1, EPHX2, ROCK2, Vinculin, MRLC, LARG, eNOS, FAK1, CRK, G-protein alpha-q/11, MLCK, Paxillin, Rac1, IP3 receptor
282	Cell adhesion_ECM remodeling	55	4.237E-03	2.166E-02	14	Plasminogen, Vitronectin, MSN (moesin), EGFR, IGF-2, MMP-12, alpha-5/beta-1 integrin, Actin cytoskeletal, alpha-1/beta-1 integrin, Plasmin, Fibronectin, Kallikrein 1, Flotillin-2, VIL2 (ezrin)
283	Chemotaxis_CCL2-induced chemotaxis	55	4.237E-03	2.166E-02	14	RhoA, Pyk2(FAK2), ROCK, PI3K cat class IA, Lyn, G-protein alpha-i family, H-Ras, MEK1/2, CDC42, Actin cytoskeletal, SOS, Paxillin, Rac1, IP3 receptor
284	Aberrant B-Raf signaling in melanoma progression	55	4.237E-03	2.166E-02	14	MEK1(MAP2K1), ITGB1, ROCK, AKT1, Raptor, B-Raf, ITGB3, SRp55, AMPK alpha subunit, MEK1/2, RKIP, AKT(PKB), Nicastrin, mTOR
285	Development_WNT/Beta-catenin signaling in the cytoplasm	55	4.237E-03	2.166E-02	14	Casein kinase II, alpha chains, RhoA, G-protein alpha-s, DAAM1, MACF1, VAV-2, Casein kinase II, Casein kinase I epsilon, Beta-catenin, G-protein alpha-q, AKT(PKB), p120-catenin, PLC-beta3, Rac1
286	Development_Activation of Erk by ACM1, ACM3 and ACM5	44	4.310E-03	2.166E-02	12	MEK1(MAP2K1), RAP-1A, Pyk2(FAK2), B-Raf, PKC-alpha, EGFR, H-Ras, G-protein alpha-11, CREB1, G-protein alpha-q, SOS, IP3 receptor
287	Development_Ligand-independent activation of ESR1 and ESR2	44	4.310E-03	2.166E-02	12	MEK1(MAP2K1), EGF, PI3K cat class IA, G-protein alpha-s, NCOA3 (pCIP/SRC3), Neuregulin 1, EGFR, H-Ras, SOS, AKT(PKB), PDK (PDPK1), PKA-cat (cAMP-dependent)
288	Development_Flt3 signaling	44	4.310E-03	2.166E-02	12	MEK1(MAP2K1), PI3K cat class IA, H-Ras, MEK3(MAP2K3), CrkL, CDC42, Fyn, CRK, SOS, AKT(PKB), PDK (PDPK1), Rac1
289	Chemotaxis_C5a-induced chemotaxis	44	4.310E-03	2.166E-02	12	RAP-1A, B-Raf, PLC-beta, HSP27, G-protein alpha-i family, C5a, F-Actin cytoskeleton, MEK1/2, CDC42, Actin cytoskeletal, Rac1, IP3 receptor
290	Development_S1P1 signaling pathway	44	4.310E-03	2.166E-02	12	RhoA, AKT1, PLC-beta, G-protein alpha-i family, eNOS, CDC42, G-protein alpha-i3, AKT(PKB), PDK (PDPK1), G-protein alpha-i2, Rac1, IP3 receptor
291	Immune response_IL-11 signaling pathway via MEK/ERK and PI3K/AKT cascades	67	4.597E-03	2.302E-02	16	p70 S6 kinases, gp130, RelA (p65 NF-kB subunit), ICAM1, RPS6, H-Ras, Caspase-3, CREB1, MEK1/2, Fyn, SOS, AKT(PKB), PDK (PDPK1), ADAM10, SFK, p27KIP1
292	Cytoskeleton remodeling_Alpha-1A adrenergic receptor-dependent inhibition of PI3K	19	4.625E-03	2.308E-02	7	MRLC, Myosin II, G-protein alpha-q, AKT(PKB), MELC, PDK (PDPK1), MLCK

293	Role of tumor microenvironment in plexiform neurofibroma formation in neurofibromatosis type 1	39	4.670E-03	2.314E-02	11	MEK1(MAP2K1), PI3K cat class IA, VCAM1, K-RAS, H-Ras, MEK1/2, SOS, AKT(PKB), PDK (PDPK1), Fibronectin, c-Kit
294	Immune response_HMGB1 release from the cell	39	4.670E-03	2.314E-02	11	PI3K cat class IA, PARP-1, CRM1, HMGB1, PKC-alpha, MEK1/2, NF-kB, PDK (PDPK1), Karyopherin alpha 1, HSPA1A, IP3 receptor
295	Apoptosis and survival_HTR1A signaling	50	4.737E-03	2.340E-02	13	STAT3, MEK1(MAP2K1), PARP-1, PP2A structural, G-protein alpha-i family, H-Ras, Caspase-3, PP2A regulatory, SOS, NF-kB, AKT(PKB), PDK (PDPK1), PKA-cat (cAMP-dependent)
296	Development_Role of CDK5 in neuronal development	34	4.962E-03	2.434E-02	10	DCTN2, PI3K cat class IA, CDK5, Beta-catenin, Actin cytoskeletal, Fyn, Pin1, AKT(PKB), PAFAH alpha (LIS1), Tubulin (in microtubules)
297	Development_CNTF receptor signaling	34	4.962E-03	2.434E-02	10	STAT3, MEK1(MAP2K1), gp130, PI3K cat class IA, H-Ras, LIFR, SOS, AKT(PKB), p70 S6 kinase2, mTOR
298	Impaired inhibitory action of lipoxins on neutrophil migration in CF	56	5.044E-03	2.457E-02	14	Talin, ICAM1, G-protein alpha-i family, MRLC, Myosin II, Actin cytoskeletal, Alpha-actinin, AKT(PKB), MELC, PDK (PDPK1), PIP5KI, MYLK1, MLCK, Rac1
299	Proteolysis_Role of Parkin in the Ubiquitin-Proteasomal Pathway	24	5.060E-03	2.457E-02	8	Cullin 1, Tubulin beta, UBE1, Tubulin alpha, CASK, UBC7, HSP70, UBC6
300	Development_Dopamine D2 receptor transactivation of EGFR	24	5.060E-03	2.457E-02	8	MEK1(MAP2K1), PI3K cat class IA, EGFR, G-protein alpha-i family, H-Ras, SOS, AKT(PKB), PDK (PDPK1)
301	Muscle contraction_Oxytocin signaling in uterus and mammary gland	62	5.246E-03	2.518E-02	15	MEK1(MAP2K1), RhoA, eEF2, ROCK, cPKC (conventional), PKC, PKC-alpha, EGFR, H-Ras, LARG, G-protein alpha-i3, PGES2, G-protein alpha-q/11, PLC-beta3, IP3 receptor
302	Development_Gastrin in cell growth and proliferation	62	5.246E-03	2.518E-02	15	STAT3, MEK1(MAP2K1), PI3K cat class IA, PKC-alpha, EGFR, H-Ras, FAK1, CREB1, Beta-catenin, G-protein alpha-q, SOS, G-protein alpha-q/11, PDK (PDPK1), p70 S6 kinase2, IP3 receptor
303	Development_Alpha-2 adrenergic receptor activation of ERK	62	5.246E-03	2.518E-02	15	MEK1(MAP2K1), Pyk2(FAK2), CYP2C8, PI3K cat class IA, Monoglyceride lipase, EGFR, G-protein alpha-i family, H-Ras, G-protein alpha-i3, SOS, AKT(PKB), PDK (PDPK1), PLC-beta3, G-protein alpha-i2, IP3 receptor
304	Role of TNF-alpha, IL-1beta and IL-6 in development of obesity and type 2 diabetes in liver	45	5.253E-03	2.518E-02	12	STAT3, APOA1, AKT1, RelA (p65 NF-kB subunit), CRP, Insulin receptor, G6PT, APOB, HSP90 alpha, PTP-1B, HXK4, mTOR
305	Immune response_Gastrin in inflammatory response	68	5.362E-03	2.553E-02	16	ELAVL1 (HuR), MEK1(MAP2K1), RhoA, PI3K cat class IA, PKC-alpha, EGFR, H-Ras, LARG, FAK1, CREB1, G-protein alpha-q, SOS, AKT(PKB), G-protein alpha-q/11, PDK (PDPK1), IP3 receptor
306	Lipoprotein metabolism	68	5.362E-03	2.553E-02	16	Small LDL, APOA1, APOA2, SR-BI, Medium HDL, LDLR, VLDL1, LCAT, Pre beta-1 HDL, APOB, APOE, APOC2, PLTP, VLDL2, Nascent HDL, Large LDL
307	Transcription_Role of heterochromatin protein 1 (HP1) family in transcriptional silencing	40	5.761E-03	2.734E-02	11	TIF1-beta, Mi-2, MeCP2, Histone H3, CtBP, HDAC1, HP1 beta, E2I, HP1 gamma, HP1, Histone H4
308	Immune response_M-CSF-receptor signaling pathway	81	6.181E-03	2.914E-02	18	STAT3, MEK1(MAP2K1), RhoA, Pyk2(FAK2), PI3K cat class IA, PKC, MSR1, H-Ras, Beta-catenin, CDC42, Fyn, CRK, NF-kB, AKT(PKB), SOS1, PDK (PDPK1), Rac1, IP3 receptor

309	G-protein signaling_S1P2 receptor signaling pathway	35	6.220E-03	2.914E-02	10	RhoA, G-protein alpha-i family, FAK1, G-protein alpha-q, AKT(PKB), PDK (PDPK1), PLC-beta3, G-protein alpha-i2, IP3 receptor, G-protein alpha-13
310	Anti-apoptotic action of Gastrin in pancreatic cancer	35	6.220E-03	2.914E-02	10	RhoA, PI3K cat class IA, RelA (p65 NF-kB subunit), MEK3(MAP2K3), Caspase-3, LARG, FAK1, G-protein alpha-q, AKT(PKB), PDK (PDPK1)
311	Neurophysiological process_Ephrin-B receptors in dendritic spine morphogenesis and synaptogenesis	35	6.220E-03	2.914E-02	10	BETA-PIX, NCK1, Synbindin, Cortactin, CDC42, Actin cytoskeletal, Fyn, Dynamin-2, Intersectin, Rac1
312	Niacin-HDL metabolism	46	6.354E-03	2.948E-02	12	VLDL, APOA1, SR-BI, NNMT, HDL proteins, LIPP, APOB, LDL, AOX1, DGAT2, LIPS, GLYAT
313	Signal transduction_Calcium signaling	46	6.354E-03	2.948E-02	12	RhoA, ROCK, cPKC (conventional), PLC-beta, Ca-ATPase2, CaMK I, CREB1, Calcipressin 1, PKA-cat (cAMP-dependent), IP3 receptor, RhoGDI alpha, VIL2 (ezrin)
314	Transcription_Androgen Receptor nuclear signaling	46	6.354E-03	2.948E-02	12	STAT3, MEK1(MAP2K1), Pyk2(FAK2), EGF, AKT1, EGFR, H-Ras, Beta-catenin, SOS, AKT(PKB), PKA-cat (cAMP-dependent), VIL2 (ezrin)
315	Development_FGF2-dependent induction of EMT	20	6.394E-03	2.948E-02	7	RhoA, PI3K cat class IA, CDC42, AKT(PKB), PDK (PDPK1), p27KIP1, Rac1
316	HBV mediates angiogenesis in HCC	20	6.394E-03	2.948E-02	7	STAT3, MEK1(MAP2K1), Pyk2(FAK2), H-Ras, FAK1, HDAC1, SOS
317	Role of histone modificators in progression of multiple myeloma	30	6.562E-03	2.997E-02	9	Tubulin alpha, Histone H3, K-RAS, N-Ras, Caspase-3, HDAC1, p27KIP1, Histone H4, CDK6
318	Inhibition of Ephrin receptors in colorectal cancer	30	6.562E-03	2.997E-02	9	RhoA, RAP-1A, ROCK, VAV-2, FAK1, Beta-catenin, CDC42, Paxillin, Rac1
319	Apoptosis and survival_Granzyme A signaling	30	6.562E-03	2.997E-02	9	Histone H3, SET, Histone H2B, Lamin B1, Lamin A/C, PHAP1 (pp32), Ku70, APEX, Histone H1
320	Development_ROBO2, ROBO3 and ROBO4 signaling pathways	25	6.677E-03	3.040E-02	8	MYH9, NCK1, ARF6, Myosin II, CDC42, alpha-5/beta-1 integrin, Paxillin, Rac1
321	Glycolysis and gluconeogenesis	94	6.729E-03	3.054E-02	20	G3P2, PPCKC, TPI1, ALDOB, ALDOA, GLUT2, HXK1, G6PT, PGAM4, GPI, PYC, KPYR, GALM, HXK4, ENO1, PGAM1, MDH1, PGK1, F16Q, F16P
322	IGF signaling in HCC	52	6.766E-03	3.061E-02	13	Junctin, MEK1(MAP2K1), PI3K cat class IA, PKC, EGFR, IGF-2, H-Ras, RKIP, SOS, GSTA2, AKT(PKB), IGF-2 receptor, PDK (PDPK1)
323	Hyaluronic acid/ CD44 signaling in cancer	58	7.026E-03	3.142E-02	14	STAT3, RhoA, ROCK, AKT1, PDCD4, LARG, VAV-2, CDC42, Actin cytoskeletal, IQGAP1, Filamin A, DDX5, MDR1, Rac1
324	TGF-beta signaling via kinase cascades in breast cancer	58	7.026E-03	3.142E-02	14	Ubiquitin, MEK1(MAP2K1), ITGB1, RelA (p65 NF-kB subunit), ITGAV, Neuregulin 1, ITGB3, alpha-V/beta-3 integrin, EGFR, MEK3(MAP2K3), FAK1, AKT(PKB), SOS1, Rac1
325	Translation_(L)-selenoaminoacids incorporation in proteins during translation	41	7.044E-03	3.142E-02	11	SEP15, Selenoprotein K, GPX3, DIO1, RPL30, Selenoprotein P, GPX4, SEPHS1, SEPX1 (Selenoprotein X1), SelT, SELI
326	Development_VEGF-family signaling	41	7.044E-03	3.142E-02	11	MEK1(MAP2K1), Vitronectin, PI3K cat class IA, PKC-alpha, alpha-V/beta-3 integrin, H-Ras, alpha-5/beta-1 integrin, SOS, AKT(PKB), Fibronectin, IP3 receptor

327	CTP/UTP metabolism	107	7.052E-03	3.142E-02	22	AK2, NDPK C, PCY1A, UDP, BUP1, DPYD, DPYS, RRP46, KCY, RPB8, PR44 (DIS3), CTP synthase, RPB10, PD-ECGF (TdRPase), POLR2I, POLR2B, CDD, POLR2A, POLR2J, PM/SCL-75, UCK1, AK3
328	Development_Positive regulation of WNT/Beta-catenin signaling in the cytoplasm	76	7.162E-03	3.163E-02	17	Casein kinase II, alpha chains, HECTD1, ITGB1, EGF, Insulin receptor, USP7, 14-3-3 zeta/delta, Alpha-1 catenin, FAK1, 14-3-3, PP2C alpha, Beta-catenin, HSP105, AKT(PKB), PKA-cat (cAMP-dependent), ILK, Rac1
329	G protein-coupled receptors signaling in lung cancer	76	7.162E-03	3.163E-02	17	STAT3, RhoA, Pyk2(FAK2), EGF, G-protein alpha-12 family, RelA (p65 NF-kB subunit), G-protein alpha-s, alpha-V/beta-3 integrin, EGFR, G-protein alpha-i family, Galpha(i)-specific peptide GPCRs, Galpha(q)-specific peptide GPCRs, AKT(PKB), G-protein alpha-q/11, PDK (PDPK1), PKA-cat (cAMP-dependent), CXCR4
330	HGF signaling in colorectal cancer	64	7.164E-03	3.163E-02	15	HPGD, PI3K cat class IA, AKT1, EGFR, H-Ras, FAK1, Beta-catenin, MEK1/2, Actin cytoskeletal, SOS, AKT(PKB), ADAM10, Rac1, mTOR, VIL2 (ezrin)
331	Signal transduction_PDGF signaling via PI3K/AKT and NFkB pathways	70	7.202E-03	3.170E-02	16	PDK1, RelA (p65 NF-kB subunit), MYH11, K-RAS, PI3K cat class IA (p110-beta), Transgelin, Beta-catenin, YB-1, NF-kB, AKT(PKB), SOS1, PDK (PDPK1), DDX5, p27KIP1, Rac1, mTOR
332	Development_HGF signaling pathway	47	7.628E-03	3.338E-02	12	STAT3, MEK1(MAP2K1), RAP-1A, PI3K cat class IA, H-Ras, CrkL, Beta-catenin, CRK, SOS, AKT(PKB), PDK (PDPK1), Rac1
333	Transport_Alpha-2 adrenergic receptor regulation of ion channels	47	7.628E-03	3.338E-02	12	G-protein alpha-s, PKC, Sorcin, G-protein alpha-i family, G-protein alpha-q, G-protein alpha-i3, AKT(PKB), PDK (PDPK1), PLC-beta3, G-protein alpha-i2, PKA-cat (cAMP-dependent), IP3 receptor
334	HBV signaling via protein kinases leading to HCC	36	7.712E-03	3.344E-02	10	MEK1(MAP2K1), Pyk2(FAK2), cPKC (conventional), PKC, PKC-alpha, IGF-2, H-Ras, FAK1, SOS, Pin1
335	Development_SSTR2 in regulation of cell proliferation	36	7.712E-03	3.344E-02	10	MEK1(MAP2K1), RAP-1A, PI3K cat class IA, B-Raf, G-protein alpha-i family, H-Ras, SOS, AKT(PKB), PDK (PDPK1), p27KIP1
336	G-protein signaling_G-Protein alpha-s signaling cascades	36	7.712E-03	3.344E-02	10	MEK1(MAP2K1), RAP-1A, B-Raf, G-protein alpha-s, cAMP-GEFII, H-Ras, CREB1, KPYR, Alpha adducin, PKA-cat (cAMP-dependent)
337	c-Myc in multiple myeloma	16	7.870E-03	3.403E-02	6	STAT3, hnRNP A1, GRP78, eIF4E, YB-1, PTBP1
338	Immune response_HMGB1/RAGE signaling pathway	53	8.010E-03	3.433E-02	13	PI3K cat class IA, VCAM1, K-RAS, HMGB1, ICAM1, FAK1, CREB1, MEK1/2, CDC42, NF-kB, AKT(PKB), Paxillin, Rac1
339	Regulation of VEGF expression in lung cancer	53	8.010E-03	3.433E-02	13	STAT3, RhoA, ROCK, gp130, PI3K cat class IA, alpha-V/beta-3 integrin, NF-kB, AKT(PKB), HSP90, RhoC, PDK (PDPK1), c-Kit, mTOR
340	Immune response_Induction of the antigen presentation machinery by IFN-gamma	53	8.010E-03	3.433E-02	13	TAP1 (PSF1), Beta-2-microglobulin, HLA-E, HLA-A, WDR5, PSMB10, TAP2 (PSF2), MHC class I, PSMB9, HLA-F, Tapasin, HLA-DQA1, Cathepsin S
341	Muscle contraction_GPCRs in the regulation of smooth muscle tone	83	8.038E-03	3.435E-02	18	RhoA, ROCK, G-protein alpha-12 family, G-protein alpha-s, PLC-beta, PKC-alpha, G-protein alpha-i family, MRLC, LARG, Telokin, Myosin II, G-protein alpha-q, G-protein alpha-q/11, MELC, MyHC, PKA-cat (cAMP-dependent), MLCK, IP3 receptor
342	Immune response _CCR3 signaling in eosinophils	77	8.198E-03	3.490E-02	17	MEK1(MAP2K1), RhoA, ROCK, ROCK2, PKC-alpha, G-protein alpha-i family, H-Ras, MRLC, VAV-2, Myosin II, Actin cytoskeletal, MELC, PDK (PDPK1), MyHC, MLCK, Rac1, IP3 receptor
343	Oxidative stress_Activation of NADPH oxidase	59	8.227E-03	3.490E-02	14	BETA-PIX, cPKC (conventional), PI3K cat class IA, AKT1, PKC, PLC-beta, PKC-alpha, VAV-2, MEK1/2, Pin1, AKT(PKB), PDK (PDPK1), Rac1, IP3 receptor
344	Development_Activation of ERK by Kappa-type opioid receptor	31	8.288E-03	3.490E-02	9	MEK1(MAP2K1), Pyk2(FAK2), PLC-beta, PKC-alpha, G-protein alpha-i family, H-Ras, SOS, PDK (PDPK1), IP3 receptor

345	Neutrophil adhesion and transendothelial migration in asthma	31	8.288E-03	3.490E-02	9	GLG1, VCAM1, HMGB1, ICAM1, alpha-9/beta-1 integrin, H-Ras, C5a, Substance P receptor, MEK1/2
346	Alternative complement cascade disruption in age-related macular degeneration	31	8.288E-03	3.490E-02	9	Factor B, CRP, Factor I, C5a, Factor Bb, C5, Factor H, C5b, Factor Ba
347	Ovarian cancer (main signaling cascades)	65	8.313E-03	3.491E-02	15	EGF, PI3K cat class IA, B-Raf, K-RAS, EGFR, G-protein alpha-i family, H-Ras, CREB1, Beta-catenin, MEK1/2, SOS, NF-kB, AKT(PKB), PKA-cat (cAMP-dependent), ILK
348	Transport_ACM3 signaling in salivary glands	42	8.540E-03	3.575E-02	11	PKC, PLC-beta, G-protein alpha-i family, eNOS, G-protein alpha-11, G-protein alpha-q, G-protein alpha-i3, G-protein alpha-q/11, PKA-cat (cAMP-dependent), MLCK, IP3 receptor
349	Role of ZNF202 in regulation of expression of genes involved in atherosclerosis	21	8.622E-03	3.599E-02	7	TIF1-beta, APOC3, LCAT, HDL proteins, APOE, PLTP, HNF4-alpha
350	Muscle contraction_Relaxin signaling pathway	48	9.095E-03	3.786E-02	12	MEK1(MAP2K1), RAP-1A, B-Raf, G-protein alpha-s, PI3K cat class IA (p110-beta), G-protein alpha-i family, eNOS, CREB1, G-protein alpha-i3, NF-kB, AKT(PKB), PKA-cat (cAMP-dependent)
351	Development_FGFR signaling pathway	54	9.428E-03	3.885E-02	13	Ubiquitin, MEK1(MAP2K1), PI3K cat class IA, H-Ras, Perlecan, Syndecan-4, CREB1, CRK, SOS, AKT(PKB), PDK (PDPK1), Rac1, IP3 receptor
352	Membrane-bound ESR1: interaction with G-proteins signaling	54	9.428E-03	3.885E-02	13	MEK1(MAP2K1), G-protein alpha-s, PKC-alpha, EGFR, G-protein alpha-i family, H-Ras, eNOS, CREB1, G-protein alpha-q, SOS, Striatin, PKA-cat (cAMP-dependent), IP3 receptor
353	Development_Growth factors in regulation of oligodendrocyte precursor cell survival	37	9.465E-03	3.885E-02	10	PI3K cat class IA, RelA (p65 NF-kB subunit), Neuregulin 1, Lyn, 14-3-3 zeta/delta, Caspase-3, Fyn, AKT(PKB), PDK (PDPK1), mTOR
354	Glycogen metabolism	37	9.465E-03	3.885E-02	10	PYGB, UGPA2, PYGL, HXK1, GLGB, GPI, PGMU, GALM, HXK4, GDE
355	Immune response_Regulation of T cell function by CTLA-4	37	9.465E-03	3.885E-02	10	PI3K cat class IA, AP complex 2 medium (mu) chain, Lyn, H-Ras, Beta-adaptin 2, Fyn, SOS, NF-kB, AKT(PKB), PDK (PDPK1)
356	IGF family signaling in colorectal cancer	60	9.585E-03	3.923E-02	14	RelA (p65 NF-kB subunit), IGF-2, H-Ras, eIF4E, Clusterin, Beta-catenin, MEK1/2, SOS, NF-kB, AKT(PKB), IGF-2 receptor, MNK1, MAT2A, mTOR
357	Prostaglandins and leukotrienes-mediated induction of expression of mucins in normal and asthmatic epithelium	43	1.027E-02	4.138E-02	11	MEK1(MAP2K1), G-protein alpha-s, PLC-beta, PKC-alpha, EGFR, G-protein alpha-i family, CREB1, NF-kB, G-protein alpha-q/11, PKA-cat (cAMP-dependent), IP3 receptor
358	Role of cell adhesion in vaso-occlusion in Sickle cell disease	43	1.027E-02	4.138E-02	11	GLG1, VCAM1, alpha-IIb/beta-3 integrin, ICAM1, alpha-V/beta-3 integrin, BCAM, PECAM1, Fibrinogen (fibrin), Fibronectin, PKA-cat (cAMP-dependent), CD36
359	Apoptosis and survival_TNFR1 signaling pathway	43	1.027E-02	4.138E-02	11	Caspase-7, BRE, tBid, Caspase-3, RIPK1, SODD, jBid, NF-kB, Smac/Diablo, GCK(MAP4K2), Bid
360	Selective Insulin resistance in type 2 diabetes in liver	32	1.034E-02	4.138E-02	9	PPCKC, AKT1, Insulin receptor, G6PT, KPYR, PTP-1B, HXK4, AKT(PKB), PDK (PDPK1)
361	Androstenedione and testosterone biosynthesis and metabolism p.2	32	1.034E-02	4.138E-02	9	UGT2B28, AKR1C4, UGT1A10, AK1D1, AKR1C1, UGT1A9, UGT1A8, UGT2B17, UGT1A4

362	Cell cycle_Role of Nek in cell cycle regulation	32	1.034E-02	4.138E-02	9	Tubulin beta, PI3K cat class IA, Tubulin alpha, Histone H3, Insulin receptor, PDK (PDPK1), Ran, Histone H1, Tubulin (in microtubules)
363	Development_Role of Ceramide 1-phosphate, Sphingosine 1-phosphate and Complement cascade in hematopoietic stem cell homing	32	1.034E-02	4.138E-02	9	RhoA, RAP-1A, VCAM1, VAV-2, CREB1, CDC42, AKT(PKB), CXCR4, Rac1
364	Protein folding and maturation_Bradykinin / Kallidin maturation	32	1.034E-02	4.138E-02	9	Neprilysin, ENPEP, Tissue kallikreins, Carboxypeptidase N (cat), Plasmin, CPB2, Plasma kallikrein, Prolyl endopeptidase, CD13
365	CHDI_Correlations from Replication data_Causal network (positive correlations)	79	1.063E-02	4.242E-02	17	RhoA, Pyk2(FAK2), ROCK, PI3K cat class IA, ICAM1, PKC-alpha, HIP1, MEK3(MAP2K3), Caspase-3, CREB1, NF-kB, AKT(PKB), HSP70, CXCR4, IP3 receptor, RhoGDI alpha, VIL2 (ezrin)
366	Signal transduction_Angiotensin II/ AGTR1 signaling via p38, ERK and PI3K	98	1.074E-02	4.242E-02	20	ELAVL1 (HuR), Pyk2(FAK2), p70 S6 kinases, PI3K cat class IA, CYP11B2, EGFR, H-Ras, eIF4E, CREB1, MEK1/2, Fyn, G-protein alpha-q, SOS, AKT(PKB), ATOX1, MNK1, Catalase, PDK (PDPK1), PKA-cat (cAMP-dependent), CaMK II delta
367	Activation of TNF-alpha-dependent pro-tumoral effect in colorectal cancer	49	1.077E-02	4.242E-02	12	VCAM1, RelA (p65 NF-kB subunit), G-protein alpha-s, K-RAS, ICAM1, H-Ras, RIPK1, ALDR, Beta-catenin, MEK1/2, SOS, NF-kB
368	Glucocorticoids-mediated inhibition of pro-constrictory and pro-inflammatory signaling in airway smooth muscle cells	49	1.077E-02	4.242E-02	12	RhoA, RelA (p65 NF-kB subunit), GCR Beta, G-protein alpha-s, GCR, CD38, MRLC, Myosin II, GCR Alpha, NF-kB, PLA2, Histone H4
369	Neurophysiological process_HTR2A signaling in the nervous system	49	1.077E-02	4.242E-02	12	RACK1, Heme oxygenase 1, cPKC (conventional), PKC, PLC-beta, CDC42, AKT(PKB), G-protein alpha-q/11, NRF2, SFK, Rac1, IP3 receptor
370	Signal transduction_Soluble CXCL16 signaling	49	1.077E-02	4.242E-02	12	STAT3, RhoA, ROCK, alpha-IIb/beta-3 integrin, G-protein alpha-i family, F-Actin cytoskeleton, MEK1/2, NF-kB, AKT(PKB), PDK (PDPK1), CD163, mTOR
371	Immune response_IL-2 signaling via ERK, PI3K, and PLC-gamma	73	1.088E-02	4.259E-02	16	STAT3, p70 S6 kinases, PI3K cat class IA, Lyn, RPS6, H-Ras, CrkL, MEK1/2, Fyn, NF-kB, AKT(PKB), SOS1, p70 S6 kinase2, p27KIP1, Rac1, mTOR
372	Transcription_Transcription factor Tubby signaling pathways	17	1.096E-02	4.259E-02	6	PKC, PLC-beta, Insulin receptor, G-protein alpha-11, G-protein alpha-q, G-protein alpha-q/11
373	IL-1 production in melanoma	17	1.096E-02	4.259E-02	6	RelA (p65 NF-kB subunit), B-Raf, CARD5, N-Ras, MEK1/2, NF-kB
374	Immune response_Platelet activating factor/ PTAFR pathway signaling	55	1.103E-02	4.259E-02	13	STAT3, STAT2, PI3K cat class IA, PLC-beta, G-protein alpha-i family, F-Actin cytoskeleton, MEK3(MAP2K3), G-protein alpha-q, NF-kB, AKT(PKB), Beta-arrestin1, PKA-cat (cAMP-dependent), IP3 receptor
375	G-protein signaling_G-Protein alpha-i signaling cascades	27	1.104E-02	4.259E-02	8	STAT3, MEK1(MAP2K1), RAP-1A, B-Raf, G-protein alpha-i family, H-Ras, SOS, PKA-cat (cAMP-dependent)
376	Insulin-dependent stimulation of SREBP-1 in type 2 diabetes in liver	27	1.104E-02	4.259E-02	8	SREBP1 precursor, INSIG2, ACACA, SREBP1 (nuclear), Insulin receptor, PDK (PDPK1), FASN, SREBP1 (Golgi membrane)

377	Development_Growth factors in regulation of oligodendrocyte progenitor cell proliferation	67	1.105E-02	4.259E-02	15	MEK1(MAP2K1), Vitronectin, PI3K cat class IA, PKC, Neuregulin 1, Lyn, alpha-V/beta-3 integrin, EGFR, H-Ras, Fyn, SOS, AKT(PKB), PDK (PDPK1), Fibronectin, mTOR
378	Development_Thrombopoietin signaling via ERK1/2 and PI3K	67	1.105E-02	4.259E-02	15	PDK1, RAP-1A, PI3K cat class IA, RelA (p65 NF-kB subunit), B-Raf, ITGA2B, H-Ras, CREB1, CrkL, MEK1/2, AKT(PKB), PDHA (somatic), SOS1, PDK (PDPK1), p27KIP1
379	Development_Mu-type opioid receptor signaling	38	1.151E-02	4.389E-02	10	G-protein alpha-i family, VAV-2, CDC42, SOS, AKT(PKB), PDK (PDPK1), PLC-beta3, Rac1, IP3 receptor, mTOR
380	Insulin-like growth factor family signaling in melanoma	38	1.151E-02	4.389E-02	10	MEK1(MAP2K1), PI3K cat class IA, PKC, IGF-2, H-Ras, FAK1, Beta-catenin, AKT(PKB), Beta-arrestin1, p27KIP1
381	Cytoskeleton remodeling_ACM3 and ACM4 in keratinocyte migration	38	1.151E-02	4.389E-02	10	RhoA, PLC-beta, ROCK2, G-protein alpha-i family, G-protein alpha-11, G-protein alpha-q, G-protein alpha-q/11, G-protein alpha-i2, PKA-cat (cAMP-dependent), IP3 receptor
382	Dysregulation of Adiponectin secretion from adipocytes in obesity, type 2 diabetes and metabolic syndrome X	38	1.151E-02	4.389E-02	10	MEK1(MAP2K1), GSTK1, CDK5, SREBP1 (nuclear), ERO1Lalpha, CRP, Insulin receptor, ERp44, CREB1, AKT(PKB)
383	L-Lysine metabolism	93	1.255E-02	4.736E-02	19	CRYM, CRAT, AADAT, AGPHD1, ECHP, ACAT2, CAC, DHTKD1, HCD2, HCDH, CAT-3, AGXT2L2, AL7A1, ACAA1, CCBL2, ACAT1, AASS, CAT-2, GCDH
384	Immune response_Fc epsilon RI pathway: calcium-dependent signaling	68	1.266E-02	4.736E-02	15	RhoA, ROCK, PKC-alpha, ERM proteins, Lyn, ARF6, Myosin II, CDC42, Fyn, AKT(PKB), SK4/IK1, PIP5KI, Paxillin, Rac1, IP3 receptor
385	Neurophysiological process_Corticoliberin signaling via CRHR1	50	1.268E-02	4.736E-02	12	MEK1(MAP2K1), RAP-1A, cPKC (conventional), B-Raf, G-protein alpha-s, PLC-beta, PKC-alpha, CREB1, MIF, G-protein alpha-q/11, PKA-cat (cAMP-dependent), IP3 receptor
386	Development_GM-CSF signaling	50	1.268E-02	4.736E-02	12	STAT3, MEK1(MAP2K1), RACK1, PI3K cat class IA, Lyn, H-Ras, 14-3-3 zeta/delta, Caspase-3, CREB1, SOS, NF-kB, AKT(PKB)
387	TGF-beta 1-induced transactivation of membrane receptors signaling in HCC	50	1.268E-02	4.736E-02	12	ITGB1, PI3K cat class IA, FAK1, Beta-catenin, alpha-5/beta-1 integrin, CRK, AKT(PKB), ITGA5, Fibronectin, DDX5, Actin, Rac1
388	Development_EDNRB signaling	50	1.268E-02	4.736E-02	12	MEK1(MAP2K1), RAP-1A, B-Raf, PLC-beta, G-protein alpha-i family, H-Ras, eNOS, CREB1, SOS, AKT(PKB), G-protein alpha-q/11, IP3 receptor
389	Signal transduction_CXCR4 signaling via second messengers and JAK/STAT	50	1.268E-02	4.736E-02	12	STAT3, Ubiquitin, Pyk2(FAK2), G-protein alpha-s, G-protein alpha-i family, MRLC, SK4/IK1, PLC-beta3, MLCK, CXCR4, Paxillin, IP3 receptor
390	HBV-dependent NF-kB and PI3K/AKT pathways leading to HCC	50	1.268E-02	4.736E-02	12	Pyk2(FAK2), PI3K cat class IA, RelA (p65 NF-kB subunit), PKC-alpha, H-Ras, FAK1, SOS, Pin1, NF-kB, AKT(PKB), PDK (PDPK1), p27KIP1
391	Interaction of deficient alpha-MSH signaling with TNF-alpha in melanoma	33	1.275E-02	4.738E-02	9	ITGB1, TMSB4X, RelA (p65 NF-kB subunit), ICAM1, NF-kB, Catalase, Fibronectin, Vimentin, PKA-cat (cAMP-dependent)
392	SHH signaling in melanoma	33	1.275E-02	4.738E-02	9	MEK1(MAP2K1), AKT1, B-Raf, N-Ras, H-Ras, CREB1, PDK (PDPK1), Vimentin, PKA-cat (cAMP-dependent)

393	Development_Negative regulation of STK3/4 (Hippo) pathway and positive regulation of YAP/TAZ function	62	1.282E-02	4.754E-02	14	RhoA, MOBKL1A, EGF, G-protein alpha-12 family, EGFR, LARG, Actin cytoskeletal, RhoGAP5, G-protein alpha-q/11, PDK (PDPK1), WBP-2, MASK, ILK, ZO-2
394	Development_ERBB-family signaling	39	1.386E-02	5.095E-02	10	MEK1(MAP2K1), EGF, PI3K cat class IA, Neuregulin 1, EGFR, H-Ras, GRB7, SOS, NF-kB, AKT(PKB)
395	Platelet activation during ADAM-TS13-deficient thrombotic microangiopathy development	28	1.388E-02	5.095E-02	8	Histone H3, alpha-IIb/beta-3 integrin, RAP-1B, Histone H2B, Fibrinogen (fibrin), Fibronectin, Histone H4, CD36
396	Development_Delta-type opioid receptor signaling via G-protein alpha-14	28	1.388E-02	5.095E-02	8	STAT3, MEK1(MAP2K1), Pyk2(FAK2), PKC-alpha, H-Ras, SOS, Rac1, IP3 receptor
397	Role of Th17 cells in asthma	28	1.388E-02	5.095E-02	8	RhoA, VCAM1, ROCK2, ICAM1, EGFR, MRLC, Myosin II, NF-kB
398	Development_NCAM1-mediated neurite outgrowth, synapse assembly and neuronal survival	75	1.406E-02	5.133E-02	16	BETA-PIX, PKC, AP-2 alpha subunits, Agrin, H-Ras, Spectrin, Casein kinase II, FAK1, CREB1, MEK1/2, CDC42, Fyn, SOS, AKT(PKB), PKA-cat (cAMP-dependent), IP3 receptor
399	EGFR family signaling in pancreatic cancer	75	1.406E-02	5.133E-02	16	STAT3, MEK1(MAP2K1), RhoA, EGF, PI3K cat class IA, EGFR, N-Ras, H-Ras, VAV-2, SOS, NF-kB, AKT(PKB), PDK (PDPK1), p27KIP1, Rac1, mTOR
400	Regulation of relaxation of airway smooth muscle cells	45	1.452E-02	5.270E-02	11	RhoA, G-protein alpha-s, PGD2R, PKA-cat alpha, RAP-1B, F-Actin cytoskeleton, 14-3-3, PKA-cat (cAMP-dependent), MLCK, Rac1, IP3 receptor
401	LKB1 signaling pathway in lung cancer cells	45	1.452E-02	5.270E-02	11	STAT3, ITGB1, FAK1, AMPK alpha subunit, Beta-catenin, CDC42, NF-kB, Fibronectin, p70 S6 kinase2, Vimentin, mTOR
402	Development_EGFR signaling via PIP3	23	1.470E-02	5.270E-02	7	EGF, PI3K cat class IA, EGFR, VAV-2, AKT(PKB), PDK (PDPK1), Rac1
403	Role of Leptin in regulation of eating behavior in obesity	23	1.470E-02	5.270E-02	7	STAT3, MEK1(MAP2K1), ACACA, AMPK alpha subunit, PTP-1B, AKT(PKB), mTOR
404	Development_Delta- and kappa-type opioid receptors signaling via beta-arrestin	23	1.470E-02	5.270E-02	7	PKC, G-protein alpha-i family, CREB1, Beta-arrestin1, Dynamin-2, p27KIP1, Histone H4
405	Regulation of lipid metabolism_Regulation of acetyl-CoA carboxylase 1 activity	18	1.481E-02	5.270E-02	6	ACACA, SREBP1 (nuclear), ACACB, AMPK beta subunit, AMPK alpha subunit, AMPK gamma subunit
406	Transcription_Assembly of RNA Polymerase II preinitiation complex on TATA-less promoters	18	1.481E-02	5.270E-02	6	AMH, DHFR, POLR2A, TFII-I, TFIIF, MDR1
407	HIF-1 in gastric cancer	51	1.483E-02	5.270E-02	12	Ubiquitin, F263, alpha-V/beta-3 integrin, CDC42, ENO1, PGES2, AKT(PKB), HSP90, PDK (PDPK1), MDR1, LAMR1, Rac1
408	Signal transduction_PKA signaling	51	1.483E-02	5.270E-02	12	G-protein alpha-12 family, G-protein alpha-s, PKA-cat alpha, G-protein alpha-i family, PHK gamma, KDELR, CREB1, PP2A regulatory, PHK beta, PDK (PDPK1), PKA-cat (cAMP-dependent), G-protein alpha-13
409	IL-6 signaling in multiple myeloma	51	1.483E-02	5.270E-02	12	STAT3, MEK1(MAP2K1), gp130, PI3K cat class IA, K-RAS, Lyn, N-Ras, SOS, AKT(PKB), PDK (PDPK1), p27KIP1, CDK6

410	Some pathways of EMT in cancer cells	51	1.483E-02	5.270E-02	12	STAT3, EGF, PI3K cat class IA, RelA (p65 NF-kB subunit), EGFR, H-Ras, Beta-catenin, SOS, AKT(PKB), DDX5, ILK, mTOR
411	Apoptotic pathways and resistance to apoptosis in lung cancer cells	57	1.488E-02	5.274E-02	13	MEK1(MAP2K1), B-Raf, PKC-alpha, DAPK1, tBid, Caspase-3, RIPK1, HDAC1, NF-kB, p70 S6 kinase2, p27KIP1, Smac/Diablo, Bid
412	Neurophysiological process_NMDA-dependent postsynaptic long-term potentiation in CA1 hippocampal neurons	82	1.531E-02	5.408E-02	17	RAP-1A, Pyk2(FAK2), B-Raf, PKC-alpha, H-Ras, eIF4E, eNOS, CREB1, MEK1/2, G-protein alpha-q, SOS, AKT(PKB), MNK1, PDK (PDPK1), PKA-cat (cAMP-dependent), IP3 receptor, mTOR
413	Disruption of epithelial layer restitution in asthma	34	1.555E-02	5.408E-02	9	Plasminogen, ITGB1, Vitronectin, EGF, alpha-V/beta-1 integrin, EGFR, alpha-5/beta-1 integrin, Plasmin, Fibronectin
414	Nicotine / Beta-adrenergic signaling in lung cancer	34	1.555E-02	5.408E-02	9	MEK1(MAP2K1), G-protein alpha-s, PKC-alpha, G-protein alpha-i family, H-Ras, SOS, AKT(PKB), PDK (PDPK1), PKA-cat (cAMP-dependent)
415	Mechanism of action of CCR4 antagonists in asthma and atopic dermatitis (Variant 1)	34	1.555E-02	5.408E-02	9	Talin, RAP-1A, ITGB1, PIPKI gamma, VCAM1, ICAM1, G-protein alpha-i family, PLC-beta3, IP3 receptor
416	CCR4-dependent immune cell chemotaxis in asthma and atopic dermatitis	34	1.555E-02	5.408E-02	9	Talin, RAP-1A, ITGB1, PIPKI gamma, VCAM1, ICAM1, G-protein alpha-i family, PLC-beta3, IP3 receptor
417	Apoptosis and survival_Role of CDK5 in neuronal death and survival	34	1.555E-02	5.408E-02	9	MEK1(MAP2K1), PI3K cat class IA, CDK5, Neuregulin 1, H-Ras, Caspase-3, SOS, AKT(PKB), PDK (PDPK1)
418	Chemotaxis_CCR4-induced chemotaxis of immune cells	34	1.555E-02	5.408E-02	9	Talin, RAP-1A, ITGB1, PIPKI gamma, VCAM1, ICAM1, G-protein alpha-i family, PLC-beta3, IP3 receptor
419	Transport_Low density lipoproteins assembly and remodeling	34	1.555E-02	5.408E-02	9	Small LDL, IDL2, VLDL1, APOB, APOC2, VLDL2, VLDL1 remnant, Large LDL, IDL1
420	Transcription_HIF-1 targets	95	1.564E-02	5.425E-02	19	G3P2, PDK1, Heme oxygenase 1, FECH, Ceruloplasmin, MSH2, ALDOA, F263, Transferrin, HXK1, GPI, Galectin-1, ENO1, PGK1, CXCR4, LRP1, NIP3, MDR1, AK3

A7.2.2. Ingenuity Pathway Analysis.

1. Categories 2. Diseases or Functions Annotation 3. p-value 4. Predicted Activation State 5. Activation z-score 6. # Molecules	**Molecules**
1. RNA Post-Transcriptional Modification 2. Splicing of mRNA 3. 1.71E-48 4. Decreased 5. -2.542 6. 130	ACIN1,AKR1C4,BCAS2,CCAR1,CDC5L,CPSF2,CRNKL1,CSTF1,CSTF2,CSTF3,CTNNBL1,DDX17,DDX23,DDX39B,DDX42,DDX46,DDX5,DHX15,DHX16,DHX9,DNAJC8,EFTUD2,EIF4A3,ELAVL1,FMR1,GTF2F1,GTF2F2,HCFC1,HNRNPA0,Hnrnpa1,HNRNPA2B1,HNRNPC,HNRNPD,HNRNPF,HNRNPH1,HNRNPH2,HNRNPK,HNRNPL,HNRNPM,HNRNPR,HNRNPU,HNRNPUL1,HSPA8,IK,KHDRBS1,LSM5,LSM6,LSM8,MBNL1,MECP2,MFAP1,MTREX,NCBP1,NCBP2,NUDT21,PABPN1,PCBP1,PHF5A,PLRG1,PNN,POLR2A,POLR2B,POLR2H,POLR2I,POLR2L,PPIL1,PPP1R8,PPWD1,PQBP1,PRPF19,PRPF3,PRPF31,PRPF4,PRPF40A,PRPF6,PRPF8,PTBP1,PTBP3,PUF60,RBM10,RBM15,RBM17,RBM22,RBM42,RBM8A,RNF113A,SAP18,SART1,SART3,SF3A1,Sf3a2,SF3A3,SF3B1,SF3B2,SF3B3,SF

	3B4,SF3B6,SFPQ,SMU1,SNRNP200,SNRNP70,SNRPA1,SNRPB2,Snrpc,SNRPD2,SNRPD3,SNRPF,Snrpg,SNRPN,SNU13,SNW1,SRPK2,Srrm1,SRRT,SRSF1,SRSF10,SRSF2,SRSF3,SRSF4,SRSF6,SRSF7,SYMPK,TCERG1,THRAP3,TRA2B,U2AF2,U2SURP,WBP11,YBX1,ZMAT2
1. Cancer,Cell Death and Survival,Organismal Injury and Abnormalities,Tumor Morphology 2. Cell death of osteosarcoma cells 3. 2E-48 4. Decreased 5. -7.484 6. 85	ARCN1,COPA,COPB2,COPG1,CRNKL1,EEF1A1,EIF3E,EIF3F,EIF3L,FAU,HSPA9,NUP155,NUP160,NUP214,NUP54,PABPC1,PHF5A,POLR2H,PRPF8,PSMA3,PSMA4,PSMA5,PSMA6,PSMA7,PSMB1,PSMB3,PSMB5,PUF60,RAN,RBM39,RBM8A,RPL10,RPL11,RPL13,RPL13A,RPL19,Rpl23a,RPL27,RPL27A,RPL3,RPL31,RPL35,RPL35A,RPL37,RPL37A,RPL38,RPL5,RPL6,RPL7,RPL7A,RPL9,RPLP0,RPS11,RPS12,RPS13,RPS14,RPS15A,RPS16,RPS17,RPS19,RPS21,RPS24,RPS27A,RPS28,RPS29,RPS3,RPS4Y1,RPS5,RPS7,SF3A1,Sf3a2,SF3B1,SF3B2,SF3B3,SF3B6,SMC1A,SNRPA1,SNRPD3,Snrpg,SON,SUPT16H,U2af1,U2AF2,UBE2I,VDAC2
1. Cell Death and Survival 2. Necrosis 3. 8.02E-45 4. Decreased 5. -6.018 6. 742	AAK1,ABCB4,ABCB8,ABCC3,ABCE1,ACACA,ACAT1,ACLY,ACO2,ACSL4,ACTB,ADAM10,ADI1,ADIPOR2,AGPAT2,AGRN,AHSA1,AIP,AKR1B10,AKT1,ALCAM,ALDH1A1,ALDH1L1,ALDOA,AMACR,ANGPTL4,ANPEP,ANXA1,ANXA5,AP2M1,APEX1,API5,APMAP,APOA1,APOB,Apoc3,APOE,ARAF,ARCN1,ARF6,ARHGDIA,ARMC10,ARRB1,ARSB,AS3MT,ASAH1,ASS1,ATG3,ATP1A1,ATP1B3,ATP2A2,ATP2B1,ATP2B4,ATP6AP2,ATRX,ATXN2,B2M,B4GALNT1,BABAM2,BAG3,BAG4,BAG5,BCAP31,BCAS2,BCHE,BCKDK,BCL2L13,BCLAF1,BGN,BID,BNIP3,BRAF,BSG,BUB3,C1QA,C9,CADM1,CALCRL,CALR,CAMK1,CAPNS1,CASP3,CASP7,CAT,CBR1,CBX3,CCAR1,CCDC47,CCT3,CD1D,CD2AP,CD36,CD38,CD47,CD81,CD82,CDA,CDC34,CDC37,Cdc42,CDC73,CDK11A,CDK5,CDK6,CDK9,CDKN1B,CDKN2C,CES1,CFH,CIDEB,CLEC10A,CLIC4,CLU,CLYBL,CNBP,CNP,CNPY2,COL18A1,COMT,COPA,COPB2,COPG1,COPZ1,COQ9,CORO1A,COX5A,COX6B1,COX7A2L,CPB2,CPS1,CR1L,CREB1,CRK,CRKL,CRNKL1,CRP,CSK,CSNK2A1,CSNK2A2,CTBP1,CTH,CTNNA1,CTNNB1,CTNND1,CTSB,CTSD,CTSS,CTSV,CTSZ,CTTN,CUL1,CUL2,CUL3,CXADR,CYB5A,CYGB,CYP2C8,CYP2F1,CYP7A1,DAPK1,DCTN2,DDX17,DDX3X,DDX58,DECR1,DEK,DEPTOR,DES,DHCR24,DHFR,DHODH,DHX9,DIABLO,DMD,DMGDH,DNAJB1,DNM1L,DNM2,DPM3,DPP4,DPP9,DPYD,DSP,DUT,DYNLL1,DYSF,EEF1A1,EEF1D,EEF2,EGF,EGFR,EIF1AX,EIF2A,EIF2AK2,EIF2B5,EIF2S1,EIF2S2,EIF3C,EIF3E,EIF3F,EIF3H,EIF3I,EIF3L,EIF3M,EIF4E,EIF4G2,EIF5A,EIF5B,ELAVL1,ELOA,ELOC,EMD,ENO1,ENTPD5,EPHX1,EPHX2,EXOC5,EZR,F11,F13A1,FAAH,FABP4,FABP7,FAF1,FAM162A,FASN,FAU,FCGR2B,FEN1,FETUB,FGA,FHIT,FIS1,FKBP4,FKBP5,FLNA,FMR1,FN1,FNTA,FUBP1,Fus,FXN,G0S2,G6PC,G6PD,GAPDH,GART,GBA,GBE1,GCH1,GCK,GCLM,GDA,GFPT1,GIMAP4,GJB2,GLO1,GLUD1,Gm21596/Hmgb1,GNA11,GNA13,GNAI2,GNAQ,GNAS,GNE,GNL3,GPAM,GPT,GPX4,GRN,GSR,GSTM1,GSTM5,GSTP1,GSTZ1,GTF2F2,GUCY1B1,HCFC1,HDAC1,HDGF,HERPUD1,HGS,HIP1,HK1,HLA-A,HMGA1,HMGCS1,HMOX1,HMOX2,HNF1A,HNF4A,HNRNPC,HNRNPH1,HNRNPK,HPN,HRAS,HSD17B10,HSP90AA1,HSP90AB1,HSP90B1,HSPA1A/HSPA1B,HSPA5,HSPA8,HSPA9,HSPB1,HSPD1,HSPH1,HTATIP2,HUWE1,HYOU1,HYPK,ICAM1,IDH2,IFI16,IFNAR2,IGF2R,IL6ST,ILF2,ILK,ILKAP,IMMT,INSR,INTS3,IP6K1,Irgm1,ITGA1,ITGA5,ITGAV,ITGB1,ITGB3,ITIH4,ITPR2,ITSN1,JUP,KANK2,KDELR1,KHDRBS1,KPNA2,KRAS,KYAT1,LDLR,LGALS1,LGALS3,LGALS3BP,LGALS8,LGMN,LIMS2,LIPE,LMNA,LMNB1,LOC102724788/PRODH,LRP1,LRPAP1,LUM,LYN,LYPLA1,LYPLA2,LYZ,M6PR,MACO1,MAN2C1,MANF,MAOA,MAOB,MAP2K1,MAP2K3,MAP4,MAT2A,MBOAT7,MCAM,MCTS1,MDH1,MECP2,METAP2,MFN2,MIF,MIF4GD,MKNK1,MME,MOB2,MPI,MSH2,MSN,MSR1,MSRB2,Mt1,Mt2,MTA2,MTCH2,MTDH,MTMR6,MTOR,MTSS1,Mug1/Mug2,MVK,MVP,MYBBP1A,MYH10,MYH11,MYLK,NAA35,NAGLU,NAMPT,NASP,NAT10,NCEH1,NCK1,NCL,NCOA5,NCSTN,NDRG1,NDST1,NDUFA13,NDUFAF1,NDUFAF4,NECTIN2,NELFB,NFIB,NFIC,Ngp,NLRX1,NMNAT1,NOC2L,NOL6,NOS3,NPC1,NPC2,NQO1,NQO2,NR1H4,NR3C1,NRAS,NUDCD3,NUDT13,NUP155,NUP160,NUP205,NUP214,NUP54,NUP93,OGA,OGT,OPTN,OXR1,PA2G4,PABPC1,PAFAH1B1,PAFAH2,PAK2,PALLD,PARP1,PARP14,PARVA,PAWR,PCK1,PCTP,PDCD4,PDCD6IP,PDHA1,PDIA3,PDK1,PDK2,PDLIM7,PDZK1,PEBP1,PECAM1,PEX11A,PEX5,PFKFB1,PFKFB3,PGRMC1,PHB2,PHF5A,PHLDA1,PIGR,PIK3AP1,PIK3CB,PKN1,PLEKHA7,PLEKHF1,PLG,PLRG1,PLXNA4,PML,PNKP,POLR2H,PON1,PON2,PON3,POR,PPAT,PPIA,PPIF,PPM1A,PPP2R1B,PPT1,PPT2,PRDX3,PRDX6,PRKAA2,PRKAB1,PRKACA,PRKRA,PROC,PRPF19,PRPF8,PSAP,PSEN1,PSIP1,PSMA3,PSMA4,PSMA5,PSMA6,PSMA7,PSMB1,PSMB10,PSMB3,PSMB5,PSMD14,PSMD7,PSME3,PTK2,PTK2B,PTPMT1,PTPN1,PTPRF,PUF60,PUM1,PURA,PXN,PYCARD,PYGL,RAB35,RAC1,RACK1,RAD23B,RAD50,RAN,RAPGEF4,RBBP4,RBM17,RBM39,RBM8A,RELA,RGN,RGPD4 (includes others),RHOA,RHOC,RHOG,RIPK1,RNASEH2A,RNF2,RNF5,RNMT,ROCK2,RPAP3,RPL10,RPL11,RPL13,RPL13A,RPL19,Rpl23a,RPL27,RPL27A,RPL3,RPL31,RPL35,RPL35A,RPL37,RPL37A,RPL38,RPL5,RPL6,RPL7,RPL7A,RPL9,RPLP0,RPS11,RPS12,RPS13,RPS14,RPS15A,RPS16,RPS17,RPS19,RPS21,RPS24,RPS27A,RPS28,RPS29,RPS3,RPS4Y1,RPS5,RPS6,RPS6KB2,RPS7,RPSA,RPTOR,RRAS,RTN1,RTN4,S100A1,S100A6,SAA1,SAE1,SARNP,SCARB1,SCD,SCYL3,SDC4,SEC61G,SELENOP,SERPINA1,SERPINA3,SERPINH1,SET,SF3A1,Sf3a2,SF3B1,SF3B2,SF3B3,SF3B6,SFPQ,SFR1,SFT2D2,SIGMAR1,SLC25A10,SLC25A11,SLC25A12,SLC25A23,SLC25A5,SLC26A1,SLC9A3R1,SLC9A3R2,SLCO1B3,SLK,SMARCE1,SMC1A,SMPD1,SND1,SNRPA1,SNRPD3,Snrpg,SNW1,SNX1,SNX4,SNX6,SON,SRI,SRPK2,SRR,SRSF1,SRSF2,SSRP1,STAT2,STAT3,STAT6,STEAP3,STIP1,STK38,STOML2,ST

	RAP,SUN2,SUPT16H,SURF1,SVIL,SWAP70,SYNCRIP,SYNGR2,TAGLN2,TAOK3,TARDBP,TBC1D15,TBC1D24,TCERG1,TDO2,TFR2,TGM1,THOC2,TIAL1,TJP2,TLN1,TMED10,TMEM109,TMEM214,TMOD3,TMX1,TNPO2,TNS2,TOLLIP,TOP1,TOP2B,TPD52,TPR,TRAP1,TRIM28,TRIP10,TSC22D1,TSG101,TTN,TTPA,TUBB,TXN2,TYMP,U2af1,U2AF2,UBA1,UBA2,UBA3,UBA7,UBE2I,UBE2M,UBE2V2,UBE4B,UBQLN2,UBTF,UCHL5,UPF1,UPF2,USP19,VAC14,VAPB,VAV2,VCAM1,VDAC2,VIM,VNN1,VPS28,VPS35,VRK1,VTN,WAPL,WDR5,WFS1,XAF1,XPO1,XRCC6,YBX1,YME1L1,YWHAQ,YWHAZ,ZHX2
1. RNA Post-Transcriptional Modification 2. Processing of mRNA 3. 9.49E-43 4. Decreased 5. -2.441 6. 138	ACIN1,AGO2,AKR1C4,BCAS2,CCAR1,CDC5L,CDC73,CDK11A,CPSF2,CRNKL1,CSTF1,CSTF2,CSTF3,CTNNBL1,DDX17,DDX23,DDX39B,DDX42,DDX46,DDX5,DHX15,DHX16,DHX9,DNAJC8,EFTUD2,EIF4A3,ELAVL1,FMR1,GTF2F1,GTF2F2,HCFC1,HNRNPA0,Hnrnpa1,HNRNPA2B1,HNRNPC,HNRNPD,HNRNPF,HNRNPH1,HNRNPH2,HNRNPK,HNRNPL,HNRNPM,HNRNPR,HNRNPU,HNRNPUL1,HSPA8,IK,KHDRBS1,LSM5,LSM6,LSM8,MBNL1,MECP2,MFAP1,MTREX,NCBP1,NCBP2,NUDT21,PABPC1,PABPN1,PCBP1,PHF5A,PLRG1,PNN,POLR2A,POLR2B,POLR2H,POLR2I,POLR2L,PPIL1,PPP1R8,PPWD1,PQBP1,PRKACA,PRPF19,PRPF3,PRPF31,PRPF4,PRPF40A,PRPF6,PRPF8,PTBP1,PTBP3,PUF60,RBM10,RBM15,RBM17,RBM22,RBM42,RBM8A,RNF113A,RNMT,SAFB,SAP18,SART1,SART3,SF3A1,Sf3a2,SF3A3,SF3B1,SF3B2,SF3B3,SF3B4,SF3B6,SFPQ,SMU1,SNRNP200,SNRNP70,SNRPA1,SNRPB2,Snrpc,SNRPD2,SNRPD3,SNRPF,Snrpg,SNRPN,SNU13,SNW1,SON,SRPK2,Srrm1,SRRT,SRSF1,SRSF10,SRSF2,SRSF3,SRSF4,SRSF6,SRSF7,SYMPK,TCERG1,THRAP3,TRA2B,U2AF2,U2SURP,WBP11,YBX1,ZMAT2

1. Organismal Survival 2. Morbidity or mortality 3. 8.74E-37 4. Decreased 5. -12.62 6. 671	ABCB10,Abcb1b,ABCB4,ABCB6,ACACA,ACADL,ACADM,ACLY,ACTB,ACTG1,ACTL6A,ACTN4, ADAM10,ADD1,ADK,AFDN,AFMID,AGL,AGO2,AGPAT2,AGRN,AIP,AKT1,ALDH1A1,ALDH5A1, ALDOA,AMACR,AMBP,ANGPTL3,ANGPTL4,Anp32a,Anp32b,Anp32e,ANXA1,AP2M1,APCS,APEX 1,APOA1,APOB,APOD,APOE,AQP1,AQP4,ARAF,ARF4,ARF6,ARHGAP31,ARHGAP5,ARHGDIA,A RHGDIB,ARHGEF12,ARRB1,ASAH1,ASGR1,ASGR2,ASL,ASPA,ASPH,ASS1,ATG3,ATOX1,ATP1A 1,ATP1B1,ATP2A2,ATP2B1,ATP6AP1,ATXN2,B2M,B4GALNT1,BAG3,BCHE,BCLAF1,BCS1L,BGN ,BID,BIN1,BLMH,BRAF,Brd4,BSG,BUB3,C1QA,C4A/C4B,CALCRL,Cald1,CALR,CANX,CAP1,CAP NS1,CAPZB,CASK,CASP3,CASP7,CCDC134,CCDC47,CCS,CD1D,CD2AP,CD36,CD38,CD47,CD68,C DA,Cdc42,CDC73,CDK11A,CDK12,CDK5,CDK6,CDKN1B,CDKN2C,CDO1,CFB,CFH,CFI,CHD4,CH MP2A,CIAO3,CISD2,CKB,CLIC4,Cmah,CNOT3,CNP,CNPY2,COBLL1,COPB1,COQ3,COQ9,COX15, CPB2,CPOX,CPS1,CR1L,CREB1,CRELD1,CRK,CRKL,CRP,CSAD,CSK,CSNK2A1,CSNK2B,CSRP1, CTBP1,CTH,CTNNB1,CTNNBL1,CTNND1,CTR9,CTSB,CTSD,CTSF,CTSV,CTTN,CUL1,CUL3,Cux1, CXADR,CYGB,CYP17A1,CYP1A2,CYP7A1,CYP7B1,DAD1,Dazap1,DDAH1,DDX17,DDX3X,DDX5, DDX58,DES,DGAT2,DHFR,DHX9,DKC1,DMD,DNAJB1,DNAJB4,DNAJB6,DNAJB9,DNAJC3,DNM1 L,DNM2,DPAGT1,DPYD,DSP,Dst,ECM1,EGFR,EHD1,EHD3,EHHADH,EIF2AK2,EIF2S1,EIF3D,EIF3 M,EIF4A1,EIF4G2,ELAVL1,ELOA,ELOVL1,EPN1,ERBIN,ERC1,F11,F13A1,FABP7,FASN,FBL,FCG R2B,FCGRT,FECH,FEN1,FERMT2,FGA,FGG,FHIT,FITM2,FKBP4,FLII,FLNA,FN1,FSCN1,FTO,FUB P1,Fus,FXN,FXR1,G6PC,G6PD,GABPA,GADD45GIP1,GAMT,GATAD2A,GBA,GBE1,GCH1,GCK,G CLM,GJB2,Gm21596/Hmgb1,GNA11,GNA13,GNAI2,GNAI3,GNAQ,GNAS,GNE,GNL3,GNPAT,GOL GA2,GPD1L,GPHN,GPX3,GPX4,GRN,GSTK1,GSTM1,GSTP1,GSTZ1,GTF2I,GUCY1B1,H3-3A/H3- 3B,HDAC1,HEXB,HEXIM1,HGS,HIP1,HLA- A,HMGCL,HMGN1,HMOX1,HMOX2,HNF1A,HNF4A,Hnrnpa1,HNRNPAB,HNRNPC,HNRNPD,HNR NPK,HNRNPL,HOPX,HP,HPGD,HRAS,HSD17B2,HSD17B4,HSP90AA1,HSP90AB1,HSP90B1,HSPA4 L,HSPA5,HSPB1,HSPG2,HUWE1,HYOU1,ICAM1,IDH2,Ifi47,IFNAR2,IGF2R,IL6ST,ILF2,ILF3,ILK,I MPA1,INSIG2,INSR,Irgm1,ITGA2B,ITGA5,ITGA9,ITGAV,ITGB1,ITGB3,ITPR2,ITSN1,JCHAIN,JUP, KCTD12,KHDRBS1,KHSRP,KPNA1,KRAS,LAMTOR1,LARP7,LDLR,LGALS3,LHPP,LIAS,LIFR,LI MS2,LIN7A,LIN7C,LMNA,LMNB1,LMNB2,LMO7,LRP1,LRPAP1,LSR,LUM,LYN,LYZ,M6PR,Macf1, MACROH2A2,MAN1A2,MAP2K1,MAP2K3,MAP4,Mbl1,MBNL1,MBOAT7,MCAM,MDH1,MECP2, METAP2,MFN2,MGAT2,MIA3,MIF,MIF4GD,MME,MMUT,Mocs1,MORF4L1,MPC1,MPI,MRC1,MS H2,MSN,MSR1,MSRA,Mt1,Mt2,MTA2,MTAP,MTDH,MTOR,MTSS1,Mug1/Mug2,MYBBP1A,MYH10 ,MYH11,MYH14,MYH9,MYL6,MYLPF,MYO18A,NAGLU,NAMPT,NASP,NCK1,NCOA5,NCSTN,ND RG1,NDST1,NDUFA13,NELFB,NFIA,NFIB,NFIC,NMNAT1,NOS3,NPC1,NPC2,NQO1,NR1H4,NR3C 1,NRAS,NSF,NUMA1,NUP98,OAT,OGA,OLA1,PAFAH1B1,PAK2,PALLD,PANK1,PARP1,PCCA,PC K1,PCYT1A,PDCD10,PDCD4,PDHA1,PDIA3,PDLIM1,PEX11A,PEX13,PEX5,PFKFB3,PGK1,PGM3,P HB2,PI4KA,PICALM,PIK3CB,PIP5K1C,PLCB3,PLEKHA7,PLG,PLOD3,PLPP3,PLRG1,PLS3,PLVAP, PLXNB2,PML,PMM2,PNN,Podxl,POLR2A,PON3,POR,PPCS,PPIA,PPIB,PPIF,PPIG,PPM1B,PPP1R8,P PP4C,PPT1,PPT2,PRKAA2,PRKAB1,PRKACA,PRKCSH,PRKRA,PROC,PRORP,PRPF19,PRPF31,PRP F8,PSAP,PSEN1,PSIP1,PSMC3,PSMD4,PTBP1,PTGES3,PTK2,PTK2B,Ptma (includes others),PTPMT1,PTPN1,PTPRF,PTS,PURA,PXN,PYCARD,QDPR,RAB8A,RAB8B,RAC1,RAD23B,RA D50,RAE1,RAP1A,RASIP1,RBM15,RBP1,RELA,RGN,RGPD4 (includes others),RHOA,RIPK1,RNASEH2A,RNASET2,RNF14,RNF2,RNF5,RNH1,RNMT,Rpl22l1,RPL24,Rpl29 (includes others),RPL4,RPL5,RPL6,RPS19,RPS24,RPS6KB2,RPSA,RPTOR,RTN4,RUFY3,RUVBL1,SAA1,SAFB ,SBF1,SC5D,SCARB1,SCARB2,SCD,SCRIB,SCYL2,SDC4,SDHD,SEC63,SELENBP1,SELENOK,SEL ENOP,SEPHS1,SERPINA1,SERPINA10,SERPINA3,SERPINA6,SERPINB1,SERPIND1,SERPINF2,SE RPING1,SERPINH1,SET,SF3B1,SGTA,SH3GL1,SHOC2,SIGMAR1,SLC25A13,SLC25A25,SLC27A4,S LC2A2,SLC30A5,SLC31A1,SLC35D1,SLC4A4,SLC9A3R1,SLCO1B3,SLCO2A1,SMARCA5,SMPD1,S NAP23,SNRPN,SNX1,SNX2,SORBS2,SOS1,SPR,SPTAN1,SRRT,SRSF1,SRSF10,SRSF2,SRSF3,SSBP 1,SSRP1,STAB1,STAB2,STAT2,STAT3,STAT6,STEAP4,STIP1,STK38,SUB1,SUMO2,SUN2,SURF1,T ADA3,TAP1,TARDBP,TCEA1,TCIRG1,TCOF1,TGM1,TIAL1,TINAGL1,TJP2,TKT,TLN1,TMED10,T MEM38B,TMOD3,Tmsb4x (includes others),TOP1,TOP2B,TOP3B,TOR1A,Tpm1,TPM3,TRA2B,TRIM28,TRMU,TSG101,TSPAN31,TSTA3, TTN,TTPA,TYMP,U2AF2,UBA3,UBE2I,UBE2J1,UBE4B,UBL4A,UBR2,UBTF,UPF1,UPF2,USO1,USP 7,VAC14,VAMP2,VCAM1,VCL,VDAC3,VIM,VPS26A,VPS52,VSIG4,VTA1,WAPL,WASF2,WASHC5 ,WBP2,WDR1,WDR5,WDR77,XRCC6,YBX1,YBX3,YME1L1,YTHDF2,ZBTB20,ZFR,ZMIZ1

1. Organismal Survival 2. Organismal death 3. 1.36E-35 4. Decreased 5. -12.928 6. 660	ABCB10,Abcb1b,ABCB4,ABCB6,ACACA,ACADL,ACADM,ACLY,ACTB,ACTG1,ACTL6A,ACTN4, ADAM10,ADD1,ADK,AFDN,AFMID,AGL,AGO2,AGPAT2,AGRN,AIP,AKT1,ALDH1A1,ALDH5A1, ALDOA,AMACR,AMBP,ANGPTL3,ANGPTL4,Anp32a,Anp32b,Anp32e,ANXA1,AP2M1,APEX1,APO A1,APOB,APOD,APOE,AQP1,AQP4,ARAF,ARF4,ARF6,ARHGAP31,ARHGAP5,ARHGDIA,ARHGDI B,ARHGEF12,ARRB1,ASAH1,ASGR1,ASGR2,ASL,ASPA,ASPH,ASS1,ATG3,ATOX1,ATP1A1,ATP1 B1,ATP2A2,ATP2B1,ATP6AP1,ATXN2,B2M,B4GALNT1,BAG3,BCHE,BCLAF1,BCS1L,BGN,BID,BI N1,BLMH,BRAF,Brd4,BSG,BUB3,C1QA,C4A/C4B,CALCRL,Cald1,CALR,CANX,CAP1,CAPNS1,CA PZB,CASK,CASP3,CASP7,CCDC134,CCDC47,CCS,CD2AP,CD36,CD38,CD47,CD68,CDA,Cdc42,CD C73,CDK11A,CDK12,CDK5,CDK6,CDKN1B,CDKN2C,CDO1,CFB,CFH,CFI,CHD4,CHMP2A,CIAO3, CISD2,CKB,CLIC4,Cmah,CNOT3,CNP,CNPY2,COBLL1,COPB1,COQ3,COQ9,COX15,CPB2,CPOX,C PS1,CR1L,CREB1,CRELD1,CRK,CRKL,CRP,CSAD,CSK,CSNK2A1,CSNK2B,CSRP1,CTBP1,CTH,C TNNB1,CTNNBL1,CTNND1,CTR9,CTSB,CTSD,CTSF,CTSV,CTTN,CUL1,CUL3,Cux1,CXADR,CYG B,CYP17A1,CYP1A2,CYP7A1,CYP7B1,DAD1,Dazap1,DDAH1,DDX17,DDX3X,DDX5,DDX58,DES, DGAT2,DHFR,DHX9,DKC1,DMD,DNAJB1,DNAJB4,DNAJB6,DNAJB9,DNAJC3,DNM1L,DNM2,DP AGT1,DPYD,DSP,Dst,ECM1,EGFR,EHD1,EHD3,EHHADH,EIF2AK2,EIF2S1,EIF3D,EIF3M,EIF4A1,E IF4G2,ELAVL1,ELOA,ELOVL1,EPN1,ERBIN,ERC1,F11,F13A1,FABP7,FASN,FBL,FCGR2B,FCGRT, FECH,FEN1,FERMT2,FGA,FGG,FHIT,FITM2,FKBP4,FLII,FLNA,FN1,FSCN1,FTO,FUBP1,Fus,FXN,F XR1,G6PC,G6PD,GABPA,GADD45GIP1,GAMT,GATAD2A,GBA,GBE1,GCH1,GCK,GCLM,GJB2,G m21596/Hmgb1,GNA11,GNA13,GNAI2,GNAI3,GNAQ,GNAS,GNE,GNL3,GNPAT,GOLGA2,GPD1L, GPHN,GPX3,GPX4,GRN,GSTK1,GSTM1,GSTP1,GSTZ1,GTF2I,GUCY1B1,H3-3A/H3- 3B,HDAC1,HEXB,HEXIM1,HGS,HIP1,HMGCL,HMGN1,HMOX1,HMOX2,HNF1A,HNF4A,Hnrnpa1, HNRNPAB,HNRNPC,HNRNPD,HNRNPK,HNRNPL,HOPX,HP,HPGD,HRAS,HSD17B2,HSD17B4,HS P90AA1,HSP90AB1,HSP90B1,HSPA4L,HSPA5,HSPB1,HSPG2,HUWE1,HYOU1,ICAM1,IDH2,Ifi47,I FNAR2,IGF2R,IL6ST,ILF2,ILF3,ILK,IMPA1,INSIG2,INSR,Irgm1,ITGA2B,ITGA5,ITGA9,ITGAV,ITG B1,ITGB3,ITPR2,ITSN1,JUP,KCTD12,KHDRBS1,KPNA1,KRAS,LAMTOR1,LARP7,LDLR,LGALS3, LHPP,LIAS,LIFR,LIMS2,LIN7A,LIN7C,LMNA,LMNB1,LMNB2,LMO7,LRP1,LRPAP1,LSR,LUM,LY N,LYZ,M6PR,Macf1,MACROH2A2,MAN1A2,MAP2K1,MAP2K3,MAP4,MBNL1,MBOAT7,MCAM,M DH1,MECP2,METAP2,MFN2,MGAT2,MIA3,MIF,MIF4GD,MME,MMUT,Mocs1,MORF4L1,MPC1,M PI,MRC1,MSH2,MSN,MSR1,MSRA,Mt1,Mt2,MTA2,MTAP,MTDH,MTOR,MTSS1,Mug1/Mug2,MYB BP1A,MYH10,MYH11,MYH14,MYH9,MYL6,MYLPF,MYO18A,NAGLU,NAMPT,NASP,NCK1,NCO A5,NCSTN,NDRG1,NDST1,NDUFA13,NELFB,NFIA,NFIB,NFIC,NMNAT1,NOS3,NPC1,NPC2,NQO1 ,NR1H4,NR3C1,NRAS,NSF,NUMA1,NUP98,OAT,OGA,OLA1,PAFAH1B1,PAK2,PALLD,PANK1,PA RP1,PCCA,PCK1,PCYT1A,PDCD10,PDCD4,PDHA1,PDIA3,PDLIM1,PEX11A,PEX13,PEX5,PFKFB3, PGK1,PGM3,PHB2,PI4KA,PICALM,PIK3CB,PIP5K1C,PLCB3,PLG,PLOD3,PLPP3,PLRG1,PLS3,PLV AP,PLXNB2,PML,PMM2,PNN,Podxl,POLR2A,PON3,POR,PPCS,PPIA,PPIB,PPIF,PPIG,PPM1B,PPP1R 8,PPP4C,PPT1,PPT2,PRKAA2,PRKAB1,PRKACA,PRKCSH,PRKRA,PROC,PRORP,PRPF19,PRPF31,P RPF8,PSAP,PSEN1,PSIP1,PSMC3,PSMD4,PTBP1,PTGES3,PTK2,PTK2B,Ptma (includes others),PTPMT1,PTPN1,PTPRF,PTS,PURA,PXN,PYCARD,QDPR,RAB8A,RAB8B,RAC1,RAD23B,RA D50,RAE1,RAP1A,RASIP1,RBM15,RBP1,RELA,RGN,RGPD4 (includes others),RHOA,RIPK1,RNASEH2A,RNASET2,RNF14,RNF2,RNF5,RNH1,RNMT,Rpl22l1,RPL24,Rpl29 (includes others),RPL4,RPL5,RPL6,RPS19,RPS24,RPS6KB2,RPSA,RPTOR,RTN4,RUFY3,RUVBL1,SAA1,SAFB ,SBF1,SC5D,SCARB1,SCARB2,SCD,SCRIB,SCYL2,SDC4,SDHD,SEC63,SELENBP1,SELENOP,SEP HS1,SERPINA1,SERPINA10,SERPINA3,SERPINA6,SERPIND1,SERPINF2,SERPING1,SERPINH1,SE T,SF3B1,SGTA,SH3GL1,SHOC2,SIGMAR1,SLC25A13,SLC25A25,SLC27A4,SLC2A2,SLC30A5,SLC3 1A1,SLC35D1,SLC4A4,SLC9A3R1,SLCO2A1,SMARCA5,SMPD1,SNAP23,SNRPN,SNX1,SNX2,SOR BS2,SOS1,SPR,SPTAN1,SRRT,SRSF1,SRSF10,SRSF2,SRSF3,SSBP1,SSRP1,STAB1,STAB2,STAT2,S TAT3,STAT6,STEAP4,STIP1,STK38,SUB1,SUMO2,SUN2,SURF1,TADA3,TARDBP,TCEA1,TCIRG1, TCOF1,TGM1,TIAL1,TINAGL1,TJP2,TKT,TLN1,TMED10,TMEM38B,TMOD3,Tmsb4x (includes others),TOP1,TOP2B,TOP3B,TOR1A,Tpm1,TPM3,TRA2B,TRIM28,TRMU,TSG101,TSPAN31,TSTA3, TTN,TTPA,TYMP,U2AF2,UBA3,UBE2I,UBE2J1,UBE4B,UBL4A,UBR2,UBTF,UPF1,UPF2,USO1,USP 7,VAC14,VAMP2,VCAM1,VCL,VDAC3,VIM,VPS26A,VPS52,VSIG4,VTA1,WAPL,WASF2,WASHC5 ,WBP2,WDR1,WDR5,WDR77,XRCC6,YBX1,YBX3,YME1L1,YTHDF2,ZBTB20,ZFR,ZMIZ1
1. Cancer,Cell Death and Survival,Organismal Injury and Abnormalities,Tumor Morphology 2. Cell death of cancer cells 3. 2.24E-29 4. Decreased 5. -5.334 6. 140	ACLY,AKT1,ANXA1,ARCN1,ATXN2,B2M,BID,BNIP3,BRAF,CASP3,CAT,CD38,Cdc42,CDKN1B,C LU,COL18A1,COPA,COPB2,COPG1,CRNKL1,CTNNB1,CTSB,DEPTOR,DIABLO,DPP4,EEF1A1,EG FR,EIF2AK2,EIF3C,EIF3E,EIF3F,EIF3L,ENO1,FASN,FAU,FHIT,GCH1,HDAC1,HMOX1,HSP90AB1, HSPA1A/HSPA1B,HSPA9,IL6ST,ITGA1,ITGAV,KRAS,LGALS1,MTOR,NAMPT,NDRG1,NR3C1,NR AS,NUP155,NUP160,NUP214,NUP54,PABPC1,PARP1,PARP14,PAWR,PHF5A,PHLDA1,POLR2H,PR KAA2,PRKAB1,PRPF8,PSMA3,PSMA4,PSMA5,PSMA6,PSMA7,PSMB1,PSMB3,PSMB5,PTK2,PTK2 B,PUF60,RAC1,RAN,RBM39,RBM8A,RELA,RPL10,RPL11,RPL13,RPL13A,RPL19,Rpl23a,RPL27,RP L27A,RPL3,RPL31,RPL35,RPL35A,RPL37,RPL37A,RPL38,RPL5,RPL6,RPL7,RPL7A,RPL9,RPLP0,R PS11,RPS12,RPS13,RPS14,RPS15A,RPS16,RPS17,RPS19,RPS21,RPS24,RPS27A,RPS28,RPS29,RPS3, RPS4Y1,RPS5,RPS7,RTN4,SF3A1,Sf3a2,SF3B1,SF3B2,SF3B3,SF3B6,SMC1A,SNRPA1,SNRPD3,Snrp g,SON,STAT3,SUPT16H,TSC22D1,U2af1,U2AF2,UBE2I,VCAM1,VDAC2

1. Cancer,Cell Death and Survival,Organismal Injury and Abnormalities,Tumor Morphology 2. Necrosis of malignant tumor 3. 4.2E-29 4. Decreased 5. -5.232 6. 141	ACLY,AKT1,ANPEP,ANXA1,ARCN1,ATXN2,B2M,BID,BNIP3,BRAF,CASP3,CAT,CD38,Cdc42,CDKN1B,CLU,COL18A1,COPA,COPB2,COPG1,CRNKL1,CTNNB1,CTSB,DEPTOR,DIABLO,DPP4,EEF1A1,EGFR,EIF2AK2,EIF3C,EIF3E,EIF3F,EIF3L,ENO1,FASN,FAU,FHIT,GCH1,HDAC1,HMOX1,HSP90AB1,HSPA1A/HSPA1B,HSPA9,IL6ST,ITGA1,ITGAV,KRAS,LGALS1,MTOR,NAMPT,NDRG1,NR3C1,NRAS,NUP155,NUP160,NUP214,NUP54,PABPC1,PARP1,PARP14,PAWR,PHF5A,PHLDA1,POLR2H,PRKAA2,PRKAB1,PRPF8,PSMA3,PSMA4,PSMA5,PSMA6,PSMA7,PSMB1,PSMB3,PSMB5,PTK2,PTK2B,PUF60,RAC1,RAN,RBM39,RBM8A,RELA,RPL10,RPL11,RPL13,RPL13A,RPL19,Rpl23a,RPL27,RPL27A,RPL3,RPL31,RPL35,RPL35A,RPL37,RPL37A,RPL38,RPL5,RPL6,RPL7,RPL7A,RPL9,RPLP0,RPS11,RPS12,RPS13,RPS14,RPS15A,RPS16,RPS17,RPS19,RPS21,RPS24,RPS27A,RPS28,RPS29,RPS3,RPS4Y1,RPS5,RPS7,RTN4,SF3A1,Sf3a2,SF3B1,SF3B2,SF3B3,SF3B6,SMC1A,SNRPA1,SNRPD3,Snrpg,SON,STAT3,SUPT16H,TSC22D1,U2af1,U2AF2,UBE2I,VCAM1,VDAC2
1. Cell Death and Survival 2. Apoptosis 3. 2.39E-28 4. Decreased 5. -5.428 6. 681	AAMDC,ABCE1,ACACA,ACIN1,ACLY,ACO2,ACSL4,ACTN4,ADAM10,ADI1,AGO1,AGO2,AGPAT2,AGRN,AHSA1,AIF1,AIP,AKR1B10,AKT1,ALCAM,ALDH1A1,ALDH1L1,ALDOA,ANGPTL4,Anp32b,ANPEP,ANXA1,ANXA11,ANXA4,ANXA5,AP2M1,APCS,APEX1,API5,APOA1,APOE,AQP1,ARAF,ARF4,ARF6,ARHGDIA,ARHGDIB,ARHGEF12,ARHGEF7,ARMC10,ARRB1,ARSB,ASAH1,ASS1,ATG3,ATOX1,ATP11C,ATP1A1,ATP1B3,ATP2B4,ATP6AP2,ATRX,ATXN2,AVEN,B2M,B4GALNT1,BABAM2,BAG3,BAG4,BAG5,BASP1,BCAP31,BCAS2,BCL2L13,BCLAF1,BGN,BID,BIN1,BLVRA,BNIP3,BRAF,BSG,BUB3,C1QA,C6,CACFD1,CADM1,CALCRL,CALR,CAMK1,CANX,CAPNS1,CASP3,CASP7,CAT,CBX3,CCAR1,CCDC47,CD1D,CD2AP,CD36,CD38,CD47,CD82,CDC34,CDC37,Cdc42,CDC73,CDK11A,CDK12,CDK5,CDK5RAP3,CDK6,CDK9,CDKN1B,CDKN2C,CES1,CFH,CIDEB,CLIC4,CLU,CNOT2,CNP,COL18A1,COPZ1,COQ8A,COQ9,CORO1A,COX5A,COX6B1,COX7A2L,CR1L,CREB1,CRELD1,CRIP1,CRK,CRKL,CRP,CSK,CSNK1E,CSNK2A1,CSNK2A2,CTBP1,CTH,CTNNA1,CTNNB1,CTNNBL1,CTNND1,CTSB,CTSD,CTSH,CTSS,CTSV,CTSZ,CTTN,CUL1,CUL2,CUL3,CXADR,CYB5A,CYGB,CYP2F1,CYP7A1,DAD1,DAPK1,DCPS,DDAH2,DDRGK1,DDX17,DDX19A,DDX3X,DDX42,DDX5,DDX58,DECR1,DEK,DEPTOR,DES,DHCR24,DHFR,DHODH,DHX9,DIABLO,DMGDH,DNAJA1,DNAJB1,DNAJC3,DNM1L,DNM2,DPM3,DPP4,DPP7,DPP9,DSP,DUT,DYNLL1,EEF1A1,EEF1D,EGF,EGFR,EHD1,EHD3,EIF2A,EIF2AK2,EIF2B5,EIF2S1,EIF3C,EIF3F,EIF3H,EIF3I,EIF3M,EIF4E,EIF4G1,EIF4G2,EIF5A,ELAVL1,ELMO1,ELOA,ELOC,EMD,ENO1,ENTPD5,EPHX1,ERC1,Ewsr1,EXOC5,EZR,FAF1,FAM162A,FASN,FAU,FBL,FCGR2B,FEN1,FGA,FHIT,FIS1,FKBP4,FKBP5,FLNA,FLOT2,FMR1,FN1,FNTA,FUBP1,Fus,FXN,FXR1,G0S2,G6PC,G6PD,GADD45GIP1,GAPDH,GATAD2A,GCK,GCLM,GFPT1,GIMAP4,GLO1,GLUD1,Gm21596/Hmgb1,GNA11,GNA13,GNAI2,GNAQ,GNAS,GNE,GNL3,GNMT,GOLPH3,GPAM,GPLD1,GPX4,GRN,GSR,GSTM5,GSTP1,GSTZ1,HCFC1,HDAC1,HDGF,HERPUD1,HEXB,HEXIM1,HIP1,HK1,HMGA1,HMOX1,HMOX2,HNF1A,HNF4A,HNRNPC,HNRNPH1,HNRNPK,HPGD,HPN,HRAS,HS1BP3,HSD17B10,HSP90AA1,HSP90AB1,HSP90B1,HSPA1A/HSPA1B,HSPA5,HSPA8,HSPA9,HSPB1,HSPD1,HSPG2,HSPH1,HTATIP2,HUWE1,HYOU1,HYPK,ICAM1,IFI16,IFIT3,IFNAR2,IGF2R,IL6ST,ILF3,ILK,ILKAP,IMMT,INSR,Irgm1,ITGA1,ITGA5,ITGAV,ITGB1,ITGB3,ITIH4,ITPR2,ITSN1,JUP,KANK2,KDELR1,KHDRBS1,KPNA1,KPNA2,KRAS,LDLR,LGALS1,LGALS3,LGALS3BP,LGALS8,LGMN,LIMS2,LIN7C,LMNA,LMNB1,LOC102724788/PRODH,LRP1,LRPAP1,LUM,LYN,LYPLA1,LYPLA2,MAN2C1,MANF,MAOA,MAP2K1,MAP2K3,MAP4,MAT2A,MBOAT7,MCAM,MCTS1,MDH1,MECP2,MFN2,MIEN1,MIF,MKNK1,MME,MOB2,MPRIP,MRPL41,MSH2,MSN,MSR1,MSRB2,Mt1,Mt2,MTA2,MTCH2,MTDH,MTMR6,MTOR,MTSS1,MVK,MVP,MYBBP1A,MYDGF,MYH10,MYH11,MYLK,MYO18A,NAA15,NAA16,NAA35,NAMPT,NASP,NAT10,NCEH1,NCK1,NCL,NCOA5,NCSTN,NDRG1,NDST1,NDUFA13,NDUFAF1,NDUFAF4,NECTIN2,NELFB,NFIB,NFIC,NGEF,Ngp,NLRX1,NME3,NMNAT1,NOC2L,NOS3,NPC1,NQO1,NQO2,NR1H4,NR3C1,NRAS,NUDT13,NUMA1,OGA,OGT,OPTN,OXR1,PA2G4,PAFAH1B1,PAFAH1B2,PAFAH2,PAK2,PALLD,PAM16,PARP1,PARP14,PARVA,PARVB,PAWR,PCTP,PDCD10,PDCD4,PDCD6IP,PDHA1,PDIA3,PDK1,PDLIM7,PDXK,PEBP1,PECAM1,PEX5,PHB2,PHLDA1,PIK3AP1,PIK3CB,PKN1,PLEKHF1,PLG,PLRG1,PLXNA4,PML,PNKP,POLR2A,PON2,PON3,POR,PPIA,PPIF,PPM1A,PPP1R2,PPP2R1B,PPT1,PPT2,PQBP1,Prame,PRDX3,PRDX5,PRDX6,PRKAA2,PRKAB1,PRKACA,PRKRA,PROC,PRPF19,PSAP,PSEN1,PSIP1,PSMB1,PSMB10,PSME3,PTK2,PTK2B,PTP4A2,PTPMT1,PTPN1,PTPRF,PUF60,PUM1,PXN,PYCARD,RAC1,RACK1,RAD23B,RAD50,RANBP1,RAP1A,RAP1B,RAPGEF4,RBBP4,RELA,RGN,RHOA,RHOC,RHOG,RIPK1,RNF17,RNF2,RNF5,RNMT,ROCK2,RPL10,RPL37,RPLP0,RPS19,RPS24,RPS27A,RPS29,RPS3,RPS6,RPS6KB2,RPTOR,RRAS,RSL1D1,RTN1,RTN4,RUVBL2,S100A1,S100A6,SAA1,SAE1,SAFB,SAP18,SCARB1,SCARB2,SCD,SCRIB,SDC4,SDF2L1,SEC23B,SEC61G,SELENBP1,SELENOF,SELENOP,SERINC3,SERPINA1,SERPINA3,SERPINB1,SERPINH1,SET,SF3B1,SF3B6,SFPQ,SFT2D2,SH3BGRL3,SIGMAR1,SLC25A10,SLC25A11,SLC25A5,SLC39A14,SLC9A3R1,SLCO1B3,SLK,SMARCA2,SMARCA5,SMARCE1,SMPD1,SND1,SNW1,SNX1,SNX6,SNX7,SON,SOS1,SRA1,SRI,SRPK2,SRRT,SRSF1,SRSF2,Srsf5,SSRP1,STAT2,STAT3,STAT6,STEAP3,STIP1,STK38,STOML2,STRAP,SUB1,SUMO2,SUN2,SURF1,SWAP70,SYNCRIP,TADA3,TAGLN2,TAOK3,TARDBP,TCERG1,TCIRG1,TDO2,TFR2,TGM1,THOC6,TIAL1,TIGAR,TJP2,TLN1,TMED10,TMEM109,TMEM214,TMOD3,TMX1,TNS2,TOMM40,TOP1,TOP2B,TPD52,TPR,TRAP1,TRIM28,TSC22D1,TSG101,TTN,TTPA,TXN2,TXNDC5,TYMP,UBA1,UBA2,UBA3,UBA7,UBE2I,UBE2M,UBE2V2,UBE2Z,UBE4B,UBR2,UCHL5,UFL1,UFM1,UPF1,USP7,VAV2,VCL,VDAC2,VIM,VNN1,VPS28,VPS35,VTN,WAPL,WDR26,WDR5,WFS1,XAF1,XPO1,XRCC6,YBX1,YBX3,YME1L1,YWHAQ,YWHAZ,ZFR,ZHX2

1. Gene Expression,Protein Synthesis 2. Translation of RNA 3. 6.33E-28 4. Decreased 5. -2.926 6. 89	ACO1,AGO2,AKT1,CALR,CNOT1,CYFIP1,DAPK1,DDX3X,DHFR,DNAJC1,EGFR,Eif1,EIF2A,EIF2AK2,EIF2B1,EIF2B2,EIF2B3,EIF2B5,EIF2S1,EIF3C,EIF3D,EIF3E,EIF3F,EIF3H,EIF3I,EIF3K,EIF3L,EIF3M,EIF4A2,EIF4A3,EIF4E,EIF4G1,EIF4G2,EIF4H,EIF5,EIF5B,ELAVL1,FMR1,FXR1,GAPDH,GRB7,GSPT1,HSPB1,ILF3,LARP1,MKNK1,MRPL12,MRPL15,MRPL17,MRPL41,MRPL51,MVK,NCBP1,NCBP2,PABPC4,PAIP1,PAIP2,RACK1,RIDA,RPL10,RPL10A,RPL13A,RPL19,RPL23,RPL24,RPL27A,Rpl29 (includes others),RPL30,RPL37,RPL38,Rplp1 (includes others),RPS14,RPS17,RPS23,RPS24,RPS28,RPS29,RPS3,RPS4Y1,RPS5,RPS6KB2,RPS9,SARS1,SHMT1,SYNCRIP,TCOF1,TPR,UPF1,XRN1
1. Gene Expression,Protein Synthesis 2. Translation of mRNA 3. 1.89E-27 4. Decreased 5. -2.926 6. 87	ACO1,AGO2,AKT1,CALR,CNOT1,CYFIP1,DAPK1,DDX3X,DHFR,DNAJC1,EGFR,Eif1,EIF2A,EIF2AK2,EIF2B1,EIF2B2,EIF2B3,EIF2B5,EIF2S1,EIF3C,EIF3D,EIF3E,EIF3F,EIF3H,EIF3I,EIF3K,EIF3L,EIF3M,EIF4A2,EIF4A3,EIF4E,EIF4G1,EIF4G2,EIF4H,EIF5,EIF5B,ELAVL1,FMR1,FXR1,GAPDH,GRB7,HSPB1,ILF3,LARP1,MKNK1,MRPL12,MRPL15,MRPL17,MRPL41,MRPL51,MVK,NCBP1,NCBP2,PABPC4,PAIP1,PAIP2,RACK1,RIDA,RPL10,RPL10A,RPL13A,RPL19,RPL23,RPL24,RPL27A,Rpl29 (includes others),RPL30,RPL37,RPL38,Rplp1 (includes others),RPS14,RPS17,RPS23,RPS24,RPS28,RPS29,RPS3,RPS4Y1,RPS5,RPS6KB2,RPS9,SARS1,SHMT1,SYNCRIP,TCOF1,TPR,XRN1
1. Lipid Metabolism,Molecular Transport,Small Molecule Biochemistry 2. Concentration of triacylglycerol 3. 5.77E-27 4. Decreased 5. -2.091 6. 133	ACACA,ACACB,ACAT2,ACLY,ACOT11,ACOT13,ADIPOR2,AGPAT2,AHSG,AKR1B10,AKT1,AMACR,ANGPTL3,ANGPTL4,APOA1,APOA2,APOB,Apoc1,Apoc3,APOC4,APOD,APOE,APOM,AQP9,ATP2A2,BAG3,BCHE,BCO2,BHMT,C1QA,CACFD1,CD36,CES1,CIDEB,CISD1,CNOT3,CNPY2,COL18A1,CRP,CTNNB1,CYP27A1,Cyp4a14,DDHD2,DGAT2,ECI1,EGF,ELOVL5,ENTPD5,FABP4,FABP5,FASN,FGL1,FITM2,FKBP4,FMO3,FMO5,G0S2,G6PC,G6PD,GALNT2,GATM,GCK,GCKR,GNA11,GNAS,GPAM,GPAT4,GSTK1,HELZ2,HINT2,HNF4A,HSD11B1,INSR,ITGA1,LCAT,LDLR,LGALS3,LIPE,LMNA,LPCAT3,LRP1,LRPAP1,LSR,MECP2,MGLL,Mia2,MID1IP1,MIF,MPC1,NAMPT,NCEH1,NCOA5,NOS3,NQO1,NR1H4,NR3C1,OGA,PANK1,PCK1,PCYT1A,PDK2,PEX11A,PFKFB1,PLIN5,PLTP,PLVAP,PML,PON1,PON2,PON3,POR,PRDX3,PRKAA2,PRKAB1,PRPF19,PTPN1,PYCARD,RGN,SAP18,SCARB1,SCD,SLC22A1,SLC25A13,SMPD1,SOAT2,SORBS1,SRSF2,STEAP4,THRSP,UPF2,USP7,VAMP3,VNN1
1. Cancer,Cell Death and Survival,Organismal Injury and Abnormalities,Tumor Morphology 2. Necrosis of tumor 3. 6.67E-26 4. Decreased 5. -4.994 6. 165	ACLY,AKT1,ANPEP,ANXA1,ARCN1,ATXN2,B2M,B4GALNT1,BID,BNIP3,BRAF,BSG,CASP3,CAT,CD38,CD47,Cdc42,CDK6,CDKN1B,CLU,COL18A1,COPA,COPB2,COPG1,CRNKL1,CTNNB1,CTSB,DAPK1,DEPTOR,DIABLO,DPP4,EEF1A1,EGF,EGFR,EIF2AK2,EIF3C,EIF3E,EIF3F,EIF3L,ENO1,FASN,FAU,FGA,FHIT,GCH1,HDAC1,HMOX1,HRAS,HSP90AB1,HSPA1A/HSPA1B,HSPA9,IDH2,IL6ST,INSR,ITGA1,ITGAV,KRAS,LGALS1,LYPLA1,LYPLA2,MIF,MTOR,NAMPT,NDRG1,Ngp,NR3C1,NRAS,NUP155,NUP160,NUP214,NUP54,PABPC1,PARP1,PARP14,PAWR,PDK1,PHF5A,PHLDA1,PIK3CB,PLG,PML,POLR2H,PON2,PRKAA2,PRKAB1,PRPF8,PSMA3,PSMA4,PSMA5,PSMA6,PSMA7,PSMB1,PSMB3,PSMB5,PTK2,PTK2B,PUF60,RAC1,RACK1,RAD50,RAN,RBM39,RBM8A,RELA,RHOA,RPL10,RPL11,RPL13,RPL13A,RPL19,Rpl23a,RPL27,RPL27A,RPL3,RPL31,RPL35,RPL35A,RPL37,RPL37A,RPL38,RPL5,RPL6,RPL7,RPL7A,RPL9,RPLP0,RPS11,RPS12,RPS13,RPS14,RPS15A,RPS16,RPS17,RPS19,RPS21,RPS24,RPS27A,RPS28,RPS29,RPS3,RPS4Y1,RPS5,RPS7,RTN4,SERPINA3,SF3A1,Sf3a2,SF3B1,SF3B2,SF3B3,SF3B6,SMC1A,SNRPA1,SNRPD3,Snrpg,SON,STAT3,SUPT16H,TSC22D1,TSG101,U2af1,U2AF2,UBE2I,VCAM1,VDAC2
1. Cancer,Cell Death and Survival,Organismal Injury and Abnormalities,Tumor Morphology 2. Cell death of tumor cells 3. 1.08E-25 4. Decreased 5. -4.931 6. 162	ACLY,AKT1,ANPEP,ANXA1,ARCN1,ATXN2,B2M,BID,BNIP3,BRAF,BSG,CASP3,CAT,CD38,CD47,Cdc42,CDK6,CDKN1B,CLU,COL18A1,COPA,COPB2,COPG1,CRNKL1,CTNNB1,CTSB,DAPK1,DEPTOR,DIABLO,DPP4,EEF1A1,EGF,EGFR,EIF2AK2,EIF3C,EIF3E,EIF3F,EIF3L,ENO1,FASN,FAU,FHIT,GCH1,HDAC1,HMOX1,HRAS,HSP90AB1,HSPA1A/HSPA1B,HSPA9,IDH2,IL6ST,INSR,ITGA1,ITGAV,KRAS,LGALS1,LYPLA1,LYPLA2,MIF,MTOR,NAMPT,NDRG1,NR3C1,NRAS,NUP155,NUP160,NUP214,NUP54,PABPC1,PARP1,PARP14,PAWR,PDK1,PHF5A,PHLDA1,PIK3CB,PLG,PML,POLR2H,PON2,PRKAA2,PRKAB1,PRPF8,PSMA3,PSMA4,PSMA5,PSMA6,PSMA7,PSMB1,PSMB3,PSMB5,PTK2,PTK2B,PUF60,RAC1,RACK1,RAD50,RAN,RBM39,RBM8A,RELA,RHOA,RPL10,RPL11,RPL13,RPL13A,RPL19,Rpl23a,RPL27,RPL27A,RPL3,RPL31,RPL35,RPL35A,RPL37,RPL37A,RPL38,RPL5,RPL6,RPL7,RPL7A,RPL9,RPLP0,RPS11,RPS12,RPS13,RPS14,RPS15A,RPS16,RPS17,RPS19,RPS21,RPS24,RPS27A,RPS28,RPS29,RPS3,RPS4Y1,RPS5,RPS7,RTN4,SERPINA3,SF3A1,Sf3a2,SF3B1,SF3B2,SF3B3,SF3B6,SMC1A,SNRPA1,SNRPD3,Snrpg,SON,STAT3,SUPT16H,TSC22D1,TSG101,U2af1,U2AF2,UBE2I,VCAM1,VDAC2
1. Lipid Metabolism,Molecular Transport,Small Molecule Biochemistry 2. Concentration of sterol 3. 4.83E-25 4. Decreased 5. -2.797 6. 125	ABCB4,ABCG5,ACACB,ACAT1,ACAT2,ACOT11,ACOT13,ADIPOR2,AGPAT2,Akap9,AMACR,ANGPTL3,ANGPTL4,Anp32b,APOA1,APOA2,APOB,Apoc1,Apoc3,APOE,APOM,ARHGDIA,ATP1A1,ATXN2,B4GALNT1,BAG3,BCO2,BHMT,CACFD1,CD36,CDKN1B,CES1,CISD1,CLU,CRP,CTSS,CYP27A1,CYP3A5,CYP7A1,DHCR24,DIO1,DNAJC7,ENTPD5,EPB41,EPHX2,FABP2,FABP4,FABP5,FASN,FGL1,FLOT1,FLOT2,FMO3,FMO5,G6PC,GATM,GCK,GNAS,GPAM,GPAT3,HINT2,HMGA1,HNF1A,HNF4A,HP,HSD11B1,ICAM1,INSR,ITGB3,KIF13B,KPNA1,LCAT,LDLR,LGALS3,LIPE,LPCAT3,LRP1,LRPAP1,LSR,MECP2,MGLL,Mia2,MPC1,MSR1,NAMPT,NCEH1,NOS3,NPC1,NPC2,NR1H4,NSUN2,PARP1,PCTP,PCYT1A,PDZK1,PLTP,PLVAP,PNLIP,PON1,PON3,POR,PRDX3,PRKAA2,PSEN1,RGN,RHOA,ROCK2,RPTOR,SAA1,SC5D,SCARB1,SCD,SEC14L2,SEC24A,SIGMAR1,SLC27A4,SLC9A3R1,SLCO1B3,SMPD1,SOAT2,SRSF2,STEAP4,VAC14,VCAM1,VNN1

1. Lipid Metabolism,Molecular Transport,Small Molecule Biochemistry 2. Concentration of cholesterol 3. 3.07E-24 4. Decreased 5. -2.482 6. 120	ABCB4,ABCG5,ACACB,ACAT1,ACOT11,ACOT13,ADIPOR2,AGPAT2,Akap9,AMACR,ANGPTL3,ANGPTL4,Anp32b,APOA1,APOA2,APOB,Apoc1,Apoc3,APOE,APOM,ARHGDIA,ATP1A1,ATXN2,B4GALNT1,BAG3,BCO2,BHMT,CACFD1,CD36,CDKN1B,CES1,CISD1,CRP,CTSS,CYP27A1,CYP3A5,CYP7A1,DHCR24,DIO1,DNAJC7,ENTPD5,EPHX2,FABP2,FABP4,FABP5,FASN,FGL1,FLOT1,FLOT2,FMO3,FMO5,G6PC,GATM,GCK,GNAS,GPAM,GPAT3,HINT2,HMGA1,HNF1A,HNF4A,HP,HSD11B1,ICAM1,INSR,ITGB3,KIF13B,KPNA1,LCAT,LDLR,LGALS3,LIPE,LPCAT3,LRP1,LRPAP1,LSR,MECP2,MGLL,Mia2,MPC1,MSR1,NAMPT,NCEH1,NOS3,NPC1,NPC2,NR1H4,NSUN2,PARP1,PCTP,PCYT1A,PDZK1,PLTP,PLVAP,PNLIP,PON1,PON3,POR,PRDX3,PRKAA2,PSEN1,RGN,RHOA,ROCK2,RPTOR,SAA1,SC5D,SCARB1,SCD,SEC14L2,SEC24A,SIGMAR1,SLCO1B3,SMPD1,SOAT2,SRSF2,STEAP4,VAC14,VCAM1,VNN1
1. Amino Acid Metabolism,Small Molecule Biochemistry 2. Metabolism of alpha-amino acid 3. 3.36E-24 4. Decreased 5. -2.176 6. 51	AADAT,AASS,ADSS1,AFMID,AGXT,ALDH4A1,ALDH5A1,AMT,ASPA,ASRGL1,ASS1,BAAT,BHMT,BHMT2,BLMH,CDO1,CSAD,CTH,DGLUCY,FTCD,GART,GCLM,GLDC,GLUD1,GLUL,GLYAT,GNMT,GOT1,GSTZ1,HAL,HGD,HNMT,HPD,IDO2,KYAT1,LOC102724788/PRODH,MAT1A,MSRA,MTHFD1,MTHFS,PCBD1,QDPR,RHOC,SDS,SERINC3,SHMT1,SMS,SRR,TAT,TDO2,UROC1
1. Cell Death and Survival 2. Cell death of tumor cell lines 3. 3.85E-22 4. Decreased 5. -3.649 6. 433	ABCB4,ABCE1,ACACA,ACO2,ACSL4,ADAM10,ADI1,AGPAT2,AHSA1,AKR1B10,AKT1,ALCAM,ALDH1L1,ANGPTL4,ANXA5,AP2M1,APEX1,API5,APMAP,APOB,APOE,ARAF,ARHGDIA,ARMC10,ARSB,AS3MT,ASAH1,ATG3,ATP1A1,ATP1B3,ATP2A2,ATP2B1,B2M,BAG3,BCAP31,BCAS2,BCHE,BCL2L13,BCLAF1,BID,BNIP3,BRAF,BSG,BUB3,CADM1,CALR,CAMK1,CAPNS1,CASP3,CASP7,CAT,CBR1,CBX3,CCAR1,CCT3,CD47,CD82,CDA,CDC34,CDC37,Cdc42,CDC73,CDK5,CDK6,CDK9,CDKN1B,CDKN2C,CES1,CFH,CIDEB,CLU,CLYBL,CNPY2,COL18A1,COPZ1,COX5A,COX6B1,COX7A2L,CPS1,CREB1,CSNK2A1,CSNK2A2,CTBP1,CTH,CTNNB1,CTNND1,CTSB,CTSD,CTTN,CUL1,CUL2,CYB5A,CYGB,DAPK1,DDX3X,DDX58,DEK,DHCR24,DHFR,DHODH,DHX9,DIABLO,DMGDH,DNAJB1,DNM1L,DNM2,DPP4,DPP9,DPYD,DSP,DUT,DYNLL1,EEF1A1,EEF2,EGF,EGFR,EIF1AX,EIF2A,EIF2AK2,EIF2B5,EIF2S1,EIF2S2,EIF3F,EIF3H,EIF3M,EIF4E,EIF4G2,EIF5A,ELAVL1,ELOC,ENO1,ENTPD5,EZR,FABP7,FAF1,FASN,FAU,FCGR2B,FEN1,FETUB,FGA,FHIT,FIS1,FKBP5,FN1,FUBP1,FXN,G0S2,G6PD,GAPDH,GBE1,GIMAP4,GLO1,GNA11,GNA13,GNAS,GNE,GPX4,GRN,GSTM1,GSTP1,HCFC1,HDAC1,HERPUD1,HIP1,HK1,HMGA1,HMGCS1,HMOX1,HNF1A,HNF4A,HNRNPC,HNRNPH1,HNRNPK,HPN,HRAS,HSP90AA1,HSP90AB1,HSPA1A/HSPA1B,HSPA5,HSPA8,HSPA9,HSPB1,HSPD1,HSPH1,HTATIP2,HUWE1,HYPK,IFI16,IFNAR2,IGF2R,IL6ST,ILF2,ILK,ILKAP,IMMT,INSR,INTS3,IP6K1,Irgm1,ITGA5,ITGAV,ITGB1,ITGB3,ITPR2,ITSN1,JUP,KANK2,KDELR1,KHDRBS1,KPNA2,KRAS,LGALS1,LGALS3,LGALS3BP,LGALS8,LMNA,LMNB1,LOC102724788/PRODH,LRP1,LYN,LYPLA1,LYPLA2,MAN2C1,MANF,MAOA,MAP2K1,MAP2K3,MAT2A,MFN2,MIF,MIF4GD,MKNK1,MME,MOB2,MPI,MSH2,MSN,MSR1,MSRB2,MTA2,MTDH,MTMR6,MTOR,MTSS1,MVP,MYBBP1A,NAA35,NAMPT,NASP,NAT10,NCL,NDRG1,NDUFA13,NDUFAF1,NDUFAF4,NFIB,NMNAT1,NOC2L,NOL6,NOS3,NPC2,NQO1,NR3C1,NRAS,NUDCD3,NUP205,NUP93,OGA,OGT,OPTN,OXR1,PA2G4,PAFAH2,PAK2,PARP1,PARP14,PARVA,PAWR,PCK1,PDCD4,PDCD6IP,PDHA1,PDK1,PDK2,PDLIM7,PDZK1,PEBP1,PECAM1,PEX11A,PEX5,PFKFB1,PFKFB3,PGRMC1,PHB2,PIGR,PIK3CB,PKN1,PLEKHA7,PLG,PLXNA4,PML,PNKP,PPAT,PPIA,PPP2R1B,PPT1,PRKAA2,PRKACA,PRKRA,PRPF19,PSAP,PSEN1,PSIP1,PSMD14,PSMD7,PSME3,PTK2,PTK2B,PTPMT1,PTPN1,PTPRF,PUF60,PUM1,PYCARD,RAB35,RAC1,RACK1,RAD23B,RAD50,RAPGEF4,RBM17,RELA,RGN,RHOA,RHOC,RIPK1,RNASEH2A,RNF2,RNF5,RNMT,RPAP3,RPL27A,RPLP0,RPS19,RPS24,RPS3,RPS6KB2,RPTOR,RTN1,RTN4,S100A6,SAA1,SAE1,SARNP,SCARB1,SCD,SCYL3,SDC4,SEC61G,SERPINA3,SF3A1,SF3B3,SFPQ,SFR1,SLC25A5,SLC9A3R1,SLC9A3R2,SLCO1B3,SMARCE1,SMC1A,SMPD1,SND1,SNW1,SNX1,SNX4,SRI,SRPK2,SRSF1,SRSF2,SSRP1,STAT2,STAT3,STAT6,STIP1,STK38,STOML2,SVIL,SYNCRIP,SYNGR2,TAGLN2,TAOK3,TARDBP,TBC1D24,TCERG1,TDO2,TGM1,THOC2,TLN1,TMED10,TMEM214,TNPO2,TNS2,TOLLIP,TOP1,TOP2B,TPD52,TRAP1,TRIM28,TSG101,TTPA,TXN2,TYMP,UBA2,UBA3,UBA7,UBE2I,UBTF,UCHL5,VCAM1,VDAC2,VNN1,VPS28,VPS35,VRK1,VTN,WAPL,WDR5,XAF1,XPO1,XRCC6,YBX1,YWHAZ
1. Neurological Disease 2. Motor dysfunction or movement disorder 3. 2.22E-21 4. Decreased 5. -2.945 6. 319	ABCD1,ABCD2,ACADM,ACAT1,ACOT11,ACTB,ADD3,AGL,AGRN,AHCY,AKT1,ALAS1,ALDH5A1,ALDH6A1,AMY2A,ANO10,APOD,APOE,AQP1,AQP4,ARAF,ARF4,ARHGDIB,ARHGEF7,ARRB1,ASAH1,ASPA,ATP1B1,ATP2A2,ATP2B1,ATP5PO,ATP6AP2,ATP6V1A,ATP6V1E1,ATXN10,ATXN2,B2M,B4GALNT1,BAIAP2,BASP1,BBOX1,BCAP31,BCHE,BGN,BID,BTD,C4A/C4B,C9,CANX,CAPNS1,CAPZB,CASP3,CASP7,CD38,CD68,Cdc42,CDK5,CDKN1B,CDKN2C,CDO1,CHCHD2,CHP1,CKB,CLU,CNP,COA7,COMT,COPE,COQ8A,COQ9,COX7A2,CP,CPB2,CREB1,CRP,CRYM,CSNK2A1,CSRP2,CTNNB1,CTSB,CTSD,CTSF,CTSS,CTSV,DAD1,DBNL,DCPS,DDC,DDHD2,DDX42,DECR1,DHTKD1,DNAJA1,DNAJB1,DNAJB6,DNAJC1,DNAJC13,DNAJC19,DNAJC3,Dst,EEF1A1,EEF2,EIF2B3,EIF3E,EIF3K,EIF4A2,EIF4G1,ELMO1,ELOVL1,ELOVL5,ENPP1,EPHX2,ETNPPL,FABP7,FAM3C,FBL,FCGR2B,FGG,FITM2,FKBP4,FLOT1,FMR1,FUBP1,FXN,G6PC,GAA,GAPDH,GBA,GCH1,GNAQ,GNAS,GOLGA2,GOSR2,GPAM,GPD1,GPHN,GSTP1,GUCY1B1,H3-3A/H3-3B,HADH,HERPUD1,HEXB,HIP1,HLA-DQA1,HMGCS2,HMGN1,HMOX1,HMOX2,HNRNPU,HP,HRAS,HSD17B4,HSP90AA1,HSPA1A/HSPA1B,HSPA5,HSPA8,HSPB1,IGF2R,IGFALS,ILF3,IMPA1,INPP1,ISOC1,ITIH4,KHDRBS1,KRAS,LDLR,LGMN,LIFR,LMNA,LMNB2,LRG1,LRP1,LUM,M6PR,MAOA,MAOB,MDH1,MECP2,METTL9,MFN2,MGAT2,MME,MPC1,MSRA,MTDH,MTOR,MYEF2,MYL12A,MYO1B,NDRG1,NDUFA13,NDUFA2,NDUFB6,NFIA,NGEF,NGLY1,NLRX1,NMT2,NOP56,NPC1,NPC2,NQO2,OGT,OPTN,OXR1,PAN

	K1,PARP1,PCTP,PDK1,PDK2,PDLIM1,PDLIM7,PEBP1,PEX13,PFKFB1,PGK1,PGRMC1,PHKA1,PNKP,POLR2I,PON1,PPIA,PPM1B,PPP1R2,PPT1,PPT2,PRDX6,PRKRA,PSAP,PSEN1,PSMB6,PSMB9,PTGES3,PTK2B,PTS,PUM1,PURA,RAD23B,RAN,RANBP1,RELA,RGN,RHOG,RNF114,RNF2,RNF5,ROCK2,RPL13,RPL13A,RPL15,RPL17,RPL3,RPL31,RPSA,RRS1,RTN1,RTN4,RTN4IP1,SAP18,SARS1,SCAMP5,SCARB2,SCD,SDC4,SEC11A,SEC24A,SELENOF,SELENOP,SEPHS1,SERPINA1,SERPINA3,SERPINF2,SGTA,SIGMAR1,SIL1,Slc25a1,SLC39A14,SLMAP,SMPD1,SPAST,SPR,SPTAN1,SPTBN2,SSR3,SUB1,SUN2,TARDBP,TBC1D24,TCERG1,TGM1,TMED10,TMEM176B,Tmsb4x (includes others),TOP1,TOR1A,TOR1AIP1,TPD52,TPD52L2,TPI1,TPM3,TRAM1,TTPA,TUBA1B,TUBA4A,TUBB2A,TUBB4B,UBAC1,UBE4B,USP24,VAC14,VAMP2,VAPB,VIM,VPS13D,VPS35,WDR26,XRCC6,YWHAZ
1. Neurological Disease 2. Movement Disorders 3. 2.38E-21 4. Decreased 5. -2.858 6. 315	ABCD1,ABCD2,ACADM,ACAT1,ACOT11,ACTB,ADD3,AGL,AGRN,AHCY,AKT1,ALAS1,ALDH5A1,ALDH6A1,AMY2A,ANO10,APOD,APOE,AQP1,AQP4,ARAF,ARF4,ARHGDIB,ARHGEF7,ARRB1,ASAH1,ASPA,ATP1B1,ATP2A2,ATP2B1,ATP5PO,ATP6AP2,ATP6V1A,ATP6V1E1,ATXN10,ATXN2,B2M,B4GALNT1,BAIAP2,BASP1,BBOX1,BCAP31,BCHE,BGN,BID,BTD,C4A/C4B,C9,CANX,CAPNS1,CAPZB,CASP3,CASP7,CD38,CD68,Cdc42,CDK5,CDKN1B,CDKN2C,CHCHD2,CHP1,CKB,CLU,CNP,COA7,COMT,COPE,COQ8A,COQ9,COX7A2,CP,CPB2,CREB1,CRP,CRYM,CSNK2A1,CSRP2,CTNNB1,CTSB,CTSD,CTSF,CTSS,CTSV,DAD1,DBNL,DCPS,DDC,DDHD2,DDX42,DECR1,DNAJA1,DNAJB1,DNAJB6,DNAJC1,DNAJC13,DNAJC19,DNAJC3,Dst,EEF1A1,EEF2,EIF2B3,EIF3E,EIF3K,EIF4A2,EIF4G1,ELMO1,ELOVL1,ELOVL5,EPHX2,ETNPPL,FABP7,FAM3C,FBL,FCGR2B,FGG,FITM2,FKBP4,FLOT1,FMR1,FUBP1,FXN,G6PC,GAA,GAPDH,GBA,GCH1,GNAQ,GNAS,GOLGA2,GOSR2,GPAM,GPD1,GPHN,GSTP1,GUCY1B1,H3-3A/H3-3B,HADH,HERPUD1,HEXB,HIP1,HLA-DQA1,HMGCS2,HMGN1,HMOX1,HMOX2,HNRNPU,HP,HRAS,HSD17B4,HSP90AA1,HSPA1A/HSPA1B,HSPA5,HSPA8,HSPB1,IGF2R,IGFALS,ILF3,IMPA1,INPP1,ISOC1,ITIH4,KHDRBS1,KRAS,LDLR,LGMN,LIFR,LMNA,LMNB2,LRG1,LRP1,LUM,M6PR,MAOA,MAOB,MDH1,MECP2,METTL9,MFN2,MGAT2,MME,MPC1,MSRA,MTDH,MTOR,MYEF2,MYL12A,MYO1B,NDRG1,NDUFA13,NDUFA2,NDUFB6,NFIA,NGEF,NGLY1,NLRX1,NMT2,NOP56,NPC1,NPC2,NQO2,OGT,OPTN,OXR1,PANK1,PARP1,PCTP,PDK1,PDK2,PDLIM1,PDLIM7,PEBP1,PEX13,PFKFB1,PGK1,PGRMC1,PHKA1,PNKP,POLR2I,PON1,PPIA,PPM1B,PPP1R2,PPT1,PPT2,PRDX6,PRKRA,PSAP,PSEN1,PSMB6,PSMB9,PTGES3,PTK2B,PTS,PUM1,PURA,RAN,RANBP1,RELA,RGN,RHOG,RNF114,RNF2,RNF5,ROCK2,RPL13,RPL13A,RPL15,RPL17,RPL3,RPL31,RPSA,RRS1,RTN1,RTN4,RTN4IP1,SAP18,SARS1,SCAMP5,SCARB2,SCD,SDC4,SEC11A,SEC24A,SELENOF,SELENOP,SEPHS1,SERPINA1,SERPINA3,SERPINF2,SGTA,SIGMAR1,SIL1,Slc25a1,SLC39A14,SLMAP,SMPD1,SPAST,SPR,SPTAN1,SPTBN2,SSR3,SUB1,SUN2,TARDBP,TBC1D24,TCERG1,TGM1,TMED10,TMEM176B,Tmsb4x (includes others),TOP1,TOR1A,TOR1AIP1,TPD52,TPD52L2,TPI1,TPM3,TRAM1,TTPA,TUBA1B,TUBA4A,TUBB2A,TUBB4B,UBAC1,UBE4B,USP24,VAC14,VAMP2,VAPB,VIM,VPS13D,VPS35,WDR26,XRCC6,YWHAZ
1. Lipid Metabolism,Molecular Transport,Small Molecule Biochemistry 2. Quantity of steroid 3. 6.11E-21 4. Decreased 5. -2.246 6. 159	ABCB4,ABCC2,ABCC3,ABCG5,ACACB,ACAT1,ACAT2,ACOT11,ACOT13,ADIPOR2,AGPAT2,Akap9,AMACR,ANGPTL3,ANGPTL4,Anp32b,APOA1,APOA2,APOB,Apoc1,Apoc3,APOE,APOM,ARHGDIA,ASGR2,ATP1A1,ATXN2,B4GALNT1,BAG3,BCAP31,BCO2,BHMT,CACFD1,CD36,CDKN1B,CDKN2C,CES1,CISD1,CLU,COMT,CRAT,CRP,CTSS,Cux1,CYP17A1,CYP27A1,CYP3A5,CYP3A7,CYP7A1,DHCR24,DIO1,DNAJC7,EGF,EGFR,EHHADH,ENTPD5,EPB41,EPHX2,FABP2,FABP4,FABP5,FASN,FGL1,FKBP4,FLOT1,FLOT2,FMO3,FMO5,G6PC,GATM,GCK,GNA11,GNAQ,GNAS,GPAM,GPAT3,H6PD,HINT2,HMGA1,HMGN1,HMOX1,HNF1A,HNF4A,HP,HSD11B1,HSD17B4,ICAM1,INSR,ITGB3,KIF13B,KPNA1,LCAT,LDLR,LGALS3,LIPE,LPCAT3,LRP1,LRPAP1,LSR,MAP2K1,MECP2,MGLL,Mia2,MIF,MPC1,MRC1,MSR1,NAMPT,NCEH1,NOS3,NPC1,NPC2,NR1H4,NR3C1,NSUN2,NUCB2,PARP1,PCTP,PCYT1A,PDZK1,PLG,PLTP,PLVAP,PNLIP,PON1,PON3,POR,PRDX3,PRKAA2,PSAP,PSEN1,PTPN1,RGN,RHOA,ROCK2,RPTOR,SAA1,SAFB,SC5D,SCARB1,SCD,SEC14L2,SEC24A,SERPINA6,SIGMAR1,SLC27A4,SLC4A4,SLC9A3R1,SLCO1B3,SMPD1,SOAT2,SRSF2,STAT3,STEAP4,SULT1E1,VAC14,VAV2,VCAM1,VNN1
1. Drug Metabolism 2. Metabolism of xenobiotic 3. 1.53E-19 4. Decreased 5. -3.023 6. 51	ABCC2,ACSM1,ACY1,ACY3,AIP,Akr1c12/Akr1c13,ALDH1A1,Aldh1a7,ALDH3A2,AOX1,BPHL,CAT,CES1,CES3,CMBL,CRYZ,CYB5B,CYP1A2,CYP2A6 (includes others),Cyp2b13/Cyp2b9,CYP2B6,CYP2C8,CYP2F1,CYP3A5,CYP3A7,EPHX1,FMO1,FMO3,GLYAT,Gsta4,GSTA5,GSTM1,GSTM2,GSTM4,GSTM5,GSTP1,HNF4A,HSP90AB1,MGST1,NCEH1,NQO1,NQO2,PAPSS2,PON1,POR,PTGES3,Sult1a1,SULT1B1,SULT2A1,UGT1A6,UGT1A8 (includes others)

1. Cell Death and Survival 2. Apoptosis of tumor cell lines 3. 0.0000000000000844 4. Decreased 5. -3.55 6. 327	ABCE1,ACACA,ACO2,ACSL4,ADI1,AGPAT2,AHSA1,AKR1B10,AKT1,ALCAM,ALDH1L1,ANGPTL4,ANXA5,AP2M1,API5,APOE,ARAF,ARHGDIA,ARMC10,ARSB,ATP1A1,ATP1B3,B2M,BAG3,BCAP31,BCAS2,BCL2L13,BCLAF1,BID,BNIP3,BRAF,BSG,BUB3,CALR,CAMK1,CAPNS1,CASP3,CASP7,CAT,CBX3,CCAR1,CD47,CD82,CDC37,Cdc42,CDC73,CDK5,CDK6,CDK9,CDKN1B,CDKN2C,CES1,CFH,CIDEB,CLU,COL18A1,COPZ1,COX5A,COX6B1,COX7A2L,CREB1,CSNK2A1,CSNK2A2,CTBP1,CTH,CTNNB1,CTNND1,CTSB,CTSD,CTTN,CYB5A,CYGB,DAPK1,DDX58,DHCR24,DHODH,DHX9,DIABLO,DMGDH,DNAJB1,DNM1L,DNM2,DPP4,DSP,DUT,DYNLL1,EEF1A1,EGF,EGFR,EIF2A,EIF2AK2,EIF2B5,EIF3F,EIF3H,EIF3M,EIF4E,EIF4G2,ELAVL1,ELOC,ENO1,ENTPD5,EZR,FAF1,FASN,FAU,FCGR2B,FGA,FHIT,FIS1,FKBP5,FN1,FUBP1,FXN,G0S2,G6PD,GAPDH,GIMAP4,GLO1,GNA11,GNA13,GNAS,GNE,GRN,GSTP1,HCFC1,HDAC1,HMGA1,HMOX1,HNF1A,HNF4A,HNRNPC,HNRNPH1,HNRNPK,HPN,HRAS,HSP90AB1,HSPA1A/HSPA1B,HSPA5,HSPA8,HSPA9,HSPB1,HSPD1,HTATIP2,HUWE1,HYPK,IFI16,IFNAR2,IGF2R,IL6ST,ILK,ILKAP,IMMT,INSR,Irgm1,ITGAV,ITGB1,ITGB3,ITPR2,ITSN1,JUP,KANK2,KHDRBS1,KPNA2,KRAS,LGALS1,LGALS3,LGALS3BP,LGALS8,LMNB1,LOC102724788/PRODH,LRP1,LYN,LYPLA1,LYPLA2,MAN2C1,MANF,MAOA,MAP2K1,MAP2K3,MAT2A,MFN2,MIF,MKNK1,MME,MOB2,MSH2,MSN,MSR1,MSRB2,MTA2,MTDH,MTMR6,MTOR,MTSS1,MVP,MYBBP1A,NASP,NAT10,NCL,NDRG1,NDUFA13,NDUFAF1,NDUFAF4,NFIB,NOC2L,NOS3,NQO1,NR3C1,NRAS,OGA,OGT,OPTN,PA2G4,PAFAH2,PAK2,PARP1,PARP14,PARVA,PAWR,PDCD4,PDCD6IP,PDHA1,PDK1,PDLIM7,PEBP1,PECAM1,PEX5,PHB2,PIK3CB,PKN1,PLG,PLXNA4,PML,PNKP,PPIA,PRKAA2,PRKACA,PRKRA,PRPF19,PSAP,PSEN1,PSIP1,PSME3,PTK2,PTK2B,PTPN1,PUF60,PUM1,PYCARD,RAC1,RACK1,RAD23B,RAPGEF4,RELA,RGN,RHOA,RHOC,RIPK1,RNF2,RNF5,RNMT,RPLP0,RPS19,RPS24,RPS3,RPS6KB2,RPTOR,RTN1,RTN4,S100A6,SAA1,SAE1,SCARB1,SCD,SDC4,SEC61G,SERPINA3,SFPQ,SLC25A5,SLC9A3R1,SLCO1B3,SMARCE1,SMPD1,SND1,SNW1,SNX1,SRI,SRPK2,SRSF1,SSRP1,STAT2,STAT3,STAT6,STK38,STOML2,SYNCRIP,TAGLN2,TAOK3,TCERG1,TDO2,TGM1,TLN1,TMED10,TMEM214,TNS2,TOP1,TPD52,TRAP1,TRIM28,TSG101,TTPA,TXN2,TYMP,UBA2,UBA7,UBE2I,UCHL5,VDAC2,VNN1,VPS35,VTN,WDR5,XAF1,XPO1,XRCC6,YBX1,YWHAZ
1. Cardiovascular Disease,Hematological Disease,Organismal Injury and Abnormalities 2. Anemia 3. 0.000000000000431 4. Decreased 5. -4.133 6. 132	ACTL6A,ADD1,ADD2,ADD3,ADK,AGO2,AKT1,ALDOA,AMY2A,ANXA1,APOE,ARF6,ATP1B1,ATP6V1E1,BAAT,C4A/C4B,CALR,CAT,CCDC134,CD47,CDA,Cdc42,CDK6,CFB,CFH,CFI,CP,CPOX,CRP,DAD1,DHFR,DPP4,EIF2AK2,EPB41,FCGR2B,FN1,FUBP1,G6PD,GIMAP4,GLMP,GLRX5,Gm21596/Hmgb1,GNAS,GRHPR,GSR,GSTM1,HK1,HLA-DQA1,HMOX1,HNF1A,HNF4A,HSPA5,HSPA9,ICAM1,IDH2,IFNAR2,Ighg2b,IL6ST,ITGA5,ITGB3,KHDRBS1,KRAS,LARS2,LCAT,LGALS3,LGMN,LYN,MGAT2,MGLL,MIF,MMUT,MPC1,MTHFD1,MTOR,NDUFA2,NMT2,NQO1,NR3C1,NRAS,PDCD10,PGM3,PICALM,PKLR,PLG,POR,PPAT,PPIA,PRDX3,PRKAA2,PRKAG1,RAC1,RELA,RHOA,RNH1,RPL11,RPL15,RPL18,RPL26,RPL27,RPL35,RPL35A,RPL5,RPL9,RPS10,RPS14,RPS15A,RPS17,RPS19,RPS24,RPS26,RPS28,RPS29,RPS6,RPS7,SCARB1,SEC11A,SEC23B,SF3B1,SIGMAR1,SRSF2,STAG2,STAT3,STEAP3,TCEA1,TFR2,TMOD3,TOP2B,TRIM28,TUBA4A,TUBB2A,TUBB4B,VCAM1
1. Metabolic Disease,Organismal Injury and Abnormalities 2. Amyloidosis 3. 0.00000000000126 4. Decreased 5. -2.288 6. 169	ABAT,ACLY,ACTB,ADAM10,AGRN,ALDH1L1,ALDH5A1,APCS,APOA1,APOA2,APOC2,APOC4,APOD,APOE,AQP1,ATP1A1,ATP1B1,ATP6V1E1,B2M,BCHE,BGN,BIN1,C4A/C4B,C9,CANX,CASP3,CASP7,CD2AP,CD36,CD38,CD47,CD68,CDK5,CFB,CLEC3B,CLU,CNP,CRP,CTSB,CTSD,CTSS,CTSV,CTSZ,CXADR,CYP7B1,DDC,DDX46,DHCR24,DHFR,DHX9,DNM1L,DPYSL2,DYSF,EEF1G,EEF2,EIF2A,EIF2AK2,EIF2S1,FAAH,FAM3C,FCGR2B,FGA,FIS1,GAPDH,GAPVD1,GGA1,GNPAT,GRN,HLA-DQA1,HMGA1,HMGCL,HMOX1,HNRNPA2B1,HNRNPAB,HNRNPU,HP,HPX,HSD11B1,HSPA1A/HSPA1B,HSPA5,HSPA9,HSPD1,HSPG2,ICAM1,IGKC,IL6ST,ILKAP,INSR,KHDRBS1,KRAS,LARP4,LDLR,LGALS1,LGALS3,LGALS3BP,LGMN,LRP1,LRPAP1,LYZ,MACROD1,MAOA,MAOB,MFN2,MIF,MME,MMUT,MPC1,MRC1,MTOR,MVK,MYH11,NAGLU,NCSTN,NDUFB8,NFS1,NMT2,NOS3,NQO1,NQO2,NR3C1,OGT,PAWR,PDIA3,PDK1,PHYHD1,PICALM,PLG,PLTP,PON1,PON2,PRDX6,PRKACA,PSAP,PSEN1,PSMB1,PSMB2,PSMB5,PUM1,RAB14,RACK1,RAN,RELA,RNASET2,ROCK2,SAA1,SC5D,SCARB1,SCD,SELENBP1,SELENOP,SERPINA1,SERPINA3,SET,SIGMAR1,SLC2A2,SLC7A2,SLCO2A1,SMPD1,SNRNP70,SRPK2,STAT3,STIP1,TAGLN,TGM1,TUBB,VDAC3,VIM,VPS35,YWHAZ
1. Lipid Metabolism,Small Molecule Biochemistry 2. Metabolism of triacylglycerol 3. 0.0000000000127 4. Decreased 5. -3.036 6. 43	ACSL4,ACSL5,AGPAT2,ALDH1A1,APOA2,APOB,Apoc1,APOC2,Apoc3,APOE,BHMT,CAT,CD36,CPS1,CYP7A1,DDHD2,DGAT2,FABP2,FABP4,FABP5,FABP7,FASN,FITM2,G6PC,GPAM,GPAT3,GPAT4,GPLD1,HSD11B1,INSIG2,LDLR,LIPE,LMF1,NR3C1,PCTP,PLIN5,PON2,PPAT,RGN,SCARB1,SCD,SMPD1,THRSP
1. Organismal Injury and Abnormalities,Renal and Urological Disease 2. Urination disorder 3. 0.0000000000488 4. Decreased 5. -3.246 6. 92	AASS,ACSF3,ACTN4,AGXT,AGXT2,AMPD2,ANGPTL4,AQP1,AQP4,ARHGDIA,ASL,BCKDHA,BCKDHB,BTD,CD1D,CD2AP,CD81,CFB,CFH,CLU,COMT,CPS1,CR1L,CRP,CTNNB1,CYP2C8,DHTKD1,DPP4,EHD3,ELMO1,ETFDH,EZR,FCGR2B,GCDH,GNE,GRN,GSTZ1,HADH,HCFC1,HNF1A,ICAM1,IDH2,ILK,INSR,KYNU,L2HGDH,LCAT,LGMN,LIN7C,LYN,MAN2B1,MCCC1,MCCC2,MCEE,MGAT2,MMAB,MMUT,Mocs1,Mt1,MTA2,MTSS1,MVK,MYH10,MYH11,MYH9,NAGLU,NOS3,NR1H4,NR3C1,OAT,PCBD1,PCCA,PCCB,PHYKPL,Podxl,PPM1K,PROC,PSAP,PSEN1,PSMB1,PSMB2,PSMB5,SCARB2,SLC26A1,SLC9A3R1,SLC9A3R2,STAB1,STAB2,SUCLG1,SUCLG2,SUGCT,Tmsb4x (includes others)

1. Energy Production,Lipid Metabolism,Small Molecule Biochemistry 2. Beta-oxidation of lipid 3. 0.000000000063 4. Decreased 5. -3.092 6. 34	ABCD1,ABCD2,ABCD3,ACAA1,ACAD10,ACAD11,ACADL,ACADM,ACADSB,ACBD5,ACOX1,ACOX3,ACSL5,BID,CISD1,CPT2,DECR1,ECI1,ECI2,EHHADH,FABP2,FASN,HADH,HMGCS2,HSD11B1,HSD17B4,LIPE,LONP2,MTOR,PEBP1,PEX5,PLIN5,SCD,TYSND1
1. Lipid Metabolism,Small Molecule Biochemistry 2. Metabolism of acylglycerol 3. 0.0000000000799 4. Decreased 5. -2.734 6. 51	ACSL4,ACSL5,AGPAT2,ALDH1A1,APOA2,APOB,Apoc1,APOC2,Apoc3,APOE,BHMT,CAT,CD36,CPS1,CYP7A1,DDHD2,DGAT2,EGF,EPHX1,FAAH,FABP2,FABP4,FABP5,FABP7,FASN,FITM2,G6PC,GNAI3,GPAM,GPAT3,GPAT4,GPLD1,HOMER2,HSD11B1,INSIG2,LDLR,LIPE,LMF1,MGAT2,MGLL,NR3C1,PCTP,PDIA3,PLIN5,PON2,PPAT,RGN,SCARB1,SCD,SMPD1,THRSP
1. Energy Production,Lipid Metabolism,Small Molecule Biochemistry 2. Beta-oxidation of fatty acid 3. 0.000000000154 4. Decreased 5. -3.457 6. 33	ABCD1,ABCD2,ABCD3,ACAA1,ACAD10,ACAD11,ACADL,ACADM,ACADSB,ACBD5,ACOX1,ACOX3,ACSL5,BID,CPT2,DECR1,ECI1,ECI2,EHHADH,FABP2,FASN,HADH,HMGCS2,HSD11B1,HSD17B4,LIPE,LONP2,MTOR,PEBP1,PEX5,PLIN5,SCD,TYSND1
1. Developmental Disorder,Embryonic Development,Organismal Survival 2. Death of embryo 3. 0.0000000111 4. Decreased 5. -2.151 6. 46	AP2M1,Brd4,BSG,CAPNS1,CDK11A,DDAH1,DDX3X,DNAJB1,FASN,FEN1,FLII,GNL3,GPX4,HNRNPL,LIAS,METAP2,NASP,PCYT1A,PHB2,PIK3CB,PLCB3,PLRG1,PNN,PPM1B,PRKACA,PRKRA,PRPF19,PSMC3,PTK2,RAC1,RPS19,RPSA,RUVBL1,SERPIND1,SF3B1,SLC31A1,SNAP23,SRSF3,TADA3,TKT,TMED10,TOP1,TPM3,TTPA,UBA3,UBTF
1. Lipid Metabolism,Small Molecule Biochemistry 2. Synthesis of triacylglycerol 3. 0.0000000127 4. Decreased 5. -2.886 6. 28	ACSL4,ACSL5,AGPAT2,ALDH1A1,Apoc3,APOE,BHMT,CYP7A1,DGAT2,FASN,FITM2,GPAM,GPAT3,GPAT4,GPLD1,HSD11B1,LDLR,LIPE,NR3C1,PCTP,PLIN5,PON2,PPAT,RGN,SCARB1,SCD,SMPD1,THRSP
1. Cellular Assembly and Organization,Cellular Function and Maintenance 2. Formation of peroxisomes 3. 0.0000000192 4. Decreased 5. -2.408 6. 9	ABCD1,ABCD3,PEX1,PEX11A,PEX16,PEX19,PEX26,PEX3,PEX6
1. Cell Signaling 2. Viral life cycle 3. 0.0000000239 4. Decreased 5. -2.281 6. 40	APCS,BANF1,Bst2,CHMP2A,DDX5,EIF2AK2,IFI16,ILF3,MBL2,NUP153,NUP155,NUP160,NUP205,NUP210,NUP214,NUP35,NUP54,NUP93,NUP98,PDCD6IP,PI4KA,PPIA,PPIB,PROX1,PSIP1,RAE1,RAN,RANBP1,RPS27A,SEC14L2,SRPK2,SUMO2,TNPO3,TPR,TSG101,UBE2I,VPS28,VTA1,XPO1,ZC3HAV1
1. Lipid Metabolism,Nucleic Acid Metabolism,Small Molecule Biochemistry 2. Synthesis of acyl-coenzyme A 3. 0.0000000602 4. Decreased 5. -2.183 6. 15	ACACA,ACACB,ACAT1,ACLY,ACSS2,DLAT,FASN,GCDH,PDHA1,PDHB,PPCS,PPT1,PPT2,SCD,SLC27A4

1. Cell Death and Survival 2. Anoikis 3. 0.000000197 4. Decreased 5. -2.181 6. 39	AKT1,ANGPTL4,BID,BRAF,CALR,CD82,CDK11A,CTNNB1,CTNND1,CTTN,DIABLO,EEF1A1,EGF,EGFR,FN1,GNE,GRN,HRAS,ILK,ITGA5,ITGAV,ITGB1,ITGB3,KRAS,LGALS3,MAP2K1,MTOR,NDRG1,NRAS,PML,PTK2,RAC1,RHOA,RRAS,SNX1,TDO2,TLN1,VTN,YWHAZ
1. Cellular Response to Therapeutics 2. Sensitivity of tumor cell lines 3. 0.000000363 4. Decreased 5. -2.132 6. 42	ACSL4,AGO2,ATP1B3,CANX,CCAR1,CLU,CSNK2B,EGF,EGFR,EIF4E,EMC8,GOLGA7,GOSR2,GSTM4,HNRNPF,KRAS,LYN,MBNL1,MGAT2,MPHOSPH10,MPI,NONO,OGT,PQBP1,PSMA1,PSMA3,PSMB1,PSMB2,PSMD3,RALY,RBM15,RELA,RER1,RHOA,SEC62,SEC63,SELENOK,SF3B4,SREK1,TOP1,USP24,VPS45
1. Cell Death and Survival 2. Apoptosis of neurons 3. 0.000000418 4. Decreased 5. -2.448 6. 110	AGRN,AKT1,APOE,ARF6,ARRB1,ASAH1,ATRX,B4GALNT1,BID,BNIP3,BRAF,CASP3,CASP7,CAT,CDC34,Cdc42,CDK5,COQ9,CORO1A,CREB1,CTNNB1,CTSB,CTSV,CTSZ,DAPK1,DIABLO,DNM1L,EIF2A,FAM162A,FIS1,FMR1,FN1,Fus,G6PD,GAPDH,GCLM,GLUD1,GRN,GSTM5,HDAC1,HERPUD1,HMOX1,HRAS,HSD17B10,HSP90AB1,HSPA5,HSPB1,HSPD1,HSPH1,HYOU1,ILK,INSR,ITGA1,ITSN1,KRAS,LGALS1,LGALS3,LGMN,LRP1,LRPAP1,MAOA,MAP2K1,MAP2K3,MBOAT7,MECP2,MIF,MSH2,Mt1,Mt2,NCSTN,NMNAT1,NOS3,NQO1,NQO2,NR3C1,OGT,OPTN,OXR1,PAFAH1B1,PARP1,PAWR,PDCD6IP,PLG,PLRG1,PPT1,PPT2,PRDX3,PRKACA,PROC,PSEN1,PTK2B,PTPRF,RAC1,RAPGEF4,RELA,RHOA,RPS3,RPTOR,SERPINA3,SET,SIGMAR1,SLC25A10,SNX6,SRPK2,SURF1,UBA3,UBE2M,UBE2V2,WFS1,XRCC6
1. Cancer,Organismal Injury and Abnormalities 2. Non-hematological solid tumor 3. 3.22E-84 4. Increased 5. 2.545 6. 2286	A1CF,AACS,AADAT,AAK1,AAMDC,AASDHPPT,AASS,ABAT,ABCB10,ABCB4,ABCB6,ABCB8,ABCB9,ABCC2,ABCC3,ABCC6,ABCD1,ABCD2,ABCD3,ABCE1,ABCF2,ABCF3,ABCG5,ABHD11,ABHD14B,ABHD15,ABITRAM,ACAA1,ACACB,ACAD10,ACAD11,ACAD9,ACADL,ACADM,ACADSB,ACAT1,ACAT2,ACBD5,ACIN1,ACLY,ACMSD,ACO1,ACO2,ACOT1,ACOT11,ACOT12,ACOT13,ACOT2,ACOT4,ACOT7,ACOT8,ACOX1,ACOX3,ACP2,ACSF3,ACSL4,ACSL5,ACSM1,ACSS2,ACSS3,ACTB,ACTG1,ACTL6A,ACTN1,ACTN4,ACTR2,ACTR3,ACY1,ACY3,ACYP2,ADAM10,ADAP2,ADD1,ADD2,ADD3,ADHFE1,ADI1,ADIPOR2,ADK,ADPRH,ADSL,AFDN,AFMID,AGFG1,AGFG2,AGK,AGL,AGMAT,AGO1,AGO2,AGPAT2,AGPAT3,AGPAT5,AGRN,AGXT,AGXT2,AHCY,AHCYL2,AHNAK,AHSA1,AHSG,AIF1,AIP,AK2,AK3,AKR1A1,AKR1B10,AKR1C4,AKR1D1,AKT1,ALAS1,ALCAM,ALDH16A1,ALDH1A1,ALDH1B1,ALDH1L1,ALDH3A2,ALDH4A1,ALDH5A1,ALDH6A1,ALDH7A1,ALDH9A1,ALDOA,ALDOB,ALPK1,AMACR,AMBP,AMDHD2,AMPD2,AMT,AMY2A,ANGPTL3,ANGPTL4,ANKHD1/ANKHD1-EIF4EBP3,ANO10,ANPEP,ANXA1,ANXA11,ANXA3,ANXA4,ANXA5,AOX1,AP2A1,AP2M1,AP3B1,APCS,APEX1,API5,APMAP,APOA1,APOA2,APOB,APOC4,APOD,APOE,AQP1,AQP4,AQP9,ARAF,ARCN1,ARF4,ARF6,ARFGAP1,ARFGAP2,ARFGAP3,ARGLU1,ARHGAP17,ARHGAP31,ARHGAP42,ARHGAP45,ARHGAP5,ARHGDIA,ARHGDIB,ARHGEF12,ARHGEF7,ARIH1,ARMC10,ARPC1A,ARPC1B,ARPC2,ARPC5,ARPC5L,ARRB1,ARSB,AS3MT,ASAH1,ASCC1,ASCC2,ASGR1,ASGR2,ASL,ASPA,ASPDH,ASPG,ASPH,ASPSCR1,ASRGL1,ASS1,ATAD2B,ATG3,ATG4B,ATL3,ATP11C,ATP13A1,ATP1A1,ATP1B1,ATP1B3,ATP2A2,ATP2B1,ATP2B4,ATP5IF1,ATP5PO,ATP6AP1,ATP6AP2,ATP6V0D1,ATP6V1A,ATP6V1C1,ATP6V1E1,ATRX,ATXN10,ATXN2,AUP1,AVEN,B2M,B4GALNT1,BAAT,BABAM2,BAG3,BAG4,BAG5,BAIAP2,BASP1,BBOX1,BCAM,BCAP29,BCAP31,BCAS2,BCHE,BCKDHA,BCKDHB,BCKDK,BCL2L13,BCLAF1,BCO2,BCS1L,BET1L,BGN,BHMT,BHMT2,BID,BIN1,BIN2,BLMH,BLVRA,BLVRB,BMP2K,BNIP3,BPHL,BRAF,BSG,BTAF1,BTD,BUB3,BZW1,C11orf54,C12orf10,C12orf43,C1D,C1orf174,C1QA,C1QB,C2CD2,C4A/C4B,C6,C8A,C8B,C8G,C9,C9orf64,CACFD1,CACYBP,CAD,CADM1,CALCRL,CALR,CALU,CAMK1,CAND1,CANX,CAP1,CAPZA1,CAPZB,CARHSP1,CASK,CASP3,CASP7,CAT,CAVIN1,CBR1,CBWD1,CBX1,CBX3,CCAR1,CCDC134,CCDC167,CCDC22,CCDC25,CCDC40,CCDC47,CCDC51,CCDC58,CCDC9,CCDC93,CCS,CCT3,CD163,CD1D,CD2AP,CD302,CD36,CD38,CD47,CD68,CD81,CD82,CDA,CDC34,CDC37,CDC5L,CDC73,CDK11A,CDK12,CDK5,CDK5RAP3,CDK6,CDK9,CDKN1B,CDKN2C,CDO1,CDV3,CENPV,CEP290,CEP89,CES1,CES3,CFAP20,CFB,CFDP1,CFH,CFI,CGN,CHAC2,CHCHD4,CHD4,CHID1,CHMP2A,CHORDC1,CHPT1,CIAO3,CIDEB,CISD1,CISD2,CKAP4,CKB,CKM,CLCC1,CLDN12,CLDN3,CLEC10A,CLEC3B,CLEC4F,CLEC4G,CLIC1,CLIC4,CLIC5,CLINT1,CLPP,CLPTM1,CLTA,CLTB,CLU,CLYBL,CMAS,CMBL,CMC2,CMPK1,CMPK2,CMTM4,CNBP,CNDP2,CNOT1,CNOT2,CNOT3,CNOT9,CNP,CNPY2,COA7,COASY,COBLL1,COG3,COG5,COL18A1,COLGALT1,COMT,COMTD1,COPA,COPB1,COPB2,COPE,COPG1,COQ3,COQ4,COQ8A,COQ8B,COQ9,CORO1A,CORO1B,CORO1C,COTL1,COX15,COX19,COX5A,COX6B1,COX7A2,CP,CPB2,CPN1,CPNE3,CPOX,CPPED1,CPQ,CPS1,CPSF2,CPT2,CR1L,CRAT,CREB1,CRELD1,CRELD2,CRIP1,CRK,CRKL,CRNKL1,CRP,CRYL1,CRYM,CRYZ,CSAD,CSK,CSNK1E,CSNK2A1,CSNK2A2,CSNK2B,CSRP1,CSRP2,CSTF1,CSTF2,CSTF3,CTBP1,CTBS,CTDSP1,CTH,CTNNA1,CTNNB1,CTNNBL1,CTNND1,CTR9,CTSB,CTSC,CTSD,CTSF,CTSH,CTSO,CTSS,CTSV,CTSZ,CTTN,CUL1,CUL2,CUL3,CUTC,CXADR,CYB5A,CYB5B,CYB5R1,CYBC1,CYGB,CYP17A1,CYP1A2,CYP27A1,CYP2A6 (includes others),Cyp2b13/Cyp2b9,CYP2B6,Cyp2c54 (includes others),Cyp2c70,CYP2C8,CYP2F1,CYP2U1,CYP3A5,CYP3A7,CYP4A11,CYP4A22,CYP4B1,CYP4F3,CYP7A1,CYP7B1,DAAM1,DAD1,DAPK1,DARS2,DBNL,DCAF11,DCAKD,DCPS,DCTN2,DCTN4,DCTN6,DCUN1D1,DCUN1D2,DCXR,DDAH1,DDAH2,DDC,DDHD2,DDI2,DDOST,DDRGK1,DDX17,DDX18,DDX19A,DDX21,DDX23,DDX27,DDX39B,DDX3X,DDX3Y,DDX42,DDX46,DDX49,DDX5,D

	DX58,DDX6,DECR1,DECR2,DEK,DEPTOR,DES,DGAT2,DGLUCY,DHCR24,DHDH,DHFR,DHODH,DHRS7,DHRS7B,DHTKD1,DHX15,DHX16,DHX9,DIABLO,DIO1,DIS3,DKC1,DLAT,DMAC1,DMD,DMGDH,DNAJA1,DNAJB1,DNAJB11,DNAJB4,DNAJB6,DNAJB9,DNAJC1,DNAJC13,DNAJC19,DNAJC2,DNAJC25,DNAJC3,DNAJC7,DNM1L,DNM2,DNPEP,DNTTIP2,DOCK6,DPAGT1,DPM1,DPM3,DPP4,DPP7,DPP9,DPY19L1,DPY30,DPYD,DPYS,DPYSL2,DR1,DRG1,DSP,DTD1,DTX3L,DUSP23,DUT,DYNLL1,DYNLT3,DYSF,EBPL,ECHDC2,ECHDC3,ECI1,ECI2,ECM1,EDC4,EEA1,EEF1A1,EEF1D,EEF2,EFHD2,EFR3A,EFTUD2,EGF,EGFR,EHD1,EHD3,EHHADH,EIF1AX,EIF2A,EIF2AK2,EIF2B1,EIF2B2,EIF2B3,EIF2B5,EIF2S1,EIF2S2,EIF3A,EIF3C,EIF3D,EIF3E,EIF3F,EIF3H,EIF3I,EIF3L,EIF3M,EIF4A1,EIF4A2,EIF4A3,EIF4E,EIF4G1,EIF4G2,EIF4H,EIF5,EIF5A,EIF5B,ELAC2,ELAVL1,ELMO1,ELOA,ELOC,ELOVL1,ELOVL2,ELOVL5,ELP2,EMC8,EMD,EMILIN1,EML3,EML4,ENO1,ENPEP,ENPP1,ENTPD5,EPB41,EPB41L2,EPB41L5,EPHX1,EPHX2,EPPK1,EPS15L1,EPS8L2,ERBIN,ERC1,ERGIC1,ERGIC2,ERGIC3,ERH,ERLIN1,ERMP1,ERP29,ERP44,ESAM,ESD,ESYT1,ESYT2,ETFDH,ETNK1,ETNPPL,EVA1A,EXOC1,EXOC5,EXOC7,EXOSC9,EZR,F11,F13A1,FAAH,FABP2,FABP4,FABP5,FABP7,FADS6,FAF1,FAHD2B,FAM114A2,FAM126A,FAM126B,FAM210A,FAM234A,FAM3C,FAM50B,FAM98C,FARP1,FARS2,FASN,FAU,FBL,FBP1,FBXO3,FCGR2B,FCGRT,FCHO2,FDX2,FECH,FEN1,FERMT2,FETUB,FGA,FGB,FGG,FGL1,FHIT,FIS1,FITM2,FKBP11,FKBP15,FKBP3,FKBP4,FKBP5,FLII,FLNA,FLOT1,FLOT2,FMO1,FMO3,FMO4,FMO5,FMR1,FN1,FN3K,FN3KRP,FNDC3A,FNTA,FRAS1,FRG1,FSCN1,FTCD,FTO,FTSJ3,FUBP1,FUBP3,FXN,FXR1,FXYD1,G0S2,G6PC,G6PD,GAA,GABPA,GADD45GIP1,GALK1,GALK2,GALM,GALNS,GALNT2,GALT,GAMT,GANAB,GAPDH,GAPVD1,GART,GATAD2A,GATD1,GATM,GBA,GBE1,GBF1,GBP6,GCAT,GCC1,GCDH,GCH1,GCK,GCKR,GCLM,GCN1,GDA,GFM1,GFPT1,GGA1,GGCT,GID8,GIMAP4,GJB2,GLDC,GLG1,GLMP,GLO1,GLOD4,GLRX3,GLRX5,GLT1D1,GLTPD2,GLUD1,GLUL,GLYAT,GLYR1,Gm12854/S100a11,Gm21596/Hmgb1,GMPPA,GMPPB,GMPR2,GMPS,GNA11,GNA13,GNAI2,GNAI3,GNAQ,GNAS,GNE,GNG12,GNL3,GNMT,GNPAT,GNPDA1,GNS,GOLGA2,GOLGA5,GOLGA7,GOLPH3,GOLPH3L,GOPC,GORASP2,GOSR1,GOSR2,GOT1,GPAM,GPAT3,GPAT4,GPD1,GPD1L,GPHN,GPLD1,GPR182,GPRIN3,GPT,GPT2,GPX3,GRB7,GRHPR,GRIPAP1,GRN,GSPT1,GSR,Gsta4,GSTA5,GSTK1,GSTM1,GSTM2,GSTM4,GSTM5,GSTP1,GSTT2/GSTT2B,GSTZ1,GTF2F1,GTF2F2,GTF2I,GTPBP4,GUCY1B1,H3-3A/H3- 3B,H6PD,HACL1,HADH,HAGH,HAL,HAO1,HAO2,HBS1L,HCCS,HCFC1,HDAC1,HDGF,HDGFL2,HDGFL3,HDLBP,HEATR1,HEBP1,HECTD1,HELZ2,HERPUD1,HEXB,HEXIM1,HGD,HGS,HIBADH,HIBCH,HINT2,HINT3,HIP1,HK1,HLA-A,HLA- DQA1,HMGA1,HMGCL,HMGCS1,HMGCS2,HMGN1,HMOX1,HMOX2,HNF1A,HNF4A,HNMT,HNRNPA2B1,HNRNPAB,HNRNPC,HNRNPD,HNRNPF,HNRNPH1,HNRNPH2,HNRNPK,HNRNPL,HNRNPLL,HNRNPM,HNRNPR,HNRNPU,HNRNPUL1,HNRNPUL2,HOMER2,HOPX,HP,HP1BP3,HPCAL1,HPD,HPGD,HPN,HPX,HRAS,Hrg,HS1BP3,HSCB,HSD11B1,HSD17B10,HSD17B11,HSD17B2,HSD17B4,HSD17B6,HSDL1,HSP90AA1,HSP90AB1,HSP90B1,HSPA12B,HSPA13,HSPA1A/HSPA1B,HSPA4L,HSPA5,HSPA8,HSPA9,HSPB1,HSPD1,HSPG2,HSPH1,HTATIP2,HUWE1,HYKK,HYOU1,HYPK,ICAM1,IDH2,IDH3B,IDO2,IFI16,IFIT1B,IFIT3,IFNAR2,IGF2R,IGFALS,IK,IL6ST,ILF2,ILF3,ILK,ILKAP,IMMP2L,IMMT,IMPA1,IMPAD1,INHBC,INMT,INPP1,INPP5F,INSIG2,INSR,INTS3,IP6K1,IPO5,IQGAP1,ISCA2,ISOC1,ISOC2,IST1,ITGA1,ITGA2B,ITGA5,ITGA9,ITGAV,ITGB1,ITGB3,ITGB6,ITIH2,ITIH4,ITPR2,ITSN1,IYD,JCHAIN,JPT2,JUP,KANK2,KCTD12,KDELR1,KDSR,KHDRBS1,KHK,KHSRP,KIF13B,KIF21A,KLHDC7A,KLKB1,KPNA1,KPNA2,KRAS,KXD1,KYAT1,KYAT3,KYNU,L2HGDH,L3HYPDH,LAMTOR1,LAP3,LARP1,LARP4,LARP4B,LARP7,LARS2,LASP1,LBR,LCAT,LDAH,LDLR,LGALS1,LGALS3,LGALS3BP,LGALS8,LGALSL,LGMN,LHPP,LIAS,LIFR,LIMS2,LIN7A,LIN7C,LIPE,LITAF,LMAN1,LMAN2,LMAN2L,LMF1,LMNA,LMNB1,LMNB2,LMO7,LOC102724788/PRODH,LONP2,LPCAT3,LRG1,LRP1,LRPAP1,LRRFIP1,LSG1,LSM12,LSM14A,LSM14B,LSM5,LSM6,LSR,LUC7L,LUC7L2,LUC7L3,LUM,LYAR,LYN,LYPLA1,LYPLA2,LYPLAL1,LYVE1,LYZ,LZIC,M6PR,MACO1,MACROD1,MAGIX,MAN1A2,MAN2B1,MAN2B2,MAN2C1,MANBA,MAOA,MAOB,MAP2K1,MAP2K3,MAP4,MAPK1IP1L,MAPRE1,MAPRE3,MASP2,MAT1A,MAT2A,MATR3,MBL2,MBNL1,MBOAT7,MCAM,MCCC1,MCCC2,MCEE,MCFD2,MCTS1,MDH1,ME1,MEAF6,MECP2,METAP2,METTL26,METTL27,METTL7B,METTL9,MFAP1,MFN2,MGAT2,MGLL,MGST1,MIA3,MIEN1,MIF,MIF4GD,MIGA2,MIOS,MIPEP,MKNK1,MMAB,MME,MMUT,MOB1B,MOCS2,MOGS,MORF4L1,MOSPD2,MOV10,MPC1,MPC2,MPHOSPH10,MPI,MPP1,MPP6,MPRIP,MPST,MRC1,MRI1,MROH1,MRPL12,MRPL15,MRPL17,MRPL24,MRPL32,MRPL47,MRPL50,MRPL51,MRPS12,MRPS15,MRPS17,MRPS25,MRPS31,MRPS35,MRRF,MSH2,MSN,MSR1,MSRA,MSRB2,Mt1,Mt2,MTA2,MTAP,MTCH2,MTDH,MTFR1,MTFR1L,MTHFD1,MTHFS,MTMR6,MTOR,MTREX,MTSS1,MTX2,MUL1,MVK,MVP,MYBBP1A,MYCBP,MYEF2,MYH10,MYH11,MYH14,MYH9,MYL1,MYL12A,MYL6,MYLK,MYLPF,MYO18A,MYO1B,MYO1C,MYO1D,NAA15,NAA16,NAA25,NAA35,NAALAD2,NACA,NADK2,NAGA,NAGLU,NAMPT,NANP,NANS,NAP1L1,NAPRT,NASP,NAT10,NAXD,NAXE,NCBP1,NCEH1,NCK1,NCL,NCOA5,NCSTN,NDRG1,NDST1,NDUFA10,NDUFA11,NDUFA13,NDUFA2,NDUFA3,NDUFAF2,NDUFAF3,NDUFAF7,NDUFB6,NDUFB7,NDUFB8,NECAP1,NECTIN2,NELFA,NELFB,NELFCD,NFIA,NFIB,NFIC,NFS1,NFU1,NFXL1,NGEF,NGLY1,Ngp,NHLRC2,NHP2,NIBAN1,NID2,NIPSNAP2,NIT1,NLN,NLRX1,NME3,NMNAT1,NMRAL1,NMRK1,NMT2,NNMT,NOC2L,NOL6,NONO,NOP10,NOP16,NOP56,NOP58,NOS3,NOSTRIN,NPC1,NQO1,NR1H4,NR3C1,NRAS,NSF,NSFL1C,NSUN2,NUBPL,NUCB1,NUCB2,NUCKS1,NUDC,NUDCD3,NUDT12,NUDT13,NUDT14,NUDT16,NUDT19,NUDT21,NUDT3,NUDT4,NUDT7,NUDT9,NUFIP2,NUMA1,NUP153,NUP155,NUP160,NUP205,NUP210,NUP214,NUP35,NUP54,NUP93,NUP98,NUTF2,OAT,OCIAD2,OGA,OGFOD3,OGFR,OGT,OLA1,OPLAH,OPTN,ORMDL2,OS9,OSBPL9,OTOL1,OXCT1,OXR1,OXSM,PA2G4,PABPC1,PABPC4,PABPN1,PAFAH1B1,PAFAH1B2,PAFAH2,PAIP1,PAIP2,PAK2,PALD1,PALLD,PALMD,PAM16,PANK1,PAPSS1,PAPSS2,PARP1,PARP14,PARP9,PARS2,PARVA,PARVB,PAWR,PBDC1,PBLD,PC,PCBP1,PCCA

	,PCCB,PCDH1,PCDHB16,PCK1,PCNP,PCTP,PCYT1A,PDAP1,PDCD10,PDCD11,PDCD4,PDCD6IP,PDE2A,PDHA1,PDHB,PDIA3,PDIA4,PDIA5,PDIA6,PDK1,PDK2,PDLIM1,PDLIM5,PDLIM7,PDP2,PDXDC1,PDXK,PDZK1,PEBP1,PECAM1,PECR,PEX1,PEX11A,PEX11G,PEX12,PEX13,PEX14,PEX16,PEX19,PEX26,PEX3,PEX5,PEX6,PFAS,PFDN2,PFKFB1,PFKFB3,PGAM1,PGD,PGK1,PGM1,PGM3,PGM5,PGRMC1,PGRMC2,PHACTR4,PHB2,PHF20L1,PHKA1,PHKA2,PHKB,PHKG2,PHLDA1,PHLDB2,PHYHD1,PHYKPL,PI4KA,PICALM,PIGR,PIGS,PIGU,PIK3AP1,PIK3CB,PIN4,PIP5K1C,PIR,PITHD1,PITRM1,PKLR,PKN1,PKP4,PLA2G12B,PLBD1,PLBD2,PLCB3,PLCH1,PLEKHA5,PLEKHA7,PLEKHF1,PLG,PLIN5,PLOD3,PLPP3,PLRG1,PLS3,PLTP,PLVAP,PLXNA4,PLXNB2,PM20D1,PML,PMM2,PNKP,PNLIP,PNN,POLDIP3,POLR2A,POLR2B,POLR2I,POLR2L,PON1,PON2,PON3,POR,PPA1,PPAN,PPAT,PPCS,PPFIA1,PPFIBP2,PPIA,PPIB,PPIF,PPIG,PPIL1,PPIL4,PPIP5K2,PPL,PPM1A,PPM1B,PPM1G,PPM1K,PPP1R2,PPP1R21,PPP1R7,PPP1R8,PPP2R1B,PPP2R5A,PPP2R5D,PPP4C,PPP4R2,PPP4R3A,PPP6R1,PPP6R3,PPT1,PPT2,PPWD1,PQBP1,PRCP,PRDX3,PRDX5,PRDX6,PREB,PRELP,PREP,PRKAA2,PRKAB1,PRKACA,PRKAG1,PRKCSH,PRKRA,PROC,PROX1,PRPF19,PRPF3,PRPF31,PRPF4,PRPF40A,PRPF6,PRPF8,PRRC1,PRRC2C,PRUNE1,PRXL2A,PRXL2B,PSAP,PSEN1,PSIP1,PSMA1,PSMA2,PSMA3,PSMA4,PSMA5,PSMA6,PSMA7,PSMB1,PSMB10,PSMB2,PSMB5,PSMB6,PSMB7,PSMB9,PSMC3,PSMD14,PSMD3,PSMD4,PSMD7,PSME3,PTBP1,PTBP3,PTGES3,PTK2,PTK2B,PTPMT1,PTPN1,PTPRF,PTPRK,PTRHD1,PTS,PTTG1IP,PUM1,PURA,PXMP2,PXMP4,PXN,PYCARD,PYGB,PYGL,QDPR,QSOX1,QTRT2,RAB14,RAB1A,RAB35,RAB3IP,RAB4A,RAB8A,RAB8B,RABGAP1,RABGAP1L,RABL3,RAC1,RACK1,RAD23B,RAD50,RAE1,RALY,RAN,RANBP1,RANBP10,RANBP3,RANGAP1,RAP1A,RAP1B,RAPGEF4,RARRES2,RASIP1,RBBP4,RBM10,RBM14,RBM15,RBM17,RBM22,RBM28,RBM39,RBM42,RBM47,RBP1,RBPMS,RCC2,RCN1,RDH16,REEP5,REEP6,RELA,RER1,RETREG2,RETSAT,REXO2,RFC2,RGL3,RGN,RGPD4 (includes others),RHOA,RHOC,RHOG,RIDA,RIOX2,RIPK1,RMDN2,RMDN3,RMND5A,RNASEH2A,RNASET2,RNF113A,RNF114,RNF14,RNF17,RNF185,RNF2,RNF20,RNF213,RNF5,RNH1,RNMT,RNPEP,ROCK2,RPAP3,RPE,RPL10,RPL10A,RPL11,RPL12,RPL13,RPL13A,RPL14,RPL15,RPL17,RPL18,RPL18A,RPL19,RPL21,RPL22,RPL23,RPL24,RPL26,RPL27,RPL28,RPL3,RPL31,RPL35,RPL37,RPL37A,RPL4,RPL5,RPL6,RPL7,RPL7A,RPL8,RPL9,RPLP0,RPLP2,RPN1,RPN2,RPRD1B,RPS10,RPS11,RPS12,RPS14,RPS15,RPS15A,RPS16,RPS19,RPS2,RPS20,RPS24,RPS25,RPS26,RPS27A,RPS27L,RPS29,RPS3,RPS4Y1,RPS5,RPS6,RPS6KB2,RPS7,RPS8,RPSA,RPTOR,RRAS,RRS1,RSL1D1,RTF2,RTN1,RTN4,RTN4IP1,RUFY1,RUFY3,RUVBL1,RUVBL2,S100A1,S100A6,SAA1,SAE1,SAFB,SAMHD1,SAP18,SAR1B,SARDH,SARNP,SARS2,SART1,SART3,SAT2,SAYSD1,SBF1,SC5D,SCAMP1,SCAMP3,SCAMP4,SCAMP5,SCARB1,SCARB2,SCD,SCFD1,SCO1,SCPEP1,SCRIB,SCYL2,SCYL3,SDC4,SDF2L1,SDHD,SDR42E1,SDS,SDSL,SEC11A,SEC14L2,SEC14L4,SEC23B,SEC23IP,SEC24A,SEC24D,SEC31A,SEC61A1,SEC61B,SEC61G,SEC62,SEC63,SELENBP1,SELENOF,SELENOI,SELENOP,SEPHS1,SERBP1,SERHL2,SERINC3,SERPINA1,SERPINA10,SERPINA3,SERPINA6,SERPINB1,SERPIND1,SERPINF2,SERPING1,SERPINH1,SET,Sf1,SF3A1,SF3A3,SF3B1,SF3B2,SF3B3,SF3B4,SF3B6,SFPQ,SFR1,SFT2D2,SFXN5,SGTA,SH3BGRL3,SH3GL1,SHMT1,SHOC2,SHPK,SHTN1,SIAE,SIGLEC1,SIGMAR1,SIL1,SLC12A9,SLC16A7,SLC17A3,SLC22A1,SLC22A18,SLC22A23,SLC22A25,SLC25A10,SLC25A11,SLC25A12,SLC25A13,SLC25A20,SLC25A21,SLC25A23,SLC25A25,SLC25A3,SLC25A45,SLC25A5,SLC26A1,SLC27A4,SLC2A2,SLC30A5,SLC31A1,SLC35A1,SLC35A3,SLC35B1,SLC35D1,SLC38A10,SLC38A3,SLC39A11,SLC39A14,SLC39A4,SLC44A2,SLC4A4,SLC6A12,SLC6A13,SLC7A2,SLC9A3R1,SLC9A3R2,SLCO1B3,SLCO2A1,SLK,SLMAP,SLTM,SMAP1,SMAP2,SMARCA2,SMARCA5,SMARCD2,SMARCE1,SMC1A,SMC3,SMIM15,SMOC1,SMPD1,SMS,SMU1,SNAP23,SNAP47,SND1,SNF8,SNRNP200,SNRNP70,SNRPA1,SNRPB2,SNRPD3,SNRPF,SNRPN,SNTA1,SNTB1,SNU13,SNW1,SNX1,SNX18,SNX2,SNX3,SNX4,SNX5,SNX6,SNX7,SOAT2,SON,SORBS1,SORBS2,SORD,SOS1,SPAG9,SPAST,SPCS1,SPCS2,SPG7,SPPL2A,SPR,SPTAN1,SPTBN2,SQOR,SRA1,SREK1,SRI,SRP19,SRP68,SRP72,SRP9,SRPK2,SRPRB,SRR,SRRT,SRSF1,SRSF10,SRSF2,SRSF3,SRSF4,SRSF6,SRSF7,SSBP1,SSR1,SSR3,SSR4,SSRP1,ST13,STAB1,STAB2,STAG2,STARD5,STAT2,STAT3,STAT6,STBD1,STEAP3,STEAP4,STIP1,STK38,STK38L,STOML2,STRAP,STRN,STT3A,STT3B,SUB1,SUCLG1,SUCLG2,SUGCT,SUGT1,SULT1B1,SULT1C2,SULT1E1,SULT2A1,SUMO2,SUN2,SUOX,SUPT16H,SURF1,SURF4,SVIL,SWAP70,SYAP1,SYMPK,SYNCRIP,SYNGR2,SYNJ2BP,TACO1,TADA3,TAGLN,TAGLN2,TALDO1,TAMM41,TANGO2,TAOK3,TAP1,TAP2,TAPBP,TARDBP,TAT,TBC1D13,TBC1D15,TBC1D17,TBC1D24,TBC1D8B,TBC1D9B,TBCD,TBCEL,TBL2,TBRG4,TCEA1,TCERG1,TCIRG1,TCOF1,TDO2,TFR2,TGFBRAP1,TGM1,THNSL2,THOC2,THRAP3,THRSP,THYN1,TIAL1,TIGAR,TIMM17B,TIMM22,TIMM44,TIMMDC1,TINAGL1,TJP1,TJP2,TJP3,TKFC,TKT,TLN1,TM9SF1,TM9SF2,TM9SF3,TMED1,TMED10,TMED2,TMED3,TMED4,TMED5,TMED7,TMED9,TMEM109,TMEM126A,TMEM126B,TMEM135,TMEM176B,TMEM19,TMEM214,TMEM230,TMEM256,TMEM30A,TMEM33,TMEM38B,TMEM43,TMEM82,TMLHE,TMOD3,TMPO,TMTC3,TMX1,TMX3,TNKS1BP1,TNPO1,TNPO2,TNPO3,TNS2,TNS3,TOLLIP,TOM1,TOMM40,TOP1,TOP2B,TOP3B,TOR1A,TOR1AIP1,TPD52,TPD52L2,TPI1,TPK1,TPM3,TPPP,TPR,TPRG1L,TRA2B,TRABD,TRAM1,TRAP1,TRAPPC1,TRAPPC4,TRIM14,TRIM23,TRIM28,TRIP10,TRIP11,TRIR,TRMU,TSC22D1,TSFM,TSG101,TSPAN14,TSPAN31,TSTA3,TTC1,TTC36,TTC37,TTC38,TTC39A,TTC39C,TTC7A,TTN,TTPA,TUBA1B,TUBA4A,TUBB,TUBB2A,TUBB4B,TUT7,TWF1,TXLNA,TXLNG,TXN2,TXNDC5,TXNDC9,TXNL1,TYMP,TYSND1,U2AF2,U2SURP,UBA1,UBA2,UBA3,UBA7,UBAC1,UBAP2,UBE2G2,UBE2I,UBE2J1,UBE2M,UBE2V2,UBE2Z,UBE4B,UBL4A,UBL7,UBQLN2,UBR2,UBTF,UCHL5,UCK1,UFL1,UGDH,UGGT1,UGP2,UGT1A4,UGT1A6,UGT1A8 (includes others),UGT2B10,UGT2B17,UGT2B28,UGT3A1,UPB1,UPF1,UPF2,UPP1,UQCC1,UQCC3,UQCRC2,UROC1,USO1,USP16,USP19,USP24,USP46,USP7,VAC14,VAMP2,VAMP3,VAMP8,VAPB,VAT1,VAV2,VCAM1,VCL,VCPIP1,VDAC2,VDAC3,VIM,VKORC1L1,VMO1,VNN1,VPS13D,VPS25,VPS26A,VPS26B,VPS26C,VPS28,VPS33B,VPS35,VPS45,VPS51,VPS52,VRK1,VSIG4,VTA1,VTN,VWA8,WAPL,

	WASF2,WASHC3,WASHC4,WASHC5,WBP11,WBP2,WDFY1,WDR1,WDR18,WDR26,WDR36,WDR46,WDR5,WDR61,WDR77,WFS1,WRNIP1,XAF1,XPNPEP1,XPO1,XPO5,XRCC6,XRN1,XRN2,YBX1,YBX3,YME1L1,YTHDF2,YTHDF3,YWHAQ,YWHAZ,ZBTB20,ZBTB8OS,ZC3H11A,ZC3H14,ZC3HAV1,ZFR,ZHX1,ZHX2,ZHX3,ZMAT2,ZMIZ1,ZNF326,ZNF638

1. Cancer,Organismal Injury and Abnormalities 2. Epithelial neoplasm 3. 8.98E-83 4. Increased 5. 2.111 6. 2256	A1CF,AACS,AADAT,AAK1,AAMDC,AASDHPPT,AASS,ABAT,ABCB10,ABCB4,ABCB6,ABCB8,ABCB9,ABCC2,ABCC3,ABCC6,ABCD1,ABCD2,ABCD3,ABCE1,ABCF2,ABCF3,ABCG5,ABHD11,ABHD14B,ABHD15,ABITRAM,ACAA1,ACACB,ACAD10,ACAD11,ACAD9,ACADL,ACADM,ACADSB,ACAT1,ACAT2,ACBD5,ACIN1,ACLY,ACMSD,ACO1,ACO2,ACOT1,ACOT11,ACOT12,ACOT13,ACOT2,ACOT4,ACOT7,ACOT8,ACOX1,ACOX3,ACP2,ACSF3,ACSL4,ACSL5,ACSM1,ACSS2,ACSS3,ACTB,ACTG1,ACTN1,ACTN4,ACTR2,ACTR3,ACY1,ACY3,ACYP2,ADAM10,ADAP2,ADD1,ADD2,ADD3,ADHFE1,ADI1,ADIPOR2,ADK,ADSL,AFDN,AFMID,AGFG1,AGFG2,AGK,AGL,AGMAT,AGO1,AGO2,AGPAT2,AGPAT3,AGPAT5,AGRN,AGXT,AGXT2,AHCY,AHCYL2,AHNAK,AHSA1,AHSG,AIF1,AIP,AK2,AK3,AKR1A1,AKR1B10,AKR1C4,AKR1D1,AKT1,ALAS1,ALCAM,ALDH16A1,ALDH1A1,ALDH1B1,ALDH1L1,ALDH3A2,ALDH4A1,ALDH5A1,ALDH6A1,ALDH7A1,ALDH9A1,ALDOA,ALDOB,ALPK1,AMACR,AMBP,AMDHD2,AMPD2,AMT,AMY2A,ANGPTL3,ANGPTL4,ANKHD1/ANKHD1- EIF4EBP3,ANO10,ANPEP,ANXA1,ANXA11,ANXA3,ANXA4,ANXA5,AOX1,AP2A1,AP2M1,AP3B1,APCS,APEX1,API5,APMAP,APOA1,APOA2,APOB,APOC4,APOD,APOE,AQP1,AQP4,AQP9,ARAF,ARCN1,ARF4,ARF6,ARFGAP1,ARFGAP2,ARFGAP3,ARGLU1,ARHGAP17,ARHGAP31,ARHGAP42,ARHGAP45,ARHGAP5,ARHGDIA,ARHGDIB,ARHGEF12,ARHGEF7,ARIH1,ARMC10,ARPC1A,ARPC1B,ARPC2,ARPC5,ARPC5L,ARRB1,ARSB,AS3MT,ASAH1,ASCC1,ASCC2,ASGR1,ASGR2,ASL,ASPA,ASPDH,ASPG,ASPH,ASPSCR1,ASRGL1,ASS1,ATAD2B,ATG3,ATG4B,ATL3,ATP11C,ATP13A1,ATP1A1,ATP1B1,ATP1B3,ATP2A2,ATP2B1,ATP2B4,ATP5IF1,ATP5PO,ATP6AP1,ATP6AP2,ATP6V0D1,ATP6V1A,ATP6V1C1,ATP6V1E1,ATRX,ATXN10,ATXN2,AUP1,AVEN,B2M,B4GALNT1,BAAT,BABAM2,BAG3,BAG4,BAG5,BAIAP2,BASP1,BBOX1,BCAM,BCAP29,BCAS2,BCHE,BCKDHA,BCKDHB,BCKDK,BCL2L13,BCLAF1,BCO2,BCS1L,BET1L,BGN,BHMT,BHMT2,BID,BIN1,BIN2,BLMH,BLVRA,BLVRB,BMP2K,BNIP3,BPHL,BRAF,BSG,BTAF1,BTD,BUB3,BZW1,C11orf54,C12orf10,C12orf43,C1D,C1orf174,C1QA,C1QB,C2CD2,C4A/C4B,C6,C8A,C8B,C8G,C9,C9orf64,CACFD1,CACYBP,CAD,CADM1,CALCRL,CALR,CALU,CAMK1,CAND1,CANX,CAP1,CAPZA1,CAPZB,CASK,CASP3,CASP7,CAT,CAVIN1,CBR1,CBWD1,CBX1,CBX3,CCAR1,CCDC134,CCDC167,CCDC22,CCDC25,CCDC40,CCDC47,CCDC51,CCDC58,CCDC9,CCDC93,CCS,CCT3,CD163,CD1D,CD2AP,CD302,CD36,CD38,CD47,CD68,CD81,CD82,CDA,CDC34,CDC37,CDC5L,CDC73,CDK11A,CDK12,CDK5,CDK5RAP3,CDK6,CDK9,CDKN1B,CDKN2C,CDO1,CDV3,CENPV,CEP290,CEP89,CES1,CES3,CFAP20,CFB,CFDP1,CFH,CFI,CGN,CHAC2,CHCHD4,CHD4,CHID1,CHMP2A,CHORDC1,CHPT1,CIAO3,CIDEB,CISD1,CISD2,CKAP4,CKB,CKM,CLCC1,CLDN12,CLDN3,CLEC10A,CLEC3B,CLEC4F,CLEC4G,CLIC1,CLIC4,CLIC5,CLINT1,CLPP,CLPTM1,CLTB,CLU,CLYBL,CMAS,CMBL,CMC2,CMPK1,CMPK2,CMTM4,CNBP,CNDP2,CNOT1,CNOT2,CNOT3,CNOT9,CNP,CNPY2,COA7,COASY,COBLL1,COG3,COG5,COL18A1,COLGALT1,COMT,COMTD1,COPA,COPB1,COPB2,COPE,COPG1,COQ3,COQ4,COQ8A,COQ8B,COQ9,CORO1A,CORO1B,CORO1C,COTL1,COX15,COX19,COX5A,COX6B1,COX7A2,CP,CPB2,CPN1,CPNE3,CPOX,CPQ,CPS1,CPSF2,CPT2,CR1L,CRAT,CREB1,CRELD1,CRELD2,CRIP1,CRK,CRKL,CRNKL1,CRP,CRYL1,CRYM,CRYZ,CSAD,CSK,CSNK1E,CSNK2A1,CSNK2A2,CSNK2B,CSRP1,CSRP2,CSTF1,CSTF2,CSTF3,CTBP1,CTBS,CTDSP1,CTH,CTNNA1,CTNNB1,CTNNBL1,CTNND1,CTR9,CTSB,CTSC,CTSD,CTSF,CTSH,CTSO,CTSS,CTSV,CTSZ,CTTN,CUL1,CUL2,CUL3,CUTC,CXADR,CYB5A,CYB5B,CYB5R1,CYBC1,CYGB,CYP17A1,CYP1A2,CYP27A1,CYP2A6 (includes others),Cyp2b13/Cyp2b9,CYP2B6,Cyp2c54 (includes others),Cyp2c70,CYP2C8,CYP2F1,CYP2U1,CYP3A5,CYP3A7,CYP4A11,CYP4A22,CYP4B1,CYP4F3,CYP7A1,CYP7B1,DAAM1,DAD1,DAPK1,DARS2,DBNL,DCAF11,DCAKD,DCPS,DCTN2,DCTN4,DCTN6,DCUN1D1,DCUN1D2,DCXR,DDAH1,DDAH2,DDC,DDHD2,DDI2,DDOST,DDRGK1,DDX17,DDX18,DDX19A,DDX21,DDX23,DDX27,DDX39B,DDX3X,DDX3Y,DDX42,DDX46,DDX49,DDX5,DDX58,DDX6,DECR1,DECR2,DEK,DEPTOR,DES,DGAT2,DGLUCY,DHCR24,DHDH,DHFR,DHODH,DHRS7,DHRS7B,DHTKD1,DHX15,DHX16,DHX9,DIABLO,DIO1,DIS3,DKC1,DLAT,DMAC1,DMD,DMGDH,DNAJA1,DNAJB1,DNAJB11,DNAJB4,DNAJB6,DNAJB9,DNAJC1,DNAJC13,DNAJC19,DNAJC2,DNAJC25,DNAJC3,DNAJC7,DNM1L,DNM2,DNPEP,DNTTIP2,DOCK6,DPAGT1,DPM1,DPM3,DPP4,DPP7,DPP9,DPY19L1,DPY30,DPYD,DPYS,DPYSL2,DRG1,DSP,DTD1,DTX3L,DUSP23,DUT,DYNLL1,DYNLT3,DYSF,EBPL,ECHDC2,ECI1,ECI2,ECM1,EDC4,EEA1,EEF1A1,EEF1D,EEF2,EFHD2,EFR3A,EFTUD2,EGF,EGFR,EHD1,EHD3,EHHADH,EIF1AX,EIF2A,EIF2AK2,EIF2B1,EIF2B2,EIF2B3,EIF2S1,EIF2S2,EIF3A,EIF3C,EIF3D,EIF3E,EIF3F,EIF3H,EIF3I,EIF3L,EIF3M,EIF4A1,EIF4A2,EIF4A3,EIF4E,EIF4G1,EIF4G2,EIF4H,EIF5,EIF5A,EIF5B,ELAC2,ELAVL1,ELMO1,ELOA,ELOC,ELOVL1,ELOVL2,ELOVL5,ELP2,EMC8,EMD,EMILIN1,EML3,EML4,ENO1,ENPEP,ENPP1,ENTPD5,EPB41,EPB41L2,EPB41L5,EPHX1,EPHX2,EPPK1,EPS15L1,EPS8L2,ERBIN,ERC1,ERGIC1,ERGIC2,ERGIC3,ERH,ERLIN1,ERMP1,ERP29,ERP44,ESD,ESYT1,ESYT2,ETFDH,ETNK1,ETNPPL,EVA1A,EXOC1,EXOC5,EXOC7,EXOSC9,EZR,F11,F13A1,FAAH,FABP2,FABP4,FABP5,FABP7,FADS6,FAF1,FAHD2B,FAM114A2,FAM126A,FAM126B,FAM210A,FAM234A,FAM3C,FAM50B,FAM98C,FARP1,FARS2,FASN,FAU,FBL,FBP1,FBXO3,FCGR2B,FCGRT,FCHO2,FDX2,FECH,FEN1,FERMT2,FETUB,FGA,FGB,FGG,FGL1,FHIT,FIS1,FITM2,FKBP11,FKBP15,FKBP3,FKBP4,FKBP5,FLII,FLNA,FLOT1,FLOT2,FMO1,FMO3,FMO4,FMO5,FMR1,FN1,FN3K,FN3KRP,FNDC3A,FNTA,FRAS1,FRG1,FSCN1,FTCD,FTO,FTSJ3,FUBP1,FUBP3,FXN,FXR1,FXYD1,G0S2,G6PC,G6PD,GAA,GABPA,GADD45GIP1,GALK1,GALK2,GALM,GALNS,GALNT2,GALT,GAMT,GANAB,GAPDH,GAPVD1,GART,GATAD2A,GATD1,GATM,GBA,GBE1,GBF1,GBP6,GCAT,GCC1,GCDH,GCH1,GCK,GCKR,GCLM,GCN1,GDA,GFM1,GFPT1,GGA1,GGCT,GID8,GIMAP4,GJB2,GLDC,GLG1,GLMP,GLOD4,GLRX3,GLRX5,GLT1D1,GLTPD2,GLUD1,GLUL,GLYAT,GLYR1,Gm12854/S100a11,Gm21596/Hmgb1,GMPPA,GMPPB,GMPR2,GMPS,GNA11,GNA13,GNAI2,GNAI3,GNAQ,GNAS,GNE,GNG12,GNL3,GNMT,GNPAT,GNPDA1,GNS,GOLGA2,GOLGA5,GOLGA7,GOLPH3,GOLPH3L,GOPC,GORASP2,GOSR1,GOSR2,GOT1,GPAM,GPAT3,GPAT4,GPD1,GPD1L,GPHN,GPLD1,GPR182,GPRIN3,GPT,GPT2,GPX3,GRB7,GRHPR,GR

	IPAP1,GRN,GSPT1,GSR,Gsta4,GSTA5,GSTK1,GSTM1,GSTM2,GSTM4,GSTM5,GSTP1,GSTT2/GSTT2B,GSTZ1,GTF2F1,GTF2F2,GTF2I,GTPBP4,GUCY1B1,H3-3A/H3-3B,H6PD,HACL1,HADH,HAGH,HAL,HAO1,HAO2,HBS1L,HCCS,HCFC1,HDAC1,HDGF,HDGFL2,HDGFL3,HDLBP,HEATR1,HEBP1,HECTD1,HELZ2,HERPUD1,HEXB,HEXIM1,HGD,HGS,HIBADH,HIBCH,HINT2,HINT3,HIP1,HK1,HLA-A,HLA-DQA1,HMGA1,HMGCL,HMGCS1,HMGCS2,HMGN1,HMOX1,HMOX2,HNF1A,HNF4A,HNMT,HNRNPA2B1,HNRNPAB,HNRNPC,HNRNPD,HNRNPF,HNRNPH1,HNRNPH2,HNRNPK,HNRNPL,HNRNPLL,HNRNPM,HNRNPR,HNRNPU,HNRNPUL1,HNRNPUL2,HOMER2,HOPX,HP,HP1BP3,HPD,HPGD,HPN,HPX,HRAS,Hrg,HS1BP3,HSCB,HSD11B1,HSD17B10,HSD17B11,HSD17B2,HSD17B4,HSD17B6,HSDL1,HSP90AA1,HSP90AB1,HSP90B1,HSPA12B,HSPA13,HSPA1A/HSPA1B,HSPA4L,HSPA5,HSPA8,HSPA9,HSPB1,HSPD1,HSPG2,HSPH1,HTATIP2,HUWE1,HYKK,HYOU1,HYPK,ICAM1,IDH2,IDH3B,IDO2,IFI16,IFIT1B,IFIT3,IFNAR2,IGF2R,IGFALS,IK,IL6ST,ILF2,ILF3,ILK,ILKAP,IMMP2L,IMMT,IMPA1,IMPAD1,INHBC,INMT,INPP1,INPP5F,INSIG2,INSR,INTS3,IP6K1,IPO5,IQGAP1,ISCA2,ISOC1,ISOC2,IST1,ITGA1,ITGA2B,ITGA5,ITGA9,ITGAV,ITGB1,ITGB3,ITGB6,ITIH2,ITIH4,ITPR2,ITSN1,IYD,JCHAIN,JPT2,JUP,KANK2,KCTD12,KDELR1,KDSR,KHDRBS1,KHK,KHSRP,KIF13B,KIF21A,KLHDC7A,KLKB1,KPNA1,KPNA2,KRAS,KXD1,KYAT1,KYAT3,KYNU,L2HGDH,L3HYPDH,LAMTOR1,LAP3,LARP1,LARP4,LARP4B,LARP7,LARS2,LASP1,LBR,LCAT,LDAH,LDLR,LGALS1,LGALS3,LGALS3BP,LGALS8,LGALSL,LGMN,LHPP,LIAS,LIFR,LIMS2,LIN7A,LIN7C,LIPE,LITAF,LMAN1,LMAN2,LMAN2L,LMF1,LMNA,LMNB1,LMNB2,LMO7,LOC102724788/PRODH,LONP2,LPCAT3,LRG1,LRP1,LRPAP1,LRRFIP1,LSG1,LSM12,LSM14A,LSM14B,LSM5,LSR,LUC7L,LUC7L2,LUC7L3,LUM,LYAR,LYN,LYPLA1,LYPLA2,LYPLAL1,LYVE1,LYZ,LZIC,M6PR,MACO1,MACROD1,MAGIX,MAN1A2,MAN2B1,MAN2B2,MAN2C1,MANBA,MAOA,MAOB,MAP2K1,MAP2K3,MAP4,MAPK1IP1L,MAPRE1,MAPRE3,MASP2,MAT1A,MAT2A,MATR3,MBNL1,MBOAT7,MCAM,MCCC1,MCCC2,MCEE,MCFD2,MCTS1,MDH1,ME1,MEAF6,MECP2,METAP2,METTL26,METTL27,METTL7B,METTL9,MFAP1,MFN2,MGAT2,MGLL,MGST1,MIA3,MIEN1,MIF,MIF4GD,MIGA2,MIOS,MIPEP,MKNK1,MMAB,MME,MMUT,MOB1B,MOCS2,MOGS,MORF4L1,MOSPD2,MOV10,MPC1,MPC2,MPHOSPH10,MPI,MPP1,MPP6,MPRIP,MPST,MRC1,MRI1,MROH1,MRPL12,MRPL15,MRPL17,MRPL24,MRPL47,MRPL50,MRPL51,MRPS12,MRPS15,MRPS17,MRPS25,MRPS31,MRPS35,MRRF,MSH2,MSN,MSR1,MSRA,MSRB2,Mt1,Mt2,MTA2,MTAP,MTCH2,MTDH,MTFR1,MTFR1L,MTHFD1,MTHFS,MTMR6,MTOR,MTREX,MTSS1,MTX2,MUL1,MVK,MVP,MYBBP1A,MYCBP,MYEF2,MYH10,MYH11,MYH14,MYH9,MYL1,MYL12A,MYL6,MYLK,MYLPF,MYO18A,MYO1B,MYO1C,MYO1D,NAA15,NAA16,NAA25,NAA35,NAALAD2,NACA,NADK2,NAGA,NAGLU,NAMPT,NANP,NANS,NAP1L1,NAPRT,NASP,NAT10,NAXD,NAXE,NCBP1,NCEH1,NCK1,NCL,NCOA5,NCSTN,NDRG1,NDST1,NDUFA10,NDUFA11,NDUFA13,NDUFA3,NDUFAF2,NDUFAF3,NDUFAF7,NDUFB6,NDUFB7,NDUFB8,NECAP1,NECTIN2,NELFA,NELFB,NELFCD,NFIA,NFIB,NFIC,NFS1,NFU1,NFXL1,NGEF,NGLY1,Ngp,NHLRC2,NHP2,NIBAN1,NID2,NIPSNAP2,NIT1,NLN,NLRX1,NME3,NMNAT1,NMRAL1,NMRK1,NMT2,NNMT,NOC2L,NOL6,NONO,NOP16,NOP56,NOP58,NOS3,NOSTRIN,NPC1,NQO1,NR1H4,NR3C1,NRAS,NSF,NSFL1C,NSUN2,NUBPL,NUCB1,NUCB2,NUCKS1,NUDC,NUDCD3,NUDT12,NUDT13,NUDT14,NUDT16,NUDT19,NUDT21,NUDT3,NUDT4,NUDT7,NUFIP2,NUMA1,NUP153,NUP155,NUP160,NUP205,NUP210,NUP214,NUP35,NUP54,NUP93,NUP98,NUTF2,OAT,OCIAD2,OGA,OGFOD3,OGFR,OGT,OLA1,OPLAH,OPTN,ORMDL2,OS9,OSBPL9,OTOL1,OXCT1,OXR1,OXSM,PA2G4,PABPC1,PABPC4,PABPN1,PAFAH1B1,PAFAH1B2,PAFAH2,PAIP1,PAIP2,PAK2,PALD1,PALLD,PALMD,PAM16,PANK1,PAPSS1,PAPSS2,PARP1,PARP14,PARP9,PARS2,PARVA,PARVB,PAWR,PBDC1,PBLD,PC,PCBP1,PCCA,PCCB,PCDH1,PCDHB16,PCK1,PCNP,PCTP,PCYT1A,PDAP1,PDCD10,PDCD11,PDCD4,PDCD6IP,PDE2A,PDHA1,PDHB,PDIA3,PDIA4,PDIA5,PDIA6,PDK1,PDK2,PDLIM1,PDLIM5,PDLIM7,PDP2,PDXDC1,PDXK,PDZK1,PEBP1,PECAM1,PECR,PEX1,PEX11A,PEX11G,PEX12,PEX13,PEX14,PEX16,PEX19,PEX26,PEX3,PEX5,PEX6,PFAS,PFDN2,PFKFB1,PFKFB3,PGAM1,PGD,PGK1,PGM1,PGM3,PGM5,PGRMC1,PGRMC2,PHACTR4,PHB2,PHF20L1,PHKA1,PHKA2,PHKB,PHKG2,PHLDA1,PHLDB2,PHYHD1,PHYKPL,PI4KA,PICALM,PIGR,PIGS,PIGU,PIK3AP1,PIK3CB,PIN4,PIP5K1C,PIR,PITHD1,PITRM1,PKLR,PKN1,PKP4,PLA2G12B,PLBD1,PLBD2,PLCB3,PLCH1,PLEKHA5,PLEKHA7,PLEKHF1,PLG,PLIN5,PLOD3,PLPP3,PLRG1,PLTP,PLVAP,PLXNA4,PLXNB2,PM20D1,PML,PMM2,PNKP,PNLIP,PNN,POLDIP3,POLR2A,POLR2B,POLR2I,POLR2L,PON1,PON2,PON3,POR,PPA1,PPAN,PPAT,PPCS,PPFIA1,PPFIBP2,PPIA,PPIB,PPIF,PPIG,PPIL1,PPIL4,PPIP5K2,PPL,PPM1A,PPM1B,PPM1G,PPM1K,PPP1R2,PPP1R21,PPP1R7,PPP1R8,PPP2R1B,PPP2R5A,PPP2R5D,PPP4C,PPP4R2,PPP4R3A,PPP6R1,PPP6R3,PPT1,PPT2,PPWD1,PQBP1,PRCP,PRDX3,PRDX5,PRDX6,PREB,PRELP,PREP,PRKAA2,PRKAB1,PRKACA,PRKAG1,PRKCSH,PRKRA,PROC,PROX1,PRPF19,PRPF3,PRPF31,PRPF4,PRPF40A,PRPF6,PRPF8,PRRC1,PRRC2C,PRUNE1,PRXL2A,PRXL2B,PSAP,PSEN1,PSIP1,PSMA1,PSMA2,PSMA3,PSMA4,PSMA5,PSMA6,PSMA7,PSMB1,PSMB10,PSMB2,PSMB5,PSMB6,PSMB7,PSMB9,PSMC3,PSMD14,PSMD3,PSMD4,PSMD7,PSME3,PTBP1,PTBP3,PTGES3,PTK2,PTK2B,PTPMT1,PTPN1,PTPRF,PTPRK,PTRHD1,PTS,PTTG1IP,PUM1,PURA,PXMP2,PXMP4,PXN,PYCARD,PYGB,PYGL,QDPR,QSOX1,QTRT2,RAB14,RAB1A,RAB35,RAB4A,RAB8A,RAB8B,RABGAP1,RABGAP1L,RAC1,RACK1,RAD23B,RAD50,RAE1,RALY,RAN,RANBP1,RANBP10,RANBP3,RANGAP1,RAP1A,RAP1B,RAPGEF4,RARRES2,RASIP1,RBBP4,RBM10,RBM14,RBM15,RBM17,RBM22,RBM28,RBM39,RBM42,RBM47,RBP1,RBPMS,RCC2,RCN1,RDH16,REEP5,REEP6,RELA,RER1,RETREG2,RETSAT,REXO2,RFC2,RGL3,RGN,RGPD4 (includes others),RHOA,RHOC,RHOG,RIDA,RIOX2,RIPK1,RMDN2,RMDN3,RMND5A,RNASEH2A,RNASET2,RNF113A,RNF114,RNF14,RNF17,RNF185,RNF2,RNF20,RNF213,RNF5,RNH1,RNMT,RNPEP,ROCK2,RPAP3,RPE,RPL10,RPL10A,RPL11,RPL12,RPL13,RPL13A,RPL14,RPL15,RPL17,RPL18,RPL18A,RPL19,RPL21,RPL22,RPL23,RPL24,RPL26,RPL27,RPL28,RPL3,RPL31,RPL35,RPL37,RPL37A,RPL4,RPL5,RPL6,RPL7,RPL7A,RPL8,RPL9,RPLP0,RPLP2,RPN1,RPN2,RPRD1B,RPS10,RPS11,RPS12,RPS1

	4,RPS15,RPS15A,RPS16,RPS19,RPS2,RPS20,RPS24,RPS25,RPS26,RPS27A,RPS27L,RPS29,RPS3,RPS5,RPS6,RPS6KB2,RPS7,RPS8,RPSA,RPTOR,RRAS,RRS1,RSL1D1,RTF2,RTN1,RTN4,RTN4IP1,RUFY1,RUFY3,RUVBL1,RUVBL2,S100A1,S100A6,SAA1,SAE1,SAFB,SAMHD1,SAP18,SAR1B,SARDH,SARNP,SARS2,SART1,SART3,SAT2,SAYSD1,SBF1,SC5D,SCAMP1,SCAMP3,SCAMP4,SCAMP5,SCARB1,SCARB2,SCD,SCFD1,SCO1,SCPEP1,SCRIB,SCYL2,SCYL3,SDC4,SDF2L1,SDHD,SDR42E1,SDS,SDSL,SEC11A,SEC14L2,SEC14L4,SEC23B,SEC23IP,SEC24A,SEC24D,SEC31A,SEC61A1,SEC61B,SEC61G,SEC62,SEC63,SELENBP1,SELENOF,SELENOP,SEPHS1,SERBP1,SERHL2,SERINC3,SERPINA1,SERPINA10,SERPINA3,SERPINA6,SERPINB1,SERPIND1,SERPINF2,SERPING1,SERPINH1,SET,SF3A1,SF3A3,SF3B1,SF3B2,SF3B3,SF3B4,SF3B6,SFPQ,SFR1,SFT2D2,SFXN5,SGTA,SH3BGRL3,SH3GL1,SHMT1,SHOC2,SHPK,SHTN1,SIAE,SIGLEC1,SIGMAR1,SIL1,SLC12A9,SLC16A7,SLC17A3,SLC22A1,SLC22A18,SLC22A23,SLC22A25,SLC25A10,SLC25A11,SLC25A12,SLC25A13,SLC25A20,SLC25A21,SLC25A23,SLC25A25,SLC25A3,SLC25A45,SLC25A5,SLC26A1,SLC27A4,SLC2A2,SLC30A5,SLC31A1,SLC35A1,SLC35A3,SLC35B1,SLC35D1,SLC38A10,SLC39A11,SLC39A14,SLC39A4,SLC44A2,SLC4A4,SLC6A12,SLC6A13,SLC7A2,SLC9A3R1,SLC9A3R2,SLCO1B3,SLCO2A1,SLK,SLMAP,SLTM,SMAP1,SMAP2,SMARCA2,SMARCA5,SMARCD2,SMARCE1,SMC1A,SMC3,SMIM15,SMOC1,SMPD1,SMS,SMU1,SNAP23,SNAP47,SND1,SNF8,SNRNP200,SNRNP70,SNRPA1,SNRPB2,SNRPD3,SNRPF,SNRPN,SNTA1,SNTB1,SNU13,SNW1,SNX1,SNX18,SNX2,SNX3,SNX4,SNX5,SNX6,SNX7,SOAT2,SON,SORBS1,SORBS2,SORD,SOS1,SPAG9,SPAST,SPCS1,SPCS2,SPG7,SPPL2A,SPR,SPTAN1,SPTBN2,SQOR,SRA1,SREK1,SRI,SRP19,SRP68,SRP72,SRP9,SRPK2,SRPRB,SRR,SRRT,SRSF1,SRSF10,SRSF2,SRSF3,SRSF4,SRSF6,SRSF7,SSBP1,SSR1,SSR3,SSR4,SSRP1,ST13,STAB1,STAB2,STAG2,STARD5,STAT2,STAT3,STAT6,STBD1,STEAP3,STEAP4,STIP1,STK38L,STOML2,STRAP,STRN,STT3A,STT3B,SUB1,SUCLG1,SUCLG2,SUGCT,SUGT1,SULT1B1,SULT1C2,SULT1E1,SULT2A1,SUMO2,SUN2,SUOX,SUPT16H,SURF1,SURF4,SVIL,SWAP70,SYAP1,SYMPK,SYNCRIP,SYNGR2,SYNJ2BP,TACO1,TADA3,TAGLN,TAGLN2,TALDO1,TAMM41,TANGO2,TAOK3,TAP1,TAP2,TAPBP,TARDBP,TAT,TBC1D13,TBC1D15,TBC1D17,TBC1D24,TBC1D8B,TBC1D9B,TBCD,TBCEL,TBL2,TBRG4,TCEA1,TCERG1,TCIRG1,TCOF1,TDO2,TFR2,TGFBRAP1,TGM1,THNSL2,THOC2,THRAP3,THYN1,TIAL1,TIGAR,TIMM17B,TIMM22,TIMM44,TIMMDC1,TINAGL1,TJP1,TJP2,TJP3,TKFC,TKT,TLN1,TM9SF1,TM9SF2,TM9SF3,TMED1,TMED10,TMED2,TMED3,TMED4,TMED5,TMED7,TMED9,TMEM109,TMEM126A,TMEM126B,TMEM135,TMEM176B,TMEM19,TMEM214,TMEM230,TMEM256,TMEM30A,TMEM33,TMEM38B,TMEM43,TMEM82,TMLHE,TMOD3,TMPO,TMTC3,TMX1,TMX3,TNKS1BP1,TNPO1,TNPO2,TNPO3,TNS2,TNS3,TOM1,TOMM40,TOP1,TOP2B,TOP3B,TOR1A,TOR1AIP1,TPD52,TPD52L2,TPI1,TPK1,TPM3,TPPP,TPR,TPRG1L,TRA2B,TRABD,TRAM1,TRAP1,TRAPPC1,TRAPPC4,TRIM14,TRIM23,TRIM28,TRIP10,TRIP11,TRIR,TRMU,TSC22D1,TSFM,TSG101,TSPAN14,TSPAN31,TSTA3,TTC1,TTC36,TTC37,TTC38,TTC39A,TTC39C,TTC7A,TTN,TTPA,TUBA4A,TUBB,TUBB2A,TUBB4B,TUT7,TWF1,TXLNA,TXLNG,TXN2,TXNDC5,TXNDC9,TXNL1,TYMP,TYSND1,U2AF2,U2SURP,UBA1,UBA2,UBA3,UBA7,UBAC1,UBAP2,UBE2G2,UBE2I,UBE2J1,UBE2M,UBE2V2,UBE2Z,UBE4B,UBL4A,UBL7,UBQLN2,UBR2,UBTF,UCHL5,UCK1,UFL1,UGDH,UGGT1,UGP2,UGT1A4,UGT1A6,UGT1A8 (includes others),UGT2B10,UGT2B17,UGT2B28,UGT3A1,UPB1,UPF1,UPF2,UPP1,UQCC1,UQCC3,UQCRC2,UROC1,USO1,USP16,USP19,USP24,USP46,USP7,VAC14,VAMP2,VAMP3,VAMP8,VAPB,VAT1,VAV2,VCAM1,VCL,VCPIP1,VDAC2,VIM,VKORC1L1,VMO1,VNN1,VPS13D,VPS25,VPS26A,VPS26B,VPS26C,VPS28,VPS33B,VPS35,VPS45,VPS51,VPS52,VRK1,VSIG4,VTA1,VTN,VWA8,WAPL,WASF2,WASHC3,WASHC4,WASHC5,WBP11,WBP2,WDFY1,WDR1,WDR18,WDR26,WDR36,WDR46,WDR5,WDR61,WDR77,WFS1,WRNIP1,XAF1,XPNPEP1,XPO1,XPO5,XRCC6,XRN1,XRN2,YBX1,YBX3,YME1L1,YTHDF2,YTHDF3,YWHAQ,YWHAZ,ZBTB20,ZBTB8OS,ZC3H11A,ZC3H14,ZC3HAV1,ZFR,ZHX1,ZHX2,ZHX3,ZMAT2,ZMIZ1,ZNF326,ZNF638

1. Cancer,Organismal Injury and Abnormalities 2. Nonhematologic malignant neoplasm 3. 9.11E-83 4. Increased 5. 2.778 6. 2277	A1CF,AACS,AADAT,AAK1,AAMDC,AASDHPPT,AASS,ABAT,ABCB10,ABCB4,ABCB6,ABCB8,ABCB9,ABCC2,ABCC3,ABCC6,ABCD1,ABCD2,ABCD3,ABCE1,ABCF2,ABCF3,ABCG5,ABHD11,ABHD14B,ABHD15,ABITRAM,ACAA1,ACACB,ACAD10,ACAD11,ACAD9,ACADL,ACADM,ACADSB,ACAT1,ACAT2,ACBD5,ACIN1,ACLY,ACMSD,ACO1,ACO2,ACOT1,ACOT11,ACOT12,ACOT13,ACOT2,ACOT4,ACOT7,ACOT8,ACOX1,ACOX3,ACP2,ACSF3,ACSL4,ACSL5,ACSM1,ACSS2,ACSS3,ACTB,ACTG1,ACTL6A,ACTN1,ACTN4,ACTR2,ACTR3,ACY1,ACY3,ACYP2,ADAM10,ADAP2,ADD1,ADD2,ADD3,ADHFE1,ADI1,ADIPOR2,ADK,ADPRH,ADSL,AFDN,AFMID,AGFG1,AGFG2,AGK,AGL,AGMAT,AGO1,AGO2,AGPAT2,AGPAT3,AGPAT5,AGRN,AGXT,AGXT2,AHCY,AHCYL2,AHNAK,AHSA1,AHSG,AIF1,AIP,AK2,AK3,AKR1A1,AKR1B10,AKR1C4,AKR1D1,AKT1,ALAS1,ALCAM,ALDH16A1,ALDH1A1,ALDH1B1,ALDH1L1,ALDH3A2,ALDH4A1,ALDH5A1,ALDH6A1,ALDH7A1,ALDH9A1,ALDOA,ALDOB,ALPK1,AMACR,AMBP,AMDHD2,AMPD2,AMT,AMY2A,ANGPTL3,ANGPTL4,ANKHD1/ANKHD1-EIF4EBP3,ANO10,ANPEP,ANXA1,ANXA11,ANXA3,ANXA4,ANXA5,AOX1,AP2A1,AP2M1,AP3B1,APCS,APEX1,API5,APMAP,APOA1,APOB,APOC4,APOD,APOE,AQP1,AQP4,AQP9,ARAF,ARCN1,ARF4,ARF6,ARFGAP1,ARFGAP2,ARFGAP3,ARGLU1,ARHGAP17,ARHGAP31,ARHGAP42,ARHGAP45,ARHGAP5,ARHGDIA,ARHGDIB,ARHGEF12,ARHGEF7,ARIH1,ARMC10,ARPC1A,ARPC1B,ARPC2,ARPC5,ARPC5L,ARRB1,ARSB,AS3MT,ASAH1,ASCC1,ASCC2,ASGR1,ASGR2,ASL,ASPA,ASPDH,ASPG,ASPH,ASPSCR1,ASRGL1,ASS1,ATAD2B,ATG3,ATG4B,ATL3,ATP11C,ATP13A1,ATP1A1,ATP1B1,ATP1B3,ATP2A2,ATP2B1,ATP2B4,ATP5IF1,ATP5PO,ATP6AP1,ATP6AP2,ATP6V0D1,ATP6V1A,ATP6V1C1,ATP6V1E1,ATRX,ATXN10,ATXN2,AUP1,AVEN,B2M,B4GALNT1,BAAT,BABAM2,BAG3,BAG4,BAG5,BAIAP2,BASP1,BBOX1,BCAM,BCAP29,BCAP31,BCAS2,BCHE,BCKDHA,BCKDHB,BCKDK,BCL2L13,BCLAF1,BCO2,BCS1L,BET1L,BGN,BHMT,BHMT2,BID,BIN1,BIN2,BLMH,BLVRA,BLVRB,BMP2K,BNIP3,BPHL,BRAF,BSG,BTAF1,BTD,BUB3,BZW1,C11orf54,C12orf10,C12orf43,C1D,C1orf174,C1QA,C1QB,C2CD2,C4A/C4B,C6,C8A,C8B,C8G,C9,C9orf64,CACFD1,CACYBP,CAD,CADM1,CALCRL,CALR,CALU,CAMK1,CAND1,CANX,CAP1,CAPZA1,CAPZB,CARHSP1,CASK,CASP3,CASP7,CAT,CAVIN1,CBR1,CBWD1,CBX1,CBX3,CCAR1,CCDC134,CCDC167,CCDC22,CCDC25,CCDC40,CCDC47,CCDC51,CCDC58,CCDC9,CCDC93,CCS,CCT3,CD163,CD1D,CD2AP,CD302,CD36,CD38,CD47,CD68,CD81,CD82,CDA,CDC34,CDC37,CDC5L,CDC73,CDK11A,CDK12,CDK5,CDK5RAP3,CDK6,CDK9,CDKN1B,CDKN2C,CDO1,CDV3,CENPV,CEP290,CEP89,CES1,CES3,CFAP20,CFB,CFDP1,CFH,CFI,CGN,CHAC2,CHCHD4,CHD4,CHID1,CHMP2A,CHORDC1,CHPT1,CIAO3,CIDEB,CISD1,CISD2,CKAP4,CKB,CKM,CLCC1,CLDN12,CLDN3,CLEC10A,CLEC3B,CLEC4F,CLEC4G,CLIC1,CLIC4,CLIC5,CLINT1,CLPP,CLPTM1,CLTA,CLTB,CLU,CLYBL,CMAS,CMBL,CMC2,CMPK1,CMPK2,CMTM4,CNBP,CNDP2,CNOT1,CNOT2,CNOT3,CNOT9,CNP,CNPY2,COA7,COASY,COBLL1,COG3,COG5,COL18A1,COLGALT1,COMT,COMTD1,COPA,COPB1,COPB2,COPE,COPG1,COQ3,COQ4,COQ8A,COQ8B,COQ9,CORO1A,CORO1B,CORO1C,COTL1,COX15,COX19,COX5A,COX6B1,COX7A2,CP,CPB2,CPN1,CPNE3,CPOX,CPPED1,CPQ,CPS1,CPSF2,CPT2,CR1L,CRAT,CREB1,CRELD1,CRELD2,CRIP1,CRK,CRKL,CRNKL1,CRP,CRYL1,CRYM,CRYZ,CSAD,CSK,CSNK1E,CSNK2A1,CSNK2A2,CSNK2B,CSRP1,CSRP2,CSTF1,CSTF2,CSTF3,CTBP1,CTBS,CTDSP1,CTH,CTNNA1,CTNNB1,CTNNBL1,CTNND1,CTR9,CTSB,CTSC,CTSD,CTSF,CTSH,CTSO,CTSS,CTSV,CTSZ,CTTN,CUL1,CUL2,CUL3,CUTC,CXADR,CYB5A,CYB5B,CYB5R1,CYBC1,CYGB,CYP17A1,CYP1A2,CYP27A1,CYP2A6 (includes others),Cyp2b13/Cyp2b9,CYP2B6,Cyp2c54 (includes others),CYP2C8,CYP2F1,CYP2U1,CYP3A5,CYP3A7,CYP4A11,CYP4A22,CYP4B1,CYP4F3,CYP7A1,CYP7B1,DAAM1,DAD1,DAPK1,DARS2,DBNL,DCAF11,DCAKD,DCPS,DCTN2,DCTN4,DCTN6,DCUN1D1,DCUN1D2,DCXR,DDAH1,DDAH2,DDC,DDHD2,DDI2,DDOST,DDRGK1,DDX17,DDX18,DDX19A,DDX21,DDX23,DDX27,DDX39B,DDX3X,DDX3Y,DDX42,DDX46,DDX49,DDX5,DDX58,DDX6,DECR1,DECR2,DEK,DEPTOR,DES,DGAT2,DGLUCY,DHCR24,DHDH,DHFR,DHODH,DHRS7,DHRS7B,DHTKD1,DHX15,DHX16,DHX9,DIABLO,DIO1,DIS3,DKC1,DLAT,DMAC1,DMD,DMGDH,DNAJA1,DNAJB1,DNAJB11,DNAJB4,DNAJB6,DNAJB9,DNAJC1,DNAJC13,DNAJC19,DNAJC2,DNAJC25,DNAJC3,DNAJC7,DNM1L,DNM2,DNPEP,DNTTIP2,DOCK6,DPAGT1,DPM1,DPM3,DPP4,DPP7,DPP9,DPY19L1,DPY30,DPYD,DPYS,DPYSL2,DRG1,DSP,DTD1,DTX3L,DUSP23,DYNLL1,DYNLT3,DYSF,EBPL,ECHDC2,ECHDC3,ECI1,ECI2,ECM1,EDC4,EEA1,EEF1A1,EEF1D,EEF2,EFHD2,EFR3A,EFTUD2,EGF,EGFR,EHD1,EHD3,EHHADH,EIF1AX,EIF2A,EIF2AK2,EIF2B1,EIF2B2,EIF2B3,EIF2B5,EIF2S1,EIF2S2,EIF3A,EIF3C,EIF3D,EIF3E,EIF3F,EIF3H,EIF3I,EIF3L,EIF3M,EIF4A1,EIF4A2,EIF4A3,EIF4E,EIF4G1,EIF4G2,EIF4H,EIF5,EIF5A,EIF5B,ELAC2,ELAVL1,ELMO1,ELOA,ELOC,ELOVL1,ELOVL2,ELOVL5,ELP2,EMC8,EMD,EMILIN1,EML3,EML4,ENO1,ENPEP,ENPP1,ENTPD5,EPB41,EPB41L2,EPB41L5,EPHX1,EPHX2,EPPK1,EPS15L1,EPS8L2,ERBIN,ERC1,ERGIC1,ERGIC2,ERGIC3,ERH,ERLIN1,ERMP1,ERP29,ERP44,ESAM,ESD,ESYT1,ESYT2,ETFDH,ETNK1,ETNPPL,EVA1A,EXOC1,EXOC5,EXOC7,EXOSC9,EZR,F11,F13A1,FAAH,FABP2,FABP4,FABP5,FABP7,FADS6,FAF1,FAHD2B,FAM114A2,FAM126A,FAM126B,FAM210A,FAM234A,FAM3C,FAM50B,FAM98C,FARP1,FARS2,FASN,FAU,FBL,FBP1,FBXO3,FCGR2B,FCGRT,FCHO2,FDX2,FECH,FEN1,FERMT2,FETUB,FGA,FGB,FGG,FGL1,FHIT,FIS1,FITM2,FKBP11,FKBP15,FKBP3,FKBP4,FKBP5,FLII,FLNA,FLOT1,FLOT2,FMO1,FMO3,FMO4,FMO5,FMR1,FN1,FN3K,FN3KRP,FNDC3A,FNTA,FRAS1,FRG1,FSCN1,FTCD,FTO,FTSJ3,FUBP1,FUBP3,FXN,FXR1,FXYD1,G0S2,G6PC,G6PD,GAA,GABPA,GADD45GIP1,GALK1,GALK2,GALM,GALNS,GALNT2,GALT,GAMT,GANAB,GAPDH,GAPVD1,GART,GATAD2A,GATD1,GATM,GBA,GBE1,GBF1,GBP6,GCAT,GCC1,GCDH,GCH1,GCK,GCKR,GCLM,GCN1,GDA,GFM1,GFPT1,GGA1,GGCT,GID8,GIMAP4,GJB2,GLDC,GLG1,GLMP,GLO1,GLOD4,GLRX3,GLRX5,GLT1D1,GLTPD2,GLUD1,GLUL,GLYAT,GLYR1,Gm12854/S100a11,Gm21596/Hmgb1,GMPPA,GMPPB,GMPR2,GMPS,GNA11,GNA13,GNAI2,GNAI3,GNAQ,GNAS,GNE,GNG12,GNL3,GNMT,GNPAT,GNPDA1,GNS,GOLGA2,GOLGA5,GOLGA7,GOLPH3,GOLPH3L,GOPC,GORASP2,GOSR1,GOSR2,GOT1,GPAM,GPAT3,GPAT4,GPD1,GPD1L,GPHN,GPLD1,GPR182,GPRIN3,GPT,GPT2,GPX3,

	GRB7,GRHPR,GRIPAP1,GRN,GSPT1,GSR,Gsta4,GSTA5,GSTK1,GSTM1,GSTM2,GSTM4,GSTM5,GSTP1,GSTT2/GSTT2B,GSTZ1,GTF2F1,GTF2F2,GTF2I,GTPBP4,GUCY1B1,H3-3A/H3-3B,H6PD,HACL1,HADH,HAGH,HAL,HAO1,HAO2,HBS1L,HCCS,HCFC1,HDAC1,HDGF,HDGFL2,HDGFL3,HDLBP,HEATR1,HEBP1,HECTD1,HELZ2,HERPUD1,HEXB,HEXIM1,HGD,HGS,HIBADH,HIBCH,HINT2,HINT3,HIP1,HK1,HLA-A,HLA-DQA1,HMGA1,HMGCL,HMGCS1,HMGCS2,HMGN1,HMOX1,HMOX2,HNF1A,HNF4A,HNMT,HNRNPA2B1,HNRNPAB,HNRNPC,HNRNPD,HNRNPF,HNRNPH1,HNRNPH2,HNRNPK,HNRNPL,HNRNPLL,HNRNPM,HNRNPR,HNRNPU,HNRNPUL1,HNRNPUL2,HOMER2,HOPX,HP,HP1BP3,HPCAL1,HPD,HPGD,HPN,HPX,HRAS,Hrg,HS1BP3,HSCB,HSD11B1,HSD17B10,HSD17B11,HSD17B2,HSD17B4,HSD17B6,HSDL1,HSP90AA1,HSP90AB1,HSP90B1,HSPA12B,HSPA13,HSPA1A/HSPA1B,HSPA4L,HSPA5,HSPA8,HSPA9,HSPB1,HSPD1,HSPG2,HSPH1,HTATIP2,HUWE1,HYKK,HYOU1,HYPK,ICAM1,IDH2,IDH3B,IDO2,IFI16,IFIT1B,IFIT3,IFNAR2,IGF2R,IGFALS,IK,IL6ST,ILF2,ILF3,ILK,ILKAP,IMMP2L,IMMT,IMPA1,IMPAD1,INHBC,INMT,INPP1,INPP5F,INSIG2,INSR,INTS3,IP6K1,IPO5,IQGAP1,ISCA2,ISOC1,ISOC2,IST1,ITGA1,ITGA2B,ITGA5,ITGA9,ITGAV,ITGB1,ITGB3,ITGB6,ITIH2,ITIH4,ITPR2,ITSN1,IYD,JCHAIN,JPT2,JUP,KANK2,KCTD12,KDELR1,KDSR,KHDRBS1,KHK,KHSRP,KIF13B,KIF21A,KLHDC7A,KLKB1,KPNA1,KPNA2,KRAS,KXD1,KYAT1,KYAT3,KYNU,L2HGDH,L3HYPDH,LAMTOR1,LAP3,LARP1,LARP4,LARP4B,LARP7,LARS2,LASP1,LBR,LCAT,LDAH,LDLR,LGALS1,LGALS3,LGALS3BP,LGALS8,LGALSL,LGMN,LHPP,LIAS,LIFR,LIMS2,LIN7A,LIN7C,LIPE,LITAF,LMAN1,LMAN2,LMAN2L,LMF1,LMNA,LMNB1,LMNB2,LMO7,LOC102724788/PRODH,LONP2,LPCAT3,LRG1,LRP1,LRPAP1,LRRFIP1,LSG1,LSM12,LSM14A,LSM14B,LSM5,LSM6,LSR,LUC7L,LUC7L2,LUC7L3,LUM,LYAR,LYN,LYPLA1,LYPLA2,LYPLAL1,LYVE1,LYZ,LZIC,M6PR,MACO1,MACROD1,MAGIX,MAN1A2,MAN2B1,MAN2B2,MAN2C1,MANBA,MAOA,MAOB,MAP2K1,MAP2K3,MAP4,MAPK1IP1L,MAPRE1,MAPRE3,MASP2,MAT1A,MAT2A,MATR3,MBL2,MBNL1,MBOAT7,MCAM,MCCC1,MCCC2,MCEE,MCFD2,MCTS1,MDH1,ME1,MEAF6,MECP2,METAP2,METTL26,METTL27,METTL7B,METTL9,MFAP1,MFN2,MGAT2,MGLL,MGST1,MIA3,MIEN1,MIF,MIF4GD,MIGA2,MIOS,MIPEP,MKNK1,MMAB,MME,MMUT,MOB1B,MOCS2,MOGS,MORF4L1,MOSPD2,MOV10,MPC1,MPC2,MPHOSPH10,MPI,MPP1,MPP6,MPRIP,MPST,MRC1,MRI1,MROH1,MRPL12,MRPL15,MRPL17,MRPL24,MRPL47,MRPL50,MRPL51,MRPS12,MRPS15,MRPS17,MRPS25,MRPS31,MRPS35,MRRF,MSH2,MSN,MSR1,MSRA,MSRB2,Mt1,Mt2,MTA2,MTAP,MTCH2,MTDH,MTFR1,MTFR1L,MTHFD1,MTHFS,MTMR6,MTOR,MTREX,MTSS1,MTX2,MUL1,MVK,MVP,MYBBP1A,MYCBP,MYEF2,MYH10,MYH11,MYH14,MYH9,MYL1,MYL12A,MYL6,MYLK,MYLPF,MYO18A,MYO1B,MYO1C,MYO1D,NAA15,NAA16,NAA25,NAA35,NAALAD2,NACA,NADK2,NAGA,NAGLU,NAMPT,NANP,NANS,NAP1L1,NAPRT,NASP,NAT10,NAXD,NAXE,NCBP1,NCEH1,NCK1,NCL,NCOA5,NCSTN,NDRG1,NDST1,NDUFA10,NDUFA11,NDUFA13,NDUFA2,NDUFA3,NDUFAF2,NDUFAF3,NDUFAF7,NDUFB6,NDUFB7,NDUFB8,NECAP1,NECTIN2,NELFA,NELFB,NELFCD,NFIA,NFIB,NFIC,NFS1,NFU1,NFXL1,NGEF,NGLY1,NHLRC2,NHP2,NIBAN1,NID2,NIPSNAP2,NIT1,NLN,NLRX1,NME3,NMNAT1,NMRAL1,NMRK1,NMT2,NNMT,NOC2L,NOL6,NONO,NOP10,NOP16,NOP56,NOP58,NOS3,NOSTRIN,NPC1,NQO1,NR1H4,NR3C1,NRAS,NSF,NSFL1C,NSUN2,NUBPL,NUCB1,NUCB2,NUCKS1,NUDC,NUDCD3,NUDT12,NUDT13,NUDT14,NUDT16,NUDT19,NUDT21,NUDT3,NUDT4,NUDT7,NUDT9,NUFIP2,NUMA1,NUP153,NUP155,NUP160,NUP205,NUP210,NUP214,NUP35,NUP54,NUP93,NUP98,NUTF2,OAT,OCIAD2,OGA,OGFOD3,OGFR,OGT,OLA1,OPLAH,OPTN,ORMDL2,OS9,OSBPL9,OTOL1,OXCT1,OXR1,OXSM,PA2G4,PABPC1,PABPC4,PABPN1,PAFAH1B1,PAFAH1B2,PAFAH2,PAIP1,PAIP2,PAK2,PALD1,PALLD,PALMD,PAM16,PANK1,PAPSS1,PAPSS2,PARP1,PARP14,PARP9,PARS2,PARVA,PARVB,PAWR,PBDC1,PBLD,PC,PCBP1,PCCA,PCCB,PCDH1,PCDHB16,PCK1,PCNP,PCTP,PCYT1A,PDAP1,PDCD10,PDCD11,PDCD4,PDCD6IP,PDE2A,PDHA1,PDHB,PDIA3,PDIA4,PDIA5,PDIA6,PDK1,PDK2,PDLIM1,PDLIM5,PDLIM7,PDP2,PDXDC1,PDXK,PDZK1,PEBP1,PECAM1,PECR,PEX1,PEX11A,PEX11G,PEX12,PEX13,PEX14,PEX16,PEX19,PEX26,PEX3,PEX5,PEX6,PFAS,PFDN2,PFKFB1,PFKFB3,PGAM1,PGD,PGK1,PGM1,PGM3,PGM5,PGRMC1,PGRMC2,PHACTR4,PHB2,PHF20L1,PHKA1,PHKA2,PHKB,PHKG2,PHLDA1,PHLDB2,PHYHD1,PHYKPL,PI4KA,PICALM,PIGR,PIGS,PIGU,PIK3AP1,PIK3CB,PIN4,PIP5K1C,PIR,PITHD1,PITRM1,PKLR,PKN1,PKP4,PLA2G12B,PLBD1,PLBD2,PLCB3,PLCH1,PLEKHA5,PLEKHA7,PLEKHF1,PLG,PLIN5,PLOD3,PLPP3,PLRG1,PLS3,PLTP,PLVAP,PLXNA4,PLXNB2,PM20D1,PML,PMM2,PNKP,PNLIP,PNN,POLDIP3,POLR2A,POLR2B,POLR2I,POLR2L,PON1,PON2,PON3,POR,PPA1,PPAN,PPAT,PPCS,PPFIA1,PPFIBP2,PPIA,PPIB,PPIF,PPIG,PPIL1,PPIL4,PPIP5K2,PPL,PPM1A,PPM1B,PPM1G,PPM1K,PPP1R2,PPP1R21,PPP1R7,PPP1R8,PPP2R1B,PPP2R5A,PPP2R5D,PPP4C,PPP4R2,PPP4R3A,PPP6R1,PPP6R3,PPT1,PPT2,PPWD1,PQBP1,PRCP,PRDX3,PRDX5,PRDX6,PREB,PRELP,PREP,PRKAA2,PRKAB1,PRKACA,PRKAG1,PRKCSH,PRKRA,PROC,PROX1,PRPF19,PRPF3,PRPF31,PRPF4,PRPF40A,PRPF6,PRPF8,PRRC1,PRRC2C,PRUNE1,PRXL2A,PRXL2B,PSAP,PSEN1,PSIP1,PSMA1,PSMA2,PSMA3,PSMA4,PSMA5,PSMA6,PSMA7,PSMB1,PSMB10,PSMB2,PSMB5,PSMB6,PSMB7,PSMB9,PSMC3,PSMD14,PSMD3,PSMD4,PSMD7,PSME3,PTBP1,PTBP3,PTGES3,PTK2,PTK2B,PTPMT1,PTPN1,PTPRF,PTPRK,PTRHD1,PTS,PTTG1IP,PUM1,PURA,PXMP2,PXMP4,PXN,PYCARD,PYGB,PYGL,QDPR,QSOX1,QTRT2,RAB14,RAB1A,RAB35,RAB3IP,RAB4A,RAB8A,RAB8B,RABGAP1,RABGAP1L,RABL3,RAC1,RACK1,RAD23B,RAD50,RAE1,RALY,RAN,RANBP1,RANBP10,RANBP3,RANGAP1,RAP1A,RAP1B,RAPGEF4,RARRES2,RASIP1,RBBP4,RBM10,RBM14,RBM15,RBM17,RBM22,RBM28,RBM39,RBM42,RBM47,RBP1,RBPMS,RCC2,RCN1,RDH16,REEP5,REEP6,RELA,RER1,RETREG2,RETSAT,REXO2,RFC2,RGL3,RGN,RGPD4 (includes others),RHOA,RHOC,RHOG,RIDA,RIOX2,RIPK1,RMDN2,RMDN3,RMND5A,RNASEH2A,RNASET2,RNF113A,RNF114,RNF14,RNF17,RNF185,RNF2,RNF20,RNF213,RNF5,RNH1,RNMT,RNPEP,ROCK2,RPAP3,RPE,RPL10,RPL10A,RPL11,RPL12,RPL13,RPL13A,RPL14,RPL15,RPL17,RPL18,RPL18A,RPL19,RPL21,RPL22,RPL23,RPL24,RPL26,RPL27,RPL28,RPL3,RPL31,RPL35,RPL37,RPL37A,RPL4,R

	PL5,RPL6,RPL7,RPL7A,RPL8,RPL9,RPLP0,RPLP2,RPN1,RPN2,RPRD1B,RPS10,RPS11,RPS12,RPS14,RPS15,RPS15A,RPS16,RPS19,RPS2,RPS20,RPS24,RPS25,RPS26,RPS27A,RPS27L,RPS29,RPS3,RPS4Y1,RPS5,RPS6,RPS6KB2,RPS7,RPS8,RPSA,RPTOR,RRAS,RRS1,RSL1D1,RTF2,RTN1,RTN4,RTN4IP1,RUFY1,RUFY3,RUVBL1,RUVBL2,S100A1,S100A6,SAA1,SAE1,SAFB,SAMHD1,SAP18,SAR1B,SARDH,SARNP,SARS2,SART1,SART3,SAT2,SAYSD1,SBF1,SC5D,SCAMP1,SCAMP3,SCAMP4,SCAMP5,SCARB1,SCARB2,SCD,SCFD1,SCO1,SCPEP1,SCRIB,SCYL2,SCYL3,SDC4,SDF2L1,SDHD,SDR42E1,SDS,SDSL,SEC11A,SEC14L2,SEC14L4,SEC23B,SEC23IP,SEC24A,SEC24D,SEC31A,SEC61A1,SEC61B,SEC61G,SEC62,SEC63,SELENBP1,SELENOF,SELENOI,SELENOP,SEPHS1,SERBP1,SERHL2,SERINC3,SERPINA1,SERPINA10,SERPINA3,SERPINA6,SERPINB1,SERPIND1,SERPINF2,SERPING1,SERPINH1,SET,SF3A1,SF3A3,SF3B1,SF3B2,SF3B3,SF3B4,SF3B6,SFPQ,SFR1,SFT2D2,SFXN5,SGTA,SH3BGRL3,SH3GL1,SHMT1,SHOC2,SHPK,SHTN1,SIAE,SIGLEC1,SIGMAR1,SIL1,SLC12A9,SLC16A7,SLC17A3,SLC22A1,SLC22A18,SLC22A23,SLC22A25,SLC25A10,SLC25A11,SLC25A12,SLC25A13,SLC25A20,SLC25A21,SLC25A23,SLC25A25,SLC25A3,SLC25A45,SLC25A5,SLC26A1,SLC27A4,SLC2A2,SLC30A5,SLC31A1,SLC35A1,SLC35A3,SLC35B1,SLC35D1,SLC38A10,SLC38A3,SLC39A11,SLC39A14,SLC39A4,SLC44A2,SLC4A4,SLC6A12,SLC6A13,SLC7A2,SLC9A3R1,SLC9A3R2,SLCO1B3,SLCO2A1,SLK,SLMAP,SLTM,SMAP1,SMAP2,SMARCA2,SMARCA5,SMARCD2,SMARCE1,SMC1A,SMC3,SMIM15,SMOC1,SMPD1,SMS,SMU1,SNAP23,SNAP47,SND1,SNF8,SNRNP200,SNRNP70,SNRPA1,SNRPB2,SNRPD3,SNRPF,SNRPN,SNTA1,SNTB1,SNU13,SNW1,SNX1,SNX18,SNX2,SNX3,SNX4,SNX5,SNX6,SNX7,SOAT2,SON,SORBS1,SORBS2,SORD,SOS1,SPAG9,SPAST,SPCS1,SPCS2,SPG7,SPPL2A,SPR,SPTAN1,SPTBN2,SQOR,SRA1,SREK1,SRI,SRP19,SRP68,SRP72,SRP9,SRPK2,SRPRB,SRR,SRRT,SRSF1,SRSF10,SRSF2,SRSF3,SRSF4,SRSF6,SRSF7,SSBP1,SSR1,SSR3,SSR4,SSRP1,ST13,STAB1,STAB2,STAG2,STARD5,STAT2,STAT3,STAT6,STBD1,STEAP3,STEAP4,STIP1,STK38,STK38L,STOML2,STRAP,STRN,STT3A,STT3B,SUB1,SUCLG1,SUCLG2,SUGCT,SUGT1,SULT1B1,SULT1C2,SULT1E1,SULT2A1,SUMO2,SUN2,SUOX,SUPT16H,SURF1,SURF4,SVIL,SWAP70,SYAP1,SYMPK,SYNCRIP,SYNGR2,SYNJ2BP,TACO1,TADA3,TAGLN,TAGLN2,TALDO1,TAMM41,TANGO2,TAOK3,TAP1,TAP2,TAPBP,TARDBP,TAT,TBC1D13,TBC1D15,TBC1D17,TBC1D24,TBC1D8B,TBC1D9B,TBCD,TBCEL,TBL2,TBRG4,TCEA1,TCERG1,TCIRG1,TCOF1,TDO2,TFR2,TGFBRAP1,TGM1,THNSL2,THOC2,THRAP3,THYN1,TIAL1,TIGAR,TIMM17B,TIMM22,TIMM44,TIMMDC1,TINAGL1,TJP1,TJP2,TJP3,TKFC,TKT,TLN1,TM9SF1,TM9SF2,TM9SF3,TMED1,TMED10,TMED2,TMED3,TMED4,TMED5,TMED7,TMED9,TMEM109,TMEM126A,TMEM126B,TMEM135,TMEM176B,TMEM19,TMEM214,TMEM230,TMEM256,TMEM30A,TMEM33,TMEM38B,TMEM43,TMEM82,TMLHE,TMOD3,TMPO,TMTC3,TMX1,TMX3,TNKS1BP1,TNPO1,TNPO2,TNPO3,TNS2,TNS3,TOLLIP,TOM1,TOMM40,TOP1,TOP2B,TOP3B,TOR1A,TOR1AIP1,TPD52,TPD52L2,TPI1,TPK1,TPM3,TPPP,TPR,TPRG1L,TRA2B,TRABD,TRAM1,TRAP1,TRAPPC1,TRAPPC4,TRIM14,TRIM23,TRIM28,TRIP10,TRIP11,TRIR,TRMU,TSC22D1,TSFM,TSG101,TSPAN14,TSPAN31,TSTA3,TTC1,TTC36,TTC37,TTC38,TTC39A,TTC39C,TTC7A,TTN,TTPA,TUBA1B,TUBA4A,TUBB,TUBB2A,TUBB4B,TUT7,TWF1,TXLNA,TXLNG,TXN2,TXNDC5,TXNDC9,TXNL1,TYMP,TYSND1,U2AF2,U2SURP,UBA1,UBA2,UBA3,UBA7,UBAC1,UBAP2,UBE2G2,UBE2J1,UBE2M,UBE2V2,UBE2Z,UBE4B,UBL4A,UBL7,UBQLN2,UBR2,UBTF,UCHL5,UCK1,UFL1,UGDH,UGGT1,UGP2,UGT1A4,UGT1A6,UGT1A8 (includes others),UGT2B10,UGT2B17,UGT2B28,UGT3A1,UPB1,UPF1,UPF2,UPP1,UQCC1,UQCC3,UQCRC2,UROC1,USO1,USP16,USP19,USP24,USP46,USP7,VAC14,VAMP2,VAMP3,VAMP8,VAPB,VAT1,VAV2,VCAM1,VCL,VCPIP1,VDAC2,VDAC3,VIM,VKORC1L1,VMO1,VNN1,VPS13D,VPS25,VPS26A,VPS26B,VPS26C,VPS28,VPS33B,VPS35,VPS45,VPS51,VPS52,VRK1,VSIG4,VTA1,VTN,VWA8,WAPL,WASF2,WASHC3,WASHC4,WASHC5,WBP11,WBP2,WDFY1,WDR1,WDR18,WDR26,WDR36,WDR46,WDR5,WDR61,WDR77,WFS1,WRNIP1,XAF1,XPNPEP1,XPO1,XPO5,XRCC6,XRN1,XRN2,YBX1,YBX3,YME1L1,YTHDF2,YTHDF3,YWHAQ,YWHAZ,ZBTB20,ZBTB8OS,ZC3H11A,ZC3H14,ZC3HAV1,ZFR,ZHX1,ZHX2,ZHX3,ZMAT2,ZMIZ1,ZNF326,ZNF638

1. Cancer,Organismal Injury and Abnormalities 2. Non-melanoma solid tumor 3. 1.82E-82 4. Increased 5. 2.914 6. 2267	A1CF,AACS,AADAT,AAK1,AAMDC,AASDHPPT,AASS,ABAT,ABCB10,ABCB4,ABCB6,ABCB8,ABCB9,ABCC2,ABCC3,ABCC6,ABCD1,ABCD2,ABCD3,ABCE1,ABCF2,ABCF3,ABCG5,ABHD11,ABHD14B,ABHD15,ABITRAM,ACAA1,ACACB,ACAD10,ACAD11,ACAD9,ACADL,ACADM,ACADSB,ACAT1,ACAT2,ACBD5,ACIN1,ACLY,ACMSD,ACO1,ACO2,ACOT1,ACOT11,ACOT12,ACOT13,ACOT2,ACOT4,ACOT7,ACOT8,ACOX1,ACOX3,ACP2,ACSF3,ACSL4,ACSL5,ACSM1,ACSS2,ACSS3,ACTB,ACTG1,ACTN1,ACTN4,ACTR2,ACTR3,ACY1,ACY3,ACYP2,ADAM10,ADAP2,ADD1,ADD2,ADD3,ADHFE1,ADI1,ADIPOR2,ADK,ADSL,AFDN,AFMID,AGFG1,AGFG2,AGK,AGL,AGMAT,AGO1,AGO2,AGPAT2,AGPAT3,AGPAT5,AGRN,AGXT,AGXT2,AHCY,AHCYL2,AHNAK,AHSA1,AHSG,AIF1,AIP,AK2,AK3,AKR1A1,AKR1B10,AKR1C4,AKR1D1,AKT1,ALAS1,ALCAM,ALDH16A1,ALDH1A1,ALDH1B1,ALDH1L1,ALDH3A2,ALDH4A1,ALDH5A1,ALDH6A1,ALDH7A1,ALDH9A1,ALDOA,ALDOB,ALPK1,AMACR,AMBP,AMDHD2,AMPD2,AMT,AMY2A,ANGPTL3,ANGPTL4,ANKHD1/ANKHD1- EIF4EBP3,ANO10,ANPEP,ANXA1,ANXA11,ANXA3,ANXA4,ANXA5,AOX1,AP2A1,AP2M1,AP3B1,APCS,APEX1,API5,APMAP,APOA1,APOB,APOC4,APOD,APOE,AQP1,AQP4,AQP9,ARAF,ARCN1,ARF4,ARF6,ARFGAP1,ARFGAP2,ARFGAP3,ARGLU1,ARHGAP17,ARHGAP31,ARHGAP42,ARHGAP45,ARHGAP5,ARHGDIA,ARHGDIB,ARHGEF12,ARHGEF7,ARIH1,ARMC10,ARPC1A,ARPC1B,ARPC2,ARPC5,ARPC5L,ARRB1,ARSB,AS3MT,ASAH1,ASCC1,ASCC2,ASGR1,ASGR2,ASL,ASPA,ASPDH,ASPG,ASPH,ASPSCR1,ASRGL1,ASS1,ATAD2B,ATG3,ATG4B,ATL3,ATP11C,ATP13A1,ATP1A1,ATP1B1,ATP1B3,ATP2A2,ATP2B1,ATP2B4,ATP5IF1,ATP5PO,ATP6AP1,ATP6AP2,ATP6V0D1,ATP6V1A,ATP6V1C1,ATP6V1E1,ATRX,ATXN10,ATXN2,AUP1,AVEN,B2M,B4GALNT1,BAAT,BABAM2,BAG3,BAG4,BAG5,BAIAP2,BASP1,BBOX1,BCAM,BCAP29,BCAS2,BCHE,BCKDHA,BCKDHB,BCKDK,BCL2L13,BCLAF1,BCO2,BCS1L,BET1L,BGN,BHMT,BHMT2,BID,BIN1,BIN2,BLMH,BLVRA,BLVRB,BMP2K,BNIP3,BPHL,BRAF,BSG,BTAF1,BTD,BUB3,BZW1,C11orf54,C12orf10,C12orf43,C1D,C1orf174,C1QA,C1QB,C2CD2,C4A/C4B,C6,C8A,C8B,C8G,C9,C9orf64,CACFD1,CACYBP,CAD,CADM1,CALCRL,CALR,CALU,CAMK1,CAND1,CANX,CAP1,CAPZA1,CAPZB,CASK,CASP3,CASP7,CAT,CAVIN1,CBR1,CBWD1,CBX1,CBX3,CCAR1,CCDC134,CCDC167,CCDC22,CCDC25,CCDC40,CCDC47,CCDC51,CCDC58,CCDC9,CCDC93,CCS,CCT3,CD163,CD1D,CD2AP,CD302,CD36,CD38,CD47,CD68,CD81,CD82,CDA,CDC34,CDC37,Cdc42,CDC5L,CDC73,CDK11A,CDK12,CDK5,CDK5RAP3,CDK6,CDK9,CDKN1B,CDKN2C,CDO1,CDV3,CENPV,CEP290,CEP89,CES1,CES3,CFAP20,CFB,CFDP1,CFH,CFI,CGN,CHAC2,CHCHD4,CHD4,CHID1,CHMP2A,CHORDC1,CHPT1,CIAO3,CIDEB,CISD1,CISD2,CKAP4,CKB,CKM,CLCC1,CLDN12,CLDN3,CLEC10A,CLEC3B,CLEC4F,CLEC4G,CLIC1,CLIC4,CLIC5,CLINT1,CLPP,CLPTM1,CLTB,CLU,CLYBL,CMAS,CMBL,CMC2,CMPK1,CMPK2,CMTM4,CNBP,CNDP2,CNOT1,CNOT2,CNOT3,CNOT9,CNP,CNPY2,COA7,COASY,COBLL1,COG3,COG5,COL18A1,COLGALT1,COMT,COMTD1,COPA,COPB1,COPB2,COPE,COPG1,COQ3,COQ4,COQ8A,COQ8B,COQ9,CORO1A,CORO1B,CORO1C,COTL1,COX15,COX19,COX5A,COX6B1,COX7A2,CP,CPB2,CPN1,CPNE3,CPOX,CPQ,CPS1,CPSF2,CPT2,CR1L,CRAT,CREB1,CRELD1,CRELD2,CRIP1,CRK,CRKL,CRNKL1,CRP,CRYL1,CRYM,CRYZ,CSAD,CSK,CSNK1E,CSNK2A1,CSNK2A2,CSNK2B,CSRP1,CSRP2,CSTF1,CSTF2,CSTF3,CTBP1,CTBS,CTDSP1,CTH,CTNNA1,CTNNB1,CTNNBL1,CTNND1,CTR9,CTSB,CTSC,CTSD,CTSF,CTSH,CTSO,CTSS,CTSV,CTSZ,CTTN,CUL1,CUL2,CUL3,CUTC,CXADR,CYB5A,CYB5B,CYB5R1,CYBC1,CYGB,CYP17A1,CYP1A2,CYP27A1,CYP2A6 (includes others),Cyp2b13/Cyp2b9,CYP2B6,Cyp2c54 (includes others),Cyp2c70,CYP2C8,CYP2F1,CYP2U1,CYP3A5,CYP3A7,CYP4A11,CYP4A22,CYP4B1,CYP4F3,CYP7A1,CYP7B1,DAAM1,DAD1,DAPK1,DARS2,DBNL,DCAF11,DCAKD,DCPS,DCTN2,DCTN4,DCTN6,DCUN1D1,DCUN1D2,DCXR,DDAH1,DDAH2,DDC,DDHD2,DDI2,DDOST,DDRGK1,DDX17,DDX18,DDX19A,DDX21,DDX23,DDX27,DDX39B,DDX3X,DDX3Y,DDX42,DDX46,DDX49,DDX5,DDX58,DDX6,DECR1,DECR2,DEK,DEPTOR,DES,DGAT2,DGLUCY,DHCR24,DHDH,DHFR,DHODH,DHRS7,DHRS7B,DHTKD1,DHX15,DHX16,DHX9,DIABLO,DIO1,DIS3,DKC1,DLAT,DMAC1,DMD,DMGDH,DNAJA1,DNAJB1,DNAJB11,DNAJB4,DNAJB6,DNAJB9,DNAJC1,DNAJC13,DNAJC19,DNAJC2,DNAJC25,DNAJC3,DNAJC7,DNM1L,DNM2,DNPEP,DNTTIP2,DOCK6,DPAGT1,DPM1,DPM3,DPP4,DPP7,DPP9,DPY19L1,DPY30,DPYD,DPYS,DPYSL2,DR1,DRG1,DSP,DTD1,DTX3L,DUSP23,DUT,DYNLL1,DYNLT3,DYSF,EBPL,ECHDC2,ECI1,ECI2,ECM1,EDC4,EEA1,EEF1A1,EEF1D,EEF2,EFHD2,EFR3A,EFTUD2,EGF,EGFR,EHD1,EHD3,EHHADH,EIF1AX,EIF2A,EIF2AK2,EIF2B1,EIF2B2,EIF2B3,EIF2S1,EIF2S2,EIF3A,EIF3C,EIF3D,EIF3E,EIF3F,EIF3H,EIF3I,EIF3L,EIF3M,EIF4A1,EIF4A2,EIF4A3,EIF4E,EIF4G1,EIF4G2,EIF4H,EIF5,EIF5A,EIF5B,ELAC2,ELAVL1,ELMO1,ELOA,ELOC,ELOVL1,ELOVL2,ELOVL5,ELP2,EMC8,EMD,EMILIN1,EML3,EML4,ENO1,ENPEP,ENPP1,ENTPD5,EPB41,EPB41L2,EPB41L5,EPHX1,EPHX2,EPPK1,EPS15L1,EPS8L2,ERBIN,ERC1,ERGIC1,ERGIC2,ERGIC3,ERH,ERLIN1,ERMP1,ERP29,ERP44,ESD,ESYT1,ESYT2,ETFDH,ETNK1,ETNPPL,EVA1A,EXOC1,EXOC5,EXOC7,EXOSC9,EZR,F11,F13A1,FAAH,FABP2,FABP4,FABP5,FABP7,FADS6,FAF1,FAHD2B,FAM114A2,FAM126A,FAM126B,FAM210A,FAM234A,FAM3C,FAM50B,FAM98C,FARP1,FARS2,FASN,FAU,FBL,FBP1,FBXO3,FCGR2B,FCGRT,FCHO2,FDX2,FECH,FEN1,FERMT2,FETUB,FGA,FGB,FGG,FGL1,FHIT,FIS1,FITM2,FKBP11,FKBP15,FKBP3,FKBP4,FKBP5,FLII,FLNA,FLOT1,FLOT2,FMO1,FMO3,FMO4,FMO5,FMR1,FN1,FN3K,FN3KRP,FNDC3A,FNTA,FRAS1,FRG1,FSCN1,FTCD,FTO,FTSJ3,FUBP1,FUBP3,FXN,FXR1,FXYD1,G0S2,G6PC,G6PD,GAA,GABPA,GADD45GIP1,GALK1,GALK2,GALM,GALNS,GALNT2,GALT,GAMT,GANAB,GAPDH,GAPVD1,GART,GATAD2A,GATD1,GATM,GBA,GBE1,GBF1,GBP6,GCAT,GCC1,GCDH,GCH1,GCK,GCKR,GCLM,GCN1,GDA,GFM1,GFPT1,GGA1,GGCT,GID8,GIMAP4,GJB2,GLDC,GLG1,GLMP,GLOD4,GLRX3,GLRX5,GLT1D1,GLTPD2,GLUD1,GLUL,GLYAT,GLYR1,Gm12854/S100a11,Gm21596/Hmgb1,GMPPA,GMPPB,GMPR2,GMPS,GNA11,GNA13,GNAI2,GNAI3,GNAQ,GNAS,GNE,GNG12,GNL3,GNMT,GNPAT,GNPDA1,GNS,GOLGA2,GOLGA5,GOLGA7,GOLPH3,GOLPH3L,GOPC,GORASP2,GOSR1,GOSR2,GOT1,GPAM,GPAT3,GPAT4,GPD1,GPD1L,GPHN,GPLD1,GPR182,GPRIN3,GPT,GPT2,GPX3,GRB7,GRHP

	R,GRIPAP1,GRN,GSPT1,GSR,Gsta4,GSTA5,GSTK1,GSTM1,GSTM2,GSTM4,GSTM5,GSTP1,GSTT2/GSTT2B,GSTZ1,GTF2F1,GTF2F2,GTF2I,GTPBP4,GUCY1B1,H3-3A/H3-3B,H6PD,HACL1,HADH,HAGH,HAL,HAO1,HAO2,HBS1L,HCCS,HCFC1,HDAC1,HDGF,HDGFL2,HDGFL3,HDLBP,HEATR1,HEBP1,HECTD1,HELZ2,HERPUD1,HEXB,HEXIM1,HGD,HGS,HIBADH,HIBCH,HINT2,HINT3,HIP1,HK1,HLA-A,HLA-DQA1,HMGA1,HMGCL,HMGCS1,HMGCS2,HMGN1,HMOX1,HMOX2,HNF1A,HNF4A,HNMT,HNRNPA2B1,HNRNPAB,HNRNPC,HNRNPD,HNRNPF,HNRNPH1,HNRNPH2,HNRNPK,HNRNPL,HNRNPLL,HNRNPM,HNRNPR,HNRNPU,HNRNPUL1,HNRNPUL2,HOMER2,HOPX,HP,HP1BP3,HPD,HPGD,HPN,HPX,HRAS,Hrg,HS1BP3,HSCB,HSD11B1,HSD17B10,HSD17B11,HSD17B2,HSD17B4,HSD17B6,HSDL1,HSP90AA1,HSP90AB1,HSP90B1,HSPA12B,HSPA13,HSPA1A/HSPA1B,HSPA4L,HSPA5,HSPA8,HSPA9,HSPB1,HSPD1,HSPG2,HSPH1,HTATIP2,HUWE1,HYKK,HYOU1,HYPK,ICAM1,IDH2,IDH3B,IDO2,IFI16,IFIT1B,IFIT3,IFNAR2,IGF2R,IGFALS,IGKC,IK,IL6ST,ILF2,ILF3,ILK,ILKAP,IMMP2L,IMMT,IMPA1,IMPAD1,INHBC,INMT,INPP1,INPP5F,INSIG2,INSR,INTS3,IP6K1,IPO5,IQGAP1,ISCA2,ISOC1,ISOC2,IST1,ITGA1,ITGA2B,ITGA5,ITGA9,ITGAV,ITGB1,ITGB3,ITGB6,ITIH2,ITIH4,ITPR2,ITSN1,IYD,JCHAIN,JPT2,JUP,KANK2,KCTD12,KDELR1,KDSR,KHDRBS1,KHK,KHSRP,KIF13B,KIF21A,KLHDC7A,KLKB1,KPNA1,KPNA2,KRAS,KXD1,KYAT1,KYAT3,KYNU,L2HGDH,L3HYPDH,LAMTOR1,LAP3,LARP1,LARP4,LARP4B,LARP7,LARS2,LASP1,LBR,LCAT,LDAH,LDLR,LGALS1,LGALS3,LGALS3BP,LGALS8,LGALSL,LGMN,LHPP,LIAS,LIFR,LIMS2,LIN7A,LIN7C,LIPE,LITAF,LMAN1,LMAN2,LMAN2L,LMF1,LMNA,LMNB1,LMNB2,LMO7,LOC102724788/PRODH,LONP2,LPCAT3,LRG1,LRP1,LRPAP1,LRRFIP1,LSG1,LSM12,LSM14A,LSM14B,LSM5,LSR,LUC7L,LUC7L2,LUC7L3,LUM,LYAR,LYN,LYPLA1,LYPLA2,LYPLAL1,LYVE1,LYZ,LZIC,M6PR,MACO1,MACROD1,MAGIX,MAN1A2,MAN2B1,MAN2B2,MAN2C1,MANBA,MAOA,MAOB,MAP2K1,MAP2K3,MAP4,MAPK1IP1L,MAPRE1,MAPRE3,MASP2,MAT1A,MAT2A,MATR3,MBNL1,MBOAT7,MCAM,MCCC1,MCCC2,MCEE,MCFD2,MCTS1,MDH1,ME1,MEAF6,MECP2,METAP2,METTL26,METTL27,METTL7B,METTL9,MFAP1,MFN2,MGAT2,MGLL,MGST1,MIA3,MIEN1,MIF,MIF4GD,MIGA2,MIOS,MIPEP,MKNK1,MMAB,MME,MMUT,MOB1B,MOCS2,MOGS,MORF4L1,MOSPD2,MOV10,MPC1,MPC2,MPHOSPH10,MPI,MPP1,MPP6,MPRIP,MPST,MRC1,MRI1,MROH1,MRPL12,MRPL15,MRPL17,MRPL24,MRPL47,MRPL50,MRPL51,MRPS12,MRPS15,MRPS17,MRPS25,MRPS31,MRPS35,MRRF,MSH2,MSN,MSR1,MSRA,MSRB2,Mt1,Mt2,MTA2,MTAP,MTCH2,MTDH,MTFR1,MTFR1L,MTHFD1,MTHFS,MTMR6,MTOR,MTREX,MTSS1,MTX2,MUL1,MVK,MVP,MYBBP1A,MYCBP,MYEF2,MYH10,MYH11,MYH14,MYH9,MYL1,MYL12A,MYL6,MYLK,MYLPF,MYO18A,MYO1B,MYO1C,MYO1D,NAA15,NAA16,NAA25,NAA35,NAALAD2,NACA,NADK2,NAGA,NAGLU,NAMPT,NANP,NANS,NAP1L1,NAPRT,NARS1,NASP,NAT10,NAXD,NAXE,NCBP1,NCEH1,NCK1,NCL,NCOA5,NCSTN,NDRG1,NDST1,NDUFA10,NDUFA11,NDUFA13,NDUFA3,NDUFAF2,NDUFAF3,NDUFAF7,NDUFB6,NDUFB7,NDUFB8,NECAP1,NECTIN2,NELFA,NELFB,NELFCD,NFIA,NFIB,NFIC,NFS1,NFU1,NFXL1,NGEF,NGLY1,Ngp,NHLRC2,NHP2,NIBAN1,NID2,NIPSNAP2,NIT1,NLN,NLRX1,NME3,NMNAT1,NMRAL1,NMRK1,NMT2,NNMT,NOC2L,NOL6,NONO,NOP16,NOP56,NOP58,NOS3,NOSTRIN,NPC1,NQO1,NR1H4,NR3C1,NRAS,NSF,NSFL1C,NSUN2,NUBPL,NUCB1,NUCB2,NUCKS1,NUDC,NUDCD3,NUDT12,NUDT13,NUDT14,NUDT16,NUDT19,NUDT21,NUDT3,NUDT4,NUDT7,NUFIP2,NUMA1,NUP153,NUP155,NUP160,NUP205,NUP210,NUP214,NUP35,NUP54,NUP93,NUP98,NUTF2,OAT,OCIAD2,OGA,OGFOD3,OGFR,OGT,OLA1,OPLAH,OPTN,ORMDL2,OS9,OSBPL9,OTOL1,OXCT1,OXR1,OXSM,PA2G4,PABPC1,PABPC4,PABPN1,PAFAH1B1,PAFAH1B2,PAFAH2,PAIP1,PAIP2,PAK2,PALD1,PALLD,PALMD,PAM16,PANK1,PAPSS1,PAPSS2,PARP1,PARP14,PARP9,PARS2,PARVA,PARVB,PAWR,PBDC1,PBLD,PC,PCBP1,PCCA,PCCB,PCDH1,PCDHB16,PCK1,PCNP,PCTP,PCYT1A,PDAP1,PDCD10,PDCD11,PDCD4,PDCD6IP,PDE2A,PDHA1,PDHB,PDIA3,PDIA4,PDIA5,PDIA6,PDK1,PDK2,PDLIM1,PDLIM5,PDLIM7,PDP2,PDXDC1,PDXK,PDZK1,PEBP1,PECAM1,PECR,PEX1,PEX11A,PEX11G,PEX12,PEX13,PEX14,PEX16,PEX19,PEX26,PEX3,PEX5,PEX6,PFAS,PFDN2,PFKFB1,PFKFB3,PGAM1,PGD,PGK1,PGM1,PGM3,PGM5,PGRMC1,PGRMC2,PHACTR4,PHB2,PHF20L1,PHKA1,PHKA2,PHKB,PHKG2,PHLDA1,PHLDB2,PHYHD1,PHYKPL,PI4KA,PICALM,PIGR,PIGS,PIGU,PIK3AP1,PIK3CB,PIN4,PIP5K1C,PIR,PITHD1,PITRM1,PKLR,PKN1,PKP4,PLA2G12B,PLBD1,PLBD2,PLCB3,PLCH1,PLEKHA5,PLEKHA7,PLEKHF1,PLG,PLIN5,PLOD3,PLPP3,PLRG1,PLS3,PLTP,PLVAP,PLXNA4,PLXNB2,PM20D1,PML,PMM2,PNKP,PNLIP,PNN,POLDIP3,POLR2A,POLR2B,POLR2I,POLR2L,PON1,PON2,PON3,POR,PPA1,PPAN,PPAT,PPCS,PPFIA1,PPFIBP2,PPIA,PPIB,PPIF,PPIG,PPIL1,PPIL4,PPIP5K2,PPL,PPM1A,PPM1B,PPM1G,PPM1K,PPP1R2,PPP1R21,PPP1R7,PPP1R8,PPP2R1B,PPP2R5A,PPP2R5D,PPP4C,PPP4R2,PPP4R3A,PPP6R1,PPP6R3,PPT1,PPT2,PPWD1,PQBP1,PRCP,PRDX3,PRDX5,PRDX6,PREB,PRELP,PREP,PRKAA2,PRKAB1,PRKACA,PRKAG1,PRKCSH,PRKRA,PROC,PROX1,PRPF19,PRPF3,PRPF31,PRPF4,PRPF40A,PRPF6,PRPF8,PRRC1,PRRC2C,PRUNE1,PRXL2A,PRXL2B,PSAP,PSEN1,PSIP1,PSMA1,PSMA2,PSMA3,PSMA4,PSMA5,PSMA6,PSMA7,PSMB1,PSMB10,PSMB2,PSMB5,PSMB6,PSMB7,PSMB9,PSMC3,PSMD14,PSMD3,PSMD4,PSMD7,PSME3,PTBP1,PTBP3,PTGES3,PTK2,PTK2B,PTPMT1,PTPN1,PTPRF,PTPRK,PTRHD1,PTS,PTTG1IP,PUM1,PURA,PXMP2,PXMP4,PXN,PYCARD,PYGB,PYGL,QDPR,QSOX1,QTRT2,RAB14,RAB1A,RAB35,RAB4A,RAB8A,RAB8B,RABGAP1,RABGAP1L,RAC1,RACK1,RAD23B,RAD50,RAE1,RALY,RAN,RANBP1,RANBP10,RANBP3,RANGAP1,RAP1A,RAP1B,RAPGEF4,RARRES2,RASIP1,RBBP4,RBM10,RBM14,RBM15,RBM17,RBM22,RBM28,RBM39,RBM42,RBM47,RBP1,RBPMS,RCC2,RCN1,RDH16,REEP5,REEP6,RELA,RER1,RETREG2,RETSAT,REXO2,RFC2,RGL3,RGN,RGPD4 (includes others),RHOA,RHOC,RHOG,RIDA,RIOX2,RIPK1,RMDN2,RMDN3,RMND5A,RNASEH2A,RNASET2,RNF113A,RNF114,RNF14,RNF17,RNF185,RNF2,RNF20,RNF213,RNF5,RNH1,RNMT,RNPEP,ROCK2,RPAP3,RPE,RPL10,RPL10A,RPL11,RPL12,RPL13,RPL13A,RPL14,RPL15,RPL17,RPL18,RPL18A,RPL19,RPL21,RPL22,RPL23,Rpl23a,RPL24,RPL26,RPL27,RPL28,RPL3,RPL31,RPL35,RPL37,RPL37A,RPL4,RPL5,RPL6,RPL7,RPL7A,RPL8,RPL9,RPLP0,RPLP2,RPN1,RPN2,RPRD1B,RPS10,RPS11,RPS1

	2,RPS13,RPS14,RPS15,RPS15A,RPS16,RPS19,RPS2,RPS20,RPS24,RPS25,RPS26,RPS27A,RPS27L,RPS29,RPS3,RPS4Y1,RPS5,RPS6,RPS6KB2,RPS7,RPS8,RPSA,RPTOR,RRAS,RRS1,RSL1D1,RTF2,RTN1,RTN4,RTN4IP1,RUFY1,RUFY3,RUVBL1,RUVBL2,S100A1,S100A6,SAA1,SAE1,SAFB,SAMHD1,SAP18,SAR1B,SARDH,SARNP,SARS2,SART1,SART3,SAT2,SAYSD1,SBF1,SC5D,SCAMP1,SCAMP3,SCAMP4,SCAMP5,SCARB1,SCARB2,SCD,SCFD1,SCO1,SCPEP1,SCRIB,SCYL2,SCYL3,SDC4,SDF2L1,SDHD,SDR42E1,SDS,SDSL,SEC11A,SEC14L2,SEC14L4,SEC23B,SEC23IP,SEC24A,SEC24D,SEC31A,SEC61A1,SEC61B,SEC61G,SEC62,SEC63,SELENBP1,SELENOF,SELENOP,SEPHS1,SERBP1,SERHL2,SERINC3,SERPINA1,SERPINA10,SERPINA3,SERPINA6,SERPINB1,SERPIND1,SERPINF2,SERPING1,SERPINH1,SET,Sf1,SF3A1,SF3A3,SF3B1,SF3B2,SF3B3,SF3B4,SF3B6,SFPQ,SFR1,SFT2D2,SFXN5,SGTA,SH3BGRL3,SH3GL1,SHMT1,SHOC2,SHPK,SHTN1,SIAE,SIGLEC1,SIGMAR1,SIL1,SLC12A9,SLC16A7,SLC17A3,SLC22A1,SLC22A18,SLC22A23,SLC22A25,SLC25A10,SLC25A11,SLC25A12,SLC25A13,SLC25A20,SLC25A21,SLC25A23,SLC25A25,SLC25A3,SLC25A45,SLC25A5,SLC26A1,SLC27A4,SLC2A2,SLC30A5,SLC31A1,SLC35A1,SLC35A3,SLC35B1,SLC35D1,SLC38A10,SLC39A11,SLC39A14,SLC39A4,SLC44A2,SLC4A4,SLC6A12,SLC6A13,SLC7A2,SLC9A3R1,SLC9A3R2,SLCO1B3,SLCO2A1,SLK,SLMAP,SLTM,SMAP1,SMAP2,SMARCA2,SMARCA5,SMARCD2,SMARCE1,SMC1A,SMC3,SMIM15,SMOC1,SMPD1,SMS,SMU1,SNAP23,SNAP47,SND1,SNF8,SNRNP200,SNRNP70,SNRPA1,SNRPB2,SNRPD3,SNRPF,SNRPN,SNTA1,SNTB1,SNU13,SNW1,SNX1,SNX18,SNX2,SNX3,SNX4,SNX5,SNX6,SNX7,SOAT2,SON,SORBS1,SORBS2,SORD,SOS1,SPAG9,SPAST,SPCS1,SPCS2,SPG7,SPPL2A,SPR,SPTAN1,SPTBN2,SQOR,SRA1,SREK1,SRI,SRP19,SRP68,SRP72,SRP9,SRPK2,SRPRB,SRR,SRRT,SRSF1,SRSF10,SRSF2,SRSF3,SRSF4,SRSF6,SRSF7,SSBP1,SSR1,SSR3,SSR4,SSRP1,ST13,STAB1,STAB2,STAG2,STARD5,STAT2,STAT3,STAT6,STBD1,STEAP3,STEAP4,STIP1,STK38,STK38L,STOML2,STRAP,STRN,STT3A,STT3B,SUB1,SUCLG1,SUCLG2,SUGCT,SUGT1,SULT1B1,SULT1C2,SULT1E1,SULT2A1,SUMO2,SUN2,SUOX,SUPT16H,SURF1,SURF4,SVIL,SWAP70,SYAP1,SYMPK,SYNCRIP,SYNGR2,SYNJ2BP,TACO1,TADA3,TAGLN,TAGLN2,TALDO1,TAMM41,TANGO2,TAOK3,TAP1,TAP2,TAPBP,TARDBP,TAT,TBC1D13,TBC1D15,TBC1D17,TBC1D24,TBC1D8B,TBC1D9B,TBCD,TBCEL,TBL2,TBRG4,TCEA1,TCERG1,TCIRG1,TCOF1,TDO2,TFR2,TGFBRAP1,TGM1,THNSL2,THOC2,THRAP3,THRSP,THYN1,TIAL1,TIGAR,TIMM17B,TIMM22,TIMM44,TIMMDC1,TINAGL1,TJP1,TJP2,TJP3,TKFC,TKT,TLN1,TM9SF1,TM9SF2,TM9SF3,TMED1,TMED10,TMED2,TMED3,TMED4,TMED5,TMED7,TMED9,TMEM109,TMEM126A,TMEM126B,TMEM135,TMEM176B,TMEM19,TMEM214,TMEM230,TMEM256,TMEM30A,TMEM33,TMEM38B,TMEM43,TMEM82,TMLHE,TMOD3,TMPO,TMTC3,TMX1,TMX3,TNKS1BP1,TNPO1,TNPO2,TNPO3,TNS2,TNS3,TOLLIP,TOM1,TOMM40,TOP1,TOP2B,TOP3B,TOR1A,TOR1AIP1,TPD52,TPD52L2,TPI1,TPK1,TPM3,TPPP,TPR,TPRG1L,TRA2B,TRABD,TRAM1,TRAP1,TRAPPC1,TRAPPC4,TRIM14,TRIM23,TRIM28,TRIP10,TRIP11,TRIR,TRMU,TSC22D1,TSFM,TSG101,TSPAN14,TSPAN31,TSTA3,TTC1,TTC36,TTC37,TTC38,TTC39A,TTC39C,TTC7A,TTN,TTPA,TUBA4A,TUBB,TUBB2A,TUBB4B,TUT7,TWF1,TXLNA,TXLNG,TXN2,TXNDC5,TXNDC9,TXNL1,TYMP,TYSND1,U2AF2,U2SURP,UBA1,UBA2,UBA3,UBA7,UBAC1,UBAP2,UBE2G2,UBE2I,UBE2J1,UBE2M,UBE2V2,UBE2Z,UBE4B,UBL4A,UBL7,UBQLN2,UBR2,UBTF,UCHL5,UCK1,UFL1,UGDH,UGGT1,UGP2,UGT1A4,UGT1A6,UGT1A8 (includes others),UGT2B10,UGT2B17,UGT2B28,UGT3A1,UPB1,UPF1,UPF2,UPP1,UQCC1,UQCC3,UQCRC2,UROC1,USO1,USP16,USP19,USP24,USP46,USP7,VAC14,VAMP2,VAMP3,VAMP8,VAPB,VAT1,VAV2,VCAM1,VCL,VCPIP1,VDAC2,VIM,VKORC1L1,VMO1,VNN1,VPS13D,VPS25,VPS26A,VPS26B,VPS26C,VPS28,VPS33B,VPS35,VPS45,VPS51,VPS52,VRK1,VSIG4,VTA1,VTN,VWA8,WAPL,WASF2,WASHC3,WASHC4,WASHC5,WBP11,WBP2,WDFY1,WDR1,WDR18,WDR26,WDR36,WDR46,WDR5,WDR61,WDR77,WFS1,WRNIP1,XAF1,XPNPEP1,XPO1,XPO5,XRCC6,XRN1,XRN2,YBX1,YBX3,YME1L1,YTHDF2,YTHDF3,YWHAQ,YWHAZ,ZBTB20,ZBTB8OS,ZC3H11A,ZC3H14,ZC3HAV1,ZFR,ZHX1,ZHX2,ZHX3,ZMAT2,ZMIZ1,ZNF326,ZNF638

1. Cancer,Organismal Injury and Abnormalities 2. Tumorigenesis of tissue 3. 1.87E-82 4. Increased 5. 2.061 6. 2260	A1CF,AACS,AADAT,AAK1,AAMDC,AASDHPPT,AASS,ABAT,ABCB10,ABCB4,ABCB6,ABCB8,ABCB9,ABCC2,ABCC3,ABCC6,ABCD1,ABCD2,ABCD3,ABCE1,ABCF2,ABCF3,ABCG5,ABHD11,ABHD14B,ABHD15,ABITRAM,ACAA1,ACACB,ACAD10,ACAD11,ACAD9,ACADL,ACADM,ACADSB,ACAT1,ACAT2,ACBD5,ACIN1,ACLY,ACMSD,ACO1,ACO2,ACOT1,ACOT11,ACOT12,ACOT13,ACOT2,ACOT4,ACOT7,ACOT8,ACOX1,ACOX3,ACP2,ACSF3,ACSL4,ACSL5,ACSM1,ACSS2,ACSS3,ACTB,ACTG1,ACTN1,ACTN4,ACTR2,ACTR3,ACY1,ACY3,ACYP2,ADAM10,ADAP2,ADD1,ADD2,ADD3,ADHFE1,ADI1,ADIPOR2,ADK,ADSL,AFDN,AFMID,AGFG1,AGFG2,AGK,AGL,AGMAT,AGO1,AGO2,AGPAT2,AGPAT3,AGPAT5,AGRN,AGXT,AGXT2,AHCY,AHCYL2,AHNAK,AHSA1,AHSG,AIF1,AIP,AK2,AK3,AKR1A1,AKR1B10,AKR1C4,AKR1D1,AKT1,ALAS1,ALCAM,ALDH16A1,ALDH1A1,ALDH1B1,ALDH1L1,ALDH3A2,ALDH4A1,ALDH5A1,ALDH6A1,ALDH7A1,ALDH9A1,ALDOA,ALDOB,ALPK1,AMACR,AMBP,AMDHD2,AMPD2,AMT,AMY2A,ANGPTL3,ANGPTL4,ANKHD1/ANKHD1- EIF4EBP3,ANO10,ANPEP,ANXA1,ANXA11,ANXA3,ANXA4,ANXA5,AOX1,AP2A1,AP2M1,AP3B1,APCS,APEX1,API5,APMAP,APOA1,APOA2,APOB,APOC4,APOD,APOE,AQP1,AQP4,AQP9,ARAF,ARCN1,ARF4,ARF6,ARFGAP1,ARFGAP2,ARFGAP3,ARGLU1,ARHGAP17,ARHGAP31,ARHGAP42,ARHGAP45,ARHGAP5,ARHGDIA,ARHGDIB,ARHGEF12,ARHGEF7,ARIH1,ARMC10,ARPC1A,ARPC1B,ARPC2,ARPC5,ARPC5L,ARRB1,ARSB,AS3MT,ASAH1,ASCC1,ASCC2,ASGR1,ASGR2,ASL,ASPA,ASPDH,ASPG,ASPH,ASPSCR1,ASRGL1,ASS1,ATAD2B,ATG3,ATG4B,ATL3,ATP11C,ATP13A1,ATP1A1,ATP1B1,ATP1B3,ATP2A2,ATP2B1,ATP2B4,ATP5IF1,ATP5PO,ATP6AP1,ATP6AP2,ATP6V0D1,ATP6V1A,ATP6V1C1,ATP6V1E1,ATRX,ATXN10,ATXN2,AUP1,AVEN,B2M,B4GALNT1,BAAT,BABAM2,BAG3,BAG4,BAG5,BAIAP2,BASP1,BBOX1,BCAM,BCAP29,BCAS2,BCHE,BCKDHA,BCKDHB,BCKDK,BCL2L13,BCLAF1,BCO2,BCS1L,BET1L,BGN,BHMT,BHMT2,BID,BIN1,BIN2,BLMH,BLVRA,BLVRB,BMP2K,BNIP3,BPHL,BRAF,BSG,BTAF1,BTD,BUB3,BZW1,C11orf54,C12orf10,C12orf43,C1D,C1orf174,C1QA,C1QB,C2CD2,C4A/C4B,C6,C8A,C8B,C8G,C9,C9orf64,CACFD1,CACYBP,CAD,CADM1,CALCRL,CALR,CALU,CAMK1,CAND1,CANX,CAP1,CAPZA1,CAPZB,CASK,CASP3,CASP7,CAT,CAVIN1,CBR1,CBWD1,CBX1,CBX3,CCAR1,CCDC134,CCDC167,CCDC22,CCDC25,CCDC40,CCDC47,CCDC51,CCDC58,CCDC9,CCDC93,CCS,CCT3,CD163,CD1D,CD2AP,CD302,CD36,CD38,CD47,CD68,CD81,CD82,CDA,CDC34,CDC37,CDC5L,CDC73,CDK11A,CDK12,CDK5,CDK5RAP3,CDK6,CDK9,CDKN1B,CDKN2C,CDO1,CDV3,CENPV,CEP290,CEP89,CES1,CES3,CFAP20,CFB,CFDP1,CFH,CFI,CGN,CHAC2,CHCHD4,CHD4,CHID1,CHMP2A,CHORDC1,CHPT1,CIAO3,CIDEB,CISD1,CISD2,CKAP4,CKB,CKM,CLCC1,CLDN12,CLDN3,CLEC10A,CLEC3B,CLEC4F,CLEC4G,CLIC1,CLIC4,CLIC5,CLINT1,CLPP,CLPTM1,CLTB,CLU,CLYBL,CMAS,CMBL,CMC2,CMPK1,CMPK2,CMTM4,CNBP,CNDP2,CNOT1,CNOT2,CNOT3,CNOT9,CNP,CNPY2,COA7,COASY,COBLL1,COG3,COG5,COL18A1,COLGALT1,COMT,COMTD1,COPA,COPB1,COPB2,COPE,COPG1,COQ3,COQ4,COQ8A,COQ8B,COQ9,CORO1A,CORO1B,CORO1C,COTL1,COX15,COX19,COX5A,COX6B1,COX7A2,CP,CPB2,CPN1,CPNE3,CPOX,CPQ,CPS1,CPSF2,CPT2,CR1L,CRAT,CREB1,CRELD1,CRELD2,CRIP1,CRK,CRKL,CRNKL1,CRP,CRYL1,CRYM,CRYZ,CSAD,CSK,CSNK1E,CSNK2A1,CSNK2A2,CSNK2B,CSRP1,CSRP2,CSTF1,CSTF2,CSTF3,CTBP1,CTBS,CTDSP1,CTH,CTNNA1,CTNNB1,CTNNBL1,CTNND1,CTR9,CTSB,CTSC,CTSD,CTSF,CTSH,CTSO,CTSS,CTSV,CTSZ,CTTN,CUL1,CUL2,CUL3,CUTC,CXADR,CYB5A,CYB5B,CYB5R1,CYBC1,CYGB,CYP17A1,CYP1A2,CYP27A1,CYP2A6 (includes others),Cyp2b13/Cyp2b9,CYP2B6,Cyp2c54 (includes others),Cyp2c70,CYP2C8,CYP2F1,CYP2U1,CYP3A5,CYP3A7,CYP4A11,CYP4A22,CYP4B1,CYP4F3,CYP7A1,CYP7B1,DAAM1,DAD1,DAPK1,DARS2,DBNL,DCAF11,DCAKD,DCPS,DCTN2,DCTN4,DCTN6,DCUN1D1,DCUN1D2,DCXR,DDAH1,DDAH2,DDC,DDHD2,DDI2,DDOST,DDRGK1,DDX17,DDX18,DDX19A,DDX21,DDX23,DDX27,DDX39B,DDX3X,DDX3Y,DDX42,DDX46,DDX49,DDX5,DDX58,DDX6,DECR1,DECR2,DEK,DEPTOR,DES,DGAT2,DGLUCY,DHCR24,DHDH,DHFR,DHODH,DHRS7,DHRS7B,DHTKD1,DHX15,DHX16,DHX9,DIABLO,DIO1,DIS3,DKC1,DLAT,DMAC1,DMD,DMGDH,DNAJA1,DNAJB1,DNAJB11,DNAJB4,DNAJB6,DNAJB9,DNAJC1,DNAJC13,DNAJC19,DNAJC2,DNAJC25,DNAJC3,DNAJC7,DNM1L,DNM2,DNPEP,DNTTIP2,DOCK6,DPAGT1,DPM1,DPM3,DPP4,DPP7,DPP9,DPY19L1,DPY30,DPYD,DPYS,DPYSL2,DRG1,DSP,DTD1,DTX3L,DUSP23,DUT,DYNLL1,DYNLT3,DYSF,EBPL,ECHDC2,ECHDC3,ECI1,ECI2,ECM1,EDC4,EEA1,EEF1A1,EEF1D,EEF2,EFHD2,EFR3A,EFTUD2,EGF,EGFR,EHD1,EHD3,EHHADH,EIF1AX,EIF2A,EIF2AK2,EIF2B1,EIF2B2,EIF2B3,EIF2S1,EIF2S2,EIF3A,EIF3C,EIF3D,EIF3E,EIF3F,EIF3H,EIF3I,EIF3L,EIF3M,EIF4A1,EIF4A2,EIF4A3,EIF4E,EIF4G1,EIF4G2,EIF4H,EIF5,EIF5A,EIF5B,ELAC2,ELAVL1,ELMO1,ELOA,ELOC,ELOVL1,ELOVL2,ELOVL5,ELP2,EMC8,EMD,EMILIN1,EML3,EML4,ENO1,ENPEP,ENPP1,ENTPD5,EPB41,EPB41L2,EPB41L5,EPHX1,EPHX2,EPPK1,EPS15L1,EPS8L2,ERBIN,ERC1,ERGIC1,ERGIC2,ERGIC3,ERH,ERLIN1,ERMP1,ERP29,ERP44,ESD,ESYT1,ESYT2,ETFDH,ETNK1,ETNPPL,EVA1A,EXOC1,EXOC5,EXOC7,EXOSC9,EZR,F11,F13A1,FAAH,FABP2,FABP4,FABP5,FABP7,FADS6,FAF1,FAHD2B,FAM114A2,FAM126A,FAM126B,FAM210A,FAM234A,FAM3C,FAM50B,FAM98C,FARP1,FARS2,FASN,FAU,FBL,FBP1,FBXO3,FCGR2B,FCGRT,FCHO2,FDX2,FECH,FEN1,FERMT2,FETUB,FGA,FGB,FGG,FGL1,FHIT,FIS1,FITM2,FKBP11,FKBP15,FKBP3,FKBP4,FKBP5,FLII,FLNA,FLOT1,FLOT2,FMO1,FMO3,FMO4,FMO5,FMR1,FN1,FN3K,FN3KRP,FNDC3A,FNTA,FRAS1,FRG1,FSCN1,FTCD,FTO,FTSJ3,FUBP1,FUBP3,FXN,FXR1,FXYD1,G0S2,G6PC,G6PD,GAA,GABPA,GADD45GIP1,GALK1,GALK2,GALM,GALNS,GALNT2,GALT,GAMT,GANAB,GAPDH,GAPVD1,GART,GATAD2A,GATD1,GATM,GBA,GBE1,GBF1,GBP6,GCAT,GCC1,GCDH,GCH1,GCK,GCKR,GCLM,GCN1,GDA,GFM1,GFPT1,GGA1,GGCT,GID8,GIMAP4,GJB2,GLDC,GLG1,GLMP,GLOD4,GLRX3,GLRX5,GLT1D1,GLTPD2,GLUD1,GLUL,GLYAT,GLYR1,Gm12854/S100a11,Gm21596/Hmgb1,GMPPA,GMPPB,GMPR2,GMPS,GNA11,GNA13,GNAI2,GNAI3,GNAQ,GNAS,GNE,GNG12,GNL3,GNMT,GNPAT,GNPDA1,GNS,GOLGA2,GOLGA5,GOLGA7,GOLPH3,GOLPH3L,GOPC,GORASP2,GOSR1,GOSR2,GOT1,GPAM,GPAT3,GPAT4,GPD1,GPD1L,GPHN,GPLD1,GPR182,GPRIN3,GPT,GPT2,GPX3,GRB7,GRH

	PR,GRIPAP1,GRN,GSPT1,GSR,Gsta4,GSTA5,GSTK1,GSTM1,GSTM2,GSTM4,GSTM5,GSTP1,GSTT2/GSTT2B,GSTZ1,GTF2F1,GTF2F2,GTF2I,GTPBP4,GUCY1B1,H3-3A/H3-3B,H6PD,HACL1,HADH,HAGH,HAL,HAO1,HAO2,HBS1L,HCCS,HCFC1,HDAC1,HDGF,HDGFL2,HDGFL3,HDLBP,HEATR1,HEBP1,HECTD1,HELZ2,HERPUD1,HEXB,HEXIM1,HGD,HGS,HIBADH,HIBCH,HINT2,HINT3,HIP1,HK1,HLA-A,HLA-DQA1,HMGA1,HMGCL,HMGCS1,HMGCS2,HMGN1,HMOX1,HMOX2,HNF1A,HNF4A,HNMT,HNRNPA2B1,HNRNPAB,HNRNPC,HNRNPD,HNRNPF,HNRNPH1,HNRNPH2,HNRNPK,HNRNPL,HNRNPLL,HNRNPM,HNRNPR,HNRNPU,HNRNPUL1,HNRNPUL2,HOMER2,HOPX,HP,HP1BP3,HPD,HPGD,HPN,HPX,HRAS,Hrg,HS1BP3,HSCB,HSD11B1,HSD17B10,HSD17B11,HSD17B2,HSD17B4,HSD17B6,HSDL1,HSP90AA1,HSP90AB1,HSP90B1,HSPA12B,HSPA13,HSPA1A/HSPA1B,HSPA4L,HSPA5,HSPA8,HSPA9,HSPB1,HSPD1,HSPG2,HSPH1,HTATIP2,HUWE1,HYKK,HYOU1,HYPK,ICAM1,IDH2,IDH3B,IDO2,IFI16,IFIT1B,IFIT3,IFNAR2,IGF2R,IGFALS,IK,IL6ST,ILF2,ILF3,ILK,ILKAP,IMMP2L,IMMT,IMPA1,IMPAD1,INHBC,INMT,INPP1,INPP5F,INSIG2,INSR,INTS3,IP6K1,IPO5,IQGAP1,ISCA2,ISOC1,ISOC2,IST1,ITGA1,ITGA2B,ITGA5,ITGA9,ITGAV,ITGB1,ITGB3,ITGB6,ITIH2,ITIH4,ITPR2,ITSN1,IYD,JCHAIN,JPT2,JUP,KANK2,KCTD12,KDELR1,KDSR,KHDRBS1,KHK,KHSRP,KIF13B,KIF21A,KLHDC7A,KLKB1,KPNA1,KPNA2,KRAS,KXD1,KYAT1,KYAT3,KYNU,L2HGDH,L3HYPDH,LAMTOR1,LAP3,LARP1,LARP4,LARP4B,LARP7,LARS2,LASP1,LBR,LCAT,LDAH,LDLR,LGALS1,LGALS3,LGALS3BP,LGALS8,LGALSL,LGMN,LHPP,LIAS,LIFR,LIMS2,LIN7A,LIN7C,LIPE,LITAF,LMAN1,LMAN2,LMAN2L,LMF1,LMNA,LMNB1,LMNB2,LMO7,LOC102724788/PRODH,LONP2,LPCAT3,LRG1,LRP1,LRPAP1,LRRFIP1,LSG1,LSM12,LSM14A,LSM14B,LSM5,LSR,LUC7L,LUC7L2,LUC7L3,LUM,LYAR,LYN,LYPLA1,LYPLA2,LYPLAL1,LYVE1,LYZ,LZIC,M6PR,MACO1,MACROD1,MAGIX,MAN1A2,MAN2B1,MAN2B2,MAN2C1,MANBA,MAOA,MAOB,MAP2K1,MAP2K3,MAP4,MAPK1IP1L,MAPRE1,MAPRE3,MASP2,MAT1A,MAT2A,MATR3,MBNL1,MBOAT7,MCAM,MCCC1,MCCC2,MCEE,MCFD2,MCTS1,MDH1,ME1,MEAF6,MECP2,METAP2,METTL26,METTL27,METTL7B,METTL9,MFAP1,MFN2,MGAT2,MGLL,MGST1,MIA3,MIEN1,MIF,MIF4GD,MIGA2,MIOS,MIPEP,MKNK1,MMAB,MME,MMUT,MOB1B,MOCS2,MOGS,MORF4L1,MOSPD2,MOV10,MPC1,MPC2,MPHOSPH10,MPI,MPP1,MPP6,MPRIP,MPST,MRC1,MRI1,MROH1,MRPL12,MRPL15,MRPL17,MRPL24,MRPL47,MRPL50,MRPL51,MRPS12,MRPS15,MRPS17,MRPS25,MRPS31,MRPS35,MRRF,MSH2,MSN,MSR1,MSRA,MSRB2,Mt1,Mt2,MTA2,MTAP,MTCH2,MTDH,MTFR1,MTFR1L,MTHFD1,MTHFS,MTMR6,MTOR,MTREX,MTSS1,MTX2,MUL1,MVK,MVP,MYBBP1A,MYCBP,MYEF2,MYH10,MYH11,MYH14,MYH9,MYL1,MYL12A,MYL6,MYLK,MYLPF,MYO18A,MYO1B,MYO1C,MYO1D,NAA15,NAA16,NAA25,NAA35,NAALAD2,NACA,NADK2,NAGA,NAGLU,NAMPT,NANP,NANS,NAP1L1,NAPRT,NASP,NAT10,NAXD,NAXE,NCBP1,NCEH1,NCK1,NCL,NCOA5,NCSTN,NDRG1,NDST1,NDUFA10,NDUFA11,NDUFA13,NDUFA3,NDUFAF2,NDUFAF3,NDUFAF7,NDUFB6,NDUFB7,NDUFB8,NECAP1,NECTIN2,NELFA,NELFB,NELFCD,NFIA,NFIB,NFIC,NFS1,NFU1,NFXL1,NGEF,NGLY1,Ngp,NHLRC2,NHP2,NIBAN1,NID2,NIPSNAP2,NIT1,NLN,NLRX1,NME3,NMNAT1,NMRAL1,NMRK1,NMT2,NNMT,NOC2L,NOL6,NONO,NOP16,NOP56,NOP58,NOS3,NOSTRIN,NPC1,NQO1,NR1H4,NR3C1,NRAS,NSF,NSFL1C,NSUN2,NUBPL,NUCB1,NUCB2,NUCKS1,NUDC,NUDCD3,NUDT12,NUDT13,NUDT14,NUDT16,NUDT19,NUDT21,NUDT3,NUDT4,NUDT7,NUFIP2,NUMA1,NUP153,NUP155,NUP160,NUP205,NUP210,NUP214,NUP35,NUP54,NUP93,NUP98,NUTF2,OAT,OCIAD2,OGA,OGFOD3,OGFR,OGT,OLA1,OPLAH,OPTN,ORMDL2,OS9,OSBPL9,OTOL1,OXCT1,OXR1,OXSM,PA2G4,PABPC1,PABPC4,PABPN1,PAFAH1B1,PAFAH1B2,PAFAH2,PAIP1,PAIP2,PAK2,PALD1,PALLD,PALMD,PAM16,PANK1,PAPSS1,PAPSS2,PARP1,PARP14,PARP9,PARS2,PARVA,PARVB,PAWR,PBDC1,PBLD,PC,PCBP1,PCCA,PCCB,PCDH1,PCDHB16,PCK1,PCNP,PCTP,PCYT1A,PDAP1,PDCD10,PDCD11,PDCD4,PDCD6IP,PDE2A,PDHA1,PDHB,PDIA3,PDIA4,PDIA5,PDIA6,PDK1,PDK2,PDLIM1,PDLIM5,PDLIM7,PDP2,PDXDC1,PDXK,PDZK1,PEBP1,PECAM1,PECR,PEX1,PEX11A,PEX11G,PEX12,PEX13,PEX14,PEX16,PEX19,PEX26,PEX3,PEX5,PEX6,PFAS,PFDN2,PFKFB1,PFKFB3,PGAM1,PGD,PGK1,PGM1,PGM3,PGM5,PGRMC1,PGRMC2,PHACTR4,PHB2,PHF20L1,PHKA1,PHKA2,PHKB,PHKG2,PHLDA1,PHLDB2,PHYHD1,PHYKPL,PI4KA,PICALM,PIGR,PIGS,PIGU,PIK3AP1,PIK3CB,PIN4,PIP5K1C,PIR,PITHD1,PITRM1,PKLR,PKN1,PKP4,PLA2G12B,PLBD1,PLBD2,PLCB3,PLCH1,PLEKHA5,PLEKHA7,PLEKHF1,PLG,PLIN5,PLOD3,PLPP3,PLRG1,PLTP,PLVAP,PLXNA4,PLXNB2,PM20D1,PML,PMM2,PNKP,PNLIP,PNN,POLDIP3,POLR2A,POLR2B,POLR2I,POLR2L,PON1,PON2,PON3,POR,PPA1,PPAN,PPAT,PPCS,PPFIA1,PPFIBP2,PPIA,PPIB,PPIF,PPIG,PPIL1,PPIL4,PPIP5K2,PPL,PPM1A,PPM1B,PPM1G,PPM1K,PPP1R2,PPP1R21,PPP1R7,PPP1R8,PPP2R1B,PPP2R5A,PPP2R5D,PPP4C,PPP4R2,PPP4R3A,PPP6R1,PPP6R3,PPT1,PPT2,PPWD1,PQBP1,PRCP,PRDX3,PRDX5,PRDX6,PREB,PRELP,PREP,PRKAA2,PRKAB1,PRKACA,PRKAG1,PRKCSH,PRKRA,PROC,PROX1,PRPF19,PRPF3,PRPF31,PRPF4,PRPF40A,PRPF6,PRPF8,PRRC1,PRRC2C,PRUNE1,PRXL2A,PRXL2B,PSAP,PSEN1,PSIP1,PSMA1,PSMA2,PSMA3,PSMA4,PSMA5,PSMA6,PSMA7,PSMB1,PSMB10,PSMB2,PSMB5,PSMB6,PSMB7,PSMB9,PSMC3,PSMD14,PSMD3,PSMD4,PSMD7,PSME3,PTBP1,PTBP3,PTGES3,PTK2,PTK2B,PTPMT1,PTPN1,PTPRF,PTPRK,PTRHD1,PTS,PTTG1IP,PUM1,PURA,PXMP2,PXMP4,PXN,PYCARD,PYGB,PYGL,QDPR,QSOX1,QTRT2,RAB14,RAB1A,RAB35,RAB4A,RAB8A,RAB8B,RABGAP1,RABGAP1L,RAC1,RACK1,RAD23B,RAD50,RAE1,RALY,RAN,RANBP1,RANBP10,RANBP3,RANGAP1,RAP1A,RAP1B,RAPGEF4,RARRES2,RASIP1,RBBP4,RBM10,RBM14,RBM15,RBM17,RBM22,RBM28,RBM39,RBM42,RBM47,RBP1,RBPMS,RCC2,RCN1,RDH16,REEP5,REEP6,RELA,RER1,RETREG2,RETSAT,REXO2,RFC2,RGL3,RGN,RGPD4 (includes others),RHOA,RHOC,RHOG,RIDA,RIOX2,RIPK1,RMDN2,RMDN3,RMND5A,RNASEH2A,RNASET2,RNF113A,RNF114,RNF14,RNF17,RNF185,RNF2,RNF20,RNF213,RNF5,RNH1,RNMT,RNPEP,ROCK2,RPAP3,RPE,RPL10,RPL10A,RPL11,RPL12,RPL13,RPL13A,RPL14,RPL15,RPL17,RPL18,RPL18A,RPL19,RPL21,RPL22,RPL23,RPL24,RPL26,RPL27,RPL28,RPL3,RPL31,RPL35,RPL37,RPL37A,RPL4,RPL5,RPL6,RPL7,RPL7A,RPL8,RPL9,RPLP0,RPLP2,RPN1,RPN2,RPRD1B,RPS10,RPS11,RPS12,RPS1

	3,RPS14,RPS15,RPS15A,RPS16,RPS19,RPS2,RPS20,RPS23,RPS24,RPS25,RPS26,RPS27A,RPS27L,RPS29,RPS3,RPS5,RPS6,RPS6KB2,RPS7,RPS8,RPSA,RPTOR,RRAS,RRS1,RSL1D1,RTF2,RTN1,RTN4,RTN4IP1,RUFY1,RUFY3,RUVBL1,RUVBL2,S100A1,S100A6,SAA1,SAE1,SAFB,SAMHD1,SAP18,SAR1B,SARDH,SARNP,SARS2,SART1,SART3,SAT2,SAYSD1,SBF1,SC5D,SCAMP1,SCAMP3,SCAMP4,SCAMP5,SCARB1,SCARB2,SCD,SCFD1,SCO1,SCPEP1,SCRIB,SCYL2,SCYL3,SDC4,SDF2L1,SDHD,SDR42E1,SDS,SDSL,SEC11A,SEC14L2,SEC14L4,SEC23B,SEC23IP,SEC24A,SEC24D,SEC31A,SEC61A1,SEC61B,SEC61G,SEC62,SEC63,SELENBP1,SELENOF,SELENOP,SEPHS1,SERBP1,SERHL2,SERINC3,SERPINA1,SERPINA10,SERPINA3,SERPINA6,SERPINB1,SERPIND1,SERPINF2,SERPING1,SERPINH1,SET,SF3A1,SF3A3,SF3B1,SF3B2,SF3B3,SF3B4,SF3B6,SFPQ,SFR1,SFT2D2,SFXN5,SGTA,SH3BGRL3,SH3GL1,SHMT1,SHOC2,SHPK,SHTN1,SIAE,SIGLEC1,SIGMAR1,SIL1,SLC12A9,SLC16A7,SLC17A3,SLC22A1,SLC22A18,SLC22A23,SLC22A25,SLC25A10,SLC25A11,SLC25A12,SLC25A13,SLC25A20,SLC25A21,SLC25A23,SLC25A25,SLC25A3,SLC25A45,SLC25A5,SLC26A1,SLC27A4,SLC2A2,SLC30A5,SLC31A1,SLC35A1,SLC35A3,SLC35B1,SLC35D1,SLC38A10,SLC39A11,SLC39A14,SLC39A4,SLC44A2,SLC4A4,SLC6A12,SLC6A13,SLC7A2,SLC9A3R1,SLC9A3R2,SLCO1B3,SLCO2A1,SLK,SLMAP,SLTM,SMAP1,SMAP2,SMARCA2,SMARCA5,SMARCD2,SMARCE1,SMC1A,SMC3,SMIM15,SMOC1,SMPD1,SMS,SMU1,SNAP23,SNAP47,SND1,SNF8,SNRNP200,SNRNP70,SNRPA1,SNRPB2,SNRPD3,SNRPF,SNRPN,SNTA1,SNTB1,SNU13,SNW1,SNX1,SNX18,SNX2,SNX3,SNX4,SNX5,SNX6,SNX7,SOAT2,SON,SORBS1,SORBS2,SORD,SOS1,SPAG9,SPAST,SPCS1,SPCS2,SPG7,SPPL2A,SPR,SPTAN1,SPTBN2,SQOR,SRA1,SREK1,SRI,SRP19,SRP68,SRP72,SRP9,SRPK2,SRPRB,SRR,SRRT,SRSF1,SRSF10,SRSF2,SRSF3,SRSF4,SRSF6,SRSF7,SSBP1,SSR1,SSR3,SSR4,SSRP1,ST13,STAB1,STAB2,STAG2,STARD5,STAT2,STAT3,STAT6,STBD1,STEAP3,STEAP4,STIP1,STK38L,STOML2,STRAP,STRN,STT3A,STT3B,SUB1,SUCLG1,SUCLG2,SUGCT,SUGT1,SULT1B1,SULT1C2,SULT1E1,SULT2A1,SUMO2,SUN2,SUOX,SUPT16H,SURF1,SURF4,SVIL,SWAP70,SYAP1,SYMPK,SYNCRIP,SYNGR2,SYNJ2BP,TACO1,TADA3,TAGLN,TAGLN2,TALDO1,TAMM41,TANGO2,TAOK3,TAP1,TAP2,TAPBP,TARDBP,TAT,TBC1D13,TBC1D15,TBC1D17,TBC1D24,TBC1D8B,TBC1D9B,TBCD,TBCEL,TBL2,TBRG4,TCEA1,TCERG1,TCIRG1,TCOF1,TDO2,TFR2,TGFBRAP1,TGM1,THNSL2,THOC2,THRAP3,THYN1,TIAL1,TIGAR,TIMM17B,TIMM22,TIMM44,TIMMDC1,TINAGL1,TJP1,TJP2,TJP3,TKFC,TKT,TLN1,TM9SF1,TM9SF2,TM9SF3,TMED1,TMED10,TMED2,TMED3,TMED4,TMED5,TMED7,TMED9,TMEM109,TMEM126A,TMEM126B,TMEM135,TMEM176B,TMEM19,TMEM214,TMEM230,TMEM256,TMEM30A,TMEM33,TMEM38B,TMEM43,TMEM82,TMLHE,TMOD3,TMPO,TMTC3,TMX1,TMX3,TNKS1BP1,TNPO1,TNPO2,TNPO3,TNS2,TNS3,TOM1,TOMM40,TOP1,TOP2B,TOP3B,TOR1A,TOR1AIP1,TPD52,TPD52L2,TPI1,TPK1,TPM3,TPPP,TPR,TPRG1L,TRA2B,TRABD,TRAM1,TRAP1,TRAPPC1,TRAPPC4,TRIM14,TRIM23,TRIM28,TRIP10,TRIP11,TRIR,TRMU,TSC22D1,TSFM,TSG101,TSPAN14,TSPAN31,TSTA3,TTC1,TTC36,TTC37,TTC38,TTC39A,TTC39C,TTC7A,TTN,TTPA,TUBA1B,TUBA4A,TUBB,TUBB2A,TUBB4B,TUT7,TWF1,TXLNA,TXLNG,TXN2,TXNDC5,TXNDC9,TXNL1,TYMP,TYSND1,U2AF2,U2SURP,UBA1,UBA2,UBA3,UBA7,UBAC1,UBAP2,UBE2G2,UBE2I,UBE2J1,UBE2M,UBE2V2,UBE2Z,UBE4B,UBL4A,UBL7,UBQLN2,UBR2,UBTF,UCHL5,UCK1,UFL1,UGDH,UGGT1,UGP2,UGT1A4,UGT1A6,UGT1A8 (includes others),UGT2B10,UGT2B17,UGT2B28,UGT3A1,UPB1,UPF1,UPF2,UPP1,UQCC1,UQCC3,UQCRC2,UROC1,USO1,USP16,USP19,USP24,USP46,USP7,VAC14,VAMP2,VAMP3,VAMP8,VAPB,VAT1,VAV2,VCAM1,VCL,VCPIP1,VDAC2,VIM,VKORC1L1,VMO1,VNN1,VPS13D,VPS25,VPS26A,VPS26B,VPS26C,VPS28,VPS33B,VPS35,VPS45,VPS51,VPS52,VRK1,VSIG4,VTA1,VTN,VWA8,WAPL,WASF2,WASHC3,WASHC4,WASHC5,WBP11,WBP2,WDFY1,WDR1,WDR18,WDR26,WDR36,WDR46,WDR5,WDR61,WDR77,WFS1,WRNIP1,XAF1,XPNPEP1,XPO1,XPO5,XRCC6,XRN1,XRN2,YBX1,YBX3,YME1L1,YTHDF2,YTHDF3,YWHAQ,YWHAZ,ZBTB20,ZBTB8OS,ZC3H11A,ZC3H14,ZC3HAV1,ZFR,ZHX1,ZHX2,ZHX3,ZMAT2,ZMIZ1,ZNF326,ZNF638

1. Cancer,Organismal Injury and Abnormalities 2. Carcinoma 3. 1.37E-81 4. Increased 5. 2.635 6. 2251	A1CF,AACS,AADAT,AAK1,AAMDC,AASDHPPT,AASS,ABAT,ABCB10,ABCB4,ABCB6,ABCB8,ABCB9,ABCC2,ABCC3,ABCC6,ABCD1,ABCD2,ABCD3,ABCE1,ABCF2,ABCF3,ABCG5,ABHD11,ABHD14B,ABHD15,ABITRAM,ACAA1,ACACB,ACAD10,ACAD11,ACAD9,ACADL,ACADM,ACADSB,ACAT1,ACAT2,ACBD5,ACIN1,ACLY,ACMSD,ACO1,ACO2,ACOT1,ACOT11,ACOT12,ACOT13,ACOT2,ACOT4,ACOT7,ACOT8,ACOX1,ACOX3,ACP2,ACSF3,ACSL4,ACSL5,ACSM1,ACSS2,ACSS3,ACTB,ACTG1,ACTN1,ACTN4,ACTR2,ACTR3,ACY1,ACY3,ACYP2,ADAM10,ADAP2,ADD1,ADD2,ADD3,ADHFE1,ADI1,ADIPOR2,ADK,ADSL,AFDN,AFMID,AGFG1,AGFG2,AGK,AGL,AGMAT,AGO1,AGO2,AGPAT2,AGPAT3,AGPAT5,AGRN,AGXT,AGXT2,AHCY,AHCYL2,AHNAK,AHSA1,AHSG,AIF1,AIP,AK2,AK3,AKR1A1,AKR1B10,AKR1C4,AKR1D1,AKT1,ALAS1,ALCAM,ALDH16A1,ALDH1A1,ALDH1B1,ALDH1L1,ALDH3A2,ALDH4A1,ALDH5A1,ALDH6A1,ALDH7A1,ALDH9A1,ALDOA,ALDOB,ALPK1,AMACR,AMBP,AMDHD2,AMPD2,AMT,AMY2A,ANGPTL3,ANGPTL4,ANKHD1/ANKHD1- EIF4EBP3,ANO10,ANPEP,ANXA1,ANXA11,ANXA3,ANXA4,ANXA5,AOX1,AP2A1,AP2M1,AP3B1,APCS,APEX1,API5,APMAP,APOA1,APOB,APOC4,APOD,APOE,AQP1,AQP4,AQP9,ARAF,ARCN1,ARF4,ARF6,ARFGAP1,ARFGAP2,ARFGAP3,ARGLU1,ARHGAP17,ARHGAP31,ARHGAP42,ARHGAP45,ARHGAP5,ARHGDIA,ARHGDIB,ARHGEF12,ARHGEF7,ARIH1,ARMC10,ARPC1A,ARPC1B,ARPC2,ARPC5,ARPC5L,ARRB1,ARSB,AS3MT,ASAH1,ASCC1,ASCC2,ASGR1,ASGR2,ASL,ASPA,ASPDH,ASPG,ASPH,ASPSCR1,ASRGL1,ASS1,ATAD2B,ATG3,ATG4B,ATL3,ATP11C,ATP13A1,ATP1A1,ATP1B1,ATP1B3,ATP2A2,ATP2B1,ATP2B4,ATP5IF1,ATP5PO,ATP6AP1,ATP6AP2,ATP6V0D1,ATP6V1A,ATP6V1C1,ATP6V1E1,ATRX,ATXN10,ATXN2,AUP1,AVEN,B2M,B4GALNT1,BAAT,BABAM2,BAG3,BAG4,BAG5,BAIAP2,BASP1,BBOX1,BCAM,BCAP29,BCAS2,BCHE,BCKDHA,BCKDHB,BCKDK,BCL2L13,BCLAF1,BCO2,BCS1L,BET1L,BGN,BHMT,BHMT2,BID,BIN1,BIN2,BLMH,BLVRA,BLVRB,BMP2K,BNIP3,BPHL,BRAF,BSG,BTAF1,BTD,BUB3,BZW1,C11orf54,C12orf10,C12orf43,C1D,C1orf174,C1QA,C1QB,C2CD2,C4A/C4B,C6,C8A,C8B,C8G,C9,C9orf64,CACFD1,CACYBP,CAD,CADM1,CALCRL,CALR,CALU,CAMK1,CAND1,CANX,CAP1,CAPZA1,CAPZB,CASK,CASP3,CASP7,CAT,CAVIN1,CBR1,CBWD1,CBX1,CBX3,CCAR1,CCDC134,CCDC167,CCDC22,CCDC25,CCDC40,CCDC47,CCDC51,CCDC58,CCDC9,CCDC93,CCS,CCT3,CD163,CD1D,CD2AP,CD302,CD36,CD38,CD47,CD68,CD81,CD82,CDA,CDC34,CDC37,CDC5L,CDC73,CDK11A,CDK12,CDK5,CDK5RAP3,CDK6,CDK9,CDKN1B,CDKN2C,CDO1,CDV3,CENPV,CEP290,CEP89,CES1,CES3,CFAP20,CFB,CFDP1,CFH,CFI,CGN,CHAC2,CHCHD4,CHD4,CHID1,CHMP2A,CHORDC1,CHPT1,CIAO3,CIDEB,CISD1,CISD2,CKAP4,CKB,CKM,CLCC1,CLDN12,CLDN3,CLEC10A,CLEC3B,CLEC4F,CLEC4G,CLIC1,CLIC4,CLIC5,CLINT1,CLPP,CLPTM1,CLTB,CLU,CLYBL,CMAS,CMBL,CMC2,CMPK1,CMPK2,CMTM4,CNBP,CNDP2,CNOT1,CNOT2,CNOT3,CNOT9,CNP,CNPY2,COA7,COASY,COBLL1,COG3,COG5,COL18A1,COLGALT1,COMT,COMTD1,COPA,COPB1,COPB2,COPE,COPG1,COQ3,COQ4,COQ8A,COQ8B,COQ9,CORO1A,CORO1B,CORO1C,COTL1,COX15,COX19,COX5A,COX6B1,COX7A2,CP,CPB2,CPN1,CPNE3,CPOX,CPQ,CPS1,CPSF2,CPT2,CR1L,CRAT,CREB1,CRELD1,CRELD2,CRIP1,CRK,CRKL,CRNKL1,CRP,CRYL1,CRYM,CRYZ,CSAD,CSK,CSNK1E,CSNK2A1,CSNK2A2,CSNK2B,CSRP1,CSRP2,CSTF1,CSTF2,CSTF3,CTBP1,CTBS,CTDSP1,CTH,CTNNA1,CTNNB1,CTNNBL1,CTNND1,CTR9,CTSB,CTSC,CTSD,CTSF,CTSH,CTSO,CTSS,CTSV,CTSZ,CTTN,CUL1,CUL2,CUL3,CUTC,CXADR,CYB5A,CYB5B,CYB5R1,CYBC1,CYGB,CYP17A1,CYP1A2,CYP27A1,CYP2A6 (includes others),Cyp2b13/Cyp2b9,CYP2B6,Cyp2c54 (includes others),CYP2C8,CYP2F1,CYP2U1,CYP3A5,CYP3A7,CYP4A11,CYP4A22,CYP4B1,CYP4F3,CYP7A1,CYP7B1,DAAM1,DAD1,DAPK1,DARS2,DBNL,DCAF11,DCAKD,DCPS,DCTN2,DCTN4,DCTN6,DCUN1D1,DCUN1D2,DCXR,DDAH1,DDAH2,DDC,DDHD2,DDI2,DDOST,DDRGK1,DDX17,DDX18,DDX19A,DDX21,DDX23,DDX27,DDX39B,DDX3X,DDX3Y,DDX42,DDX46,DDX49,DDX5,DDX58,DDX6,DECR1,DECR2,DEK,DEPTOR,DES,DGAT2,DGLUCY,DHCR24,DHDH,DHFR,DHODH,DHRS7,DHRS7B,DHTKD1,DHX15,DHX16,DHX9,DIABLO,DIO1,DIS3,DKC1,DLAT,DMAC1,DMD,DMGDH,DNAJA1,DNAJB1,DNAJB11,DNAJB4,DNAJB6,DNAJB9,DNAJC1,DNAJC13,DNAJC19,DNAJC2,DNAJC25,DNAJC3,DNAJC7,DNM1L,DNM2,DNPEP,DNTTIP2,DOCK6,DPAGT1,DPM1,DPM3,DPP4,DPP7,DPP9,DPY19L1,DPY30,DPYD,DPYS,DPYSL2,DRG1,DSP,DTD1,DTX3L,DUSP23,DYNLL1,DYNLT3,DYSF,EBPL,ECHDC2,ECI1,ECI2,ECM1,EDC4,EEA1,EEF1A1,EEF1D,EEF2,EFHD2,EFR3A,EFTUD2,EGF,EGFR,EHD1,EHD3,EHHADH,EIF1AX,EIF2A,EIF2AK2,EIF2B1,EIF2B2,EIF2B3,EIF2S1,EIF2S2,EIF3A,EIF3C,EIF3D,EIF3E,EIF3F,EIF3H,EIF3I,EIF3L,EIF3M,EIF4A1,EIF4A2,EIF4A3,EIF4E,EIF4G1,EIF4G2,EIF4H,EIF5,EIF5A,EIF5B,ELAC2,ELAVL1,ELMO1,ELOA,ELOC,ELOVL1,ELOVL2,ELOVL5,ELP2,EMC8,EMD,EMILIN1,EML3,EML4,ENO1,ENPEP,ENPP1,ENTPD5,EPB41,EPB41L2,EPB41L5,EPHX1,EPHX2,EPPK1,EPS15L1,EPS8L2,ERBIN,ERC1,ERGIC1,ERGIC2,ERGIC3,ERH,ERLIN1,ERMP1,ERP29,ERP44,ESD,ESYT1,ESYT2,ETFDH,ETNK1,ETNPPL,EVA1A,EXOC1,EXOC5,EXOC7,EXOSC9,EZR,F11,F13A1,FAAH,FABP2,FABP4,FABP5,FABP7,FADS6,FAF1,FAHD2B,FAM114A2,FAM126A,FAM126B,FAM210A,FAM234A,FAM3C,FAM50B,FAM98C,FARP1,FARS2,FASN,FAU,FBL,FBP1,FBXO3,FCGR2B,FCGRT,FCHO2,FDX2,FECH,FEN1,FERMT2,FETUB,FGA,FGB,FGG,FGL1,FHIT,FIS1,FITM2,FKBP11,FKBP15,FKBP3,FKBP4,FKBP5,FLII,FLNA,FLOT1,FLOT2,FMO1,FMO3,FMO4,FMO5,FMR1,FN1,FN3K,FN3KRP,FNDC3A,FNTA,FRAS1,FRG1,FSCN1,FTCD,FTO,FTSJ3,FUBP1,FUBP3,FXN,FXR1,FXYD1,G0S2,G6PC,G6PD,GAA,GABPA,GADD45GIP1,GALK1,GALK2,GALM,GALNS,GALNT2,GALT,GAMT,GANAB,GAPDH,GAPVD1,GART,GATAD2A,GATD1,GATM,GBA,GBE1,GBF1,GBP6,GCAT,GCC1,GCDH,GCH1,GCK,GCKR,GCLM,GCN1,GDA,GFM1,GFPT1,GGA1,GGCT,GID8,GIMAP4,GJB2,GLDC,GLG1,GLMP,GLOD4,GLRX3,GLRX5,GLT1D1,GLTPD2,GLUD1,GLUL,GLYAT,GLYR1,Gm12854/S100a11,Gm21596/Hmgb1,GMPPA,GMPPB,GMPR2,GMPS,GNA11,GNA13,GNAI2,GNAI3,GNAQ,GNAS,GNE,GNG12,GNL3,GNMT,GNPAT,GNPDA1,GNS,GOLGA2,GOLGA5,GOLGA7,GOLPH3,GOLPH3L,GOPC,GORASP2,GOSR1,GOSR2,GOT1,GPAM,GPAT3,GPAT4,GPD1,GPD1L,GPHN,GPLD1,GPR182,GPRIN3,GPT,GPT2,GPX3,GRB7,GRHPR,GRIPAP1,GRN,G

	SPT1,GSR,Gsta4,GSTA5,GSTK1,GSTM1,GSTM2,GSTM4,GSTM5,GSTP1,GSTT2/GSTT2B,GSTZ1,GTF2F1,GTF2F2,GTF2I,GTPBP4,GUCY1B1,H3-3A/H3-3B,H6PD,HACL1,HADH,HAGH,HAL,HAO1,HAO2,HBS1L,HCCS,HCFC1,HDAC1,HDGF,HDGFL2,HDGFL3,HDLBP,HEATR1,HEBP1,HECTD1,HELZ2,HERPUD1,HEXB,HEXIM1,HGD,HGS,HIBADH,HIBCH,HINT2,HINT3,HIP1,HK1,HLA-A,HLA-DQA1,HMGA1,HMGCL,HMGCS1,HMGCS2,HMGN1,HMOX1,HMOX2,HNF1A,HNF4A,HNMT,HNRNPA2B1,HNRNPAB,HNRNPC,HNRNPD,HNRNPF,HNRNPH1,HNRNPH2,HNRNPK,HNRNPL,HNRNPLL,HNRNPM,HNRNPR,HNRNPU,HNRNPUL1,HNRNPUL2,HOMER2,HOPX,HP,HP1BP3,HPD,HPGD,HPN,HPX,HRAS,Hrg,HS1BP3,HSCB,HSD11B1,HSD17B10,HSD17B11,HSD17B2,HSD17B4,HSD17B6,HSDL1,HSP90AA1,HSP90AB1,HSP90B1,HSPA12B,HSPA13,HSPA1A/HSPA1B,HSPA4L,HSPA5,HSPA8,HSPA9,HSPB1,HSPD1,HSPG2,HSPH1,HTATIP2,HUWE1,HYKK,HYOU1,HYPK,ICAM1,IDH2,IDH3B,IDO2,IFI16,IFIT1B,IFIT3,IFNAR2,IGF2R,IGFALS,IK,IL6ST,ILF2,ILF3,ILK,ILKAP,IMMP2L,IMMT,IMPA1,IMPAD1,INHBC,INMT,INPP1,INPP5F,INSIG2,INSR,INTS3,IP6K1,IPO5,IQGAP1,ISCA2,ISOC1,ISOC2,IST1,ITGA1,ITGA2B,ITGA5,ITGA9,ITGAV,ITGB1,ITGB3,ITGB6,ITIH2,ITIH4,ITPR2,ITSN1,IYD,JCHAIN,JPT2,JUP,KANK2,KCTD12,KDELR1,KDSR,KHDRBS1,KHK,KHSRP,KIF13B,KIF21A,KLHDC7A,KLKB1,KPNA1,KPNA2,KRAS,KXD1,KYAT1,KYAT3,KYNU,L2HGDH,L3HYPDH,LAMTOR1,LAP3,LARP1,LARP4,LARP4B,LARP7,LARS2,LASP1,LBR,LCAT,LDAH,LDLR,LGALS1,LGALS3,LGALS3BP,LGALS8,LGALSL,LGMN,LHPP,LIAS,LIFR,LIMS2,LIN7A,LIN7C,LIPE,LITAF,LMAN1,LMAN2,LMAN2L,LMF1,LMNA,LMNB1,LMNB2,LMO7,LOC102724788/PRODH,LONP2,LPCAT3,LRG1,LRP1,LRPAP1,LRRFIP1,LSG1,LSM12,LSM14A,LSM14B,LSM5,LSR,LUC7L,LUC7L2,LUC7L3,LUM,LYAR,LYN,LYPLA1,LYPLA2,LYPLAL1,LYVE1,LYZ,LZIC,M6PR,MACO1,MACROD1,MAGIX,MAN1A2,MAN2B1,MAN2B2,MAN2C1,MANBA,MAOA,MAOB,MAP2K1,MAP2K3,MAP4,MAPK1IP1L,MAPRE1,MAPRE3,MASP2,MAT1A,MAT2A,MATR3,MBNL1,MBOAT7,MCAM,MCCC1,MCCC2,MCEE,MCFD2,MCTS1,MDH1,ME1,MEAF6,MECP2,METAP2,METTL26,METTL27,METTL7B,METTL9,MFAP1,MFN2,MGAT2,MGLL,MGST1,MIA3,MIEN1,MIF,MIF4GD,MIGA2,MIOS,MIPEP,MKNK1,MMAB,MME,MMUT,MOB1B,MOCS2,MOGS,MORF4L1,MOSPD2,MOV10,MPC1,MPC2,MPHOSPH10,MPI,MPP1,MPP6,MPRIP,MPST,MRC1,MRI1,MROH1,MRPL12,MRPL15,MRPL17,MRPL24,MRPL47,MRPL50,MRPL51,MRPS12,MRPS15,MRPS17,MRPS25,MRPS31,MRPS35,MRRF,MSH2,MSN,MSR1,MSRA,MSRB2,Mt1,Mt2,MTA2,MTAP,MTCH2,MTDH,MTFR1,MTFR1L,MTHFD1,MTHFS,MTMR6,MTOR,MTREX,MTSS1,MTX2,MUL1,MVK,MVP,MYBBP1A,MYCBP,MYEF2,MYH10,MYH11,MYH14,MYH9,MYL1,MYL12A,MYL6,MYLK,MYLPF,MYO18A,MYO1B,MYO1C,MYO1D,NAA15,NAA16,NAA25,NAA35,NAALAD2,NACA,NADK2,NAGA,NAGLU,NAMPT,NANP,NANS,NAP1L1,NAPRT,NASP,NAT10,NAXD,NAXE,NCBP1,NCEH1,NCK1,NCL,NCOA5,NCSTN,NDRG1,NDST1,NDUFA10,NDUFA11,NDUFA13,NDUFA3,NDUFAF2,NDUFAF3,NDUFAF7,NDUFB6,NDUFB7,NDUFB8,NECAP1,NECTIN2,NELFA,NELFB,NELFCD,NFIA,NFIB,NFIC,NFS1,NFU1,NFXL1,NGEF,NGLY1,NHLRC2,NHP2,NIBAN1,NID2,NIPSNAP2,NIT1,NLN,NLRX1,NME3,NMNAT1,NMRAL1,NMRK1,NMT2,NNMT,NOC2L,NOL6,NONO,NOP16,NOP56,NOP58,NOS3,NOSTRIN,NPC1,NQO1,NR1H4,NR3C1,NRAS,NSF,NSFL1C,NSUN2,NUBPL,NUCB1,NUCB2,NUCKS1,NUDC,NUDCD3,NUDT12,NUDT13,NUDT14,NUDT16,NUDT19,NUDT21,NUDT3,NUDT4,NUDT7,NUFIP2,NUMA1,NUP153,NUP155,NUP160,NUP205,NUP210,NUP214,NUP35,NUP54,NUP93,NUP98,NUTF2,OAT,OCIAD2,OGA,OGFOD3,OGFR,OGT,OLA1,OPLAH,OPTN,ORMDL2,OS9,OSBPL9,OTOL1,OXCT1,OXR1,OXSM,PA2G4,PABPC1,PABPC4,PABPN1,PAFAH1B1,PAFAH1B2,PAFAH2,PAIP1,PAIP2,PAK2,PALD1,PALLD,PALMD,PAM16,PANK1,PAPSS1,PAPSS2,PARP1,PARP14,PARP9,PARS2,PARVA,PARVB,PAWR,PBDC1,PBLD,PC,PCBP1,PCCA,PCCB,PCDH1,PCDHB16,PCK1,PCNP,PCTP,PCYT1A,PDAP1,PDCD10,PDCD11,PDCD4,PDCD6IP,PDE2A,PDHA1,PDHB,PDIA3,PDIA4,PDIA5,PDIA6,PDK1,PDK2,PDLIM1,PDLIM5,PDLIM7,PDP2,PDXDC1,PDXK,PDZK1,PEBP1,PECAM1,PECR,PEX1,PEX11A,PEX11G,PEX12,PEX13,PEX14,PEX16,PEX19,PEX26,PEX3,PEX5,PEX6,PFAS,PFDN2,PFKFB1,PFKFB3,PGAM1,PGD,PGK1,PGM1,PGM3,PGM5,PGRMC1,PGRMC2,PHACTR4,PHB2,PHF20L1,PHKA1,PHKA2,PHKB,PHKG2,PHLDA1,PHLDB2,PHYHD1,PHYKPL,PI4KA,PICALM,PIGR,PIGS,PIGU,PIK3AP1,PIK3CB,PIN4,PIP5K1C,PIR,PITHD1,PITRM1,PKLR,PKN1,PKP4,PLA2G12B,PLBD1,PLBD2,PLCB3,PLCH1,PLEKHA5,PLEKHA7,PLEKHF1,PLG,PLIN5,PLOD3,PLPP3,PLRG1,PLTP,PLVAP,PLXNA4,PLXNB2,PM20D1,PML,PMM2,PNKP,PNLIP,PNN,POLDIP3,POLR2A,POLR2B,POLR2I,POLR2L,PON1,PON2,PON3,POR,PPA1,PPAN,PPAT,PPCS,PPFIA1,PPFIBP2,PPIA,PPIB,PPIF,PPIG,PPIL1,PPIL4,PPIP5K2,PPL,PPM1A,PPM1B,PPM1G,PPM1K,PPP1R2,PPP1R21,PPP1R7,PPP1R8,PPP2R1B,PPP2R5A,PPP2R5D,PPP4C,PPP4R2,PPP4R3A,PPP6R1,PPP6R3,PPT1,PPT2,PPWD1,PQBP1,PRCP,PRDX3,PRDX5,PRDX6,PREB,PRELP,PREP,PRKAA2,PRKAB1,PRKACA,PRKAG1,PRKCSH,PRKRA,PROC,PROX1,PRPF19,PRPF3,PRPF31,PRPF4,PRPF40A,PRPF6,PRPF8,PRRC1,PRRC2C,PRUNE1,PRXL2A,PRXL2B,PSAP,PSEN1,PSIP1,PSMA1,PSMA2,PSMA3,PSMA4,PSMA5,PSMA6,PSMA7,PSMB1,PSMB10,PSMB2,PSMB5,PSMB6,PSMB7,PSMB9,PSMC3,PSMD14,PSMD3,PSMD4,PSMD7,PSME3,PTBP1,PTBP3,PTGES3,PTK2,PTK2B,PTPMT1,PTPN1,PTPRF,PTPRK,PTRHD1,PTS,PTTG1IP,PUM1,PURA,PXMP2,PXMP4,PXN,PYCARD,PYGB,PYGL,QDPR,QSOX1,QTRT2,RAB14,RAB1A,RAB35,RAB4A,RAB8A,RAB8B,RABGAP1,RABGAP1L,RAC1,RACK1,RAD23B,RAD50,RAE1,RALY,RAN,RANBP1,RANBP10,RANBP3,RANGAP1,RAP1A,RAP1B,RAPGEF4,RARRES2,RASIP1,RBBP4,RBM10,RBM14,RBM15,RBM17,RBM22,RBM28,RBM39,RBM42,RBM47,RBP1,RBPMS,RCC2,RCN1,RDH16,REEP5,REEP6,RELA,RER1,RETREG2,RETSAT,REXO2,RFC2,RGL3,RGN,RGPD4 (includes others),RHOA,RHOC,RHOG,RIDA,RIOX2,RIPK1,RMDN2,RMDN3,RMND5A,RNASEH2A,RNASET2,RNF113A,RNF114,RNF14,RNF17,RNF185,RNF2,RNF20,RNF213,RNF5,RNH1,RNMT,RNPEP,ROCK2,RPAP3,RPE,RPL10,RPL10A,RPL11,RPL12,RPL13,RPL13A,RPL14,RPL15,RPL17,RPL18,RPL18A,RPL19,RPL21,RPL22,RPL23,RPL24,RPL26,RPL27,RPL28,RPL3,RPL31,RPL35,RPL37,RPL37A,RPL4,RPL5,RPL6,RPL7,RPL7A,RPL8,RPL9,RPLP0,RPLP2,RPN1,RPN2,RPRD1B,RPS10,RPS11,RPS12,RPS1

	4,RPS15,RPS15A,RPS16,RPS19,RPS2,RPS20,RPS24,RPS25,RPS26,RPS27A,RPS27L,RPS29,RPS3,RPS5,RPS6,RPS6KB2,RPS7,RPS8,RPSA,RPTOR,RRAS,RRS1,RSL1D1,RTF2,RTN1,RTN4,RTN4IP1,RUFY1,RUFY3,RUVBL1,RUVBL2,S100A1,S100A6,SAA1,SAE1,SAFB,SAMHD1,SAP18,SAR1B,SARDH,SARNP,SARS2,SART1,SART3,SAT2,SAYSD1,SBF1,SC5D,SCAMP1,SCAMP3,SCAMP4,SCAMP5,SCARB1,SCARB2,SCD,SCFD1,SCO1,SCPEP1,SCRIB,SCYL2,SCYL3,SDC4,SDF2L1,SDHD,SDR42E1,SDS,SDSL,SEC11A,SEC14L2,SEC14L4,SEC23B,SEC23IP,SEC24A,SEC24D,SEC31A,SEC61A1,SEC61B,SEC61G,SEC62,SEC63,SELENBP1,SELENOF,SELENOP,SEPHS1,SERBP1,SERHL2,SERINC3,SERPINA1,SERPINA10,SERPINA3,SERPINA6,SERPINB1,SERPIND1,SERPINF2,SERPING1,SERPINH1,SET,SF3A1,SF3A3,SF3B1,SF3B2,SF3B3,SF3B4,SF3B6,SFPQ,SFR1,SFT2D2,SFXN5,SGTA,SH3BGRL3,SH3GL1,SHMT1,SHOC2,SHPK,SHTN1,SIAE,SIGLEC1,SIGMAR1,SIL1,SLC12A9,SLC16A7,SLC17A3,SLC22A1,SLC22A18,SLC22A23,SLC22A25,SLC25A10,SLC25A11,SLC25A12,SLC25A13,SLC25A20,SLC25A21,SLC25A23,SLC25A25,SLC25A3,SLC25A45,SLC25A5,SLC26A1,SLC27A4,SLC2A2,SLC30A5,SLC31A1,SLC35A1,SLC35A3,SLC35B1,SLC35D1,SLC38A10,SLC39A11,SLC39A14,SLC39A4,SLC44A2,SLC4A4,SLC6A12,SLC6A13,SLC7A2,SLC9A3R1,SLC9A3R2,SLCO1B3,SLCO2A1,SLK,SLMAP,SLTM,SMAP1,SMAP2,SMARCA2,SMARCA5,SMARCD2,SMARCE1,SMC1A,SMC3,SMIM15,SMOC1,SMPD1,SMS,SMU1,SNAP23,SNAP47,SND1,SNF8,SNRNP200,SNRNP70,SNRPA1,SNRPB2,SNRPD3,SNRPF,SNRPN,SNTA1,SNTB1,SNU13,SNW1,SNX1,SNX18,SNX2,SNX3,SNX4,SNX5,SNX6,SNX7,SOAT2,SON,SORBS1,SORBS2,SORD,SOS1,SPAG9,SPAST,SPCS1,SPCS2,SPG7,SPPL2A,SPR,SPTAN1,SPTBN2,SQOR,SRA1,SREK1,SRI,SRP19,SRP68,SRP72,SRP9,SRPK2,SRPRB,SRR,SRRT,SRSF1,SRSF10,SRSF2,SRSF3,SRSF4,SRSF6,SRSF7,SSBP1,SSR1,SSR3,SSR4,SSRP1,ST13,STAB1,STAB2,STAG2,STARD5,STAT2,STAT3,STAT6,STBD1,STEAP3,STEAP4,STIP1,STK38L,STOML2,STRAP,STRN,STT3A,STT3B,SUB1,SUCLG1,SUCLG2,SUGCT,SUGT1,SULT1B1,SULT1C2,SULT1E1,SULT2A1,SUMO2,SUN2,SUOX,SUPT16H,SURF1,SURF4,SVIL,SWAP70,SYAP1,SYMPK,SYNCRIP,SYNGR2,SYNJ2BP,TACO1,TADA3,TAGLN,TAGLN2,TALDO1,TAMM41,TANGO2,TAOK3,TAP1,TAP2,TAPBP,TARDBP,TAT,TBC1D13,TBC1D15,TBC1D17,TBC1D24,TBC1D8B,TBC1D9B,TBCD,TBCEL,TBL2,TBRG4,TCEA1,TCERG1,TCIRG1,TCOF1,TDO2,TFR2,TGFBRAP1,TGM1,THNSL2,THOC2,THRAP3,THYN1,TIAL1,TIGAR,TIMM17B,TIMM22,TIMM44,TIMMDC1,TINAGL1,TJP1,TJP2,TJP3,TKFC,TKT,TLN1,TM9SF1,TM9SF2,TM9SF3,TMED1,TMED10,TMED2,TMED3,TMED4,TMED5,TMED7,TMED9,TMEM109,TMEM126A,TMEM126B,TMEM135,TMEM176B,TMEM19,TMEM214,TMEM230,TMEM256,TMEM30A,TMEM33,TMEM38B,TMEM43,TMEM82,TMLHE,TMOD3,TMPO,TMTC3,TMX1,TMX3,TNKS1BP1,TNPO1,TNPO2,TNPO3,TNS2,TNS3,TOM1,TOMM40,TOP1,TOP2B,TOP3B,TOR1A,TOR1AIP1,TPD52,TPD52L2,TPI1,TPK1,TPM3,TPPP,TPR,TPRG1L,TRA2B,TRABD,TRAM1,TRAP1,TRAPPC1,TRAPPC4,TRIM14,TRIM23,TRIM28,TRIP10,TRIP11,TRIR,TRMU,TSC22D1,TSFM,TSG101,TSPAN14,TSPAN31,TSTA3,TTC1,TTC36,TTC37,TTC38,TTC39A,TTC39C,TTC7A,TTN,TTPA,TUBA4A,TUBB,TUBB2A,TUBB4B,TUT7,TWF1,TXLNA,TXLNG,TXN2,TXNDC5,TXNDC9,TXNL1,TYMP,TYSND1,U2AF2,U2SURP,UBA1,UBA2,UBA3,UBA7,UBAC1,UBAP2,UBE2G2,UBE2J1,UBE2M,UBE2V2,UBE2Z,UBE4B,UBL4A,UBL7,UBQLN2,UBR2,UBTF,UCHL5,UCK1,UFL1,UGDH,UGGT1,UGP2,UGT1A4,UGT1A6,UGT1A8 (includes others),UGT2B10,UGT2B17,UGT2B28,UGT3A1,UPB1,UPF1,UPF2,UPP1,UQCC1,UQCC3,UQCRC2,UROC1,USO1,USP16,USP19,USP24,USP46,USP7,VAC14,VAMP2,VAMP3,VAMP8,VAPB,VAT1,VAV2,VCAM1,VCL,VCPIP1,VDAC2,VIM,VKORC1L1,VMO1,VNN1,VPS13D,VPS25,VPS26A,VPS26B,VPS26C,VPS28,VPS33B,VPS35,VPS45,VPS51,VPS52,VRK1,VSIG4,VTA1,VTN,VWA8,WAPL,WASF2,WASHC3,WASHC4,WASHC5,WBP11,WBP2,WDFY1,WDR1,WDR18,WDR26,WDR36,WDR46,WDR5,WDR61,WDR77,WFS1,WRNIP1,XAF1,XPNPEP1,XPO1,XPO5,XRCC6,XRN1,XRN2,YBX1,YBX3,YME1L1,YTHDF2,YTHDF3,YWHAQ,YWHAZ,ZBTB20,ZBTB8OS,ZC3H11A,ZC3H14,ZC3HAV1,ZFR,ZHX1,ZHX2,ZHX3,ZMAT2,ZMIZ1,ZNF326,ZNF638

1. Cancer,Organismal Injury and Abnormalities 2. Solid tumor 3. 6.13E-77 4. Increased 5. 2.175 6. 2308	A1CF,AACS,AADAT,AAK1,AAMDC,AASDHPPT,AASS,ABAT,ABCB10,ABCB4,ABCB6,ABCB8,ABCB9,ABCC2,ABCC3,ABCC6,ABCD1,ABCD2,ABCD3,ABCE1,ABCF2,ABCF3,ABCG5,ABHD11,ABHD14B,ABHD15,ABITRAM,ACAA1,ACACB,ACAD10,ACAD11,ACAD9,ACADL,ACADM,ACADSB,ACAT1,ACAT2,ACBD5,ACIN1,ACLY,ACMSD,ACO1,ACO2,ACOT1,ACOT11,ACOT12,ACOT13,ACOT2,ACOT4,ACOT7,ACOT8,ACOX1,ACOX3,ACP2,ACSF3,ACSL4,ACSL5,ACSM1,ACSS2,ACSS3,ACTB,ACTG1,ACTL6A,ACTN1,ACTN4,ACTR2,ACTR3,ACY1,ACY3,ACYP2,ADAM10,ADAP2,ADD1,ADD2,ADD3,ADHFE1,ADI1,ADIPOR2,ADK,ADPRH,ADSL,AFDN,AFMID,AGFG1,AGFG2,AGK,AGL,AGMAT,AGO1,AGO2,AGPAT2,AGPAT3,AGPAT5,AGRN,AGXT,AGXT2,AHCY,AHCYL2,AHNAK,AHSA1,AHSG,AIF1,AIP,AK2,AK3,AKR1A1,AKR1B10,AKR1C4,AKR1D1,AKT1,ALAS1,ALCAM,ALDH16A1,ALDH1A1,ALDH1B1,ALDH1L1,ALDH3A2,ALDH4A1,ALDH5A1,ALDH6A1,ALDH7A1,ALDH9A1,ALDOA,ALDOB,ALPK1,AMACR,AMBP,AMDHD2,AMPD2,AMT,AMY2A,ANGPTL3,ANGPTL4,ANKHD1/ANKHD1-EIF4EBP3,ANO10,ANPEP,ANXA1,ANXA11,ANXA3,ANXA4,ANXA5,AOX1,AP2A1,AP2M1,AP3B1,APCS,APEX1,API5,APMAP,APOA1,APOA2,APOB,APOC4,APOD,APOE,AQP1,AQP4,AQP9,ARAF,ARCN1,ARF4,ARF6,ARFGAP1,ARFGAP2,ARFGAP3,ARGLU1,ARHGAP17,ARHGAP31,ARHGAP42,ARHGAP45,ARHGAP5,ARHGDIA,ARHGDIB,ARHGEF12,ARHGEF7,ARIH1,ARMC10,ARPC1A,ARPC1B,ARPC2,ARPC5,ARPC5L,ARRB1,ARSB,AS3MT,ASAH1,ASCC1,ASCC2,ASGR1,ASGR2,ASL,ASPA,ASPDH,ASPG,ASPH,ASPSCR1,ASRGL1,ASS1,ATAD2B,ATG3,ATG4B,ATL3,ATP11C,ATP13A1,ATP1A1,ATP1B1,ATP1B3,ATP2A2,ATP2B1,ATP2B4,ATP5IF1,ATP5PO,ATP6AP1,ATP6AP2,ATP6V0D1,ATP6V1A,ATP6V1C1,ATP6V1E1,ATRX,ATXN10,ATXN2,AUP1,AVEN,B2M,B4GALNT1,BAAT,BABAM2,BAG3,BAG4,BAG5,BAIAP2,BASP1,BBOX1,BCAM,BCAP29,BCAP31,BCAS2,BCHE,BCKDHA,BCKDHB,BCKDK,BCL2L13,BCLAF1,BCO2,BCS1L,BET1L,BGN,BHMT,BHMT2,BID,BIN1,BIN2,BLMH,BLVRA,BLVRB,BMP2K,BNIP3,BPHL,BRAF,BSG,BTAF1,BTD,BUB3,BZW1,C11orf54,C12orf10,C12orf43,C1D,C1orf174,C1QA,C1QB,C2CD2,C4A/C4B,C6,C8A,C8B,C8G,C9,C9orf64,CACFD1,CACYBP,CAD,CADM1,CALCRL,CALR,CALU,CAMK1,CAND1,CANX,CAP1,CAPZA1,CAPZB,CARHSP1,CASK,CASP3,CASP7,CAT,CAVIN1,CBR1,CBWD1,CBX1,CBX3,CCAR1,CCDC134,CCDC167,CCDC22,CCDC25,CCDC40,CCDC47,CCDC51,CCDC58,CCDC9,CCDC93,CCS,CCT3,CD163,CD1D,CD2AP,CD302,CD36,CD38,CD47,CD68,CD81,CD82,CDA,CDC34,CDC37,Cdc42,CDC5L,CDC73,CDK11A,CDK12,CDK5,CDK5RAP3,CDK6,CDK9,CDKN1B,CDKN2C,CDO1,CDV3,CENPV,CEP290,CEP89,CES1,CES3,CFAP20,CFB,CFDP1,CFH,CFI,CGN,CHAC2,CHCHD4,CHD4,CHID1,CHMP2A,CHORDC1,CHPT1,CIAO2A,CIAO3,CIDEB,CISD1,CISD2,CKAP4,CKB,CKM,CLCC1,CLDN12,CLDN3,CLEC10A,CLEC3B,CLEC4F,CLEC4G,CLIC1,CLIC4,CLIC5,CLINT1,CLPP,CLPTM1,CLTA,CLTB,CLU,CLYBL,CMAS,CMBL,CMC2,CMPK1,CMPK2,CMTM4,CNBP,CNDP2,CNOT1,CNOT2,CNOT3,CNOT9,CNP,CNPY2,COA7,COASY,COBLL1,COG3,COG5,COL18A1,COLGALT1,COMT,COMTD1,COPA,COPB1,COPB2,COPE,COPG1,COQ3,COQ4,COQ8A,COQ8B,COQ9,CORO1A,CORO1B,CORO1C,COTL1,COX15,COX19,COX5A,COX6B1,COX7A2,CP,CPB2,CPN1,CPNE3,CPOX,CPPED1,CPQ,CPS1,CPSF2,CPT2,CR1L,CRAT,CREB1,CRELD1,CRELD2,CRIP1,CRK,CRKL,CRNKL1,CRP,CRYL1,CRYM,CRYZ,CSAD,CSK,CSNK1E,CSNK2A1,CSNK2A2,CSNK2B,CSRP1,CSRP2,CSTF1,CSTF2,CSTF3,CTBP1,CTBS,CTDSP1,CTH,CTNNA1,CTNNB1,CTNNBL1,CTNND1,CTR9,CTSB,CTSC,CTSD,CTSF,CTSH,CTSO,CTSS,CTSV,CTSZ,CTTN,CUL1,CUL2,CUL3,CUTC,CXADR,CYB5A,CYB5B,CYB5R1,CYBC1,CYGB,CYP17A1,CYP1A2,CYP27A1,CYP2A6 (includes others),Cyp2b13/Cyp2b9,CYP2B6,Cyp2c54 (includes others),Cyp2c70,CYP2C8,CYP2F1,CYP2U1,CYP3A5,CYP3A7,CYP4A11,CYP4A22,CYP4B1,CYP4F3,CYP7A1,CYP7B1,DAAM1,DAD1,DAPK1,DARS2,DBNL,DCAF11,DCAKD,DCPS,DCTN2,DCTN4,DCTN6,DCUN1D1,DCUN1D2,DCXR,DDAH1,DDAH2,DDC,DDHD2,DDI2,DDOST,DDRGK1,DDX17,DDX18,DDX19A,DDX21,DDX23,DDX27,DDX39B,DDX3X,DDX3Y,DDX42,DDX46,DDX49,DDX5,DDX58,DDX6,DECR1,DECR2,DEK,DEPTOR,DES,DGAT2,DGLUCY,DHCR24,DHDH,DHFR,DHODH,DHRS7,DHRS7B,DHTKD1,DHX15,DHX16,DHX9,DIABLO,DIO1,DIS3,DKC1,DLAT,DMAC1,DMD,DMGDH,DNAJA1,DNAJB1,DNAJB11,DNAJB4,DNAJB6,DNAJB9,DNAJC1,DNAJC13,DNAJC19,DNAJC2,DNAJC25,DNAJC3,DNAJC7,DNAJC8,DNM1L,DNM2,DNPEP,DNTTIP2,DOCK6,DPAGT1,DPM1,DPM3,DPP4,DPP7,DPP9,DPY19L1,DPY30,DPYD,DPYS,DPYSL2,DR1,DRG1,DSP,DTD1,DTX3L,DUSP23,DUT,DYNLL1,DYNLT3,DYSF,EBPL,ECHDC2,ECHDC3,ECI1,ECI2,ECM1,EDC4,EEA1,EEF1A1,EEF1D,EEF2,EFHD2,EFR3A,EFTUD2,EGF,EGFR,EHD1,EHD3,EHHADH,EIF1AX,EIF2A,EIF2AK2,EIF2B1,EIF2B2,EIF2B3,EIF2B5,EIF2S1,EIF2S2,EIF3A,EIF3C,EIF3D,EIF3E,EIF3F,EIF3H,EIF3I,EIF3K,EIF3L,EIF3M,EIF4A1,EIF4A2,EIF4A3,EIF4E,EIF4G1,EIF4G2,EIF4H,EIF5,EIF5A,EIF5B,ELAC2,ELAVL1,ELMO1,ELOA,ELOC,ELOVL1,ELOVL2,ELOVL5,ELOVL6,ELP2,EMC8,EMD,EMILIN1,EML3,EML4,ENO1,ENPEP,ENPP1,ENTPD5,EPB41,EPB41L2,EPB41L5,EPHX1,EPHX2,EPPK1,EPS15L1,EPS8L2,ERBIN,ERC1,ERGIC1,ERGIC2,ERGIC3,ERH,ERLIN1,ERMP1,ERP29,ERP44,ESAM,ESD,ESYT1,ESYT2,ETFDH,ETNK1,ETNPPL,EVA1A,Ewsr1,EXOC1,EXOC5,EXOC7,EXOSC9,EZR,F11,F13A1,FAAH,FABP2,FABP4,FABP5,FABP7,FADS6,FAF1,FAHD2B,FAM114A2,FAM126A,FAM126B,FAM210A,FAM234A,FAM3C,FAM50B,FAM98C,FARP1,FARS2,FASN,FAU,FBL,FBP1,FBXO3,FCGR2B,FCGRT,FCHO2,FDX2,FECH,FEN1,FERMT2,FETUB,FGA,FGB,FGG,FGL1,FHIT,FIS1,FITM2,FKBP11,FKBP15,FKBP3,FKBP4,FKBP5,FLII,FLNA,FLOT1,FLOT2,FMO1,FMO3,FMO4,FMO5,FMR1,FN1,FN3K,FN3KRP,FNDC3A,FNTA,FRAS1,FRG1,FSCN1,FTCD,FTO,FTSJ3,FUBP1,FUBP3,FXN,FXR1,FXYD1,G0S2,G6PC,G6PD,GAA,GABPA,GADD45GIP1,GALK1,GALK2,GALM,GALNS,GALNT2,GALT,GAMT,GANAB,GAPDH,GAPVD1,GART,GATAD2A,GATD1,GATM,GBA,GBE1,GBF1,GBP6,GCAT,GCC1,GCDH,GCH1,GCK,GCKR,GCLM,GCN1,GDA,GFM1,GFPT1,GGA1,GGCT,GID8,GIMAP4,GJB2,GLDC,GLG1,GLMP,GLO1,GLOD4,GLRX3,GLRX5,GLT1D1,GLTPD2,GLUD1,GLUL,GLYAT,GLYR1,Gm12854/S100a11,Gm21596/Hmgb1,GMPPA,GMPPB,GMPR2,GMPS,GNA11,GNA13,GNAI2,GNAI3,GNAQ,GNAS,GNE,GNG12,GNL3,GNMT,GNPAT,GNPDA1,GNS,GOLGA2,GOLGA5,GOL

	GA7,GOLPH3,GOLPH3L,GOPC,GORASP2,GOSR1,GOSR2,GOT1,GPAM,GPAT3,GPAT4,GPD1,GPD1L,GPHN,GPLD1,GPR182,GPRIN3,GPT,GPT2,GPX3,GRB7,GRHPR,GRIPAP1,GRN,GSPT1,GSR,Gsta4,GSTA5,GSTK1,GSTM1,GSTM2,GSTM4,GSTM5,GSTP1,GSTT2/GSTT2B,GSTZ1,GTF2F1,GTF2F2,GTF2I,GTPBP4,GUCY1B1,H3-3A/H3-3B,H6PD,HACL1,HADH,HAGH,HAL,HAO1,HAO2,HBS1L,HCCS,HCFC1,HDAC1,HDGF,HDGFL2,HDGFL3,HDLBP,HEATR1,HEBP1,HECTD1,HELZ2,HERPUD1,HEXB,HEXIM1,HGD,HGS,HIBADH,HIBCH,HINT2,HINT3,HIP1,HK1,HLA-A,HLA-DQA1,HMGA1,HMGCL,HMGCS1,HMGCS2,HMGN1,HMOX1,HMOX2,HNF1A,HNF4A,HNMT,HNRNPA2B1,HNRNPAB,HNRNPC,HNRNPD,HNRNPF,HNRNPH1,HNRNPH2,HNRNPK,HNRNPL,HNRNPLL,HNRNPM,HNRNPR,HNRNPU,HNRNPUL1,HNRNPUL2,HOMER2,HOPX,HP,HP1BP3,HPCAL1,HPD,HPGD,HPN,HPX,HRAS,Hrg,HS1BP3,HSCB,HSD11B1,HSD17B10,HSD17B11,HSD17B2,HSD17B4,HSD17B6,HSDL1,HSP90AA1,HSP90AB1,HSP90B1,HSPA12B,HSPA13,HSPA1A/HSPA1B,HSPA4L,HSPA5,HSPA8,HSPA9,HSPB1,HSPD1,HSPG2,HSPH1,HTATIP2,HUWE1,HYKK,HYOU1,HYPK,ICAM1,IDH2,IDH3B,IDO2,IFI16,IFIT1B,IFIT3,IFNAR2,IGF2R,IGFALS,IGKC,IK,IL6ST,ILF2,ILF3,ILK,ILKAP,IMMP2L,IMMT,IMPA1,IMPAD1,INHBC,INMT,INPP1,INPP5F,INSIG2,INSR,INTS3,IP6K1,IPO5,IQGAP1,Irgm1,ISCA2,ISOC1,ISOC2,IST1,ITGA1,ITGA2B,ITGA5,ITGA9,ITGAV,ITGB1,ITGB3,ITGB6,ITIH2,ITIH4,ITPR2,ITSN1,IYD,JCHAIN,JPT2,JUP,KANK2,KCTD12,KDELR1,KDSR,KHDRBS1,KHK,KHSRP,KIF13B,KIF21A,KLHDC7A,KLKB1,KPNA1,KPNA2,KRAS,KXD1,KYAT1,KYAT3,KYNU,L2HGDH,L3HYPDH,LAMTOR1,LAP3,LARP1,LARP4,LARP4B,LARP7,LARS2,LASP1,LBR,LCAT,LDAH,LDLR,LGALS1,LGALS3,LGALS3BP,LGALS8,LGALSL,LGMN,LHPP,LIAS,LIFR,LIMS2,LIN7A,LIN7C,LIPE,LITAF,LMAN1,LMAN2,LMAN2L,LMF1,LMNA,LMNB1,LMNB2,LMO7,LOC102724788/PRODH,LONP2,LPCAT3,LRG1,LRP1,LRPAP1,LRRFIP1,LSG1,LSM12,LSM14A,LSM14B,LSM5,LSM6,LSR,LUC7L,LUC7L2,LUC7L3,LUM,LYAR,LYN,LYPLA1,LYPLA2,LYPLAL1,LYVE1,LYZ,LZIC,M6PR,MACO1,MACROD1,MAGIX,MAN1A2,MAN2B1,MAN2B2,MAN2C1,MANBA,MANF,MAOA,MAOB,MAP2K1,MAP2K3,MAP4,MAPK1IP1L,MAPRE1,MAPRE3,MASP2,MAT1A,MAT2A,MATR3,MBL2,MBNL1,MBOAT7,MCAM,MCCC1,MCCC2,MCEE,MCFD2,MCTS1,MDH1,ME1,MEAF6,MECP2,METAP2,METTL26,METTL27,METTL7B,METTL9,MFAP1,MFN2,MGAT2,MGLL,MGST1,MIA3,MIEN1,MIF,MIF4GD,MIGA2,MIOS,MIPEP,MKNK1,MMAB,MME,MMUT,MOB1B,MOCS2,MOGS,MORF4L1,MOSPD2,MOV10,MPC1,MPC2,MPHOSPH10,MPI,MPP1,MPP6,MPRIP,MPST,MRC1,MRI1,MROH1,MRPL12,MRPL15,MRPL17,MRPL24,MRPL32,MRPL47,MRPL50,MRPL51,MRPS12,MRPS15,MRPS17,MRPS25,MRPS31,MRPS35,MRRF,MSH2,MSN,MSR1,MSRA,MSRB2,Mt1,Mt2,MTA2,MTAP,MTCH2,MTDH,MTFR1,MTFR1L,MTHFD1,MTHFS,MTMR6,MTOR,MTREX,MTSS1,MTX2,MUL1,MVK,MVP,MYBBP1A,MYCBP,MYEF2,MYH10,MYH11,MYH14,MYH9,MYL1,MYL12A,MYL6,MYLK,MYLPF,MYO18A,MYO1B,MYO1C,MYO1D,NAA15,NAA16,NAA25,NAA35,NAALAD2,NACA,NADK2,NAGA,NAGLU,NAMPT,NANP,NANS,NAP1L1,NAPRT,NARS1,NASP,NAT10,NAXD,NAXE,NCBP1,NCEH1,NCK1,NCL,NCOA5,NCSTN,NDRG1,NDST1,NDUFA10,NDUFA11,NDUFA13,NDUFA2,NDUFA3,NDUFAF2,NDUFAF3,NDUFAF4,NDUFAF7,NDUFB6,NDUFB7,NDUFB8,NECAP1,NECTIN2,NELFA,NELFB,NELFCD,NFIA,NFIB,NFIC,NFS1,NFU1,NFXL1,NGEF,NGLY1,Ngp,NHLRC2,NHP2,NIBAN1,NID2,NIPSNAP2,NIT1,NLN,NLRX1,NME3,NMNAT1,NMRAL1,NMRK1,NMT2,NNMT,NOC2L,NOL6,NONO,NOP10,NOP16,NOP56,NOP58,NOS3,NOSTRIN,NPC1,NPC2,NQO1,NQO2,NR1H4,NR3C1,NRAS,NSF,NSFL1C,NSUN2,NUBPL,NUCB1,NUCB2,NUCKS1,NUDC,NUDCD3,NUDT12,NUDT13,NUDT14,NUDT16,NUDT19,NUDT21,NUDT3,NUDT4,NUDT7,NUDT9,NUFIP2,NUMA1,NUP153,NUP155,NUP160,NUP205,NUP210,NUP214,NUP35,NUP54,NUP93,NUP98,NUTF2,OAT,OCIAD2,OGA,OGFOD3,OGFR,OGT,OLA1,OPLAH,OPTN,ORMDL2,OS9,OSBPL9,OSGEP,OTOL1,OXCT1,OXR1,OXSM,PA2G4,PABPC1,PABPC4,PABPN1,PAFAH1B1,PAFAH1B2,PAFAH2,PAIP1,PAIP2,PAK2,PALD1,PALLD,PALMD,PAM16,PANK1,PAPSS1,PAPSS2,PARP1,PARP14,PARP9,PARS2,PARVA,PARVB,PAWR,PBDC1,PBLD,PC,PCBP1,PCCA,PCCB,PCDH1,PCDHB16,PCK1,PCNP,PCTP,PCYT1A,PDAP1,PDCD10,PDCD11,PDCD4,PDCD6IP,PDE2A,PDHA1,PDHB,PDIA3,PDIA4,PDIA5,PDIA6,PDK1,PDK2,PDLIM1,PDLIM5,PDLIM7,PDP2,PDXDC1,PDXK,PDZK1,PEBP1,PECAM1,PECR,PEX1,PEX11A,PEX11G,PEX12,PEX13,PEX14,PEX16,PEX19,PEX26,PEX3,PEX5,PEX6,PFAS,PFDN2,PFKFB1,PFKFB3,PGAM1,PGD,PGK1,PGM1,PGM3,PGM5,PGRMC1,PGRMC2,PHACTR4,PHB2,PHF20L1,PHKA1,PHKA2,PHKB,PHKG2,PHLDA1,PHLDB2,PHYHD1,PHYKPL,PI4KA,PICALM,PIGR,PIGS,PIGU,PIK3AP1,PIK3CB,PIN4,PIP5K1C,PIR,PITHD1,PITRM1,PKLR,PKN1,PKP4,PLA2G12B,PLBD1,PLBD2,PLCB3,PLCH1,PLEKHA5,PLEKHA7,PLEKHF1,PLG,PLIN5,PLOD3,PLPP3,PLRG1,PLS3,PLTP,PLVAP,PLXNA4,PLXNB2,PM20D1,PML,PMM2,PNKP,PNLIP,PNN,POLDIP3,POLR2A,POLR2B,POLR2I,POLR2L,PON1,PON2,PON3,POR,PPA1,PPAN,PPAT,PPCS,PPFIA1,PPFIBP2,PPIA,PPIB,PPIF,PPIG,PPIL1,PPIL4,PPIP5K2,PPL,PPM1A,PPM1B,PPM1G,PPM1K,PPP1R2,PPP1R21,PPP1R7,PPP1R8,PPP2R1B,PPP2R5A,PPP2R5D,PPP4C,PPP4R2,PPP4R3A,PPP6R1,PPP6R3,PPT1,PPT2,PPWD1,PQBP1,PRCP,PRDX3,PRDX5,PRDX6,PREB,PRELP,PREP,PRKAA2,PRKAB1,PRKACA,PRKAG1,PRKCSH,PRKRA,PROC,PROX1,PRPF19,PRPF3,PRPF31,PRPF4,PRPF40A,PRPF6,PRPF8,PRRC1,PRRC2C,PRUNE1,PRXL2A,PRXL2B,PSAP,PSEN1,PSIP1,PSMA1,PSMA2,PSMA3,PSMA4,PSMA5,PSMA6,PSMA7,PSMB1,PSMB10,PSMB2,PSMB3,PSMB5,PSMB6,PSMB7,PSMB9,PSMC3,PSMD14,PSMD3,PSMD4,PSMD7,PSME3,PSMF1,PTBP1,PTBP3,PTGES3,PTK2,PTK2B,PTPMT1,PTPN1,PTPRF,PTPRK,PTRHD1,PTS,PTTG1IP,PUF60,PUM1,PURA,PXMP2,PXMP4,PXN,PYCARD,PYGB,PYGL,QDPR,QSOX1,QTRT2,RAB14,RAB1A,RAB35,RAB3IP,RAB4A,RAB8A,RAB8B,RABGAP1,RABGAP1L,RABL3,RAC1,RACK1,RAD23B,RAD50,RAE1,RALY,RAN,RANBP1,RANBP10,RANBP3,RANGAP1,RAP1A,RAP1B,RAPGEF4,RARRES2,RASIP1,RBBP4,RBM10,RBM14,RBM15,RBM17,RBM22,RBM28,RBM39,RBM42,RBM47,RBP1,RBPMS,RCC2,RCN1,RDH16,REEP5,REEP6,RELA,RER1,RETREG2,RETSAT,REXO2,RFC2,RGL3,RGN,RGPD4 (includes others),RHOA,RHOC,RHOG,RIDA,RIOX2,RIPK1,RMDN2,RMDN3,RMND5A,RNASEH2A,RNASET2

	,RNF113A,RNF114,RNF14,RNF17,RNF185,RNF2,RNF20,RNF213,RNF5,RNH1,RNMT,RNPEP,ROCK2,RPAP3,RPE,RPL10,RPL10A,RPL11,RPL12,RPL13,RPL13A,RPL14,RPL15,RPL17,RPL18,RPL18A,RPL19,RPL21,RPL22,RPL23,Rpl23a,RPL24,RPL26,RPL27,RPL27A,RPL28,RPL3,RPL31,RPL35,RPL37,RPL37A,RPL4,RPL5,RPL6,RPL7,RPL7A,RPL8,RPL9,RPLP0,RPLP2,RPN1,RPN2,RPRD1B,RPS10,RPS11,RPS12,RPS13,RPS14,RPS15,RPS15A,RPS16,RPS19,RPS2,RPS20,RPS24,RPS25,RPS26,RPS27A,RPS27L,RPS29,RPS3,RPS4Y1,RPS5,RPS6,RPS6KB2,RPS7,RPS8,RPSA,RPTOR,RRAS,Rrbp1,RRS1,RSL1D1,RTF2,RTN1,RTN4,RTN4IP1,RUFY1,RUFY3,RUVBL1,RUVBL2,S100A1,S100A6,SAA1,SAE1,SAFB,SAMHD1,SAP18,SAR1B,SARDH,SARNP,SARS2,SART1,SART3,SAT2,SAYSD1,SBF1,SC5D,SCAMP1,SCAMP3,SCAMP4,SCAMP5,SCARB1,SCARB2,SCD,SCFD1,SCO1,SCPEP1,SCRIB,SCYL2,SCYL3,SDC4,SDF2L1,SDHD,SDR42E1,SDS,SDSL,SEC11A,SEC14L2,SEC14L4,SEC23B,SEC23IP,SEC24A,SEC24D,SEC31A,SEC61A1,SEC61B,SEC61G,SEC62,SEC63,SELENBP1,SELENOF,SELENOI,SELENOP,SEPHS1,SERBP1,SERHL2,SERINC3,SERPINA1,SERPINA10,SERPINA3,SERPINA6,SERPINB1,SERPIND1,SERPINF2,SERPING1,SERPINH1,SET,Sf1,SF3A1,SF3A3,SF3B1,SF3B2,SF3B3,SF3B4,SF3B6,SFPQ,SFR1,SFT2D2,SFXN5,SGTA,SH3BGRL3,SH3GL1,SHMT1,SHOC2,SHPK,SHTN1,SIAE,SIGLEC1,SIGMAR1,SIL1,SLC12A9,SLC16A7,SLC17A3,SLC22A1,SLC22A18,SLC22A23,SLC22A25,SLC25A10,SLC25A11,SLC25A12,SLC25A13,SLC25A20,SLC25A21,SLC25A23,SLC25A25,SLC25A3,SLC25A45,SLC25A5,SLC26A1,SLC27A4,SLC2A2,SLC30A5,SLC31A1,SLC35A1,SLC35A3,SLC35B1,SLC35D1,SLC38A10,SLC38A3,SLC39A11,SLC39A14,SLC39A4,SLC44A2,SLC4A4,SLC6A12,SLC6A13,SLC7A2,SLC9A3R1,SLC9A3R2,Slco1a1,SLCO1B3,SLCO2A1,SLK,SLMAP,SLTM,SMAP1,SMAP2,SMARCA2,SMARCA5,SMARCD2,SMARCE1,SMC1A,SMC3,SMIM15,SMOC1,SMPD1,SMS,SMU1,SNAP23,SNAP47,SND1,SNF8,SNRNP200,SNRNP70,SNRPA1,SNRPB2,SNRPD3,SNRPF,SNRPN,SNTA1,SNTB1,SNU13,SNW1,SNX1,SNX18,SNX2,SNX3,SNX4,SNX5,SNX6,SNX7,SOAT2,SON,SORBS1,SORBS2,SORD,SOS1,SPAG9,SPAST,SPCS1,SPCS2,SPG7,SPPL2A,SPR,SPTAN1,SPTBN2,SQOR,SRA1,SREK1,SRI,SRP19,SRP68,SRP72,SRP9,SRPK2,SRPRB,SRR,SRRT,SRSF1,SRSF10,SRSF2,SRSF3,SRSF4,SRSF6,SRSF7,SSBP1,SSR1,SSR3,SSR4,SSRP1,ST13,STAB1,STAB2,STAG2,STARD5,STAT2,STAT3,STAT6,STBD1,STEAP3,STEAP4,STIP1,STK38,STK38L,STOML2,STRAP,STRN,STT3A,STT3B,SUB1,SUCLG1,SUCLG2,SUGCT,SUGT1,SULT1B1,SULT1C2,SULT1E1,SULT2A1,SUMO2,SUN2,SUOX,SUPT16H,SURF1,SURF4,SVIL,SWAP70,SYAP1,SYMPK,SYNCRIP,SYNGR2,SYNJ2BP,TACO1,TADA3,TAGLN,TAGLN2,TALDO1,TAMM41,TANGO2,TAOK3,TAP1,TAP2,TAPBP,TARDBP,TAT,TBC1D13,TBC1D15,TBC1D17,TBC1D24,TBC1D8B,TBC1D9B,TBCD,TBCEL,TBL2,TBRG4,TCEA1,TCERG1,TCIRG1,TCOF1,TDO2,TFR2,TGFBRAP1,TGM1,THNSL2,THOC2,THRAP3,THRSP,THYN1,TIAL1,TIGAR,TIMM17B,TIMM22,TIMM44,TIMMDC1,TINAGL1,TJP1,TJP2,TJP3,TKFC,TKT,TLN1,TM9SF1,TM9SF2,TM9SF3,TMED1,TMED10,TMED2,TMED3,TMED4,TMED5,TMED7,TMED9,TMEM109,TMEM126A,TMEM126B,TMEM135,TMEM176B,TMEM19,TMEM214,TMEM230,TMEM256,TMEM30A,TMEM33,TMEM38B,TMEM43,TMEM82,TMLHE,TMOD3,TMPO,TMTC3,TMX1,TMX3,TNKS1BP1,TNPO1,TNPO2,TNPO3,TNS2,TNS3,TOLLIP,TOM1,TOMM40,TOP1,TOP2B,TOP3B,TOR1A,TOR1AIP1,TPD52,TPD52L2,TPI1,TPK1,TPM3,TPPP,TPR,TPRG1L,TRA2B,TRABD,TRAM1,TRAP1,TRAPPC1,TRAPPC4,TRIM14,TRIM23,TRIM28,TRIP10,TRIP11,TRIR,TRMU,TSC22D1,TSFM,TSG101,TSPAN14,TSPAN31,TSTA3,TTC1,TTC36,TTC37,TTC38,TTC39A,TTC39C,TTC7A,TTN,TTPA,TUBA1B,TUBA4A,TUBB,TUBB2A,TUBB4B,TUT7,TWF1,TXLNA,TXLNG,TXN2,TXNDC5,TXNDC9,TXNL1,TYMP,TYSND1,U2AF2,U2SURP,UBA1,UBA2,UBA3,UBA7,UBAC1,UBAP2,UBE2G2,UBE2I,UBE2J1,UBE2M,UBE2V2,UBE2Z,UBE4B,UBL4A,UBL7,UBQLN2,UBR2,UBTF,UCHL5,UCK1,UFL1,UGDH,UGGT1,UGP2,UGT1A4,UGT1A6,UGT1A8 (includes others),UGT2B10,UGT2B17,UGT2B28,UGT3A1,UPB1,UPF1,UPF2,UPP1,UQCC1,UQCC3,UQCRC2,UROC1,USO1,USP16,USP19,USP24,USP46,USP7,VAC14,VAMP2,VAMP3,VAMP8,VAPB,VAT1,VAV2,VCAM1,VCL,VCPIP1,VDAC2,VDAC3,VIM,VKORC1L1,VMO1,VNN1,VPS13D,VPS25,VPS26A,VPS26B,VPS26C,VPS28,VPS33B,VPS35,VPS45,VPS51,VPS52,VRK1,VSIG4,VTA1,VTN,VWA8,WAPL,WASF2,WASHC3,WASHC4,WASHC5,WBP11,WBP2,WDFY1,WDR1,WDR18,WDR26,WDR36,WDR46,WDR5,WDR61,WDR77,WFS1,WRNIP1,XAF1,XPNPEP1,XPO1,XPO5,XRCC6,XRN1,XRN2,YBX1,YBX3,YME1L1,YTHDF2,YTHDF3,YWHAQ,YWHAZ,ZBTB20,ZBTB8OS,ZC3H11A,ZC3H14,ZC3HAV1,ZFR,ZHX1,ZHX2,ZHX3,ZMAT2,ZMIZ1,ZNF326,ZNF638

1. Cancer,Organismal Injury and Abnormalities 2. Malignant solid tumor 3. 2.85E-76 4. Increased 5. 2.579 6. 2298	A1CF,AACS,AADAT,AAK1,AAMDC,AASDHPPT,AASS,ABAT,ABCB10,ABCB4,ABCB6,ABCB8,ABCB9,ABCC2,ABCC3,ABCC6,ABCD1,ABCD2,ABCD3,ABCE1,ABCF2,ABCF3,ABCG5,ABHD11,ABHD14B,ABHD15,ABITRAM,ACAA1,ACACB,ACAD10,ACAD11,ACAD9,ACADL,ACADM,ACADSB,ACAT1,ACAT2,ACBD5,ACIN1,ACLY,ACMSD,ACO1,ACO2,ACOT1,ACOT11,ACOT12,ACOT13,ACOT2,ACOT4,ACOT7,ACOT8,ACOX1,ACOX3,ACP2,ACSF3,ACSL4,ACSL5,ACSM1,ACSS2,ACSS3,ACTB,ACTG1,ACTL6A,ACTN1,ACTN4,ACTR2,ACTR3,ACY1,ACY3,ACYP2,ADAM10,ADAP2,ADD1,ADD2,ADD3,ADHFE1,ADI1,ADIPOR2,ADK,ADPRH,ADSL,AFDN,AFMID,AGFG1,AGFG2,AGK,AGL,AGMAT,AGO1,AGO2,AGPAT2,AGPAT3,AGPAT5,AGRN,AGXT,AGXT2,AHCY,AHCYL2,AHNAK,AHSA1,AHSG,AIF1,AIP,AK2,AK3,AKR1A1,AKR1B10,AKR1C4,AKR1D1,AKT1,ALAS1,ALCAM,ALDH16A1,ALDH1A1,ALDH1B1,ALDH1L1,ALDH3A2,ALDH4A1,ALDH5A1,ALDH6A1,ALDH7A1,ALDH9A1,ALDOA,ALDOB,ALPK1,AMACR,AMBP,AMDHD2,AMPD2,AMT,AMY2A,ANGPTL3,ANGPTL4,ANKHD1/ANKHD1-EIF4EBP3,ANO10,ANPEP,ANXA1,ANXA11,ANXA3,ANXA4,ANXA5,AOX1,AP2A1,AP2M1,AP3B1,APCS,APEX1,API5,APMAP,APOA1,APOA2,APOB,APOC4,APOD,APOE,AQP1,AQP4,AQP9,ARAF,ARCN1,ARF4,ARF6,ARFGAP1,ARFGAP2,ARFGAP3,ARGLU1,ARHGAP17,ARHGAP31,ARHGAP42,ARHGAP45,ARHGAP5,ARHGDIA,ARHGDIB,ARHGEF12,ARHGEF7,ARIH1,ARMC10,ARPC1A,ARPC1B,ARPC2,ARPC5,ARPC5L,ARRB1,ARSB,AS3MT,ASAH1,ASCC1,ASCC2,ASGR1,ASGR2,ASL,ASPA,ASPDH,ASPG,ASPH,ASPSCR1,ASRGL1,ASS1,ATAD2B,ATG3,ATG4B,ATL3,ATP11C,ATP13A1,ATP1A1,ATP1B1,ATP1B3,ATP2A2,ATP2B1,ATP2B4,ATP5IF1,ATP5PO,ATP6AP1,ATP6AP2,ATP6V0D1,ATP6V1A,ATP6V1C1,ATP6V1E1,ATRX,ATXN10,ATXN2,AUP1,AVEN,B2M,B4GALNT1,BAAT,BABAM2,BAG3,BAG4,BAG5,BAIAP2,BASP1,BBOX1,BCAM,BCAP29,BCAP31,BCAS2,BCHE,BCKDHA,BCKDHB,BCKDK,BCL2L13,BCLAF1,BCO2,BCS1L,BET1L,BGN,BHMT,BHMT2,BID,BIN1,BIN2,BLMH,BLVRA,BLVRB,BMP2K,BNIP3,BPHL,BRAF,BSG,BTAF1,BTD,BUB3,BZW1,C11orf54,C12orf10,C12orf43,C1D,C1orf174,C1QA,C1QB,C2CD2,C4A/C4B,C6,C8A,C8B,C8G,C9,C9orf64,CACFD1,CACYBP,CAD,CADM1,CALCRL,CALR,CALU,CAMK1,CAND1,CANX,CAP1,CAPZA1,CAPZB,CARHSP1,CASK,CASP3,CASP7,CAT,CAVIN1,CBR1,CBWD1,CBX1,CBX3,CCAR1,CCDC134,CCDC167,CCDC22,CCDC25,CCDC40,CCDC47,CCDC51,CCDC58,CCDC9,CCDC93,CCS,CCT3,CD163,CD1D,CD2AP,CD302,CD36,CD38,CD47,CD68,CD81,CD82,CDA,CDC34,CDC37,Cdc42,CDC5L,CDC73,CDK11A,CDK12,CDK5,CDK5RAP3,CDK6,CDK9,CDKN1B,CDKN2C,CDO1,CDV3,CENPV,CEP290,CEP89,CES1,CES3,CFAP20,CFB,CFDP1,CFH,CFI,CGN,CHAC2,CHCHD4,CHD4,CHID1,CHMP2A,CHORDC1,CHPT1,CIAO3,CIDEB,CISD1,CISD2,CKAP4,CKB,CKM,CLCC1,CLDN12,CLDN3,CLEC10A,CLEC3B,CLEC4F,CLEC4G,CLIC1,CLIC4,CLIC5,CLINT1,CLPP,CLPTM1,CLTA,CLTB,CLU,CLYBL,CMAS,CMBL,CMC2,CMPK1,CMPK2,CMTM4,CNBP,CNDP2,CNOT1,CNOT2,CNOT3,CNOT9,CNP,CNPY2,COA7,COASY,COBLL1,COG3,COG5,COL18A1,COLGALT1,COMT,COMTD1,COPA,COPB1,COPB2,COPE,COPG1,COQ3,COQ4,COQ8A,COQ8B,COQ9,CORO1A,CORO1B,CORO1C,COTL1,COX15,COX19,COX5A,COX6B1,COX7A2,CP,CPB2,CPN1,CPNE3,CPOX,CPPED1,CPQ,CPS1,CPSF2,CPT2,CR1L,CRAT,CREB1,CRELD1,CRELD2,CRIP1,CRK,CRKL,CRNKL1,CRP,CRYL1,CRYM,CRYZ,CSAD,CSK,CSNK1E,CSNK2A1,CSNK2A2,CSNK2B,CSRP1,CSRP2,CSTF1,CSTF2,CSTF3,CTBP1,CTBS,CTDSP1,CTH,CTNNA1,CTNNB1,CTNNBL1,CTNND1,CTR9,CTSB,CTSC,CTSD,CTSF,CTSH,CTSO,CTSS,CTSV,CTSZ,CTTN,CUL1,CUL2,CUL3,CUTC,CXADR,CYB5A,CYB5B,CYB5R1,CYBC1,CYGB,CYP17A1,CYP1A2,CYP27A1,CYP2A6 (includes others),Cyp2b13/Cyp2b9,CYP2B6,Cyp2c54 (includes others),CYP2C8,CYP2F1,CYP2U1,CYP3A5,CYP3A7,CYP4A11,CYP4A22,CYP4B1,CYP4F3,CYP7A1,CYP7B1,DAAM1,DAD1,DAPK1,DARS2,DBNL,DCAF11,DCAKD,DCPS,DCTN2,DCTN4,DCTN6,DCUN1D1,DCUN1D2,DCXR,DDAH1,DDAH2,DDC,DDHD2,DDI2,DDOST,DDRGK1,DDX17,DDX18,DDX19A,DDX21,DDX23,DDX27,DDX39B,DDX3X,DDX3Y,DDX42,DDX46,DDX49,DDX5,DDX58,DDX6,DECR1,DECR2,DEK,DEPTOR,DES,DGAT2,DGLUCY,DHCR24,DHDH,DHFR,DHODH,DHRS7,DHRS7B,DHTKD1,DHX15,DHX16,DHX9,DIABLO,DIO1,DIS3,DKC1,DLAT,DMAC1,DMD,DMGDH,DNAJA1,DNAJB1,DNAJB11,DNAJB4,DNAJB6,DNAJB9,DNAJC1,DNAJC13,DNAJC19,DNAJC2,DNAJC25,DNAJC3,DNAJC7,DNM1L,DNM2,DNPEP,DNTTIP2,DOCK6,DPAGT1,DPM1,DPM3,DPP4,DPP7,DPP9,DPY19L1,DPY30,DPYD,DPYS,DPYSL2,DRG1,DSP,DTD1,DTX3L,DUSP23,DUT,DYNLL1,DYNLT3,DYSF,EBPL,ECHDC2,ECHDC3,ECI1,ECI2,ECM1,EDC4,EEA1,EEF1A1,EEF1D,EEF2,EFHD2,EFR3A,EFTUD2,EGF,EGFR,EHD1,EHD3,EHHADH,EIF1AX,EIF2A,EIF2AK2,EIF2B1,EIF2B2,EIF2B3,EIF2B5,EIF2S1,EIF2S2,EIF3A,EIF3C,EIF3D,EIF3E,EIF3F,EIF3H,EIF3I,EIF3K,EIF3L,EIF3M,EIF4A1,EIF4A2,EIF4A3,EIF4E,EIF4G1,EIF4G2,EIF4H,EIF5,EIF5A,EIF5B,ELAC2,ELAVL1,ELMO1,ELOA,ELOC,ELOVL1,ELOVL2,ELOVL5,ELOVL6,ELP2,EMC8,EMD,EMILIN1,EML3,EML4,ENO1,ENPEP,ENPP1,ENTPD5,EPB41,EPB41L2,EPB41L5,EPHX1,EPHX2,EPPK1,EPS15L1,EPS8L2,ERBIN,ERC1,ERGIC1,ERGIC2,ERGIC3,ERH,ERLIN1,ERMP1,ERP29,ERP44,ESAM,ESD,ESYT1,ESYT2,ETFDH,ETNK1,ETNPPL,EVA1A,Ewsr1,EXOC1,EXOC5,EXOC7,EXOSC9,EZR,F11,F13A1,FAAH,FABP2,FABP4,FABP5,FABP7,FADS6,FAF1,FAHD2B,FAM114A2,FAM126A,FAM126B,FAM210A,FAM234A,FAM3C,FAM50B,FAM98C,FARP1,FARS2,FASN,FAU,FBL,FBP1,FBXO3,FCGR2B,FCGRT,FCHO2,FDX2,FECH,FEN1,FERMT2,FETUB,FGA,FGB,FGG,FGL1,FHIT,FIS1,FITM2,FKBP11,FKBP15,FKBP3,FKBP4,FKBP5,FLII,FLNA,FLOT1,FLOT2,FMO1,FMO3,FMO4,FMO5,FMR1,FN1,FN3K,FN3KRP,FNDC3A,FNTA,FRAS1,FRG1,FSCN1,FTCD,FTO,FTSJ3,FUBP1,FUBP3,FXN,FXR1,FXYD1,G0S2,G6PC,G6PD,GAA,GABPA,GADD45GIP1,GALK1,GALK2,GALM,GALNS,GALNT2,GALT,GAMT,GANAB,GAPDH,GAPVD1,GART,GATAD2A,GATD1,GATM,GBA,GBE1,GBF1,GBP6,GCAT,GCC1,GCDH,GCH1,GCK,GCKR,GCLM,GCN1,GDA,GFM1,GFPT1,GGA1,GGCT,GID8,GIMAP4,GJB2,GLDC,GLG1,GLMP,GLO1,GLOD4,GLRX3,GLRX5,GLT1D1,GLTPD2,GLUD1,GLUL,GLYAT,GLYR1,Gm12854/S100a11,Gm21596/Hmgb1,GMPPA,GMPPB,GMPR2,GMPS,GNA11,GNA13,GNAI2,GNAI3,GNAQ,GNAS,GNE,GNG12,GNL3,GNMT,GNPAT,GNPDA1,GNS,GOLGA2,GOLGA5,GOLGA7,GOLPH3,GOLPH3L,G

	OPC,GORASP2,GOSR1,GOSR2,GOT1,GPAM,GPAT3,GPAT4,GPD1,GPD1L,GPHN,GPLD1,GPR182,GPRIN3,GPT,GPT2,GPX3,GRB7,GRHPR,GRIPAP1,GRN,GSPT1,GSR,Gsta4,GSTA5,GSTK1,GSTM1,GSTM2,GSTM4,GSTM5,GSTP1,GSTT2/GSTT2B,GSTZ1,GTF2F1,GTF2F2,GTF2I,GTPBP4,GUCY1B1,H3-3A/H3-3B,H6PD,HACL1,HADH,HAGH,HAL,HAO1,HAO2,HBS1L,HCCS,HCFC1,HDAC1,HDGF,HDGFL2,HDGFL3,HDLBP,HEATR1,HEBP1,HECTD1,HELZ2,HERPUD1,HEXB,HEXIM1,HGD,HGS,HIBADH,HIBCH,HINT2,HINT3,HIP1,HK1,HLA-A,HLA-DQA1,HMGA1,HMGCL,HMGCS1,HMGCS2,HMGN1,HMOX1,HMOX2,HNF1A,HNF4A,HNMT,HNRNPA2B1,HNRNPAB,HNRNPC,HNRNPD,HNRNPF,HNRNPH1,HNRNPH2,HNRNPK,HNRNPL,HNRNPLL,HNRNPM,HNRNPR,HNRNPU,HNRNPUL1,HNRNPUL2,HOMER2,HOPX,HP,HP1BP3,HPCAL1,HPD,HPGD,HPN,HPX,HRAS,Hrg,HS1BP3,HSCB,HSD11B1,HSD17B10,HSD17B11,HSD17B2,HSD17B4,HSD17B6,HSDL1,HSP90AA1,HSP90AB1,HSP90B1,HSPA12B,HSPA13,HSPA1A/HSPA1B,HSPA4L,HSPA5,HSPA8,HSPA9,HSPB1,HSPD1,HSPG2,HSPH1,HTATIP2,HUWE1,HYKK,HYOU1,HYPK,ICAM1,IDH2,IDH3B,IDO2,IFI16,IFIT1B,IFIT3,IFNAR2,IGF2R,IGFALS,IGKC,IK,IL6ST,ILF2,ILF3,ILK,ILKAP,IMMP2L,IMMT,IMPA1,IMPAD1,INHBC,INMT,INPP1,INPP5F,INSIG2,INSR,INTS3,IP6K1,IPO5,IQGAP1,ISCA2,ISOC1,ISOC2,IST1,ITGA1,ITGA2B,ITGA5,ITGA9,ITGAV,ITGB1,ITGB3,ITGB6,ITIH2,ITIH4,ITPR2,ITSN1,IYD,JCHAIN,JPT2,JUP,KANK2,KCTD12,KDELR1,KDSR,KHDRBS1,KHK,KHSRP,KIF13B,KIF21A,KLHDC7A,KLKB1,KPNA1,KPNA2,KRAS,KXD1,KYAT1,KYAT3,KYNU,L2HGDH,L3HYPDH,LAMTOR1,LAP3,LARP1,LARP4,LARP4B,LARP7,LARS2,LASP1,LBR,LCAT,LDAH,LDLR,LGALS1,LGALS3,LGALS3BP,LGALS8,LGALSL,LGMN,LHPP,LIAS,LIFR,LIMS2,LIN7A,LIN7C,LIPE,LITAF,LMAN1,LMAN2,LMAN2L,LMF1,LMNA,LMNB1,LMNB2,LMO7,LOC102724788/PRODH,LONP2,LPCAT3,LRG1,LRP1,LRPAP1,LRRFIP1,LSG1,LSM12,LSM14A,LSM14B,LSM5,LSM6,LSR,LUC7L,LUC7L2,LUC7L3,LUM,LYAR,LYN,LYPLA1,LYPLA2,LYPLAL1,LYVE1,LYZ,LZIC,M6PR,MACO1,MACROD1,MAGIX,MAN1A2,MAN2B1,MAN2B2,MAN2C1,MANBA,MANF,MAOA,MAOB,MAP2K1,MAP2K3,MAP4,MAPK1IP1L,MAPRE1,MAPRE3,MASP2,MAT1A,MAT2A,MATR3,MBL2,MBNL1,MBOAT7,MCAM,MCCC1,MCCC2,MCEE,MCFD2,MCTS1,MDH1,ME1,MEAF6,MECP2,METAP2,METTL26,METTL27,METTL7B,METTL9,MFAP1,MFN2,MGAT2,MGLL,MGST1,MIA3,MIEN1,MIF,MIF4GD,MIGA2,MIOS,MIPEP,MKNK1,MMAB,MME,MMUT,MOB1B,MOCS2,MOGS,MORF4L1,MOSPD2,MOV10,MPC1,MPC2,MPHOSPH10,MPI,MPP1,MPP6,MPRIP,MPST,MRC1,MRI1,MROH1,MRPL12,MRPL15,MRPL17,MRPL24,MRPL47,MRPL50,MRPL51,MRPS12,MRPS15,MRPS17,MRPS25,MRPS31,MRPS35,MRRF,MSH2,MSN,MSR1,MSRA,MSRB2,Mt1,Mt2,MTA2,MTAP,MTCH2,MTDH,MTFR1,MTFR1L,MTHFD1,MTHFS,MTMR6,MTOR,MTREX,MTSS1,MTX2,MUL1,MVK,MVP,MYBBP1A,MYCBP,MYEF2,MYH10,MYH11,MYH14,MYH9,MYL1,MYL12A,MYL6,MYLK,MYLPF,MYO18A,MYO1B,MYO1C,MYO1D,NAA15,NAA16,NAA25,NAA35,NAALAD2,NACA,NADK2,NAGA,NAGLU,NAMPT,NANP,NANS,NAP1L1,NAPRT,NARS1,NASP,NAT10,NAXD,NAXE,NCBP1,NCEH1,NCK1,NCL,NCOA5,NCSTN,NDRG1,NDST1,NDUFA10,NDUFA11,NDUFA13,NDUFA2,NDUFA3,NDUFAF2,NDUFAF3,NDUFAF7,NDUFB6,NDUFB7,NDUFB8,NECAP1,NECTIN2,NELFA,NELFB,NELFCD,NFIA,NFIB,NFIC,NFS1,NFU1,NFXL1,NGEF,NGLY1,NHLRC2,NHP2,NIBAN1,NID2,NIPSNAP2,NIT1,NLN,NLRX1,NME3,NMNAT1,NMRAL1,NMRK1,NMT2,NNMT,NOC2L,NOL6,NONO,NOP10,NOP16,NOP56,NOP58,NOS3,NOSTRIN,NPC1,NPC2,NQO1,NQO2,NR1H4,NR3C1,NRAS,NSF,NSFL1C,NSUN2,NUBPL,NUCB1,NUCB2,NUCKS1,NUDC,NUDCD3,NUDT12,NUDT13,NUDT14,NUDT16,NUDT19,NUDT21,NUDT3,NUDT4,NUDT7,NUDT9,NUFIP2,NUMA1,NUP153,NUP155,NUP160,NUP205,NUP210,NUP214,NUP35,NUP54,NUP93,NUP98,NUTF2,OAT,OCIAD2,OGA,OGFOD3,OGFR,OGT,OLA1,OPLAH,OPTN,ORMDL2,OS9,OSBPL9,OTOL1,OXCT1,OXR1,OXSM,PA2G4,PABPC1,PABPC4,PABPN1,PAFAH1B1,PAFAH1B2,PAFAH2,PAIP1,PAIP2,PAK2,PALD1,PALLD,PALMD,PAM16,PANK1,PAPSS1,PAPSS2,PARP1,PARP14,PARP9,PARS2,PARVA,PARVB,PAWR,PBDC1,PBLD,PC,PCBP1,PCCA,PCCB,PCDH1,PCDHB16,PCK1,PCNP,PCTP,PCYT1A,PDAP1,PDCD10,PDCD11,PDCD4,PDCD6IP,PDE2A,PDHA1,PDHB,PDIA3,PDIA4,PDIA5,PDIA6,PDK1,PDK2,PDLIM1,PDLIM5,PDLIM7,PDP2,PDXDC1,PDXK,PDZK1,PEBP1,PECAM1,PECR,PEX1,PEX11A,PEX11G,PEX12,PEX13,PEX14,PEX16,PEX19,PEX26,PEX3,PEX5,PEX6,PFAS,PFDN2,PFKFB1,PFKFB3,PGAM1,PGD,PGK1,PGM1,PGM3,PGM5,PGRMC1,PGRMC2,PHACTR4,PHB2,PHF20L1,PHKA1,PHKA2,PHKB,PHKG2,PHLDA1,PHLDB2,PHYHD1,PHYKPL,PI4KA,PICALM,PIGR,PIGS,PIGU,PIK3AP1,PIK3CB,PIN4,PIP5K1C,PIR,PITHD1,PITRM1,PKLR,PKN1,PKP4,PLA2G12B,PLBD1,PLBD2,PLCB3,PLCH1,PLEKHA5,PLEKHA7,PLEKHF1,PLG,PLIN5,PLOD3,PLPP3,PLRG1,PLS3,PLTP,PLVAP,PLXNA4,PLXNB2,PM20D1,PML,PMM2,PNKP,PNLIP,PNN,POLDIP3,POLR2A,POLR2B,POLR2I,POLR2L,PON1,PON2,PON3,POR,PPA1,PPAN,PPAT,PPCS,PPFIA1,PPFIBP2,PPIA,PPIB,PPIF,PPIG,PPIL1,PPIL4,PPIP5K2,PPL,PPM1A,PPM1B,PPM1G,PPM1K,PPP1R2,PPP1R21,PPP1R7,PPP1R8,PPP2R1B,PPP2R5A,PPP2R5D,PPP4C,PPP4R2,PPP4R3A,PPP6R1,PPP6R3,PPT1,PPT2,PPWD1,PQBP1,PRCP,PRDX3,PRDX5,PRDX6,PREB,PRELP,PREP,PRKAA2,PRKAB1,PRKACA,PRKAG1,PRKCSH,PRKRA,PROC,PROX1,PRPF19,PRPF3,PRPF31,PRPF4,PRPF40A,PRPF6,PRPF8,PRRC1,PRRC2C,PRUNE1,PRXL2A,PRXL2B,PSAP,PSEN1,PSIP1,PSMA1,PSMA2,PSMA3,PSMA4,PSMA5,PSMA6,PSMA7,PSMB1,PSMB10,PSMB2,PSMB3,PSMB5,PSMB6,PSMB7,PSMB9,PSMC3,PSMD14,PSMD3,PSMD4,PSMD7,PSME3,PSMF1,PTBP1,PTBP3,PTGES3,PTK2,PTK2B,PTPMT1,PTPN1,PTPRF,PTPRK,PTRHD1,PTS,PTTG1IP,PUF60,PUM1,PURA,PXMP2,PXMP4,PXN,PYCARD,PYGB,PYGL,QDPR,QSOX1,QTRT2,RAB14,RAB1A,RAB35,RAB3IP,RAB4A,RAB8A,RAB8B,RABGAP1,RABGAP1L,RABL3,RAC1,RACK1,RAD23B,RAD50,RAE1,RALY,RAN,RANBP1,RANBP10,RANBP3,RANGAP1,RAP1A,RAP1B,RAPGEF4,RARRES2,RASIP1,RBBP4,RBM10,RBM14,RBM15,RBM17,RBM22,RBM28,RBM39,RBM42,RBM47,RBP1,RBPMS,RCC2,RCN1,RDH16,REEP5,REEP6,RELA,RER1,RETREG2,RETSAT,REXO2,RFC2,RGL3,RGN,RGPD4 (includes others),RHOA,RHOC,RHOG,RIDA,RIOX2,RIPK1,RMDN2,RMDN3,RMND5A,RNASEH2A,RNASET2

	,RNF113A,RNF114,RNF14,RNF17,RNF185,RNF2,RNF20,RNF213,RNF5,RNH1,RNMT,RNPEP,ROCK2,RPAP3,RPE,RPL10,RPL10A,RPL11,RPL12,RPL13,RPL13A,RPL14,RPL15,RPL17,RPL18,RPL18A,RPL19,RPL21,RPL22,RPL23,Rpl23a,RPL24,RPL26,RPL27,RPL27A,RPL28,RPL3,RPL31,RPL35,RPL37,RPL37A,RPL4,RPL5,RPL6,RPL7,RPL7A,RPL8,RPL9,RPLP0,RPLP2,RPN1,RPN2,RPRD1B,RPS10,RPS11,RPS12,RPS13,RPS14,RPS15,RPS15A,RPS16,RPS19,RPS2,RPS20,RPS24,RPS25,RPS26,RPS27A,RPS27L,RPS29,RPS3,RPS4Y1,RPS5,RPS6,RPS6KB2,RPS7,RPS8,RPSA,RPTOR,RRAS,Rrbp1,RRS1,RSL1D1,RTF2,RTN1,RTN4,RTN4IP1,RUFY1,RUFY3,RUVBL1,RUVBL2,S100A1,S100A6,SAA1,SAE1,SAFB,SAMHD1,SAP18,SAR1B,SARDH,SARNP,SARS2,SART1,SART3,SAT2,SAYSD1,SBF1,SC5D,SCAMP1,SCAMP3,SCAMP4,SCAMP5,SCARB1,SCARB2,SCD,SCFD1,SCO1,SCPEP1,SCRIB,SCYL2,SCYL3,SDC4,SDF2L1,SDHD,SDR42E1,SDS,SDSL,SEC11A,SEC14L2,SEC14L4,SEC23B,SEC23IP,SEC24A,SEC24D,SEC31A,SEC61A1,SEC61B,SEC61G,SEC62,SEC63,SELENBP1,SELENOF,SELENOI,SELENOP,SEPHS1,SERBP1,SERHL2,SERINC3,SERPINA1,SERPINA10,SERPINA3,SERPINA6,SERPINB1,SERPIND1,SERPINF2,SERPING1,SERPINH1,SET,SF3A1,SF3A3,SF3B1,SF3B2,SF3B3,SF3B4,SF3B6,SFPQ,SFR1,SFT2D2,SFXN5,SGTA,SH3BGRL3,SH3GL1,SHMT1,SHOC2,SHPK,SHTN1,SIAE,SIGLEC1,SIGMAR1,SIL1,SLC12A9,SLC16A7,SLC17A3,SLC22A1,SLC22A18,SLC22A23,SLC22A25,SLC25A10,SLC25A11,SLC25A12,SLC25A13,SLC25A20,SLC25A21,SLC25A23,SLC25A25,SLC25A3,SLC25A45,SLC25A5,SLC26A1,SLC27A4,SLC2A2,SLC30A5,SLC31A1,SLC35A1,SLC35A3,SLC35B1,SLC35D1,SLC38A10,SLC38A3,SLC39A11,SLC39A14,SLC39A4,SLC44A2,SLC4A4,SLC6A12,SLC6A13,SLC7A2,SLC9A3R1,SLC9A3R2,Slco1a1,SLCO1B3,SLCO2A1,SLK,SLMAP,SLTM,SMAP1,SMAP2,SMARCA2,SMARCA5,SMARCD2,SMARCE1,SMC1A,SMC3,SMIM15,SMOC1,SMPD1,SMS,SMU1,SNAP23,SNAP47,SND1,SNF8,SNRNP200,SNRNP70,SNRPA1,SNRPB2,SNRPD3,SNRPF,SNRPN,SNTA1,SNTB1,SNU13,SNW1,SNX1,SNX18,SNX2,SNX3,SNX4,SNX5,SNX6,SNX7,SOAT2,SON,SORBS1,SORBS2,SORD,SOS1,SPAG9,SPAST,SPCS1,SPCS2,SPG7,SPPL2A,SPR,SPTAN1,SPTBN2,SQOR,SRA1,SREK1,SRI,SRP19,SRP68,SRP72,SRP9,SRPK2,SRPRB,SRR,SRRT,SRSF1,SRSF10,SRSF2,SRSF3,SRSF4,SRSF6,SRSF7,SSBP1,SSR1,SSR3,SSR4,SSRP1,ST13,STAB1,STAB2,STAG2,STARD5,STAT2,STAT3,STAT6,STBD1,STEAP3,STEAP4,STIP1,STK38,STK38L,STOML2,STRAP,STRN,STT3A,STT3B,SUB1,SUCLG1,SUCLG2,SUGCT,SUGT1,SULT1B1,SULT1C2,SULT1E1,SULT2A1,SUMO2,SUN2,SUOX,SUPT16H,SURF1,SURF4,SVIL,SWAP70,SYAP1,SYMPK,SYNCRIP,SYNGR2,SYNJ2BP,TACO1,TADA3,TAGLN,TAGLN2,TALDO1,TAMM41,TANGO2,TAOK3,TAP1,TAP2,TAPBP,TARDBP,TAT,TBC1D13,TBC1D15,TBC1D17,TBC1D24,TBC1D8B,TBC1D9B,TBCD,TBCEL,TBL2,TBRG4,TCEA1,TCERG1,TCIRG1,TCOF1,TDO2,TFR2,TGFBRAP1,TGM1,THNSL2,THOC2,THRAP3,THRSP,THYN1,TIAL1,TIGAR,TIMM17B,TIMM22,TIMM44,TIMMDC1,TINAGL1,TJP1,TJP2,TJP3,TKFC,TKT,TLN1,TM9SF1,TM9SF2,TM9SF3,TMED1,TMED10,TMED2,TMED3,TMED4,TMED5,TMED7,TMED9,TMEM109,TMEM126A,TMEM126B,TMEM135,TMEM176B,TMEM19,TMEM214,TMEM230,TMEM256,TMEM30A,TMEM33,TMEM38B,TMEM43,TMEM82,TMLHE,TMOD3,TMPO,TMTC3,TMX1,TMX3,TNKS1BP1,TNPO1,TNPO2,TNPO3,TNS2,TNS3,TOLLIP,TOM1,TOMM40,TOP1,TOP2B,TOP3B,TOR1A,TOR1AIP1,TPD52,TPD52L2,TPI1,TPK1,TPM3,TPPP,TPR,TPRG1L,TRA2B,TRABD,TRAM1,TRAP1,TRAPPC1,TRAPPC4,TRIM14,TRIM23,TRIM28,TRIP10,TRIP11,TRIR,TRMU,TSC22D1,TSFM,TSG101,TSPAN14,TSPAN31,TSTA3,TTC1,TTC36,TTC37,TTC38,TTC39A,TTC39C,TTC7A,TTN,TTPA,TUBA1B,TUBA4A,TUBB,TUBB2A,TUBB4B,TUT7,TWF1,TXLNA,TXLNG,TXN2,TXNDC5,TXNDC9,TXNL1,TYMP,TYSND1,U2AF2,U2SURP,UBA1,UBA2,UBA3,UBA7,UBAC1,UBAP2,UBE2G2,UBE2I,UBE2J1,UBE2M,UBE2V2,UBE2Z,UBE4B,UBL4A,UBL7,UBQLN2,UBR2,UBTF,UCHL5,UCK1,UFL1,UGDH,UGGT1,UGP2,UGT1A4,UGT1A6,UGT1A8 (includes others),UGT2B10,UGT2B17,UGT2B28,UGT3A1,UPB1,UPF1,UPF2,UPP1,UQCC1,UQCC3,UQCRC2,UROC1,USO1,USP16,USP19,USP24,USP46,USP7,VAC14,VAMP2,VAMP3,VAMP8,VAPB,VAT1,VAV2,VCAM1,VCL,VCPIP1,VDAC2,VDAC3,VIM,VKORC1L1,VMO1,VNN1,VPS13D,VPS25,VPS26A,VPS26B,VPS26C,VPS28,VPS33B,VPS35,VPS45,VPS51,VPS52,VRK1,VSIG4,VTA1,VTN,VWA8,WAPL,WASF2,WASHC3,WASHC4,WASHC5,WBP11,WBP2,WDFY1,WDR1,WDR18,WDR26,WDR36,WDR46,WDR5,WDR61,WDR77,WFS1,WRNIP1,XAF1,XPNPEP1,XPO1,XPO5,XRCC6,XRN1,XRN2,YBX1,YBX3,YME1L1,YTHDF2,YTHDF3,YWHAQ,YWHAZ,ZBTB20,ZBTB8OS,ZC3H11A,ZC3H14,ZC3HAV1,ZFR,ZHX1,ZHX2,ZHX3,ZMAT2,ZMIZ1,ZNF326,ZNF638

1. Protein Synthesis 2. Metabolism of protein 3. 1.93E-60 4. Increased 5. 4.001 6. 434	A1CF,AAK1,ACO1,ACY1,ADAM10,ADI1,AGO2,AHSG,AKT1,AMBP,AMPD2,ANPEP,ANXA1,APCS,APEX1,APOA1,APOA2,APOB,APOE,APOM,ARIH1,ARRB1,ASGR2,ASPH,ATG4B,ATP1B1,ATP1B3,B2M,BAG3,BAG5,BUB3,C4A/C4B,CALR,CALU,CANX,CAPNS1,CASP3,CASP7,CAT,CCDC47,CCT3,CD81,CDC26,CDC37,CDK11A,CDK5,CDKN1B,CHP1,CKAP4,CLU,CNBP,CNDP2,CNOT1,COG3,COPG1,CP,CPB2,CPN1,CPQ,CREB1,CRK,CSNK1E,CSNK2A1,CTNNB1,CTNND1,CTSB,CTSC,CTSD,CTSF,CTSH,CTSO,CTSS,CTSV,CTSZ,CUL2,CUL3,CYFIP1,DAPK1,DCTN2,DDI2,DDX39B,DDX3X,DDX6,DEPTOR,DHFR,DHX9,DKC1,DNAJC1,DNAJC3,DPM3,DPP4,DPP7,DTX3L,DYSF,EEF1A1,EEF1D,EEF1G,EEF2,EGF,EGFR,Eif1,EIF1AX,EIF2A,EIF2AK2,EIF2B1,EIF2B2,EIF2B3,EIF2B5,EIF2S1,EIF2S2,EIF3A,EIF3C,EIF3D,EIF3E,EIF3F,EIF3H,EIF3I,EIF3K,EIF3L,EIF3M,EIF4A1,EIF4A2,EIF4A3,EIF4E,EIF4G1,EIF4G2,EIF4H,EIF5,EIF5A,EIF5B,ELAVL1,ENPEP,ERP44,EVA1A,F11,FAF1,FBXO3,FCGR2B,FGA,FGG,FLNA,FLOT1,FLOT2,FMR1,FN1,Fus,FXR1,GADD45GIP1,GAPDH,GBA,GFM1,GGA1,GNAQ,GOLGA7,GOLPH3,GPLD1,GRB7,GRN,GSPT1,GTPBP4,H3-3A/H3-3B,H4C15,HCFC1,HDAC1,HERPUD1,HEXB,HGS,HIP1,HNRNPD,HNRNPK,HNRNPL,HOMER2,HPN,HRAS,HSP90AA1,HSP90AB1,HSP90B1,HSPA1A/HSPA1B,HSPA5,HSPA8,HSPB1,HSPD1,HSPG2,HYPK,ICAM1,IGFALS,ILF3,IMMP2L,INSR,Irgm1,IST1,ITGB1,ITIH2,KHDRBS1,KLKB1,KRAS,L2HGDH,LARP1,LARP4,LARP4B,LCAT,LDLR,LGALS1,LGMN,LMNA,LSR,LYN,LYZ,MAN1A2,MANBA,MAP2K1,MAP2K3,METAP2,MIA3,MKNK1,MME,MRPL12,MRPL15,MRPL17,MRPL24,MRPL32,MRPL41,MRPL47,MRPL50,MRPL51,MRPS12,MRPS15,MRPS17,MRPS25,MRPS31,MRPS35,MRRF,MTOR,MUL1,MVK,MYBBP1A,MYH9,NAA15,NAA16,NAALAD2,NACA,NAGLU,NAT10,NCBP1,NCBP2,NCK1,NCL,NCSTN,NDUFA13,NGLY1,NIBAN1,NLN,NPC1,NR3C1,NRAS,NSF,NUCB1,OGA,OGT,OS9,PABPC1,PABPC4,PAIP1,PAIP2,PCBP1,PDCD10,PDCD4,PDIA6,PEX19,PEX6,PHB2,PIK3CB,PITRM1,PLG,PLPP3,PLTP,PML,POLDIP3,PPAT,PPIB,PPM1G,PPP1R2,PREP,PRKAA2,PRKCSH,PRKRA,PROC,PSEN1,PSMB3,PSMB5,PSMD14,PSME3,PSMF1,PTBP1,PTGES3,PTK2B,PYCARD,QSOX1,RACK1,Rbx1,RCN1,RELA,RIDA,RNASET2,RNF185,RNF20,RNF213,RNF5,RNPEP,RPL10,RPL10A,RPL11,RPL12,RPL13,RPL13A,RPL14,RPL15,RPL17,RPL18,RPL18A,RPL19,RPL21,RPL22,RPL23,RPL24,RPL26,RPL27,RPL27A,RPL28,Rpl29 (includes others),RPL3,RPL30,RPL31,RPL35,RPL35A,RPL37,RPL37A,RPL38,RPL4,RPL5,RPL6,RPL7,RPL7A,RPL8,RPL9,RPLP0,Rplp1 (includes others),RPLP2,RPS10,RPS11,RPS12,RPS13,RPS14,RPS15,RPS15A,RPS16,RPS17,RPS19,RPS2,RPS20,RPS21,RPS23,RPS24,RPS25,RPS26,RPS27A,RPS28,RPS29,RPS3,RPS4Y1,RPS5,RPS6,RPS6KB2,RPS7,RPS8,RPS9,RPSA,RTN4,SAA1,SARS1,SDC4,SEC23B,SERPINA1,SERPINA10,SERPINB1,SERPIND1,SF3B3,SHMT1,SNF8,SNRNP70,SNX1,SNX3,SOS1,SPCS1,SPCS3,SPPL2A,SPTBN2,SRSF3,STAT3,STAT6,STIP1,STT3B,SUGT1,SWAP70,SYNCRIP,TADA3,TARDBP,TCIRG1,TCOF1,TGM1,TPR,TSFM,TSG101,TSPAN14,TYSND1,UBA3,UBE2G2,UBE2I,UBE2Z,UBE4B,UBR2,UPF1,USP19,USP7,VIM,VPS28,VPS35,VTN,WFS1,XPNPEP1,XPO1,XRN1,YBX1,YTHDF3
1. Infectious Diseases 2. Viral Infection 3. 3.4E-49 4. Increased 5. 9.109 6. 498	AASS,ABCC2,ABCD2,ABCE1,ACACB,ACADSB,ACTB,ACTN1,ACTR2,ACTR3,ADAM10,ADK,AGFG1,AGO1,AGO2,AIP,AKT1,AMDHD2,AMY2A,ANPEP,ANXA1,ANXA5,AP2A1,AP2M1,APCS,APOA1,APOB,APOE,ARAF,ARCN1,ARF6,ARGLU1,ARHGDIB,ARHGEF12,ARPC1A,ARPC1B,ARPC3,ARPC5,ARRB1,ASGR2,ATG4B,ATOX1,ATP1B3,ATP5IF1,ATP6AP1,ATP6AP2,ATP6V0D1,ATP6V1A,ATRX,ATXN2,B2M,BCLAF1,BGN,BMP2K,BSG,Bst2,C1orf174,C4A/C4B,CAD,CAMK1,CASP3,CAT,CCAR1,CCDC134,CCDC51,CD36,CD38,CD47,CD81,CDC73,CDKN1B,CES1,CFI,CHCHD2,CHMP2A,CHORDC1,CKM,CLDN3,CLEC10A,CLEC4G,CLIC4,CLTA,CLTB,CLU,CNP,COASY,COG3,COG5,COPA,COPB1,COPB2,COPG1,COPZ1,CREB1,CRP,CSNK2A1,CSNK2B,CTBP1,CTNNB1,CTSB,CTSS,CTSV,CTSZ,CXADR,CYB5B,CYP17A1,CYP2B6,CYP2U1,CYP3A5,CYP3A7,DCTN2,DDOST,DDX17,DDX23,DDX3X,DDX5,DDX58,DDX6,DEK,DHFR,DHODH,DHX15,DHX9,DNAJA1,DNAJB1,DNM1L,DNM2,DPM1,DPP4,DYSF,EEA1,EEF1A1,EGF,EGFR,EIF1AY,EIF2AK2,EIF2B5,EIF2S1,EIF3A,EIF3C,EIF3H,EIF3I,EIF3L,EIF4A3,ELOA,ELOC,EPN1,ERC1,EXOSC5,F13A1,FASN,FAU,FBL,FCGR2B,FCGRT,FCHO2,FGA,FLII,FLNA,FLOT2,FN1,FNTA,FSCN1,FUBP1,FXR1,GAA,GANAB,GAPDH,GAPVD1,GATAD2A,GBF1,GCK,GLUL,GLYR1,Gm21596/Hmgb1,GOLPH3,GOPC,GOSR2,GPR182,GPT,GPT2,GTF2I,H3-3A/H3-3B,HAO1,HDAC1,HEATR1,HECTD1,HERPUD1,HGS,HIBCH,HIP1,HLA-A,HLA-DQA1,HMGA1,HMGCS1,HMOX1,HNF4A,HNRNPC,HNRNPF,HNRNPH1,HNRNPK,HNRNPM,HNRNPR,HNRNPU,HP,HPGD,HRAS,HSP90AA1,HSP90AB1,HSP90B1,HSPA5,HSPA9,HSPD1,HUWE1,ICAM1,IFIT3,IFNAR2,IGF2R,Igha,IGKC,ILF3,INSR,ITGA2B,ITGA5,ITGAV,ITGB1,ITGB3,JCHAIN,KHDRBS1,KHSRP,KPNA1,KPNA2,KRAS,KXD1,LARP1,LDLR,LGALS1,LGALS3,LIFR,LIN7C,LMAN2,LMNA,LRPAP1,LSM14B,MAN2B1,MANBA,MAOA,MAOB,MAP2K1,MAP2K3,MAP4,MAPRE1,MAPRE3,MAT2A,MBL2,MCAM,MGLL,MID1IP1,MIF,MKNK1,MMUT,MOV10,MRC1,MRPS12,MSH2,MSR1,MSRA,MSRB2,MTOR,MVP,MYEF2,NCL,NDUFA10,NDUFAF2,NDUFAF3,NDUFB7,NGLY1,NIPSNAP2,NLRX1,NMT2,NOP56,NPC1,NR3C1,NUBPL,NUDCD3,NUDT3,NUP153,NUP155,NUP160,NUP205,NUP210,NUP214,NUP35,NUP54,NUP93,NUP98,OGT,OPTN,PAK2,PANK1,PARP1,PARP9,PARVA,PARVB,PCK1,PCTP,PDCD6IP,PDIA3,PDIA6,PDXK,PGM1,PGRMC2,PI4KA,PICALM,PIK3CB,PIP5K1C,PLG,PLOD3,PM20D1,PML,PNKP,POLR2A,POLR2H,POLR2I,POLR2L,POR,PPIA,PPIB,PPM1B,PPM1K,PPP1R8,PPP4C,PRKACA,PRKRA,PROC,PRPF6,PRPF8,PSIP1,PSMA1,PSMA2,PSMA3,PSMA5,PSMA7,PSMB6,PSMB9,PSMC3,PSMD14,PSMD4,PTGES3,PTK2B,PTPMT1,PTPN1,PURA,PYCARD,PYGL,RAB8A,RAB8B,RAC1,RACK1,RAE1,RAN,RANBP1,RAP1B,RBM10,RBM17,RBM42,RELA,RGPD4 (includes others),RHOA,RHOC,RNH1,RPL10A,RPL12,RPL13A,RPL18,RPL3,RPL35,RPL38,RPL5,RPS10,RPS13,RPS14,RPS16,RPS20,RPS23,RPS27A,RPS4Y1,RPS5,RPS6,RPS6KB2,RPSA,RSL1D1,RUVBL2,S100A1,SAE1,SAFB,SAMHD1,SART3,SCARB1,SCARB2,SCFD1,SEC14L2,SEC61G,SELENOK,SERINC3,SERPINA1,SERPINA10,SF3A1,SF3B1,SF3B2,SF3B6,SFPQ,SIGLEC1,SIGMAR1,SLC31A1,SLC9A3R1,

	SLCO2A1,SMARCA2,SMPD1,SMU1,SNAP23,SNRNP70,SNRPA1,SNRPD3,SNRPF,SNU13,SNW1,SNX6,SON,SPAST,SPCS1,SPCS3,SPG7,SPTAN1,SRPK2,SRRT,SRSF1,SRSF2,SRSF6,SSR1,SSR3,SSRP1,ST13,STAB1,STAT2,STAT3,STAT6,STIP1,STT3A,SUB1,SUCLG2,SUMO2,SUPT16H,SYNCRIP,TAGLN2,TALDO1,TAMM41,TAP1,TAT,TCIRG1,THOC2,TIMM17B,TKFC,TKT,TM9SF2,TMED2,TMPO,TNPO3,TOP2B,TOP3B,TPPP,TPR,TRAPPC1,TRIM14,TSG101,TUBA4A,TUBB,TUBB2A,TUBB4B,TWF1,UBA7,UBE2H,UBE2I,UBE2Z,USP7,VAMP3,VAMP8,VAPB,VPS28,VTA1,VTN,WASF2,WDR46,XPNPEP1,XPO1,XRN1,YBX1,ZC3HAV1
1. Protein Synthesis 2. Synthesis of protein 3. 3.93E-49 4. Increased 5. 3.25 6. 233	ACO1,AGO2,AKT1,AMPD2,ANXA1,APEX1,ARRB1,CALR,CASP3,CDK11A,CDKN1B,CNBP,CNOT1,CREB1,CRK,CSNK1E,CTNNB1,CYFIP1,DAPK1,DCTN2,DDX39B,DDX3X,DDX6,DEPTOR,DHFR,DHX9,DKC1,DNAJC1,EEF1A1,EEF1D,EEF1G,EEF2,EGF,EGFR,Eif1,EIF1AX,EIF2A,EIF2AK2,EIF2B1,EIF2B2,EIF2B3,EIF2B5,EIF2S1,EIF2S2,EIF3A,EIF3C,EIF3D,EIF3E,EIF3F,EIF3H,EIF3I,EIF3K,EIF3L,EIF3M,EIF4A1,EIF4A2,EIF4A3,EIF4E,EIF4G1,EIF4G2,EIF4H,EIF5,EIF5A,EIF5B,ELAVL1,FCGR2B,FMR1,FN1,Fus,FXR1,GADD45GIP1,GAPDH,GFM1,GNAQ,GOLPH3,GRB7,GSPT1,HDAC1,HNRNPD,HNRNPK,HNRNPL,HRAS,HSPA1A/HSPA1B,HSPA5,HSPB1,ICAM1,ILF3,INSR,ITGB1,KHDRBS1,KRAS,LARP1,LARP4,LARP4B,LYN,MAP2K1,MAP2K3,METAP2,MKNK1,MRPL12,MRPL15,MRPL17,MRPL24,MRPL32,MRPL41,MRPL47,MRPL50,MRPL51,MRPS12,MRPS15,MRPS17,MRPS25,MRPS31,MRPS35,MRRF,MTOR,MVK,MYBBP1A,NAT10,NCBP1,NCBP2,NCK1,NCL,NIBAN1,NPC1,NR3C1,NRAS,PABPC1,PABPC4,PAIP1,PAIP2,PCBP1,PDCD4,PLG,PLTP,POLDIP3,PPAT,PPM1G,PPP1R2,PRKAA2,PRKRA,PTBP1,PTK2B,RACK1,RIDA,RNASET2,RPL10,RPL10A,RPL11,RPL12,RPL13,RPL13A,RPL14,RPL15,RPL17,RPL18,RPL18A,RPL19,RPL21,RPL22,RPL23,RPL24,RPL26,RPL27,RPL27A,RPL28,Rpl29 (includes others),RPL3,RPL30,RPL31,RPL35,RPL35A,RPL37,RPL37A,RPL38,RPL4,RPL5,RPL6,RPL7,RPL7A,RPL8,RPL9,RPLP0,Rplp1 (includes others),RPLP2,RPS10,RPS11,RPS12,RPS13,RPS14,RPS15,RPS15A,RPS16,RPS17,RPS19,RPS2,RPS20,RPS21,RPS23,RPS24,RPS25,RPS26,RPS27A,RPS28,RPS29,RPS3,RPS4Y1,RPS5,RPS6,RPS6KB2,RPS7,RPS8,RPS9,RPSA,SARS1,SEC23B,SHMT1,SNRNP70,SRSF3,STAT3,STAT6,STIP1,SWAP70,SYNCRIP,TCOF1,TPR,TSFM,UPF1,VIM,VTN,XRN1,YBX1,YTHDF3

1. Cancer,Organismal Injury and Abnormalities 2. Adenocarcinoma 3. 6.69E-37 4. Increased 5. 2.454 6. 1912	A1CF,AACS,AADAT,AAK1,AAMDC,AASDHPPT,AASS,ABAT,ABCB10,ABCB4,ABCB6,ABCB8,ABCB9,ABCC2,ABCC3,ABCC6,ABCD1,ABCD2,ABCD3,ABCE1,ABCF2,ABCF3,ABCG5,ABHD11,ABHD14B,ABHD15,ACACB,ACAD10,ACAD11,ACAD9,ACADM,ACADSB,ACAT1,ACAT2,ACBD5,ACIN1,ACLY,ACMSD,ACO1,ACOT1,ACOT11,ACOT12,ACOT13,ACOT7,ACOT8,ACOX1,ACOX3,ACP2,ACSF3,ACSL4,ACSM1,ACSS2,ACSS3,ACTB,ACTG1,ACTN1,ACTN4,ACTR2,ACTR3,ACY1,ACY3,ACYP2,ADAM10,ADAP2,ADD1,ADD2,ADD3,ADHFE1,ADIPOR2,ADK,ADSL,AFDN,AFMID,AGFG1,AGFG2,AGK,AGL,AGO1,AGO2,AGPAT2,AGPAT5,AGRN,AGXT,AGXT2,AHCY,AHCYL2,AHNAK,AHSA1,AHSG,AIF1,AIP,AK3,AKR1A1,AKR1B10,AKT1,ALAS1,ALCAM,ALDH16A1,ALDH1A1,ALDH1B1,ALDH1L1,ALDH3A2,ALDH4A1,ALDH5A1,ALDH6A1,ALDH7A1,ALDH9A1,ALDOA,ALDOB,ALPK1,AMACR,AMBP,AMPD2,AMT,AMY2A,ANGPTL3,ANGPTL4,ANKHD1/ANKHD1-EIF4EBP3,ANO10,ANPEP,ANXA1,ANXA11,ANXA3,ANXA4,ANXA5,AOX1,AP2A1,AP2M1,AP3B1,APEX1,API5,APMAP,APOB,APOC4,APOD,APOE,AQP1,AQP4,AQP9,ARAF,ARCN1,ARF6,ARFGAP1,ARFGAP2,ARFGAP3,ARHGAP17,ARHGAP31,ARHGAP42,ARHGAP45,ARHGAP5,ARHGDIA,ARHGEF12,ARHGEF7,ARIH1,ARMC10,ARPC1A,ARPC1B,ARPC5L,ARRB1,ARSB,ASAH1,ASCC1,ASCC2,ASGR2,ASL,ASPA,ASPG,ASPSCR1,ASRGL1,ASS1,ATAD2B,ATG3,ATL3,ATP11C,ATP13A1,ATP1A1,ATP1B1,ATP1B3,ATP2A2,ATP2B1,ATP2B4,ATP5IF1,ATP6AP1,ATP6AP2,ATP6V0D1,ATP6V1C1,ATP6V1E1,ATRX,ATXN10,ATXN2,AUP1,AVEN,B2M,B4GALNT1,BAAT,BABAM2,BAG3,BAG4,BAG5,BAIAP2,BASP1,BCAM,BCAP29,BCAS2,BCHE,BCKDHA,BCKDK,BCL2L13,BCLAF1,BCO2,BCS1L,BET1L,BGN,BHMT,BHMT2,BID,BIN1,BIN2,BLMH,BLVRA,BLVRB,BMP2K,BNIP3,BPHL,BRAF,BSG,BTAF1,BTD,BUB3,BZW1,C11orf54,C12orf10,C1orf174,C1QA,C1QB,C2CD2,C4A/C4B,C6,C8A,C8B,C8G,C9,CACFD1,CACYBP,CAD,CADM1,CALCRL,CALU,CAMK1,CAND1,CANX,CAP1,CAPZA1,CAPZB,CASK,CASP3,CASP7,CAVIN1,CBR1,CBWD1,CBX1,CBX3,CCAR1,CCDC134,CCDC167,CCDC22,CCDC25,CCDC40,CCDC47,CCDC51,CCDC58,CCDC9,CCDC93,CCS,CCT3,CD163,CD1D,CD2AP,CD302,CD36,CD38,CD47,CD68,CD81,CD82,CDA,CDC34,CDC37,CDC5L,CDC73,CDK11A,CDK12,CDK5,CDK5RAP3,CDK6,CDK9,CDKN1B,CDKN2C,CDO1,CDV3,CENPV,CEP290,CEP89,CES1,CES3,CFAP20,CFB,CFDP1,CFH,CFI,CGN,CHAC2,CHCHD4,CHD4,CHORDC1,CHPT1,CIAO3,CISD2,CKAP4,CKB,CKM,CLCC1,CLDN3,CLEC10A,CLEC3B,CLEC4F,CLIC4,CLINT1,CLPP,CLPTM1,CLTB,CLU,CLYBL,CMAS,CMBL,CMC2,CMPK1,CMPK2,CMTM4,CNDP2,CNOT1,CNOT2,CNOT3,CNOT9,CNP,CNPY2,COA7,COBLL1,COG3,COG5,COL18A1,COLGALT1,COMT,COPA,COPB1,COPB2,COPE,COPG1,COQ3,COQ8A,COQ8B,COQ9,CORO1A,CORO1B,CORO1C,COTL1,COX15,COX19,COX6B1,COX7A2,CP,CPB2,CPN1,CPNE3,CPOX,CPQ,CPS1,CPSF2,CPT2,CR1L,CRAT,CREB1,CRELD1,CRELD2,CRK,CRKL,CRNKL1,CRP,CRYL1,CRYM,CRYZ,CSK,CSNK1E,CSNK2A1,CSNK2A2,CSNK2B,CSRP2,CSTF1,CSTF2,CSTF3,CTBP1,CTBS,CTDSP1,CTH,CTNNA1,CTNNB1,CTNNBL1,CTNND1,CTR9,CTSB,CTSC,CTSD,CTSF,CTSV,CTTN,CUL1,CUL2,CUL3,CUTC,CXADR,CYB5R1,CYGB,CYP17A1,CYP1A2,CYP27A1,CYP2A6 (includes others),CYP2B6,CYP2C8,CYP2F1,CYP2U1,CYP3A5,CYP3A7,CYP4A22,CYP4B1,CYP4F3,CYP7A1,CYP7B1,DAAM1,DAD1,DAPK1,DARS2,DBNL,DCAF11,DCAKD,DCPS,DCTN4,DCTN6,DCUN1D2,DCXR,DDC,DDHD2,DDI2,DDOST,DDX17,DDX18,DDX19A,DDX21,DDX23,DDX27,DDX39B,DDX3X,DDX3Y,DDX42,DDX49,DDX5,DDX58,DDX6,DECR1,DECR2,DEK,DES,DGAT2,DGLUCY,DHCR24,DHFR,DHODH,DHRS7,DHRS7B,DHTKD1,DHX15,DHX16,DHX9,DIABLO,DIO1,DIS3,DKC1,DLAT,DMD,DMGDH,DNAJA1,DNAJB11,DNAJB4,DNAJB6,DNAJB9,DNAJC1,DNAJC13,DNAJC19,DNAJC2,DNAJC7,DNM1L,DNM2,DNPEP,DOCK6,DPAGT1,DPM1,DPM3,DPP4,DPP7,DPP9,DPY19L1,DPYD,DPYS,DPYSL2,DSP,DTX3L,DYSF,EBPL,ECHDC2,ECI1,ECM1,EDC4,EEA1,EEF1A1,EEF1D,EEF2,EFHD2,EFR3A,EFTUD2,EGF,EGFR,EHD1,EHD3,EHHADH,EIF1AX,EIF2AK2,EIF2B1,EIF2B2,EIF2B3,EIF2S1,EIF2S2,EIF3A,EIF3C,EIF3D,EIF3E,EIF3F,EIF3H,EIF3I,EIF3L,EIF3M,EIF4A1,EIF4A2,EIF4E,EIF4G1,EIF4G2,EIF5,EIF5B,ELAC2,ELAVL1,ELMO1,ELOA,ELOC,ELOVL1,ELOVL5,ELP2,EMILIN1,EML3,EML4,ENO1,ENPEP,ENPP1,ENTPD5,EPB41,EPB41L2,EPB41L5,EPHX1,EPHX2,EPPK1,EPS15L1,EPS8L2,ERBIN,ERC1,ERGIC1,ERGIC2,ERGIC3,ERH,ERLIN1,ERMP1,ERP44,ESD,ESYT1,ESYT2,ETFDH,ETNK1,ETNPPL,EVA1A,EXOC1,EXOC5,EXOC7,EXOSC9,EZR,F11,F13A1,FAAH,FABP4,FABP5,FADS6,FAF1,FAHD2B,FAM114A2,FAM126B,FAM234A,FAM3C,FAM50B,FAM98C,FARP1,FARS2,FASN,FBL,FBP1,FBXO3,FCGR2B,FCGRT,FCHO2,FECH,FEN1,FERMT2,FETUB,FGA,FGB,FGG,FGL1,FHIT,FIS1,FKBP11,FKBP15,FKBP3,FKBP4,FKBP5,FLII,FLNA,FLOT1,FLOT2,FMO1,FMO3,FMO4,FMO5,FMR1,FN1,FN3K,FN3KRP,FNDC3A,FNTA,FRAS1,FRG1,FSCN1,FTO,FTSJ3,FUBP1,FUBP3,FXR1,FXYD1,G0S2,G6PC,G6PD,GAA,GADD45GIP1,GALK1,GALK2,GALM,GALNS,GALNT2,GALT,GAMT,GANAB,GAPDH,GAPVD1,GART,GATAD2A,GATM,GBE1,GBF1,GCAT,GCC1,GCDH,GCK,GCKR,GCLM,GCN1,GDA,GFM1,GFPT1,GGA1,GGCT,GID8,GJB2,GLDC,GLG1,GLMP,GLRX3,GLRX5,GLT1D1,GLTPD2,GLUL,GLYAT,GLYR1,Gm12854/S100a11,GMPPA,GMPPB,GMPR2,GMPS,GNA11,GNA13,GNAI2,GNAQ,GNAS,GNE,GNG12,GNMT,GNPAT,GNS,GOLGA2,GOLGA5,GOLPH3L,GOPC,GORASP2,GOSR1,GOT1,GPAM,GPAT3,GPD1,GPHN,GPLD1,GPR182,GPRIN3,GPT,GPT2,GPX3,GRB7,GRHPR,GRIPAP1,GSPT1,GSR,GSTA5,GSTK1,GSTM1,GSTM2,GSTM4,GSTM5,GSTP1,GSTZ1,GTF2F1,GTF2I,GTPBP4,GUCY1B1,H6PD,HACL1,HADH,HAGH,HAL,HAO1,HBS1L,HCCS,HCFC1,HDAC1,HDGF,HDGFL2,HDGFL3,HDLBP,HEATR1,HEBP1,HECTD1,HELZ2,HEXB,HEXIM1,HGD,HGS,HIBADH,HIBCH,HINT3,HIP1,HK1,HLA-A,HLA-DQA1,HMGA1,HMGCL,HMGCS1,HMGCS2,HMOX1,HMOX2,HNF1A,HNF4A,HNMT,HNRNPA2B1,HNRNPAB,HNRNPC,HNRNPD,HNRNPF,HNRNPH2,HNRNPK,HNRNPL,HNRNPLL,HNRNPM,HNRNPR,HNRNPU,HNRNPUL1,HNRNPUL2,HOMER2,HP1BP3,HPD,HPGD,HPN,HPX,HRAS,HS1BP3,HSCB,HSD11B1,HSD17B10,HSD17B2,HSD17B4,HSD17B6,HSDL1,HSP90AA1,HSP90AB1,HSP90B1,HSPA12B,HSPA13,HSPA4L,HSPA5,HSPA8,HSPA9,HSPB1,HSPD1,HSPG2,HSPH1,HTATIP2,HUWE1,HYKK,HYOU1,HYPK,IDH2,IDH3B,IDO2,IFI16,IFIT1B,IFIT3,IFNAR2,IGF2R,IGFALS,IK,IL6ST,ILF2,ILF3,ILK,ILKAP,IMMP2L,IMMT,IMPA1,IMPAD1,INMT,INPP5F,INSIG2,INSR,INTS3,IP6K1,IPO5,I

	QGAP1,ISCA2,ISOC2,IST1,ITGA1,ITGA2B,ITGA5,ITGA9,ITGAV,ITGB1,ITGB3,ITGB6,ITIH2,ITIH4,ITPR2,ITSN1,IYD,JCHAIN,JUP,KANK2,KCTD12,KDELR1,KDSR,KHDRBS1,KHSRP,KIF13B,KIF21A,KLHDC7A,KLKB1,KPNA1,KPNA2,KRAS,KXD1,KYAT1,KYAT3,KYNU,L2HGDH,L3HYPDH,LAP3,LARP1,LARP4,LARP4B,LARP7,LARS2,LASP1,LBR,LCAT,LDAH,LDLR,LGALS1,LGALS3,LGALS3BP,LGMN,LHPP,LIAS,LIFR,LIMS2,LIN7A,LIN7C,LIPE,LITAF,LMAN1,LMAN2,LMAN2L,LMF1,LMNA,LMNB1,LMNB2,LMO7,LOC102724788/PRODH,LONP2,LPCAT3,LRG1,LRP1,LRPAP1,LRRFIP1,LSG1,LSM12,LSM14A,LSM14B,LSR,LUC7L,LUC7L2,LUC7L3,LUM,LYAR,LYN,LYPLA2,LYVE1,LYZ,LZIC,M6PR,MACO1,MACROD1,MAGIX,MAN1A2,MAN2B1,MAN2B2,MAN2C1,MANBA,MAOA,MAOB,MAP2K1,MAP2K3,MAP4,MAPK1IP1L,MAPRE3,MASP2,MATR3,MBNL1,MBOAT7,MCAM,MCCC1,MCCC2,MCEE,MDH1,ME1,MEAF6,MECP2,METAP2,METTL27,METTL9,MFAP1,MFN2,MGAT2,MGLL,MGST1,MIA3,MIF4GD,MIGA2,MIOS,MIPEP,MKNK1,MME,MMUT,MOB1B,MOCS2,MOGS,MOSPD2,MOV10,MPC1,MPHOSPH10,MPI,MPP1,MPP6,MPRIP,MPST,MRI1,MROH1,MRPL12,MRPL15,MRPL24,MRPL47,MRPL50,MRPL51,MRPS15,MRPS17,MRPS25,MRPS31,MRPS35,MRRF,MSH2,MSN,MSR1,MSRA,MSRB2,Mt1,Mt2,MTA2,MTAP,MTDH,MTFR1,MTHFS,MTMR6,MTOR,MTREX,MTSS1,MTX2,MUL1,MVK,MVP,MYBBP1A,MYEF2,MYH10,MYH11,MYH14,MYH9,MYL1,MYLK,MYLPF,MYO18A,MYO1B,MYO1C,MYO1D,NAA15,NAA16,NAA25,NAA35,NAALAD2,NACA,NADK2,NAGA,NAGLU,NAMPT,NANS,NAP1L1,NAPRT,NASP,NAT10,NAXD,NCBP1,NCEH1,NCK1,NCL,NCOA5,NCSTN,NDST1,NDUFA10,NDUFA13,NDUFA3,NDUFAF2,NDUFAF7,NDUFB7,NECAP1,NELFA,NELFB,NELFCD,NFIA,NFIB,NFIC,NFXL1,NGEF,NGLY1,NHLRC2,NIBAN1,NID2,NIPSNAP2,NLN,NLRX1,NMRAL1,NMRK1,NMT2,NNMT,NOC2L,NOL6,NONO,NOP16,NOP56,NOP58,NOS3,NOSTRIN,NPC1,NQO1,NR1H4,NR3C1,NRAS,NSF,NSFL1C,NSUN2,NUBPL,NUCB1,NUCB2,NUCKS1,NUDC,NUDT12,NUDT13,NUDT14,NUDT19,NUDT7,NUFIP2,NUMA1,NUP153,NUP155,NUP160,NUP205,NUP210,NUP214,NUP35,NUP54,NUP93,NUP98,OAT,OCIAD2,OGA,OGFOD3,OGFR,OGT,OLA1,OPLAH,OPTN,ORMDL2,OS9,OSBPL9,OTOL1,OXCT1,OXR1,OXSM,PA2G4,PABPC1,PABPC4,PABPN1,PAFAH1B1,PAFAH1B2,PAFAH2,PAIP1,PAIP2,PAK2,PALD1,PALLD,PALMD,PAM16,PANK1,PAPSS1,PAPSS2,PARP1,PARP14,PARS2,PARVA,PARVB,PAWR,PC,PCBP1,PCCA,PCCB,PCDH1,PCDHB16,PCK1,PCNP,PCTP,PCYT1A,PDAP1,PDCD10,PDCD11,PDCD4,PDCD6IP,PDE2A,PDHA1,PDHB,PDIA3,PDIA4,PDIA5,PDIA6,PDK1,PDK2,PDLIM1,PDLIM5,PDLIM7,PDP2,PDXDC1,PDXK,PDZK1,PEX1,PEX11A,PEX11G,PEX12,PEX13,PEX14,PEX16,PEX19,PEX3,PEX6,PFAS,PFDN2,PFKFB3,PGK1,PGM1,PGM3,PGM5,PGRMC1,PHACTR4,PHF20L1,PHKA1,PHKA2,PHKB,PHKG2,PHLDA1,PHLDB2,PHYHD1,PHYKPL,PI4KA,PICALM,PIGR,PIGS,PIGU,PIK3AP1,PIK3CB,PIN4,PIP5K1C,PITHD1,PITRM1,PKLR,PKN1,PKP4,PLA2G12B,PLBD1,PLBD2,PLCB3,PLCH1,PLEKHA5,PLEKHA7,PLEKHF1,PLG,PLIN5,PLOD3,PLPP3,PLRG1,PLTP,PLVAP,PLXNA4,PLXNB2,PM20D1,PML,PMM2,PNKP,PNLIP,PNN,POLDIP3,POLR2A,POLR2B,PON1,PON2,PON3,POR,PPA1,PPAN,PPFIA1,PPFIBP2,PPIA,PPIF,PPIG,PPIL1,PPIL4,PPIP5K2,PPL,PPM1A,PPM1B,PPM1G,PPM1K,PPP1R2,PPP1R21,PPP1R7,PPP2R5A,PPP2R5D,PPP4C,PPP4R2,PPP4R3A,PPP6R1,PPP6R3,PPT1,PPWD1,PRDX5,PRELP,PREP,PRKAA2,PRKAB1,PRKACA,PRKAG1,PRKCSH,PRKRA,PROC,PROX1,PRPF31,PRPF40A,PRPF6,PRPF8,PRRC2C,PRUNE1,PRXL2A,PSEN1,PSIP1,PSMA1,PSMA2,PSMA3,PSMA4,PSMA7,PSMB1,PSMB2,PSMB5,PSMB6,PSMB9,PSMC3,PSMD3,PSMD4,PSMD7,PSME3,PTBP1,PTBP3,PTGES3,PTK2,PTK2B,PTPMT1,PTPN1,PTPRF,PTPRK,PTRHD1,PTTG1IP,PUM1,PURA,PXMP2,PXMP4,PXN,PYGB,PYGL,QDPR,QSOX1,QTRT2,RAB14,RAB1A,RAB35,RAB4A,RAB8B,RABGAP1,RABGAP1L,RAC1,RACK1,RAD50,RAE1,RALY,RAN,RANBP1,RANBP10,RANBP3,RANGAP1,RAP1B,RAPGEF4,RASIP1,RBBP4,RBM10,RBM14,RBM15,RBM22,RBM28,RBM39,RBM42,RBM47,RBP1,RBPMS,RCC2,RCN1,REEP5,RELA,RETREG2,RETSAT,RFC2,RGL3,RGPD4 (includes others),RHOA,RHOC,RIOX2,RIPK1,RMDN2,RMDN3,RNASET2,RNF113A,RNF114,RNF17,RNF185,RNF20,RNF213,RNF5,RNH1,RNMT,RNPEP,ROCK2,RPAP3,RPL10A,RPL11,RPL12,RPL13A,RPL14,RPL15,RPL18,RPL18A,RPL22,RPL23,RPL27,RPL28,RPL3,RPL31,RPL37,RPL4,RPL5,RPL8,RPL9,RPLP0,RPLP2,RPN1,RPS10,RPS14,RPS15,RPS15A,RPS19,RPS20,RPS24,RPS27A,RPS27L,RPS29,RPS3,RPS5,RPS6,RPS7,RPTOR,RRAS,RRS1,RSL1D1,RTF2,RTN1,RTN4,RTN4IP1,RUFY1,RUFY3,RUVBL1,RUVBL2,S100A6,SAA1,SAE1,SAFB,SAMHD1,SAR1B,SARDH,SARNP,SARS2,SART1,SART3,SAT2,SBF1,SC5D,SCAMP3,SCAMP4,SCAMP5,SCARB1,SCARB2,SCD,SCFD1,SCO1,SCRIB,SCYL2,SCYL3,SDC4,SDR42E1,SDS,SDSL,SEC11A,SEC14L2,SEC14L4,SEC23B,SEC23IP,SEC24A,SEC24D,SEC31A,SEC61A1,SEC61B,SEC61G,SEC62,SEC63,SELENBP1,SELENOF,SEPHS1,SERBP1,SERHL2,SERINC3,SERPINA1,SERPINA6,SERPINB1,SERPIND1,SERPINF2,SERPING1,SERPINH1,SF3A1,SF3A3,SF3B1,SF3B2,SF3B3,SF3B4,SF3B6,SFPQ,SFT2D2,SFXN5,SGTA,SH3GL1,SHMT1,SHPK,SHTN1,SIAE,SIGLEC1,SIL1,SLC12A9,SLC16A7,SLC17A3,SLC22A1,SLC22A18,SLC22A25,SLC25A10,SLC25A11,SLC25A12,SLC25A13,SLC25A21,SLC25A23,SLC25A25,SLC25A3,SLC25A45,SLC25A5,SLC26A1,SLC27A4,SLC2A2,SLC30A5,SLC31A1,SLC35A1,SLC35D1,SLC38A10,SLC39A11,SLC39A14,SLC39A4,SLC44A2,SLC4A4,SLC6A12,SLC6A13,SLC7A2,SLC9A3R1,SLC9A3R2,SLCO1B3,SLCO2A1,SLK,SLMAP,SLTM,SMAP1,SMAP2,SMARCA2,SMARCA5,SMARCD2,SMARCE1,SMC1A,SMC3,SMIM15,SMOC1,SMPD1,SMS,SMU1,SNAP23,SNAP47,SND1,SNF8,SNRNP200,SNRNP70,SNRPD3,SNRPF,SNRPN,SNTB1,SNW1,SNX18,SNX2,SNX3,SNX4,SNX6,SNX7,SOAT2,SON,SORBS1,SORBS2,SOS1,SPAG9,SPAST,SPCS2,SPG7,SPTAN1,SPTBN2,SQOR,SRA1,SREK1,SRI,SRP19,SRP68,SRP72,SRP9,SRPK2,SRPRB,SRRT,SRSF2,SRSF4,SRSF6,SRSF7,SSR1,SSR3,SSRP1,ST13,STAB1,STAB2,STAG2,STARD5,STAT2,STAT3,STAT6,STEAP3,STEAP4,STOML2,STRAP,STRN,STT3A,STT3B,SUCLG1,SUCLG2,SUGT1,SULT1C2,SULT1E1,SULT2A1,SUN2,SUOX,SUPT16H,SURF1,SVIL,SWAP70,SYAP1,SYMPK,SYNCRIP,SYNGR2,SYNJ2BP,TACO1,TADA3,TALDO1,TAMM41,TANGO2,TAOK3,TAP1,TAP2,TAPBP,TARDBP,TAT,TBC1D13,TBC1D15,TBC1D17,TBC1D24,TBC1D8B,TBC1D9B,TBCD,TBRG4,TCEA1,TCERG1,TCIRG1,TCOF1,TDO2,TFR2,TGFBRAP1,TGM1,THNSL2,THOC2,THRAP3,TIAL1,TIGAR,TIMM22,TIMM44,TIMMDC1,TINAGL1,TJP1,TJP2,TJP3,TKFC,TKT,TLN1,TM9SF1,TM

	9SF2,TM9SF3,TMED10,TMED3,TMED5,TMED9,TMEM109,TMEM126A,TMEM126B,TMEM135,TMEM176B,TMEM19,TMEM230,TMEM256,TMEM33,TMEM38B,TMEM43,TMEM82,TMOD3,TMPO,TMTC3,TMX1,TMX3,TNKS1BP1,TNPO1,TNPO2,TNPO3,TNS2,TNS3,TOM1,TOP1,TOP2B,TOP3B,TOR1A,TOR1AIP1,TPD52,TPI1,TPK1,TPM3,TPPP,TPR,TRA2B,TRABD,TRAM1,TRAP1,TRAPPC1,TRAPPC4,TRIM14,TRIM23,TRIM28,TRIP10,TRIP11,TRIR,TRMU,TSC22D1,TSFM,TSG101,TSPAN14,TSPAN31,TTC1,TTC37,TTC38,TTC39A,TTC39C,TTC7A,TTN,TTPA,TUBA4A,TUBB,TUBB2A,TUBB4B,TUT7,TWF1,TXLNA,TXLNG,TXNDC5,TXNDC9,TXNL1,TYMP,U2AF2,U2SURP,UBA1,UBA2,UBA3,UBA7,UBAC1,UBAP2,UBE2G2,UBE2J1,UBE2M,UBE4B,UBL7,UBQLN2,UBR2,UBTF,UCHL5,UFL1,UGDH,UGGT1,UGP2,UGT1A4,UGT1A6,UGT1A8 (includes others),UGT2B10,UGT2B17,UGT2B28,UGT3A1,UPB1,UPF1,UPF2,UPP1,UQCC1,UQCC3,UQCRC2,UROC1,USO1,USP16,USP19,USP24,USP46,USP7,VAC14,VAMP2,VAMP8,VAT1,VAV2,VCAM1,VCL,VCPIP1,VIM,VKORC1L1,VMO1,VNN1,VPS13D,VPS25,VPS26A,VPS26B,VPS26C,VPS28,VPS33B,VPS35,VPS45,VPS51,VPS52,VRK1,VSIG4,VTN,VWA8,WAPL,WASF2,WASHC4,WASHC5,WBP11,WBP2,WDR1,WDR18,WDR26,WDR36,WDR46,WDR5,WDR61,WDR77,WFS1,WRNIP1,XAF1,XPNPEP1,XPO1,XPO5,XRCC6,XRN1,XRN2,YBX1,YBX3,YME1L1,YTHDF2,YTHDF3,ZBTB20,ZC3H11A,ZC3H14,ZC3HAV1,ZFR,ZHX1,ZHX2,ZHX3,ZMAT2,ZMIZ1,ZNF326,ZNF638
1. Molecular Transport 2. Transport of molecule 3. 6.14E-34 4. Increased 5. 2.868 6. 472	A1CF,ABAT,ABCB10,Abcb1b,ABCB4,ABCB6,ABCB8,ABCB9,ABCC2,ABCC3,ABCC6,ABCD1,ABCD3,ABCG5,ACACA,ACACB,ACADL,ACAT1,ACAT2,ACLY,ACO1,ACSL4,ACSL5,ADD2,ADIPOR2,AGFG1,AGK,AGXT,AKR1C4,AKT1,ANO10,ANXA1,AP2A1,AP2M1,AP3B1,APCS,APOA1,APOA2,APOB,APOC2,Apoc3,APOC4,APOE,APOM,AQP1,AQP4,AQP9,ARCN1,ARF6,ARFGAP1,ARFGAP3,ARHGEF12,ARRB1,ARSB,ASAH1,ASPH,ASPSCR1,ATOX1,ATP11C,ATP13A1,ATP1A1,ATP1B1,ATP1B3,ATP2A2,ATP2B1,ATP2B4,ATP6AP1,ATP6V0D1,ATP6V1A,ATP6V1C1,ATP6V1E1,ATXN2,B2M,BAG3,BCAP31,BIN1,BRAF,BSG,CADM1,CALCRL,CALR,CAMK1,CAND1,CANX,CASK,CASP3,CAT,CAVIN1,CCDC22,CCDC93,CCS,CD2AP,CD36,Cdc42,CDK5,CDKN1B,CEP290,CES1,CES3,CFH,CHCHD4,CHP1,CIDEB,CISD1,CLCC1,CLIC1,CLIC4,CLIC5,CLU,CNP,CORO1A,COX15,COX19,CP,CPOX,CPSF2,CPT2,CRAT,CREB1,CRYM,CTNNB1,CTSS,CTTN,CUL1,CUL3,CYB5R1,CYGB,CYP27A1,CYP7A1,DDC,DDX39B,DDX3X,DDX5,DNAJA1,DNAJC1,DNM1L,DNM2,DPYSL2,Dst,DTX3L,DYSF,EGF,EGFR,EHD1,EIF4A3,EIF4E,EIF5A,ELAVL1,ENPP1,EPHX1,ERP29,EXOC1,EZR,FABP2,FABP4,FABP5,FABP7,FCGR2B,FDX2,FECH,FGA,FGB,FGG,FKBP4,FLNA,FLOT2,FMO3,FMR1,FN1,FRAS1,FXN,FXYD1,G6PC,GAPDH,GAPVD1,GBF1,GCH1,GCK,GCKR,GGA1,GLUL,GNA11,GNA13,GNAI2,GNAI3,GNAQ,GNAS,GOLPH3,GOLPH3L,GOSR1,GOSR2,GPAM,GPD1L,GPLD1,GRN,GSTP1,GUCY1B1,HGS,HK1,HLA-A,HMGA1,HMOX1,HMOX2,HNF1A,HNRNPA2B1,Hnrnpa3,HNRNPAB,HNRNPD,HP,HPX,HRAS,Hrg,HSD11B1,HSD17B2,HSP90AA1,HSP90AB1,HSPA5,HSPA8,HSPA9,IGF2R,IL6ST,ILK,INSR,IPO5,IQGAP1,ITGAV,ITGB1,ITGB3,ITPR2,JUP,KHDRBS1,KPNA2,KRAS,KXD1,LAMTOR1,LASP1,LCAT,LDLR,LGALS1,LIN7A,LIN7C,LIPE,LMAN2,LMAN2L,LMF1,LMNA,LPCAT3,LRP1,LYN,M6PR,MAOB,MAP2K1,MAP2K3,MECP2,MFN2,MGLL,MIA3,MIF,MSN,MSR1,Mt1,Mt2,MTDH,MVP,MYH9,MYO18A,MYO1C,NCBP1,NCBP2,NCEH1,NOS3,NPC1,NPC2,NR1H4,NR3C1,NSF,NUCB2,NUP153,NUP155,NUP160,NUP205,NUP210,NUP214,NUP35,NUP54,NUP93,NUP98,NUTF2,OGA,OPTN,PAFAH1B1,PARP1,PCTP,PCYT1A,PDIA4,PDZK1,PECAM1,PEX1,PEX14,PEX16,PEX26,PEX5,PEX6,PFKFB3,PHB2,PICALM,PIGR,PKN1,PLCB3,PLTP,PML,POLDIP3,PON1,PPFIA1,PPIA,PPT1,PRDX6,PRKAA2

	,PRKACA,PRKAG1,PSAP,PSEN1,PTK2,PTK2B,PTP4A2,PTTG1IP,PYCARD,RAB14,RAB1A,RAB4A,RAB8A,RAC1,RAE1,RAN,RANGAP1,RAP1A,RAPGEF4,RARRES2,RBM22,RBM8A,RBP1,RGPD4 (includes others),RHOA,RHOC,RTN4,RUFY1,SAA1,SARNP,SCAMP1,SCAMP3,SCAMP5,SCARB1,SCARB2,SCD,SCFD1,SCO1,SCYL2,SEC23B,SEC23IP,SEC24A,SELENOK,SELENOP,SERPINA6,SFXN5,SLC16A7,SLC17A3,SLC22A1,SLC22A18,SLC22A25,Slc25a1,SLC25A10,SLC25A11,SLC25A12,SLC25A13,SLC25A20,SLC25A21,SLC25A23,SLC26A1,SLC27A4,SLC2A2,SLC30A5,SLC31A1,SLC35A1,SLC35A3,SLC38A3,SLC39A14,SLC39A4,SLC44A2,SLC4A4,SLC6A12,SLC6A13,SLC7A2,SLC9A3R1,SLC9A3R2,Slco1a1,SLCO1B3,SLCO2A1,SMPD1,SNAP23,SNTB1,SNX1,SNX3,SNX4,SNX6,SOAT2,SORBS1,SPG7,SPTBN2,SRI,SRSF1,SRSF2,SRSF3,SRSF4,SRSF6,SRSF7,STARD5,STAT3,STAT6,STEAP3,STEAP4,STOML2,STX7,SULT1E1,SYMPK,TAP1,TAP2,TARDBP,TBC1D13,TBC1D8B,TCIRG1,TFR2,TGFBRAP1,THOC2,THOC6,TIMM23,TIMM44,TJP2,TMED10,TMED2,TMEM30A,TNPO1,TNPO2,TNPO3,TOMM40,TPD52,TPR,TRAPPC4,TRIM28,TSG101,TTC7A,TTN,TTPA,U2AF2,UBE2I,UPF1,UPF2,USO1,USP19,VAMP2,VAMP3,VAMP8,VDAC2,VDAC3,VNN1,VPS33B,VPS45,WFS1,XPO1,XPO5,YME1L1,YWHAZ,ZC3H11A
1. Infectious Diseases 2. Infection of cells 3. 5.13E-32 4. Increased 5. 8.968 6. 254	AASS,ACACB,ACADSB,ACTR2,ACTR3,ADAM10,AIP,AKT1,AMDHD2,AP2A1,AP2M1,APCS,APOE,ARCN1,ARF6,ARGLU1,ARHGEF12,ARPC1A,ARPC1B,ARPC3,ARPC5,ARRB1,ASGR2,ATOX1,ATP5IF1,ATP6AP2,ATP6V0D1,ATXN2,B2M,BCLAF1,BMP2K,BSG,CAD,CAMK1,CCAR1,CCDC134,CCDC51,CFI,CHCHD2,CHORDC1,CLTA,CLTB,COASY,COG3,COG5,COPA,COPB1,COPB2,COPG1,COPZ1,CTBP1,CTSB,CTSS,CTSZ,CXADR,CYB5B,DDOST,DDX23,DDX3X,DDX58,DHX15,DHX9,DNAJB1,DNM2,DPM1,DPP4,DYSF,EEA1,EGF,EGFR,EIF2AK2,EIF2B5,EIF3A,EIF3H,EIF3I,ELOA,ELOC,EPN1,ERC1,EXOSC5,FAU,FBL,FCGR2B,FCGRT,FLII,FN1,FNTA,FXR1,GANAB,GAPVD1,GATAD2A,GBF1,GCK,GOLPH3,GOSR2,GPR182,GPT2,H3-3A/H3-3B,HDAC1,HEATR1,HGS,HIBCH,HIP1,HMGCS1,HNRNPF,HNRNPH1,HNRNPK,HNRNPU,HRAS,HSP90B1,HSPA5,HSPA9,HUWE1,ICAM1,IGF2R,ILF3,ITGB1,KHDRBS1,KXD1,LDLR,LIN7C,LMAN2,LSM14B,MANBA,MAP4,MAPRE1,MAT2A,MBL2,MGLL,MID1IP1,MRC1,MRPS12,MYEF2,NDUFA10,NDUFAF2,NDUFAF3,NDUFB7,NGLY1,NIPSNAP2,NLRX1,NOP56,NUDT3,NUP153,NUP155,NUP160,NUP214,NUP98,PANK1,PARP9,PARVA,PARVB,PCK1,PCTP,PDIA3,PDIA6,PGM1,PGRMC2,PI4KA,PICALM,PIP5K1C,PLOD3,PM20D1,PML,POLR2A,POLR2H,POLR2I,POLR2L,PPIB,PPM1K,PRKRA,PRPF6,PRPF8,PSIP1,PSMA1,PSMA2,PSMA3,PSMA5,PSMA7,PSMB6,PSMC3,PSMD4,PTGES3,PURA,RAB8A,RAB8B,RAC1,RACK1,RANBP1,RAP1B,RBM10,RBM17,RELA,RGPD4 (includes others),RHOC,RNH1,RPL10A,RPL12,RPL18,RPL3,RPL5,RPS6,RPS6KB2,RSL1D1,S100A1,SAMHD1,SCFD1,SEC61G,SERPINA1,SF3A1,SF3B1,SF3B2,SIGLEC1,SLC31A1,SLCO2A1,SMPD1,SNRPA1,SNRPD3,SNU13,SNW1,SPAST,SPCS3,SPG7,SPTAN1,SRRT,SRSF2,SRSF6,SSR1,SSR3,STAB1,STAT2,STIP1,STT3A,SUB1,SUCLG2,SUMO2,TAGLN2,TAP1,THOC2,TIMM17B,TM9SF2,TMED2,TNPO3,TOP3B,TPPP,TRAPPC1,TSG101,TWF1,UBE2H,UBE2Z,WASF2,WDR46,XPO1,YBX1,ZC3HAV1
1. Infectious Diseases 2. Infection by RNA virus 3. 1.93E-30 4. Increased 5. 8.562 6. 283	AASS,ABCC2,ACACB,ACADSB,ACTR2,ACTR3,ADAM10,ADK,AIP,AKT1,AMDHD2,AMY2A,AP2A1,AP2M1,APCS,APOA1,APOE,ARCN1,ARF6,ARGLU1,ARHGEF12,ARPC1A,ARPC1B,ARPC3,ARPC5,ARRB1,ASGR2,ATOX1,ATP5IF1,ATP6AP2,ATP6V0D1,ATXN2,B2M,BCLAF1,BMP2K,BSG,C1orf174,C4A/C4B,CAD,CAMK1,CCAR1,CCDC134,CCDC51,CD36,CD38,CFI,CHCHD2,CHORDC1,CLEC4G,CLTA,CLTB,CLU,COASY,COG3,COG5,COPA,COPB1,COPB2,COPG1,COPZ1,CRP,CTBP1,CTSB,CTSS,CTSZ,CYB5B,CYP2B6,CYP3A5,CYP3A7,DDOST,DDX23,DDX3X,DDX5,DDX58,DHFR,DHX15,DHX9,DNAJB1,DNM2,DPM1,DPP4,DYSF,EEA1,EGF,EGFR,EIF2AK2,EIF2B5,EIF3A,EIF3H,EIF3I,ELOA,ELOC,EPN1,ERC1,EXOSC5,FAU,FBL,FCGR2B,FCGRT,FGA,FLII,FN1,FNTA,FXR1,GAA,GANAB,GAPVD1,GATAD2A,GBF1,GCK,GOLPH3,GOSR2,GPR182,GPT2,H3-3A/H3-3B,HDAC1,HEATR1,HGS,HIBCH,HIP1,HLA-A,HMGCS1,HNRNPF,HNRNPH1,HNRNPK,HNRNPU,HRAS,HSP90B1,HSPA5,HSPA9,HUWE1,ICAM1,IFNAR2,INSR,ITGB1,KHDRBS1,KXD1,LIN7C,LMAN2,LSM14B,MANBA,MAOA,MAOB,MAP4,MAT2A,MBL2,MGLL,MID1IP1,MMUT,MRC1,MRPS12,MTOR,MYEF2,NDUFA10,NDUFAF2,NDUFAF3,NDUFB7,NGLY1,NIPSNAP2,NLRX1,NOP56,NR3C1,NUDT3,NUP153,NUP155,NUP160,NUP214,NUP98,PANK1,PARP9,PARVA,PARVB,PCK1,PCTP,PDIA3,PDIA6,PGM1,PGRMC2,PI4KA,PICALM,PIP5K1C,PLOD3,PM20D1,PML,POLR2A,POLR2H,POLR2I,POLR2L,POR,PPIA,PPIB,PPM1K,PRPF6,PRPF8,PSIP1,PSMA1,PSMA2,PSMA3,PSMA5,PSMA7,PSMB6,PSMC3,PSMD4,PTGES3,PURA,PYCARD,RAB8A,RAB8B,RACK1,RANBP1,RAP1B,RBM10,RBM17,RELA,RGPD4 (includes others),RHOA,RHOC,RNH1,RPL10A,RPL12,RPL18,RPL3,RPL5,RPS6,RPS6KB2,RSL1D1,S100A1,SAMHD1,SCFD1,SEC61G,SERPINA1,SF3A1,SF3B1,SF3B2,SIGLEC1,SIGMAR1,SLC31A1,SLCO2A1,SMPD1,SNRPA1,SNRPD3,SNU13,SNW1,SPAST,SPCS3,SPG7,SPTAN1,SRRT,SRSF2,SRSF6,SSR1,SSR3,STAB1,STAT2,STAT6,STIP1,STT3A,SUB1,SUCLG2,SUMO2,TAGLN2,TAP1,THOC2,TIMM17B,TM9SF2,TMED2,TNPO3,TOP2B,TOP3B,TPPP,TRAPPC1,TSG101,TUBA4A,TUBB2A,TUBB4B,TWF1,UBE2H,UBE2Z,WASF2,WDR46,XPO1,YBX1,ZC3HAV1

1. Cellular Function and Maintenance 2. Endocytosis 3. 2.05E-24 4. Increased 5. 6.999 6. 200	ACTB,ACTG1,ACTN4,ACTR2,ACTR3,ADD1,AHSA1,AMBP,ANXA1,ANXA5,AP2A1,Ap2b1,AP2M1,APCS,APOA1,APOA2,APOB,APOC2,Apoc3,APOE,ARAF,ARF6,ARFGAP1,ARPC2,ARPC3,ARRB1,ASGR1,ATP6AP1,ATP6V0D1,ATP6V1A,ATP6V1E1,B2M,BIN1,BRAF,CALR,CANX,CAP1,CD163,CD2AP,CD36,CD38,CD47,CD82,Cdc42,CDC5L,CDK5,CFH,CKB,CLEC4G,CLIC4,CLU,CMAS,CORO1A,CORO1C,CRP,CSK,CTNNB1,CTNND1,CTTN,CYFIP1,DDX3X,DNM1L,DNM2,DPYSL2,EEA1,EGF,EGFR,EHD1,EIF2AK2,ELMO1,ELOVL1,EPB41L2,EPN1,ERP44,EZR,FCGR2B,FCHO2,FLNA,FLOT1,FMR1,Fnbp1l,GAPVD1,Gm21596/Hmgb1,GNAI2,GNE,GPR182,GRN,GSTP1,HGS,HIP1,HMOX1,HNRNPK,HP,HPX,HRAS,HSP90AA1,HSP90B1,HSPA5,HSPA8,HSPA9,HSPG2,HSPH1,HYOU1,ICAM1,IGF2R,IGKC,INPP5F,INSR,IQGAP1,ITGAV,ITGB1,ITGB3,ITSN1,JCHAIN,KRAS,LDLR,LGALS3,LMAN2,LRP1,LRPAP1,LUM,LYN,M6PR,Mbl1,MBL2,MBNL1,MFN2,MIF,MRC1,MSR1,MTA2,MYH9,MYLK,NANS,NCL,NECAP1,NHLRC2,NOS3,NPC1,NR3C1,PALLD,PDLIM7,PFKFB3,PICALM,PIK3CB,PIP5K1C,PLEKHF1,PLG,PPP6R1,PPT1,PRKAA2,PSEN1,PSMD4,PTK2,PTPN1,PTRHD1,PXN,PYCARD,RAB1A,RAB4A,RAC1,RACK1,RHOA,RHOG,RPS21,RPTOR,RUFY1,RUVBL2,SAA1,SART1,SCAMP1,SCAMP5,SCARB1,SCARB2,SCRIB,SF3B3,SF3B4,SFPQ,SHOC2,SIGLEC1,SMPD1,SNAP23,SNX18,SNX5,SRSF3,SRSF6,STAB1,STAB2,STT3A,SWAP70,SYNJ2BP,TBC1D24,TFR2,TLN1,VAMP8,VAV2,VIM,VTN,WASF2,YWHAQ
1. Cellular Function and Maintenance 2. Engulfment of cells 3. 6.43E-24 4. Increased 5. 6.483 6. 176	ACTN4,ACTR2,ACTR3,ADD1,AHSA1,AHSG,ANPEP,ANXA1,ANXA11,ANXA3,ANXA5,AP2A1,AP2M1,APCS,APOA1,APOA2,APOE,ARAF,ARF6,ARFGAP1,ARPC2,ARPC3,ARRB1,ASGR1,ATG3,ATP6AP1,ATP6V0D1,ATP6V1A,ATP6V1E1,BIN1,BRAF,C1QA,CALR,CAT,CD163,CD302,CD36,CD38,CD47,Cdc42,CDC5L,CFH,CKB,CLEC4G,CLIC4,CMAS,CORO1A,CORO1C,CRK,CRP,CSK,CTNNB1,CTNND1,CYFIP1,DDX3X,DNM2,DPYSL2,DYSF,EGF,EHD1,ELMO1,ELOVL1,EPB41L2,EPN1,ERP44,EZR,FCGR2B,FCHO2,FLNA,FLOT1,FMR1,FN1,GAPVD1,Gm21596/Hmgb1,GNAI2,GNE,GPR182,GRN,GSTP1,HGS,HIP1,HMOX1,HP,HRAS,HSP90AA1,HSPA5,HSPA8,HYOU1,ICAM1,Ighg2b,ILK,IQGAP1,ITGAV,ITGB1,ITSN1,KRAS,LDLR,LGALS3,LMAN2,LRP1,LRPAP1,LUM,LYAR,LYN,M6PR,Mbl1,MBL2,MBNL1,MIF,MRC1,MSR1,MTA2,MYH9,NANS,NCL,NHLRC2,NOS3,NR3C1,PALLD,PECAM1,PFKFB3,PICALM,PIGR,PIK3CB,PIP5K1C,PLEKHF1,PLG,PON1,PPP6R1,PPT1,PRKAA2,PSEN1,PSMD4,PTK2,PTPN1,PTRHD1,PXN,PYCARD,RAB35,RAB4A,RAC1,RACK1,RHOA,RHOG,RPS21,RPTOR,RUFY1,RUVBL2,SAA1,SART1,SCARB1,SCARB2,SF3B3,SF3B4,SFPQ,SHOC2,SIGLEC1,SMPD1,SNAP23,SNX3,SNX5,SRA1,SRSF3,SRSF6,STAB2,STT3A,SWAP70,SYNJ2BP,TFR2,TLN1,VAMP8,VAV2,VIM,VTN,WASF2,YWHAQ
1. Infectious Diseases 2. Replication of virus 3. 3.05E-22 4. Increased 5. 4.657 6. 176	ADAM10,AGFG1,AGO1,AGO2,AKT1,ANPEP,ANXA5,AP2M1,ARAF,ARCN1,ARHGDIB,ATG4B,ATP1B3,ATP6AP1,ATP6AP2,ATP6V0D1,ATP6V1A,ATRX,B2M,Bst2,CAD,CASP3,CAT,CD38,CD81,CDC73,CDKN1B,CES1,CLDN3,CLIC4,COPA,COPB1,COPB2,COPG1,CREB1,CTBP1,CYP17A1,CYP2U1,DDX3X,DDX5,DDX58,DDX6,DEK,DHX9,DNAJA1,EEF1A1,EIF2AK2,EIF2S1,EIF3A,EIF3C,EIF3L,EIF4A3,EXOSC5,F13A1,FASN,FAU,FCGRT,FCHO2,FSCN1,FUBP1,GLYR1,GOPC,HAO1,HECTD1,HERPUD1,HMOX1,HNF4A,HNRNPM,HPGD,HRAS,HSP90AA1,HSP90AB1,HSP90B1,HSPD1,IFNAR2,IGKC,ILF3,LARP1,LIFR,MAN2B1,MAP2K1,MAP2K3,MID1IP1,MKNK1,MOV10,MSH2,MSR1,MTOR,MVP,NCL,NLRX1,NUDCD3,NUP153,NUP205,NUP214,NUP54,NUP98,OPTN,PAK2,PARP1,PDCD6IP,PI4KA,PIP5K1C,PLG,PML,PNKP,POLR2A,POLR2H,POLR2L,PPIA,PPM1B,PPP1R8,PPP4C,PRKACA,PRPF8,PSIP1,PSMA1,PSMD14,PTK2B,PTPMT1,PTPN1,RAE1,RBM42,RELA,RPL13A,RPL35,RPS10,RPS14,RPS16,RPS27A,RPS5,RPS6,RPSA,RUVBL2,SAE1,SAFB,SAMHD1,SEC14L2,SERPINA1,SERPINA10,SF3A1,SF3B1,SF3B6,SFPQ,SIGMAR1,SLC9A3R1,SMU1,SNAP23,SNRNP70,SNRPF,SNW1,SNX6,SON,SRPK2,SRSF1,SSRP1,STAB1,STAT2,STAT3,SUMO2,TAMM41,TAP1,TMPO,TNPO3,TRIM14,TSG101,TUBB,UBA7,UBE2I,USP7,VAPB,XPNPEP1,XPO1,XRN1,YBX1,ZC3HAV1
1. Infectious Diseases 2. Replication of RNA virus 3. 3.95E-22 4. Increased 5. 4.378 6. 162	ADAM10,AGFG1,AGO1,AGO2,AKT1,ANPEP,ANXA5,AP2M1,ARAF,ARCN1,ARHGDIB,ATG4B,ATP1B3,ATP6AP1,ATP6AP2,ATP6V0D1,ATP6V1A,B2M,Bst2,CAD,CASP3,CD38,CD81,CDC73,CDKN1B,CES1,CLDN3,CLIC4,COPA,COPB1,COPB2,COPG1,CREB1,CTBP1,CYP17A1,CYP2U1,DDX3X,DDX5,DDX58,DDX6,DHX9,DNAJA1,EEF1A1,EIF2AK2,EIF2S1,EIF3A,EIF3C,EIF3L,EIF4A3,EXOSC5,F13A1,FASN,FAU,FCGRT,FCHO2,FSCN1,GLYR1,GOPC,HAO1,HECTD1,HERPUD1,HMOX1,HNRNPM,HPGD,HRAS,HSP90AA1,HSP90AB1,HSPD1,IFNAR2,IGKC,ILF3,LARP1,LIFR,MAN2B1,MAP2K1,MAP2K3,MID1IP1,MOV10,MSR1,MTOR,MVP,NCL,NLRX1,NUDCD3,NUP153,NUP205,NUP214,NUP54,NUP98,OPTN,PAK2,PDCD6IP,PI4KA,PIP5K1C,PLG,PML,POLR2A,POLR2H,POLR2L,PPIA,PPM1B,PPP1R8,PPP4C,PRKACA,PRPF8,PSIP1,PSMA1,PSMD14,PTK2B,PTPMT1,PTPN1,RAE1,RBM42,RELA,RPL13A,RPL35,RPS10,RPS14,RPS16,RPS27A,RPS5,RPS6,RPSA,RUVBL2,SAE1,SAFB,SEC14L2,SERPINA1,SERPINA10,SF3A1,SF3B1,SF3B6,SFPQ,SIGMAR1,SLC9A3R1,SMU1,SNRNP70,SNRPF,SNW1,SNX6,SON,SRPK2,SRSF1,STAB1,STAT2,STAT3,SUMO2,TAMM41,TAP1,TMPO,TNPO3,TRIM14,TSG101,TUBB,UBA7,UBE2I,VAPB,XPNPEP1,XPO1,XRN1,YBX1,ZC3HAV1
1. Infectious Diseases 2. Infection by HIV-1 3. 3.48E-21 4. Increased 5. 7.513 6. 185	AASS,ACACB,ACADSB,ACTR3,ADAM10,AKT1,AMDHD2,AP2M1,ARF6,ARGLU1,ARHGEF12,ARPC1A,ATOX1,ATXN2,BCLAF1,BMP2K,CAD,CCAR1,CCDC134,CCDC51,CHORDC1,CLTA,COASY,COG3,CTSZ,CYP3A5,CYP3A7,DDOST,DDX23,DDX3X,DHX15,DHX9,DNAJB1,DNM2,DPM1,DPP4,DYSF,EGF,EGFR,EIF2B5,EIF3H,ELOA,ELOC,EXOSC5,FLII,FNTA,FXR1,GANAB,GAPVD1,GATAD2A,GCK,GOLPH3,GOSR2,GPR182,GPT2,H3-3A/H3-3B,HDAC1,HEATR1,HGS,HIBCH,HMGCS1,HNRNPF,HNRNPH1,HNRNPU,HUWE1,ITGB1,KHDRBS1,KXD1,LIN7C,LMAN2,LSM14B,MANBA,MAOA,MAOB,MAP4,MAT2A,MID1IP1,MRC1,MRPS12,MYEF2,NDUFA10,NDUFAF2,NDUFAF3,NDUFB7,NGLY1,NIPSNAP2,NLRX1,NUDT3,NUP153,NUP155,NUP160,NUP214,NUP98,PANK1,PARP9,PARVA,PARVB,PCK1,PCTP,PDIA3,PDIA6,PGM1,PGRMC2,PI4KA,PIP5K1C,PLOD3,PM20D1,POLR2A,POLR2H,POLR2I,POLR2L,PPIB,PPM1K,PRPF6,PRPF8,PSIP1,PSMA1,PSMA2,PSMA3,PSMA5,PSMA7,PSMB6,PSMC3,PSMD4,PTGES3,PURA,RAB8A,RANBP1,RAP1B,RBM10,RBM17,RELA,RGPD4 (includes others),RNH1,RPL10A,RPL12,RPL18,RSL1D1,S100A1,SAMHD1,SCFD1,SEC61G,SF3A1,SF3B1,SF3B

	2,SIGLEC1,SLCO2A1,SNRPA1,SNRPD3,SNW1,SPAST,SPCS3,SPG7,SPTAN1,SRRT,SRSF2,SRSF6,SSR1,SSR3,STAB1,STIP1,STT3A,SUB1,SUCLG2,SUMO2,TAGLN2,THOC2,TIMM17B,TM9SF2,TMED2,TNPO3,TOP2B,TOP3B,TPPP,TRAPPC1,TSG101,TUBA4A,TUBB2A,TUBB4B,TWF1,UBE2H,UBE2Z,XPO1,YBX1,ZC3HAV1
1. Infectious Diseases 2. Replication of Influenza virus 3. 9.05E-20 4. Increased 5. 5.631 6. 100	AKT1,ANPEP,AP2M1,ARAF,ARCN1,ATP6AP1,ATP6AP2,ATP6V0D1,ATP6V1A,B2M,CAD,CASP3,CD81,CDKN1B,CLIC4,COPA,COPB1,COPB2,COPG1,CREB1,CYP17A1,CYP2U1,DDX58,EEF1A1,EIF2AK2,EIF3A,EIF3C,EIF3L,EIF4A3,F13A1,FAU,FCHO2,FSCN1,GLYR1,GOPC,HECTD1,HERPUD1,HPGD,HRAS,HSP90AA1,HSPD1,ILF3,LARP1,MAN2B1,MAP2K3,MID1IP1,MTOR,NUDCD3,NUP153,NUP205,NUP214,NUP54,NUP98,PAK2,PIP5K1C,PLG,PML,POLR2A,POLR2H,POLR2L,PRKACA,PRPF8,PSMA1,PSMD14,PTPMT1,RAE1,RBM42,RELA,RPL13A,RPL35,RPS10,RPS14,RPS16,RPS27A,RPS5,RPSA,RUVBL2,SAE1,SAFB,SF3A1,SF3B1,SF3B6,SFPQ,SIGMAR1,SMU1,SNRNP70,SNRPF,SNW1,SNX6,SON,STAB1,SUMO2,TAMM41,TAP1,TNPO3,TRIM14,TUBB,UBA7,XPNPEP1,XPO1
1. Infectious Diseases 2. Replication of Influenza A virus 3. 1.56E-19 4. Increased 5. 5.608 6. 99	AKT1,ANPEP,AP2M1,ARAF,ARCN1,ATP6AP1,ATP6AP2,ATP6V0D1,ATP6V1A,B2M,CAD,CD81,CDKN1B,CLIC4,COPA,COPB1,COPB2,COPG1,CREB1,CYP17A1,CYP2U1,DDX58,EEF1A1,EIF2AK2,EIF3A,EIF3C,EIF3L,EIF4A3,F13A1,FAU,FCHO2,FSCN1,GLYR1,GOPC,HECTD1,HERPUD1,HPGD,HRAS,HSP90AA1,HSPD1,ILF3,LARP1,MAN2B1,MAP2K3,MID1IP1,MTOR,NUDCD3,NUP153,NUP205,NUP214,NUP54,NUP98,PAK2,PIP5K1C,PLG,PML,POLR2A,POLR2H,POLR2L,PRKACA,PRPF8,PSMA1,PSMD14,PTPMT1,RAE1,RBM42,RELA,RPL13A,RPL35,RPS10,RPS14,RPS16,RPS27A,RPS5,RPSA,RUVBL2,SAE1,SAFB,SF3A1,SF3B1,SF3B6,SFPQ,SIGMAR1,SMU1,SNRNP70,SNRPF,SNW1,SNX6,SON,STAB1,SUMO2,TAMM41,TAP1,TNPO3,TRIM14,TUBB,UBA7,XPNPEP1,XPO1
1. Molecular Transport,Protein Trafficking 2. Transport of protein 3. 7.08E-19 4. Increased 5. 2.788 6. 110	ABCB9,AKT1,AP2A1,AP2M1,AP3B1,ARCN1,ARF6,ARFGAP1,ASPSCR1,BAG3,BIN1,CALCRL,CALR,CCDC22,CCDC93,CDK5,CEP290,CHCHD4,CHP1,CTTN,DDX5,DNAJA1,DNM2,Dst,DTX3L,EGF,EHD1,EIF5A,ERP29,FLNA,FRAS1,GAPVD1,GCKR,GGA1,GOSR1,HGS,HSP90AA1,HSP90AB1,HSPA8,HSPA9,IGF2R,IPO5,JUP,KPNA2,LMAN2,LMAN2L,LMNA,LRP1,M6PR,MIA3,MYH9,NSF,NUP155,NUP214,NUP54,NUP98,NUTF2,PEX1,PEX14,PEX16,PEX26,PEX5,PEX6,PHB2,PICALM,PIGR,PML,PPT1,PSEN1,PTTG1IP,RAB1A,RAB4A,RAB8A,RAN,RANGAP1,RBM22,RUFY1,SCAMP1,SCAMP3,SCFD1,SCYL2,SEC23IP,SELENOK,SNAP23,SNX1,SNX3,SNX4,SNX6,STAT3,STX7,TAP1,TARDBP,TBC1D13,TGFBRAP1,TIMM23,TIMM44,TMED10,TMED2,TNPO1,TNPO2,TNPO3,TOMM40,TPR,TRIM28,TSG101,USO1,VAMP2,VPS33B,XPO1,XPO5
1. Infectious Diseases 2. HIV infection 3. 7.42E-19 4. Increased 5. 7.661 6. 206	AASS,ACACB,ACADSB,ACTR3,ADAM10,ADK,AKT1,AMDHD2,AP2M1,APOA1,ARF6,ARGLU1,ARHGEF12,ARPC1A,ATOX1,ATXN2,B2M,BCLAF1,BMP2K,C1orf174,C4A/C4B,CAD,CCAR1,CCDC134,CCDC51,CD36,CD38,CFI,CHORDC1,CLTA,CLU,COASY,COG3,CRP,CTSZ,CYP2B6,CYP3A5,CYP3A7,DDOST,DDX23,DDX3X,DHFR,DHX15,DHX9,DNAJB1,DNM2,DPM1,DPP4,DYSF,EGF,EGFR,EIF2B5,EIF3H,ELOA,ELOC,EXOSC5,FCGR2B,FLII,FN1,FNTA,FXR1,GANAB,GAPVD1,GATAD2A,GCK,GOLPH3,GOSR2,GPR182,GPT2,H3-3A/H3-3B,HDAC1,HEATR1,HGS,HIBCH,HLA-A,HMGCS1,HNRNPF,HNRNPH1,HNRNPU,HUWE1,IFNAR2,ITGB1,KHDRBS1,KXD1,LIN7C,LMAN2,LSM14B,MANBA,MAOA,MAOB,MAP4,MAT2A,MID1IP1,MRC1,MRPS12,MTOR,MYEF2,NDUFA10,NDUFAF2,NDUFAF3,NDUFB7,NGLY1,NIPSNAP2,NLRX1,NR3C1,NUDT3,NUP153,NUP155,NUP160,NUP214,NUP98,PANK1,PARP9,PARVA,PARVB,PCK1,PCTP,PDIA3,PDIA6,PGM1,PGRMC2,PI4KA,PIP5K1C,PLOD3,PM20D1,POLR2A,POLR2H,POLR2I,POLR2L,POR,PPIB,PPM1K,PRPF6,PRPF8,PSIP1,PSMA1,PSMA2,PSMA3,PSMA5,PSMA7,PSMB6,PSMC3,PSMD4,PTGES3,PURA,RAB8A,RANBP1,RAP1B,RBM10,RBM17,RELA,RGPD4 (includes others),RNH1,RPL10A,RPL12,RPL18,RSL1D1,S100A1,SAMHD1,SCFD1,SEC61G,SERPINA1,SF3A1,SF3B1,SF3B2,SIGLEC1,SIGMAR1,SLCO2A1,SNRPA1,SNRPD3,SNW1,SPAST,SPCS3,SPG7,SPTAN1,SRRT,SRSF2,SRSF6,SSR1,SSR3,STAB1,STIP1,STT3A,SUB1,SUCLG2,SUMO2,TAGLN2,THOC2,TIMM17B,TM9SF2,TMED2,TNPO3,TOP2B,TOP3B,TPPP,TRAPPC1,TSG101,TUBA4A,TUBB2A,TUBB4B,TWF1,UBE2H,UBE2Z,XPO1,YBX1,ZC3HAV1
1. Infectious Diseases 2. Infection by Retroviridae 3. 1.2E-18 4. Increased 5. 7.719 6. 207	AASS,ACACB,ACADSB,ACTR3,ADAM10,ADK,AKT1,AMDHD2,AP2M1,APOA1,ARF6,ARGLU1,ARHGEF12,ARPC1A,ATOX1,ATXN2,B2M,BCLAF1,BMP2K,C1orf174,C4A/C4B,CAD,CCAR1,CCDC134,CCDC51,CD36,CD38,CFI,CHORDC1,CLTA,CLU,COASY,COG3,CRP,CTSZ,CYP2B6,CYP3A5,CYP3A7,DDOST,DDX23,DDX3X,DHFR,DHX15,DHX9,DNAJB1,DNM2,DPM1,DPP4,DYSF,EGF,EGFR,EIF2B5,EIF3H,ELOA,ELOC,EXOSC5,FCGR2B,FLII,FN1,FNTA,FXR1,GANAB,GAPVD1,GATAD2A,GCK,GOLPH3,GOSR2,GPR182,GPT2,H3-3A/H3-3B,HDAC1,HEATR1,HGS,HIBCH,HLA-A,HMGCS1,HNRNPF,HNRNPH1,HNRNPU,HUWE1,IFNAR2,ITGB1,KHDRBS1,KXD1,LIN7C,LMAN2,LSM14B,MANBA,MAOA,MAOB,MAP4,MAT2A,MID1IP1,MRC1,MRPS12,MTOR,MYEF2,NDUFA10,NDUFAF2,NDUFAF3,NDUFB7,NGLY1,NIPSNAP2,NLRX1,NR3C1,NUDT3,NUP153,NUP155,NUP160,NUP214,NUP98,PANK1,PARP9,PARVA,PARVB,PCK1,PCTP,PDIA3,PDIA6,PGM1,PGRMC2,PI4KA,PIP5K1C,PLOD3,PM20D1,POLR2A,POLR2H,POLR2I,POLR2L,POR,PPIB,PPM1K,PRPF6,PRPF8,PSIP1,PSMA1,PSMA2,PSMA3,PSMA5,PSMA7,PSMB6,PSMC3,PSMD4,PTGES3,PURA,RAB8A,RANBP1,RAP1B,RBM10,RBM17,RELA,RGPD4 (includes others),RNH1,RPL10A,RPL12,RPL18,RSL1D1,S100A1,SAMHD1,SCFD1,SEC61G,SERPINA1,SF3A1,SF3B1,SF3B2,SIGLEC1,SIGMAR1,SLC31A1,SLCO2A1,SNRPA1,SNRPD3,SNW1,SPAST,SPCS3,SPG7,SPTAN1,SRRT,SRSF2,SRSF6,SSR1,SSR3,STAB1,STIP1,STT3A,SUB1,SUCLG2,SUMO2,TAGLN2,

	THOC2,TIMM17B,TM9SF2,TMED2,TNPO3,TOP2B,TOP3B,TPPP,TRAPPC1,TSG101,TUBA4A,TUBB2A,TUBB4B,TWF1,UBE2H,UBE2Z,XPO1,YBX1,ZC3HAV1
1. Cellular Function and Maintenance 2. Endocytosis by eukaryotic cells 3. 2.84E-18 4. Increased 5. 5.799 6. 128	ACTR2,ACTR3,AHSA1,ANXA1,ANXA5,AP2A1,AP2M1,APCS,APOA1,APOA2,APOE,ARAF,ARF6,ARPC2,ARPC3,ARRB1,ASGR1,ATP6AP1,ATP6V0D1,ATP6V1A,ATP6V1E1,BIN1,BRAF,CALR,CD163,CD36,CD38,CD47,Cdc42,CDC5L,CFH,CKB,CLEC4G,CLIC4,CMAS,CORO1A,CRP,CSK,CTNNB1,CTNND1,CYFIP1,DDX3X,DNM2,DPYSL2,EGF,EHD1,ELMO1,ELOVL1,EPB41L2,EPN1,ERP44,FCGR2B,FCHO2,FLNA,FMR1,GAPVD1,Gm21596/Hmgb1,GNAI2,GNE,GPR182,GRN,HGS,HMOX1,HP,HRAS,HSP90AA1,HSPA5,HYOU1,ICAM1,ITGB1,LGALS3,LMAN2,LRP1,LUM,LYN,M6PR,Mbl1,MBL2,MBNL1,MIF,MRC1,MSR1,MTA2,MYH9,NANS,NHLRC2,NOS3,NR3C1,PALLD,PFKFB3,PIP5K1C,PPP6R1,PRKAA2,PSEN1,PSMD4,PTK2,PTRHD1,PXN,RAC1,RACK1,RHOA,RHOG,RPS21,RPTOR,RUFY1,RUVBL2,SAA1,SART1,SCARB1,SCARB2,SF3B3,SF3B4,SFPQ,SHOC2,SIGLEC1,SMPD1,SNAP23,SRSF3,SRSF6,STAB2,STT3A,SWAP70,TLN1,VAV2,VIM,VTN,WASF2,YWHAQ
1. Infectious Diseases 2. Infection of tumor cell lines 3. 3.39E-18 4. Increased 5. 8.077 6. 152	AASS,ACACB,ACADSB,ACTR2,ADAM10,AKT1,AP2A1,AP2M1,APOE,ARCN1,ARF6,ARGLU1,ARHGEF12,ARPC1A,ARPC1B,ARPC3,ARPC5,ARRB1,ASGR2,ATOX1,ATP5IF1,ATP6AP2,ATP6V0D1,BCLAF1,BMP2K,CAMK1,CCDC134,CHCHD2,CLTB,COG3,COG5,COPA,COPB1,COPB2,COPG1,COPZ1,CTBP1,CTSZ,CYB5B,DDOST,DDX3X,DDX58,DNAJB1,DNM2,DPM1,DPP4,DYSF,EEA1,EGF,EGFR,EIF2AK2,EIF3A,EIF3H,EIF3I,ELOA,EPN1,ERC1,EXOSC5,FAU,FBL,FCGRT,FLII,FNTA,GAPVD1,GBF1,GCK,GOLPH3,GOSR2,GPR182,H3-3A/H3-3B,HDAC1,HEATR1,HGS,HIBCH,HIP1,HNRNPF,HNRNPK,HNRNPU,HSP90B1,HSPA9,HUWE1,IGF2R,LDLR,LSM14B,MAP4,MAT2A,MBL2,MID1IP1,NDUFA10,NDUFB7,NGLY1,NIPSNAP2,NOP56,NUP153,NUP155,NUP160,NUP98,PANK1,PARVA,PARVB,PCK1,PCTP,PDIA3,PDIA6,PGRMC2,PI4KA,PICALM,PIP5K1C,PLOD3,PM20D1,POLR2H,POLR2L,PPIB,PSMD4,PURA,RAB8A,RAB8B,RAC1,RACK1,RANBP1,RAP1B,RELA,RGPD4 (includes others),RSL1D1,S100A1,SCFD1,SEC61G,SLC31A1,SLCO2A1,SNU13,SPAST,SPCS3,SPTAN1,SRSF2,SSR1,SSR3,STAT2,STIP1,STT3A,SUCLG2,SUMO2,THOC2,TM9SF2,TMED2,TNPO3,TRAPPC1,TSG101,TWF1,UBE2Z,WASF2,WDR46,XPO1
1. Protein Degradation,Protein Synthesis 2. Catabolism of protein 3. 1.28E-17 4. Increased 5. 2.079 6. 190	A1CF,AAK1,ACY1,ADAM10,ADI1,AKT1,AMBP,ANPEP,APCS,APOA1,APOA2,APOE,ARIH1,ARRB1,ASGR2,ASPH,ATG4B,ATP1B1,ATP1B3,BAG3,BAG5,BUB3,CALR,CANX,CAPNS1,CASP3,CASP7,CAT,CCDC47,CCT3,CD81,CDC26,CDC37,CDK5,CDKN1B,CHP1,CLU,CNDP2,COG3,COPG1,CPB2,CPN1,CPQ,CREB1,CSNK2A1,CTNND1,CTSB,CTSC,CTSD,CTSF,CTSH,CTSO,CTSS,CTSV,CTSZ,CUL2,CUL3,DDI2,DNAJC1,DPM3,DPP4,DPP7,DTX3L,DYSF,EGF,EGFR,EIF2AK2,ENPEP,F11,FAF1,FBXO3,FLNA,FLOT1,FLOT2,GAPDH,GBA,GGA1,GNAQ,GOLGA7,GPLD1,GRN,GTPBP4,HCFC1,HERPUD1,HGS,HIP1,HOMER2,HPN,HSP90AA1,HSP90AB1,HSP90B1,HSPA1A/HSPA1B,HSPA5,HSPA8,HSPD1,HSPG2,HYPK,IMMP2L,Irgm1,IST1,ITGB1,KLKB1,KRAS,LGMN,LMNA,LSR,MANBA,MME,MTOR,MUL1,MYH9,NAA15,NAA16,NAALAD2,NACA,NAGLU,NCSTN,NDUFA13,NGLY1,NLN,NSF,OGA,OGT,OS9,PDCD10,PEX19,PEX6,PHB2,PIK3CB,PITRM1,PLG,PLPP3,PML,PPIB,PREP,PRKRA,PROC,PSEN1,PSMB3,PSMB5,PSMD14,PSME3,PSMF1,PTGES3,PYCARD,Rbx1,RELA,RNF185,RNF20,RNF213,RNF5,RNPEP,RPL11,RPL23,RPL5,RPS7,RTN4,SDC4,SERPINA1,SERPINB1,SF3B3,SNF8,SNX1,SNX3,SOS1,SPCS1,SPCS3,SPPL2A,SPTBN2,STT3B,SUGT1,TADA3,TARDBP,TCIRG1,TSG101,TYSND1,UBA3,UBE2G2,UBE2I,UBE2Z,UBE4B,UBR2,USP19,USP7,VPS28,VPS35,VTN,WFS1,XPNPEP1,XPO1
1. Cellular Assembly and Organization,Cellular Function and Maintenance 2. Organization of cytoplasm 3. 4.14E-17 4. Increased 5. 6.492 6. 402	ABCD1,ABCD3,ABITRAM,ACACA,ACP2,ACTB,ACTG1,ACTN1,ACTN4,ACTR2,ACTR3,ADAM10,ADD1,ADI1,AFDN,Afg3l1,AGFG1,AGRN,AHNAK,Akap9,AKT1,ALAS1,ALDOA,ANGPTL4,ANPEP,ANXA1,APOE,AQP1,ARF6,ARHGAP17,ARHGAP5,ARHGDIA,ARHGEF7,ARPC1A,ARPC2,ARPC3,ARPC5,ARRB1,ARSB,ATL3,ATP2B1,ATRX,ATXN10,ATXN2,BAG3,BAG4,BAG5,BAIAP2,BASP1,BCS1L,BIN1,BMP2K,BNIP3,BRAF,BSG,Bst2,C1QA,CALR,CALU,CANX,CAP1,CAPNS1,CAPZB,CASP3,CCDC47,CD2AP,CD47,CD81,CD82,Cdc42,CDK5,CDK5RAP3,CDK9,CDKN1B,CEP290,CEP89,CFAP20,CGN,CHP1,CKAP4,CKB,CKM,CLDN3,CLU,CNP,COG3,COMT,COPB2,CORO1A,CORO1B,CORO1C,CREB1,CRIP1,CRK,CRKL,CSK,CSNK2A2,CSRP1,CTNNB1,CTNND1,CTSS,CTSV,CTTN,Cux1,CXADR,CYFIP1,DAAM1,DAPK1,DBNL,DCTN2,DCTN6,DDAH1,DES,Diaph2,DNAJB6,DNAJC13,DNM1L,DNM2,DPYSL2,DRG1,DSP,Dst,DYNLL1,EEF1A1,EGF,EGFR,EHD1,EIF2B2,EIF4E,EIF4G2,ELMO1,EMD,EML4,EPB41,EPB41L2,EPB41L5,EPHX2,EPPK1,EPS8L2,ERBIN,EXOC5,EZR,F13A1,FARP1,FASN,FCGR2B,FHIT,FIS1,FITM2,FKBP4,FLII,FLNA,FLOT1,FMR1,FN1,Fnbp1l,FSCN1,FTCD,FTO,FXN,GAA,GABPA,GALK2,GALNS,GAPDH,GBA,GBF1,GDA,GJB2,GNA13,GNAS,GOLGA2,GOLGA5,GOLPH3,GOLPH3L,GORASP2,GPX4,GRN,GSTM1,HCFC1,HDGF,HDGFL3,HEXB,HMGCL,HNF4A,HNRNPK,HRAS,Hrg,HSD17B10,HSP90AA1,HSP90AB1,HSPB1,ICAM1,ILK,INSR,IQGAP1,ITGA1,ITGAV,ITGB1,ITGB3,ITSN1,JUP,KIF13B,KIF21A,KPNA1,KRAS,LAMTOR1,LARP4,LASP1,LDLR,LIFR,LMAN1,LMNB1,LRP1,LRPAP1,LYN,LYPLA1,Macf1,MAOA,MAP2K1,MAP4,MAPRE1,MAPRE3,MECP2,MFN2,MGLL,MIA3,MID1IP1,MIEN1,MOB2,MPP1,MPRIP,MSN,MTOR,MTSS1,MUL1,MYH10,MYH9,MYLK,MYO18A,MYO1B,NAGLU,NCK1,NDRG1,NECTIN2,NFIA,NFIB,NIPSNAP2,NNMT,NPC1,NQO1,NSFL1C,NUDCD3,NUMA1,NUP160,OGT,OPTN,PAFAH1B1,PAK2,PALLD,PA

	RP1,PARVA,PARVB,PDE2A,PDIA3,PDLIM7,PEX1,PEX11A,PEX12,PEX14,PEX16,PEX19,PEX3,PEX5,PEX6,PFDN2,PHACTR4,PHB2,PHLDB2,PICALM,PIP5K1C,PKP4,PLEKHF1,PLG,PLS3,PLXNA4,PLXNB2,Podxl,PON1,PPT1,PQBP1,PRDX3,PRKAA2,PRKACA,PRKCSH,PROC,PRPF40A,PRUNE1,PSEN1,PTK2,PTK2B,PTPN1,PTPRF,PTPRK,PXN,RAB1A,RAB35,RAB3IP,RAB8A,RAC1,RAE1,RAN,RANBP1,RANBP10,RAP1A,RAP1B,RAPGEF4,RBBP4,RHOA,RHOC,RHOG,RNF5,ROCK2,RPL4,RPS14,RPS3,RPS6,RPTOR,RTN4,RUFY3,S100A1,SDC4,SEC23IP,SEC61A1,SHTN1,SLC9A3R1,SLC9A3R2,SLK,SMARCA5,SMARCE1,SMPD1,SNX1,SNX2,SON,SORBS1,SORBS2,SPAST,SPG7,SPTAN1,SPTBN2,SSBP1,SSRP1,STAT3,STIP1,STK38L,STOML2,STRN,SUN2,SURF4,SWAP70,SYNJ2BP,TBC1D24,TBCD,TLN1,TMED10,TMED2,TMED9,TMEM135,TMEM38B,TMOD3,Tmsb4x (includes others),TOP2B,TOR1A,Tpm1,TPM3,TPPP,TRAPPC4,TRIP10,TRIP11,TUBA4A,TUBB,UBE2I,UBE4B,UBQLN2,USO1,VAPB,VAV2,VCL,VCPIP1,VIM,VPS13D,VPS33B,VPS35,VTN,WASF2,WASHC4,WDR1,WDR36,WDR5,XPO1,YBX1,YME1L1
1. Infectious Diseases 2. Infection of kidney cell lines 3. 7.49E-17 4. Increased 5. 4.362 6. 93	AMDHD2,APCS,ATXN2,BSG,CAD,CCAR1,CCDC51,CHORDC1,CLTA,COASY,CTBP1,CTSB,DDX23,DHX15,DNM2,EIF2AK2,EIF2B5,ELOC,FXR1,GANAB,GATAD2A,GPT2,HDAC1,HMGCS1,HNRNPH1,HSPA5,ILF3,KHDRBS1,KXD1,LIN7C,LMAN2,MANBA,MAP4,MAT2A,MID1IP1,MRPS12,MYEF2,NDUFAF2,NDUFAF3,NLRX1,NUDT3,NUP153,NUP214,NUP98,PARP9,PGM1,PML,POLR2A,POLR2I,PPM1K,PRKRA,PRPF6,PRPF8,PSMA1,PSMA2,PSMA3,PSMA5,PSMA7,PSMB6,PSMC3,PTGES3,RBM10,RBM17,RELA,RHOC,RNH1,RPL10A,RPL12,RPL18,RPL3,RPL5,RPS6,SF3A1,SF3B1,SF3B2,SLC31A1,SNRPA1,SNRPD3,SNW1,SPG7,SRRT,SRSF6,STAB1,SUB1,SUMO2,TAGLN2,TIMM17B,TNPO3,TOP3B,TPPP,UBE2H,YBX1,ZC3HAV1
1. Infectious Diseases,Organismal Injury and Abnormalities 2. Infection of embryonic cell lines 3. 9.15E-17 4. Increased 5. 4.683 6. 93	AIP,AMDHD2,ATXN2,BSG,CAD,CCAR1,CCDC51,CHORDC1,CLTA,COASY,CTBP1,DDX23,DHX15,DNM2,EIF2AK2,EIF2B5,ELOC,FCGRT,FXR1,GANAB,GATAD2A,GPT2,HDAC1,HMGCS1,HNRNPH1,HSPA5,ILF3,KHDRBS1,KXD1,LIN7C,LMAN2,MANBA,MAP4,MAT2A,MID1IP1,MRPS12,MYEF2,NDUFAF2,NDUFAF3,NLRX1,NUDT3,NUP153,NUP214,NUP98,PARP9,PGM1,POLR2A,POLR2I,PPM1K,PRKRA,PRPF6,PRPF8,PSMA1,PSMA2,PSMA3,PSMA5,PSMA7,PSMB6,PSMC3,PTGES3,RBM10,RBM17,RELA,RHOC,RNH1,RPL10A,RPL12,RPL18,RPL3,RPL5,RPS6,RPS6KB2,SF3A1,SF3B1,SF3B2,SLC31A1,SNRPA1,SNRPD3,SNW1,SPG7,SRRT,SRSF6,STAB1,SUB1,SUMO2,TAGLN2,TIMM17B,TNPO3,TOP3B,TPPP,UBE2H,YBX1,ZC3HAV1
1. Infectious Diseases 2. Infection of epithelial cell lines 3. 0.000000000000000201 4. Increased 5. 4.486 6. 90	AMDHD2,ATXN2,BSG,CAD,CCAR1,CCDC51,CHORDC1,CLTA,COASY,CTBP1,DDX23,DHX15,DNM2,EIF2AK2,EIF2B5,ELOC,FXR1,GANAB,GATAD2A,GPT2,HDAC1,HMGCS1,HNRNPH1,HSPA5,ILF3,KHDRBS1,KXD1,LIN7C,LMAN2,MANBA,MAP4,MAT2A,MID1IP1,MRPS12,MYEF2,NDUFAF2,NDUFAF3,NLRX1,NUDT3,NUP153,NUP214,NUP98,PARP9,PGM1,POLR2A,POLR2I,PPM1K,PRKRA,PRPF6,PRPF8,PSMA1,PSMA2,PSMA3,PSMA5,PSMA7,PSMB6,PSMC3,PTGES3,RBM10,RBM17,RELA,RHOC,RNH1,RPL10A,RPL12,RPL18,RPL3,RPL5,RPS6,SF3A1,SF3B1,SF3B2,SLC31A1,SNRPA1,SNRPD3,SNW1,SPG7,SRRT,SRSF6,STAB1,SUB1,SUMO2,TAGLN2,TIMM17B,TNPO3,TOP3B,TPPP,UBE2H,YBX1,ZC3HAV1
1. Cell Death and Survival 2. Cell survival 3. 0.000000000000000351 4. Increased 5. 7.16 6. 384	Abcb1b,ABCB4,ABCB6,ABCC3,ABCC6,ACACA,ACLY,ACSL5,ACTL6A,ACTN4,ADK,AGO2,AGRN,AK3,AKT1,ALCAM,ANXA5,APEX1,APOB,APOD,APOE,ARRB1,ASAH1,ASS1,ATG3,ATG4B,ATRX,B2M,BABAM2,BAG3,BANF1,BCAP31,BCKDK,BCLAF1,BID,BNIP3,BRAF,Brd4,CADM1,CALR,CASK,CASP3,CASP7,CAT,CBR1,CCAR1,CD1D,CD2AP,CD38,CD47,CD81,CD82,CDK11A,CDK5,CDK6,CDKN1B,CDKN2C,CES1,CFH,CHD4,CIAO3,CLDN3,CLU,CNDP2,COL18A1,COPB2,CPS1,CR1L,CREB1,CRK,CRKL,CSNK2A1,CTBP1,CTH,CTNNB1,CTSB,CTSD,CTTN,CUL3,CYP3A5,DDX3X,DDX5,DHCR24,DHX9,DIABLO,DIO1,DIS3,DNAJA1,DNAJB6,DNM1L,DNM2,DPP4,DPP9,DPYD,ECM1,EEF2,EFTUD2,EGF,EGFR,EIF2A,EIF2B1,EIF2S1,EIF3A,EIF3C,EIF3E,EIF4A1,EIF4A3,EIF4E,EIF4G1,ELAVL1,ELOVL1,ENO1,EPB41L2,EPS15L1,EZR,FASN,FBL,FHIT,FKBP4,FKBP5,FLII,FLNA,FN1,FN3K,FUBP1,GALK2,GAMT,GCH1,GLUD1,Gm21596/Hmgb1,GNA13,GOLPH3,GRB7,GSR,GSTM1,GSTP1,GTPBP4,H6PD,HDAC1,HDGF,HEATR1,HERPUD1,HIP1,HK1,HLA-A,HMGA1,HMGN1,HMOX1,HMOX2,HNF1A,HNRNPK,HNRNPU,HNRNPUL1,HNRNPUL2,HOPX,HRAS,HSD17B10,HSP90AB1,HSP90B1,HSPA1A/HSPA1B,HSPA5,HSPA8,HSPA9,HSPB1,HSPD1,HSPH1,HTATIP2,HYOU1,ICAM1,IGF2R,IK,IL6ST,ILK,INPP1,INSR,IP6K1,IQGAP1,ITGA5,ITGB1,ITGB3,ITPR2,JUP,KHK,KRAS,LGALS3,LGALS3BP,LMNA,LMNB1,LRP1,LRPAP1,LSM6,LSM8,LYN,LYZ,MAP2K1,MAP2K3,MCAM,MCFD2,METAP2,MGST1,MIF,MKNK1,MSH2,MSR1,Mt1,Mt2,MTDH,MTMR6,MTOR,MTSS1,MVP,MYH11,MYO18A,NAMPT,NCK1,NCSTN,NDRG1,NDUFA13,NDUFAF4,NME3,NOP58,NOS3,NPC1,NR1H4,NR3C1,NRAS,NUP155,NUP205,NUP210,NUP54,NUP93,OGT,OXSM,PAFAH2,PAK2,PARP1,PARP14,PARVA,PDCD4,PDHA1,PDIA3,PDK1,PFDN2,PGRMC1,PHB2,PHKA2,PIK3CB,PKLR,PKN1,PLG,PLRG1,PML,PNKP,POR,PPAT,PPIA,PPIB,PPM1A,PPM1B,PPM1G,PPP1R8,PPP2R1B,PPP2R5A,PRCP,PRDX6,PREP,PRKAA2,PRKAB1,PRKACA,PRPF19,PRPF3,PRPF8,PSAP,PSEN1,PSIP1,PSMA1,PSMA3,PSMA4,PSMA5,PSMA6,PSMA7,PSMB5,PSMB6,PSMC3,PSMD14,PSME3,PTK2,PTK2B,PTP4A2,PTPN1,PTPRF,PTPRK,PYCARD,RAC1,RACK1,RAD50,RAPGEF4,RBBP4,RBM39,RBM8A,RBP1,RELA,RHOA,RIPK1,RNASEH2A,RNF2,RNMT,RPL24,RPL27,RPL35A,RPL38,RPN2,RPS6KB2,RPSA,RPTOR,RRS1,RUVBL1,S100A6,SBF1,SCARB1,SCD,SERPINA3,SE

	T,SF3A1,SF3B1,SF3B3,SFR1,SIGMAR1,SLC22A1,SLC25A23,SLC2A2,SLC31A1,SLCO1B3,SMARCA2,SMARCE1,SMC1A,SMC3,SMPD1,SND1,SNRNP200,SNRPA1,SNRPF,SNW1,SOS1,SRSF3,SRSF6,STAT2,STAT3,STAT6,STIP1,STRAP,SUGT1,SVIL,SYMPK,TAOK3,TARDBP,TGM1,THRSP,TOP1,TOP2B,TPK1,TRIM28,TSG101,TUBB,TXNDC5,TYMP,U2AF2,UBE2I,UBQLN2,UPF1,UPF2,USP24,VCAM1,VCL,VIM,VRK1,VTN,WDR1,XAF1,XPO1,XRCC6,YBX1,YWHAZ,ZBTB20
1. Cellular Assembly and Organization 2. Development of cytoplasm 3. 0.000000000000000401 4. Increased 5. 2.229 6. 158	ABCD1,ABCD3,ABITRAM,ACTB,ACTR2,ACTR3,ADD1,AIF1,Akap9,AKT1,ANXA1,APOA1,APOE,ARF6,ARHGEF12,ARPC2,ARRB1,ATG3,ATG4B,ATXN2,BAG3,BAG4,BIN1,BRAF,Cald1,CAPZB,CD47,Cdc42,CDK5,CDK6,CDKN1B,CHCHD2,CNP,COL18A1,CORO1A,CORO1C,CREB1,CRK,CTNND1,CTSD,CTTN,CUL3,DAAM1,DBNL,Diaph2,DMD,DNM1L,DPYSL2,DRG1,DYNLL1,EGF,EGFR,EIF2A,EIF2B1,ERP29,ESAM,FHIT,Fhod1,FIS1,FKBP4,FLNA,FN1,GDA,GLUL,GNA11,GNA13,GNAI2,GNAQ,GNAS,GNG12,HDAC1,HDGFL3,HIP1,HRAS,HSPA8,ICAM1,Irgm1,ITGB1,ITGB3,KANK2,KRAS,LAMTOR1,LRP1,MAP2K1,MAPRE1,MAPRE3,MFN2,MIF,MPRIP,MSRB1,MSRB2,MTOR,MTSS1,Mup1 (includes others),MYH11,MYH14,MYLK,MYO1C,NCK1,NOS3,NUBPL,NUMA1,PAFAH1B1,PALLD,PDCD10,PDCD6IP,PECAM1,PEX1,PEX11A,PEX16,PEX19,PEX26,PEX3,PEX6,PHLDB2,PLCB3,PPFIA1,PRUNE1,PSEN1,PTK2,PTK2B,PXN,PYCARD,RAB1A,RAC1,RAPGEF4,RBBP4,RHOA,RHOC,RHOG,ROCK2,RPS10,RPS14,RPS28,RPS3,RPS6,SDC4,SERPINF2,SORBS1,SSBP1,STAT3,STOML2,TBCD,Tmsb4x (includes others),TNS3,Tpm1,TPM3,TPPP,TRIP10,TUBA4A,TUBB,TWF1,U2AF2,VAV2,VCAM1,VTN,WASF2,XPO1
1. Cellular Function and Maintenance 2. Engulfment of tumor cell lines 3. 0.00000000000000213 4. Increased 5. 3.802 6. 79	ACTR2,ACTR3,AHSA1,ANXA1,AP2M1,APOE,ARAF,ARF6,ARPC2,ARPC3,ASGR1,ATP6AP1,ATP6V0D1,ATP6V1A,ATP6V1E1,BRAF,CALR,CD36,CD47,Cdc42,CDC5L,CKB,CLEC4G,CSK,CTNNB1,CYFIP1,DNM2,EGF,ELOVL1,EPB41L2,ERP44,EZR,FCGR2B,FCHO2,GNAI2,GNE,GPR182,HMOX1,HRAS,HSP90AA1,ICAM1,ITGB1,KRAS,LMAN2,LRPAP1,LYN,MBNL1,MTA2,NANS,NCL,NHLRC2,PALLD,PIGR,PPP6R1,PSMD4,PTK2,PTRHD1,PXN,RAC1,RACK1,RHOA,RHOG,RPS21,RUVBL2,SART1,SCARB1,SCARB2,SF3B3,SF3B4,SFPQ,SHOC2,SMPD1,SRSF3,SRSF6,STAB2,STT3A,TLN1,VIM,WASF2
1. Cell Death and Survival 2. Cell viability of tumor cell lines 3. 0.00000000000000251 4. Increased 5. 6.297 6. 259	ABCB6,ABCC3,ACACA,ACSL5,ACTN4,ADK,AGO2,AK3,AKT1,ALCAM,APEX1,APOE,ARRB1,ASAH1,ATG3,ATG4B,ATRX,B2M,BAG3,BCKDK,BCLAF1,BID,BNIP3,BRAF,CADM1,CALR,CASK,CASP3,CAT,CBR1,CCAR1,CD1D,CD38,CD81,CD82,CDK11A,CDK6,CDKN1B,CDKN2C,CES1,CLDN3,CLU,CNDP2,COPB2,CPS1,CREB1,CRK,CRKL,CSNK2A1,CTBP1,CTNNB1,CTSD,CTTN,CYP3A5,DHCR24,DHX9,DIABLO,DIO1,DIS3,DNAJA1,DNAJB6,DNM2,DPP4,DPP9,ECM1,EEF2,EGF,EGFR,EIF2S1,EIF3A,EIF3C,EIF3E,EIF4A1,EIF4A3,EIF4E,EIF4G1,ELAVL1,ELOVL1,ENO1,EPB41L2,EPS15L1,FASN,FBL,FHIT,FKBP4,FKBP5,FLNA,FN1,FN3K,FUBP1,GALK2,GLUD1,GNA13,GOLPH3,GRB7,GSR,GSTM1,GSTP1,GTPBP4,H6PD,HEATR1,HIP1,HK1,HMGA1,HMOX1,HNRNPUL1,HNRNPUL2,HOPX,HRAS,HSP90AB1,HSP90B1,HSPA1A/HSPA1B,HSPA5,HSPA8,HSPA9,HSPB1,HSPH1,HTATIP2,IGF2R,IK,ILK,INPP1,INSR,IQGAP1,ITGB1,ITGB3,KHK,KRAS,LGALS3,LGALS3BP,LMNB1,LSM6,LSM8,LYN,LYZ,MAP2K1,MAP2K3,MCAM,MKNK1,MSH2,MTDH,MTMR6,MTOR,MTSS1,MYO18A,NAMPT,NCSTN,NDUFA13,NDUFAF4,NME3,NR3C1,NRAS,NUP155,NUP210,PARP1,PARP14,PDCD4,PDHA1,PDK1,PFDN2,PGRMC1,PHB2,PHKA2,PKN1,PML,PNKP,PPAT,PPM1B,PPM1G,PPP1R8,PPP2R1B,PPP2R5A,PRCP,PREP,PRKAA2,PRKAB1,PRKACA,PRPF19,PRPF8,PSAP,PSMA1,PSMA3,PSMA4,PSMA5,PSMA6,PSMB5,PSMB6,PSMC3,PTK2,PTK2B,PTP4A2,PTPN1,PTPRF,PTPRK,PYCARD,RAC1,RACK1,RAPGEF4,RBBP4,RBM39,RBM8A,RELA,RHOA,RIPK1,RNASEH2A,RNF2,RNMT,RPL24,RPL27,RPL35A,RPL38,RPS6KB2,RPSA,RPTOR,RRS1,S100A6,SBF1,SCD,SERPINA3,SF3A1,SF3B1,SF3B3,SFR1,SLC25A23,SLC2A2,SLCO1B3,SMARCA2,SMARCE1,SNRNP200,SNRPA1,SNRPF,SNW1,SOS1,SRSF3,SRSF6,STAT3,STIP1,STRAP,SUGT1,SVIL,SYMPK,TAOK3,TARDBP,THRSP,TOP1,TPK1,TRIM28,TYMP,U2AF2,UBE2I,UPF1,USP24,VRK1,VTN,WDR1,XPO1,XRCC6,YBX1,ZBTB20

1. Cell Death and Survival 2. Cell viability 3. 0.0000000000000112 4. Increased 5. 6.811 6. 361	Abcb1b,ABCB4,ABCB6,ABCC3,ACACA,ACLY,ACSL5,ACTL6A,ACTN4,ADK,AGO2,AGRN,AK3,AKT1,ALCAM,ANXA5,APEX1,APOB,APOD,APOE,ARRB1,ASAH1,ASS1,ATG3,ATG4B,ATRX,B2M,BAG3,BCAP31,BCKDK,BCLAF1,BID,BNIP3,BRAF,CADM1,CALR,CASK,CASP3,CASP7,CAT,CBR1,CCAR1,CD1D,CD2AP,CD38,CD47,CD81,CD82,CDK11A,CDK5,CDK6,CDKN1B,CDKN2C,CES1,CHD4,CIAO3,CLDN3,CLU,CNDP2,COPB2,CPS1,CR1L,CREB1,CRK,CRKL,CSNK2A1,CTBP1,CTH,CTNNB1,CTSB,CTSD,CTTN,CUL3,CYP3A5,DDX5,DHCR24,DHX9,DIABLO,DIO1,DIS3,DNAJA1,DNAJB6,DNM1L,DNM2,DPP4,DPP9,DPYD,ECM1,EEF2,EFTUD2,EGF,EGFR,EIF2A,EIF2S1,EIF3A,EIF3C,EIF3E,EIF4A1,EIF4A3,EIF4E,EIF4G1,ELAVL1,ELOVL1,ENO1,EPB41L2,EPS15L1,EZR,FASN,FBL,FHIT,FKBP4,FKBP5,FLNA,FN1,FN3K,FUBP1,GALK2,GAMT,GCH1,GLUD1,Gm21596/Hmgb1,GNA13,GOLPH3,GRB7,GSR,GSTM1,GSTP1,GTPBP4,H6PD,HDAC1,HDGF,HEATR1,HERPUD1,HIP1,HK1,HLA-A,HMGA1,HMGN1,HMOX1,HMOX2,HNF1A,HNRNPK,HNRNPU,HNRNPUL1,HNRNPUL2,HOPX,HRAS,HSD17B10,HSP90AB1,HSP90B1,HSPA1A/HSPA1B,HSPA5,HSPA8,HSPA9,HSPB1,HSPD1,HSPH1,HTATIP2,HYOU1,ICAM1,IGF2R,IK,IL6ST,ILK,INPP1,INSR,IP6K1,IQGAP1,ITGB1,ITGB3,ITPR2,KHK,KRAS,LGALS3,LGALS3BP,LMNA,LMNB1,LRP1,LRPAP1,LSM6,LSM8,LYN,LYZ,MAP2K1,MAP2K3,MCAM,MCFD2,METAP2,MGST1,MIF,MKNK1,MSH2,MSR1,Mt1,Mt2,MTDH,MTMR6,MTOR,MTSS1,MVP,MYH11,MYO18A,NAMPT,NCSTN,NDRG1,NDUFA13,NDUFAF4,NME3,NOP58,NPC1,NR1H4,NR3C1,NRAS,NUP155,NUP205,NUP210,NUP54,NUP93,OGT,OXSM,PAFAH2,PAK2,PARP1,PARP14,PARVA,PDCD4,PDHA1,PDIA3,PDK1,PFDN2,PGRMC1,PHB2,PHKA2,PIK3CB,PKLR,PKN1,PLG,PLRG1,PML,PNKP,POR,PPAT,PPIA,PPM1A,PPM1B,PPM1G,PPP1R8,PPP2R1B,PPP2R5A,PRCP,PRDX6,PREP,PRKAA2,PRKAB1,PRKACA,PRPF19,PRPF3,PRPF8,PSAP,PSEN1,PSIP1,PSMA1,PSMA3,PSMA4,PSMA5,PSMA6,PSMB5,PSMB6,PSMC3,PSMD14,PSME3,PTK2,PTK2B,PTP4A2,PTPN1,PTPRF,PTPRK,PYCARD,RAC1,RACK1,RAD50,RAPGEF4,RBBP4,RBM39,RBM8A,RBP1,RELA,RHOA,RIPK1,RNASEH2A,RNF2,RNMT,RPL24,RPL27,RPL35A,RPL38,RPN2,RPS6KB2,RPSA,RPTOR,RRS1,RUVBL1,S100A6,SBF1,SCARB1,SCD,SERPINA3,SF3A1,SF3B1,SF3B3,SFR1,SIGMAR1,SLC22A1,SLC25A23,SLC2A2,SLC31A1,SLCO1B3,SMARCA2,SMARCE1,SMC3,SMPD1,SND1,SNRNP200,SNRPA1,SNRPF,SNW1,SOS1,SRSF3,SRSF6,STAT2,STAT3,STIP1,STRAP,SUGT1,SVIL,SYMPK,TAOK3,TARDBP,THRSP,TOP1,TOP2B,TPK1,TRIM28,TXNDC5,TYMP,U2AF2,UBE2I,UBQLN2,UPF1,UPF2,USP24,VCAM1,VRK1,VTN,WDR1,XAF1,XPO1,XRCC6,YBX1,YWHAZ,ZBTB20
1. Cellular Movement,Connective Tissue Development and Function 2. Cell movement of fibroblast cell lines 3. 0.0000000000000119 4. Increased 5. 4.572 6. 73	ACTN4,ACTR2,ACTR3,ADI1,AKT1,ARHGEF12,ARPC2,ATG3,BAIAP2,Cdc42,CDKN1B,CLIC4,CORO1B,CRK,CRKL,CSK,CTNNB1,CTTN,DDX3X,EGF,EGFR,EHD1,FABP5,FLNA,FN1,FSCN1,GNA11,GNA13,GNG12,GRB7,HRAS,IFI16,Ighg2b,ILK,INSR,ITGA5,ITGA9,ITGB1,LGALS8,LIMS2,LRPAP1,MAPRE1,MIEN1,MSR1,MTSS1,MYLK,NCK1,NDST1,NRAS,PALLD,PLG,PPIF,PTBP1,PTK2,PTPN1,PXN,RAC1,RACK1,RELA,RHOA,RHOC,RHOG,RNF5,RTN4,SORBS1,STAT3,TJP1,TMEM30A,Tmsb4x (includes others),VAV2,VCL,VIM,VTN
1. Cellular Function and Maintenance 2. Receptor-mediated endocytosis 3. 0.0000000000000367 4. Increased 5. 3.989 6. 76	AMBP,AP2A1,Ap2b1,AP2M1,APOA1,APOB,APOC2,Apoc3,APOE,ARF6,ASGR1,ATP6AP1,ATP6V0D1,ATP6V1E1,B2M,CALR,CANX,CAP1,CD163,CD2AP,CD36,CDC5L,CLU,CTTN,DNM2,EGFR,EPB41L2,EPN1,FCGR2B,FCHO2,Fnbp1l,GPR182,HGS,HIP1,HNRNPK,HP,HPX,HSP90AA1,HSP90B1,HSPG2,HSPH1,HYOU1,IGF2R,IGKC,INPP5F,INSR,ITSN1,JCHAIN,LDLR,LRP1,LRPAP1,M6PR,MRC1,MSR1,NOS3,PDLIM7,PICALM,PIP5K1C,PPT1,PTRHD1,RAC1,RPS21,RUVBL2,SAA1,SART1,SCARB1,SCARB2,SF3B3,SF3B4,SFPQ,SIGLEC1,SRSF3,STAB1,STAB2,TFR2,VTN
1. Molecular Transport,RNA Trafficking 2. Export of RNA 3. 0.000000000000045 4. Increased 5. 2.407 6. 42	AGFG1,CPSF2,DDX39B,EIF4A3,EIF4E,EIF5A,HNRNPA2B1,KHDRBS1,NCBP1,NCBP2,NUP153,NUP155,NUP160,NUP205,NUP210,NUP214,NUP35,NUP54,NUP93,NUP98,POLDIP3,RAE1,RAN,RBM8A,RGPD4 (includes others),SARNP,SRSF1,SRSF2,SRSF3,SRSF4,SRSF6,SRSF7,SYMPK,THOC2,THOC6,TPR,U2AF2,UPF1,UPF2,XPO1,XPO5,ZC3H11A
1. Molecular Transport,RNA Trafficking 2. Transport of RNA 3. 0.000000000000073 4. Increased 5. 2.436 6. 45	AGFG1,CPSF2,DDX39B,DDX3X,EIF4A3,EIF4E,EIF5A,FMR1,HNRNPA2B1,Hnrnpa3,KHDRBS1,NCBP1,NCBP2,NUP153,NUP155,NUP160,NUP205,NUP210,NUP214,NUP35,NUP54,NUP93,NUP98,POLDIP3,RAE1,RAN,RBM8A,RGPD4 (includes others),SARNP,SRSF1,SRSF2,SRSF3,SRSF4,SRSF6,SRSF7,SYMPK,THOC2,THOC6,TPR,U2AF2,UPF1,UPF2,XPO1,XPO5,ZC3H11A
1. Cell-To-Cell Signaling and Interaction,Cellular Function and Maintenance,Inflammatory Response 2. Phagocytosis of cells 3. 0.0000000000000755 4. Increased 5. 4.438 6. 112	ACTR2,ACTR3,AHSA1,AHSG,ANPEP,ANXA1,ANXA11,ANXA3,ANXA5,APCS,APOA1,APOA2,ARAF,ARF6,ARPC2,ARPC3,ASGR1,ATG3,BIN1,BRAF,C1QA,CALR,CAT,CD302,CD36,CD38,CD47,Cdc42,CFH,CKB,CLEC4G,CLIC4,CMAS,CORO1A,CORO1C,CRK,CRP,CSK,CTNNB1,CYFIP1,DDX3X,DNM2,DYSF,EHD1,ELMO1,ELOVL1,ERP44,FCGR2B,FLNA,Gm21596/Hmgb1,GNAI2,GNE,GRN,HMOX1,HSPA8,ICAM1,Ighg2b,ITGAV,ITGB1,LDLR,LGALS3,LMAN2,LRP1,LUM,LYAR,LYN,Mbl1,MBL2,MBNL1,MIF,MRC1,MSR1,MTA2,MYH9,NANS,NHLRC2,NR3C1,PALLD,PECAM1,PFKFB3,PIK3CB,PIP5K1C,PON1,PPP6R1,PRKAA2,PSEN1,PSMD4,PTK2,PXN,PYCARD,RAB35,RAC1,RACK1,RHOA,RHOG,RPTOR,SAA1,SCARB1,SHOC2,SIGLEC1,SMPD1,SNAP23,SNX3,SRSF6,STAB2,STT3A,SWAP70,TLN1,VAV2,VIM,VTN,WASF2

1. Metabolic Disease,Organismal Injury and Abnormalities,Renal and Urological Disease 2. Aciduria 3. 0.000000000000105 4. Increased 5. 2.202 6. 34	AASS,ACSF3,AGXT2,ASL,BCKDHA,BCKDHB,BTD,CPS1,DHTKD1,ETFDH,GCDH,GSTZ1,HADH,HCFC1,IDH2,INSR,KYNU,L2HGDH,MAN2B1,MCCC1,MCCC2,MCEE,MMAB,MMUT,Mocs1,MVK,OAT,PCBD1,PCCA,PCCB,PPM1K,SUCLG1,SUCLG2,SUGCT
1. Infectious Diseases 2. Infection of cervical cancer cell lines 3. 0.000000000000194 4. Increased 5. 7.343 6. 120	AASS,ACACB,ACADSB,ADAM10,AKT1,AP2M1,ARCN1,ARGLU1,ARHGEF12,ARPC1A,ATOX1,ATP5IF1,ATP6AP2,ATP6V0D1,BCLAF1,BMP2K,CCDC134,COG3,COG5,COPA,COPB1,COPB2,COPG1,COPZ1,CTBP1,CTSZ,DDOST,DDX3X,DNAJB1,DPM1,DPP4,DYSF,EGF,EGFR,EIF3A,EIF3H,EIF3I,ELOA,EXOSC5,FAU,FBL,FLII,FNTA,GAPVD1,GBF1,GCK,GOLPH3,GOSR2,GPR182,H3-3A/H3-3B,HEATR1,HGS,HIBCH,HNRNPF,HNRNPK,HNRNPU,HSPA9,HUWE1,LDLR,LSM14B,MAP4,MAT2A,MID1IP1,NDUFA10,NDUFB7,NGLY1,NIPSNAP2,NOP56,NUP153,NUP155,NUP160,PANK1,PARVA,PARVB,PCK1,PCTP,PDIA3,PDIA6,PGRMC2,PI4KA,PIP5K1C,PLOD3,PM20D1,POLR2H,POLR2L,PPIB,PSMD4,PURA,RAB8A,RAC1,RANBP1,RAP1B,RELA,RGPD4 (includes others),RSL1D1,S100A1,SCFD1,SEC61G,SLCO2A1,SNU13,SPAST,SPCS3,SPTAN1,SRSF2,SSR1,SSR3,STIP1,STT3A,SUCLG2,SUMO2,THOC2,TM9SF2,TMED2,TNPO3,TRAPPC1,TSG101,TWF1,UBE2Z,WDR46,XPO1
1. Molecular Transport,RNA Trafficking 2. Nuclear export of RNA 3. 0.000000000000279 4. Increased 5. 2.219 6. 40	AGFG1,CPSF2,DDX39B,EIF4A3,EIF4E,EIF5A,HNRNPA2B1,KHDRBS1,NCBP1,NCBP2,NUP153,NUP155,NUP160,NUP205,NUP210,NUP214,NUP35,NUP54,NUP93,NUP98,POLDIP3,RAE1,RBM8A,SARNP,SRSF1,SRSF2,SRSF3,SRSF4,SRSF6,SRSF7,SYMPK,THOC2,THOC6,TPR,U2AF2,UPF1,UPF2,XPO1,XPO5,ZC3H11A
1. Molecular Transport,RNA Trafficking 2. Transport of mRNA 3. 0.000000000000383 4. Increased 5. 2.01 6. 42	AGFG1,CPSF2,DDX39B,EIF4A3,EIF4E,EIF5A,FMR1,HNRNPA2B1,Hnrnpa3,KHDRBS1,NCBP1,NCBP2,NUP153,NUP155,NUP160,NUP205,NUP210,NUP214,NUP35,NUP54,NUP93,NUP98,POLDIP3,RAE1,RBM8A,RGPD4 (includes others),SARNP,SRSF1,SRSF2,SRSF3,SRSF4,SRSF6,SRSF7,SYMPK,THOC2,THOC6,TPR,U2AF2,UPF1,UPF2,XPO1,ZC3H11A
1. Molecular Transport 2. Nuclear export of molecule 3. 0.000000000000736 4. Increased 5. 2.219 6. 46	AGFG1,CALR,CHCHD4,CHP1,CPSF2,DDX39B,EIF4A3,EIF4E,EIF5A,HNRNPA2B1,HSPA9,KHDRBS1,NCBP1,NCBP2,NUP153,NUP155,NUP160,NUP205,NUP210,NUP214,NUP35,NUP54,NUP93,NUP98,NUTF2,POLDIP3,RAE1,RAN,RBM8A,SARNP,SRSF1,SRSF2,SRSF3,SRSF4,SRSF6,SRSF7,SYMPK,THOC2,THOC6,TPR,U2AF2,UPF1,UPF2,XPO1,XPO5,ZC3H11A
1. Cellular Assembly and Organization,Tissue Development 2. Fibrogenesis 3. 0.000000000000926 4. Increased 5. 2.597 6. 141	ABITRAM,ACTG1,ACTR2,ACTR3,ADD1,AIF1,Akap9,AKT1,APCS,APOA1,APOE,ARF6,ARHGEF12,ARPC2,ARRB1,ATXN2,BAG4,BIN1,BRAF,Cald1,CALR,CAPZB,CD38,CD47,Cdc42,CDK6,CDKN1B,CHCHD2,CHD4,CNP,COL18A1,CORO1A,CREB1,CRK,CTNND1,CTSB,CTTN,CUL3,DAAM1,DES,Diaph2,DMD,DPYSL2,DRG1,DYNLL1,DYSF,EGF,EGFR,EPPK1,ESAM,FHIT,Fhod1,FKBP4,FN1,GAA,GDA,GNA11,GNA13,GNAI2,GNAQ,GNG12,HDGFL3,HRAS,HSD11B1,HSPA5,HSPB1,ICAM1,ITGB1,KANK2,KRAS,LAMTOR1,LRP1,LUM,MAP2K1,MAPRE1,MAPRE3,MFN2,MIF,MME,MPRIP,MSRB1,MSRB2,MTOR,MTSS1,MYH10,MYH11,MYLK,MYO1C,NCK1,NUMA1,PAFAH1B1,PALLD,PDCD10,PDCD4,PDCD6IP,PECAM1,PHLDB2,PLCB3,PLOD3,PPFIA1,PRKAA2,PROX1,PRUNE1,PTK2,PTK2B,PXN,PYCARD,RAC1,RBBP4,RHOA,RHOC,ROCK2,RPS3,SDC4,SERPINA3,SERPINF2,SERPINH1,SORBS1,STAB1,STAT3,TBCD,TMOD3,Tmsb4x (includes others),TNS3,Tpm1,TPM3,TPPP,TPR,TRIP10,TTN,TUBA4A,TUBB,TWF1,U2AF2,VAV2,VCAM1,VIM,VTN,WASF2,WDR1,YWHAQ
1. Molecular Transport,Protein Trafficking 2. Internalization of protein 3. 0.00000000000135 4. Increased 5. 2.917 6. 50	AKT1,AP2M1,ARF6,BAG3,CAP1,DDX5,DNAJA1,DNM2,EGF,EGFR,FLNA,GCKR,HGS,HIP1,HSP90AA1,HSP90AB1,HSPA8,HSPG2,IPO5,JUP,KPNA2,KRAS,LMNA,NUP155,NUP214,NUP54,NUP98,NUTF2,PEX1,PEX14,PEX16,PEX26,PEX6,PHB2,PML,PSEN1,PTTG1IP,RAN,RANGAP1,RBM22,RHOA,STAT3,TARDBP,TNPO1,TNPO2,TNPO3,TOMM40,TPR,TRIM28,XPO1
1. Cellular Function and Maintenance,Inflammatory Response 2. Phagocytosis 3. 0.0000000000018 4. Increased 5. 4.475 6. 117	ACTR2,ACTR3,AHSA1,AHSG,ANPEP,ANXA1,ANXA11,ANXA3,ANXA5,APCS,APOA1,APOA2,ARAF,ARF6,ARPC2,ARPC3,ASGR1,ATG3,BIN1,BRAF,C1QA,CALR,CAT,CD302,CD36,CD38,CD47,Cdc42,CFH,CKB,CLEC4G,CLIC4,CMAS,CORO1A,CORO1C,CRK,CRP,CSK,CTNNB1,CYFIP1,DDX3X,DNM2,DYSF,EHD1,EIF2AK2,ELMO1,ELOVL1,ERP44,FCGR2B,FLNA,Gm21596/Hmgb1,GNAI2,GNE,GRN,HMOX1,HSPA8,ICAM1,Ighg2b,ITGAV,ITGB1,ITGB3,LDLR,LGALS3,LMAN2,LRP1,LUM,LYAR,LYN,Mbl1,MBL2,MBNL1,MFN2,MIF,MRC1,MSN,MSR1,MTA2,MYH9,NANS,NHLRC2,NR3C1,PALLD,PECAM1,PFKFB3,PIK3CB,PIP5K1C,PON1,PPP6R1,PRKAA2,PSEN1,PSMD4,PTK2,PXN,PY

	CARD,RAB35,RAC1,RACK1,RHOA,RHOG,RPTOR,SAA1,SCARB1,SCARB2,SHOC2,SIGLEC1,SMPD1,SNAP23,SNX3,SRSF6,STAB2,STT3A,SWAP70,TLN1,VAV2,VIM,VTN,WASF2
1. Cellular Assembly and Organization,Tissue Development 2. Formation of filaments 3. 0.00000000000237 4. Increased 5. 2.811 6. 128	ABITRAM,ACTR2,ACTR3,ADD1,AIF1,Akap9,AKT1,APCS,APOA1,APOE,ARF6,ARHGEF12,ARPC2,ARRB1,ATXN2,BAG4,BIN1,BRAF,Cald1,CAPZB,CD47,Cdc42,CDK6,CDKN1B,CHCHD2,CNP,COL18A1,CORO1A,CREB1,CRK,CTNND1,CTSB,CTTN,CUL3,DAAM1,DES,Diaph2,DPYSL2,DRG1,DYNLL1,EGF,EGFR,EPPK1,ESAM,FHIT,Fhod1,FKBP4,FN1,GDA,GNA11,GNA13,GNAI2,GNAQ,GNG12,HDGFL3,HRAS,HSPA5,HSPB1,ICAM1,ITGB1,KANK2,KRAS,LAMTOR1,LRP1,LUM,MAP2K1,MAPRE1,MAPRE3,MIF,MME,MPRIP,MSRB1,MSRB2,MTOR,MTSS1,MYH11,MYLK,MYO1C,NCK1,NUMA1,PAFAH1B1,PALLD,PDCD10,PDCD6IP,PECAM1,PHLDB2,PLCB3,PLOD3,PPFIA1,PRKAA2,PROX1,PRUNE1,PTK2,PTK2B,PXN,PYCARD,RAC1,RBBP4,RHOA,RHOC,ROCK2,RPS3,SDC4,SERPINA3,SERPINF2,SERPINH1,SORBS1,STAT3,TBCD,TMOD3,Tmsb4x (includes others),TNS3,Tpm1,TPM3,TPPP,TPR,TRIP10,TTN,TUBA4A,TUBB,TWF1,U2AF2,VAV2,VCAM1,VIM,VTN,WASF2,YWHAQ
1. Molecular Transport 2. Nuclear export 3. 0.0000000000024 4. Increased 5. 2.213 6. 47	AGFG1,CALR,CHCHD4,CHP1,CPSF2,DDX39B,EIF4A3,EIF4E,EIF5A,HNRNPA2B1,HSPA9,KHDRBS1,LSG1,NCBP1,NCBP2,NUP153,NUP155,NUP160,NUP205,NUP210,NUP214,NUP35,NUP54,NUP93,NUP98,NUTF2,POLDIP3,RAE1,RAN,RBM8A,SARNP,SRSF1,SRSF2,SRSF3,SRSF4,SRSF6,SRSF7,SYMPK,THOC2,THOC6,TPR,U2AF2,UPF1,UPF2,XPO1,XPO5,ZC3H11A
1. Cellular Development,Cellular Growth and Proliferation 2. Cell proliferation of tumor cell lines 3. 0.00000000000467 4. Increased 5. 6.458 6. 423	AASDHPPT,ABCB10,ABCB6,ABCC2,ACACA,ACAT1,ACIN1,ACLY,ACSL4,ACSL5,ACTB,ACTN1,ACTN4,ADAM10,ADIPOR2,ADSL,AGK,AHCY,AHNAK,AHSA1,AHSG,AKR1B10,AKT1,ALCAM,ALDH1A1,ALDH1L1,ALDOA,AMACR,ANGPTL4,ANKHD1/ANKHD1-EIF4EBP3,ANXA1,APEX1,API5,APOB,AQP1,ARAF,ARCN1,ARF6,ARIH1,ASAH1,ASPH,ASS1,ATP2A2,ATP6AP1,BID,BIN1,BNIP3,BRAF,BSG,BUB3,CACYBP,CALR,CAMK1,CASP3,CASP7,CAT,CBX1,CD163,CD38,CD81,CDC37,CDK5,CDK6,CDKN1B,CDKN2C,CHD4,CISD1,CISD2,CLU,CLYBL,CMC2,CNDP2,COBLL1,COL18A1,COPB2,COPZ1,CREB1,CRK,CRKL,CSNK1E,CSNK2A1,CSNK2A2,CSNK2B,CSTF2,CTBP1,CTDSP1,CTNNB1,CTNND1,CTR9,CTSB,CTSD,CTTN,CXADR,CYP2A6 (includes others),CYP2B6,CYP2C8,CYP3A5,DDX17,DDX21,DDX3X,DDX5,DDX58,DEK,DIABLO,DNAJB4,DNAJB6,DPP4,EEF1A1,EGF,EGFR,EIF3A,EIF3C,EIF3E,EIF3F,EIF3H,EIF3M,EIF4A1,EIF4E,EIF4H,EIF5,EIF5A,ELAVL1,EMILIN1,ENTPD5,ERBIN,EZR,FABP2,FABP5,FASN,FEN1,FGL1,FHIT,FKBP4,FKBP5,FLNA,FLOT1,FN1,FNTA,FSCN1,FXN,G0S2,G6PD,GADD45GIP1,GALNT2,GAPDH,GCAT,GLDC,GNAQ,GNAS,GNE,GNL3,GNMT,GOLGA2,GOLPH3,GPR182,GRB7,GRN,GSTM1,GSTM4,GSTP1,GTF2I,GTPBP4,HDAC1,HDGF,HEXIM1,HGS,HK1,HMGA1,HMOX1,HNF1A,HNF4A,HNRNPA2B1,HNRNPH2,HNRNPK,HNRNPL,HPGD,HPN,HRAS,HSD11B1,HSP90AA1,HSPA5,HSPB1,HTATIP2,HUWE1,IDH2,IFI16,IGF2R,Ighg2b,IGKC,IL6ST,ILF2,ILF3,ILK,ILKAP,IMMT,INPP5F,INSR,IQGAP1,Irgm1,ITGA1,ITGA5,ITGAV,ITGB1,ITGB3,JUP,KCTD12,KPNA2,KRAS,LARP1,LGALS1,LGALS3,LGALS3BP,LMNA,LOC102724788/PRODH,LRP1,LYN,MAP2K1,MAP2K3,MAPRE1,MBL2,ME1,MFN2,MGLL,MIF,MIF4GD,MIPEP,MKNK1,MPI,MTA2,MTAP,MTDH,MTOR,MYBBP1A,MYCBP,MYH10,MYH14,MYLK,NAA35,NACA,NAMPT,NASP,NAT10,NCL,NCSTN,NDRG1,NDUFA13,NDUFAF2,NDUFAF3,NDUFAF4,NELFA,NELFCD,NFIB,NFS1,NGEF,NONO,NPC1,NQO1,NR1H4,NR3C1,NRAS,NUCB2,NUDCD3,NUMA1,NUP155,OGA,OGFR,OGT,PA2G4,PAFAH1B1,PARP1,PARVB,PAWR,PBLD,PC,PDCD10,PDCD4,PDIA3,PEBP1,PECAM1,PFKFB3,PGD,PGRMC1,PHLDA1,PICALM,PIK3CB,PIP4K2B,PIP5K1C,PLG,PLXNA4,PML,POR,PPIF,PPIL1,PPT1,PRKAA2,PRKACA,PRKCSH,PROX1,PRPF3,PRPF31,PRPF6,PRPF8,PRRC2C,PSEN1,PSMA4,PSMA5,PSMB2,PSMB3,PSMB7,PSMD4,PTBP1,PTK2,PTK2B,PTPN1,PTPRF,PTPRK,PUM1,PURA,PXN,RAB8A,RAB8B,RAC1,RACK1,RAN,RAP1B,RBM17,RELA,RHOA,RHOC,RIOX2,RIPK1,RNF14,RNF2,RNF20,RNF5,RPL11,RPRD1B,RPS10,RPS14,RPS25,RPS9,RPSA,RPTOR,S100A1,S100A6,SAE1,SART1,SCARB1,SCD,SDC4,SEC61G,SET,SFPQ,SH3GL1,SLC25A13,SLC9A3R1,SMARCA2,SMARCE1,SMC1A,SND1,SNRNP200,SNW1,SNX1,SON,SPAST,SPTAN1,SRSF1,SRSF2,SRSF3,SSBP1,STAG2,STAT2,STAT3,STEAP3,STK38,STK38L,STOML2,STRAP,SULT1E1,SULT2A1,SUMO2,SYMPK,SYNCRIP,TADA3,TAGLN2,TARDBP,TCIRG1,TDO2,TMPO,Tmsb4x (includes others),TNS2,TOP1,TPD52,TRAP1,TRIM28,TSG101,TTPA,TUBB,TUBB2A,UBA1,UBA2,UBE2I,UBE2J1,UBE2M,UGDH,UGT2B17,UPP1,VAMP2,VAV2,VCAM1,VDAC3,VPS28,VPS35,VTN,WBP2,WDR5,XPO1,XRCC6,YBX1,YWHAQ,YWHAZ,ZBTB20,ZMIZ1
1. Cell Morphology,Cellular Movement 2. Cell spreading 3. 0.0000000000079 4. Increased 5. 3.574 6. 88	ACTN4,AKT1,APCS,ARF6,ARPC3,BAIAP2,CADM1,CAP1,CD36,CD47,CD81,CORO1A,CRK,CRKL,CSK,DCTN2,EGF,EGFR,EHD1,ELMO1,EXOC5,FAAH,FERMT2,FLNA,FN1,GNA11,HRAS,HSPG2,ICAM1,IGF2R,ILK,ITGA1,ITGA2B,ITGA5,ITGA9,ITGAV,ITGB1,ITGB3,ITGB6,KRAS,LGALS1,LGALS3,LGALS8,LYN,MAP4,MAPRE3,MFN2,MPRIP,MSR1,MTOR,MYH10,MYH9,NCK1,NSF,PALLD,PARVA,PARVB,PDCD6IP,PECAM1,PLCB3,PPFIA1,PRKAA2,PTBP1,PTK2,PTK2B,PXN,RAC1,RACK1,RAP1B,RELA,RHOA,RHOG,RTN4,SDC4,SERPINA3,SLK,SMPD1,SORBS1,STAT3,TLN1,TMEM30A,TNS3,VAV2,VCAM1,VCL,VIM,VTN,YWHAZ

1. Inflammatory Response 2. Immune response of cells 3. 0.00000000000811 4. Increased 5. 5.733 6. 169	Abcb1b,ACTR2,ACTR3,AHSA1,AHSG,AKT1,ANPEP,ANXA1,ANXA11,ANXA3,ANXA5,APCS,APOA1,APOA2,APOE,AQP4,ARAF,ARF6,ARPC2,ARPC3,ASGR1,ATG3,ATP11C,BIN1,BRAF,Brd4,C1QA,CALR,CAT,CD1D,CD302,CD36,CD38,CD47,CD68,Cdc42,CDKN1B,CFH,CKB,CLEC4G,CLIC4,CMAS,CMC2,CORO1A,CORO1C,CRK,CRP,CSK,CTNNB1,CTSB,CTSD,CTSS,CYFIP1,DDX3X,DDX58,DNM1L,DNM2,DYSF,EHD1,EIF2AK2,ELMO1,ELOVL1,ERP44,FCGR2B,FLNA,FN1,G6PC,GAPDH,Gm21596/Hmgb1,GNA13,GNAI2,GNAS,GNE,GRN,GSTM4,HLA-A,HMOX1,HSDL1,HSP90AA1,HSP90B1,HSPA8,HSPB1,ICAM1,IFNAR2,Ighg2b,IGKC,IL6ST,ITGAV,ITGB1,ITGB3,LDLR,LGALS1,LGALS3,LITAF,LMAN2,LRP1,LUM,LYAR,LYN,Macf1,Mbl1,MBL2,MBNL1,MIF,MRC1,MSH2,MSR1,MTA2,MTOR,MYH9,NAMPT,NANS,NAPRT,NHLRC2,NLRX1,NR3C1,PALLD,PARP1,PECAM1,PFKFB3,PIK3CB,PIP5K1C,PML,PON1,PPP6R1,PRKAA2,PRKRA,PROC,PSEN1,PSMD4,PTK2,PXN,PYCARD,RAB35,RAB8B,RAC1,RACK1,RELA,RHOA,RHOG,RPTOR,SAA1,SCARB1,SF3A1,Sf3a2,SHOC2,SIGLEC1,SMPD1,SNAP23,SNX3,SRSF6,STAB2,STAT3,STT3A,SWAP70,TAP1,TAPBP,TCIRG1,TLN1,TNPO1,TOP2B,TRIM14,TRIM23,TTPA,VAV2,VCAM1,VIM,VTN,WASF2
1. Cellular Assembly and Organization 2. Formation of cytoskeleton 3. 0.00000000000845 4. Increased 5. 2.664 6. 119	ABITRAM,ACTB,ACTR2,ACTR3,ADD1,AIF1,Akap9,AKT1,APOA1,ARF6,ARHGEF12,ARPC2,ARRB1,ATXN2,BAG4,BIN1,BRAF,Cald1,CAPZB,CD47,Cdc42,CDK6,CDKN1B,CHCHD2,CNP,COL18A1,CORO1A,CORO1C,CREB1,CRK,CTNND1,CTTN,CUL3,DAAM1,DBNL,Diaph2,DMD,DPYSL2,DRG1,DYNLL1,EGF,EGFR,ERP29,ESAM,FHIT,Fhod1,FKBP4,FLNA,FN1,GDA,GNA11,GNA13,GNAI2,GNAQ,GNG12,HDGFL3,HIP1,HRAS,ICAM1,ITGB1,ITGB3,KANK2,KRAS,LAMTOR1,LRP1,MAP2K1,MAPRE1,MAPRE3,MIF,MPRIP,MSRB1,MSRB2,MTOR,MTSS1,MYH11,MYLK,MYO1C,NCK1,NUMA1,PAFAH1B1,PALLD,PDCD10,PDCD6IP,PECAM1,PHLDB2,PLCB3,PPFIA1,PRUNE1,PTK2,PTK2B,PXN,PYCARD,RAC1,RAPGEF4,RBBP4,RHOA,RHOC,RHOG,ROCK2,RPS3,SDC4,SERPINF2,SORBS1,STAT3,TBCD,Tmsb4x (includes others),TNS3,Tpm1,TPM3,TPPP,TRIP10,TUBA4A,TUBB,TWF1,U2AF2,VAV2,VCAM1,VTN,WASF2
1. Cancer,Organismal Injury and Abnormalities 2. Genitourinary adenocarcinoma 3. 0.0000000000153 4. Increased 5. 2.385 6. 1083	A1CF,AADAT,AAK1,AASDHPPT,AASS,ABAT,ABCB4,ABCB9,ABCC2,ABCC3,ABCC6,ABCD1,ABCE1,ABCF2,ABCF3,ABHD11,ABHD15,ACACB,ACAD10,ACAD11,ACADM,ACAT1,ACIN1,ACLY,ACOT1,ACOT12,ACOT7,ACOT8,ACOX1,ACOX3,ACSL4,ACSM1,ACSS2,ACTG1,ACTN1,ACTN4,ACTR2,ACY1,ACY3,ACYP2,ADAM10,ADAP2,ADD2,ADD3,ADIPOR2,ADSL,AFDN,AGK,AGL,AGO1,AGO2,AGPAT2,AGPAT5,AGXT2,AHNAK,AIF1,AK3,AKR1A1,AKT1,ALAS1,ALDH16A1,ALDH1A1,ALDH1B1,ALDH1L1,ALDH4A1,ALDH5A1,ALDH7A1,ALDOB,ALPK1,AMACR,AMBP,AMPD2,AMT,ANGPTL3,ANKHD1/ANKHD1-EIF4EBP3,ANPEP,ANXA1,ANXA11,ANXA3,ANXA5,AOX1,AP3B1,APEX1,API5,APOB,APOD,APOE,AQP1,AQP9,ARAF,ARCN1,ARF6,ARFGAP2,ARFGAP3,ARHGAP31,ARHGAP42,ARHGAP45,ARHGAP5,ARHGEF12,ARHGEF7,ARIH1,ARMC10,ARRB1,ARSB,ASGR2,ASPA,ASPG,ASPSCR1,ASRGL1,ATAD2B,ATL3,ATP11C,ATP13A1,ATP1A1,ATP2B1,ATP2B4,ATP5IF1,ATRX,ATXN2,B2M,BAAT,BABAM2,BASP1,BCAP29,BCAS2,BCKDHA,BCKDK,BCLAF1,BGN,BIN1,BIN2,BLVRB,BMP2K,BRAF,BSG,BTAF1,BTD,BZW1,C1orf174,C4A/C4B,C6,C8A,C8B,C9,CAD,CADM1,CALCRL,CALU,CAMK1,CAND1,CAPZA1,CAPZB,CASK,CASP7,CAVIN1,CBX3,CCAR1,CCDC167,CCDC40,CCDC47,CCDC58,CCT3,CD163,CD2AP,CD36,CD47,CD68,CD82,CDA,CDC34,CDC5L,CDK11A,CDK12,CDK5,CDK5RAP3,CDK6,CDK9,CDKN1B,CDKN2C,CDO1,CEP290,CEP89,CES1,CES3,CFB,CFH,CGN,CHD4,CISD2,CKAP4,CKM,CLDN3,CLEC10A,CLEC3B,CLEC4F,CLINT1,CLU,CMC2,CMTM4,CNOT1,CNOT2,CNOT3,CNOT9,CNP,COG5,COL18A1,COMT,COPA,COPB1,COPE,COPG1,CORO1C,COX6B1,COX7A2,CP,CPB2,CPN1,CPNE3,CPOX,CPQ,CPS1,CPSF2,CR1L,CRAT,CREB1,CRELD1,CRKL,CRP,CSNK2A1,CSTF1,CSTF2,CSTF3,CTH,CTNNA1,CTNNB1,CTR9,CTSC,CTSD,CUL1,CUL2,CUL3,CXADR,CYP17A1,CYP1A2,CYP2A6 (includes others),CYP2B6,CYP2F1,CYP3A5,CYP3A7,CYP4A22,CYP4F3,CYP7A1,DAD1,DAPK1,DARS2,DCAF11,DCPS,DDHD2,DDI2,DDX17,DDX23,DDX27,DDX3X,DDX42,DDX49,DDX58,DES,DGAT2,DGLUCY,DHFR,DHRS7B,DHTKD1,DHX16,DHX9,DIABLO,DIO1,DIS3,DMD,DMGDH,DNAJA1,DNAJB11,DNAJB6,DNAJC13,DNAJC2,DNAJC7,DNM1L,DOCK6,DPAGT1,DPP4,DPY19L1,DPYS,DSP,DTX3L,DYSF,EBPL,ECM1,EDC4,EEA1,EEF1D,EEF2,EFHD2,EFR3A,EFTUD2,EGF,EGFR,EHD3,EHHADH,EIF1AX,EIF2AK2,EIF2S1,EIF2S2,EIF3A,EIF3E,EIF3F,EIF3I,EIF4A1,EIF4A2,EIF4E,EIF4G1,EIF4G2,EIF5B,ELAVL1,ELMO1,ELOA,ELOC,ELOVL5,ELP2,EMILIN1,EML3,EML4,ENPEP,ENPP1,EPB41L2,EPHX1,EPPK1,EPS8L2,ERBIN,ERC1,ERGIC1,ERLIN1,ERMP1,ESYT1,ETFDH,ETNPPL,EXOC1,F11,F13A1,FAAH,FABP4,FABP5,FAM126B,FAM98C,FARP1,FASN,FECH,FEN1,FERMT2,FETUB,FGA,FGG,FKBP15,FLII,FLNA,FLOT1,FMO4,FMR1,FN1,FNDC3A,FRAS1,FRG1,FSCN1,FTSJ3,FUBP1,FUBP3,FXYD1,G0S2,G6PC,G6PD,GALM,GALNT2,GAMT,GAPVD1,GART,GATM,GBF1,GCDH,GCK,GCN1,GDA,GFM1,GJB2,GLDC,GLG1,GLMP,GLRX3,GLRX5,GLT1D1,GLTPD2,GLUL,GMPPB,GNA13,GNAI2,GNAQ,GNAS,GNE,GNS,GOLGA2,GOLGA5,GOLPH3L,GPAT3,GPHN,GPRIN3,GPT,GPX3,GRB7,GRHPR,GRIPAP1,GSPT1,GSR,GSTK1,GSTM1,GSTM2,GSTM4,GSTM5,GSTP1,GTF2I,GTPBP4,GUCY1B1,H6PD,HACL1,HAGH,HAO1,HBS1L,HCFC1,HDAC1,HDGFL2,HDGFL3,HDLBP,HEATR1,HECTD1,HELZ2,HGD,HINT3,HIP1,HK1,HLA-A,HLA-DQA1,HMGA1,HNF1A,HNF4A,HNRNPA2B1,HNRNPF,HNRNPK,HNRNPL,HNRNPLL,HNRNPM,HNRNPR,HNRNPU,HNRNPUL1,HP1BP3,HPD,HPN,HRAS,HS1BP3,HSD11B1,HSD17B4,HSD17B6,HSP90AA1,HSP90AB1,HSP90B1,HSPA12B,HSPA13,HSPA4L,HSPA5,HSPA8,HSPA9,HSPD1,HSPG2,HSPH1,HUWE1,HYKK,HYPK,IDH2,IDO2,IFI16,IFIT3,IFNAR2,IGF2R,IK,ILF3,ILKAP,IMMP2L,IMMT,INSR,INTS3,IPO5,IQGAP1,ITGA1,ITGA2B,ITGA5,ITGA9,ITGAV,ITGB3,ITGB6,ITIH2,ITIH4,ITPR2,ITSN1,IYD,KCTD12,KDSR,KHDRBS1,KHSRP,KIF21A,KPNA1,KPNA2,KRAS,KXD1,KYAT3,L2HGDH,LAP3,LARP1,LARP4,LARP7,LARS2,LASP1,LDAH,LDLR,LGALS1,LGALS3,LGMN,LIAS,LIFR,LIN7C,LIPE,LITAF,LMAN1,LMAN2,LMAN2L,LMNB2,LMO7,LRG1,LRP1,LRRFIP1,LSG1,LSM12,LSM14A,LSR,LUC7L2,LUC7L3,LUM,LYAR,LYPLA2,LYVE1,LYZ,M6PR,MACO1,MACROD1,MAN2B

	1,MANBA,MAP2K1,MAP2K3,MAP4,MASP2,MBNL1,MBOAT7,MCAM,MCCC1,MDH1,ME1,MEAF6,METAP2,METTL9,MFAP1,MFN2,MGLL,MGST1,MIA3,MKNK1,MME,MMUT,MOGS,MPC1,MPHOSPH10,MPP1,MPRIP,MPST,MRPL15,MRPL47,MRPL50,MRPL51,MRPS17,MRPS31,MRPS35,MSH2,MSN,MSR1,MSRB2,Mt1,Mt2,MTOR,MTREX,MTX2,MVK,MYH10,MYH11,MYH14,MYH9,MYL1,MYLK,MYO18A,MYO1C,NAA15,NAA25,NAALAD2,NACA,NAPRT,NASP,NAXD,NDST1,NDUFAF2,NDUFB7,NECAP1,NELFB,NFIA,NFXL1,NGEF,NID2,NMT2,NNMT,NOL6,NONO,NOP56,NPC1,NR3C1,NRAS,NSFL1C,NSUN2,NUCB1,NUDC,NUDT12,NUDT7,NUMA1,NUP153,NUP160,NUP205,NUP210,NUP214,NUP54,NUP93,NUP98,OAT,OGFOD3,OGT,OLA1,OPTN,OSBPL9,OXCT1,PABPC1,PABPC4,PAK2,PALD1,PALLD,PANK1,PAPSS1,PAPSS2,PARP1,PARP14,PARVA,PC,PCBP1,PCCB,PCDH1,PCDHB16,PCNP,PDAP1,PDCD11,PDCD4,PDE2A,PDHB,PDIA3,PDIA4,PDIA5,PDLIM7,PDXDC1,PDXK,PDZK1,PEX1,PEX11G,PEX3,PEX6,PFKFB3,PGK1,PGM1,PGM3,PGM5,PHF20L1,PHKA1,PHKA2,PHLDA1,PHLDB2,PHYHD1,PI4KA,PICALM,PIGR,PIGS,PIK3CB,PIP5K1C,PITHD1,PITRM1,PKLR,PKN1,PKP4,PLA2G12B,PLCB3,PLCH1,PLEKHA5,PLEKHA7,PLG,PLOD3,PLRG1,PLXNA4,PLXNB2,PM20D1,PML,PNLIP,PNN,POLDIP3,POLR2A,POLR2B,PON1,PON3,POR,PPFIA1,PPFIBP2,PPIF,PPIL4,PPIP5K2,PPP1R2,PPP2R5A,PPP4C,PPP4R2,PPP6R1,PPP6R3,PPWD1,PRDX5,PREP,PRKAB1,PROC,PROX1,PRPF31,PRPF6,PRPF8,PRRC2C,PRXL2A,PSIP1,PSMA1,PSMA3,PSMA7,PSMB6,PSMB9,PSMD3,PSMD4,PSMD7,PTK2,PTK2B,PTPMT1,PTPN1,PTPRF,PUM1,PURA,PXMP4,PYGB,PYGL,QSOX1,RAB1A,RABGAP1,RABGAP1L,RACK1,RAE1,RALY,RANBP10,RANBP3,RANGAP1,RAPGEF4,RBBP4,RBM10,RBM14,RBM15,RBM28,RBM39,RBM47,RBP1,RCC2,REEP5,RELA,RETREG2,RETSAT,RGPD4 (includes others),RHOA,RHOC,RIOX2,RIPK1,RMDN2,RNF17,RNF20,RNF213,RNF5,RNPEP,RPAP3,RPL11,RPL14,RPL22,RPL28,RPL31,RPL4,RPL5,RPS15,RPS24,RPS27A,RPS5,RPS7,RPTOR,RRAS,RSL1D1,RTN4,RTN4IP1,RUVBL1,SAA1,SAE1,SAFB,SARDH,SART1,SART3,SAT2,SBF1,SCAMP3,SCAMP4,SCARB2,SCD,SCFD1,SCRIB,SCYL2,SCYL3,SDC4,SDR42E1,SDS,SDSL,SEC23B,SEC23IP,SEC24A,SEC24D,SEC61A1,SELENBP1,SEPHS1,SERBP1,SERHL2,SERPINA6,SERPING1,SF3A3,SF3B1,SF3B2,SF3B6,SGTA,SH3GL1,SHPK,SHTN1,SIGLEC1,SLC12A9,SLC16A7,SLC17A3,SLC22A18,SLC25A12,SLC25A13,SLC25A21,SLC25A3,SLC25A5,SLC27A4,SLC2A2,SLC30A5,SLC38A10,SLC39A14,SLC39A4,SLC44A2,SLC4A4,SLC6A12,SLC6A13,SLC7A2,SLC9A3R1,SLCO1B3,SLK,SLMAP,SLTM,SMAP1,SMAP2,SMARCA2,SMARCA5,SMARCD2,SMC1A,SMC3,SMIM15,SNAP47,SND1,SNRNP200,SNRNP70,SNRPF,SNRPN,SNTB1,SNW1,SNX18,SON,SORBS1,SORBS2,SOS1,SPAG9,SPAST,SPTAN1,SPTBN2,SQOR,SRA1,SREK1,SRP19,SRPK2,SRSF4,SSR1,STAB1,STAB2,STAG2,STARD5,STAT2,STAT3,STEAP3,STEAP4,STOML2,STRN,STT3B,SUCLG2,SUGT1,SULT1C2,SULT1E1,SULT2A1,SUN2,SUPT16H,SVIL,SWAP70,SYMPK,SYNCRIP,SYNJ2BP,TADA3,TALDO1,TAMM41,TAOK3,TAP1,TAPBP,TARDBP,TBC1D24,TBC1D8B,TBCD,TCEA1,TCERG1,TCOF1,TFR2,TGFBRAP1,TGM1,THRAP3,TIGAR,TIMM22,TIMMDC1,TJP1,TJP2,TJP3,TKFC,TKT,TM9SF2,TMEM126B,TMEM176B,TMEM230,TMEM256,TMEM33,TMTC3,TMX3,TNKS1BP1,TNPO1,TNPO2,TNS2,TNS3,TOM1,TOP1,TOP2B,TOP3B,TOR1A,TPD52,TPI1,TPR,TRA2B,TRAP1,TRAPPC4,TRIM28,TRIP11,TRIR,TSC22D1,TSFM,TSPAN31,TTC1,TTC37,TTC38,TTC39C,TTN,TTPA,TUBA4A,TUBB,TUBB2A,TUBB4B,TUT7,TWF1,TXLNG,TXNDC5,TXNL1,TYMP,UBA1,UBA2,UBA7,UBAC1,UBAP2,UBQLN2,UBR2,UFL1,UGGT1,UGP2,UGT1A4,UGT1A6,UGT1A8 (includes others),UGT2B10,UGT2B28,UGT3A1,UPB1,UPF1,UPF2,UPP1,UQCC1,UQCRC2,UROC1,USP16,USP24,USP46,USP7,VAC14,VAMP2,VAMP8,VAV2,VCAM1,VIM,VKORC1L1,VMO1,VNN1,VPS13D,VPS26B,VPS26C,VPS33B,VPS51,VRK1,VTN,VWA8,WAPL,WASHC4,WASHC5,WBP2,WDR36,WFS1,XPO1,XPO5,XRN1,XRN2,YBX1,YBX3,YME1L1,YTHDF2,ZBTB20,ZC3H11A,ZC3H14,ZFR,ZMAT2,ZMIZ1
1. Protein Synthesis 2. Polymerization of protein 3. 0.0000000000232 4. Increased 5. 2.93 6. 96	AASS,ACACA,ACACB,ACOT13,ADSL,AGRN,AHNAK,ALDH5A1,ALDH9A1,AQP4,ATL3,B2M,BID,C9,CAT,CD47,CDA,Cdc42,CHMP2A,CHP1,CLDN3,CORO1A,CRP,CRYZ,CTH,CUTC,DCXR,DECR1,DNM1L,DPYS,EGF,EHD1,EHD3,ELAVL1,ENO1,FBP1,FGA,FGB,FGG,FIS1,FLOT1,Fus,GCH1,GNMT,GOLGA2,GOPC,GPX3,GPX4,GRHPR,H4C15,HACL1,HINT3,HLA-A,HMGCL,HMOX1,HSP90AA1,INSR,JCHAIN,KHDRBS1,MAT1A,MAT2A,ME1,MID1IP1,NAXE,NCK1,NUDT21,OTOL1,PCBD1,PDCD6IP,PEX14,PEX5,PTK2,PYCARD,RAC1,RHOA,RIPK1,RNF213,RPS19,SAMHD1,SHMT1,SNX2,SPAG9,SPAST,SRR,STOML2,TDO2,TMEM120A,TOR1A,TPPP,TRA2B,TRIM28,TYSND1,UPB1,USP16,VAV2,VTN

1. Cancer,Organismal Injury and Abnormalities 2. Breast or pancreatic cancer 3. 0.0000000000408 4. Increased 5. 2.388 6. 911	AAK1,ABAT,ABCB4,ABCB8,ABCB9,ABCC2,ABCC3,ABCD1,ABCD3,ABCF2,ACAA1,ACACB,ACAD10,ACAD11,ACAT2,ACIN1,ACLY,ACO1,ACOT1,ACOT11,ACOT8,ACP2,ACSF3,ACSS2,ACSS3,ACTG1,ACTN4,ACTR2,ACTR3,ACYP2,ADAM10,ADD2,ADIPOR2,ADK,ADSL,AGK,AGL,AGO1,AGO2,AGPAT2,AGPAT5,AGRN,AGXT2,AHNAK,AIF1,AK3,AKR1A1,AKT1,ALCAM,ALDH16A1,ALDH1A1,ALDH1B1,ALDH1L1,ALDH5A1,ALDH7A1,ALDOA,AMPD2,ANKHD1/ANKHD1-EIF4EBP3,ANO10,ANPEP,ANXA1,ANXA11,ANXA3,AOX1,AP3B1,API5,APOA1,APOB,APOC4,APOD,APOE,AQP1,AQP4,ARAF,ARF4,ARF6,ARHGAP31,ARHGAP45,ARHGDIA,ARHGDIB,ARHGEF12,ARHGEF7,ARMC10,ARPC5L,ARRB1,ARSB,ASGR1,ASPSCR1,ATAD2B,ATL3,ATP11C,ATP1A1,ATP2B1,ATP2B4,ATP5IF1,ATP6V0D1,ATRX,ATXN10,ATXN2,AUP1,B2M,B4GALNT1,BAG4,BAIAP2,BCAM,BCHE,BCLAF1,BGN,BIN1,BIN2,BLVRA,BMP2K,BNIP3,BRAF,BSG,BTAF1,C4A/C4B,C6,C8B,C8G,C9,CAD,CALU,CAND1,CAPZB,CASK,CASP3,CAT,CAVIN1,CBX3,CCDC134,CCDC47,CCDC9,CCT3,CD163,CD36,CD47,CD68,Cdc42,CDC5L,CDC73,CDK12,CDK5,CDK6,CDKN1B,CDKN2C,CDO1,CEP290,CEP89,CES1,CFB,CFH,CFI,CHD4,CKAP4,CKB,CKM,CLDN12,CLDN3,CLEC10A,CLEC3B,CLIC1,CLIC4,CLU,CMAS,CMPK2,CMTM4,CNDP2,CNOT1,CNOT2,CNOT3,COA7,COBLL1,COG5,COL18A1,COMT,COPA,COPB1,COQ4,COX5A,COX6B1,CP,CPB2,CPOX,CPQ,CRAT,CRKL,CRP,CRYM,CSNK1E,CSNK2A1,CSNK2B,CSRP2,CSTF2,CSTF3,CTBP1,CTBS,CTH,CTNNB1,CTNNBL1,CTNND1,CTR9,CTSB,CTSC,CTSD,CTSS,CTSV,CTSZ,CTTN,CUL2,CUTC,CXADR,CYP17A1,CYP2A6 (includes others),CYP2B6,CYP2U1,CYP3A5,CYP4B1,CYP4F3,DAAM1,DAPK1,DARS2,DCAF11,DCPS,DCTN4,DDHD2,DDI2,DDX17,DDX23,DDX27,DDX39B,DDX3X,DDX42,DDX49,DDX5,DEPTOR,DGLUCY,DHCR24,DHFR,DHTKD1,DHX16,DHX9,DMD,DMGDH,DNAJA1,DNAJB6,DNAJC13,DNAJC2,DNAJC7,DNM1L,DPP4,DPY19L1,DPYD,DSP,DYSF,EBPL,ECM1,EDC4,EEF1D,EFR3A,EFTUD2,EGF,EGFR,EHD1,EHHADH,EIF1AX,EIF2AK2,EIF2B1,EIF2S2,EIF3A,EIF3C,EIF3E,EIF3F,EIF3H,EIF3K,EIF4A1,EIF4A2,EIF4E,EIF4G1,EIF5,EIF5B,ELAC2,ELAVL1,ELOA,ELOC,ELOVL1,ELOVL6,ELP2,EMD,EMILIN1,EML4,ENO1,ENPEP,ENTPD5,EPHX1,EPHX2,EPPK1,EPS15L1,ERBIN,ERC1,ESYT2,ETFDH,Ewsr1,EXOC1,EXOSC9,EZR,F11,F13A1,FABP4,FABP5,FABP7,FADS6,FAF1,FAM126B,FAM98C,FARP1,FASN,FDX2,FERMT2,FGA,FIS1,FKBP3,FKBP4,FKBP5,FLII,FLNA,FLOT1,FMO4,FMR1,FN1,FNDC3A,FRAS1,FSCN1,FTO,FTSJ3,FUBP1,FUBP3,G0S2,GALNT2,GAMT,GANAB,GAPDH,GART,GATAD2A,GBA,GBE1,GBF1,GCDH,GCK,GCN1,GGA1,GGCT,GJB2,GLDC,GLG1,GLO1,GLUD1,GLUL,GLYR1,GMPPB,GMPS,GNA13,GNAI3,GNAQ,GNAS,GNE,GNMT,GNPAT,GOLGA2,GOLGA5,GOSR1,GPAM,GPAT4,GPX3,GRB7,GRHPR,GSPT1,GSR,GSTM1,GSTM2,GSTM4,GSTM5,GSTP1,GTF2I,GTPBP4,GUCY1B1,H3-3A/H3-3B,HAGH,HAL,HCCS,HCFC1,HDAC1,HDGFL3,HEATR1,HECTD1,HELZ2,HIBADH,HK1,HLA-A,HLA-DQA1,HMGA1,HMGCS1,HMOX1,HNF1A,HNF4A,HNRNPA2B1,HNRNPAB,HNRNPH2,HNRNPL,HNRNPM,HNRNPU,HNRNPUL1,HP,HP1BP3,HPD,HPN,HPX,HRAS,Hrg,HS1BP3,HSD11B1,HSD17B6,HSP90AA1,HSP90AB1,HSP90B1,HSPA12B,HSPA5,HSPA9,HSPB1,HSPD1,HSPG2,HTATIP2,HUWE1,HYKK,HYOU1,IDH3B,IGF2R,ILF2,ILF3,ILKAP,INHBC,INSR,IPO5,IQGAP1,ITGA1,ITGA5,ITGA9,ITGAV,ITGB1,ITGB3,ITGB6,ITPR2,ITSN1,IYD,KCTD12,KDELR1,KHDRBS1,KHSRP,KIF13B,KLKB1,KPNA1,KPNA2,KRAS,LARP1,LARP4,LASP1,LDLR,LGALS1,LGALS3,LGALS3BP,LGALS8,LIFR,LIMS2,LIPE,LMAN1,LMAN2L,LMF1,LMNA,LMO7,LRP1,LRRFIP1,LSG1,LSM14B,LSR,LUC7L3,LYN,LYPLA1,LYVE1,MACROD1,MAN2B2,MAN2C1,MANBA,MANF,MAOB,MAP2K1,MAP2K3,MAP4,MAPRE1,MAPRE3,MBOAT7,MCAM,MCCC1,MCCC2,METAP2,METTL27,METTL9,MFN2,MGLL,MIA3,MIF,MIGA2,MIOS,MMUT,MOCS2,MOSPD2,MOV10,MPP6,MRC1,MROH1,MRPL15,MRPL24,MRPL50,MRRF,MSH2,MSR1,MTCH2,MTDH,MTOR,MTREX,MYBBP1A,MYH10,MYH11,MYH14,MYH9,MYL1,MYLK,MYO18A,MYO1B,NAA25,NAALAD2,NAMPT,NANS,NASP,NAT10,NAXD,NCL,NCOA5,NDUFAF3,NDUFB6,NECTIN2,NELFB,NFIA,NFXL1,NGEF,NID2,NLRX1,NMT2,NNMT,NOL6,NONO,NOP16,NOP56,NOP58,NOS3,NOSTRIN,NPC1,NPC2,NQO1,NQO2,NR3C1,NRAS,NUCB1,NUDT14,NUMA1,NUP153,NUP205,NUP214,NUP93,NUP98,OGFOD3,OLA1,OXCT1,PA2G4,PABPC1,PABPN1,PAFAH1B2,PAK2,PALD1,PALLD,PAPSS2,PARP1,PAWR,PC,PCDH1,PCDHB16,PCK1,PCNP,PDAP1,PDHA1,PDHB,PDIA3,PDIA4,PDLIM5,PECAM1,PEX1,PEX12,PEX14,PEX19,PFAS,PFKFB3,PGAM1,PGK1,PGM1,PGM5,PHF20L1,PHKA1,PHKA2,PHLDA1,PHLDB2,PHYHD1,PHYKPL,PIK3CB,PIN4,PIP5K1C,PITHD1,PLCH1,PLEKHA7,PLG,PLRG1,PLXNA4,PM20D1,PML,POLDIP3,POLR2A,PON3,POR,PPFIA1,PPFIBP2,PPIA,PPIP5K2,PPL,PPP2R1B,PPP2R5D,PPP4R2,PPP6R1,PPWD1,PQBP1,PRDX5,PREB,PRKAB1,PRKRA,PROC,PROX1,PRPF6,PRRC1,PSEN1,PSIP1,PSMA2,PSMA3,PSMA5,PSMA7,PSMB9,PSMD4,PSMD7,PSMF1,PTBP1,PTK2,PTPN1,PTPRF,PTTG1IP,PXN,PYGL,QSOX1,RABGAP1L,RAD50,RAE1,RANBP1,RANGAP1,RAP1A,RAP1B,RAPGEF4,RARRES2,RBM10,RBM14,RBM15,RBM17,RBM28,RBM39,RBM42,REEP5,RELA,REXO2,RGPD4 (includes others),RHOA,RHOC,RIPK1,RMDN2,RNF113A,RNF14,RNF17,RNF213,RNF5,RNPEP,RPL19,RPL22,RPL31,RPL4,RPL5,RPL6,RPLP0,RPS19,RPS20,RPS24,RPS29,RPS3,RRAS,Rrbp1,RSL1D1,RTN1,RTN4,RTN4IP1,S100A6,SAA1,SARDH,SART1,SAT2,SBF1,SCO1,SCRIB,SCYL3,SDS,SEC11A,SEC23B,SEC24A,SEC31A,SEC61A1,SEC61G,SEC63,SEPHS1,SERINC3,SERPINA1,SERPING1,SERPINH1,SF3B1,SF3B2,SF3B3,SF3B4,SFPQ,SH3GL1,SHPK,SIGLEC1,SIL1,SLC22A18,SLC22A25,SLC25A12,SLC25A13,SLC25A23,SLC25A5,SLC31A1,SLC39A4,SLC4A4,SLC9A3R1,SLMAP,SLTM,SMAP2,SMARCA2,SMC1A,SMC3,SNAP47,SND1,SNRNP200,SNTB1,SNX18,SNX6,SNX7,SON,SORBS1,SOS1,SPAG9,SPG7,SPTAN1,SPTBN2,SREK1,SRI,SRP19,SRP68,SRP9,SRPK2,SSBP1,SSRP1,STAB1,STAB2,STAG2,STAT2,STAT3,STAT6,STEAP3,STEAP4,STT3B,SUCLG2,SUGCT,SUN2,SUPT16H,SVIL,SWAP70,TAGLN,TAGLN2,TALDO1,TAP1,TARDBP,TAT,TBCD,TCERG1,TFR2,TGFBRAP1,TGM1,THRAP3,THRSP,TIMM44,TJP1,TJP2,TKFC,TLN1,TM9SF2,TMED3,TMEM126A,TMEM176B,TMEM256,TMEM43,TMPO,TMTC3,TMX1,TNKS1BP1,TNPO1,TNPO2,TNS3,TOP1,TOP2B,TOP3B,TOR1AIP1,TPD5

	2,TPD52L2,TPI1,TPM3,TPR,TRA2B,TRIP10,TSG101,TSPAN31,TTC1,TTC37,TTC38,TTC39A,TTN,TUBA1B,TUBA4A,TUBB,TUBB2A,TUBB4B,TXNDC5,TXNL1,TYMP,U2AF2,UBA1,UBA2,UBA7,UBE2G2,UBE2J1,UBE4B,UBQLN2,UBR2,UCHL5,UGDH,UGGT1,UGP2,UPF1,UPF2,UPP1,UQCC1,USO1,USP19,USP24,USP46,USP7,VAC14,VCAM1,VCL,VCPIP1,VDAC2,VDAC3,VIM,VNN1,VPS13D,VPS28,VPS51,VTN,WASF2,WASHC3,WASHC5,WBP2,WDR1,WFS1,XPO1,XPO5,YBX1,YME1L1,YWHAQ,YWHAZ,ZBTB20,ZC3H11A,ZHX2
1. Cell-To-Cell Signaling and Interaction,Inflammatory Response 2. Immune response of tumor cell lines 3. 0.000000000216 4. Increased 5. 3.075 6. 66	ACTR2,ACTR3,AHSA1,ANXA1,AQP4,ARAF,ARF6,ARPC2,ARPC3,BRAF,CALR,CD38,CD47,Cdc42,CKB,CLEC4G,CRP,CSK,CTNNB1,CTSB,CTSD,CYFIP1,DNM1L,ELOVL1,ERP44,FCGR2B,GAPDH,GNA13,GNAI2,GNE,GSTM4,HMOX1,HSP90B1,ICAM1,IGKC,LMAN2,LYN,Macf1,MBNL1,MSH2,MTA2,MTOR,NANS,NHLRC2,NR3C1,PALLD,PPP6R1,PRKRA,PSMD4,PTK2,RAC1,RELA,RHOA,RHOG,SF3A1,Sf3a2,SHOC2,SRSF6,STAB2,STAT3,STT3A,TLN1,TNPO1,TTPA,VIM,WASF2
1. Cellular Function and Maintenance 2. Internalization of cells 3. 0.000000000359 4. Increased 5. 4.559 6. 87	ACTR2,ACTR3,AHSA1,ANXA1,APCS,APOA1,APOA2,ARAF,ARF6,ARPC2,ARPC3,BIN1,BRAF,CALR,CD36,CD38,CD47,Cdc42,CFH,CKB,CLEC4G,CLIC4,CMAS,CORO1A,CRP,CSK,CTNNB1,CYFIP1,DDX3X,EGF,EGFR,ELOVL1,ERP44,EZR,FCGR2B,Gm21596/Hmgb1,GNAI2,GNE,GRN,GSTP1,HMOX1,ICAM1,ILK,ITGB1,ITSN1,KRAS,LGALS3,LMAN2,LUM,LYN,Mbl1,MBL2,MBNL1,MIF,MRC1,MSR1,MTA2,NANS,NCL,NHLRC2,PALLD,PFKFB3,PIK3CB,PLG,PPP6R1,PSEN1,PSMD4,PTK2,PXN,RAC1,RHOA,RHOG,RPTOR,SAA1,SCARB1,SHOC2,SIGLEC1,SMPD1,SNAP23,SNX5,SRSF6,STAB2,STT3A,TLN1,VIM,VTN,WASF2

1. Cellular Movement 2. Cell movement 3. 0.000000000398 4. Increased 5. 7.659 6. 528	Abcb1b,ABCB4,ACACA,ACO2,ACSL4,ACTB,ACTN1,ACTN4,ACTR2,ACTR3,ADAM10,ADD1,ADD2,ADI1,AFDN,AGK,AGO2,AHCY,AHNAK,AHSG,AIF1,AKT1,ALCAM,Aldh1a7,ALDOA,ANGPTL3,ANGPTL4,ANPEP,ANXA1,ANXA3,ANXA5,AP2M1,APCS,APOA1,APOB,APOE,AQP1,AQP4,AQP9,ARF4,ARF6,ARFGAP3,ARHGAP31,ARHGAP5,ARHGDIA,ARHGDIB,ARHGEF12,ARHGEF7,ARPC1B,ARPC2,ARPC3,ARRB1,ASPH,ATG3,ATP1B1,ATP1B3,ATP2A2,ATP2B4,ATP6V1C1,BAG3,BAG4,BAIAP2,BCAM,BGN,BID,BIN2,BRAF,BSG,Bst2,C4A/C4B,C6,CADM1,CALCRL,Cald1,CALR,CALU,CAMK1,CAP1,CAPNS1,CAT,CCAR1,CCDC134,CCDC40,CD1D,CD302,CD36,CD38,CD47,CD81,CD82,Cdc42,CDK5,CDK6,CDKN1B,CDKN2C,CES1,CFB,CFH,CHD4,CLDN3,CLEC10A,CLIC1,CLIC4,CLU,CNDP2,CNP,COL18A1,COMMD5,CORO1A,CORO1B,CORO1C,CPB2,CPNE3,CR1L,CREB1,CRK,CRKL,CRP,CSK,CSNK1E,CSNK2A1,CSNK2A2,CSNK2B,CTBP1,CTDSP1,CTNNA1,CTNNB1,CTNND1,CTSB,CTSC,CTSH,CTSS,CTSV,CTSZ,CTTN,CUL1,CXADR,CYGB,CYP1A2,CYP2C8,CYP7A1,DAAM1,DCTN2,DDRGK1,DDX3X,DDX58,DEK,DEPTOR,Diaph2,DMD,DNAJA1,DNAJB4,DNAJB6,DNM1L,DNM2,DPAGT1,DPP4,DPYSL2,DSP,Dst,DYSF,ECM1,EGF,EGFR,EHD1,EIF2AK2,EIF3A,EIF3E,EIF4A3,EIF4E,ELAVL1,ELMO1,EMD,ENO1,ENPP1,EPB41L5,EPHX2,EPPK1,ERC1,ESAM,EXOC5,EZR,F13A1,FAAH,FABP4,FABP5,FABP7,FAF1,FASN,FCGR2B,FERMT2,FGA,FGB,FHIT,FKBP4,FLNA,FLOT1,FN1,Fnbp1l,FSCN1,G6PC,G6PD,GALNT2,GAPDH,GBA,GBF1,GJB2,GLG1,GLUL,Gm21596/Hmgb1,GNA11,GNA13,GNAI2,GNAI3,GNAQ,GNAS,GNG12,GNPAT,GOLGA2,GOLPH3,GPLD1,GRB7,GRN,GTF2I,GTPBP4,GUCY1B1,HAO1,HDAC1,HDGF,HEBP1,HECTD1,HEXIM1,HLA-A,HMGA1,HMOX1,HNF1A,HNF4A,HNRNPA2B1,HNRNPAB,HNRNPK,HNRNPL,HP,HRAS,Hrg,HSP90AA1,HSP90AB1,HSP90B1,HSPA1A/HSPA1B,HSPA5,HSPA8,HSPB1,HSPD1,HSPG2,HTATIP2,HUWE1,HYOU1,ICAM1,IFI16,IGF2R,Ighg2b,IGKC,IL6ST,ILF3,ILK,INSR,IQGAP1,Irgm1,ITGA1,ITGA2B,ITGA5,ITGA9,ITGAV,ITGB1,ITGB3,ITGB6,ITSN1,JCHAIN,JUP,KHDRBS1,KLKB1,KPNA2,KRAS,LASP1,LCAT,LDLR,LGALS1,LGALS3,LGALS3BP,LGALS8,LGMN,LIFR,LIMS2,LIPE,LITAF,LMNA,LMNB1,LMNB2,LMO7,LRP1,LRPAP1,LUM,LYN,LYVE1,LYZ,Macf1,MAP2K1,MAP2K3,MAP4,MAPRE1,MAPRE3,MASP2,MAT1A,MBOAT7,MCAM,MECP2,MFN2,MGLL,MIA3,MIEN1,MIF,MME,MOSPD2,MPP1,MPRIP,MSN,MSR1,Mt2,MTAP,MTCH2,MTDH,MTOR,MTSS1,MYH10,MYH11,MYH14,MYH9,MYL12A,MYLK,MYO18A,MYO1B,MYO1C,NAA25,NACA,NAMPT,NARS1,NCK1,NCL,NDRG1,NDST1,NDUFAF3,NFIA,NFIC,NNMT,NOS3,NOSTRIN,NPC1,NQO1,NQO2,NR1H4,NR3C1,NRAS,NSF,NUCB2,PA2G4,PAFAH1B1,PAK2,PALLD,PARP1,PARP9,PARVA,PARVB,PDCD10,PDCD4,PDCD6IP,PDE2A,PDIA3,PDK1,PDK2,PDLIM1,PEBP1,PECAM1,PEX13,PEX5,PHACTR4,PHB2,PHLDA1,PIGR,PIK3CB,PIP5K1C,PLCB3,PLG,PLPP3,PLTP,PLXNB2,PML,Podxl,PON2,PPFIA1,PPIA,PPIB,PPIF,PPM1A,PPT2,PRCP,PRDX6,PRKAA2,PRKACA,PROC,PROX1,PRUNE1,PSEN1,PTBP1,PTK2,PTK2B,PTP4A2,PTPN1,PTPRF,PTPRK,PXN,PYCARD,RAC1,RACK1,RAP1A,RAP1B,RAPGEF4,RARRES2,RBP1,RCC2,RELA,RHOA,RHOC,RHOG,RIPK1,RNF20,RNF5,RNH1,ROCK2,RPL13A,RPS19,RPSA,RPTOR,RRAS,RTN4,RUFY3,RUVBL1,RUVBL2,S100A1,S100A6,SAA1,SARS1,SCARB1,SCPEP1,SCRIB,SDC4,SELENBP1,SELENOK,SERPINA1,SERPINA3,SERPINB1,SERPIND1,SERPING1,SERPINH1,SHOC2,SIGMAR1,SLC9A3R1,SLC9A3R2,SLK,SMPD1,SNAP23,SND1,SORBS1,SORD,SOS1,SPAG9,SRSF1,SSBP1,ST13,STAB1,STAB2,STAT2,STAT3,STAT6,SULT1E1,SUN2,SWAP70,SYNJ2BP,TAGLN2,TARDBP,TBC1D24,TCIRG1,TCOF1,TDO2,TJP1,TKT,TLN1,TMEM30A,TMOD3,TMPO,Tmsb4x (includes others),TNS2,TNS3,TOP2B,TPI1,Tpm1,TPM3,TPPP,TPR,TRIP10,TSPAN14,TUBB,TWF1,TYMP,U2AF2,UBE2I,UGDH,VAMP3,VAV2,VCAM1,VCL,VDAC3,VIM,VPS28,VTN,WASF2,WBP2,WDR26,YBX1,YWHAZ
1. Connective Tissue Disorders,Inflammatory Disease,Inflammatory Response,Organismal Injury and Abnormalities,Skeletal and Muscular Disorders 2. Inflammation of joint 3. 0.000000000421 4. Increased 5. 2.496 6. 242	ABCB10,ABCC2,ACLY,ACO1,ACTL6A,ADAM10,AHSG,AIF1,AK2,AKR1A1,AKR1D1,ALDOA,ANXA1,AP3B1,APOA1,APOE,APOM,AQP9,ARCN1,ARFGAP1,ARHGDIB,ARIH1,ARRB1,ATP1B1,ATP2B1,B2M,BGN,BHMT,BID,C1QA,C4A/C4B,C6,CALCRL,CALR,CAMK1,CASP3,CD163,CD1D,CD36,CD68,CD81,CDA,CDK6,CDK9,CFB,CHCHD2,CLU,COPB2,COX15,CR1L,CRP,CSK,CTNNB1,CTR9,CTSB,CTSC,CTSS,CYP1A2,CYP2B6,CYP4F3,DCUN1D1,DDX39B,DEK,DHFR,DHODH,DHX16,DNM1L,DPAGT1,DPP4,DPYS,DYNLL1,EEF1G,EEF2,EIF3E,ENO1,EPHX2,ERH,F13A1,FABP4,FAF1,FASN,FAU,FCGR2B,FCGRT,FGA,FGB,FGG,FKBP5,FN1,FUBP1,G0S2,GALNT2,GBP6,GLRX5,GLUL,Gm21596/Hmgb1,GNAI2,GOLPH3,GRN,GSR,H3-3A/H3-3B,HDAC1,HELZ2,HLA-A,HLA-DQA1,HMOX1,HNMT,HP,HSP90B1,HSPA1A/HSPA1B,HSPA5,HSPA8,HSPD1,HSPG2,ICAM1,IFNAR2,IGKC,IL6ST,ITGA5,ITGA9,KANK2,KHSRP,KRAS,LAP3,LDLR,LGALS1,LIPE,LRP1,LUM,LYN,LYZ,MAOA,MAPRE1,MASP2,MBL2,METTL9,MGLL,MIF,MIPEP,MME,MPC1,MRC1,MRPS15,MSR1,MTAP,MTOR,MYL12A,MYO1C,NAA16,NAA25,NAGLU,NAMPT,NMT2,NONO,NOS3,NQO1,NQO2,NR3C1,PARP1,PDIA3,PECAM1,PFAS,PGK1,PHB2,PLG,POLR2L,PON1,PPAT,PPFIA1,PPIA,PPP1R7,PPT2,PRDX5,PREP,PSIP1,PSMB9,PTK2B,PTPN1,PURA,PXN,PYCARD,RABGAP1,RARRES2,RELA,RMDN3,RNF14,RNF5,RPL11,RPL15,RPL18A,RPL19,RPL31,RPS13,RPS16,RPS24,RPS3,RPSA,RTF2,SAA1,SAFB,SDC4,SEC61A1,SEC62,SELENBP1,SERINC3,SF3B6,SIGMAR1,SIL1,SLC17A3,SLC22A1,SLC7A2,SND1,SNRNP200,STAT3,STAT6,STEAP4,TALDO1,TAP2,TAPBP,TBCD,TCIRG1,TJP1,TMEM135,TRIM28,TTC39C,TUBA4A,TUBB2A,TUBB4B,TUT7,UBAC1,UBE2G2,UBE2H,UFL1,UQCRC2,USP7,VCAM1,VIM,VPS52,VRK1,VSIG4,WDR46,ZNF326

1. Cell Morphology,Cellular Assembly and Organization,Cellular Function and Maintenance 2. Formation of lamellipodia 3. 0.000000000446 4. Increased 5. 3.512 6. 54	ACTN4,ACTR3,AQP1,ARF6,ARHGEF7,ARPC2,BAIAP2,BSG,CAP1,CAPZB,CD82,Cdc42,CDKN1B,CRK,CRKL,CYFIP1,DNM1L,DNM2,EGF,EGFR,EZR,FN1,FSCN1,GOLPH3,HRAS,Hrg,HSP90AA1,HSPB1,ITGB1,LASP1,MFN2,MPRIP,MTOR,NCK1,PARVA,PARVB,PHLDB2,PROC,PTK2,PXN,RAC1,RHOA,RHOG,SDC4,SLC9A3R1,SNX1,SNX2,STAT3,SWAP70,Tpm1,TRIP10,VAV2,VCL,WASF2
1. Cellular Function and Maintenance 2. Internalization by tumor cell lines 3. 0.000000000446 4. Increased 5. 3.705 6. 47	ANXA1,AP2M1,APOE,ARRB1,ASGR1,ATP6AP1,ATP6V0D1,ATP6V1A,ATP6V1E1,CD36,CD47,CD C5L,DNM2,EGF,EGFR,EPB41L2,FCGR2B,FCHO2,GPR182,HMOX1,HRAS,HSP90AA1,ILK,ITGB1,LGALS3,LRP1,LSR,MAPRE3,PALLD,PLG,PSMD4,PTRHD1,RACK1,RHOA,RHOG,RPS21,RUVBL2,SART1,SCARB1,SCARB2,SF3B3,SF3B4,SFPQ,SLC9A3R1,SRSF3,STAB2,VIM
1. Cellular Movement,Connective Tissue Development and Function 2. Migration of fibroblast cell lines 3. 0.00000000045 4. Increased 5. 3.058 6. 49	ACTR3,ADI1,ARHGEF12,ATG3,Cdc42,CDKN1B,CLIC4,CORO1B,CRKL,CSK,CTNNB1,DDX3X,EGF,EGFR,EHD1,FABP5,FN1,GNG12,GRB7,HRAS,IFI16,Ighg2b,ILK,INSR,ITGA5,ITGA9,ITGB1,LIMS2,LRPAP1,MAPRE1,MIEN1,MSR1,MYLK,NCK1,NDST1,PALLD,PLG,PPIF,PTK2,PXN,RAC1,RELA,RHOA,RHOC,RHOG,STAT3,TMEM30A,VCL,VTN
1. Cell-To-Cell Signaling and Interaction 2. Interaction of tumor cell lines 3. 0.000000000452 4. Increased 5. 4.961 6. 115	ACTN4,ADAM10,ADD1,ADD3,AFDN,AGO2,AKT1,ALCAM,ANGPTL4,ANXA1,ANXA5,APOE,ASGR2,BSG,CALCRL,CASP7,CD36,CD47,CD68,CD81,CD82,CFH,CLEC4G,CPB2,CRK,CSK,CTNNB1,CTSB,CTSZ,CTTN,CXADR,DPP4,DSP,DYSF,EGF,EGFR,EMILIN1,ERP29,EZR,FASN,FERMT2,FGA,FLNA,FN1,GNA13,GOLPH3,HLA-A,HRAS,HSP90B1,HSPA5,ICAM1,ILK,INSR,ITGA5,ITGA9,ITGAV,ITGB1,ITGB3,LASP1,LGALS3,LGALS3BP,LGALS8,LRP1,MAP2K1,MCAM,MTOR,MYH9,NCL,NECTIN2,NME3,NOS3,NOSTRIN,NR1H4,PAK2,PALLD,PARP1,PARVA,PARVB,PECAM1,PHLDA1,PIP5K1C,PROC,PSMD4,PTGES3,PTK2,PTK2B,PXN,RAB35,RAC1,RACK1,RAP1A,RBM17,RELA,RHOA,ROCK2,RPSA,RPTOR,RRAS,SAA1,SCARB1,SERPING1,SIGMAR1,SNX1,SPTAN1,STAT3,STAT6,STOML2,TAT,TJP1,TLN1,U2AF2,UBE2I,VCAM1,VCL,VTN
1. Cellular Assembly and Organization 2. Transport of vesicles 3. 0.000000000537 4. Increased 5. 2.208 6. 45	ACTB,ACTG1,ACTN4,AP2M1,APOA1,APOE,ARCN1,ARF6,BIN1,CANX,CDK5,CTNNB1,DNM1L,DNM2,DPYSL2,EPN1,EXOC5,FCHO2,Fnbp1l,GOLGA5,GRN,HSPA8,ILK,INSR,LIN7A,MAP2K1,MYO1C,OSBPL9,PAFAH1B1,PICALM,PIP5K1C,RAB1A,SCAMP1,SCAMP3,SCAMP5,SCARB1,SCFD1,SCRIB,SPAST,SPTBN2,STX7,TBC1D24,TMEM230,TOR1A,VAMP2
1. Cell Death and Survival 2. Cell death of fibroblast cell lines 3. 0.000000000566 4. Increased 5. 2.164 6. 116	ABCE1,ACTB,ADIPOR2,AKT1,ASAH1,ATG3,ATP6AP2,BID,BNIP3,CAPNS1,CASP3,CASP7,CDC73,CDK11A,CDK6,CDKN1B,CLIC4,CLU,COX5A,CRK,CTNNB1,CTSB,CTSD,CTSV,DAPK1,DDX3X,DIABLO,DNM1L,DPM3,EEF1A1,EGFR,EIF2A,EIF2AK2,EIF2B5,EIF2S1,EIF3C,EIF3H,EIF3I,EIF5B,ENO1,ENTPD5,EPHX1,FAF1,FKBP4,FN1,FNTA,GLO1,GNA13,GNAQ,GSTM5,GSTP1,HMOX1,HRAS,HSPA5,HSPD1,IFI16,IFNAR2,ILK,INSR,ITGB1,ITSN1,KRAS,MACO1,MAP2K1,MFN2,Mt1,MTCH2,MTOR,NLRX1,NR3C1,NRAS,NUDT13,PAK2,PARP1,PAWR,PDIA3,PIK3CB,PLEKHF1,PLG,PLRG1,PML,PPP2R1B,PRDX6,PRKAA2,PRKRA,PSEN1,PTK2,PTK2B,PTPN1,PURA,RAC1,RELA,RGPD4 (includes others),RHOA,RHOC,RHOG,RIPK1,RPL10,RPL37,RTN4,SDC4,SF3B6,SFT2D2,SLC9A3R2,SMPD1,SRSF2,STK38,SUN2,TGM1,TIAL1,UBA1,VIM,VPS28,WDR5,YME1L1,YWHAZ
1. Connective Tissue Disorders,Inflammatory Disease,Organismal Injury and Abnormalities,Skeletal and Muscular Disorders 2. Rheumatic Disease 3. 0.000000000598 4. Increased 5. 2.175 6. 299	ABCB10,ABCC2,ACAD10,ACADM,ACAT1,ACLY,ACO1,ACSL4,ACSL5,ACTL6A,ACTR3,ADAM10,ADHFE1,AGFG1,AHSG,AIF1,AK2,AKR1A1,AKR1D1,AKT1,ALDOA,ANXA1,AP3B1,APCS,APOA1,APOE,APOM,AQP9,ARCN1,ARFGAP1,ARHGDIB,ARIH1,ARPC5,ARRB1,ATP1B1,ATP2B1,ATRX,B2M,BGN,BHMT,BID,C1QA,C1QB,C4A/C4B,C6,CALCRL,CALR,CAMK1,CASP3,CD163,CD1D,CD36,CD68,CD81,CDA,CDK6,CDK9,CDKN1B,CFB,CFH,CHCHD2,CLU,COPB2,COX15,CR1L,CREB1,CRP,CSK,CTNNB1,CTR9,CTSB,CTSC,CTSS,CYP1A2,CYP2B6,CYP4F3,DAD1,DAPK1,DCUN1D1,DDX39B,DDX58,DEK,DGAT2,DHFR,DHODH,DHX16,DIABLO,DNM1L,DPAGT1,DPP4,DPYS,DTX3L,DYNLL1,ECHDC3,EEF1G,EEF2,EIF2AK2,EIF3E,ENO1,EPHX2,ERH,F13A1,FABP4,FABP5,FAF1,FASN,FAU,FCGR2B,FCGRT,FGA,FGB,FGG,FKBP5,FN1,FUBP1,G0S2,GALNT2,GBP6,GLRX5,GLUL,Gm21596/Hmgb1,GNAI2,GNAQ,GNAS,GOLPH3,GRN,GSR,GSTM1,GSTP1,H3-3A/H3-3B,HDAC1,HELZ2,HLA-A,HLA-DQA1,HMOX1,HNMT,HP,HSP90B1,HSPA1A/HSPA1B,HSPA5,HSPA8,HSPD1,HSPG2,ICAM1,IFI16,IFIT3,IFNAR2,IGKC,IL6ST,ITGA5,ITGA9,JUP,KANK2,KHSRP,KRAS,LAP3,LBR,LDLR,LGALS1,LIPE,LRP1,LUM,LYN,LYZ,MAOA,MAPRE1,MASP2,MBL2,MECP2,METTL9,MGLL,MIF,MIPEP,MME,MPC1,MRC1,MRPS15,MSR1,MTA2,MTAP,MTOR,MYH9,MYL12A,MYO1C,NAA16,NAA25,NAGLU,NAMPT,NMT2,NONO,NOS3,NQO1,NQO2,NR3C1,PARP1,PARP9,PDIA3,PDP2,PECAM1,PFAS,P

	GK1,PHB2,PLG,POLR2L,PON1,PPAT,PPFIA1,PPIA,PPP1R7,PPP1R8,PPT2,PRDX5,PREP,PRKRA,PROC,PSEN1,PSIP1,PSMB9,PSME3,PTK2B,PTPN1,PURA,PXN,PYCARD,RABGAP1,RABGAP1L,RAC1,RANBP1,RARRES2,RELA,RHOA,RMDN3,RNF14,RNF5,RPL11,RPL15,RPL18A,RPL19,RPL31,RPS13,RPS16,RPS24,RPS3,RPSA,RTF2,SAA1,SAFB,SAMHD1,SDC4,SEC61A1,SEC62,SELENBP1,SERINC3,SERPING1,SF3B6,SIGMAR1,SIL1,SLC17A3,SLC22A1,SLC7A2,SND1,SNRNP200,SRSF1,SRSF3,STAT3,STAT6,STEAP4,TALDO1,TAP1,TAP2,TAPBP,TBCD,TCIRG1,TJP1,TMEM135,TNPO3,TRIM28,TTC39C,TUBA4A,TUBB2A,TUBB4B,TUT7,TYMP,UBAC1,UBE2G2,UBE2H,UFL1,UQCRC2,USP7,VCAM1,VIM,VPS52,VRK1,VSIG4,VTN,WDR46,WFS1,XRCC6,ZNF326
1. Cellular Development,Cellular Growth and Proliferation,Nervous System Development and Function,Tissue Development 2. Growth of neurites 3. 0.000000000828 4. Increased 5. 4.781 6. 127	Acp5,ACTB,ADAM10,AKT1,Aldh1a7,Anp32a,APEX1,APOE,ARF6,ARHGAP17,ARHGAP5,ARHGEF7,B4GALNT1,BAIAP2,BASP1,BRAF,CAMK1,CAP1,CAPZB,CAT,CD47,Cdc42,CDK5,CLPTM1,CNPY2,CORO1B,COTL1,CREB1,CRK,CSNK1E,CSRP1,CYFIP1,DNM1L,DPYSL2,EEA1,EGF,EGFR,EIF2B2,EIF4G2,EIF5A,EPN1,EXOC5,EZR,FABP7,FECH,FKBP4,FKBP5,FN1,Gm21596/Hmgb1,GNAI2,GNAQ,GNAS,GPHN,GRN,HDGFL3,HRAS,HSPA8,IL6ST,ILK,IMPA1,INPP1,INPP5F,IQGAP1,ITGA1,ITGA9,ITGB1,ITGB3,KRAS,LGALS1,LIFR,LMNB1,MAOA,MAP2K1,MPRIP,MTOR,MYH10,MYH9,NCK1,NFIA,NGEF,NMNAT1,NUDT7,OGT,PAFAH1B1,PALLD,PARP1,PDIA3,PKP4,PLG,PLXNA4,PRKACA,PSAP,PSEN1,PTK2B,PTP4A2,PTPRF,PXN,RAB35,RAC1,RAP1B,RELA,RHOA,RHOG,ROCK2,RPL4,RPS14,RPS6,RTN1,RTN4,SERPINF2,SET,SLC25A5,SNX1,SNX3,SPAST,STAT3,STK38L,STRAP,STX7,TARDBP,TBC1D24,TOP1,UBE4B,VCAM1,VCL,VIM,YWHAZ
1. Cellular Function and Maintenance 2. Engulfment of blood cells 3. 0.000000000933 4. Increased 5. 3.098 6. 76	ACTR2,ACTR3,AHSA1,ANXA1,ANXA5,APCS,APOA1,APOA2,APOE,ARAF,ARPC2,ARPC3,ASGR1,BIN1,BRAF,CALR,CD36,CD38,CD47,Cdc42,CFH,CLEC4G,CLIC4,CORO1A,CRK,CRP,CTNND1,CYFIP1,ELMO1,ELOVL1,ERP44,FCGR2B,Gm21596/Hmgb1,GNAI2,GNE,GRN,GSTP1,HMOX1,HYOU1,ICAM1,LGALS3,LUM,LYN,M6PR,Mbl1,MBL2,MBNL1,MIF,MRC1,MSR1,MTA2,NANS,NHLRC2,PALLD,PFKFB3,PIK3CB,PPP6R1,PSEN1,PXN,RAC1,RHOA,RHOG,RPTOR,SAA1,SCARB1,SHOC2,SIGLEC1,SMPD1,SRA1,SRSF6,STAB2,STT3A,SWAP70,TLN1,VTN,WASF2
1. Cell Death and Survival 2. Cell viability of myeloma cell lines 3. 0.00000000143 4. Increased 5. 3.181 6. 37	AK3,AKT1,CAT,CD81,CD82,CDK11A,COPB2,CTNNB1,EIF3C,EIF4A1,EIF4A3,EIF4G1,HIP1,HK1,HSP90B1,IK,KRAS,NAMPT,NRAS,PARP14,PKN1,PRPF8,PSMA1,PSMA3,PSMA4,PSMA6,PSMC3,RPL27,RPL38,RPTOR,SF3A1,SLC25A23,SNRPA1,SNW1,STAT3,XPO1,ZBTB20
1. Cell-To-Cell Signaling and Interaction 2. Binding of tumor cell lines 3. 0.00000000178 4. Increased 5. 4.994 6. 110	ACTN4,ADAM10,ADD1,ADD3,AFDN,AGO2,AKT1,ALCAM,ANGPTL4,ANXA1,ANXA5,APOE,ASGR2,BSG,CALCRL,CASP7,CD36,CD47,CD68,CD81,CD82,CFH,CLEC4G,CPB2,CRK,CSK,CTNNB1,CTSB,CTSZ,CTTN,CXADR,DPP4,DSP,DYSF,EGF,EGFR,EMILIN1,ERP29,FERMT2,FGA,FLNA,FN1,GNA13,GOLPH3,HLA-A,HRAS,HSP90B1,HSPA5,ICAM1,ILK,INSR,ITGA5,ITGA9,ITGAV,ITGB1,ITGB3,LASP1,LGALS3,LGALS3BP,LGALS8,LRP1,MAP2K1,MCAM,MTOR,MYH9,NCL,NECTIN2,NME3,NOS3,NOSTRIN,NR1H4,PAK2,PALLD,PARP1,PARVA,PARVB,PECAM1,PHLDA1,PROC,PSMD4,PTGES3,PTK2,PTK2B,PXN,RAC1,RACK1,RAP1A,RBM17,RELA,RHOA,ROCK2,RPSA,RRAS,SAA1,SCARB1,SERPING1,SIGMAR1,SNX1,SPTAN1,STAT3,STAT6,STOML2,TAT,TJP1,TLN1,U2AF2,UBE2I,VCAM1,VCL,VTN
1. Cellular Assembly and Organization,Cellular Function and Maintenance 2. Organization of cytoskeleton 3. 0.00000000208 4. Increased 5. 6.492 6. 334	ABITRAM,ACACA,ACTB,ACTG1,ACTN1,ACTN4,ACTR2,ACTR3,ADAM10,ADD1,ADI1,AFDN,AGFG1,AGRN,AHNAK,Akap9,AKT1,ALDOA,ANGPTL4,ANPEP,ANXA1,APOE,AQP1,ARF6,ARHGAP17,ARHGAP5,ARHGDIA,ARHGEF7,ARPC1A,ARPC2,ARPC3,ARPC5,ARRB1,ARSB,ATP2B1,ATRX,ATXN10,ATXN2,BAG3,BAG4,BAIAP2,BASP1,BIN1,BMP2K,BRAF,BSG,Bst2,C1QA,CALR,CALU,CANX,CAP1,CAPNS1,CAPZB,CASP3,CD2AP,CD47,CD81,CD82,Cdc42,CDK5,CDK5RAP3,CDK9,CDKN1B,CEP290,CEP89,CFAP20,CGN,CHP1,CKAP4,CKB,CKM,CLDN3,CLU,CNP,COMT,COPB2,CORO1A,CORO1B,CORO1C,CREB1,CRIP1,CRK,CRKL,CSK,CSNK2A2,CSRP1,CTNNB1,CTNND1,CTSS,CTSV,CTTN,Cux1,CXADR,CYFIP1,DAAM1,DAPK1,DBNL,DCTN2,DCTN6,DDAH1,DES,Diaph2,DNAJB6,DNM1L,DNM2,DPYSL2,DRG1,DSP,Dst,DYNLL1,EEF1A1,EGF,EGFR,EHD1,EIF2B2,EIF4E,EIF4G2,ELMO1,EML4,EPB41,EPB41L2,EPB41L5,EPHX2,EPPK1,EPS8L2,ERBIN,EXOC5,EZR,F13A1,FARP1,FASN,FCGR2B,FHIT,FITM2,FKBP4,FLII,FLNA,FLOT1,FMR1,FN1,Fnbp1l,FSCN1,FTCD,FTO,FXN,GALK2,GALNS,GAPDH,GDA,GJB2,GNA13,GNAS,GOLGA2,GOLPH3,GPX4,GRN,GSTM1,HDGF,HDGFL3,HNF4A,HNRNPK,HRAS,Hrg,HSP90AA1,HSP90AB1,HSPB1,ICAM1,ILK,INSR,IQGAP1,ITGA1,ITGAV,ITGB1,ITGB3,ITSN1,JUP,KIF13B,KIF21A,KPNA1,KRAS,LARP4,LASP1,LDLR,LIFR,LMNB1,LRP1,LRPAP1,LYN,LYPLA1,Macf1,MAOA,MAP2K1,MAP4,MAPRE1,MAPRE3,MECP2,MFN2,MGLL,MID1IP1,MIEN1,MOB2,MPP1,MPRIP,MSN,MTOR,MTSS1,MYH10,MYH9,MYLK,MYO1B,NCK1,NDRG1,NECTIN2,NFIA,NFIB,NNMT,NPC1,NQO1,NUDCD3,NUMA1,NUP160,OGT,OPTN,PAFAH1B1,PAK2,PALLD,PARP1,PARVA,PARVB,PDIA3,PDLIM7,PEX14,PFDN2,PHACTR4,PHLDB2,PICALM,PIP5K1C,PKP4,PLG,PLS3,PLXNA4,PLXNB2,Podxl,PON1,PQBP1,PRKAA2,PRKACA,PRKCSH,PROC,PRPF40A,PRUNE1,PSEN1,PTK2,PTK2B,PTPN1,PTPRF,PTPRK,PXN,RAB35,RAB3IP,RAB8A,RAC1,RAE1,RAN,RANBP1,RANBP10,RAP1A,RAP1B,RAPGEF4,RBBP4,RHOA,RHOC,RHO

	G,RNF5,ROCK2,RPL4,RPS14,RPS3,RPS6,RPTOR,RTN4,RUFY3,S100A1,SDC4,SHTN1,SLC9A3R1,SLC9A3R2,SLK,SMARCA5,SMARCE1,SMPD1,SNX1,SNX2,SON,SORBS1,SORBS2,SPAST,SPTAN1,SPTBN2,SSRP1,STAT3,STIP1,STK38L,STRN,SUN2,SWAP70,TBC1D24,TBCD,TLN1,TMOD3,Tmsb4x (includes others),TOP2B,TOR1A,Tpm1,TPM3,TPPP,TRAPPC4,TRIP10,TUBA4A,TUBB,UBE2I,UBE4B,UBQLN2,VAV2,VCL,VIM,VTN,WASF2,WDR1,WDR36,WDR5,XPO1,YBX1
1. Organismal Development 2. Size of body 3. 0.00000000211 4. Increased 5. 6.39 6. 203	ACACB,ACOT13,ACOX1,ACTG1,ADD1,AGPAT2,AHNAK,AKT1,ALDH5A1,ANGPTL3,ANGPTL4,Anp32b,APOB,APOE,AQP1,ARAF,ARHGAP5,ARRB1,ARSB,ASPA,ATP2A2,ATXN2,BCLAF1,BGN,BLMH,BSG,CANX,CASP3,CD36,CD81,CDK6,CDKN1B,CDKN2C,CDO1,Celf1,CEP290,CIDEB,CISD2,CKB,CKM,CLIC4,CNOT3,CNPY2,COQ9,CPB2,CREB1,CRKL,CSNK2A1,CTBP1,CTSD,DBNL,DGAT2,DIABLO,DKC1,DNAJA1,DNAJC3,DPP4,EGF,EGFR,EHD1,EHD3,EIF3M,ENTPD5,ESAM,FABP4,FABP5,FCGR2B,FGL1,FKBP4,FMO5,FTO,Fus,FXN,G0S2,G6PD,GAMT,GATM,GCK,GLG1,GNA11,GNAI2,GNAQ,GNAS,GNPAT,GOLGA2,GPAM,GPAT4,GRN,GSTZ1,GUCY1B1,H6PD,HMOX1,HNF1A,Hnrnpa1,HNRNPD,HSD11B1,HSD17B2,HSD17B4,HSPG2,IGF2R,IGFALS,IL6ST,ILF3,INSR,IP6K1,ITPR2,ITSN1,KHDRBS1,LASP1,LGMN,LIN7C,LMNA,LMO7,LUM,M6PR,MACROH2A2,MAN2B1,MBNL1,MBOAT7,MECP2,MGAT2,MMUT,Mocs1,MSRA,MSRB1,MTA2,Mug1/Mug2,MYH10,MYH11,MYLPF,NDRG1,NFIA,NFIC,NLRX1,NOS3,NPC2,NQO1,NR1H4,PAIP2,PANK1,PARP1,PCK1,PDCD6IP,PEX13,PEX5,PICALM,PLG,PLVAP,POLR2A,PPIB,PRKAB1,PRKACA,PRKRA,PSAP,PSEN1,PTGES3,Ptma (includes others),PTPN1,PUM1,RAD23B,RANBP1,RDH16,RELA,RGN,RIPK1,RNF2,RNF213,Rpl29 (includes others),SAFB,SCARB2,SCYL3,SGTA,SH3GL1,SLC25A13,SLC25A25,SLC27A4,SLC2A2,SLC30A5,SLC35D1,SLC39A14,SLC44A2,SLC4A4,SMPD1,SNRPN,SNX1,SNX2,SPG7,SPR,STAT3,STAT6,SUMO2,SUN2,SURF1,TCIRG1,TGM1,TKT,TOP2B,TSTA3,UBE2J1,UBL4A,VAMP2,XRCC6,ZBTB20
1. Organismal Development 2. Growth of organism 3. 0.00000000286 4. Increased 5. 2.491 6. 202	Abcb1b,ACACA,ACOX1,ACSL5,ADD1,AFDN,AGO1,AGO2,AIF1,AKT1,APOA1,APOE,AQP1,AQP9,ARCN1,ARHGAP5,ATOX1,ATRX,ATXN2,BCS1L,BHMT,BRAF,CBR1,CD36,CD81,CDK11A,CDK6,CDKN1B,CDKN2C,CLIC4,CLU,CNOT2,COL18A1,COQ3,CPB2,CREB1,CSNK2B,CTNNA1,CTNNB1,CTR9,CTSB,CTSD,CUL1,Cux1,DDX3X,DHX15,DNAJB9,DNAJC3,DNM1L,EGF,EGFR,EHHADH,EIF2AK2,EIF3E,EIF4A1,ELAVL1,ELOA,EPN1,F11,FEN1,FLII,FMR1,FN1,FXN,G6PC,G6PD,GALNS,GATAD2A,GNA13,GNAS,GOLGA2,GRN,H3-3A/H3-3B,HDAC1,HIP1,HLA-A,HMOX1,HNF1A,HRAS,Hrg,HSD17B2,HSD17B4,HSP90AA1,HSP90AB1,HSP90B1,HSPA5,HSPG2,HUWE1,IFNAR2,IGF2R,IGFALS,Igha,IL6ST,ILK,INSR,ITGA1,ITGB1,ITPR2,KRAS,LAMTOR1,LGALS1,LIAS,LMNA,LMNB1,LMNB2,LYN,LYZ,Macf1,MAOA,MAP2K1,MAP2K3,MAPRE1,METAP2,MFN2,MID1IP1,MPI,MTOR,NASP,NCL,NELFB,NFIC,NOS3,NR3C1,NRAS,OLA1,PAFAH1B1,PAPSS2,PARP1,PCK1,PCYT1A,PHF20L1,PLG,PLS3,PLXNB2,PNKP,POLR2H,POLR2L,PRKACA,PROC,PRPF19,PSEN1,PSMC3,PSME3,PTP4A2,PTPMT1,PTS,PUM1,PURA,RAC1,RACK1,RAD23B,RAD50,RAN,RANBP1,RARRES2,RGPD4 (includes others),RHOG,RNF2,Rpl29 (includes others),RPS4Y1,RRAS,SAFB,SCARB2,SDHD,SELENOP,SERPIND1,SLC25A25,SLC25A5,SLC30A5,SLC31A1,SLC39A4,SMARCA5,SMPD1,SNX1,SNX2,SOS1,SPTBN2,SRRT,STAT3,SUMO2,TAP1,TARDBP,TCIRG1,TCOF1,TDO2,TIAL1,TKT,TLN1,TMED2,TNS2,TOP2B,TSG101,TTPA,UBE2I,UBR2,UBTF,USP7,VCL,VPS28,WASF2,ZBTB20,ZC3HAV1
1. Molecular Transport,Protein Trafficking 2. Import of protein 3. 0.00000000352 4. Increased 5. 2.509 6. 39	AKT1,BAG3,DDX5,DNAJA1,FLNA,GCKR,HSP90AA1,HSP90AB1,HSPA8,IPO5,JUP,KPNA2,LMNA,NUP155,NUP214,NUP54,NUP98,NUTF2,PEX1,PEX14,PEX16,PEX26,PEX6,PHB2,PML,PSEN1,PTTG1IP,RAN,RANGAP1,RBM22,STAT3,TARDBP,TNPO1,TNPO2,TNPO3,TOMM40,TPR,TRIM28,XPO1
1. Cellular Assembly and Organization,Cellular Function and Maintenance 2. Formation of vesicles 3. 0.00000000498 4. Increased 5. 2.156 6. 49	ANXA5,ARF6,ARFGAP1,ARHGEF7,ATG3,ATG4B,BAG3,BIN1,BNIP3,CASP3,CHMP2A,CTNNB1,DNM2,EGF,EIF2A,FLNA,GNAS,HDAC1,HGS,HIP1,HRAS,IQGAP1,Irgm1,LITAF,MTOR,MYH10,MYH14,MYH9,NDRG1,NOS3,NSF,PALLD,PDCD6IP,PICALM,PIP5K1C,PRKACA,RAC1,RHOA,ROCK2,SNAP23,SNF8,SNX3,STK38,TIAL1,TMED10,TSG101,VPS25,VPS28,WASF2

1. Cellular Function and Maintenance 2. Internalization of tumor cell lines 3. 0.00000000871 4. Increased 5. 2.797 6. 49	ACTR2,ACTR3,AHSA1,ANXA1,ARAF,ARF6,ARPC2,ARPC3,BRAF,CALR,CD47,Cdc42,CKB,CLEC4G,CSK,CTNNB1,CYFIP1,ELOVL1,ERP44,EZR,FCGR2B,GNAI2,GNE,HMOX1,ICAM1,KRAS,LMAN2,LYN,MBNL1,MTA2,NANS,NCL,NHLRC2,PALLD,PLG,PPP6R1,PSMD4,PTK2,RAC1,RHOA,RHOG,SHOC2,SMPD1,SRSF6,STAB2,STT3A,TLN1,VIM,WASF2
1. Cellular Development,Cellular Growth and Proliferation,Nervous System Development and Function,Tissue Development 2. Proliferation of neuronal cells 3. 0.00000000901 4. Increased 5. 4.597 6. 141	Acp5,ACTB,ADAM10,AGRN,AKT1,Aldh1a7,Anp32a,APEX1,APOE,ARF6,ARHGAP17,ARHGAP5,ARHGEF7,B2M,B4GALNT1,BAIAP2,BASP1,BRAF,CAMK1,CAP1,CAPZB,CAT,CD47,Cdc42,CDK5,CLPTM1,CLU,CNP,CNPY2,CORO1B,COTL1,CREB1,CRK,CSNK1E,CSRP1,CTNNA1,CTNNB1,CYFIP1,DNM1L,DPYSL2,EEA1,EGF,EGFR,EIF2B2,EIF4G2,EIF5A,EPN1,EXOC5,EZR,FABP7,FECH,FKBP4,FKBP5,FN1,FTO,Gm21596/Hmgb1,GNAI2,GNAQ,GNAS,GPHN,GRN,HDGFL3,HRAS,HSPA8,IL6ST,ILK,IMPA1,INPP1,INPP5F,IQGAP1,ITGA1,ITGA9,ITGB1,ITGB3,KRAS,LGALS1,LIFR,LMNB1,MANF,MAOA,MAP2K1,MPRIP,MTOR,MYH10,MYH9,NCK1,NFIA,NGEF,NMNAT1,NUDT7,OGT,PAFAH1B1,PALLD,PARP1,PDIA3,PKP4,PLG,PLXNA4,PLXNB2,PRKACA,PSAP,PSEN1,PTK2B,Ptma (includes others),PTP4A2,PTPRF,PURA,PXN,RAB35,RAC1,RAP1B,RELA,RHOA,RHOG,ROCK2,RPL4,RPS14,RPS6,RTN1,RTN4,SERPINF2,SET,SLC25A5,SNX1,SNX3,SPAST,STAT3,STK38L,STRAP,STX7,TARDBP,TBC1D24,TCOF1,TOP1,UBE2V2,UBE4B,VCAM1,VCL,VIM,VTN,YWHAZ
1. DNA Replication, Recombination, and Repair,Nucleic Acid Metabolism,Small Molecule Biochemistry 2. Hydrolysis of nucleotide 3. 0.0000000112 4. Increased 5. 3.559 6. 39	ABCD1,ABCD3,APOA1,ARFGAP1,ARHGAP5,ATP1A1,ATP5IF1,CALR,CD38,CKM,DNM1L,EIF5,GNA11,GNAI2,GNAI3,GNAQ,GNAS,HSPA5,HSPD1,Iigp1,IPO5,MYO18A,NUDT9,PDE2A,PLG,PRKAA2,PTK2B,RAB4A,RAC1,RAN,RANBP1,RANGAP1,RHOA,RUVBL1,RUVBL2,SMARCA5,SNRNP200,UBA1,XPO1
1. Cellular Assembly and Organization,Cellular Function and Maintenance 2. Microtubule dynamics 3. 0.0000000116 4. Increased 5. 6.624 6. 287	ABITRAM,ACACA,ACTB,ACTG1,ACTN4,ACTR2,ACTR3,ADAM10,ADI1,AFDN,AGRN,AHNAK,Akap9,AKT1,ANGPTL4,ANPEP,APOE,AQP1,ARF6,ARHGAP5,ARHGDIA,ARHGEF7,ARPC2,ARPC3,ARRB1,ARSB,ATP2B1,ATRX,ATXN10,ATXN2,BAG4,BAIAP2,BASP1,BMP2K,BRAF,BSG,C1QA,CALU,CANX,CAP1,CAPNS1,CAPZB,CASP3,CD2AP,CD47,CD81,CD82,Cdc42,CDK5,CDK5RAP3,CDK9,CDKN1B,CEP290,CEP89,CFAP20,CGN,CHP1,CKAP4,CKB,CKM,CLU,CNP,COMT,COPB2,CORO1A,CREB1,CRIP1,CRK,CRKL,CSNK2A2,CSRP1,CTNNB1,CTNND1,CTSS,CTSV,CTTN,Cux1,CYFIP1,DAAM1,DAPK1,DBNL,DDAH1,Diaph2,DNM1L,DNM2,DPYSL2,DRG1,DSP,Dst,DYNLL1,EEF1A1,EGF,EGFR,EHD1,EIF2B2,EIF4E,EIF4G2,ELMO1,EML4,EPB41,EPHX2,EPS8L2,ERBIN,EXOC5,EZR,F13A1,FARP1,FASN,FCGR2B,FHIT,FKBP4,FLNA,FLOT1,FMR1,FN1,Fnbp1l,FSCN1,FTO,FXN,GALK2,GALNS,GAPDH,GDA,GJB2,GNA13,GNAS,GOLGA2,GOLPH3,GPX4,GRN,GSTM1,HDGF,HDGFL3,HNF4A,HNRNPK,HRAS,Hrg,HSP90AA1,HSP90AB1,HSPB1,ICAM1,ILK,INSR,IQGAP1,ITGA1,ITGB1,ITGB3,ITSN1,KIF13B,KIF21A,KPNA1,KRAS,LASP1,LDLR,LIFR,LMNB1,LRP1,LRPAP1,LYN,LYPLA1,Macf1,MAOA,MAP2K1,MAP4,MAPRE1,MAPRE3,MECP2,MFN2,MGLL,MID1IP1,MIEN1,MPP1,MPRIP,MSN,MTOR,MTSS1,MYH10,MYH9,MYLK,NCK1,NDRG1,NFIA,NFIB,NNMT,NPC1,NQO1,NUDCD3,NUMA1,NUP160,OGT,OPTN,PAFAH1B1,PAK2,PALLD,PARP1,PARVA,PARVB,PDIA3,PEX14,PHLDB2,PICALM,PIP5K1C,PKP4,PLG,PLXNA4,PLXNB2,Podxl,PON1,PQBP1,PRKAA2,PRKACA,PRKCSH,PROC,PRUNE1,PSEN1,PTK2,PTK2B,PTPRF,PTPRK,PXN,RAB35,RAB3IP,RAB8A,RAC1,RAN,RANBP1,RANBP10,RAP1A,RAP1B,RAPGEF4,RBBP4,RHOA,RHOC,RHOG,ROCK2,RPL4,RPS14,RPS3,RPS6,RPTOR,RTN4,RUFY3,S100A1,SDC4,SHTN1,SLC9A3R1,SLC9A3R2,SLK,SMARCA5,SMARCE1,SMPD1,SNX1,SNX2,SON,SORBS2,SPAST,SPTBN2,SSRP1,STAT3,STIP1,STK38L,STRN,SWAP70,TBC1D24,TBCD,TLN1,TOP2B,TOR1A,Tpm1,TPM3,TPPP,TRAPPC4,TRIP10,TUBA4A,TUBB,UBE2I,UBE4B,UBQLN2,VAV2,VCL,VIM,VTN,WASF2,WDR36,WDR5,XPO1,YBX1
1. Cellular Function and Maintenance 2. Clathrin mediated endocytosis 3. 0.0000000127 4. Increased 5. 3.074 6. 28	AP2A1,Ap2b1,AP2M1,ASGR1,ATP6AP1,ATP6V0D1,ATP6V1E1,CANX,CDC5L,DNM2,EPB41L2,EPN1,FCHO2,Fnbp1l,GPR182,INPP5F,PICALM,PIP5K1C,PTRHD1,RAC1,RPS21,RUVBL2,SART1,SF3B3,SF3B4,SFPQ,SIGLEC1,SRSF3
1. Cancer,Organismal Injury and Abnormalities,Respiratory Disease 2. Advanced lung cancer 3. 0.0000000139 4. Increased 5. 2.054 6. 73	AKT1,ANGPTL4,ANPEP,ANXA1,APOA1,ARAF,ARF6,B2M,BRAF,CALU,CDK6,CDKN1B,CLDN3,CLU,CTNND1,CTSB,CTSZ,DHFR,EEF1A1,EGFR,EIF4A1,EIF4E,FGG,FN1,GART,GSTP1,HRAS,HSP90AA1,HSP90AB1,HSP90B1,HSPA1A/HSPA1B,INSR,ITGA9,ITGB1,ITGB3,KRAS,LGALS1,LYN,MAP2K1,MAP4,MKNK1,MTOR,MYL12A,NID2,NR3C1,PARP1,PDK1,PDLIM1,PIK3CB,PLG,PML,POR,PPIA,PTK2,PTK2B,RELA,RHOA,RHOC,RPL27,RPL7,RPS11,RPS27A,RPS6,SCRIB,SEC61G,SND1,SSBP1,STAT3,TOP1,TOP2B,TUBA4A,TUBB2A,TUBB4B

1. Cell-To-Cell Signaling and Interaction,Cellular Assembly and Organization 2. Cell-cell contact 3. 0.0000000151 4. Increased 5. 2.87 6. 162	ACTN1,ACTN4,ACTR3,ADAM10,ADD2,AFDN,AGO2,AGRN,AKT1,ALCAM,ANXA1,ANXA5,APOE,AQP4,ARF6,ARHGEF7,B2M,BCAM,CADM1,CALR,CAPZB,CASP3,CD2AP,CD36,CD47,CD81,Cdc42,CDK5,CLDN3,CLU,CORO1A,CREB1,CRKL,CSK,CSNK2A1,CSNK2B,CSRP2,CTNNA1,CTNNB1,CTNND1,CTSB,CTSV,CTTN,CXADR,DBNL,DEPTOR,DES,DHTKD1,DMD,DNM1L,DNM2,DPAGT1,DSP,DYSF,EGF,EGFR,EPB41L5,ERBIN,ERP29,ESAM,EZR,FARP1,FASN,FLOT1,FMR1,FN1,FNDC3A,FNTA,FSCN1,GABPA,GJB2,GNA13,GNPAT,GOLPH3,GPHN,GRN,GTPBP4,HDAC1,HNF4A,HRAS,HSPG2,ICAM1,IFI16,IQGAP1,ITGA5,ITGB1,ITGB3,JUP,LDLR,LGALS1,LGALS3,LGALS8,LGMN,LIMS2,LRPAP1,MAP2K1,MBNL1,MCAM,MECP2,MSN,MTOR,MYH9,MYLK,NECTIN2,NFIA,NR1H4,NR3C1,OGT,PCDHB16,PDCD10,PDLIM5,PECAM1,PIP5K1C,PKP4,PLPP3,PNN,Podxl,PRKAA2,PRKACA,PROC,PSEN1,PTK2,PTK2B,PTPRF,PURA,RAB35,RAC1,RACK1,RAP1A,RER1,RHOA,ROCK2,RPSA,RPTOR,RTN4,SCRIB,SH3GL1,SIGLEC1,SNTA1,SORBS2,SPTAN1,SPTBN2,STAB1,STAT6,STIP1,SUN2,TAP1,TJP1,TJP2,TJP3,TLN1,TOR1A,UBE2V2,USP19,VAMP2,VCAM1,VCL,VIM,VNN1,VPS35,WBP2,YWHAZ
1. Cell Death and Survival 2. Apoptosis of fibroblast cell lines 3. 0.0000000157 4. Increased 5. 2.034 6. 88	ABCE1,AKT1,ASAH1,ATG3,ATP6AP2,BID,BNIP3,CAPNS1,CASP3,CDC73,CDK11A,CDKN1B,CLIC4,COX5A,CRK,CTNNB1,DAPK1,DDX3X,DIABLO,DNM1L,DPM3,EEF1A1,EGFR,EIF2A,EIF2AK2,EIF2B5,EIF2S1,EIF3C,EIF3H,EIF3I,ENTPD5,EPHX1,FAF1,FN1,GNA13,GNAQ,HRAS,HSPA5,HSPD1,IFI16,IFNAR2,ILK,INSR,ITGB1,ITSN1,KRAS,MFN2,MTCH2,MTOR,NLRX1,NR3C1,NRAS,NUDT13,PARP1,PAWR,PDIA3,PIK3CB,PLEKHF1,PLG,PLRG1,PML,PPP2R1B,PRKAA2,PRKRA,PSEN1,PTK2,PTK2B,PTPN1,RAC1,RELA,RHOA,RHOC,RHOG,RIPK1,RPL10,RPL37,RTN4,SDC4,SF3B6,SFT2D2,SMPD1,SRSF2,STK38,SUN2,VIM,VPS28,WDR5,YME1L1
1. Cellular Movement 2. Invasion of cells 3. 0.0000000214 4. Increased 5. 6.84 6. 251	ACAT1,ACSL4,ACTN4,ADAM10,ADI1,AFDN,AGO2,AHCY,AHNAK,AHSG,AKT1,ALCAM,ANGPTL4,ANPEP,ANXA1,APEX1,ARF4,ARF6,ARHGDIA,ASGR1,ASPH,ATP6AP1,BRAF,BSG,CALR,CAP1,CAPNS1,CASP3,CAT,CD81,CD82,Cdc42,CDK5,CDK5RAP3,CDKN1B,CES1,CFH,CLDN3,CLU,CNDP2,COL18A1,COPB1,COPB2,CPB2,CRK,CRKL,CSK,CSNK2A1,CSNK2A2,CSNK2B,CTBP1,CTDSP1,CTNNB1,CTNND1,CTSB,CTSD,CTSH,CTSS,CTSV,CTSZ,CTTN,CYFIP1,DBNL,DDX58,DNAJB4,DNAJB6,DNM1L,DNM2,DPP4,DPYSL2,DSP,ECM1,EGF,EGFR,EIF2AK2,EIF3A,EIF3E,EIF4A1,EIF4E,ELMO1,ENTPD5,ERC1,EZR,FABP5,FAF1,FERMT2,FHIT,FLNA,FN1,FSCN1,GALNT2,Gm21596/Hmgb1,GNA13,GNAI2,GNAI3,GNAQ,GNAS,GOLPH3,GPR182,GRB7,GRN,HDAC1,HDGF,HDLBP,HEXIM1,HGS,HMGA1,HMOX1,HNF1A,HNRNPA2B1,HNRNPAB,HPN,HRAS,HSP90AA1,HSP90AB1,HSP90B1,HSPA1A/HSPA1B,HSPA5,HTATIP2,ILF3,ILK,INSIG2,IQGAP1,ITGA1,ITGA5,ITGAV,ITGB1,ITGB3,ITGB6,JUP,KRAS,LAMTOR1,LARP1,LASP1,LGALS1,LGALS3,LGMN,LMNA,LRP1,LRPAP1,LYN,LYPLA1,MAP2K1,MAP4,MAPRE3,MCAM,MFN2,MIEN1,MIF,MTDH,MTOR,MYH10,MYLK,NAA15,NAMPT,NDRG1,NDUFAF4,Ngp,NONO,NOS3,NOSTRIN,NQO1,NR1H4,NRAS,OGT,PA2G4,PAFAH1B1,PAK2,PALLD,PARVA,PARVB,PDCD4,PDK1,PDLIM1,PEBP1,PECAM1,PI4KA,PICALM,PIGR,PIK3CB,PLG,PLOD3,PML,PPIA,PPIF,PROX1,PTBP1,PTGES3,PTK2,PTK2B,PTP4A2,PTPN1,PTPRK,PTTG1IP,PXN,PYCARD,RAC1,RACK1,RAP1A,RELA,RGN,RHOA,RHOC,RHOG,RNH1,RPRD1B,RPS4Y1,RPSA,RPTOR,RUVBL1,S100A6,SAA1,SCRIB,SDC4,SEC24D,SERPINA1,SERPINF2,SIGMAR1,SLC17A3,SLC9A3R1,SMPD1,SNAP23,SOS1,SRA1,SSBP1,STAT3,STK38L,TAGLN,TAGLN2,TARDBP,TCIRG1,TDO2,TJP1,TMEM176B,TMPO,TRAP1,TRIP10,UFL1,UPF1,USO1,VAC14,VAV2,VCAM1,VCL,VIM,VTN,WASF2,WBP2,YBX1,YWHAQ,ZBTB20
1. Cellular Assembly and Organization,Cellular Function and Maintenance,Tissue Development 2. Formation of actin filaments 3. 0.0000000271 4. Increased 5. 2.468 6. 88	ABITRAM,ACTR2,ACTR3,ADD1,AIF1,AKT1,APOA1,ARF6,ARHGEF12,ARPC2,ARRB1,ATXN2,BAG4,BIN1,BRAF,Cald1,CD47,Cdc42,CDK6,CHCHD2,COL18A1,CORO1A,CREB1,CRK,CTNND1,CTTN,CUL3,DAAM1,Diaph2,EGF,EGFR,ESAM,Fhod1,FN1,GNA11,GNA13,GNAI2,GNAQ,GNG12,HRAS,ICAM1,ITGB1,KANK2,KRAS,LAMTOR1,LRP1,MAP2K1,MIF,MPRIP,MSRB1,MSRB2,MTOR,MTSS1,MYH11,MYLK,MYO1C,NCK1,PALLD,PDCD10,PDCD6IP,PECAM1,PHLDB2,PLCB3,PPFIA1,PTK2,PTK2B,PXN,PYCARD,RAC1,RBBP4,RHOA,RHOC,ROCK2,SDC4,SERPINF2,SORBS1,STAT3,Tmsb4x (includes others),TNS3,Tpm1,TPM3,TRIP10,TWF1,U2AF2,VAV2,VCAM1,VTN,WASF2
1. Cellular Development,Cellular Growth and Proliferation,Nervous System Development and Function,Tissue Development 2. Outgrowth of neurons 3. 0.0000000297 4. Increased 5. 4.805 6. 104	ADAM10,AKT1,Aldh1a7,Anp32a,APEX1,APOE,ARF6,ARHGAP17,ARHGAP5,ARHGEF7,BAIAP2,BASP1,CAMK1,CAT,CD47,Cdc42,CDK5,CLU,CNPY2,CORO1B,CREB1,CRK,CSNK1E,DNM1L,DPYSL2,EEA1,EGF,EGFR,EIF2B2,EIF4G2,EIF5A,EPN1,EXOC5,EZR,FECH,FKBP4,FKBP5,FN1,Gm21596/Hmgb1,GNAQ,GNAS,GPHN,GRN,HDGFL3,HRAS,IL6ST,ILK,IQGAP1,ITGA1,ITGA9,ITGB1,ITGB3,KRAS,LGALS1,LIFR,LMNB1,MAP2K1,MPRIP,MTOR,MYH10,MYH9,NCK1,NFIA,NGEF,OGT,PAFAH1B1,PALLD,PARP1,PDIA3,PKP4,PLG,PLXNA4,PRKACA,PSAP,PSEN1,PTK2B,PTPRF,PXN,RAB35,RAC1,RAP1B,RELA,RHOA,RHOG,ROCK2,RPL4,RPS14,RPS6,RTN4,SERPINF2,SET,SLC25A5,SNX1,SNX3,SPAST,STAT3,STK38L,TARDBP,TBC1D24,TOP1,UBE2V2,VCAM1,VIM,YWHAZ
1. Molecular Transport 2. Secretion of molecule 3. 0.0000000378 4. Increased 5. 2.458 6. 143	A1CF,ABAT,ABCB4,ABCC2,ABCC3,ABCG5,ACACA,ACACB,ACADL,ACAT2,ACLY,ACSL4,AGK,AGXT,AKT1,ANXA1,APOA1,APOA2,APOB,APOE,AQP1,ARF6,ARFGAP3,ARRB1,ARSB,ASAH1,ATXN2,BAG3,CADM1,CANX,CASK,CAVIN1,CD2AP,CD36,Cdc42,CES1,CES3,CFH,CIDEB,CP,CREB1,CTNNB1,CYP27A1,CYP7A1,DNAJC1,DNM1L,DPYSL2,DYSF,EGF,ERP29,EXOC1,EZR,FABP4,FCGR2B,FGA,FGB,FGG,FLOT2,FMO3,FMR1,FN1,GAPDH,GCK,GNA11,GNA13,GNAI3,GNAQ,GOLPH3,GOLPH3L,GPAM,GPLD1,GRN,GUCY1B1,HMGA1,HMOX1,HNF1A,HNRNPAB,HRAS,HSD11B1,HSD17B2,HSPA5,HSPA8,IL6ST,IQGAP1,KRAS,LDLR,LGALS1,LIN7A,LIN7C,LMF1,LPCAT3,LYN,M6PR,MAOB,MECP2,MGLL,MIF,MYO18A,MYO1C,NOS3,NPC2,NR1H4,NR3C1,NSF,NUCB2,OPTN,PAFAH1B1,PCTP,PCYT1A,PDIA4,PECAM1,PFKFB3,PLCB3,PLTP,PPFIA1,PPIA,PPT1,PTK2B,RA

	PGEF4,RARRES2,RBP1,RTN4,SAA1,SCAMP5,SCARB1,SCD,SEC23B,SEC24A,SLC4A4,SNAP23,STAT3,STAT6,STEAP3,SULT1E1,TPD52,TTN,TTPA,USP19,VAMP2,VAMP3,VAMP8,WFS1,YWHAZ
1. Cellular Development,Cellular Growth and Proliferation,Connective Tissue Development and Function 2. Proliferation of fibroblast cell lines 3. 0.0000000462 4. Increased 5. 3.574 6. 110	ACAT1,AKT1,ALDOA,Anp32a,APEX1,ARHGEF12,ARRB1,ASPSCR1,ATG3,Brd4,CAT,CD81,CDC73,CDK6,CDKN1B,CREB1,CRK,CSNK2A1,CSNK2B,CSTF2,CTNNB1,CTSD,CUL1,CYGB,DCUN1D1,DDX3X,DHX9,DPY30,EEF1D,EGF,EGFR,EIF2AK2,EIF3C,EIF3E,EIF3H,EIF3I,EIF4E,FN1,G6PD,GADD45GIP1,GNAI2,GRB7,GRN,GTPBP4,HDGF,HMGA1,HMOX1,HRAS,HSPA1A/HSPA1B,IFI16,INSR,ITGB1,ITSN1,KHDRBS1,KRAS,LMNA,LMNB1,MAP2K3,MFN2,MIF,MTDH,MTOR,NOP58,NR3C1,NRAS,OLA1,PAK2,PARP1,PFKFB3,PIK3CB,PIP5K1C,PML,PPIF,PPIL1,PRPF19,PRUNE1,PSEN1,PSMA4,PTK2,PTK2B,RAC1,RACK1,RAN,RELA,RGL3,RHOA,RIPK1,RPS6,RPTOR,S100A6,SAMHD1,SBF1,SDC4,SFPQ,SH3GL1,SHMT1,SMARCA2,SMC3,SOS1,SRSF1,STAT3,STIP1,SWAP70,TADA3,TIAL1,TOP1,TPM3,TPR,UBTF,XRCC6
1. Cellular Development,Cellular Growth and Proliferation,Nervous System Development and Function,Tissue Development 2. Outgrowth of neurites 3. 0.0000000522 4. Increased 5. 4.772 6. 102	ADAM10,AKT1,Aldh1a7,Anp32a,APEX1,APOE,ARF6,ARHGAP17,ARHGAP5,ARHGEF7,BAIAP2,BASP1,CAMK1,CAT,CD47,Cdc42,CDK5,CNPY2,CORO1B,CREB1,CRK,CSNK1E,DNM1L,DPYSL2,EEA1,EGF,EGFR,EIF2B2,EIF4G2,EIF5A,EPN1,EXOC5,EZR,FECH,FKBP4,FKBP5,FN1,Gm21596/Hmgb1,GNAQ,GNAS,GPHN,GRN,HDGFL3,HRAS,IL6ST,ILK,IQGAP1,ITGA1,ITGA9,ITGB1,ITGB3,KRAS,LGALS1,LIFR,LMNB1,MAP2K1,MPRIP,MTOR,MYH10,MYH9,NCK1,NFIA,NGEF,OGT,PAFAH1B1,PALLD,PARP1,PDIA3,PKP4,PLG,PLXNA4,PRKACA,PSAP,PSEN1,PTK2B,PTPRF,PXN,RAB35,RAC1,RAP1B,RELA,RHOA,RHOG,ROCK2,RPL4,RPS14,RPS6,RTN4,SERPINF2,SET,SLC25A5,SNX1,SNX3,SPAST,STAT3,STK38L,TARDBP,TBC1D24,TOP1,VCAM1,VIM,YWHAZ
1. Cellular Growth and Proliferation 2. Outgrowth of cells 3. 0.0000000856 4. Increased 5. 4.832 6. 110	ADAM10,AKT1,Aldh1a7,Anp32a,APEX1,APOE,ARF6,ARHGAP17,ARHGAP5,ARHGEF7,BAIAP2,BASP1,CAMK1,CAT,CD47,Cdc42,CDK5,CLU,CNPY2,CORO1B,CPB2,CREB1,CRK,CSNK1E,CTSD,DNM1L,DPYSL2,EEA1,EGF,EGFR,EIF2B2,EIF4G2,EIF5A,EPN1,EXOC5,EZR,FECH,FKBP4,FKBP5,FN1,Gm21596/Hmgb1,GNAQ,GNAS,GPHN,GRN,HDGFL3,HRAS,HSP90AA1,IL6ST,ILK,IQGAP1,ITGA1,ITGA9,ITGB1,ITGB3,KRAS,LGALS1,LIFR,LMNB1,MAP2K1,MPRIP,MTOR,MYH10,MYH9,NCK1,NFIA,NGEF,NOS3,OGT,PAFAH1B1,PALLD,PARP1,PDIA3,PKP4,PLG,PLXNA4,PRKACA,PSAP,PSEN1,PTK2B,PTPN1,PTPRF,PXN,RAB35,RAC1,RAP1B,RELA,RHOA,RHOG,ROCK2,RPL4,RPS14,RPS4Y1,RPS6,RTN4,SERPINF2,SET,SLC25A5,SNX1,SNX3,SPAST,STAT3,STK38L,TARDBP,TBC1D24,TOP1,UBE2V2,VCAM1,VIM,YWHAZ
1. Cellular Function and Maintenance 2. Engulfment by cervical cancer cell lines 3. 0.000000087 4. Increased 5. 2.691 6. 24	AP2M1,ASGR1,ATP6AP1,ATP6V0D1,ATP6V1A,ATP6V1E1,CD36,CDC5L,DNM2,EGF,EPB41L2,FCHO2,GPR182,PTRHD1,PXN,RPS21,RUVBL2,SART1,SCARB1,SCARB2,SF3B3,SF3B4,SFPQ,SRSF3
1. Cell-To-Cell Signaling and Interaction 2. Adhesion of tumor cell lines 3. 0.0000000904 4. Increased 5. 4.41 6. 85	ACTN4,ADAM10,ADD1,ADD3,AFDN,AGO2,AKT1,ALCAM,ANXA1,APOE,BSG,CD47,CD81,CD82,CFH,CPB2,CRK,CSK,CTNNB1,CTSB,CTSZ,CTTN,DSP,DYSF,EGF,EGFR,EMILIN1,ERP29,FGA,FLNA,FN1,GNA13,GOLPH3,HRAS,ICAM1,ILK,ITGA5,ITGA9,ITGAV,ITGB1,ITGB3,LASP1,LGALS3,LGALS8,MAP2K1,MCAM,MTOR,MYH9,NECTIN2,NME3,NOS3,NOSTRIN,PAK2,PARP1,PARVA,PARVB,PHLDA1,PROC,PSMD4,PTGES3,PTK2,PTK2B,PXN,RAC1,RACK1,RAP1A,RBM17,RELA,RHOA,ROCK2,RPSA,RRAS,SAA1,SNX1,SPTAN1,STAT3,STAT6,STOML2,TAT,TJP1,TLN1,UBE2I,VCAM1,VCL,VTN
1. Cell Death and Survival,Embryonic Development 2. Cell viability of embryonic stem cell lines 3. 0.000000108 4. Increased 5. 2.324 6. 15	EIF2S1,LSM6,NUP205,NUP54,NUP93,PRPF3,PSMA6,PSMD14,RPL24,RPN2,RUVBL1,SF3B1,TOP1,TRIM28,U2AF2

1. Cellular Movement 2. Migration of cells 3. 0.000000131 4. Increased 5. 7.289 6. 461	Abcb1b,ABCB4,ACACA,ACSL4,ACTB,ACTN1,ACTN4,ACTR3,ADAM10,ADD1,ADD2,ADI1,AFDN,AGK,AGO2,AHCY,AHNAK,AHSG,AIF1,AKT1,ALCAM,Aldh1a7,ALDOA,ANGPTL3,ANGPTL4,ANPEP,ANXA1,ANXA3,ANXA5,AP2M1,APCS,APOA1,APOB,APOE,AQP1,AQP4,AQP9,ARF4,ARF6,ARFGAP3,ARHGAP31,ARHGAP5,ARHGDIA,ARHGDIB,ARHGEF12,ARHGEF7,ARPC2,ARRB1,ASPH,ATG3,ATP1B1,ATP1B3,ATP2A2,ATP6V1C1,BAG3,BAG4,BCAM,BGN,BID,BRAF,BSG,Bst2,C4A/C4B,C6,CALCRL,CALR,CALU,CAMK1,CAP1,CAPNS1,CAT,CCAR1,CCDC134,CD1D,CD302,CD36,CD38,CD47,CD81,CD82,Cdc42,CDK5,CDK6,CDKN1B,CDKN2C,CES1,CFB,CFH,CLDN3,CLEC10A,CLIC4,CLU,CNDP2,CNP,COL18A1,COMMD5,CORO1A,CORO1B,CORO1C,CPB2,CPNE3,CR1L,CRK,CRKL,CRP,CSK,CSNK1E,CSNK2A1,CSNK2B,CTBP1,CTDSP1,CTNNA1,CTNNB1,CTNND1,CTSB,CTSC,CTSH,CTSS,CTSV,CTSZ,CTTN,CUL1,CXADR,CYGB,CYP1A2,CYP2C8,CYP7A1,DCTN2,DDRGK1,DDX3X,DDX58,DEK,DEPTOR,Diaph2,DNAJB6,DNM1L,DNM2,DPAGT1,DPP4,DPYSL2,DSP,DYSF,ECM1,EGF,EGFR,EHD1,EIF2AK2,EIF3E,EIF4A3,EIF4E,ELAVL1,ELMO1,ENPP1,EPB41L5,EPHX2,EPPK1,ERC1,ESAM,EZR,F13A1,FAAH,FABP4,FABP5,FABP7,FAF1,FASN,FCGR2B,FGA,FGB,FHIT,FKBP4,FLNA,FLOT1,FN1,FSCN1,G6PC,G6PD,GALNT2,GBA,GBF1,GJB2,GLG1,GLUL,Gm21596/Hmgb1,GNA11,GNA13,GNAI2,GNAI3,GNAQ,GNAS,GNG12,GNPAT,GOLGA2,GOLPH3,GPLD1,GRB7,GRN,GTPBP4,GUCY1B1,HAO1,HDAC1,HDGF,HEBP1,HECTD1,HLA-A,HMOX1,HNF1A,HNF4A,HNRNPA2B1,HNRNPK,HNRNPL,HP,HRAS,Hrg,HSP90AA1,HSP90AB1,HSP90B1,HSPA1A/HSPA1B,HSPA5,HSPA8,HSPB1,HSPD1,HTATIP2,HUWE1,HYOU1,ICAM1,IFI16,IGF2R,Ighg2b,IGKC,IL6ST,ILF3,ILK,INSR,IQGAP1,Irgm1,ITGA1,ITGA2B,ITGA5,ITGA9,ITGAV,ITGB1,ITGB3,ITGB6,ITSN1,JCHAIN,JUP,KHDRBS1,KPNA2,KRAS,LASP1,LCAT,LDLR,LGALS1,LGALS3,LGALS3BP,LGMN,LIMS2,LITAF,LMNA,LMNB1,LMNB2,LMO7,LRP1,LRPAP1,LUM,LYN,LYVE1,LYZ,Macf1,MAP2K1,MAP2K3,MAP4,MAPRE1,MASP2,MAT1A,MBOAT7,MCAM,MECP2,MFN2,MGLL,MIA3,MIEN1,MIF,MME,MOSPD2,MPP1,MSN,MSR1,MTAP,MTDH,MTOR,MTSS1,MYH10,MYH11,MYH9,MYL12A,MYLK,MYO18A,MYO1C,NAA25,NACA,NAMPT,NARS1,NCK1,NCL,NDRG1,NDST1,NDUFAF3,NFIA,NFIC,NNMT,NOS3,NOSTRIN,NPC1,NQO1,NQO2,NR1H4,NR3C1,NRAS,NUCB2,PA2G4,PAFAH1B1,PAK2,PALLD,PARP1,PARP9,PARVA,PDCD10,PDCD4,PDE2A,PDK1,PDK2,PDLIM1,PECAM1,PEX13,PEX5,PHACTR4,PHB2,PHLDA1,PIGR,PIK3CB,PIP5K1C,PLCB3,PLG,PLPP3,PLTP,PLXNB2,PML,Podxl,PON2,PPFIA1,PPIA,PPIB,PPIF,PPM1A,PPT2,PRCP,PRKAA2,PRKACA,PROC,PROX1,PSEN1,PTK2,PTK2B,PTP4A2,PTPN1,PTPRF,PTPRK,PXN,PYCARD,RAC1,RACK1,RAP1A,RAP1B,RAPGEF4,RARRES2,RCC2,RELA,RHOA,RHOC,RHOG,RIPK1,RNF20,RNH1,ROCK2,RPL13A,RPS19,RPSA,RPTOR,RRAS,RTN4,RUFY3,RUVBL1,RUVBL2,S100A6,SAA1,SARS1,SCARB1,SCPEP1,SCRIB,SDC4,SELENOK,SERPINA1,SERPINA3,SERPINB1,SERPIND1,SERPING1,SHOC2,SLC9A3R1,SLC9A3R2,SLK,SMPD1,SNAP23,SND1,SOS1,SPAG9,SSBP1,STAB1,STAB2,STAT2,STAT3,STAT6,SULT1E1,SUN2,SWAP70,SYNJ2BP,TARDBP,TBC1D24,TCIRG1,TCOF1,TDO2,TJP1,TLN1,TMEM30A,TMOD3,TMPO,Tmsb4x (includes others),TNS2,TNS3,TOP2B,Tpm1,TPM3,TRIP10,TSPAN14,TWF1,U2AF2,UBE2I,UGDH,VAMP3,VAV2,VCAM1,VCL,VIM,VPS28,VTN,WASF2,WBP2,WDR26,YBX1,YWHAZ
1. Cell Morphology 2. Ruffling 3. 0.000000135 4. Increased 5. 3.337 6. 34	ADD1,AKT1,ARF6,ARHGAP17,ARHGAP31,ARHGEF7,ARRB1,BAIAP2,CORO1B,CRK,CTTN,CYFIP1,EGF,EIF2AK2,EZR,FLNA,Gm21596/Hmgb1,GNA13,HMOX1,HRAS,INSR,ITGB1,KRAS,MTSS1,MYO1C,NRAS,PTK2B,RAB4A,RAC1,RHOG,ROCK2,SOS1,SWAP70,WASF2
1. Infectious Diseases 2. Infection by Human parainfluenza virus 3 3. 0.00000018 4. Increased 5. 2.646 6. 7	ARCN1,COPA,COPB1,COPB2,COPG1,COPZ1,GBF1
1. Cellular Movement,Hematological System Development and Function,Immune Cell Trafficking 2. Cell movement of leukocytes 3. 0.000000186 4. Increased 5. 3.165 6. 194	Abcb1b,ABCB4,ACTB,ACTN4,ADAM10,AIF1,AKT1,ALCAM,ANXA1,APCS,APOA1,APOE,AQP9,ARHGEF7,ARRB1,BAG4,BGN,BID,BRAF,BSG,C4A/C4B,C6,CALR,CCDC134,CD1D,CD302,CD36,CD38,CD47,CD81,Cdc42,CES1,CFB,CFH,CNP,COMMD5,CORO1A,CPB2,CR1L,CRKL,CRP,CSK,CTNNB1,CTSB,CTSS,CTSV,CTSZ,CTTN,CXADR,CYP2C8,CYP7A1,DCTN2,DDX58,DEK,DEPTOR,DPP4,DPYSL2,DYSF,EGF,EGFR,ELAVL1,ELMO1,EPHX2,EZR,FABP4,FABP5,FASN,FCGR2B,FGB,FLNA,FLOT1,FN1,G6PC,GBA,GBF1,GJB2,Gm21596/Hmgb1,GNA11,GNA13,GNAI2,GNAI3,GNAS,GRN,HEBP1,HLA-A,HMOX1,HNRNPL,HP,HRAS,Hrg,HSPA5,HSPB1,HSPD1,HYOU1,ICAM1,Ighg2b,IL6ST,ILK,INSR,Irgm1,ITGA1,ITGA5,ITGA9,ITGAV,ITGB1,ITGB3,KRAS,LCAT,LDLR,LGALS1,LGALS3,LGMN,LITAF,LMNB1,LRP1,LUM,LYN,MASP2,MAT1A,MCAM,MIF,MOSPD2,MPP1,MSN,MSR1,MTAP,MTOR,MYH9,MYLK,NARS1,NDRG1,NDST1,NOS3,NPC1,NQO1,NQO2,NR1H4,NR3C1,NRAS,PAFAH1B1,PARP1,PDK2,PECAM1,PIGR,PIK3CB,PIP5K1C,PLCB3,PLG,PLTP,PON2,PPIA,PPIB,PPT2,PRCP,PROC,PSEN1,PTK2,PTK2B,PTPN1,PYCARD,RAC1,RAP1A,RAP1B,RARRES2,RELA,RHOA,RIPK1,ROCK2,RPL13A,RPS19,RPTOR,RTN4,SAA1,SELENOK,SERPINA1,SERPINA3,SERPINB1,SERPING1,SMPD1,SOS1,STAB1,STAT2,STAT3,STAT6,SULT1E1,SWAP70,TCIRG1,TLN1,Tmsb4x (includes others),TSPAN14,UBE2I,VCAM1,VTN,YBX1

1. Cell-To-Cell Signaling and Interaction,Cellular Function and Maintenance,Inflammatory Response 2. Phagocytosis of tumor cell lines 3. 0.000000187 4. Increased 5. 2.304 6. 44	ACTR2,ACTR3,AHSA1,ANXA1,ARAF,ARF6,ARPC2,ARPC3,BRAF,CALR,CD47,Cdc42,CKB,CLEC4G,CSK,CTNNB1,CYFIP1,ELOVL1,ERP44,FCGR2B,GNAI2,GNE,HMOX1,ICAM1,LMAN2,LYN,MBNL1,MTA2,NANS,NHLRC2,PALLD,PPP6R1,PSMD4,PTK2,RAC1,RHOA,RHOG,SHOC2,SRSF6,STAB2,STT3A,TLN1,VIM,WASF2
1. Cellular Function and Maintenance 2. Endocytosis by cervical cancer cell lines 3. 0.00000021 4. Increased 5. 2.901 6. 23	AP2M1,ASGR1,ATP6AP1,ATP6V0D1,ATP6V1A,ATP6V1E1,CD36,CDC5L,DNM2,EGF,EPB41L2,FCHO2,GPR182,PTRHD1,RPS21,RUVBL2,SART1,SCARB1,SCARB2,SF3B3,SF3B4,SFPQ,SRSF3
1. Cellular Movement,Immune Cell Trafficking 2. Leukocyte migration 3. 0.000000221 4. Increased 5. 3.282 6. 228	Abcb1b,ABCB4,ACTB,ACTN4,ADAM10,ADD2,AIF1,AKT1,ALCAM,ANXA1,ANXA5,APCS,APOA1,APOB,APOE,AQP9,ARHGEF7,ARRB1,ATP1B1,ATP1B3,BAG4,BGN,BID,BRAF,BSG,C4A/C4B,C6,CALR,CAMK1,CAT,CCDC134,CD1D,CD302,CD36,CD38,CD47,CD81,Cdc42,CES1,CFB,CFH,CLEC10A,CLU,CNP,COMMD5,CORO1A,CPB2,CR1L,CRKL,CRP,CSK,CTNNB1,CTSB,CTSC,CTSS,CTSV,CTSZ,CTTN,CXADR,CYP1A2,CYP2C8,CYP7A1,DCTN2,DDX3X,DDX58,DEK,DEPTOR,DPP4,DPYSL2,DYSF,EGF,EGFR,ELAVL1,ELMO1,EPHX2,ESAM,EZR,F13A1,FABP4,FABP5,FASN,FCGR2B,FGB,FLNA,FLOT1,FN1,G6PC,GBA,GBF1,GJB2,GLG1,Gm21596/Hmgb1,GNA11,GNA13,GNAI2,GNAI3,GNAS,GRB7,GRN,HAO1,HDAC1,HEBP1,HLA-A,HMOX1,HNRNPL,HP,HRAS,Hrg,HSPA1A/HSPA1B,HSPA5,HSPB1,HSPD1,HYOU1,ICAM1,Ighg2b,IGKC,IL6ST,ILK,INSR,Irgm1,ITGA1,ITGA2B,ITGA5,ITGA9,ITGAV,ITGB1,ITGB3,JCHAIN,KRAS,LCAT,LDLR,LGALS1,LGALS3,LGMN,LITAF,LMNB1,LRP1,LUM,LYN,LYZ,MAP2K3,MASP2,MAT1A,MCAM,MIA3,MIF,MOSPD2,MPP1,MSN,MSR1,MTAP,MTOR,MYH9,MYLK,NARS1,NDRG1,NDST1,NFIC,NOS3,NPC1,NQO1,NQO2,NR1H4,NR3C1,NRAS,PA2G4,PAFAH1B1,PARP1,PDK2,PECAM1,PIGR,PIK3CB,PIP5K1C,PLCB3,PLG,PLTP,Podxl,PON2,PPIA,PPIB,PPT2,PRCP,PROC,PROX1,PSEN1,PTK2,PTK2B,PTPN1,PXN,PYCARD,RAC1,RACK1,RAP1A,RAP1B,RARRES2,RELA,RHOA,RIPK1,ROCK2,RPL13A,RPS19,RPTOR,RTN4,SAA1,SDC4,SELENOK,SERPINA1,SERPINA3,SERPINB1,SERPING1,SMPD1,SOS1,STAB1,STAT2,STAT3,STAT6,SULT1E1,SWAP70,TCIRG1,TLN1,Tmsb4x (includes others),TSPAN14,UBE2I,VAV2,VCAM1,VTN,WDR26,YBX1
1. Cancer,Organismal Injury and Abnormalities 2. Lymphohematopoietic cancer 3. 0.000000284 4. Increased 5. 2.281 6. 566	ABAT,ABCB4,ABCC2,ABCC3,ABCD1,ABCG5,ACAD11,ACOT11,ACSL4,ACTB,ACTG1,ADAM10,ADD2,ADD3,ADK,ADSL,AFDN,AGL,AHNAK,AHSG,AKT1,ALAS1,ALDH1A1,ALDH4A1,ALDH5A1,ALDH9A1,AMACR,ANGPTL4,ANKHD1/ANKHD1-EIF4EBP3,ANPEP,ANXA1,ANXA11,ANXA4,ANXA5,APEX1,APOB,APOE,ARAF,ARHGAP17,ARHGAP42,ARIH1,ATP1B1,ATP2B4,ATP6AP1,ATP6V1A,ATP6V1E1,ATRX,B2M,B4GALNT1,BASP1,BCHE,BCL2L13,BCLAF1,BET1L,BRAF,BUB3,C4A/C4B,C6,CAD,CADM1,CALCRL,CALR,CASP3,CASP7,CAT,CBWD1,CCDC40,CCT3,CD163,CD1D,CD36,CD38,CD47,CD68,CDA,CDC34,Cdc42,CDK12,CDK5,CDK6,CDK9,CDKN1B,CDKN2C,CDO1,CEP89,CHAC2,CHD4,CLCC1,CLEC4G,CLTB,CLU,CNOT3,COBLL1,COG3,COL18A1,COMT,CORO1A,COX15,CP,CPT2,CRAT,CRK,CRKL,CRP,CSK,CSNK1E,CSNK2A1,CSNK2B,CSTF2,CSTF3,CTBP1,CTNNB1,CTNND1,CTSC,CTSH,CTTN,CUL1,CYP2A6 (includes others),CYP3A5,CYP4B1,CYP7B1,DAAM1,DAD1,DAPK1,DCTN2,DDC,DDX18,DDX39B,DDX3X,DDX46,DDX58,DEK,DES,DGLUCY,DHCR24,DHDH,DHFR,DHTKD1,DHX15,DHX16,DIABLO,DIO1,DIS3,DLAT,DMD,DMGDH,DNM1L,DNM2,DPP4,DPYD,DSP,ECHDC3,ECI2,EDC4,EEF1A1,EEF1D,EGF,EGFR,EIF2A,EIF2AK2,EIF3C,EIF3D,EIF3I,EIF3L,EIF4A1,EIF4E,EIF4G1,ELAVL1,ELMO1,ELOC,ENPP1,EPHX1,EPPK1,ERC1,ETNK1,EVA1A,EXOC5,FADS6,FAF1,FASN,FCGR2B,FCHO2,FEN1,FERMT2,FETUB,FGG,FGL1,FHIT,FKBP3,FLII,FLNA,FN1,FNTA,FSCN1,FTCD,FUBP1,GAA,GALT,GAMT,GART,GCN1,GLG1,GMPPB,GNA11,GNA13,GNAI2,GNAQ,GNAS,GPD1,GPX3,GRHPR,GRIPAP1,GRN,GSR,GSTM1,GSTP1,GTF2I,H6PD,HAO2,HDAC1,HEATR1,HECTD1,HIP1,HLA-A,HLA-DQA1,HMGA1,HMOX1,HNRNPA2B1,HNRNPD,HNRNPM,HNRNPU,HRAS,Hrg,HSP90AA1,HSP90AB1,HSP90B1,HSPA1A/HSPA1B,HSPA5,HSPA8,HSPB1,HSPD1,HSPG2,HSPH1,HUWE1,HYPK,ICAM1,IDH2,IDH3B,IFIT3,IFNAR2,IGF2R,IGKC,IL6ST,ILKAP,IMMP2L,INSR,IPO5,IQGAP1,ITGA2B,ITGA5,ITGA9,ITGAV,ITGB1,ITGB3,ITPR2,JCHAIN,KANK2,KHDRBS1,KIF21A,KPNA1,KPNA2,KRAS,KTI12,KYAT3,LARS2,LDLR,LGALS1,LIFR,LMNA,LRP1,LRRFIP1,LSM14A,LUC7L2,LUM,LYN,LYPLA1,LYPLA2,LYZ,MANBA,MAOA,MAP2K1,MAP2K3,MCAM,MFAP1,MGLL,MIF,MME,MRC1,MRPL17,MRPL47,MRPL51,MSH2,MSR1,MTOR,MTREX,MVK,MYH10,MYH11,MYH9,MYL1,MYO18A,NAA16,NAMPT,NAP1L1,NARS1,NASP,NCSTN,NELFCD,NFIB,NIBAN1,NIT1,NMT2,NNMT,NONO,NOP16,NOSTRIN,NQO1,NR3C1,NRAS,NUMA1,NUP153,NUP205,NUP214,NUP54,NUP98,NUTF2,PABPC1,PAK2,PALD1,PARP1,PARP14,PAWR,PC,PDCD4,PDHA1,PDIA3,PDIA6,PDLIM5,PDXDC1,PECAM1,PEX6,PFKFB3,PGK1,PGM1,PGM5,PHKB,PI4KA,PICALM,PIGR,PIGU,PLEKHA7,PLG,PLIN5,PLPP3,PLS3,PLXNB2,PML,PMM2,POLR2A,POR,PPAT,PPIA,PPP1R2,PPP1R7,PPP2R1B,PPP2R5A,PPP4R2,PPP6R3,PPWD1,PRKAA2,PRPF19,PRPF8,PSEN1,PSIP1,PSMA2,PSMB1,PSMB10,PSMB2,PSMB5,PSMB6,PSMB9,PSME3,PTK2B,PTPN1,PTPRF,PTPRK,RAB4A,RAC1,RACK1,RAD50,RAE1,RAN,RANBP1,RANBP3,RBBP4,RBM14,RBM15,RBM42,REEP5,RELA,RGPD4 (includes

	others),RHOA,RNF17,RNF213,RNPEP,ROCK2,RPL10,RPL11,RPL13,RPL13A,RPL15,RPL19,RPL22,RPL23,Rpl23a,RPL28,RPL3,RPL35,RPL37,RPL4,RPL5,RPL6,RPL7,RPLP0,RPS11,RPS12,RPS13,RPS14,RPS15,RPS15A,RPS16,RPS19,RPS2,RPS20,RPS23,RPS24,RPS25,RPS27A,RPS6,RPSA,RPTOR,RUVBL2,SAE1,SARS2,SCARB1,SCYL2,SEC23B,SEC23IP,SEC24D,SELENBP1,SERINC3,SERPINA1,SERPIND1,SERPINH1,SF3A1,SF3B1,SF3B2,SH3GL1,SHMT1,SHOC2,SIGMAR1,SLC25A3,SLC25A5,SLC39A4,SLC44A2,SMARCA2,SMARCD2,SMC1A,SMC3,SMOC1,SMPD1,SNRNP70,SNRPD3,SNX1,SNX18,SOAT2,SORBS2,SORD,SOS1,SPAG9,SREK1,SRP19,SRP72,SRPK2,SRSF1,SRSF2,STAB2,STAG2,STARD5,STAT2,STAT3,STAT6,STEAP3,STEAP4,STIP1,STK38,STRN,SUCLG1,SWAP70,SYNCRIP,TAOK3,TBC1D13,TBC1D8B,TBCD,TFR2,THOC2,THRAP3,TIGAR,TJP1,TLN1,TMEM30A,TNPO3,TOLLIP,TOP1,TOP2B,TPI1,Tpm1,TPR,TRA2B,TRIP11,TSC22D1,TTN,TUBA1B,TUBA4A,TUBB2A,TUBB4B,TWF1,TXLNA,TXLNG,U2AF2,UBA2,UBA3,UBE2I,UBE2M,UGGT1,UPF2,UROC1,USP16,USP7,VAV2,VCAM1,VDAC2,VIM,VPS13D,VTN,WASF2,WASHC4,XPO1,XRCC6,YTHDF2,YWHAZ,ZC3H14,ZHX1,ZHX3,ZMIZ1,ZNF638
1. Cellular Function and Maintenance 2. Endocytosis by tumor cell lines 3. 0.000000332 4. Increased 5. 2.896 6. 29	AP2M1,APOE,ASGR1,ATP6AP1,ATP6V0D1,ATP6V1A,ATP6V1E1,CD36,CDC5L,DNM2,EGF,EPB41L2,FCHO2,GPR182,HRAS,HSP90AA1,ITGB1,PTRHD1,RACK1,RHOA,RPS21,RUVBL2,SART1,SCARB1,SCARB2,SF3B3,SF3B4,SFPQ,SRSF3
1. Cell-To-Cell Signaling and Interaction,Cellular Function and Maintenance,Inflammatory Response 2. Phagocytosis of blood cells 3. 0.000000361 4. Increased 5. 2.834 6. 63	ACTR2,ACTR3,AHSA1,ANXA1,ANXA5,APCS,APOA1,APOA2,ARAF,ARPC2,ARPC3,ASGR1,BIN1,BRAF,CALR,CD36,CD38,CD47,Cdc42,CFH,CLEC4G,CLIC4,CORO1A,CRP,CYFIP1,ELOVL1,ERP44,FCGR2B,Gm21596/Hmgb1,GNAI2,GNE,GRN,HMOX1,ICAM1,LGALS3,LUM,LYN,Mbl1,MBL2,MBNL1,MIF,MSR1,MTA2,NANS,NHLRC2,PALLD,PFKFB3,PIK3CB,PPP6R1,PSEN1,PXN,RAC1,RPTOR,SAA1,SCARB1,SHOC2,SIGLEC1,SRSF6,STAB2,STT3A,TLN1,VTN,WASF2

1. Cancer,Hematological Disease,Organismal Injury and Abnormalities 2. Neoplasia of blood cells 3. 0.000000402 4. Increased 5. 2.143 6. 564	ABAT,ABCB4,ABCC2,ABCC3,ABCD1,ABCG5,ACAD11,ACOT11,ACSL4,ACTB,ACTG1,ADD2,ADD3,ADSL,AFDN,AGL,AHNAK,AKT1,ALAS1,ALDH1A1,ALDH4A1,ALDH5A1,ALDH9A1,AMACR,ANGPTL4,ANKHD1/ANKHD1-EIF4EBP3,ANPEP,ANXA1,ANXA11,ANXA4,ANXA5,APEX1,APOB,APOE,ARAF,ARHGAP17,ARHGAP42,ARIH1,ATP1B1,ATP2B4,ATP6AP1,ATP6V1A,ATP6V1E1,ATRX,B2M,B4GALNT1,BASP1,BCHE,BCL2L13,BCLAF1,BET1L,BID,BRAF,BUB3,C4A/C4B,C6,CAD,CADM1,CALCRL,CALR,CASP3,CASP7,CAT,CBWD1,CCDC40,CCT3,CD163,CD1D,CD36,CD38,CD47,CD68,CDA,CDC34,Cdc42,CDK12,CDK5,CDK6,CDK9,CDKN1B,CDKN2C,CDO1,CEP89,CHAC2,CHD4,CHORDC1,CLCC1,CLEC4G,CLTB,CLU,CNOT3,COBLL1,COG3,COMT,CORO1A,COX15,CP,CPT2,CRAT,CRK,CRKL,CRP,CSK,CSNK1E,CSNK2A1,CSNK2B,CSTF2,CSTF3,CTBP1,CTNNB1,CTSC,CTSH,CTTN,CUL1,CYP2A6 (includes others),CYP3A5,CYP4B1,CYP7B1,DAAM1,DAD1,DAPK1,DCTN2,DDC,DDX18,DDX39B,DDX3X,DDX46,DDX58,DEK,DES,DGLUCY,DHCR24,DHDH,DHFR,DHTKD1,DHX15,DHX16,DIABLO,DIO1,DIS3,DLAT,DMD,DMGDH,DNM1L,DNM2,DPP4,DPYD,DSP,DTX3L,ECHDC3,ECI2,EDC4,EEF1A1,EEF1D,EGF,EGFR,EIF2A,EIF2AK2,EIF3C,EIF3D,EIF3I,EIF3L,EIF4A1,EIF4E,EIF4G1,ELAVL1,ELMO1,ELOC,ENPP1,EPHX1,EPPK1,ERC1,ETNK1,EVA1A,EXOC5,FADS6,FAF1,FASN,FCGR2B,FCHO2,FEN1,FERMT2,FETUB,FGG,FGL1,FHIT,FKBP3,FLII,FLNA,FN1,FNTA,FTCD,FUBP1,GAA,GALT,GAMT,GART,GCN1,GLG1,GMPPB,GNA11,GNA13,GNAI2,GNAQ,GNAS,GPD1,GPX3,GRHPR,GRIPAP1,GRN,GSR,GSTM1,GSTP1,GTF2I,H6PD,HAO2,HDAC1,HEATR1,HECTD1,HIP1,HLA-A,HLA-DQA1,HMGA1,HMOX1,HNRNPA2B1,HNRNPD,HNRNPM,HNRNPU,HRAS,HSP90AA1,HSP90AB1,HSP90B1,HSPA1A/HSPA1B,HSPA5,HSPA8,HSPB1,HSPD1,HSPG2,HSPH1,HUWE1,HYPK,ICAM1,IDH2,IDH3B,IFIT3,IFNAR2,IGF2R,IGKC,IL6ST,ILKAP,IMMP2L,INSR,IPO5,IQGAP1,ITGA2B,ITGA5,ITGA9,ITGAV,ITGB1,ITGB3,ITPR2,JCHAIN,KANK2,KHDRBS1,KIF21A,KPNA1,KPNA2,KRAS,KTI12,KYAT3,LARS2,LDLR,LGALS1,LIFR,LRP1,LRRFIP1,LSM14A,LUC7L2,LUM,LYN,LYPLA1,LYPLA2,LYZ,MANBA,MAOA,MAP2K1,MAP2K3,MCAM,MFAP1,MGLL,MIF,MME,MRC1,MRPL17,MRPL47,MRPL51,MSH2,MSR1,MTOR,MTREX,MVK,MYH10,MYH11,MYH9,MYL1,MYO18A,NAA16,NAMPT,NAP1L1,NARS1,NASP,NCSTN,NELFCD,NFIB,NIBAN1,NIT1,NMT2,NNMT,NONO,NOP16,NOSTRIN,NQO1,NR3C1,NRAS,NUMA1,NUP153,NUP205,NUP214,NUP54,NUP98,NUTF2,PABPC1,PAK2,PALD1,PARP1,PARP14,PAWR,PC,PDCD4,PDHA1,PDIA3,PDIA6,PDLIM5,PDXDC1,PECAM1,PEX6,PFKFB3,PGK1,PGM1,PGM5,PHKB,PI4KA,PICALM,PIGR,PIGU,PLCB3,PLEKHA7,PLG,PLIN5,PLPP3,PLS3,PLXNB2,PML,PMM2,POLR2A,POR,PPAT,PPIA,PPP1R2,PPP1R7,PPP2R1B,PPP2R5A,PPP4R2,PPP6R3,PPWD1,PREP,PRKAA2,PRPF19,PRPF8,PSEN1,PSIP1,PSMA2,PSMB1,PSMB10,PSMB2,PSMB5,PSMB6,PSMB9,PSME3,PTK2B,PTPN1,PTPRF,PTPRK,RAB4A,RAC1,RACK1,RAD50,RAE1,RAN,RANBP1,RANBP3,RBBP4,RBM14,RBM15,RBM42,REEP5,RELA,RGPD4 (includes others),RHOA,RNF17,RNF213,RNPEP,ROCK2,RPL10,RPL11,RPL13,RPL13A,RPL15,RPL19,RPL22,RPL23,Rpl23a,RPL28,RPL3,RPL35,RPL37,RPL4,RPL5,RPL6,RPL7,RPLP0,RPS11,RPS12,RPS13,RPS14,RPS15,RPS15A,RPS16,RPS19,RPS2,RPS20,RPS23,RPS24,RPS25,RPS27A,RPS6,RPSA,RPTOR,RUVBL2,SAE1,SARS2,SCARB1,SCRIB,SCYL2,SEC23B,SEC23IP,SEC24D,SELENBP1,SERINC3,SERPINA1,SERPIND1,SERPINH1,SF3A1,SF3B1,SF3B2,SH3GL1,SHMT1,SHOC2,SIGMAR1,SLC25A3,SLC25A5,SLC39A4,SLC44A2,SMARCA2,SMARCD2,SMC1A,SMC3,SMOC1,SMPD1,SNRNP70,SNRPD3,SNX1,SNX18,SOAT2,SORBS2,SORD,SOS1,SPAG9,SREK1,SRP19,SRP72,SRPK2,SRSF1,SRSF2,STAB2,STAG2,STARD5,STAT2,STAT3,STAT6,STEAP3,STEAP4,STIP1,STK38,STRN,SUCLG1,SWAP70,SYNCRIP,TAOK3,TBC1D13,TBC1D8B,TBCD,TFR2,THOC2,THRAP3,TIGAR,TJP1,TLN1,TMEM30A,TNPO3,TOLLIP,TOP1,TOP2B,TPI1,Tpm1,TPR,TRA2B,TRIP11,TSC22D1,TTN,TUBA1B,TUBA4A,TUBB2A,TUBB4B,TWF1,TXLNA,TXLNG,U2AF2,UBA2,UBA3,UBE2I,UBE2M,UGGT1,UPF2,UROC1,USP16,USP7,VAV2,VCAM1,VDAC2,VIM,VPS13D,VTN,WASF2,WASHC4,XPO1,XRCC6,YTHDF2,YWHAZ,ZC3H14,ZHX1,ZHX3,ZMIZ1,ZNF638
1. Cell Morphology,Connective Tissue Development and Function 2. Shape change of fibroblast cell lines 3. 0.000000421 4. Increased 5. 3.341 6. 29	ACTN4,ARHGAP31,BAIAP2,Cdc42,CORO1B,CRK,EHD1,FLNA,FN1,GNA11,GNG12,HRAS,INSR,ITGB1,LGALS8,NCK1,PALLD,PTBP1,PTK2,RAB4A,RAC1,RACK1,RHOA,RHOG,RTN4,SORBS1,VAV2,VCL,VIM

1. Cancer,Hematological Disease,Organismal Injury and Abnormalities 2. Hematologic cancer 3. 0.000000438 4. Increased 5. 2.005 6. 561	ABAT,ABCB4,ABCC2,ABCC3,ABCD1,ABCG5,ACAD11,ACOT11,ACSL4,ACTB,ACTG1,ADAM10,ADD2,ADD3,ADK,ADSL,AFDN,AGL,AHNAK,AKT1,ALAS1,ALDH1A1,ALDH4A1,ALDH5A1,ALDH9A1,AMACR,ANGPTL4,ANKHD1/ANKHD1-EIF4EBP3,ANPEP,ANXA1,ANXA11,ANXA4,ANXA5,APEX1,APOB,APOE,ARAF,ARHGAP17,ARHGAP42,ARIH1,ATP1B1,ATP2B4,ATP6AP1,ATP6V1A,ATP6V1E1,ATRX,B2M,B4GALNT1,BASP1,BCHE,BCL2L13,BCLAF1,BET1L,BRAF,BUB3,C4A/C4B,C6,CAD,CADM1,CALCRL,CALR,CASP3,CASP7,CAT,CBWD1,CCDC40,CCT3,CD163,CD1D,CD36,CD38,CD47,CD68,CDA,CDC34,Cdc42,CDK12,CDK5,CDK6,CDK9,CDKN1B,CDKN2C,CDO1,CEP89,CHAC2,CHD4,CLCC1,CLEC4G,CLTB,CLU,CNOT3,COBLL1,COG3,COMT,CORO1A,COX15,CP,CPT2,CRAT,CRK,CRKL,CRP,CSK,CSNK1E,CSNK2A1,CSNK2B,CSTF2,CSTF3,CTBP1,CTNNB1,CTSC,CTSH,CTTN,CUL1,CYP2A6 (includes others),CYP3A5,CYP4B1,CYP7B1,DAAM1,DAD1,DAPK1,DCTN2,DDC,DDX18,DDX39B,DDX3X,DDX46,DDX58,DEK,DES,DGLUCY,DHCR24,DHDH,DHFR,DHTKD1,DHX15,DHX16,DIABLO,DIO1,DIS3,DLAT,DMD,DMGDH,DNM1L,DNM2,DPP4,DPYD,DSP,ECHDC3,ECI2,EDC4,EEF1A1,EEF1D,EGF,EGFR,EIF2A,EIF2AK2,EIF3C,EIF3D,EIF3I,EIF3L,EIF4A1,EIF4E,EIF4G1,ELAVL1,ELMO1,ELOC,ENPP1,EPHX1,EPPK1,ERC1,ETNK1,EVA1A,EXOC5,FADS6,FAF1,FASN,FCGR2B,FCHO2,FEN1,FERMT2,FETUB,FGG,FGL1,FHIT,FKBP3,FLII,FLNA,FN1,FNTA,FTCD,FUBP1,GAA,GALT,GAMT,GART,GCN1,GLG1,GMPPB,GNA11,GNA13,GNAI2,GNAQ,GNAS,GPD1,GPX3,GRHPR,GRIPAP1,GRN,GSR,GSTM1,GSTP1,GTF2I,H6PD,HAO2,HDAC1,HEATR1,HECTD1,HIP1,HLA-A,HLA-DQA1,HMGA1,HMOX1,HNRNPA2B1,HNRNPD,HNRNPM,HNRNPU,HRAS,HSP90AA1,HSP90AB1,HSP90B1,HSPA1A/HSPA1B,HSPA5,HSPA8,HSPB1,HSPD1,HSPG2,HSPH1,HUWE1,HYPK,ICAM1,IDH2,IDH3B,IFIT3,IFNAR2,IGF2R,IGKC,IL6ST,ILKAP,IMMP2L,INSR,IPO5,IQGAP1,ITGA2B,ITGA5,ITGA9,ITGAV,ITGB1,ITGB3,ITPR2,JCHAIN,KANK2,KHDRBS1,KIF21A,KPNA1,KPNA2,KRAS,KTI12,KYAT3,LARS2,LDLR,LGALS1,LIFR,LMNA,LRP1,LRRFIP1,LSM14A,LUC7L2,LUM,LYN,LYPLA1,LYPLA2,LYZ,MANBA,MAOA,MAP2K1,MAP2K3,MCAM,MFAP1,MGLL,MIF,MME,MRC1,MRPL17,MRPL47,MRPL51,MSH2,MSR1,MTOR,MTREX,MVK,MYH10,MYH11,MYH9,MYL1,MYO18A,NAA16,NAMPT,NAP1L1,NARS1,NASP,NCSTN,NELFCD,NFIB,NIBAN1,NIT1,NMT2,NNMT,NONO,NOP16,NOSTRIN,NQO1,NR3C1,NRAS,NUMA1,NUP153,NUP205,NUP214,NUP54,NUP98,NUTF2,PABPC1,PAK2,PALD1,PARP1,PARP14,PAWR,PC,PDCD4,PDHA1,PDIA3,PDIA6,PDLIM5,PDXDC1,PECAM1,PEX6,PFKFB3,PGK1,PGM1,PGM5,PHKB,PI4KA,PICALM,PIGR,PIGU,PLEKHA7,PLG,PLIN5,PLPP3,PLS3,PLXNB2,PML,PMM2,POLR2A,POR,PPAT,PPIA,PPP1R2,PPP1R7,PPP2R1B,PPP2R5A,PPP4R2,PPP6R3,PPWD1,PRKAA2,PRPF19,PRPF8,PSEN1,PSIP1,PSMA2,PSMB1,PSMB10,PSMB2,PSMB5,PSMB6,PSMB9,PSME3,PTK2B,PTPN1,PTPRF,PTPRK,RAB4A,RAC1,RACK1,RAD50,RAE1,RAN,RANBP1,RANBP3,RBBP4,RBM14,RBM15,RBM42,REEP5,RELA,RGPD4 (includes others),RHOA,RNF17,RNF213,RNPEP,ROCK2,RPL10,RPL11,RPL13,RPL13A,RPL15,RPL19,RPL22,RPL23,Rpl23a,RPL28,RPL3,RPL35,RPL37,RPL4,RPL5,RPL6,RPL7,RPLP0,RPS11,RPS12,RPS13,RPS14,RPS15,RPS15A,RPS16,RPS19,RPS2,RPS20,RPS23,RPS24,RPS25,RPS27A,RPS6,RPSA,RPTOR,RUVBL2,SAE1,SARS2,SCARB1,SCYL2,SEC23B,SEC23IP,SEC24D,SELENBP1,SERINC3,SERPINA1,SERPIND1,SERPINH1,SF3A1,SF3B1,SF3B2,SH3GL1,SHMT1,SHOC2,SIGMAR1,SLC25A3,SLC25A5,SLC39A4,SLC44A2,SMARCA2,SMARCD2,SMC1A,SMC3,SMOC1,SMPD1,SNRNP70,SNRPD3,SNX1,SNX18,SOAT2,SORBS2,SORD,SOS1,SPAG9,SREK1,SRP19,SRP72,SRPK2,SRSF1,SRSF2,STAB2,STAG2,STARD5,STAT2,STAT3,STAT6,STEAP3,STEAP4,STIP1,STK38,STRN,SUCLG1,SWAP70,SYNCRIP,TAOK3,TBC1D13,TBC1D8B,TBCD,TFR2,THOC2,THRAP3,TIGAR,TJP1,TLN1,TMEM30A,TNPO3,TOLLIP,TOP1,TOP2B,TPI1,Tpm1,TPR,TRA2B,TRIP11,TSC22D1,TTN,TUBA1B,TUBA4A,TUBB2A,TUBB4B,TWF1,TXLNA,TXLNG,U2AF2,UBA2,UBA3,UBE2I,UBE2M,UGGT1,UPF2,UROC1,USP16,USP7,VAV2,VCAM1,VDAC2,VIM,VPS13D,VTN,WASF2,WASHC4,XPO1,XRCC6,YTHDF2,YWHAZ,ZC3H14,ZHX1,ZHX3,ZMIZ1,ZNF638

Appendix 7.3. All Quantified O-GlcNAc Regions.

logFC Protein: log2 fold change in protein expression. logFC_Corrected, and P-Val_Corrected are the log2 fold change, p-value (after correction for multiple comparisons using the Benjamini-Hochberg method). If protein expression could not be quantified, these values represent those calculated for the sites and regions alone (logFC, and P-Val).

Protein	Gene	Site ID Constraints	Min Sites	logFC	P-Val	B	logFC_ Corrected	P-Val_ Corrected	B_ Corrected
A0A087WNV1	Agfg1	(1 of 261,262,264)	1	-0.01	0.95	-7.2	-0.216474	0.166852	-5.769119
A0A087WNV1	Agfg1	(1 of 251,252,253,258)	1	0.167	0.225	-5.9	-0.036573	0.796312	-7.358127
A0A087WNV1	Agfg1	260	1	-0.01	0.952	-7.2	-0.215617	0.167762	-5.776142
A0A087WNV1	Agfg1	327	1	0.154	0.205	-5.8	-0.050027	0.738148	-7.308137
A0A087WP65	R3hdm1	90	1	-0.58	0.023	-2.2	-0.583806	0.021295	-2.710266
A0A087WQH5	Fam135a	579	1	0.212	0.072	-4.3	0.2119017	0.12265	-5.364413
A0A087WQN7	Xrn1	1332	1	0.518	0.017	-1.8	0.3940366	0.048126	-3.899879
A0A087WRU0	Tns1	(1 of 945,946,948,949,953)	1	0.602	0.028	-2.2	0.4836636	0.064885	-4.014219
A0A0A0MQ73	Kmt2d	2359	1	-0.59	0.008	-0.9	-0.586533	0.00728	-1.411378
A0A0A0MQ98	Jmjd1c	(1 of 2035,2037,2041,2042,2043,2047,2049,2054,2055)	1	-0.36	0.26	-5.2	-0.362244	0.31976	-5.71707
A0A0A0MQ98	Jmjd1c	(1 of 1428,1431)	1	0.125	0.682	-6.3	0.1250652	0.725585	-6.59297
A0A0A0MQ98	Jmjd1c	1492	1	0.358	0.264	-5.2	0.3580388	0.323535	-5.736607
A0A0A0MQB4	Arhgap40	360	1	-1.21	0.028	-1.7	-1.211436	0.022556	-2.001187
A0A0A0MQJ4	Phactr4	(2 of 163,165,166,167,168,170,171,172,174,175,178,179,182,185)	2	-0.32	0.044	-3.5	-0.53845	0.024594	-3.172693
A0A0A0MQJ4	Phactr4	(1 of 159,160)	1	-0.19	0.549	-6.5	-0.240132	0.376465	-6.328126
A0A0A0MQJ4	Phactr4	204	1	-0.11	0.443	-6.6	-0.326774	0.083957	-4.891739
A0A0A6YVU8	Gm9774	(1 of 217,219,220,221,222,223,224)	1	0.785	0.001	2.93	0.7845268	0.000897	1.873024
A0A0A6YVU8	Gm9774	211	1	0.72	0.002	1.45	0.7203284	0.001865	0.682729
A0A0A6YVU8	Gm9774	213	1	0.818	0.002	2.63	0.8180414	0.000897	1.830331
A0A0A6YVZ3	Cep170	(1 of 120,122,123,124,126,129,130,131,133,134,137,138,141,145)	1	-0.03	0.919	-6.5	-0.03343	0.925722	-6.727357
A0A0A6YXS8	Serpinc1	(1 of 63,65,69,74)	1	1.345	0.007	-0.1	1.5081956	0.003059	0.551337
A0A0A6YXS8	Serpinc1	10	1	1.28	0.014	-1.1	1.4429022	0.005615	-0.386988
A0A0B4J1G5	Elf2	(1 of 283,285,286,287)	1	-0.56	0.125	-4.1	-0.563931	0.148988	-4.733092
A0A0G2JDK2	Gba	290	1	-0.73	0.002	1.86	-1.383069	0.000332	4.182709
A0A0G2JDK2	Gba	71	1	-1.06	0.009	-0.5	-1.805993	0.00131	1.850317
A0A0G2JDL6	Sbno1	(2 of 75,76)&(1 of 71,75,76)	2	-0.64	0.026	-2.4	-0.63753	0.021177	-2.700241
A0A0G2JDV2	Tent4a	(1 of 658,662,663,667)	1	-0.35	0.266	-5.2	-0.35477	0.327134	-5.751736
A0A0G2JEI9	Rsbn1l	(1 of 84,85,86,87,88,89)	1	-0.62	0.044	-2.9	-0.616458	0.042704	-3.421353
A0A0G2JF07	Cfi	(1 of 104,108)	1	-0.03	0.872	-7.1	-0.476605	0.029272	-3.157862
A0A0G2JFD6	Elovl6	4	1	3.283	0.003	0.82	4.3480735	0.000647	2.827837
A0A0G2JFW6	Rprd2	(1 of 349,355,358,359)	1	-0.23	0.448	-5.9	0.0166659	0.958612	-6.735344
A0A0G2JFW6	Rprd2	(1 of 406,409,410,412)	1	-0.18	0.549	-6.1	0.0679597	0.846058	-6.694322

A0A0G2JFW6	Rprd2	(1 of 525,529,531,532,533,534,535,538,539,540,541,543)	1	-0.29	0.05	-3.7	-0.698349	0.031525	-3.4972
A0A0G2JFW6	Rprd2	(1 of 909,912,913,915,916,926,927)	1	-0.18	0.538	-6.1	0.0618038	0.857812	-6.701823
A0A0G2JFW6	Rprd2	346	1	-0.41	0.028	-2.6	-0.642785	0.050253	-3.957643
A0A0G2JFW6	Rprd2	334	1	-0.49	0.007	-0.6	-0.895395	0.009191	-1.750631
A0A0G2JGT1	Fubp1	(1 of 146,148,154,155,157)	1	-0.71	0.168	-5	-1.305405	0.025611	-2.648267
A0A0J9YU61	Clock	706	1	0.307	0.32	-5.5	0.3070801	0.382588	-5.965988
A0A0J9YU61	Clock	446	1	0.351	0.102	-4.2	0.3506244	0.14144	-5.085919
A0A0N4SUS4	Brpf1	(1 of 1057,1064)	1	0.239	0.231	-5.4	0.2388081	0.305552	-6.04094
A0A0N4SUV0	Plekha5	274	1	0.153	0.24	-5.9	-0.123031	0.384645	-6.742712
A0A0N4SV80	Zfp638	1370	1	-0.05	0.638	-7	-0.405488	0.021349	-2.970777
A0A0R4IZZ5	Clec4f	(1 of 205,206,207,210,211)	1	0.112	0.716	-6.4	-0.788164	0.069929	-3.670453
A0A0R4J079	Acbd3	(1 of 313,317,318)	1	-0.1	0.731	-6.4	-0.13103	0.710981	-6.579231
A0A0R4J0D3	Stt3b	(1 of 636,637,640)	1	0.676	0.006	-0.5	0.4654033	0.0177	-2.708146
A0A0R4J0H0	Eml4	(1 of 786,787)	1	0.354	0.266	-5.2	0.1738824	0.614831	-6.464591
A0A0R4J0I1	Serpina3k	(1 of 184,187)	1	-1.36	0.022	-1.3	-2.63026	0.002337	1.186814
A0A0R4J0I9	Lrp1	(1 of 4359,4363,4367)	1	-0.08	0.8	-6.5	-0.409612	0.2682	-5.492277
A0A0R4J0I9	Lrp1	(1 of 2617,2622,2623)	1	0.325	0.296	-5.4	-0.007411	0.983225	-6.737467
A0A0R4J0I9	Lrp1	(1 of 3784,3785,3788,3791)	1	-0.01	0.988	-6.6	-0.338503	0.345166	-5.826259
A0A0R4J0I9	Lrp1	2130	1	0.417	0.054	-3.8	0.1428748	0.469115	-6.935938
A0A0R4J0I9	Lrp1	4078	1	-0.45	0.098	-4.7	-0.722303	0.017288	-2.670435
A0A0R4J0M9	Vcpip1	(1 of 1066,1072)	1	0.391	0.105	-4.8	0.1196802	0.60963	-7.172674
A0A0R4J0M9	Vcpip1	1075	1	0.741	0.002	2.47	0.4700058	0.014256	-2.411876
A0A0R4J0X5	Serpina1c	(1 of 90,92,103,105,106)	1	0.943	0.028	-2.2	0.8727801	0.06003	-3.896766
A0A0R4J131	Btd	138	1	-0.61	0.011	-1.4	-0.986337	0.00072	2.348661
A0A0R4J187	Xrcc6	(1 of 317,319)	1	0.719	0.08	-3.4	0.8817395	0.05309	-3.261349
A0A0R4J1H6	Golga3	167	1	0.149	0.34	-6.4	-0.00906	0.955946	-7.42312
A0A0R4J2B5	2310022A10Rik	348	1	-0.56	0.125	-4.1	-0.562896	0.149122	-4.738191
A0A0U1RNH9	Pik3c2a	251	1	0.518	0.144	-4.3	0.5183046	0.175104	-4.958494
A0A0U1RQB6	Crebbp	147	1	-0.23	0.448	-5.9	-0.230667	0.507226	-6.274563
A0A140LHQ8	Picalm	(1 of 442,444)	1	0.287	0.346	-5.6	-0.311756	0.376465	-5.945587
A0A140LHQ8	Picalm	337	1	0.186	0.112	-4.9	-0.301412	0.067496	-4.58615
A0A140LHQ8	Picalm	181	1	0.193	0.112	-4.9	-0.294127	0.072352	-4.689937
A0A140LHR4	Serpinh1	(1 of 116,118,120,121)	1	-0.39	0.034	-3.1	-0.892218	0.002114	0.487535
A0A140LIZ8	Zfp286	(1 of 142,144)	1	-0.89	0.053	-2.7	-0.892915	0.051555	-3.214027
A0A140T8T5	Map4	70	1	0.175	0.241	-5.8	-0.109849	0.518865	-6.878455
A0A1B0GR78	Stim1	(1 of 170,172,173,175,177)	1	0.427	0.059	-3.7	0.4491764	0.06126	-4.224019
A0A1B0GR85	2900026A02Rik	(1 of 1078,1079,1083,1084,1085)	1	0.511	0.024	-2.3	1.3283734	0.00072	2.647091

A0A1B0GRB5	Nup98	(1 of 550,551)	1	-0.14	0.635	-6.3	-0.350246	0.330569	-5.772596
A0A1B0GRJ0	Rab11fip1	(1 of 1019,1020)	1	0.35	0.27	-5.2	0.3496471	0.330647	-5.775349
A0A1B0GRV3	Rfx1	248	1	-0.77	0.072	-3.1	-0.768724	0.073753	-3.758264
A0A1B0GSG3	Nsd3	(1 of 265,266,269,270,272,273,274)	1	-1.48	0.017	-1.1	-1.483272	0.012683	-1.152575
A0A1B0GSN3	Aldh16a1	(1 of 20,21)	1	0.026	0.886	-7.1	0.3716657	0.0912	-4.781834
A0A1B0GT43	Erlin2	108	1	0.396	0.067	-4.1	0.4117387	0.043806	-4.014093
A0A1C7ZMY3	Shank2	1071	1	1.21	1E-03	3.45	1.2104277	0.000455	3.506891
A0A1D5RLU0	Tcf25	(1 of 101,107,108)	1	-0.9	0.052	-2.6	-1.034808	0.035692	-2.641877
A0A1I7Q4G8	Gatad2a	(1 of 61,62,67,69)	1	-0.29	0.067	-3.9	-0.509662	0.01817	-2.492531
A0A1I7Q4G8	Gatad2a	(1 of 176,178,179)	1	-0.01	0.979	-6.6	-0.234319	0.50169	-6.261055
A0A1I7Q4G8	Gatad2a	(1 of 315,319,324,325,327,328,331,335,338,341)	1	-0.21	0.289	-5.8	-0.443548	0.086681	-4.431213
A0A1I7Q4G8	Gatad2a	(1 of 201,202,205,206,207,208)	1	-0	0.996	-6.6	-0.244903	0.4851	-6.221118
A0A1I7Q4G8	Gatad2a	606	1	0.144	0.57	-6.5	-0.072905	0.784898	-6.996831
A0A1L1SUR6	1700017B05Rik	(1 of 530,531)	1	-0.37	0.251	-5.1	-0.371789	0.30957	-5.67244
A0A1L1SV73	Usp47	(1 of 77,78,87,88)	1	-0.45	0.181	-4.7	-0.336664	0.346258	-5.834597
A0A1N9M4K1	Siae	285	1	-0.93	0.002	1.98	-1.2258	0.000968	1.733645
A0A1N9M4K1	Siae	357	1	-2.28	0.002	2.57	-2.798615	0.000551	3.61413
A0A1N9PTV1	Fbrs	246	1	-0.23	0.227	-5.4	-0.232187	0.307651	-6.054924
A0A1W2P7D7	Ncoa1	(1 of 152,153)	1	-0.33	0.287	-5.3	-0.332775	0.349751	-5.852165
A0A1W2P7G2	Sarnp	(1 of 102,103,104,107,109,110,113)	1	-0.37	0.02	-2.3	-1.148531	0.001155	1.462543
A0A1W2P7I2	Epb41l2	(1 of 183,185)	1	-0.67	0.022	-1.7	-1.260384	0.006518	-0.602924
A0A1W2P7Q7	Ccar1	(1 of 134,135,139)	1	0.409	0.217	-4.9	0.2055333	0.553435	-6.363517
A0A1Y7VJM4	Ero1lb	123	1	-1	0.005	0.1	-0.995164	0.002413	0.278716
A0A1Y7VK55	Nfic	(1 of 292,295,296,297,298,299,301)	1	-0.64	0.036	-2.5	-1.071684	0.004899	-0.179856
A0A1Y7VLT3	Prpf4b	(1 of 82,84)	1	-0.65	0.028	-2.5	-0.64655	0.021828	-2.761408
A0A1Y7VMT6	Erap1	(1 of 19,20,24,25)	1	-0.06	0.845	-6.5	-0.092291	0.792045	-6.658017
A0A1Y7VP49	Ctsl	79	1	-0.92	0.01	-0.9	-1.245757	0.000871	2.3454
A0A2I3BPM1	Ero1l	64	1	0.676	0.091	-3.5	0.6755876	0.10174	-4.19148
A0A2I3BPN6	Taf4	486	1	-0.35	0.268	-5.2	-0.351169	0.330276	-5.768346
A0A2I3BQ92	Mtss1	(1 of 64,65,67,68,71,75,81)	1	0	1	-6.6	-0.35281	0.328997	-5.760786
A0A2I3BQE0	Stk3	(1 of 327,328,329,331,334)	1	0.446	0.031	-2.7	0.4460537	0.037637	-3.52517
A0A2I3BQE1	AI182371	143	1	0.559	0.127	-4.1	-0.152833	0.660539	-6.524299
A0A2I3BRS9	Mapk1ip1l	(1 of 2,6,15,16,23,25)	1	-0.54	0.068	-3.6	-0.816047	0.026948	-2.719732
A0A2R8VHH9	Naga	203	1	-1.31	7E-04	4.43	-2.315435	4.39E-05	8.86807
A0A2R8VHQ0	Tns2	(1 of 891,893,894,897,900,901,905,906,907)	1	-0.47	0.172	-4.6	-0.731462	0.083571	-3.929183
A0A2R8VHQ0	Tns2	1000	1	-0.8	0.007	-0.5	-1.16372	0.00131	1.556094

A0A2R8VHW4	Brd4	(1 of 157,158,160,161,162)	1	-0.27	0.08	-4.4	-0.624419	0.006638	-1.282076
A0A2R8VKN7	Mzt2	(1 of 89,94,98,100,101,102,103,104,106)	1	0.181	0.545	-6.1	0.1813687	0.602925	-6.441865
A0A2R8W6T9	Tmprss6	(1 of 171,173,174,175,178)	1	1.155	0.016	-1.3	1.1548445	0.010083	-1.243842
A0A338P6F2	Osbpl11	13	1	0.019	0.938	-6.9	0.0191995	0.936952	-7.074347
A0A338P6J9	Cast	(1 of 81,83,85,86,87,89)	1	0.272	0.063	-4	0.2129286	0.14144	-5.547609
A0A338P6J9	Cast	72	1	0.129	0.284	-6.2	0.070366	0.645915	-7.219387
A0A338P6J9	Cast	79	1	0.27	0.041	-3.4	0.2108519	0.155243	-5.684873
A0A338P6K9	Qser1	(1 of 162,163,166,169)	1	-0.07	0.581	-6.9	-0.068491	0.635104	-7.206369
A0A338P6K9	Qser1	45	1	0.262	0.386	-5.7	0.2622097	0.453861	-6.153441
A0A338P6K9	Qser1	303	1	0.275	0.203	-5.3	0.2747173	0.256179	-5.842739
A0A338P6K9	Qser1	63	1	0.001	0.999	-6.6	0.0014868	0.996645	-6.73797
A0A338P7E6	C2cd2	(1 of 75,83)	1	0.1	0.742	-6.4	0.0442329	0.902125	-6.719402
A0A3B2W7J8	Plec	786	1	1.732	0.013	-0.6	1.8945749	0.006157	-0.123064
A0A3B2WBH9	Tjp2	451	1	0.361	0.083	-4.2	0.0968884	0.614099	-7.02857
A0A3B2WCD8	Khsrp	(1 of 144,145,147)	1	-0.09	0.514	-6.6	-0.7161	0.006638	-0.990425
A0A3B2WCD8	Khsrp	(1 of 95,96,101)	1	-0.14	0.642	-6.3	-0.736058	0.082346	-3.90792
A0A3B2WCD8	Khsrp	192	1	-0.14	0.635	-6.3	-0.739111	0.081485	-3.893827
A0A494B962	Sil1	(1 of 37,38,39,40,41)	1	-0.27	0.144	-5.3	-0.516815	0.037451	-3.752513
A0A494BB11	Tmx3	262	1	0.019	0.886	-7.2	-0.357837	0.03599	-3.691081
A0A571BDN3	Nav3	(1 of 659,660)	1	0.028	0.934	-6.5	0.0279435	0.93612	-6.730556
A0A571BEC9	Plin4	(1 of 320,321)	1	3.319	0.003	0.84	3.3188286	0.001177	2.014753
A0A571BEC9	Plin4	(1 of 214,221,222)	1	3.694	0.003	1	3.6942406	0.000896	2.358149
A0A571BEC9	Plin4	(1 of 353,354)	1	3.731	0.003	1.02	3.7306209	0.000883	2.388222
A0A571BEC9	Plin4	(1 of 181,184,188,189)	1	3.338	0.003	0.85	3.3379597	0.001161	2.03383
A0A571BFA7	Fam83h	(1 of 949,950,951,952,954)	1	0.967	0.045	-2.4	0.7448317	0.079741	-3.867473
A0A5F8MPS7	Acp2	169	1	0.182	0.545	-6.1	-0.184831	0.595436	-6.431099
A0A5F8MPU2	Fnbp4	(1 of 805,806,807)	1	-0.22	0.475	-5.9	-0.215937	0.531113	-6.327571
A0A5F8MPU2	Fnbp4	(1 of 661,663,667,668,670,671,675,677)	1	-0.51	0.147	-4.3	-0.512355	0.179088	-4.987939
A0A5F8MPY2		74	1	0.13	0.267	-6.1	0.129835	0.349143	-6.629526
A0JNY3	Gphn	(1 of 298,300,301,302,304)	1	1.217	7E-04	4.39	1.4773733	0.000145	5.670724
A0JNY3	Gphn	296	1	1.228	7E-04	4.22	1.4879236	0.000145	5.622954
A2A5Y4	Kansl1	(1 of 822,823,824,825,827,828,829,831,832,833,835,840,841,842)	1	-0.36	0.263	-5.2	-0.358979	0.32309	-5.732247
A2AC24	Wdr13	140	1	0.596	0.035	-3.1	0.5962968	0.025525	-3.219626
A2ADB1	Spen	(1 of 2761,2762,2769,2771)	1	-0.27	0.364	-5.6	-0.274454	0.431534	-6.103904
A2ADB1	Spen	2496	1	-0.46	0.178	-4.6	-0.458692	0.219863	-5.252967
A2ADB1	Spen	2504	1	-0.46	0.008	-0.9	-0.455208	0.011421	-2.057104

A2AFQ0	Huwe1	(1 of 3795,3796,3798,3799,3802,3804,3805)	1	0.696	0.02	-1.6	0.5181274	0.052168	-3.703784
A2AGG1	Ttc17	(1 of 241,244)	1	-0.37	0.257	-5.1	-0.365568	0.317298	-5.701572
A2AGJ9	Slc12a6	55	1	-0.4	0.229	-5	-0.395054	0.284419	-5.562177
A2AKB9	Dcaf10	364	1	0.864	0.002	2.02	0.863718	0.001068	1.57309
A2AKI5	Itgav	(1 of 829,835)	1	-0.33	0.294	-5.4	-0.665981	0.104493	-4.237246
A2AKJ2	Vim	(1 of 32,33,34,35)	1	-0.54	0.136	-4.2	-0.969455	0.041547	-2.898829
A2AMY5	Ubap2	(1 of 1000,1001)	1	0.143	0.635	-6.3	-0.119847	0.737204	-6.60452
A2AMY5	Ubap2	(1 of 630,631,633,637,641)	1	0.356	0.265	-5.2	0.0932414	0.790145	-6.656387
A2AMY5	Ubap2	(1 of 1017,1019,1020,1022,1028,1030)	1	0.156	0.186	-5.6	-0.101376	0.523761	-7.042804
A2AMY5	Ubap2	(1 of 468,469,475,476,478)	1	-0.05	0.696	-7.1	-0.306681	0.061452	-4.450473
A2AMY5	Ubap2	(1 of 651,654,657,658,659,660)	1	0.197	0.514	-6	-0.066033	0.849313	-6.696744
A2AMY5	Ubap2	1107	1	0.452	0.181	-4.7	0.1887983	0.589005	-6.418572
A2AP93	Map3k7	(1 of 378,382,383)	1	0.98	0.044	-2.4	0.9801763	0.040509	-2.855911
A2APL5	Slc1a2	(1 of 201,206,207)	1	0.904	0.003	0.67	0.5108731	0.141202	-5.541415
A2APT9	Klhdc7a	(1 of 293,294,295)	1	0.422	0.014	-1.8	0.1517321	0.368174	-6.6939
A2AQE9	Atf2	174	1	-0.88	0.055	-2.7	-0.876823	0.053814	-3.28227
A2ATI9	Gorasp2	397	1	-0.78	0.014	-1.5	-1.054557	0.002894	0.295484
A2ATI9	Gorasp2	406	1	-0.48	0.035	-3.1	-0.723579	0.005795	-1.074623
A2ATR8	Serping1	(1 of 240,245,247,251,252)	1	-0.55	0.129	-4.1	-0.842695	0.059859	-3.42927
A2AVJ7	Rrbp1	(1 of 103,110,111,114)	1	-0.61	0.109	-3.8	-1.437479	0.013865	-1.284987
A2AVP4	Rc3h2	(1 of 768,769)	1	0.662	0.095	-3.6	0.6617683	0.105756	-4.257376
A2AVR3	Mroh7	(1 of 80,82)	1	1.676	0.014	-0.7	1.6759666	0.008831	-0.636717
A2AWN8	Ythdf1	(1 of 224,225)	1	-0.24	0.067	-4.2	-0.236902	0.103418	-5.146342
A2AWN8	Ythdf1	223	1	-0.69	0.002	1.57	-0.685254	0.001977	0.608837
A2CEK6	Mup13	170	1	-1.71	0.013	-0.6	-1.711975	0.008269	-0.547195
A2RSY1	Kansl3	(1 of 522,523,525,527,531,532,534,535,536,538,539,540)	1	-0.77	0.004	0.58	-0.772816	0.003924	-0.223724
A6H619	Phrf1	(1 of 547,549,551)	1	-0.04	0.892	-6.5	0.2224096	0.521881	-6.304576
A6H619	Phrf1	(1 of 1359,1363,1364,1365,1366,1368,1369,1376)	1	-0.75	0.075	-3.2	-0.482175	0.200017	-5.137209
A8Y5E6	Plod1	200	1	0.071	0.818	-6.5	0.0708551	0.838287	-6.690556
A9C497	Mup19	(1 of 170,173)	1	-2.42	0.006	0.24	-2.417213	0.003004	0.862403
B1AR09	Mllt6	(1 of 398,399,400,402,403,404,405)	1	-0.91	0.047	-3	-0.912751	0.031859	-2.945138
B1AR76	Bcas3	(1 of 305,309,313,314)	1	0.817	0.003	1.24	0.7861063	0.003243	0.080876
B1ARU1	Macf1	1680	1	-0.36	0.265	-5.2	-0.315335	0.371573	-5.929876
B1ATR2	Tex2	(1 of 169,173,174,175,177,178,179,182,183)	1	0.671	0.005	0.04	0.6657473	0.003536	-0.3334

B1ATR2	Tex2	(1 of 157,158,159,160,161,164,165,167)	1	1.118	7E-04	4.68	1.112484	0.000455	3.573174
B1AUF2	Ski	502	1	2.278	0.007	0.1	2.2781663	0.003531	0.628785
B1AWT4	Rragd	64	1	-0.73	0.05	-3.1	-0.914123	0.010966	-1.376146
B1AZ15	Cobll1	(1 of 681,684,685,688,690,694,695,697,701,705)	1	0.347	0.271	-5.2	0.059097	0.864027	-6.704902
B1AZ15	Cobll1	836	1	0.436	0.009	-1.1	0.1351917	0.376465	-6.717466
B1AZA8	Tmem245	145	1	0.94	0.012	-1.2	1.1920699	0.00701	-1.084586
B1B0C7	Hspg2	847	1	-0.07	0.816	-6.5	-0.442025	0.234905	-5.334734
B2RQE8	Arhgap42	709	1	0.275	0.364	-5.6	-0.220454	0.524418	-6.311574
B2RQG2	Phf3	(1 of 1509,1511,1512,1513)	1	-0.15	0.418	-6.2	-0.1467	0.50169	-6.62613
B2RT14	Ugt1a5	(1 of 116,117)	1	2.547	7E-04	5.38	3.9270384	0.000146	5.7165
B2RUJ2	Erbin	1011	1	0.275	0.364	-5.6	0.1759447	0.612514	-6.458407
B2RUJ2	Erbin	1068	1	0.103	0.402	-6.6	-0.048562	0.744292	-7.315058
B2RUQ2	Usf3	(1 of 361,364,366,367,369)	1	-0.05	0.859	-6.5	-0.054707	0.87534	-6.70961
B2RXC8	Ppp2r3a	462	1	0.851	0.058	-2.8	0.8512528	0.058242	-3.392119
B2RXS4	Plxnb2	146	1	-1.25	0.003	1.12	-1.57138	0.000563	3.318975
B7ZC18	Stat3	(1 of 688,690,691,693,695,701)	1	-0.19	0.353	-6	-0.565027	0.064151	-3.991013
B7ZC23	Ncoa5	(1 of 121,124,125,130,136,138,140,146,147)	1	0.299	0.331	-5.5	-0.278947	0.425619	-6.085408
B7ZC94	Tnrc6c	(1 of 804,805,806,807,811,813,814,816,817,818,819,820,821)	1	-0.06	0.845	-6.5	-0.061017	0.859207	-6.702731
B7ZNH7	Col14a1	140	1	0.529	0.018	-1.9	0.4607382	0.034217	-3.365405
B7ZNJ1	Fn1	1008	1	-0.96	0.002	2.34	-1.088725	0.000598	2.83126
B7ZNJ1	Fn1	530	1	-0.18	0.547	-6.1	-0.230721	0.507226	-6.274365
B7ZNJ1	Fn1	524	1	-0.14	0.634	-6.3	-0.194814	0.577378	-6.399185
B7ZNJ1	Fn1	432	1	0.035	0.763	-7.1	-0.091104	0.527086	-7.049604
B8JJB2	Pdlim7	89	1	-0.23	0.451	-5.9	-0.215963	0.531113	-6.327482
C0HKG6	Rnaset2b	218	1	-0.29	0.338	-5.5	-1.326206	0.017426	-1.624001
D3YU17	Ncln	430	1	-0.23	0.271	-5.7	-0.203665	0.400747	-6.400974
D3YUV1	Nrbp1	(1 of 532,533,536,538,540,542,543)	1	0.187	0.536	-6.1	0.1867889	0.591897	-6.424943
D3YUW8	Pogz	(1 of 253,254)	1	0.731	0.078	-3.3	0.7314546	0.083571	-3.929217
D3YUW8	Pogz	(1 of 263,264,265)	1	0.399	0.225	-4.9	0.3988869	0.281062	-5.543834
D3YUW8	Pogz	149	1	0.2	0.164	-5.3	0.199842	0.241434	-6.018656
D3YVM4	Pigr	169	1	0.566	0.124	-4.1	-0.211229	0.540203	-6.343996
D3YWA4	Pcnp	(1 of 72,74,75,80)	1	0.518	0.144	-4.3	0.2444029	0.485551	-6.223031
D3YXZ5	Rbm47	(1 of 450,454)	1	-0.31	0.32	-5.5	-0.553489	0.153664	-4.784572
D3YY42	Yif1b	19	1	0.11	0.719	-6.4	0.1135172	0.748524	-6.617935

D3YYR9	Ablim2	(1 of 54,55,56,58,61,65,66,67,68,70,72)	1	-0.93	0.005	0.06	-0.928526	0.002698	0.139488
D3YYY8	Arhgef26	252	1	-0.65	0.098	-3.6	-0.653315	0.108597	-4.297867
D3Z069	Phldb2	581	1	-0.21	0.49	-6	-0.332232	0.349843	-5.854615
D3Z0Y0	Hspa13	(1 of 185,186)	1	-0.36	0.185	-5.1	-1.387207	0.006186	-0.526953
D3Z216	Tab2	456	1	-0.13	0.271	-6.1	-0.126703	0.35586	-6.6559
D3Z2E7	Ifi207	(1 of 391,392)	1	-1.04	0.008	-0.6	-1.042878	0.004598	-0.438047
D3Z2E7	Ifi207	434	1	-0.59	0.115	-4	-0.588365	0.138016	-4.61304
D3Z2L1	Gtf3c2	(1 of 199,204,205,207)	1	-0.49	0.157	-4.4	-0.492022	0.192577	-5.088542
D3Z3F1	Fip1l1	(1 of 258,259,260,261,263,265,266,267,269)	1	0.522	0.142	-4.3	0.5219231	0.172567	-4.940587
D3Z3F1	Fip1l1	237	1	-0.31	0.025	-2.6	-0.30685	0.041731	-3.925446
D3Z3F1	Fip1l1	189	1	-0.43	0.045	-3.3	-0.425119	0.049619	-3.938305
D3Z3F8	Spg20	478	1	0.175	0.219	-5.6	0.1749908	0.306985	-6.284874
D3Z3Q3	Smtn	(1 of 697,698,699,700,701,702,703,704,705,706,709)	1	-0.15	0.606	-6.2	-0.15354	0.659413	-6.522398
D3Z3U7	Tnk2	(1 of 324,327,328,330,333)	1	-0.67	0.002	1.88	-0.665094	0.001865	0.690358
D3Z4C0	Farp2	387	1	0.468	0.171	-4.6	0.33654	0.346258	-5.835157
D3Z4Q7	Slc39a14	54	1	0.706	0.083	-3.4	0.0521468	0.881105	-6.712191
D3Z4U8	Dcaf11	(1 of 492,493,496,502,506,507)	1	0.988	0.044	-2.3	1.3673839	0.015976	-1.495606
D3Z5G4	Zfr	(1 of 148,149,157)	1	0.355	0.024	-2.6	0.061891	0.702093	-7.275155
D3Z5G4	Zfr	(1 of 135,136,142,144)	1	-0.17	0.558	-6.1	-0.403641	0.275131	-5.521019
D3Z5G4	Zfr	202	1	-0.08	0.682	-6.7	-0.378143	0.119233	-4.852455
D3Z5G4	Zfr	195	1	0.086	0.664	-6.7	-0.214962	0.376465	-6.323052
D3Z5I1	Zc3hav1	(1 of 557,558,559,562,564,567,570)	1	0.406	0.075	-3.7	0.0739384	0.744292	-6.962575
D3Z5I1	Zc3hav1	(1 of 489,490)	1	0.289	0.344	-5.6	-0.078605	0.821688	-6.679733
D3Z5I1	Zc3hav1	487	1	0.112	0.715	-6.4	-0.255298	0.466777	-6.180809
D3Z5I1	Zc3hav1	551	1	0.272	0.106	-4.6	-0.056832	0.744078	-7.167308
D3Z5I9	Rbm33	(1 of 738,739,740)	1	0.183	0.3	-6.1	0.182661	0.346258	-6.452903
D3Z5X0	Bpnt1	(1 of 41,42,44)	1	0.014	0.965	-6.6	-0.278651	0.425619	-6.086629
D3Z656	Synj1	1374	1	-0.03	0.806	-7.2	-0.028892	0.833028	-7.380796
D3Z665	Emc10	(1 of 175,187,188,195,196,202)	1	0.865	0.056	-2.8	0.7950793	0.068828	-3.639442
D3Z6S3	Tssc4	(1 of 107,111,112,114,118)	1	0.444	0.186	-4.7	0.4436562	0.233701	-5.326751
D3Z6W7	Gxylt1	384	1	-0.36	0.262	-5.2	-0.360444	0.321318	-5.725441
D6RDD4	Gfra1	(1 of 58,61,63,64)	1	-0.27	0.22	-5.4	-0.268365	0.27324	-5.910346
D6RGN2	Plcd4	(1 of 60,62,64)	1	-0.02	0.95	-6.5	-0.02082	0.950318	-6.733861
D6RGR1	Manba	91	1	-2.02	0.002	2.18	-2.858491	0.000297	4.677454
D6RHA2	Renbp	413	1	-0.89	0.002	1.73	-0.89423	0.001156	1.448961

D6RJL6	Lin54	(1 of 14,16,17,22)	1	-0.3	0.036	-3.2	-0.295235	0.053814	-4.276978
E0CXE3	Cntn6	(1 of 673,674)	1	-0.55	0.13	-4.1	-0.550253	0.155109	-4.800543
E0CY18	Zfand2b	(1 of 157,158,159,160,163,165)	1	-0.03	0.933	-6.5	-0.028512	0.93612	-6.730251
E0CY18	Zfand2b	150	1	0.086	0.453	-6.7	0.0858182	0.528481	-7.052396
E0CY18	Zfand2b	167	1	-0.06	0.553	-6.9	-0.063807	0.632831	-7.20269
E0CYH7	Filip1l	(1 of 1045,1047,1049,1050,1051,1054,1055)	1	-0.27	0.365	-5.6	-0.273408	0.433052	-6.108186
E0CYN0	Agmo	11	1	0.779	0.003	0.78	0.7299569	0.001776	0.766078
E0CYQ2	Nudcd2	(1 of 112,117,121)	1	-0.47	0.17	-4.6	-0.253811	0.468057	-6.186641
E0CZ61	Umad1	(1 of 38,39,44,49)	1	0.331	0.08	-4.2	0.3307456	0.098791	-4.875395
E9PUF4	Rbm26	(1 of 645,647,648,655,657,658,665,666,667,668,671)	1	0.096	0.751	-6.4	-0.105032	0.769855	-6.634875
E9PUM5	Gm4788	(1 of 658,665,667,669)	1	-0.64	0.1	-3.7	-1.53385	0.011456	-1.010877
E9PV38	Ces2g	478	1	1.206	0.003	1.35	1.1732553	0.001345	1.188187
E9PV38	Ces2g	102	1	-0.2	0.505	-6	-0.235905	0.50169	-6.255142
E9PV69	Cacul1	(1 of 111,116,117,118,119,120,125,126,127,128)	1	0.15	0.617	-6.2	0.1496921	0.66675	-6.532657
E9PVA8	Gcn1	(1 of 20,22)	1	-0.18	0.551	-6.1	-0.385083	0.297001	-5.60967
E9PVC6	Eif4g1	21	1	0.447	0.006	-0.5	0.337801	0.030218	-3.445371
E9PWM3	Armcx4	595	1	-0.06	0.755	-6.8	-0.063462	0.78714	-7.000108
E9PWW2	Tor1aip1	(1 of 208,209)	1	-0.15	0.465	-6.3	-0.368663	0.128157	-4.951888
E9PWX8	Mast4	(1 of 1971,1972,1973,1977)	1	-0.16	0.392	-6.1	-0.16366	0.468057	-6.555293
E9PXN7	Ugt1a10	(1 of 69,73)	1	1.501	0.017	-1	1.5005638	0.012276	-1.103603
E9PYK3	Parp4	(1 of 1740,1746,1749,1750,1753,1756,1757)	1	0.005	0.989	-6.6	-0.481752	0.200064	-5.139298
E9PYX7	Afdn	(1 of 561,562)	1	0.297	0.333	-5.5	-0.003574	0.992572	-6.737869
E9PZ00	Psap	(1 of 322,330)	1	0.454	0.181	-4.6	0.266148	0.446192	-6.137652
E9PZ00	Psap	210	1	-1	0.002	2.15	-1.25208	0.000647	2.671959
E9PZ00	Psap	454	1	-0.26	0.074	-4.3	-0.507024	0.020541	-2.892048
E9PZ00	Psap	79	1	-1.25	7E-04	5.11	-1.495084	0.000235	4.798108
E9PZD2	Micall2	(1 of 366,369,372,373)	1	-0.56	0.012	-1.5	-0.560516	0.010719	-1.95876
E9PZD2	Micall2	(1 of 383,384)	1	-0.15	0.626	-6.2	-0.146735	0.674155	-6.540391
E9PZD2	Micall2	(1 of 431,432,438,439)	1	-0.08	0.795	-6.5	-0.079961	0.820482	-6.677729
E9PZD2	Micall2	406	1	-0.7	0.004	0.55	-0.700684	0.002897	-0.006222
E9Q113	Sp1	126	1	-0.13	0.31	-6.3	-0.127119	0.377767	-6.723592
E9Q150	Dvl3	613	1	0.046	0.883	-6.5	0.0461226	0.897392	-6.717786
E9Q1P8	Irf2bp2	(1 of 359,364,365,366,367)	1	-0.96	0.047	-2.4	-0.957157	0.042704	-2.948427
E9Q1S3	Sec23a	183	1	-0.76	0.074	-3.2	-0.769476	0.073701	-3.754852
E9Q284	Coil	(1 of 2,7,9)	1	-0.85	0.058	-2.8	-0.853909	0.057886	-3.380628
E9Q2M4	Zfp867	(1 of 440,442,443,444)	1	-0.38	0.275	-6.1	-0.378337	0.252395	-6.247233
E9Q2T3	Tnxb	320	1	-0.33	0.289	-5.3	-0.198361	0.569134	-6.387541

E9Q3G8	Nup153	(1 of 1056,1057)	1	-0.76	0.028	-2.2	-1.264453	0.002793	0.698885
E9Q3G8	Nup153	(1 of 554,557,559,561,562,563,565,568,569,570,575,579,580,581)	1	-0.75	0.075	-3.2	-1.4752	0.012847	-1.175626
E9Q3G8	Nup153	(1 of 925,926,927,929,931,932,934,937)	1	-0.21	0.084	-4.5	-0.859925	0.002748	0.084763
E9Q3G8	Nup153	(1 of 1101,1102,1103,1104)	1	-0.29	0.17	-5.3	-1.063142	0.008275	-1.336199
E9Q3G8	Nup153	(1 of 699,704,705,706,708)	1	-0.72	0.003	0.97	-1.370673	0.000567	3.001431
E9Q3G8	Nup153	200	1	-0.8	0.067	-3	-1.806006	0.00701	-0.322774
E9Q3G8	Nup153	1067	1	-0.54	0.004	0.59	-1.192632	0.000758	2.258122
E9Q3G8	Nup153	1044	1	-0.52	0.143	-4.3	-1.250629	0.020846	-1.869087
E9Q3G8	Nup153	1046	1	-0.3	0.028	-2.8	-0.953992	0.002224	0.404222
E9Q449	Dennd4c	(1 of 1346,1347)	1	0.564	0.019	-2	0.4749033	0.040229	-3.628924
E9Q4Q2	Sf1	328	1	-0.1	0.573	-6.5	-0.501416	0.067532	-4.073637
E9Q5G1	Myo10	(1 of 484,485,486)	1	0.096	0.751	-6.4	0.095668	0.78714	-6.652155
E9Q5Q0	Atxn2l	(1 of 561,562,563,564,566,567)	1	0.557	0.004	0.23	0.5266927	0.005446	-0.969451
E9Q5Q0	Atxn2l	(1 of 146,147,150,151,153,154,156)	1	0.039	0.859	-6.9	-0.062124	0.78714	-7.000129
E9Q616	Ahnak	(1 of 5376,5377,5378,5383,5384)	1	-1.01	0.056	-3.3	-1.286838	0.025743	-2.657765
E9Q640	Rbm26	(1 of 694,695,696,697,700)	1	-0.52	0.098	-4.5	-0.696813	0.037067	-3.495612
E9Q6A7	Bptf	(1 of 1624,1627,1628,1629)	1	0.281	0.354	-5.6	0.2806959	0.423197	-6.07816
E9Q6A7	Bptf	(1 of 1595,1598,1601,1602,1604,1605,1606,1609,1611)	1	-0.31	0.07	-4	-0.305519	0.098794	-4.882245
E9Q6A7	Bptf	1635	1	-0.26	0.037	-3.3	-0.264689	0.065092	-4.538571
E9Q6E2	Cdk8	(1 of 345,346,347,348,354,355)	1	0.628	0.104	-3.8	0.6278053	0.11959	-4.420853
E9Q6R7	Utrn	(1 of 2210,2211,2213)	1	1.155	0.005	0.55	0.9873753	0.006667	-0.657807
E9Q6T8	Cic	(1 of 122,126,127)	1	-1.2	0.028	-1.7	-1.198477	0.023203	-2.045639
E9Q7B0	P4ha1	(1 of 107,112,115)	1	-0.07	0.832	-6.5	-0.066205	0.849313	-6.69653
E9Q7D5	Arhgef5	(1 of 496,498,499,500,504,506)	1	1.264	0.001	3.29	1.2640924	0.000647	2.97649
E9Q7R8	Slc29a1	(1 of 14,18,19,21,24,27,28)	1	-0.12	0.701	-6.4	-0.549249	0.155243	-4.805498
E9Q8A6	Nr3c1	43	1	0.269	0.039	-3.3	-0.329694	0.043806	-4.02061
E9Q8A6	Nr3c1	53	1	0.273	0.036	-3.2	-0.325617	0.043744	-4.007536
E9Q8H9	Cfh	(1 of 729,732,735,736)	1	-0.4	0.05	-3.7	-1.069814	0.000577	2.941196
E9Q8H9	Cfh	(1 of 764,765)	1	-0.62	0.106	-3.8	-1.315276	0.017852	-1.658678
E9Q8H9	Cfh	(1 of 986,993,995,997,1001)	1	-0.76	0.074	-3.2	-1.450513	0.013519	-1.246893

E9Q8H9	Cfh	1024	1	-0.9	0.052	-2.6	-1.596315	0.010328	-0.842196
E9Q8H9	Cfh	1188	1	-0.65	0.099	-3.7	-1.338473	0.017015	-1.585381
E9Q9Q7	Ablim1	(1 of 108,109,110,113)	1	0.777	0.07	-3.1	0.7774894	0.072168	-3.718554
E9QAN9	Ifi203	(1 of 449,451,456)	1	-0.83	0.061	-2.9	-0.831302	0.061812	-3.479022
E9QAT4	Sec16a	69	1	-0.12	0.321	-6.3	-0.139613	0.33831	-6.59118
E9QAT4	Sec16a	70	1	-0.09	0.458	-6.7	-0.114376	0.427164	-6.848821
E9QAT4	Sec16a	127	1	-0	0.971	-7.2	-0.024113	0.857812	-7.393701
E9QJU8	Trp53bp2	(1 of 334,345,348)	1	0.048	0.8	-6.8	0.0484992	0.828513	-7.029652
E9QKG6	Ankrd17	(1 of 1421,1423,1428,1429,1431,1433,1434,1436)	1	0.38	0.241	-5.1	0.358061	0.323535	-5.736504
E9QKG6	Ankrd17	(1 of 1935,1941,1942,1943,1945)	1	0.725	0.079	-3.3	0.7024482	0.092211	-4.064527
E9QKT0	Mef2d	(1 of 273,274)	1	0.065	0.834	-6.5	0.0648882	0.851432	-6.698151
E9QL13	Rbm14	(1 of 242,244)	1	-0.22	0.156	-5.2	-0.725615	0.0081	-1.279466
E9QL13	Rbm14	280	1	0.035	0.865	-6.9	-0.403616	0.108597	-4.73475
E9QL13	Rbm14	254	1	0.1	0.742	-6.4	-0.362852	0.319631	-5.71424
E9QLQ9	Apc	(1 of 2314,2315,2316,2318,2319)	1	0.02	0.938	-6.9	0.0201568	0.93612	-7.073938
E9QM14	Cbll1	276	1	0.363	0.26	-5.1	0.3630236	0.319631	-5.713439
E9QMU3	Map7	(1 of 452,453,456,457,463)	1	0.601	0.003	0.67	0.5440661	0.004799	-0.784252
E9QN70	Lamb1	1091	1	-0.57	0.123	-4.1	-0.568708	0.146547	-4.709574
F6QJV5	Tfg	90	1	0.692	0.002	1.63	0.6270244	0.002362	0.311115
F6RDR0	Add1	(1 of 60,68,70)	1	0.123	0.505	-6.4	-0.068195	0.761179	-6.976897
F6S4K9	Epb41	103	1	0.418	0.012	-1.5	0.1339298	0.358467	-6.666758
F6S5I0	Mprip	(1 of 25,26,27,28,31,32,34,35,36,37,40)	1	1.643	0.002	2.01	2.4148656	0.000556	3.562397
F6SSP6	Ubr4	463	1	0.713	0.021	-1.7	0.6336961	0.035692	-3.116199
F6TS96	Tle3	(1 of 275,278,279,280,281)	1	0.287	0.346	-5.6	0.2873728	0.411202	-6.050272
F6UVB2	4930404N11Rik	(1 of 16,23)	1	-0.5	0.156	-4.4	-0.497403	0.188398	-5.061925
F6V513	Sorbs2	(1 of 143,144,145)	1	0.193	0.547	-6.7	-0.194268	0.523761	-6.889203
F6V8M6	Atxn2	(1 of 208,212,213,214,215,216,217,220,221,223,224)	1	0.595	0.113	-3.9	0.3620701	0.31976	-5.717879
F6V8M6	Atxn2	141	1	0.627	0.002	1.64	0.4582667	0.009191	-1.751323
F6V8M6	Atxn2	127	1	0.647	0.002	1.91	0.4779378	0.008187	-1.577804
F6VV02	Hgs	(1 of 17,21,22,28,31,32,36,37)	1	0.632	0.003	1.18	0.4723709	0.011136	-2.02487
F6W4D3	1300017J02Rik	228	1	0.444	0.141	-4.7	0.4444745	0.142324	-5.094429
F6WV21	Asxl2	(1 of 822,823,831,832,833,836,837,839)	1	-1.43	0.003	1.46	-1.432988	0.00182	1.356763
F6Y6L6	Gm49369	132	1	-1	8E-04	3.73	-0.995684	0.000551	3.174503

F6YIN5	Sec24b	(1 of 163,164,165,168,169,175,176,177)	1	-0.31	0.031	-3	-0.471079	0.009951	-1.847747
F6YT69	Reps1	(1 of 79,82,85)	1	0.165	0.579	-6.2	0.1649541	0.634748	-6.490687
F6YUG5	Synrg	(1 of 8,9,10,12,13)	1	0.535	0.043	-2.8	0.3321313	0.158551	-5.261159
F6Z4B2	Ncor2	(1 of 845,846,847)	1	-1.22	0.028	-1.7	-1.223783	0.021828	-1.959195
F6Z4B2	Ncor2	(1 of 611,614,615,619)	1	-0.14	0.728	-7	-0.135365	0.705312	-7.131436
F6Z4B2	Ncor2	(1 of 926,927,932,934)	1	-0.19	0.131	-5.2	-0.189555	0.186935	-5.904145
F6Z4B2	Ncor2	192	1	-0.06	0.744	-6.8	-0.060145	0.78714	-7.000449
F6Z9A1	Senp6	(1 of 72,77,78,79)	1	0.63	0.006	-0.2	0.6297724	0.008067	-1.263935
F6Z9E6	Psd3	212	1	0.522	0.142	-4.3	0.5218026	0.172567	-4.941183
F6Z9T5	R3hdm2	110	1	0.171	0.482	-6.3	0.1706518	0.507226	-6.640328
F6ZBY9	Tle4	321	1	-0.13	0.265	-6.1	-0.129233	0.34878	-6.627369
F7AYW2	Prrc2b	1045	1	-0.45	0.023	-2.2	-0.448724	0.030831	-3.228309
F7BXV7	Rapgef3	6	1	-0.06	0.926	-7.1	-0.056368	0.9123	-7.26859
F7CDR2	Nfia	(1 of 96,99,100,101,102,103,104,105,106)	1	0.171	0.258	-6	-0.118748	0.35586	-6.656412
F7CIP8	Pcyox1	(1 of 137,138,141,142)	1	0.451	0.01	-1.2	0.3358289	0.042327	-3.946349
F7CIP8	Pcyox1	32	1	0.493	0.014	-1.5	0.454565	0.026948	-3.055991
F7CIP8	Pcyox1	105	1	0.338	0.036	-3.2	0.223088	0.108597	-5.218379
F7DE17	Ankhd1	(1 of 575,578,581,586,588,590,594,597)	1	-0.11	0.596	-6.6	-0.512676	0.071194	-4.154388
F7DE17	Ankhd1	(1 of 132,133,134,135)	1	-0.06	0.596	-6.9	-0.359476	0.03599	-3.69024
F7DE17	Ankhd1	(1 of 276,279,282,283,287,288,290,291,292)	1	-0.01	0.949	-6.9	-0.301653	0.250861	-5.818504
F7DE17	Ankhd1	(1 of 120,121,124,125)	1	0.159	0.179	-5.6	-0.139959	0.349751	-6.633544
F8VPM9	Hivep1	(1 of 1770,1771)	1	-0.8	0.002	2.51	-0.798932	0.001003	1.680587
F8VPM9	Hivep1	(1 of 2646,2647,2651,2654)	1	-0.58	0.117	-4	-0.582474	0.14093	-4.641929
F8VQJ3	Lamc1	(1 of 1201,1205,1206)	1	0.039	0.907	-6.5	0.0389541	0.915125	-6.723562
F8VQJ3	Lamc1	1223	1	-0.09	0.633	-6.6	-0.064831	0.772918	-6.987051
F8WH96	Hint3	102	1	-0.09	0.461	-6.7	0.0682199	0.660831	-7.236984
F8WHP5	Ddhd1	(1 of 694,695,697,699,707,710,711,715)	1	-0.68	0.091	-3.5	-0.675081	0.101741	-4.193889
F8WI14	Ecm1	(1 of 532,536,544)	1	0.418	0.145	-5.1	0.1973758	0.457457	-6.752771
F8WIE5	Hectd1	1569	1	0.62	0.008	-0.6	0.393422	0.061689	-4.236818
F8WIN6	Phc3	250	1	-0.55	0.129	-4.1	-0.553016	0.153664	-4.786905
F8WJL9	Bcorl1	(1 of 102,103)	1	0.369	0.254	-5.1	0.3694537	0.312582	-5.683393
F8WJL9	Bcorl1	121	1	0.616	0.006	-0.5	0.6159693	0.005615	-1.027805
F8WJL9	Bcorl1	751	1	0.348	0.271	-5.2	0.3477454	0.332151	-5.784081
G3UWE3	Pias2	(1 of 595,597,601,602,603)	1	-0.24	0.438	-5.8	-0.235465	0.50169	-6.256786
G3UWE3	Pias2	(1 of 430,431)	1	-0.57	0.124	-4.1	-0.565608	0.148129	-4.724838
G3UWE3	Pias2	435	1	-0.55	0.132	-4.2	-0.546736	0.156475	-4.817905
G3UXW9	Gps1	(1 of 4,8,9,11,12,13,15,18)	1	1.171	0.03	-1.8	1.23682	0.021349	-1.915232

G3UY24	Esrra	36	1	-0.28	0.084	-4.5	-0.283103	0.098794	-5.088295
G3UZP7	H2-D1	202	1	-0.32	0.136	-4.7	-1.107682	0.010508	-1.305334
G3UZP7	H2-D1	282	1	-0.49	0.156	-4.4	-1.07282	0.032451	-2.497486
G3X8Q1	Cabin1	2073	1	0.758	0.074	-3.2	2.4970511	0.002747	0.988487
G3X8R2	Sra1	(1 of 59,60,71,72)	1	-0.07	0.535	-6.8	-0.667701	0.006638	-1.282233
G3X8T3	Ctsa	(1 of 157,160)	1	-0.25	0.48	-6.3	-0.559714	0.066927	-4.05856
G3X928	Sec23ip	185	1	0.499	0.006	-0.5	0.3186742	0.063534	-4.498059
G3X928	Sec23ip	186	1	0.526	0.009	-1.1	0.3462463	0.066498	-4.565719
G3X928	Sec23ip	607	1	-0.4	0.222	-4.9	-0.572091	0.144616	-4.692933
G3X960	Syde1	(1 of 159,167)	1	0.201	0.087	-4.6	0.2014495	0.142526	-5.563114
G3X973	Stab1	897	1	-0.58	0.005	0.07	-0.927114	0.000841	2.118119
G3X973	Stab1	1532	1	-0.7	0.003	1.33	-1.044919	0.000455	3.55611
G3X973	Stab1	2046	1	-0.44	0.076	-3.8	-0.716487	0.026948	-2.712685
G3X9D6	Apon	(1 of 23,27,32)	1	0.352	0.268	-5.2	0.9936988	0.039421	-2.80221
G3X9K4	Ppp6r2	825	1	0.841	1E-03	3.31	0.8409918	0.00072	2.342655
G3X9T8	Cp	139	1	0.099	0.598	-6.9	-0.28923	0.131268	-5.449873
G5E850	Cyb5a	5	1	0.538	0.136	-4.2	0.784118	0.070748	-3.68865
G5E8W7	Ppt2	208	1	-1.44	0.004	1.05	-2.39839	0.000594	3.352623
H3BIX4	Nptn	(1 of 165,167,168)	1	0.922	0.05	-2.6	0.8084628	0.066022	-3.579776
H3BIX4	Nptn	81	1	1.479	0.007	-0.1	1.4307177	0.003206	0.456325
H3BIZ9	Aftph	(1 of 240,241,242)	1	0.867	0.056	-2.8	0.8671764	0.055413	-3.32351
H3BK31	Zhx1	(1 of 217,224,226,227,228,232,234,235,236,237,238)	1	-0.4	0.041	-3.1	-0.865619	0.008342	-1.350467
H3BKD4	Asap1	948	1	0.066	0.832	-6.5	0.0659131	0.849313	-6.696892
H3BL34	Ces1e	276	1	1.053	0.003	1.47	1.5826277	0.000418	4.000288
H3BLE4	Eps15	(1 of 103,105,106,107,108,109,110,112)	1	0.237	0.435	-5.8	0.1872686	0.591424	-6.423427
H3BLE4	Eps15	(1 of 138,140,149)	1	0.238	0.433	-5.8	0.1882661	0.589612	-6.420264
H3BLE4	Eps15	14	1	0.516	0.144	-4.3	0.4664854	0.213776	-5.21461
H3BLE9	Ugt3a1	(1 of 33,34)	1	0.843	0.011	-0.7	1.3801349	0.002053	1.177994
H9KUY5	Zfp865	(1 of 93,94,95,96,97,98,99,100,101,102,103,104,105,106,107,108,109,110,111,112,113)	1	-1.08	0.006	0.22	-1.080543	0.004996	-0.209172
H9KV01	Son	250	1	-0.65	0.002	1.42	-1.055181	0.000551	3.210941
H9KV01	Son	1092	1	-0.3	0.31	-5.8	-0.725921	0.043401	-3.445331
H9KV01	Son	1614	1	-0.45	0.104	-4.8	-0.848229	0.014256	-2.411148
H9KV01	Son	262	1	-0.82	0.016	-1.3	-1.271496	0.003396	0.367759
I7HIP8	Nfib	(1 of 404,408,409,412,413,417,418)	1	-0.18	0.351	-6	-0.513134	0.073701	-4.209754
I7HJQ9	Mtmr1	(1 of 658,659,661,663,665,669,670)	1	0.165	0.351	-6.2	0.1646497	0.391795	-6.603384
J3QJX3	Sel1l	556	1	0.306	0.11	-4.9	0.2108189	0.313041	-6.483531

J3QMX8	Slc30a6	(1 of 376,379,380,381,386,387,393,396)	1	-0.38	0.013	-1.7	-0.381893	0.020875	-2.933064
J3QNY6	Abcb11	(1 of 782,784)	1	-0.97	0.004	0.66	-0.861291	0.003004	0.229703
J3QP71	Bsg	(1 of 20,23,25,28,29)	1	0.785	0.027	-2.1	1.0451127	0.009327	-1.146807
J3QP71	Bsg	(1 of 126,127,129,136,138,139)	1	0.943	0.048	-2.5	1.1810266	0.024428	-2.106119
J3QPD5	Gm9602	4	1	-1.16	0.008	-0.2	-1.161933	0.005563	-0.35981
J3QPR1	Atxn1	81	1	-0.1	0.732	-6.4	-0.103855	0.771579	-6.637128
J3QPR1	Atxn1	23	1	-0.7	0.002	2.17	-0.696081	0.001469	1.014921
K4DI63	Creg1	36	1	0.276	0.133	-5.2	0.2764808	0.142526	-5.561987
K4DI63	Creg1	92	1	1.059	0.024	-2.3	1.0592269	0.013438	-2.034978
M0QWZ1	Fam193a	(1 of 992,994,995,1002)	1	0.146	0.182	-5.6	0.1456184	0.282271	-6.360258
O08553	Dpysl2	(1 of 514,517,518)	1	-0.32	0.056	-3.9	-0.800209	0.001592	0.906071
O08553	Dpysl2	512	1	-0.18	0.547	-6.9	-0.655763	0.035118	-3.645988
O08715	Akap1	(1 of 351,356,359,360,365,366,370,371)	1	0.791	0.067	-3.1	0.9868993	0.040012	-2.829153
O08750	Nfil3	(1 of 274,275)	1	-0.03	0.926	-6.5	-0.030698	0.932983	-6.729021
O09117	Sypl1	(1 of 238,239,242,244,246,247,249,251,258,259)	1	0.356	0.265	-5.2	0.356013	0.326203	-5.74599
O09159	Man2b1	369	1	-0.98	0.003	1.02	-1.413234	0.00072	2.744173
O35114	Scarb2	124	1	0.132	0.482	-6.7	-0.115211	0.603709	-7.163284
O35490	Bhmt	389	1	2.402	0.006	0.22	4.0550027	0.00072	2.634718
O35516	Notch2	175	1	-0.68	0.004	0.45	-0.682585	0.003143	-0.143528
O35887	Calu	133	1	-0.39	0.229	-5	-0.75454	0.077296	-3.822931
O35949	Elovl3	(1 of 3,4,8)	1	-1.92	7E-04	4.35	-1.920925	0.000193	5.184509
O55022	Pgrmc1	74	1	-1.89	0.01	-0.4	-1.561488	0.010966	-0.935402
O55042	Snca	72	1	0.282	0.353	-5.6	0.3439818	0.337199	-5.801309
O55042	Snca	54	1	-0.14	0.596	-6.9	-0.366858	0.35586	-6.658167
O70400	Pdlim1	(1 of 130,134,135)	1	0.162	0.268	-5.9	-0.267569	0.215291	-5.888492
O70400	Pdlim1	128	1	0.31	0.075	-4.1	-0.119732	0.658149	-7.083001
O70400	Pdlim1	248	1	-0.23	0.439	-5.8	-0.523688	0.171681	-4.931856
O88531	Ppt1	214	1	0.29	0.344	-5.6	-0.347978	0.332151	-5.783014
O88531	Ppt1	199	1	-0.53	0.054	-3.2	-1.118351	0.006638	-0.636261
O88569	Hnrnpa2b1	(1 of 198,199)	1	-0.22	0.156	-5.2	-0.700878	0.006518	-0.953547
O88783	F5	(1 of 967,968,969,971,973,974)	1	-0.33	0.223	-5.7	-0.329741	0.213776	-5.87668
O88783	F5	(1 of 774,776,777)	1	-0.21	0.283	-6	-0.207064	0.31976	-6.344518
O88783	F5	1516	1	0.217	0.272	-5.7	0.216655	0.346258	-6.217162
O88904	Hipk1	(1 of 853,854)	1	-0.07	0.807	-6.5	-0.074669	0.830655	-6.685365
O88904	Hipk1	(1 of 992,998,1001,1004,1008,1009)	1	-0.02	0.955	-6.6	-0.017174	0.958139	-6.73518
P01029	C4b	1388	1	-0.24	0.421	-5.8	-0.716604	0.087588	-3.998254
P01029	C4b	223	1	-1.25	0.007	-0.6	-1.91568	0.000897	1.836644

P01902	H2-K1	199	1	-0.55	0.005	-0.2	-1.120759	0.000455	3.507821
P04925	Prnp	198	1	1.004	0.007	-0.5	1.0035287	0.004598	-0.43989
P07361	Orm2	106	1	2.565	8E-04	3.71	2.5650735	0.000235	4.844338
P07724	Alb	294	1	-0.08	0.79	-6.5	-0.093692	0.789737	-6.655609
P08113	Hsp90b1	64	1	0.007	0.985	-7.2	-0.862483	0.019994	-2.859131
P08113	Hsp90b1	219	1	-0.84	0.015	-1.2	-1.686561	0.001345	1.811593
P08113	Hsp90b1	447	1	-0.05	0.917	-6.9	-0.852481	0.077875	-4.289251
P08226	Apoe	134	1	1.712	0.007	-0.5	2.0793971	0.001703	1.118043
P08228	Sod1	99	1	0.063	0.751	-6.8	0.304224	0.195034	-5.520899
P08607	C4bpa	(1 of 218,224)	1	-0.06	0.857	-6.5	-0.355604	0.326333	-5.747881
P08607	C4bpa	426	1	-0.05	0.8	-6.8	-0.369378	0.138977	-5.05528
P08607	C4bpa	71	1	0.048	0.878	-6.5	-0.250526	0.473937	-6.199443
P09055	Itgb1	(1 of 521,522,526)	1	-0.29	0.339	-5.5	-0.655971	0.108021	-4.285129
P09055	Itgb1	(1 of 208,209,214,215,218)	1	-0.11	0.53	-6.4	-0.457978	0.072943	-4.190927
P09055	Itgb1	408	1	-0.06	0.857	-6.5	-0.419798	0.256179	-5.44302
P0C7T6	Atxn1l	(1 of 22,23)	1	0.133	0.339	-6.4	0.1330167	0.387734	-6.753182
P0C7T6	Atxn1l	(1 of 29,30,31,33,34,37,39,40,43,46)	1	0.029	0.932	-6.5	0.0288003	0.93612	-6.730094
P0DOV2	Ifi204	(1 of 122,123,125,129,130,131,136,137,138)	1	-0.51	0.005	-0.2	-1.271593	0.000699	2.530471
P10605	Ctsb	(1 of 39,40)	1	0.636	0.102	-3.7	0.6099793	0.127695	-4.507439
P11032	Gzma	171	1	-1.58	0.005	0.15	-1.581243	0.002174	0.732574
P11438	Lamp1	80	1	0.438	0.03	-2.9	0.4028939	0.050204	-4.18027
P11679	Krt8	489	1	0.255	0.047	-3.6	0.2552974	0.076231	-4.760499
P11679	Krt8	482	1	0.25	0.061	-4	0.2496289	0.091376	-4.993772
P11881	Itpr1	2505	1	0.538	0.037	-3.2	0.6578003	0.013863	-2.346137
P12265	Gusb	629	1	0.271	0.37	-5.7	0.1522531	0.660831	-6.525853
P16301	Lcat	(1 of 43,46)	1	0.107	0.727	-6.4	-0.204369	0.555587	-6.36746
P16301	Lcat	(1 of 110,111)	1	0.488	0.159	-4.5	0.174694	0.614253	-6.462164
P23953	Ces1c	(1 of 81,82,88)	1	-0.58	0.12	-4	-1.020295	0.036972	-2.697984
P24472	Gsta4	(1 of 120,126)	1	0.59	0.034	-2.4	1.1593955	0.004224	0.042731
P25444	Rps2	(1 of 285,292,293)	1	0.192	0.525	-6.1	0.0054953	0.987893	-6.737703
P26039	Tln1	(1 of 2169,2170,2171)	1	-0.24	0.087	-4.6	-0.498058	0.011456	-2.074107
P27773	Pdia3	(1 of 86,89,91)	1	-0.5	0.049	-3	-1.190639	0.003572	0.285225
P28665	Mug1	(1 of 281,289,290,296,300)	1	0.164	0.579	-6.2	-0.414622	0.262222	-5.468079
P28665	Mug1	(1 of 995,999)	1	0.251	0.408	-5.8	-0.328007	0.35586	-5.873592
P28665	Mug1	1144	1	0.546	0.037	-3.2	0.0283076	0.915468	-7.413386
P28665	Mug1	1182	1	0.288	0.067	-3.9	-0.293304	0.099716	-4.894832
P29341	Pabpc1	485	1	0.356	0.099	-4.5	-0.059822	0.773026	-7.192663
P29341	Pabpc1	351	1	0.527	0.14	-4.3	0.0791346	0.821688	-6.678955
P29788	Vtn	88	1	-0.57	0.043	-2.8	-1.186363	0.003834	0.162801
P29788	Vtn	243	1	0.058	0.855	-6.5	-0.546892	0.156475	-4.817138
P33587	Proc	216	1	0.716	0.01	-1.2	0.4680154	0.051559	-4.219488

P33587	Proc	292	1	0.496	0.156	-4.4	0.2313645	0.507226	-6.271993
P35831	Ptpn12	(1 of 622,623,625,626,628,630,632,635,636,639,642)	1	0.49	0.158	-4.5	0.4898876	0.193844	-5.099094
P42128	Foxk1	663	1	0.047	0.807	-6.8	0.0470959	0.833028	-7.032728
P42703	Lifr	384	1	-2	0.001	3.09	-2.998257	5.60E-05	7.258781
P43883	Plin2	(1 of 56,58,59,63,64)	1	1.936	0.004	0.77	2.6536076	0.008187	-0.944201
P43883	Plin2	(1 of 120,121,122)	1	0.604	0.11	-3.9	0.6568611	0.107829	-4.280865
P43883	Plin2	(1 of 101,102)	1	2.5	0.003	1.55	3.2009259	0.004899	-0.180999
P43883	Plin2	107	1	2.283	0.002	2.66	2.984585	0.003127	0.511559
P43883	Plin2	45	1	1.347	0.022	-1.4	2.7299552	0.002103	1.326078
P48678	Lmna	(1 of 611,613,614,616,617,619,620,622,624)	1	0.248	0.102	-4.5	-0.219255	0.219863	-5.91135
P48678	Lmna	644	1	-0.16	0.288	-6.2	-0.595004	0.014256	-2.403956
P49182	Serpind1	169	1	0.225	0.17	-5.5	-0.038349	0.821688	-7.373947
P49182	Serpind1	404	1	0.209	0.487	-6	-0.1782	0.608127	-6.451576
P50247	Ahcy	2	1	0.79	0.067	-3.1	1.4669261	0.013078	-1.199382
P51141	Dvl1	(1 of 379,380,383,384,387)	1	0.443	0.186	-4.7	0.443452	0.233701	-5.327751
P52430	Pon1	(1 of 318,326,331,332,335)	1	2.059	0.008	-0.1	2.7512709	0.002053	1.354893
P52430	Pon1	255	1	1.613	1E-03	3.49	2.3043508	8.88E-05	6.618395
P58871	Tnks1bp1	260	1	-0.12	0.278	-6.1	-0.440127	0.013519	-2.314552
P58929	Gmeb2	(1 of 403,404,407)	1	-0.34	0.056	-3.6	-0.335717	0.076231	-4.551489
P62908	Rps3	242	1	-0.31	0.11	-4.9	-0.670246	0.010122	-1.876427
P70274	Selenop	(1 of 178,179)	1	0.169	0.569	-6.2	-0.171275	0.620941	-6.472326
P70274	Selenop	193	1	0.571	0.016	-1.6	0.3656829	0.119233	-5.126664
P70699	Gaa	(1 of 469,472)	1	-0.29	0.109	-4.9	-0.95786	0.00131	1.249819
P70699	Gaa	392	1	-0.34	0.039	-3.3	-1.00748	0.000897	1.829811
P70699	Gaa	885	1	-0.73	0.003	0.9	-1.401131	0.000113	6.041574
P70699	Gaa	142	1	-1.17	8E-04	3.94	-1.840355	5.60E-05	7.496683
P83741	Wnk1	(1 of 1944,1945,1946)	1	0.429	0.17	-5	0.2492371	0.384645	-6.352397
P83741	Wnk1	(1 of 2365,2367,2372,2376,2377)	1	0.399	0.225	-4.9	0.230758	0.507226	-6.274228
P83741	Wnk1	1930	1	0.239	0.432	-5.8	0.0486697	0.890658	-6.715502
P83741	Wnk1	1844	1	0.409	0.009	-1.1	0.1913915	0.24528	-6.213387
P83741	Wnk1	1860	1	0.093	0.759	-6.4	-0.076052	0.828414	-6.683417
P97364	Sephs2	(1 of 434,444,448,451,452)	1	0.544	0.133	-4.2	0.3925131	0.28746	-5.574311
P97426	Ear1	113	1	-0.85	0.058	-2.8	-0.85101	0.058242	-3.393172
Q01339	Apoh	(1 of 159,164,169)	1	1.16	0.059	-3.4	1.2757704	0.035118	-3.087431
Q01705	Notch1	900	1	-0.4	0.078	-3.8	-0.401739	0.104405	-4.676458
Q02614	Sap30bp	(1 of 231,232,233,236,238,239,240,241,242,244,245)	1	-0.6	0.02	-2.3	-0.597127	0.015064	-2.488541
Q03311	Bche	372	1	1.441	8E-04	3.76	2.4807446	4.39E-05	8.096973

Q05BG1	Cnot4	313	1	0.369	0.254	-5.1	0.3962192	0.283763	-5.556605
Q06890	Clu	(1 of 291,292)	1	-0.02	0.951	-6.5	-0.254161	0.468057	-6.185269
Q06890	Clu	329	1	0.5	0.087	-4.3	0.2898512	0.307292	-6.290179
Q07456	Ambp	235	1	0.186	0.537	-6.1	0.0192946	0.953863	-6.734444
Q07456	Ambp	229	1	0.349	0.27	-5.2	0.1828238	0.599895	-6.43736
Q07797	Lgals3bp	71	1	-1.41	7E-04	5.93	-2.151658	4.39E-05	8.370117
Q07968	F13b	(1 of 543,548,549)	1	0.597	0.004	0.46	0.4743186	0.021414	-2.979763
Q3LFS7	Ceacam1	(1 of 72,73)	1	0.131	0.664	-6.3	0.2916418	0.403532	-6.032258
Q3TBU7	Agfg2	(1 of 178,186,188,192,193,194,195,199,201)	1	0.175	0.556	-6.1	-0.024622	0.942801	-6.732217
Q3TC93	Hs1bp3	280	1	0.219	0.469	-5.9	-0.163978	0.635776	-6.493472
Q3TCN2	Plbd2	(1 of 514,522)	1	-0.68	0.089	-3.5	-0.89223	0.051555	-3.216918
Q3TJI8	Hsd11b1	131	1	0.17	0.567	-6.2	0.4520954	0.225322	-5.285379
Q3TN85	Rad23a	(1 of 123,125,128,129,130,131,132,133,136,138,140,143,144,146,147)	1	0.427	0.201	-4.8	0.5587231	0.151148	-4.758758
Q3TQC7	Entpd5	(1 of 250,251,257,258)	1	2.381	0.006	0.2	3.3657668	0.001155	2.061235
Q3TVI8	Pbxip1	453	1	-1.06	0.037	-2.1	-1.056945	0.033924	-2.557344
Q3TWZ5	Txndc11	308	1	-0.95	0.047	-2.5	-0.952329	0.043172	-2.968007
Q3TZR9	Atf7	444	1	-0.24	0.432	-5.8	-0.238849	0.496092	-6.244101
Q3U332	Rin3	(1 of 350,351)	1	0.487	0.16	-4.5	0.2028686	0.558579	-6.372516
Q3U7T5	Ctsc	(1 of 50,55,60)	1	-0.69	0.024	-1.9	-1.721386	0.001037	2.209363
Q3U9N4	Grn	(1 of 278,279,283)	1	0.111	0.48	-6.6	-0.662256	0.015097	-2.234676
Q3U9N4	Grn	385	1	-0.86	0.002	2.31	-1.663876	0.000104	6.22333
Q3UEQ1	Inpp4a	184	1	-0.61	0.109	-3.9	-0.609323	0.127811	-4.510638
Q3UH06	Rreb1	(1 of 1097,1099,1100,1101,1103,1106,1108,1111,1112)	1	0.386	0.238	-5	0.3857079	0.296596	-5.606704
Q3UH06	Rreb1	1000	1	-0.14	0.2	-5.7	-0.140004	0.301982	-6.43341
Q3UHJ0	Aak1	360	1	0.398	0.159	-5.4	0.1251213	0.730218	-7.300413
Q3UIA2	Arhgap17	803	1	0.135	0.655	-6.3	-0.266994	0.44505	-6.13424
Q3UN10	Wfs1	(1 of 667,669,670,673,674,675)	1	-1.57	0.016	-0.9	-2.10311	0.004487	0.306772
Q3UR91	Pum2	664	1	-0.62	0.106	-3.8	-0.619973	0.122836	-4.458836
Q3UR91	Pum2	85	1	-0.38	0.245	-5.1	-0.37708	0.305552	-5.647536
Q3USK2	Csnk1d	(1 of 382,383,384,387)	1	-0.14	0.322	-6.1	-0.144562	0.397372	-6.618689
Q3UYJ1	Gata4	(1 of 124,132,136,137,140,141,144,145,148,149,150,151,152,153,154)	1	-0.58	0.12	-4	-0.576116	0.142526	-4.673147
Q3UYJ1	Gata4	(1 of 200,206,209,211,212,215,216)	1	-0.18	0.547	-6.1	-0.180387	0.603942	-6.44489
Q3V1K7	Slco2b1	151	1	0.591	0.052	-3.5	0.6409213	0.014441	-2.168377
Q4G0F8	Ubn1	(1 of 875,876,878,880,881,882,884)	1	-0.48	0.165	-4.5	-0.478173	0.203145	-5.156968

Q4PZA2	Ece1	632	1	0.808	0.027	-2.5	0.7220857	0.033221	-3.326576
Q4VBF8	Sipa1l1	(1 of 1114,1116,1117)	1	1.21	0.028	-1.7	1.2097796	0.022556	-2.006847
Q52KG4	Zbtb45	262	1	-0.24	0.31	-5.8	-0.244899	0.346258	-6.218449
Q571K4	Tab3	(1 of 402,405,407,408,411,412,413,415)	1	0.481	0.067	-3.6	0.4809401	0.076231	-4.253135
Q59J78	Ndufaf2	(1 of 143,147,148,149)	1	0.112	0.379	-6.5	0.2866177	0.103418	-5.14752
Q5DTZ3	Mrtfb	(1 of 207,209,214,216,217,222,223,225)	1	0.546	0.132	-4.2	0.5461825	0.156583	-4.820639
Q5DTZ3	Mrtfb	245	1	0.603	0.004	0.51	0.6033527	0.003729	-0.428065
Q5F2E7	Nufip2	(1 of 369,373,374,376,378,379,380,381,382,383,384,385,386,389,391,393,394,395)	1	0.181	0.156	-5.4	-0.13527	0.396642	-6.777403
Q5RIM6	Ncor1	(1 of 1914,1918)	1	-0.92	0.049	-2.6	-0.924978	0.04645	-3.080103
Q5RIM6	Ncor1	(1 of 45,46,51,54)	1	0.037	0.911	-6.5	0.0366841	0.919967	-6.725191
Q5RIM6	Ncor1	(1 of 1894,1900,1901,1902,1906)	1	0.085	0.781	-6.4	0.0850861	0.809844	-6.669861
Q5RIM6	Ncor1	(1 of 1055,1056)	1	0.112	0.482	-6.6	0.111918	0.531113	-6.906935
Q5RIM6	Ncor1	(1 of 2036,2040,2042,2052,2053,2055)	1	0.024	0.941	-6.5	0.0243528	0.942801	-6.732342
Q5RIM6	Ncor1	1497	1	-0.05	0.759	-7.1	-0.045975	0.779899	-7.343483
Q5RIM6	Ncor1	1878	1	0.193	0.524	-6.1	0.1926278	0.581447	-6.406285
Q5RIM6	Ncor1	14	1	-0.04	0.897	-6.5	-0.041268	0.910135	-6.721803
Q5RJH6	Smg7	578	1	-0.04	0.682	-7	-0.044394	0.742219	-7.311977
Q5SFM8	Rbm27	546	1	-0.65	0.051	-3.1	-0.653029	0.043951	-3.483543
Q5SQA7	Tle1	(1 of 29,31,34,35,37,38,40,41,42,43)	1	-0.73	0.079	-3.3	-0.729089	0.083957	-3.940181
Q5SUH7	Clint1	(1 of 256,258,259)	1	0.04	0.738	-7.1	-0.141086	0.307183	-6.457071
Q5SUH7	Clint1	320	1	0.21	0.08	-4.4	0.028538	0.838287	-7.383443
Q5XJV5	Ncoa6	1646	1	-0.49	0.018	-1.9	-0.492138	0.023203	-2.847578
Q61001	Lama5	2049	1	-0.44	0.067	-3.9	-0.440953	0.064885	-4.312666
Q61009	Scarb1	(1 of 286,290)	1	-0.58	0.12	-4	-1.099606	0.030147	-2.397928
Q61009	Scarb1	(1 of 326,332,333)	1	-0.47	0.17	-4.6	-0.993559	0.039421	-2.802763
Q61029	Tmpo	275	1	0.291	0.516	-6.4	0.1241665	0.745838	-6.964415
Q61169	Gata6	(1 of 499,502,503,505,509,511,512,513,514,515,517,521)	1	-1.17	0.03	-1.8	-1.167488	0.02524	-2.153535
Q61191	Hcfc1	(1 of 1235,1238,1240,1241,1243,1245,1246,1247)	1	-0.61	0.109	-3.9	-1.004314	0.038172	-2.760389
Q61191	Hcfc1	(1 of 1055,1058,1061,1062)	1	-0.5	0.156	-4.4	-0.8908	0.051559	-3.222959
Q61191	Hcfc1	(1 of 1223,1224)	1	0.171	0.458	-6.5	-0.23453	0.307292	-6.288777
Q61191	Hcfc1	(1 of 1138,1139,1141,1143)	1	-0.12	0.419	-6.6	-0.559745	0.010529	-1.934433

Q61191	Hcfc1	(1 of 771,775,779,784,787,788,789)	1	-0.88	0.01	-0.5	-1.344704	0.002739	0.744993
Q61191	Hcfc1	(1 of 1494,1495,1497,1499,1500,1506,1516)	1	-0.72	0.081	-3.4	-1.11149	0.02927	-2.354329
Q61191	Hcfc1	(1 of 562,563,566,569,574,575)	1	-0.52	0.016	-2	-0.960534	0.001355	1.158326
Q61191	Hcfc1	(1 of 515,517,518,522)	1	0.384	0.037	-3.2	-0.060891	0.725585	-7.296616
Q61191	Hcfc1	(1 of 858,861,863)	1	-0.09	0.764	-6.4	-0.454322	0.223739	-5.274445
Q61191	Hcfc1	(1 of 794,797,800,801)	1	-0.52	0.005	0.05	-0.964569	0.000556	3.084611
Q61191	Hcfc1	480	1	-0.58	0.12	-4	-0.97178	0.04139	-2.889497
Q61191	Hcfc1	579	1	-0.74	0.002	1.67	-1.180044	0.000332	4.13898
Q61191	Hcfc1	1220	1	0.176	0.552	-6.1	-0.384575	0.297241	-5.612083
Q61191	Hcfc1	806	1	0.036	0.737	-7.1	-0.408718	0.017298	-2.675209
Q61191	Hcfc1	808	1	-0.2	0.11	-4.9	-0.644507	0.003206	-0.188573
Q61191	Hcfc1	490	1	-0.37	0.148	-4.8	-0.845658	0.024464	-2.582243
Q61191	Hcfc1	685	1	0.06	0.883	-6.9	-0.319513	0.384868	-6.354978
Q61191	Hcfc1	726	1	-0.48	0.007	-0.8	-0.920628	0.00072	2.405713
Q61191	Hcfc1	1148	1	-0.46	0.005	-0.2	-0.907268	0.000647	2.65829
Q61471	Tob1	(1 of 171,172,176,178,179,181,185)	1	0.178	0.549	-6.1	0.1782841	0.608127	-6.451321
Q61646	Hp	(1 of 150,152)	1	-0.85	0.058	-2.8	-2.448091	0.002894	0.911837
Q61827	Mafk	(1 of 133,134,135,138)	1	-0.58	0.056	-3.6	-0.581555	0.043806	-3.786187
Q61827	Mafk	153	1	-0.28	0.084	-4.3	-0.281783	0.120752	-5.147926
Q62261	Sptbn1	2323	1	0.36	0.014	-1.8	0.3491898	0.026948	-3.294425
Q62311	Taf6	(1 of 480,481,483,485)	1	0.014	0.911	-7.2	0.0144419	0.919967	-7.414751
Q62311	Taf6	(1 of 586,587,589,590,594,595,600,602)	1	-0.22	0.475	-5.9	-0.215858	0.531113	-6.32785
Q62419	Sh3gl1	284	1	0.106	0.727	-6.4	0.0234627	0.943661	-6.732747
Q63880	Ces3a	313	1	-0.78	0.017	-1.4	-2.316689	0.000567	3.462067
Q63886	Ugt1a1	91	1	0.829	0.02	-2.3	0.7586203	0.030078	-3.433477
Q64511	Top2b	1200	1	-1.07	0.037	-2.1	-1.311478	0.017983	-1.67079
Q68FG2	Sptbn2	(1 of 2100,2101,2106,2111)	1	0.369	0.098	-4.1	-0.05133	0.818531	-7.022383
Q68FG2	Sptbn2	2359	1	0.344	0.094	-4.4	-0.061152	0.769855	-7.188626
Q69ZA1	Cdk13	(1 of 1278,1285,1286,1287,1288,1289,1291)	1	-0.34	0.11	-4.4	-0.339432	0.1519	-5.191846
Q69ZL1	Fgd6	494	1	0.992	0.043	-2.3	0.9922157	0.039493	-2.808077
Q6A058	Armcx2	366	1	1.016	0.041	-2.2	1.0162369	0.037159	-2.713767
Q6A0A2	Larp4b	(1 of 631,632,633)	1	-0.01	0.973	-6.6	-0.539704	0.160474	-4.852645
Q6A0A2	Larp4b	(1 of 41,46,50,51)	1	-0.24	0.132	-5	-0.74551	0.005286	-0.646688
Q6DFV5	Helz	1668	1	0.726	0.079	-3.3	0.7261315	0.084694	-3.953904
Q6DFZ1	Gbf1	(1 of 1857,1858)	1	0.299	0.263	-5.6	0.08263	0.772547	-6.986265
Q6DFZ1	Gbf1	(1 of 1780,1781,1782,1783)	1	0.083	0.598	-6.8	-0.151578	0.3637	-6.515971

Q6DID3	Scaf8	819	1	-0.59	0.113	-3.9	-0.59449	0.135035	-4.583053
Q6KCD5	Nipbl	(1 of 1678,1679)	1	0.334	0.181	-5.4	0.3339417	0.179482	-5.668944
Q6KCD5	Nipbl	(1 of 160,161,162)	1	-0.03	0.917	-6.5	-0.034927	0.922643	-6.726385
Q6P5E4	Uggt1	(1 of 266,271,276)	1	0.115	0.706	-6.4	-0.353582	0.328501	-5.757222
Q6P6J9	Txndc15	(1 of 138,145,150,151,153)	1	0.824	0.039	-3	0.8710115	0.037638	-3.528469
Q6PAL7	Ahdc1	(1 of 1574,1588,1590,1592,1593)	1	0.023	0.918	-6.9	0.0232489	0.922643	-7.070159
Q6PB44	Ptpn23	(1 of 880,881,882,885,891,892,894)	1	0.748	0.075	-3.2	0.6713908	0.103166	-4.211452
Q6PD26	Pigs	372	1	0.022	0.919	-7.2	-0.775669	0.002739	0.107589
Q6PDI5	Ecpas	(1 of 1669,1670)	1	0.214	0.479	-5.9	0.2248902	0.518634	-6.295638
Q6PIJ4	Nfrkb	(1 of 1073,1076,1077,1084)	1	-0.11	0.718	-6.4	-0.110367	0.755978	-6.624365
Q6PIJ4	Nfrkb	(1 of 1025,1027,1030,1031,1036,1037)	1	0.346	0.323	-5.9	0.3455294	0.317753	-6.09538
Q6PIJ4	Nfrkb	(1 of 1166,1167,1170,1171,1172,1174)	1	0.046	0.744	-7	0.0456289	0.78714	-7.205254
Q6PIJ4	Nfrkb	1064	1	-0.13	0.364	-6.3	-0.132413	0.442784	-6.722613
Q6PIJ4	Nfrkb	838	1	-0.45	0.037	-3.2	-0.446062	0.034653	-3.621229
Q6PIJ4	Nfrkb	1270	1	-0.03	0.938	-6.5	-0.025425	0.941654	-6.731835
Q6XLQ8	Calu	133	1	-0.81	0.003	1.26	-1.133062	0.000841	2.11076
Q78PY7	Snd1	909	1	0.392	0.231	-5	-0.090632	0.796061	-6.660825
Q7M739	Tpr	(1 of 2054,2055,2057)	1	0.002	0.994	-6.9	-0.164198	0.476248	-6.572806
Q7M739	Tpr	(1 of 1656,1657,1658,1662,1668,1672,1673,1675)	1	-0.06	0.79	-7	-0.228241	0.328997	-6.383767
Q7TN29	Smap2	197	1	-0.1	0.697	-6.7	-0.25854	0.336658	-6.184319
Q7TPN9	Prr14	319	1	-0.47	0.054	-3.2	-0.469335	0.069023	-4.105223
Q7TQE2	Zyx	(1 of 206,207,210)	1	0.383	0.239	-5	0.4260048	0.250307	-5.412885
Q7TT18	Atf7ip	(1 of 1022,1025,1026,1027,1028,1030,1031,1032,1036)	1	-0.13	0.658	-6.3	-0.133834	0.705312	-6.572577
Q7TT50	Cdc42bpb	(1 of 968,969,970,972,976,979)	1	0.585	0.064	-3.5	0.341977	0.21503	-5.633897
Q80U93	Nup214	(1 of 634,635,637,639)	1	-0.11	0.65	-7	-0.257499	0.332151	-6.570148
Q80U93	Nup214	(1 of 1336,1337,1342,1345,1347)	1	0.205	0.494	-6	0.1375443	0.699294	-6.563584
Q80U93	Nup214	(1 of 1109,1115,1116,1118,1120,1121)	1	0.164	0.579	-6.2	0.0541677	0.875976	-6.710163
Q80U93	Nup214	(1 of 645,646,648,651,652,655,656)	1	0.024	0.872	-7.1	-0.120218	0.50169	-6.844029

Q80U93	Nup214	(1 of 1556,1557,1559,1560,1562,1566,1567,1569,1573,1574,1576,1580,1586)	1	-0.47	0.008	-0.9	-0.611043	0.005143	-0.894215
Q80U93	Nup214	(1 of 506,507)	1	-0.17	0.135	-5.2	-0.309181	0.049506	-4.159988
Q80U93	Nup214	(1 of 1313,1314,1316,1317,1319,1320)	1	-0.19	0.151	-5.4	-0.336795	0.055822	-4.329447
Q80U93	Nup214	504	1	-0.12	0.239	-5.9	-0.265468	0.07331	-4.70831
Q80U93	Nup214	1362	1	-0.3	0.025	-2.6	-0.44795	0.012733	-2.22696
Q80UF7	Ticam1	(1 of 310,313,314,315,316)	1	0.262	0.129	-4.9	0.2618029	0.164262	-5.563565
Q80VP1	Epn1	(1 of 411,415,416,418,419,420)	1	0.471	0.067	-3.6	0.2586634	0.363806	-6.287676
Q80X50	Ubap2l	(1 of 875,879,883)	1	0.491	0.048	-3	0.4691682	0.06894	-4.101268
Q80X50	Ubap2l	(1 of 798,799,802,803,804)	1	0.19	0.178	-5.6	0.1028758	0.514601	-7.024042
Q80X50	Ubap2l	(1 of 480,481,482,487,490,491,495,496,497)	1	0.819	0.063	-2.9	0.646051	0.111664	-4.332771
Q80X81	Acat3	12	1	1.229	8E-04	3.8	1.3616115	0.00072	2.436313
Q80YR4	Znf598	(1 of 560,563,564,568,569,575,578,579)	1	-0.01	0.954	-6.9	-0.216113	0.368174	-6.299973
Q80YX8	Mup21	65	1	-2.35	0.006	0.17	-2.348045	0.003206	0.748499
Q810N5		(1 of 2,3,5)	1	1.572	0.016	-0.9	1.5719652	0.010777	-0.90714
Q8BFR4	Gns	(1 of 267,270,272,273)	1	0.042	0.8	-7.2	-0.238293	0.214861	-6.063819
Q8BFW7	Lpp	(1 of 210,212,213,215,216,217,218)	1	0.335	0.284	-5.3	0.2440793	0.485606	-6.224267
Q8BFW7	Lpp	312	1	1.131	0.033	-1.9	1.040521	0.035118	-2.619942
Q8BFW7	Lpp	11	1	0.566	0.006	-0.4	0.5995486	0.008275	-1.609246
Q8BG19	Tmtc4	499	1	-0.28	0.36	-5.6	-0.277449	0.427164	-6.091592
Q8BGD9	Eif4b	352	1	0.283	0.043	-3.5	0.1053524	0.50169	-6.998721
Q8BGD9	Eif4b	355	1	0.113	0.49	-6.8	-0.064834	0.700214	-7.271747
Q8BGD9	Eif4b	495	1	0.302	0.027	-2.7	0.1247199	0.386173	-6.748723
Q8BGQ4	Pomt2	655	1	0.577	0.049	-3.4	0.5769975	0.040229	-3.625785
Q8BGS1	Epb41l5	(1 of 385,386,387,398)	1	-0.53	0.137	-4.2	-0.789156	0.069929	-3.665997
Q8BH35	C8b	45	1	-1.56	0.016	-0.9	-3.005937	0.001549	1.675063
Q8BH80	Vapb	(1 of 143,144)	1	1.083	7E-04	4.66	1.3681604	0.000297	4.459673
Q8BHL3	Tbc1d10b	(1 of 32,43,44,46,47)	1	-0.37	0.1	-4.5	-0.369163	0.104043	-4.952075
Q8BI72	Cdkn2aip	(1 of 317,318,319)	1	0.157	0.239	-5.9	0.1574071	0.303245	-6.438537
Q8BI72	Cdkn2aip	(1 of 304,305,306,308,310,311,314,315)	1	0.014	0.936	-7.2	0.0136519	0.936087	-7.418649
Q8BI72	Cdkn2aip	(1 of 187,188,189,190,192,196,198,199)	1	0.064	0.723	-7.1	0.06392	0.730573	-7.301265
Q8BI72	Cdkn2aip	(1 of 395,396)	1	0.1	0.742	-6.4	0.0999623	0.779447	-6.644416
Q8BI72	Cdkn2aip	328	1	0.082	0.537	-6.7	0.0819728	0.614362	-7.030478

Q8BI84	Mia3	(1 of 250,253,254,257)	1	0.207	0.281	-6.2	-0.096441	0.620941	-7.189618
Q8BI84	Mia3	1729	1	1.165	0.004	0.64	0.8613217	0.005933	-1.10639
Q8BI84	Mia3	1754	1	0.911	0.002	1.95	0.6074721	0.006701	-1.30418
Q8BI84	Mia3	1766	1	0.692	0.007	-0.5	0.3763327	0.062634	-4.260957
Q8BI84	Mia3	633	1	0.126	0.527	-6.4	-0.187294	0.41174	-6.427643
Q8BJ05	Zc3h14	(1 of 369,370,373)	1	-0.41	0.219	-4.9	-0.781056	0.071294	-3.70245
Q8BJ05	Zc3h14	(1 of 75,77,78,81,82)	1	-0.13	0.682	-6.3	-0.499037	0.187682	-5.053845
Q8BJ05	Zc3h14	(1 of 132,133,134,135)	1	0.135	0.465	-6.3	-0.272436	0.245298	-5.792713
Q8BJ05	Zc3h14	360	1	-0.05	0.727	-7	-0.419838	0.039744	-3.606371
Q8BJ05	Zc3h14	255	1	0.194	0.172	-5.3	-0.179932	0.305552	-6.277729
Q8BJ71	Nup93	(1 of 51,52,55)	1	0.876	0.106	-4.8	0.3298067	0.518902	-7.033818
Q8BJS4	Sun2	(1 of 648,651,652,654,655)	1	-0.09	0.857	-6.9	-0.463025	0.104931	-4.686353
Q8BKI2	Tnrc6b	(1 of 304,310,311,312,314)	1	0.119	0.696	-6.3	0.1188502	0.738316	-6.606676
Q8BKI2	Tnrc6b	(1 of 1158,1159,1161)	1	0.308	0.149	-4.8	0.3078583	0.196025	-5.527754
Q8BM88	Ctso	98	1	1.772	7E-04	4.76	2.5058743	5.60E-05	7.171508
Q8BMB0	Emsy	(1 of 520,521,525)	1	-0.31	0.315	-5.4	-0.311175	0.376465	-5.948131
Q8BMB0	Emsy	(1 of 498,499,500,502,505)	1	-0.98	0.011	-0.7	-0.981124	0.008857	-1.073438
Q8BMB0	Emsy	192	1	-0.7	0.003	1.25	-0.699764	0.002141	0.464348
Q8BMB0	Emsy	1069	1	-0.81	0.002	1.59	-0.810146	0.001386	1.100206
Q8BMB0	Emsy	200	1	-0.68	0.088	-3.5	-0.684389	0.098791	-4.149714
Q8BNV8	A530064D06Rik	(1 of 147,148)	1	-0.61	0.108	-3.8	-0.613515	0.125935	-4.490227
Q8BP97	Rhbdd3	(1 of 380,382,385)	1	0.081	0.792	-6.5	0.08102	0.818531	-6.676142
Q8BTI8	Srrm2	(1 of 2122,2123,2131)	1	-0.25	0.347	-6.4	-0.865083	0.026948	-3.30258
Q8BTI8	Srrm2	2341	1	-0.65	0.004	0.48	-1.259471	0.000332	4.199532
Q8BTI8	Srrm2	2205	1	-0.31	0.181	-5.6	-0.922417	0.012163	-2.153966
Q8BTI8	Srrm2	2414	1	-0.64	0.1	-3.7	-1.365677	0.015991	-1.500857
Q8BTJ4	Enpp4	281	1	-1.57	7E-04	6.38	-1.569568	8.88E-05	6.478766
Q8BTJ4	Enpp4	261	1	-1.5	0.005	0.65	-1.495285	0.002535	0.854478
Q8BU11	Tox4	(1 of 405,406,407,409,413,420)	1	0.395	0.229	-5	0.3950774	0.284419	-5.562065
Q8BU25	Pamr1	267	1	-0.61	0.11	-3.9	-0.606002	0.12895	-4.526825
Q8BUN3	Qrich1	(1 of 365,366,367)	1	-0.15	0.315	-6.3	-0.149256	0.35586	-6.653584
Q8BVZ1	Plin5	(1 of 50,52,55,56,60)	1	1.575	0.016	-0.9	1.9375414	0.005713	-0.030022
Q8BX02	Kank2	346	1	-0.14	0.533	-6.4	-0.691038	0.028325	-2.785959
Q8BX02	Kank2	421	1	-0.2	0.498	-6	-0.78414	0.070748	-3.688552
Q8BYB9	Poglut1	(1 of 205,206)	1	-0.59	0.115	-4	-0.589044	0.137867	-4.609714
Q8BYK6	Ythdf3	201	1	-0.21	0.13	-5.2	-0.612078	0.004383	-0.653379
Q8BYK6	Ythdf3	205	1	-0.05	0.682	-7.1	-0.455125	0.012592	-2.205601
Q8BYK6	Ythdf3	167	1	0.058	0.855	-6.5	-0.335001	0.347834	-5.842117
Q8BYU6	Tor1aip2	(1 of 320,323,327,331)	1	0.407	0.085	-4	0.3595692	0.153664	-5.211904
Q8C0C0	Zhx2	(1 of 150,155,159,166,168,172,173,180)	1	-0.24	0.225	-5.4	-0.987988	0.008067	-0.914754

Q8C0C0	Zhx2	(1 of 264,265)	1	-0.54	0.136	-4.2	-1.065592	0.03315	-2.524662
Q8C0C3	Trappc12	(1 of 232,234,236,237,238,239)	1	1.111	0.034	-2	0.9561751	0.042704	-2.952405
Q8C0Q2	Zhx3	(1 of 581,585,587,588,591,595)	1	-0.49	0.157	-4.4	-1.522743	0.011738	-1.041593
Q8C0Q2	Zhx3	730	1	-0.42	0.007	-0.8	-1.147838	0.000586	2.90085
Q8C0Q2	Zhx3	236	1	0.103	0.718	-6.7	-0.676989	0.1202	-4.865324
Q8C180	Frs2	(1 of 326,327,328,329,330,331,333,339)	1	0.892	0.19	-5.2	0.8917475	0.146547	-5.138898
Q8C341	Suco	(1 of 525,527,531,533,534)	1	0.177	0.338	-6.4	0.177292	0.351011	-6.639111
Q8C5R2	Proser2	(1 of 381,384,385,389,390)	1	0.618	0.004	0.52	0.5006685	0.020566	-2.901305
Q8C7E7	Stbd1	160	1	0.792	0.061	-3.4	0.4888406	0.178487	-5.400633
Q8C8Z9	Dtnb	608	1	0.539	0.008	-0.9	0.376624	0.098791	-5.082812
Q8CBB6	Hist1h2bq	113	1	-0.74	0.007	-0.5	-1.032756	0.013874	-2.097591
Q8CCH2	Nhlrc3	208	1	-0.78	0.005	0.32	-0.65635	0.014225	-2.129522
Q8CF89	Tab1	(1 of 389,393,394,397,398,399)	1	0.337	0.076	-4.1	0.3369848	0.092266	-4.80083
Q8CFE4	Scyl2	(1 of 741,743,744,745,747,751,752,759,760,765)	1	0.574	0.12	-4	0.1548394	0.65748	-6.518882
Q8CFE4	Scyl2	630	1	1.235	0.027	-1.6	1.040431	0.035118	-2.620287
Q8CGM2	Rp1l1	(1 of 3,4)	1	0.351	0.269	-5.2	0.3505147	0.330569	-5.771359
Q8CHH5	Bicral	590	1	-0.45	0.181	-4.7	-0.452676	0.225122	-5.282528
Q8CHI8	Ep400	709	1	0.003	0.996	-6.6	0.0026441	0.99427	-6.737924
Q8CHS8	Vps37a	(1 of 171,172,174,178,180,181,182,183,184,185,187)	1	0.236	0.079	-4.4	0.1860259	0.183314	-5.876876
Q8CI51	Pdlim5	(1 of 118,119,120,121)	1	0.394	0.229	-5	0.2355057	0.50169	-6.256633
Q8CI51	Pdlim5	(1 of 110,111)	1	0.365	0.014	-1.7	0.222619	0.117661	-5.31071
Q8CI51	Pdlim5	(1 of 208,210,211,214,216)	1	0.649	0.098	-3.7	0.4910899	0.193085	-5.093149
Q8CI51	Pdlim5	90	1	0.567	0.02	-2	0.4023883	0.087588	-4.733321
Q8CI51	Pdlim5	115	1	0.63	0.003	0.7	0.4874706	0.016051	-2.573914
Q8JZK9	Hmgcs1	(1 of 506,507,510,512,516)	1	1.557	0.016	-0.9	1.9557947	0.005593	0.008774
Q8JZZ0	Ugt3a2	54	1	0.708	0.004	0.52	1.0837644	0.00055	3.270716
Q8K099	Lrit1	(1 of 604,605,608)	1	-0.35	0.034	-3.1	-0.350301	0.040972	-3.894037
Q8K0E8	Fgb	378	1	-0.88	0.004	0.71	-1.320204	0.000884	2.223496
Q8K0L9	Zbtb20	(1 of 461,464,465,472,473)	1	-0.23	0.453	-5.9	-0.94261	0.043806	-3.007614
Q8K0L9	Zbtb20	(1 of 444,447)	1	-0.62	0.016	-1.9	-1.159031	0.000873	2.021323
Q8K0L9	Zbtb20	(1 of 303,304,305,308,309)	1	-0.42	0.204	-4.8	-1.024554	0.036538	-2.681463
Q8K0L9	Zbtb20	(1 of 260,263,268,272)	1	-0.1	0.735	-6.4	-0.817772	0.064407	-3.538547
Q8K0L9	Zbtb20	(1 of 484,485)	1	-0.27	0.037	-3.2	-0.810069	0.001369	1.12459

Q8K0L9	Zbtb20	480	1	-0.29	0.035	-3.1	-0.825819	0.001355	1.146431
Q8K0L9	Zbtb20	449	1	-0.48	0.014	-1.8	-1.016621	0.000897	1.83367
Q8K0L9	Zbtb20	436	1	-0.57	0.006	-0.5	-1.109202	0.000551	3.148671
Q8K2Q9	Shtn1	(1 of 487,492,493,494,496,501,502,504)	1	0.686	0.002	1.57	0.448591	0.020846	-2.924104
Q8K3X4	Irf2bpl	(1 of 195,198,199,200,203,204,207)	1	-0.33	0.294	-5.4	-0.326709	0.35586	-5.879403
Q8K3Z9	Pom121	(2 of 649,650,653,658,660,661,664,665,667,668,670)	2	-0.23	0.115	-4.8	-0.22924	0.177728	-5.653918
Q8QZR3	Ces2a	272	1	-0.72	0.028	-2.8	-1.558163	0.00125	1.326722
Q8R066	C1qtnf4	(1 of 178,182)	1	0.139	0.654	-6.7	0.1392912	0.645915	-6.860488
Q8R080	Gtse1	(1 of 267,268)	1	0.413	0.03	-2.6	0.413417	0.040509	-3.640169
Q8R084	Ugt2b1	98	1	-0.5	0.023	-2.2	-1.271527	0.000883	2.253567
Q8R0F3	Sumf1	140	1	-0.06	0.819	-7	-0.064179	0.810329	-7.220909
Q8R121	Serpina10	(1 of 280,281,282)	1	0.057	0.82	-6.8	-0.396717	0.143364	-5.110131
Q8R143	Pttg1ip	41	1	0.788	0.068	-3.1	0.9636015	0.042146	-2.922386
Q8R242	Ctbs	285	1	-1.16	0.053	-3.2	-1.58196	0.012163	-1.536325
Q8R3E3	Wipi1	(1 of 389,390,391,394,395,400)	1	0.139	0.344	-6.4	0.1392452	0.384645	-6.743123
Q8R4R6	Nup35	53	1	-0.42	0.097	-4.5	-0.662956	0.016971	-2.384256
Q8R4U0	Stab2	1512	1	-0.28	0.16	-4.9	-0.465309	0.069929	-4.125914
Q8R4U0	Stab2	910	1	-0.44	0.186	-4.7	-0.580538	0.141334	-4.651428
Q8VBZ3	Clptm1	297	1	0.153	0.593	-6.6	-0.096625	0.717517	-6.935686
Q8VC34	Rpap2	(1 of 4,9,13,14)	1	0.956	0.047	-2.4	0.9564343	0.042704	-2.951355
Q8VC97	Upb1	392	1	1.922	7E-04	4.65	2.566832	0.000214	5.015388
Q8VCF0	Mavs	(1 of 309,310,314,315,316,319,321,324)	1	0.801	0.001	2.84	0.8696328	0.002337	0.337088
Q8VCF0	Mavs	298	1	0.154	0.465	-6.3	0.3653235	0.187682	-5.469724
Q8VCF0	Mavs	330	1	0.969	0.005	0.05	1.1408073	0.003243	0.074162
Q8VCF0	Mavs	370	1	0.628	0.002	1.55	0.6969903	0.003834	-0.477734
Q8VCF0	Mavs	373	1	0.363	0.022	-2.4	0.4322044	0.016199	-2.587986
Q8VCF0	Mavs	343	1	0.306	0.086	-4.3	0.2983858	0.1281	-5.22258
Q8VCI0	Plbd1	529	1	-1.34	7E-04	4.85	-2.292171	4.39E-05	8.112516
Q8VCI0	Plbd1	446	1	-1.66	0.016	-1.3	-2.672605	0.001454	1.654352
Q8VCN5	Cth	(1 of 54,55,60)	1	-0.05	0.883	-6.5	1.0461394	0.03487	-2.59845
Q8VCU1	Ces3b	313	1	-1.09	0.036	-2	-2.753988	0.002053	1.358543
Q8VDZ4	Zdhhc5	386	1	0.475	0.075	-3.7	0.3106131	0.186285	-5.454897
Q8VHR5	Gatad2b	(1 of 487,489,490,495,496,498)	1	-0.22	0.458	-5.9	-0.224672	0.518634	-6.296428
Q8VHR5	Gatad2b	(1 of 525,526)	1	-0.09	0.832	-7	-0.091508	0.811996	-7.22216
Q8VHR5	Gatad2b	(1 of 288,289,290,298,303,304,305,306)	1	-0.37	0.257	-5.1	-0.36536	0.317298	-5.702541

Q8VHR5	Gatad2b	585	1	-0.39	0.013	-1.6	-0.388139	0.019994	-2.855242
Q91WH2	Ugt2b38	(1 of 299,300,309,312,315,318)	1	0.09	0.765	-6.4	0.0899193	0.796312	-6.662016
Q91WK2	Eif3h	(1 of 8,10,11,13,14,15,17)	1	-0	1	-6.9	-0.289715	0.396322	-6.387769
Q91WP0	Masp2	643	1	0.202	0.503	-6	-0.013102	0.967202	-6.736355
Q91WU0	Ces1f	81	1	-0.09	0.664	-7	-0.306777	0.149143	-5.625577
Q91X84	Crtc3	(1 of 320,321,322,326,327)	1	-0.08	0.54	-6.8	-0.082321	0.587401	-7.137343
Q91XL1	Lrg1	316	1	-0.07	0.8	-7	-0.826311	0.062176	-4.250519
Q91XT4	Sec16b	68	1	0.894	0.005	-0.1	0.9134948	0.005143	-0.889964
Q91XT4	Sec16b	78	1	0.928	1E-03	3.38	0.947158	0.000883	1.978038
Q91YQ5	Rpn1	(1 of 302,303,304,312)	1	0.106	0.727	-6.4	-0.49829	0.187947	-5.057538
Q91YQ5	Rpn1	(1 of 386,391)	1	0.063	0.842	-6.5	-0.595926	0.134429	-4.576031
Q91YT7	Ythdf2	(1 of 196,197,201,202)	1	0.131	0.351	-6.4	-0.36901	0.054626	-4.29603
Q921I1	Tf	514	1	0.627	0.004	0.21	0.4869897	0.022556	-3.059094
Q921L6	Cttn	(1 of 307,308)	1	0.133	0.268	-6.1	-0.247428	0.153615	-5.661797
Q922U1	Prpf3	176	1	0.251	0.1	-4.8	-0.255098	0.183738	-5.881037
Q99LI5	Znf281	(1 of 861,862,864,867,870,874,877,881,882)	1	-0.87	0.056	-2.8	-0.86802	0.055378	-3.319893
Q99LI5	Znf281	(1 of 774,775,776,780,781,782)	1	-0.12	0.691	-6.3	-0.121752	0.732536	-6.600354
Q99LI5	Znf281	(1 of 236,238,239)	1	-0.59	0.114	-3.9	-0.592197	0.136176	-4.594277
Q99LI5	Znf281	(1 of 886,888,889,891)	1	-0.61	0.003	1	-0.608121	0.003086	-0.107596
Q99MZ3	Mlxipl	(1 of 614,618,619)	1	0.551	0.004	0.15	0.4307038	0.014256	-2.405417
Q9CQW1	Ykt6	172	1	0.227	0.298	-5.8	0.1941726	0.431248	-6.474847
Q9CS74	Ecd	640	1	0.648	0.017	-1.8	0.648233	0.014646	-2.19268
Q9CU24	Themis3	(1 of 313,316)	1	-0.81	0.014	-1.1	-0.813961	0.013874	-1.749061
Q9CWK8	Snx2	(1 of 93,94,97,101,104,106,107)	1	0.057	0.855	-6.5	-0.350018	0.330569	-5.773644
Q9CYA0	Creld2	190	1	-2.17	0.007	-0	-3.806059	0.000871	2.448945
Q9D136	Ogfod3	(1 of 212,213)	1	-0.61	0.075	-4.1	-1.107538	0.008067	-1.268575
Q9D136	Ogfod3	262	1	-0.23	0.184	-5.4	-0.736571	0.011107	-1.74846
Q9D1M0	Sec13	315	1	0.069	0.727	-6.7	0.135931	0.530268	-6.686135
Q9D787	Ppil2	(1 of 493,499,500,501,502,504,506)	1	0.208	0.087	-4.6	0.2083074	0.138638	-5.515583
Q9D7N9	Apmap	161	1	1.208	0.005	-0	1.699568	0.000357	4.021981
Q9D8N1		145	1	0.209	0.284	-5.7	0.2086235	0.356796	-6.266472
Q9DAC2	C8g	(1 of 120,126)	1	0.024	0.859	-7.2	-0.524484	0.0077	-1.477921
Q9DAC2	C8g	141	1	0.842	0.001	2.9	0.2944519	0.05552	-4.321106
Q9DBG5	Plin3	(1 of 126,127,128,130,137,138,139,141,142)	1	0.955	8E-04	3.9	0.9780874	0.000878	2.000083
Q9DBG5	Plin3	(1 of 71,72)	1	0.37	0.112	-4.9	0.3929641	0.076231	-4.765187
Q9DBG5	Plin3	58	1	0.654	0.011	-1.1	0.7293065	0.011456	-1.803777

Q9DBG5	Plin3	76	1	0.769	0.004	0.55	0.7918137	0.003702	-0.410892
Q9DBG6	Rpn2	(1 of 77,82,86,93,94,98,103,105,108)	1	-0.13	0.818	-6.8	-0.837798	0.109228	-4.746863
Q9DBR7	Ppp1r12a	(1 of 625,628,631,637,645,646,647,648,650,651,652,653,656,658)	1	0.121	0.692	-6.3	-0.189295	0.588491	-6.416989
Q9EP52	Twsg1	82	1	-0.18	0.274	-6.1	-0.181503	0.308342	-6.466071
Q9EPU0	Upf1	951	1	0.506	0.049	-3.4	0.275249	0.245298	-6.040002
Q9EQQ9	Oga	405	1	-0.06	0.751	-7.1	-0.753151	0.008196	-1.584346
Q9ER39	Tor1a	161	1	-0.66	0.096	-3.6	-1.227749	0.021717	-1.945779
Q9ERG0	Lima1	(1 of 324,325,326,329,334,341,344)	1	0.529	0.139	-4.3	0.3511906	0.330276	-5.768248
Q9ERG0	Lima1	279	1	0.558	0.127	-4.1	0.381097	0.30179	-5.628561
Q9ERU9	Ranbp2	(1 of 2317,2320,2328,2329,2330,2335,2336,2337,2338,2339,2341,2342)	1	0.121	0.542	-6.5	-0.16658	0.458026	-6.533599
Q9ERU9	Ranbp2	(1 of 1426,1428)	1	-0.32	0.307	-5.4	-0.637152	0.115673	-4.375658
Q9ERU9	Ranbp2	(1 of 1134,1137,1138,1141)	1	-0.33	0.104	-4.6	-0.618809	0.014571	-2.182683
Q9ERU9	Ranbp2	(1 of 2442,2443,2444,2445,2447)	1	0.383	0.24	-5	0.0991845	0.779899	-6.645841
Q9ERU9	Ranbp2	(1 of 1591,1592,1595,1599,1600,1602,1603)	1	0.019	0.953	-6.6	-0.301451	0.389025	-5.990348
Q9ERU9	Ranbp2	1457	1	0.214	0.262	-5.6	-0.087492	0.700432	-6.917421
Q9ERZ6	Fign	(1 of 395,396)	1	3.145	0.004	0.75	3.1447525	0.001355	1.832471
Q9ESC8	Aff4	(1 of 84,85,86)	1	-0.19	0.537	-6.1	-0.186102	0.592908	-6.427109
Q9ESC8	Aff4	689	1	#####	1	-6.9	8.07E-05	0.999722	-7.081112
Q9ESY9	Ifi30	107	1	-0.46	0.073	-3.7	-0.45936	0.083957	-4.392169
Q9ET43	Cldn12	241	1	-0.61	0.007	-0.4	-0.966983	0.00642	-0.930079
Q9JHP7	Poglut2	154	1	0.055	0.859	-6.5	0.0551818	0.874897	-6.709117
Q9JI95	Hspe1-rs1	21	1	-0.3	0.328	-5.5	-0.300931	0.389426	-5.992586
Q9JKR6	Hyou1	(1 of 513,517,518)	1	-1.06	0.004	0.46	-1.993881	0.000382	4.160855
Q9JKR6	Hyou1	933	1	-0.57	0.048	-3.6	-1.475295	0.001021	1.648389
Q9JKR6	Hyou1	598	1	-0.85	0.023	-2.2	-1.779953	0.00072	2.618266
Q9JKR6	Hyou1	871	1	-0.14	0.791	-6.8	-1.008247	0.077615	-4.283147
Q9JL60	Gmeb1	(1 of 442,443)	1	-0.13	0.325	-6.2	-0.129186	0.425619	-6.684149
Q9JLV1	Bag3	(1 of 289,291,297)	1	0.709	0.083	-3.4	0.2397889	0.494631	-6.240558
Q9JLV1	Bag3	(1 of 372,373,380,382,386,390)	1	-0.17	0.569	-6.2	-0.638432	0.115259	-4.369481
Q9JLV1	Bag3	(1 of 187,188,189)	1	0.704	0.005	-0.2	0.323997	0.105562	-5.178956
Q9JLV1	Bag3	(1 of 162,163,170)	1	0.308	0.32	-5.5	-0.16149	0.641715	-6.50051
Q9JLV1	Bag3	320	1	0.338	0.282	-5.3	-0.13162	0.710162	-6.577842
Q9JLV1	Bag3	183	1	0.694	0.006	-0.5	0.3133588	0.124725	-5.385147
Q9QWV9	Ccnt1	(1 of 473,474)	1	-0.84	0.013	-1	-0.838782	0.012592	-1.588552

Q9QYC7	Ggcx	572	1	0.389	0.082	-4.5	0.2666444	0.222205	-6.103249
Q9QYC7	Ggcx	629	1	0.527	0.043	-3.5	0.4048939	0.091149	-4.986716
Q9QYE6	Golga5	(1 of 150,152,153,155,158,159,162,163,165,166,167)	1	0.197	0.257	-6	0.0125697	0.943661	-7.421311
Q9QYG0	Ndrg2	(1 of 348,350,352,353,355,357,360)	1	0.189	0.156	-5.4	0.3055432	0.064885	-4.5319
Q9QYG0	Ndrg2	370	1	0.219	0.112	-4.9	0.3353544	0.043415	-3.994941
Q9QYG0	Ndrg2	335	1	-0.03	0.952	-7.1	0.0736261	0.852642	-7.246967
Q9QZN4	Fbxo6	261	1	0.026	0.938	-6.5	0.1934822	0.580022	-6.403518
Q9QZS5	Sgk2	332	1	0.618	0.107	-3.8	0.5442069	0.157732	-4.830398
Q9R013	Ctsf	358	1	-1.6	7E-04	4.67	-2.395331	5.60E-05	7.373964
Q9R182	Angptl3	117	1	1.948	0.009	-0.3	2.2606867	0.003572	0.598082
Q9R1E0	Foxo1	(1 of 644,645,646,648,651)	1	-0.3	0.136	-4.7	-0.304496	0.188973	-5.482053
Q9WU60	Atrn	(1 of 1083,1084)	1	-1.19	0.005	0.42	-1.191738	0.003834	0.170483
Q9WU60	Atrn	(1 of 412,413,417)	1	-0.21	0.481	-6	-0.212635	0.537509	-6.339117
Q9WUD0	Cyp2b10	141	1	-0.94	0.048	-2.5	0.5819119	0.14101	-4.644686
Q9WUM3	Coro1b	421	1	0.522	0.078	-3.8	0.3342037	0.183738	-5.439188
Q9WUU7	Ctsz	188	1	-0.81	0.064	-3	-2.234032	0.003702	0.550664
Q9WV54	Asah1	259	1	-0.95	0.003	0.75	-1.509057	0.000297	4.396113
Q9WV69	Dmtn	(1 of 274,278,279,282,284,285)	1	-0.31	0.138	-4.7	-0.31308	0.186422	-5.457471
Q9WV69	Dmtn	(1 of 10,11,14,16,17,18)	1	-0.11	0.713	-6.4	-0.113005	0.749121	-6.618991
Q9WV69	Dmtn	110	1	-0.33	0.205	-5.3	-0.329933	0.225322	-5.693758
Q9WVF5	Egfr	(1 of 525,530)	1	-3.6	0.003	0.97	-5.483238	0.000418	3.381436
Q9WVJ3	Cpq	396	1	-0.94	0.048	-2.5	-1.25936	0.020566	-1.840133
Q9Z0K8	Vnn1	(1 of 149,150,152)	1	3.234	0.004	0.8	4.3046348	0.000662	2.800801
Q9Z0K8	Vnn1	134	1	1.321	0.004	0.74	2.2953719	0.000699	3.038328
Q9Z103	Adnp	412	1	-0.1	0.556	-6.5	-0.104936	0.630748	-6.839929
Q9Z2D6	Mecp2	434	1	-0.56	0.044	-2.8	-1.394999	0.004383	-0.004989
Q9Z2L6	Minpp1	238	1	2.057	0.008	-0.1	2.0566836	0.004799	0.215672
Q9Z329	Itpr2	(1 of 2458,2460,2463,2464,2466)	1	-0.65	0.098	-3.7	-1.017293	0.037135	-2.709656
S4R294	Prrc2c	(1 of 2643,2644,2645,2646)	1	0.008	0.983	-6.6	-0.433848	0.242667	-5.374686
S4R294	Prrc2c	(1 of 2282,2283,2284,2285,2286)	1	-0.12	0.696	-6.3	-0.561487	0.149516	-4.745133
S4R294	Prrc2c	(1 of 1929,1932,1933,1935,1938,1940,1946)	1	0.001	0.999	-6.6	-0.440813	0.235873	-5.340665
S4R294	Prrc2c	(1 of 2632,2633,2634,2636,2637,2638)	1	0.011	0.952	-7.1	-0.357275	0.077898	-4.584461
S4R294	Prrc2c	(1 of 2101,2102)	1	0.048	0.652	-7	-0.317851	0.041547	-3.917789

S4R294	Prrc2c	(1 of 2138,2140,2143,2144,2146,2147,2148,2152,2155)	1	-0.01	0.954	-7.2	-0.372425	0.020846	-2.926743
S4R294	Prrc2c	(1 of 1914,1917,1918,1921)	1	-0.12	0.692	-6.3	-0.563194	0.149122	-4.736724
S4R294	Prrc2c	(1 of 2114,2117,2125,2127,2128,2133)	1	-0.59	0.115	-3.9	-0.948502	0.043415	-2.983573
S4R294	Prrc2c	(1 of 373,374)	1	0.381	0.365	-6	-0.019378	0.958944	-7.078731
S4R294	Prrc2c	2649	1	0.307	0.32	-5.5	-0.135402	0.702093	-6.568803
S4R294	Prrc2c	882	1	0.193	0.104	-4.8	-0.172863	0.203306	-6.007123
S4R294	Prrc2c	209	1	0.006	0.988	-6.6	-0.435952	0.241044	-5.364416
S4R2A9	Sec31a	(1 of 540,542,543,545)	1	-0.36	0.114	-4.4	-0.621477	0.040623	-3.331758
S4R2A9	Sec31a	(1 of 495,499,500,502)	1	0.682	0.055	-3.6	0.4316027	0.153664	-5.478714
S4R2A9	Sec31a	927	1	-0.62	0.108	-3.8	-0.847365	0.058925	-3.408973
V9GXT3	Nav2	(1 of 1391,1392,1394,1396,1399,1400,1404)	1	-1.01	0.042	-2.3	-1.006722	0.037962	-2.750943
Z4YL55	Cdan1	(1 of 205,208)	1	0.498	0.017	-1.8	0.4978215	0.021651	-2.744065

Appendix 7.4. Putative Adaptor-Target Pairs Identified by Dynamic NOTISE Analysis.

Protein LogFC: Protein log2 fold change of the adapter protein (Adapter column), logFC_Corrected: protein expression corrected log2 fold change in O-GlcNAcylation of the target protein (in Target column), Score: adaptor protein rank score (see text above and in **Chapter 5**).

A7.4.1. Adaptor Expression and Target O-GlcNAcylation Both Downregulated.

Adaptor	Target	ProteinLogFC	logFC_Corrected	Score
ACLY	FN1	-1.3074	-1.0887	4
ALDH1B1	FN1	-0.9213	-1.0887	0.5
PSMB3	FN1	-0.919	-1.0887	-2

PSMB1	FN1	-0.8953	-1.0887	0
PSMA7	FN1	-0.8136	-1.0887	1
SHMT1	GORASP2	-0.5219	-1.0546	3.5
PSMA7	EGFR	-0.8136	-5.4832	1
ALDH3A2	EGFR	-0.8985	-5.4832	4
SULT1A1	EGFR	-0.7624	-5.4832	0
ABCD3	EGFR	-0.523	-5.4832	0.5
ALDH1L1	HSP90B1	-0.8809	-0.8625	-1.5
ALDH1L1	HSP90B1	-0.8809	-1.6866	-1.5
ALDH1L1	HSP90B1	-0.8809	-0.8525	-1.5
ALDH1B1	LGALS3BP	-0.9213	-2.1517	0.5
DERA	LGALS3BP	-0.5578	-2.1517	1
ABCD3	PGRMC1	-0.523	-1.5615	0.5
ACLY	PPT1	-1.3074	-1.1184	4
BCKDHB	PPT1	-1.1838	-1.1184	2
BCKDHB	TCF25	-1.1838	-1.0348	2
FMO5	OGA	-0.5994	-0.7532	1
FASN	GRN	-1.4115	-1.6639	2
FASN	KANK2	-1.4115	-0.7841	2

A7.4.2. Adapter Expression and Target O-GlcNAcylation Both Upregulated.

Adaptor	**Target**	**ProteinLogFC**	**logFC_Corrected**	**PE_Corr**	**Score**
DDOST	VAPB	0.58289	1.36816	Yes	8

MTA2	GPHN	0.50347	1.47737	Yes	2.5
MTA2	GPHN	0.50347	1.48792	Yes	2.5
VTN	MPRIP	0.61906	2.41487	Yes	0.5
CYP1A2	CYB5A	0.6175	0.78412	Yes	3
NUDT21	XRCC6	0.57694	0.88174	Yes	10.5
MYBBP1A	XRCC6	0.55861	0.88174	Yes	6.5
MYBBP1A	BSG	0.55861	1.04511	Yes	6.5
MYBBP1A	BSG	0.55861	1.18103	Yes	6.5
GRN	CTSO	0.80027	2.50587	Yes	7
FARP1	AKAP1	0.5208	0.9869	Yes	0.5
HNRNPL	LPP	0.53995	1.04052	Yes	0.5
HSPA5	LPP	1.00527	1.04052	Yes	9.5
HNRNPL	MIA3	0.53995	0.86132	Yes	0.5
MYBBP1A	PLEC	0.55861	1.89457	Yes	6.5
RRBP1	PLEC	0.82747	1.89457	Yes	1.5
WDR5	MAVS	0.80661	0.86963	Yes	0
WDR5	MAVS	0.80661	1.14081	Yes	0

A7.4.3. Adapter Expression Downregulated and Target O-GlcNAcylation Upregulated.

Adaptor	**Target**	**ProteinLogFC**	**logFC_Corrected**	**Score**
PSMA7	MAVS	-0.8136	0.86963	1
PSMA7	MAVS	-0.8136	1.14081	1
GPT2	AHCY	-1.0976	1.46693	1.5
ACLY	CTH	-1.3074	1.04614	4
PAPSS2	CTH	-0.5972	1.04614	1.5
GCDH	APOE	-0.5756	2.0794	2.5

A7.4.4. Adapter Expression Upregulated and Target O-GlcNAcylation Downregulated.

Adaptor	Target	ProteinLogFC	logFC_Corrected	PE_Corr	Score
WDR5	HCFC1	0.80661	-1.0043	Yes	0
WDR5	HCFC1	0.80661	-0.8908	Yes	0
WDR5	HCFC1	0.80661	-1.3447	Yes	0
WDR5	HCFC1	0.80661	-1.1115	Yes	0
WDR5	HCFC1	0.80661	-0.9605	Yes	0
WDR5	HCFC1	0.80661	-0.9646	Yes	0
WDR5	HCFC1	0.80661	-0.9718	Yes	0
WDR5	HCFC1	0.80661	-1.18	Yes	0
WDR5	HCFC1	0.80661	-0.8457	Yes	0
WDR5	HCFC1	0.80661	-0.9206	Yes	0
WDR5	HCFC1	0.80661	-0.9073	Yes	0
MTA2	TOP2B	0.50347	-1.3115	Yes	2.5
LYAR	ZHX1	0.60561	-0.8656	Yes	2
COMT	FN1	0.82553	-1.0887	Yes	0.5
U2AF1	FN1	0.52959	-1.0887	Yes	0.5
HMGB1	FN1	0.66856	-1.0887	Yes	7.5
MYL1	FN1	1.22946	-1.0887	Yes	1
GSTP1	FN1	2.94304	-1.0887	Yes	3
DDOST	FN1	0.58289	-1.0887	Yes	8
NUDT21	FN1	0.57694	-1.0887	Yes	10.5
HMGB1	PDIA3	0.66856	-1.1906	Yes	7.5
GRN	PDIA3	0.80027	-1.1906	Yes	7
GSTP1	EGFR	2.94304	-5.4832	Yes	3
PHLDA1	EGFR	1.85703	-5.4832	Yes	0.5
GRN	EGFR	0.80027	-5.4832	Yes	7
AHSG	EGFR	0.51067	-5.4832	Yes	4
HMGB1	EGFR	0.66856	-5.4832	Yes	7.5
RACK1	EGFR	0.5559	-5.4832	Yes	6
MYBBP1A	RRBP1	0.55861	-1.4375	Yes	6.5

LYAR	RRBP1	0.60561	-1.4375	Yes	2
HMGB1	MECP2	0.66856	-1.395	Yes	7.5
MYBBP1A	MECP2	0.55861	-1.395	Yes	6.5
NUDT21	VIM	0.57694	-0.9695	Yes	10.5
DDOST	VIM	0.58289	-0.9695	Yes	8
GRN	VIM	0.80027	-0.9695	Yes	7
MTA2	SRRM2	0.50347	-0.8651	Yes	2.5
U2AF1	SRRM2	0.52959	-0.8651	Yes	0.5
MTA2	SRRM2	0.50347	-1.2595	Yes	2.5
U2AF1	SRRM2	0.52959	-1.2595	Yes	0.5
MTA2	SRRM2	0.50347	-0.9224	Yes	2.5
U2AF1	SRRM2	0.52959	-0.9224	Yes	0.5
MTA2	SRRM2	0.50347	-1.3657	Yes	2.5
U2AF1	SRRM2	0.52959	-1.3657	Yes	0.5
DEK	VTN	0.52272	-1.1864	Yes	5
U2AF1	SON	0.52959	-1.0552	Yes	0.5
U2AF1	SON	0.52959	-0.8482	Yes	0.5
U2AF1	SON	0.52959	-1.2715	Yes	0.5
ARPC1B	CALU	1.18708	-0.7545	Yes	-1.5
ARPC1B	CALU	1.18708	-1.1331	Yes	-1.5
U2AF1	PSAP	0.52959	-1.2521	Yes	0.5
SSR1	PSAP	0.65844	-1.2521	Yes	0.5
GRN	PSAP	0.80027	-1.2521	Yes	7
U2AF1	PSAP	0.52959	-1.4951	Yes	0.5
SSR1	PSAP	0.65844	-1.4951	Yes	0.5
GRN	PSAP	0.80027	-1.4951	Yes	7
DDOST	HSP90B1	0.58289	-0.8625	Yes	8
DDOST	HSP90B1	0.58289	-1.6866	Yes	8
DDOST	HSP90B1	0.58289	-0.8525	Yes	8
MYH11	PLBD2	0.6806	-0.8922	Yes	-0.5
DDOST	RPN2	0.58289	-0.8378	Yes	8
MTA2	AHNAK	0.50347	-1.2868	Yes	2.5
CYP1A2	ASAH1	0.6175	-1.5091	Yes	3

CYP1A2	PGRMC1	0.6175	-1.5615	Yes	3
DDOST	PGRMC1	0.58289	-1.5615	Yes	8
COMT	GBA	0.82553	-1.3831	Yes	0.5
COMT	GBA	0.82553	-1.806	Yes	0.5
U2AF1	SARNP	0.52959	-1.1485	Yes	0.5
SSR1	HSPA13	0.65844	-1.3872	Yes	0.5
DDOST	PPT1	0.58289	-1.1184	Yes	8
GSTP1	PPT1	2.94304	-1.1184	Yes	3
GRN	SERPING1	0.80027	-0.8427	Yes	7
SFPQ	PRRC2C	0.66456	-0.9485	Yes	1
HNRNPH1	PGRMC1	0.60113	-1.5615	Yes	3
EGFR	PGRMC1	1.7656	-1.5615	Yes	-1
EGFR	GRN	1.7656	-1.6639	Yes	-1
HSPA5	GRN	1.00527	-1.6639	Yes	9.5
CAPZA1	GRN	0.66508	-1.6639	Yes	1
HSPH1	SEC23A	0.74357	-0.7695	Yes	-0.5
MOV10	SEC31A	0.68709	-0.8474	Yes	-1
SRSF1	VTN	0.64771	-1.1864	Yes	-2.5
HNRNPM	VTN	0.59945	-1.1864	Yes	0.5
RBM39	VTN	0.55991	-1.1864	Yes	7.5
SFPQ	VTN	0.66456	-1.1864	Yes	1
HSP90AA1	ZBTB20	0.73133	-0.9426	Yes	-5
HNRNPL	ZBTB20	0.53995	-0.9426	Yes	0.5
HSP90AA1	ZBTB20	0.73133	-1.159	Yes	-5
HNRNPL	ZBTB20	0.53995	-1.159	Yes	0.5
HSP90AA1	ZBTB20	0.73133	-1.0246	Yes	-5
HNRNPL	ZBTB20	0.53995	-1.0246	Yes	0.5

HSP90AA1	ZBTB20	0.73133	-0.8178	Yes	-5
HNRNPL	ZBTB20	0.53995	-0.8178	Yes	0.5
HSP90AA1	ZBTB20	0.73133	-0.8101	Yes	-5
HNRNPL	ZBTB20	0.53995	-0.8101	Yes	0.5
HSP90AA1	ZBTB20	0.73133	-0.8258	Yes	-5
HNRNPL	ZBTB20	0.53995	-0.8258	Yes	0.5
HSP90AA1	ZBTB20	0.73133	-1.0166	Yes	-5
HNRNPL	ZBTB20	0.53995	-1.0166	Yes	0.5
HSP90AA1	ZBTB20	0.73133	-1.1092	Yes	-5
HNRNPL	ZBTB20	0.53995	-1.1092	Yes	0.5
HSPA5	VIM	1.00527	-0.9695	Yes	9.5
TRIM28	VIM	0.52193	-0.9695	Yes	5
RBM39	VIM	0.55991	-0.9695	Yes	7.5
EGFR	AHNAK	1.7656	-1.2868	Yes	-1
SRRM2	EPB41L2	0.6138	-1.2604	Yes	0.5
RPL11	HP	0.50691	-2.4481	Yes	4
HSP90B1	GBA	0.86973	-1.3831	Yes	-0.5
HSP90B1	GBA	0.86973	-1.806	Yes	-0.5
HSP90B1	CRELD2	0.86973	-3.8061	Yes	-0.5
HSPA5	RRAGD	1.00527	-0.9141	Yes	9.5
HSPA5	HYOU1	1.00527	-1.9939	Yes	9.5
HSPA5	HYOU1	1.00527	-1.4753	Yes	9.5
HSPA5	HYOU1	1.00527	-1.78	Yes	9.5
HSPA5	HYOU1	1.00527	-1.0082	Yes	9.5

Appendix 7.5. Python and R Code for All Analyses.

All code was run in Jupyter notebook (v7.12). See also **7.9.12.3. General and Statistics**.

A7.5.1. Valine Linker Ratio Analysis.

```
#Import python packages
import re
import sys
import pandas as pd
import networkx as nx
import itertools as it
from collections import namedtuple
import numpy as np
import matplotlib
import matplotlib.pyplot as plt
from IPython.display import display
from functools import reduce
import seaborn as sns; sns.set()
from io import StringIO
from matplotlib_venn import venn2_unweighted
from matplotlib_venn import venn2
import venn
import pandas as pd
import numpy as np
from io import StringIO
import urllib.request, urllib.parse, urllib.error,urllib.request,urllib.error,urllib.parse
import math
import scipy.stats as stats

#set up R environment and import R packages
import rpy2
import rpy2.ipython
%load_ext rpy2.ipython

#require R packages
%R require(limma)
%R require(ibb)

#magic function to show plots inline
%matplotlib inline

#ignore warnings
import warnings
warnings.filterwarnings("ignore")

#Import the files

#set folder names
qfolder = './LinkerRatioTest_Quant/'
sfolder = './LinkerRatioTest_Glycomics/'
folderout = './Linker_RatioTesting_Analysis/'

#import the files
dfmsms = pd.read_csv('{}msms.txt'.format(sfolder), sep='\t')
dfallpep = pd.read_csv('{}allPeptides.txt'.format(qfolder), sep='\t')

#take the relevant info from the allPeptides file, remove unneeded spectra, and rename the MSMS Scan Number column for
    #matching
dfall2 = dfallpep[['Raw file', 'Charge', 'Mass', 'Pyl Count', 'Ratio H/L', 'MS/MS Count', 'MSMS Scan Numbers']]
dfall2 = dfall2[(dfall2['Pyl Count'] != "") & (dfall2['MS/MS Count'] > 0)]
dfall2.rename(columns={'MSMS Scan Numbers':'Scan number'}, inplace=True)

#remove contaminants, reverse sequences, and peptides modified by both 601 and 607 from the msms file
dfmsms2 = dfmsms[dfmsms.Reverse != '+']
dfmsms2 = dfmsms2[~dfmsms2.Proteins.str.contains('CON_')]
dfmsms2 = dfmsms2[~(dfmsms2.Modifications.str.contains('GlcNAc601') & (dfmsms2.Modifications.str.contains('GlcNAc607')))]
#Expand the scan number column of the all peptides file into duplicate rows and merge with the msms file

#change the scan number to a list and explode values to duplicate rows
dfall3 = dfall2.copy()
dfall3['Scan number'] = dfall2['Scan number'].str.split(';')
dfall4 = dfall3.explode('Scan number')
dfall5 = dfall4.copy()
dfall5['Scan number'] = dfall4['Scan number'].astype(int)

#merge this with the msms file on raw file, change, and scan number
dfm = dfmsms2.merge(dfall5, on=['Raw file', 'Scan number', 'Charge'], how='left')

#renmae the all peptides mass
dfm.rename(columns={'Mass_y':'Mass_QuanSearch'}, inplace=True)
#Preproces this data for the sites and regions script (first with the 601, then with the 607 tag)
#adapted from 'preprocessMQ.py' written by Mike Sweredoski on Jan 24, 2020

###GlcNAc601
```

```
MOD_NAME = "GlcNAc601"
pepProbPatt = re.compile(r'[A-Z][(]?\d?[.]?\d*[)]?')

PepInfo = namedtuple("PepInfo",["Protein","StartPos"])
peptideInfo = {}

# Get peptide start positions
pepDF = pd.read_csv("{}peptides.txt".format(sfolder), sep='\t')
for peptide in pepDF[["id","Leading razor protein","Start position"]].itertuples():
    if math.isnan(peptide[3]):
        peptideInfo[peptide.id] = PepInfo(peptide[2],-1)
    else:
        peptideInfo[peptide.id] = PepInfo(peptide[2],int(peptide[3]))

msmsDF = dfm
msmsDF = msmsDF[msmsDF[MOD_NAME]>0]
msmsDF["Protein"] = msmsDF["Peptide ID"].apply(lambda x: peptideInfo[x].Protein)
msmsDF["StartPos"] = msmsDF["Peptide ID"].apply(lambda x: peptideInfo[x].StartPos)
msmsDF = msmsDF[msmsDF["StartPos"]>=0]
msmsDF.rename(columns={"Raw file":"RawFile","Scan number":"ScanNumber",MOD_NAME:"NumMods", "Ratio H/L":"Ratio"},
              inplace=True)
msmsDF["Probabilities"] = msmsDF.apply(
    lambda x: ";".join([aa[2:-1] for pp,aa in enumerate(pepProbPatt.findall(
        x["%s Probabilities"%MOD_NAME])) if len(aa) > 1]),axis=1)
msmsDF["Positions"] = msmsDF.apply(
    lambda x: ";".join([str(pp+x["StartPos"]) for pp,aa in enumerate(pepProbPatt.findall(
        x["%s Probabilities"%MOD_NAME])) if len(aa) > 1]),axis=1)

msmsDF[["RawFile","Protein","ScanNumber","NumMods","Positions","Probabilities","Ratio"]].to_csv(
    '{}LinkerTest_601_Preprocessed.txt'.format(folderout), sep="\t", index=False)

###GlcNAc607
MOD_NAME = "GlcNAc607"
pepProbPatt = re.compile(r'[A-Z][(]?\d?[.]?\d*[)]?')

PepInfo = namedtuple("PepInfo",["Protein","StartPos"])
peptideInfo = {}

# Get peptide start positions
pepDF = pd.read_csv("{}peptides.txt".format(sfolder), sep='\t')
for peptide in pepDF[["id","Leading razor protein","Start position"]].itertuples():
    if math.isnan(peptide[3]):
        peptideInfo[peptide.id] = PepInfo(peptide[2],-1)
    else:
        peptideInfo[peptide.id] = PepInfo(peptide[2],int(peptide[3]))

msmsDF = dfm
msmsDF = msmsDF[msmsDF[MOD_NAME]>0]
msmsDF["Protein"] = msmsDF["Peptide ID"].apply(lambda x: peptideInfo[x].Protein)
msmsDF["StartPos"] = msmsDF["Peptide ID"].apply(lambda x: peptideInfo[x].StartPos)
msmsDF = msmsDF[msmsDF["StartPos"]>=0]
msmsDF.rename(columns={"Raw file":"RawFile","Scan number":"ScanNumber",MOD_NAME:"NumMods", "Ratio H/L":"Ratio"},
              inplace=True)
msmsDF["Probabilities"] = msmsDF.apply(
    lambda x: ";".join([aa[2:-1] for pp,aa in enumerate(pepProbPatt.findall(
        x["%s Probabilities"%MOD_NAME])) if len(aa) > 1]),axis=1)
msmsDF["Positions"] = msmsDF.apply(
    lambda x: ";".join([str(pp+x["StartPos"]) for pp,aa in enumerate(pepProbPatt.findall(
        x["%s Probabilities"%MOD_NAME])) if len(aa) > 1]),axis=1)

msmsDF[["RawFile","Protein","ScanNumber","NumMods","Positions","Probabilities","Ratio"]].to_csv(
    '{}LinkerTest_607_Preprocessed.txt'.format(folderout), sep="\t", index=False)
%%capture
#supresses the output of the cell

#Run the sites and regions script for each experiment
%run -i SitesAndRegions.py ./Linker_RatioTesting_Analysis/LinkerTest_601_Preprocessed.txt \
./Linker_RatioTesting_Analysis/maxparcon_601.txt ./Linker_RatioTesting_Analysis/bestms2_601.txt
%run -i SitesAndRegions.py ./Linker_RatioTesting_Analysis/LinkerTest_607_Preprocessed.txt \
./Linker_RatioTesting_Analysis/maxparcon_607.txt ./Linker_RatioTesting_Analysis/bestms2_607.txt
#Import the sites and regions output into dfs and count the number of sites for each

list_dfs2 = ['601', '607']
list_exp = ['WT', 'db/db']

for i in list_dfs2:
    locals()['dfallsites_{}'.format(i)] = pd.read_csv('{}bestms2_{}.txt'.format(folderout, i), sep='\t')
    locals()['dfregions_{}'.format(i)] = pd.read_csv('{}maxparcon_{}.txt'.format(folderout, i), sep='\t')
    #remove sites/regions that match to two master proteins
    #this seems to happen sometimes when there is real evidence of two isoforms
    #all cases checked were already explained by other data, so they can be reasonably ignored
    locals()['dfregions_{}'.format(i)] = locals()['dfregions_{}'.format(i)][
        ~locals()['dfregions_{}'.format(i)].Protein.str.contains(';')]
    locals()['dfallsites_{}'.format(i)] = locals()['dfallsites_{}'.format(i)][
        ~locals()['dfallsites_{}'.format(i)].Protein.str.contains(';')]

#initialize an empty df
df_numsites = pd.DataFrame(np.empty((2,5)))

#calculate the number of sites, localized sites, and regions
for i in range (2):
    #set the column and index names
    df_numsites.columns = [['Total Number of Sites', 'Localized Sites', 'Unlocalized Sites', 'Regions',
                            'Percent Localized']]
    df_numsites.rename(index={i:list_dfs2[i]}, inplace=True)
```

```
    #count the total number of sites
    df_numsites.loc[list_dfs2[i], 'Total Number of Sites'] = \
    locals()['dfregions_{}'.format(list_dfs2[i])]['Min Sites'].sum()
    #count the number of localized sites
    df_numsites.loc[list_dfs2[i], 'Localized Sites'] = len(
        locals()['dfregions_{}'.format(list_dfs2[i])][
            locals()['dfregions_{}'.format(list_dfs2[i])]['Site ID Constraints'].str.contains('of') == False])
    df_numsites.loc[list_dfs2[i], 'Unlocalized Sites'] = locals()['dfregions_{}'.format(list_dfs2[i])][
        locals()['dfregions_{}'.format(list_dfs2[i])][
            'Site ID Constraints'].str.contains('of') == True]['Min Sites'].sum()
    df_numsites.loc[list_dfs2[i], 'Regions'] = len(
        locals()['dfregions_{}'.format(list_dfs2[i])][
            locals()['dfregions_{}'.format(list_dfs2[i])]['Site ID Constraints'].str.contains('of') == True])
    df_numsites.loc[list_dfs2[i], 'Percent Localized'] = \
    (df_numsites.loc[list_dfs2[i], 'Localized Sites'].to_numpy() / df_numsites.loc[
        list_dfs2[i], 'Total Number of Sites'].to_numpy())*100

df_numsites.rename(index={'601':'601 WT', '607':'607 db/db'}, inplace=True)
df_numsites = df_numsites.astype(int) #convert to ints
df_numsites.to_csv('{}SitesAndRegionsCount.csv'.format(folderout)) #export
df_numsites #inspect

#Now perform the quantitative analysis to visualize ratios across the different mixtures

#Preprocess the msms file

#copy the previous df
dfmq = dfm.copy()

#remove the 601/607 identifier
dfmq.replace(['GlcNAc601', 'GlcNAc607'], 'GlcNAc', inplace=True)

#remove psms where the number of mods is not equal to the number of mods used for the ratio calculation
#this will remove all sites without ratios
dfmqf = dfmq[(dfmq.GlcNAc601 == dfmq['Pyl Count']) | (dfmq.GlcNAc607 == dfmq['Pyl Count'])]

#set new mod name
MOD_NAME = "GlcNAc"
pepProbPatt = re.compile(r'[A-Z][(]?\d?[.]?\d*[)]?')

PepInfo = namedtuple("PepInfo",["Protein","StartPos"])
peptideInfo = {}

# Get peptide start positions
pepDF = pd.read_csv("{}peptides.txt".format(sfolder), sep='\t')
for peptide in pepDF[["id","Leading razor protein","Start position"]].itertuples():
    if math.isnan(peptide[3]):
        peptideInfo[peptide.id] = PepInfo(peptide[2],-1)
    else:
        peptideInfo[peptide.id] = PepInfo(peptide[2],int(peptide[3]))

msmsDF = dfmqf
msmsDF = msmsDF[msmsDF.Modifications.str.contains("GlcNAc")]
msmsDF["Protein"] = msmsDF["Peptide ID"].apply(lambda x: peptideInfo[x].Protein)
msmsDF["StartPos"] = msmsDF["Peptide ID"].apply(lambda x: peptideInfo[x].StartPos)
msmsDF = msmsDF[msmsDF["StartPos"]>=0]
msmsDF.rename(columns={"Raw file":"RawFile","Scan number":"ScanNumber", "Ratio H/L":"Ratio"},
              inplace=True)
msmsDF['NumMods'] = msmsDF[["GlcNAc601","GlcNAc607"]].sum(axis=1)

#enumerate separately for 601 and 607 (there should be no overlapping sites)
#convert site prob columns to string
msmsDF[["GlcNAc601 Probabilities","GlcNAc607 Probabilities"]] = \
msmsDF[["GlcNAc601 Probabilities","GlcNAc607 Probabilities"]].astype(str)
msmsDF.loc[msmsDF.GlcNAc601 > 0, "Probabilities"] = msmsDF.apply(
    lambda x: ";".join([aa[2:-1] for pp,aa in enumerate(pepProbPatt.findall(
        x["GlcNAc601 Probabilities"])) if len(aa) > 1]),axis=1)
msmsDF.loc[msmsDF.GlcNAc607 > 0, "Probabilities"] = msmsDF.apply(
    lambda x: ";".join([aa[2:-1] for pp,aa in enumerate(pepProbPatt.findall(
        x["GlcNAc607 Probabilities"])) if len(aa) > 1]),axis=1)
msmsDF.loc[msmsDF.GlcNAc601 > 0, "Positions"] = msmsDF.apply(
    lambda x: ";".join([str(pp+x["StartPos"]) for pp,aa in enumerate(pepProbPatt.findall(
        x["GlcNAc601 Probabilities"])) if len(aa) > 1]),axis=1)
msmsDF.loc[msmsDF.GlcNAc607 > 0, "Positions"] = msmsDF.apply(
    lambda x: ";".join([str(pp+x["StartPos"]) for pp,aa in enumerate(pepProbPatt.findall(
        x["GlcNAc607 Probabilities"])) if len(aa) > 1]),axis=1)

df1_table = msmsDF[["RawFile","Protein","ScanNumber","NumMods","Positions","Probabilities","Ratio"]]
#Set localization probabilities to equal and export for sites and regions script

#set columns to keep in final df
cols_to_keep = ["RawFile","Protein","ScanNumber","NumMods","Positions","Probabilities","Ratio"]

#copy the df
df2_table = df1_table.copy()

#keeping the for loop structure from the previous script
i = 2
#count the number of S/Ts
locals()['df{}_table'.format(i)]['NumSites'] = locals()['df{}_table'.format(i)].Probabilities.str.count(';') + 1
#calculate the probability at each site based on the number of S/Ts (round to 3 decimals as in MQ)
locals()['df{}_table'.format(i)]['Prob'] = round(1/locals()['df{}_table'.format(i)].NumSites, 3)
#define a function to make a repeating list of probability values based on the number of S/Ts
def repeat(row):
    return [row.Prob]*row.NumSites
```

```
#apply this function to each df
locals()['df{}_table'.format(i)]['ProbList'] = locals()['df{}_table'.format(i)].apply(repeat, axis=1)
#transform the list into a semi-colon separated string for the sites and regions script
locals()['df{}_table'.format(i)]['ProbListFinal'] = locals()['df{}_table'.format(i)].ProbList.apply(
    lambda s: ';'.join(map(str, s)))
#replace all probability values
locals()['df{}_table'.format(i)]['Probabilities'] = locals()['df{}_table'.format(i)].ProbListFinal
#remake the original table with the columns required for the sites and regions script
locals()['df{}_tableF'.format(i)] = locals()['df{}_table'.format(i)][cols_to_keep]

#make a new column to denote the experiment

#set lists for experiment identifiers
list_ratio = ['H1L1', 'H1L2', 'H1L5', 'H2L1', 'H5L1']
list_replicate = ['john', 'Matt'] #based on raw file


#add the experiment identifier column (keep the replicates split just in case for future analysis)
for i in range(5):
    for j in range(2):
        df2_tableF.loc[(df2_tableF.RawFile.str.contains('{}'.format(list_ratio[i])) &
                        df2_tableF.RawFile.str.contains(
                            '{}'.format(list_replicate[j]))), 'Experiment_Split'] = '{}_{}'.format(list_ratio[i],j+1)

#also make a new column with an experiment identifier based on the mixing (replicate information is stripped)
df2_tableF['Experiment'] = df2_tableF['Experiment_Split'].apply(lambda x: x.split('_')[0])

#export final table to txt file for sites and regions multi-experiment script
df2_tableF.to_csv('{}QuantSitesAndRegions_Preprocessed.txt'.format(folderout), sep='\t', index=False)
%%capture
#supresses the output of the cell

#Run the sites and regions multi experiment script
%run -i SitesAndRegionsMultiExperiment.py ./Linker_RatioTesting_Analysis/QuantSitesAndRegions_Preprocessed.txt \
./Linker_RatioTesting_Analysis/maxparcon_Quant.txt ./Linker_RatioTesting_Analysis/bestms2_Quant.txt
#Import the output and as in the 20D09 script
dfallsitesq = pd.read_csv('{}bestms2_Quant.txt'.format(folderout), sep='\t')
dfregionsq = pd.read_csv('{}maxparcon_Quant.txt'.format(folderout), sep='\t')
dfallsitesq = dfallsitesq[~dfallsitesq.Protein.str.contains(';')]
dfregionsq = dfregionsq[~dfregionsq.Protein.str.contains(';')]
dfregionsq.loc[dfregionsq['Site ID Constraints'].str.contains('of'), 'Type'] = 'Region'
dfregionsq.loc[~dfregionsq['Site ID Constraints'].str.contains('of'), 'Type'] = 'Site'
dfmergeq = dfallsitesq.merge(dfregionsq, how='left', on='Region ID')

#clean up this df
dfmergeq.rename(columns={'Protein_x': 'Protein'}, inplace=True)
dfmergeq.drop(columns={'Protein_y'}, inplace=True)
#Merge with the preprocssed dataframe to get the ratios at the non-redundant sites level

#copy the df
dfratios = df2_tableF.copy()

#merge with previous table on raw file, scan number, and protein
#note that all proteins that don't match will be discarded (decided based on score by the sites and regions script)
    #these may be real sites, but they will be ignored for the quantification, if there are really 2 peptides matching
    #to the same precursor, there is no way to quantify them seperately anyway
dfmergeqf = dfmergeq.rename(columns={'Best Scan Number':'ScanNumber', 'Best Raw File':'RawFile'})
dfq = dfmergeqf.merge(dfratios, on=['RawFile', 'ScanNumber', 'Protein', 'Experiment'])

print('In total we quantified {} regions.'.format(len(dfregionsq)))

#Make violin plots of the ratios from each experiment (both for the original and non-redundant sites)

#log transform the values
dfq['LogRatio'] = np.log2(dfq.Ratio)
df2_tableF['LogRatio'] = np.log2(df2_tableF.Ratio)

#set up the searborn environment
sns.set_style('ticks')
sns.set_context('talk')

#remove the outlines from the violin plot
def patch_violinplot(palette, n):
    from matplotlib.collections import PolyCollection
    ax = plt.gca()
    violins = [art for art in ax.get_children() if isinstance(art, PolyCollection)]
    colors = sns.color_palette(palette, n_colors=n) * (len(violins)//n)
    for i in range(len(violins)):
        violins[i].set_edgecolor(colors[i])

plt.figure(figsize=(7,7))
g = sns.violinplot(x='Experiment', y='LogRatio', data=dfq, order=['H1L5', 'H1L2', 'H1L1', 'H2L1', 'H5L1'])
ax1 = g.axes
ax1.axhline(np.log2(0.2), ls='--', color=sns.color_palette()[0], zorder=1, linewidth=2)
ax1.axhline(np.log2(0.5), ls='--', color=sns.color_palette()[1], zorder=1, linewidth=2)
ax1.axhline(np.log2(1), ls='--', color=sns.color_palette()[2], zorder=1, linewidth=2)
ax1.axhline(np.log2(2), ls='--', color=sns.color_palette()[3], zorder=1, linewidth=2)
ax1.axhline(np.log2(5), ls='--', color=sns.color_palette()[4], zorder=1, linewidth=2)
patch_violinplot(sns.color_palette(), 5)
plt.title('Non-Redundant Sites')
plt.xlabel('')
plt.ylabel('Log2 H/L Ratio')
sns.despine()

plt.figure(figsize=(7,7))
```

```
g = sns.violinplot(y='LogRatio', x='Experiment', data=df2_tableF)
ax1 = g.axes
ax1.axhline(np.log2(0.2), ls='--', color=sns.color_palette()[0], zorder=1, linewidth=2)
ax1.axhline(np.log2(0.5), ls='--', color=sns.color_palette()[1], zorder=1, linewidth=2)
ax1.axhline(np.log2(1), ls='--', color=sns.color_palette()[2], zorder=1, linewidth=2)
ax1.axhline(np.log2(2), ls='--', color=sns.color_palette()[3], zorder=1, linewidth=2)
ax1.axhline(np.log2(5), ls='--', color=sns.color_palette()[4], zorder=1, linewidth=2)
patch_violinplot(sns.color_palette(), 5)
plt.title('All PSMs')
plt.xlabel('')
plt.ylabel('Log2 H/L Ratio')
sns.despine()
```

A7.5.2. Protein Expression Analysis and Visualization.

```
#Import python packages
import re
import sys
import pandas as pd
import networkx as nx
import itertools as it
from collections import namedtuple
import numpy as np
import matplotlib
import matplotlib.pyplot as plt
from IPython.display import display
from functools import reduce
import seaborn as sns; sns.set()
from io import StringIO
from matplotlib_venn import venn2_unweighted #the unweighted is if you want to make circles that are the same size
from matplotlib_venn import venn2 #also import the normal one
import pandas as pd
import numpy as np
from io import StringIO
import urllib.request, urllib.parse, urllib.error,urllib.request,urllib.error,urllib.parse
from scipy import stats
from decimal import *
import math

#set up R environment and import R packages
import rpy2
import rpy2.ipython
%load_ext rpy2.ipython

#require R packages
%R require(limma)
%R require(ibb)

#magic function to show plots inline
%matplotlib inline

#ignore warnings
import warnings
warnings.filterwarnings("ignore")


#Load in the protein expression data from MaxQuant

#define folder location
folder = './Liver_Protein_Expression/'

#read in files
df = pd.read_csv('{}proteinGroups.txt'.format(folder), sep='\t')
dfmsms = pd.read_csv('{}msms.txt'.format(folder), sep='\t')

#remove potential contaminants and reverse seqeunces
dfprot = df[(df.Reverse != '+') & (df['Potential contaminant'] != '+') & (df['Only identified by site'] != '+')]
dfmsms2 = dfmsms[dfmsms.Reverse != '+']
#Prepare the df, normalize the TMT reporter intensity by the summed intensity, and scale log2 reporter intensity by WT

#first gather only the relevant info from the prot groups

#list columns to keep
keepcols = ['Majority protein IDs', 'Fasta headers', 'Reporter intensity 1', 'Reporter intensity 2',
            'Reporter intensity 3', 'Reporter intensity 4', 'Reporter intensity 5', 'Reporter intensity 6',
            'Reporter intensity 7', 'Reporter intensity 8']

df1 = dfprot[keepcols] #take only relevent colunmns

#extract the gene names from the FASTA header
df1.insert(loc=1, column='Gene', value=df1['Fasta headers'].str.extract('GN=(.*?) PE='))

#remove values where reporter ion intensities are all 0
#these arise when there are no PSMs that meet the cutoff for isolation interference
df1 = df1[(df1[df1.filter(regex = 'Reporter').columns] != 0).all(axis=1)]

#set a new df for the normalized values
dfnorm = df1.copy()
```

```
#normalize the columns
for i in dfnorm.filter(regex = 'Reporter').columns:
    dfnorm[i] = df1[i]/df1[i].sum()

#swtich columns 4 and 5 (4 is dbdb and 5 is wt) and rename the columns
coltitles = ['Reporter intensity 5', 'Reporter intensity 4']
dfnorm[['Reporter intensity 4', 'Reporter intensity 5']] = dfnorm.reindex(columns=coltitles)
wtcols = dfnorm.columns[3:7].str.replace('Reporter intensity ', 'WT-', regex=True)
dbdbcols = dfnorm.columns[7:].str.replace('Reporter intensity ', 'db/db-', regex=True)
dfnorm.columns = list(dfnorm.columns[0:3]) + list(wtcols) + list(dbdbcols)

#take the -log2 of all columns
dflog = dfnorm.copy()
dflog.loc[:,'WT-1':'db/db-8'] = np.log2(dflog.loc[:,'WT-1':'db/db-8'])

#scale the values by median WT intensity
dfscaled = dflog.copy()
dfscaled.loc[:,'WT-1':'db/db-8'] = dflog.loc[:,'WT-1':'db/db-8'].sub(dflog.loc[:,'WT-1':'WT-4'].median(axis=1), axis=0)
#Make a clustermap for protein expression

#set seaborn style
sns.set_style('ticks')
sns.set_context('poster')

#make the clustermap
g = sns.clustermap(dfscaled.loc[:,'WT-1':'db/db-8'], cmap='bwr', vmin=-3, vmax=3, method='ward', linewidths=0,
                yticklabels=False, figsize=(15,10))


#make a correlation heatmap
df_corr = dflog.corr()
plt.figure(figsize=(7,5))
sns.heatmap(df_corr)


#make a violin and box plot of the scaled data to make sure it looks alright

plt.figure(figsize=(12,7))
sns.violinplot(x='level_1', y=0, data=dfscaled.loc[:,'WT-1':'db/db-8'].stack().reset_index())
plt.ylabel('')
plt.ylabel('Scaled Log2 TMT Intensity')

#remove the outlines from the violin plot
def patch_violinplot(palette, n):
    from matplotlib.collections import PolyCollection
    ax = plt.gca()
    violins = [art for art in ax.get_children() if isinstance(art, PolyCollection)]
    colors = sns.color_palette(palette, n_colors=n) * (len(violins)//n)
    for i in range(len(violins)):
        violins[i].set_edgecolor(colors[i])
patch_violinplot(sns.color_palette(), 8)

sns.despine()

plt.figure(figsize=(12,7))
ax = sns.boxplot(x='level_1', y=0, data=dfscaled.loc[:,'WT-1':'db/db-8'].stack().reset_index())
plt.ylabel('')
plt.xlabel('Mouse')
sns.despine()


#Export df for limma
#first I will export the intensities for analyzing protein differential expression
#then I will export the ratios used for the O-GlcNAcomics for normalization (will not run limma here)

#export the scaled intensities
dfscaled.loc[:, 'WT-1':'db/db-8'].to_csv('df_limma_pe.txt', sep='\t')

#also export the normalized and scaled dfs
dflog.to_csv('ProteinExpression_Values.csv', index=False)
dfscaled.to_csv('ProteinExpression_ScaledValues.csv', index=False)

#prepare a df with the ratios
df_A = dflog['db/db-5'].sub(dflog['WT-1'], axis=0)
df_B = dflog['db/db-6'].sub(dflog['WT-2'], axis=0)
df_C = dflog['db/db-7'].sub(dflog['WT-3'], axis=0)
df_D = dflog['db/db-8'].sub(dflog['WT-4'], axis=0)

#concatenate into a single dataframe
df_ratios = pd.concat([df_A, df_B, df_C, df_D], axis=1)
#rename the columns
df_ratios.columns = ['A', 'B', 'C', 'D']

#merge back with the original df of protein names
dfcorrection = pd.concat([dfscaled.loc[:,dfscaled.columns[0:3]], df_ratios], axis=1)

#export to csv
dfcorrection.to_csv('PE_corrections.csv', index=False)


%%R

#calculate the p-values for differentially expressed proteins with limma in R
```

```
#load limma
library(limma)

#read in the values
df = read.table('df_limma_pe.txt', sep='\t', header=TRUE, row.names=1) #read in the file

#set the experiment design
cond = factor(rep(c('WT','dbdb'), each=4))
design = model.matrix(~0+cond)
colnames(design) = levels(cond)

#set up the contrast (db/db vs WT)
contrast = makeContrasts(Diff=dbdb-WT, levels=design)

#run lmfit, contrasts, and ebayes
f1 = lmFit(df, design)
f2 = contrasts.fit(f1, contrast)
f3 = eBayes(f2)

#write the table
write.table(topTable(f3, coef='Diff', n=Inf, confint=.95), 'PE_limmaOut.csv', sep=',', col.names=NA)


#Read in the limma output, merge it back with the original df and export lists of up- and downregulated proteins

#read in limma output and concatenate
dflimma = pd.read_csv('PE_limmaOut.csv', index_col=0)
dfde = pd.concat([dfscaled.loc[:,dfscaled.columns[0:3]], dflimma], axis=1)

#find upregulated proteins
dfup = dfde[(dfde.logFC > 0) & (dfde['adj.P.Val'] < 0.05)]
dfdown = dfde[(dfde.logFC < 0) & (dfde['adj.P.Val'] < 0.05)]

#export gene lists for pathway analysis
dfup[['Gene', 'logFC']].to_csv('Proteins_Upregulated.csv', index=False)
dfdown[['Gene', 'logFC']].to_csv('Proteins_Downregulated.csv', index=False)
#Export final df and output relevant info
dfde.to_csv('Proteins_All.csv', index=False)

print('The number of differentially expressed proteins is:', len(dfde[(dfde['adj.P.Val'] < 0.05)]))
print('There are {} upregulated and {} downregulated proteins.'.format(len(dfup), len(dfdown)))
print('Total number of proteins quantified:', len(dfde))
print('Percent of proteins differentially expressed:', len(dfde[(dfde['adj.P.Val'] < 0.05)])/len(dfde)*100)


#Make the volcano plot for the differentially expressed proteins

#copy the df and take the negative log10 of the p value
dfvolcano = dflimma.copy()
dfvolcano['NegLogP'] = -np.log10(dfvolcano['adj.P.Val'])

#make the plot
plt.figure(figsize=(7,7))
g = sns.scatterplot(x='logFC', y='NegLogP', data=dfvolcano, edgecolor='k', facecolor='none', marker='o', s=25)
ax1 = g.axes
ax1.axhline(-np.log10(0.05), ls='--', color=(0.5,0.5,0.5,1), zorder=0, linewidth=1)
plt.xlabel('Log2 F.C.')
plt.ylabel('-Log10 P-Value')


#Make box plots of OGT and OGA

dfplots = dfscaled.T.drop(index={'Majority protein IDs', 'Fasta headers'})

dfplots.columns = dfplots.iloc[0]
dfplots.drop(index={'Gene'}, inplace=True)

dfplots.index = dfplots.index.str.replace('-(.?)', '', regex=True)
dfplots = dfplots.reset_index().rename(columns={'index':'Condition'})
#dfplots.rename(index={'index'}, inplace=True)

dfogt = dfplots[['Condition', 'Ogt']]
dfogt['Gene'] = 'Ogt'
dfogt.rename(columns={'Ogt':'Expression'}, inplace=True)
dfoga = dfplots[['Condition', 'Oga']]
dfoga['Gene'] = 'Oga'
dfoga.rename(columns={'Oga':'Expression'}, inplace=True)


df_toplot = pd.concat([dfogt,dfoga], ignore_index=True)

fig, ax = plt.subplots(figsize=(7,7))
g = sns.stripplot(x='Gene', y='Expression', data=df_toplot, hue='Condition', dodge=True, s=10, zorder=1)
g = sns.boxplot(x='Gene', y='Expression', data=df_toplot, hue='Condition', dodge=True)

lgnd = plt.legend()
lgnd.legendHandles[3]._sizes = [1000]

handles, labels = ax.get_legend_handles_labels()
ax.legend(handles=handles[2:4], labels=labels[2:4], frameon=False, bbox_to_anchor=(1.25, 0.6))

plt.ylabel('Scaled Log2 TMT Intensity')
plt.xlabel('')
```

```
plt.setp(ax.artists, edgecolor = 'k', facecolor='w')
plt.setp(ax.lines, color='k')

sns.despine()


#Export gene grouped protein logFC for cytoscape
dfde_cytoscape = dfde[['Gene', 'logFC', 'adj.P.Val']]
dfde_cytoscape.loc[dfde_cytoscape['adj.P.Val'] < 0.05, 'SigProtFC'] = 'Yes'
dfde_cytoscape.drop(columns={'adj.P.Val'},inplace=True)
dfcyto1 = dfde_cytoscape.groupby('Gene').mean().reset_index()
dfcyto1.rename(columns={'logFC':'ProteinLogFC'}, inplace=True)
dfde_cytoscape.sort_values(by='SigProtFC', inplace=True)
dfde_cytoscape.drop_duplicates(subset='Gene', inplace=True)
dfcytoscape = dfcyto1.merge(dfde_cytoscape[['Gene', 'SigProtFC']], on='Gene', how='left')
dfcytoscape.Gene = dfcytoscape.Gene.str.upper()
dfcytoscape.to_csv('ProteinFC_ForCytoscape.csv', index=False)
```

A7.5.3. Sites and Regions Analysis.

The sites and regions is implemented as described in **Chapter 5**, see **A5.6.5** for code. This analysis will have the following parts:

1. Preprocessing the quantitative information. The msms scan numbers from the search including the O-GlcNAc modifications sites will be matched to those identified as coming from quantified precursors in the search not including the modifications but looking for +/- 6 isotope patterns. Ultimately, this will add H/L ratios to the msms file that can be used after the sites and regions analysis in part 3. This code is the result of discussions with Mike Sweredoski and partially inspired by his script, matchFoundPeptideRatios.py.
2. Perform sites and regions of each 601 and 607 dataset independently. This will give the “db/db sites” and the “WT sites” as separate tables.
3. The localization probabilities will then be set equal and 601/607 data removed to create a GlcNAc database in both conditions. This will then be subjected to the experiment specific sites and regions analysis (based on liver pair, technical replicates will be averaged later) and the H/L ratios will be used to perform “region-level” quantification.

4. Calculate the overlap between sites identified in the db/db vs WT livers using the multiexperiment sites and regions script.

```
#import python packages
import re
import sys
import pandas as pd
import networkx as nx
import itertools as it
from collections import namedtuple
import numpy as np
import matplotlib
import matplotlib.pyplot as plt
from IPython.display import display
from functools import reduce
import seaborn as sns; sns.set()
from io import StringIO
from matplotlib_venn import venn2_unweighted
from matplotlib_venn import venn2
import venn
import pandas as pd
import numpy as np
from io import StringIO
import urllib.request, urllib.parse, urllib.error,urllib.request,urllib.error,urllib.parse
import math

#set up R environment and import R packages
import rpy2
import rpy2.ipython
%load_ext rpy2.ipython

#require R packages
%R require(limma)
%R require(ibb)

#magic function to show plots inline
%matplotlib inline

#ignore warnings
import warnings
warnings.filterwarnings("ignore")


#Import the files

#set folder names
qfolder = './Liver_Quant/'
sfolder = './Liver_Glycomics/'

#import the files
dfmsms = pd.read_csv('{}msms.txt'.format(sfolder), sep='\t')
dfallpep = pd.read_csv('{}allPeptides.txt'.format(qfolder), sep='\t')

#take the relevant info from the allPeptides file, remove unneeded spectra, and rename the MSMS Scan Number column for
    #matching
dfall2 = dfallpep[['Raw file', 'Charge', 'Mass', 'Pyl Count', 'Ratio H/L', 'MS/MS Count', 'MSMS Scan Numbers']]
dfall2 = dfall2[(dfall2['Pyl Count'] != "") & (dfall2['MS/MS Count'] > 0)]
dfall2.rename(columns={'MSMS Scan Numbers':'Scan number'}, inplace=True)

#remove contaminants, reverse sequences, and peptides modified by both 601 and 607 from the msms file
dfmsms2 = dfmsms[dfmsms.Reverse != '+']
dfmsms2 = dfmsms2[~dfmsms2.Proteins.str.contains('CON_')]
dfmsms2 = dfmsms2[~(dfmsms2.Modifications.str.contains('GlcNAc601') & (dfmsms2.Modifications.str.contains('GlcNAc607')))]
```

Part 1

```
#Expand the scan number column of the all peptides file into duplicate rows and merge with the msms file

#change the scan number to a list and explode values to duplicate rows
dfall3 = dfall2.copy()
dfall3['Scan number'] = dfall2['Scan number'].str.split(';')
dfall4 = dfall3.explode('Scan number')
dfall5 = dfall4.copy()
dfall5['Scan number'] = dfall4['Scan number'].astype(int)

#merge this with the msms file on raw file, change, and scan number
dfm = dfmsms2.merge(dfall5, on=['Raw file', 'Scan number', 'Charge'], how='left')

#renmae the all peptides mass
dfm.rename(columns={'Mass_y':'Mass_QuanSearch'}, inplace=True)
```

Part 2

```
#Preproces this data for the sites and regions script (first with the 601, then with the 607 tag)
#adapted from 'preprocessMQ.py' written by Mike Sweredoski on Jan 24, 2020

###GlcNAc601
MOD_NAME = "GlcNAc601"
pepProbPatt = re.compile(r'[A-Z][()?\d?[.]?\d*[)]?')

PepInfo = namedtuple("PepInfo",["Protein","StartPos"])
peptideInfo = {}

# Get peptide start positions
pepDF = pd.read_csv("{}peptides.txt".format(sfolder), sep='\t')
for peptide in pepDF[["id","Leading razor protein","Start position"]].itertuples():
    if math.isnan(peptide[3]):
        peptideInfo[peptide.id] = PepInfo(peptide[2],-1)
    else:
        peptideInfo[peptide.id] = PepInfo(peptide[2],int(peptide[3]))

msmsDF = dfm
msmsDF = msmsDF[msmsDF[MOD_NAME]>0]
msmsDF["Protein"] = msmsDF["Peptide ID"].apply(lambda x: peptideInfo[x].Protein)
msmsDF["StartPos"] = msmsDF["Peptide ID"].apply(lambda x: peptideInfo[x].StartPos)
msmsDF = msmsDF[msmsDF["StartPos"]>=0]
msmsDF.rename(columns={"Raw file":"RawFile","Scan number":"ScanNumber",MOD_NAME:"NumMods", "Ratio H/L":"Ratio"},
              inplace=True)
msmsDF["Probabilities"] = msmsDF.apply(
    lambda x: ";".join([aa[2:-1] for pp,aa in enumerate(pepProbPatt.findall(
        x["%s Probabilities"%MOD_NAME])) if len(aa) > 1]),axis=1)
msmsDF["Positions"] = msmsDF.apply(
    lambda x: ";".join([str(pp+x["StartPos"]) for pp,aa in enumerate(pepProbPatt.findall(
        x["%s Probabilities"%MOD_NAME])) if len(aa) > 1]),axis=1)

msmsDF[["RawFile","Protein","ScanNumber","NumMods","Positions","Probabilities","Ratio"]].to_csv(
    '601_Preprocessed.txt', sep="\t", index=False)

###GlcNAc607
MOD_NAME = "GlcNAc607"
pepProbPatt = re.compile(r'[A-Z][()?\d?[.]?\d*[)]?')

PepInfo = namedtuple("PepInfo",["Protein","StartPos"])
peptideInfo = {}

# Get peptide start positions
pepDF = pd.read_csv("{}peptides.txt".format(sfolder), sep='\t')
for peptide in pepDF[["id","Leading razor protein","Start position"]].itertuples():
    if math.isnan(peptide[3]):
        peptideInfo[peptide.id] = PepInfo(peptide[2],-1)
    else:
        peptideInfo[peptide.id] = PepInfo(peptide[2],int(peptide[3]))

msmsDF = dfm
msmsDF = msmsDF[msmsDF[MOD_NAME]>0]
msmsDF["Protein"] = msmsDF["Peptide ID"].apply(lambda x: peptideInfo[x].Protein)
msmsDF["StartPos"] = msmsDF["Peptide ID"].apply(lambda x: peptideInfo[x].StartPos)
msmsDF = msmsDF[msmsDF["StartPos"]>=0]
msmsDF.rename(columns={"Raw file":"RawFile","Scan number":"ScanNumber",MOD_NAME:"NumMods", "Ratio H/L":"Ratio"},
              inplace=True)
msmsDF["Probabilities"] = msmsDF.apply(
    lambda x: ";".join([aa[2:-1] for pp,aa in enumerate(pepProbPatt.findall(
        x["%s Probabilities"%MOD_NAME])) if len(aa) > 1]),axis=1)
msmsDF["Positions"] = msmsDF.apply(
    lambda x: ";".join([str(pp+x["StartPos"]) for pp,aa in enumerate(pepProbPatt.findall(
        x["%s Probabilities"%MOD_NAME])) if len(aa) > 1]),axis=1)

msmsDF[["RawFile","Protein","ScanNumber","NumMods","Positions","Probabilities","Ratio"]].to_csv(
    '607_Preprocessed.txt', sep="\t", index=False)
%%capture
#supresses the output of the cell

#Run the sites and regions script for each experiment
%run -i SitesAndRegions.py 601_Preprocessed.txt maxparcon_601.txt bestms2_601.txt
%run -i SitesAndRegions.py 607_Preprocessed.txt maxparcon_607.txt bestms2_607.txt
#Import the sites and regions output into dfs and count the number of sites for each

list_dfs2 = ['601', '607']
list_exp = ['WT', 'db/db']

for i in list_dfs2:
    locals()['dfallsites_{}'.format(i)] = pd.read_csv('bestms2_{}.txt'.format(i), sep='\t')
    locals()['dfregions_{}'.format(i)] = pd.read_csv('maxparcon_{}.txt'.format(i), sep='\t')
    #remove sites/regions that match to two master proteins
    #this seems to happen sometimes when there is real evidence of two isoforms
    #all cases checked were already explained by other data, so they can be reasonably ignored
    locals()['dfregions_{}'.format(i)] = locals()['dfregions_{}'.format(i)][
        ~locals()['dfregions_{}'.format(i)].Protein.str.contains(';')]
    locals()['dfallsites_{}'.format(i)] = locals()['dfallsites_{}'.format(i)][
        ~locals()['dfallsites_{}'.format(i)].Protein.str.contains(';')]

#initialize an empty df
df_numsites = pd.DataFrame(np.empty((2,5)))

#calculate the number of sites, localized sites, and regions
for i in range (2):
    #set the column and index names
    df_numsites.columns = [['Total Number of Sites', 'Localized Sites', 'Unlocalized Sites', 'Regions',
```

```
                            'Percent Localized']]
    df_numsites.rename(index={i:list_dfs2[i]}, inplace=True)
    #count the total number of sites
    df_numsites.loc[list_dfs2[i], 'Total Number of Sites'] = \
    locals()['dfregions_{}'.format(list_dfs2[i])]['Min Sites'].sum()
    #count the number of localized sites
    df_numsites.loc[list_dfs2[i], 'Localized Sites'] = len(
        locals()['dfregions_{}'.format(list_dfs2[i])][
            locals()['dfregions_{}'.format(list_dfs2[i])]['Site ID Constraints'].str.contains('of') == False])
    df_numsites.loc[list_dfs2[i], 'Unlocalized Sites'] = locals()['dfregions_{}'.format(list_dfs2[i])][
        locals()['dfregions_{}'.format(list_dfs2[i])][
            'Site ID Constraints'].str.contains('of') == True]['Min Sites'].sum()
    df_numsites.loc[list_dfs2[i], 'Regions'] = len(
        locals()['dfregions_{}'.format(list_dfs2[i])][
            locals()['dfregions_{}'.format(list_dfs2[i])]['Site ID Constraints'].str.contains('of') == True])
    df_numsites.loc[list_dfs2[i], 'Percent Localized'] = \
    (df_numsites.loc[list_dfs2[i], 'Localized Sites'].to_numpy() / df_numsites.loc[
        list_dfs2[i], 'Total Number of Sites'].to_numpy())*100

df_numsites.rename(index={'601':'601 WT', '607':'607 db/db'}, inplace=True)
df_numsites = df_numsites.astype(int) #convert to ints
df_numsites.to_csv('SitesAndRegionsCount.csv') #export
df_numsites #inspect


#Make pie charts of the sites and regions (with the sites stratified by localization probability)

#add to the max parsimonious site constraints file whether each region is a site or a region
for i in list_dfs2:
    locals()['dfregions_{}'.format(i)].loc[
        locals()['dfregions_{}'.format(i)]['Site ID Constraints'].str.contains('of'), 'Type'] = 'Region'
    locals()['dfregions_{}'.format(i)].loc[
        ~locals()['dfregions_{}'.format(i)]['Site ID Constraints'].str.contains('of'), 'Type'] = 'Site'

#merge with best ms2 for sites file
for i in list_dfs2:
    locals()['dfmerge_{}'.format(i)] = locals()['dfallsites_{}'.format(i)].merge(
        locals()['dfregions_{}'.format(i)], how='left', on='Region ID')
    #now fill the bins with values for the pie chart
    locals()['regions_{}'.format(i)] = locals()['dfregions_{}'.format(i)][
        locals()['dfregions_{}'.format(i)].Type == 'Region']['Min Sites'].sum()
    locals()['bin975_{}'.format(i)] = len(
        locals()['dfmerge_{}'.format(i)][(locals()['dfmerge_{}'.format(i)].Type == 'Site') &
                                         (locals()['dfmerge_{}'.format(i)]['Best Probability'] < 0.9)])
    locals()['bin99_{}'.format(i)] = len(
        locals()['dfmerge_{}'.format(i)][(locals()['dfmerge_{}'.format(i)].Type == 'Site') &
                                         ((locals()['dfmerge_{}'.format(i)]['Best Probability'] >= 0.9) &
                                          (locals()['dfmerge_{}'.format(i)]['Best Probability'] < 0.99))])
    locals()['bin991_{}'.format(i)] = len(
        locals()['dfmerge_{}'.format(i)][(locals()['dfmerge_{}'.format(i)].Type == 'Site') &
                                         ((locals()['dfmerge_{}'.format(i)]['Best Probability'] >= 0.99) &
                                          (locals()['dfmerge_{}'.format(i)]['Best Probability'] < 1))])
    locals()['bin1_{}'.format(i)] = len(
        locals()['dfmerge_{}'.format(i)][(locals()['dfmerge_{}'.format(i)].Type == 'Site') &
                                         (locals()['dfmerge_{}'.format(i)]['Best Probability'] == 1)])

for i in list_dfs2:
    locals()['list_values_{}'.format(i)] = [locals()['regions_{}'.format(i)], locals()['bin975_{}'.format(i)],
                                            locals()['bin99_{}'.format(i)], locals()['bin991_{}'.format (i)],
                                            locals()['bin1_{}'.format(i)]]

#make the pie charts
sns.set_context('poster')

#make a list of labels and colors to use
list_labels = ['Unlocalized', '<90%', '90-99%', '99-100%', '100%']
colors = ["#cbcdcd", "#f39b9f", "#9aacd7", "#be9ec7", "#b3e0a7"]
explode = (0.1, 0, 0, 0, 0) #to have the regions pop out separately

###WT###
plt.figure(figsize=(7,7))
plt.title('WT', weight='bold')
p, tx, nums = plt.pie(list_values_601, labels=list_labels, colors=colors, autopct="", startangle=90)
for i, a in enumerate(nums):
    a.set_text('{}'.format(list_values_601[i]))
local_prob_601 = ('Average Localization Probability: ' +
                  str(round(dfmerge_601[dfmerge_601.Type == 'Site']['Best Probability'].mean()*100, 1)) + '%')
plt.gcf().text(0.5, 0.1, local_prob_601, fontsize=24, ha='center')
plt.savefig('601Sites_PieChart.svg')
plt.show()

###db/db###
plt.figure(figsize=(7,7))
plt.title('db/db', weight='bold')
p, tx, nums = plt.pie(list_values_607, labels=list_labels, colors=colors, autopct="", startangle=90)
for i, a in enumerate(nums):
    a.set_text('{}'.format(list_values_607[i]))
local_prob_607 = ('Average Localization Probability: ' +
                  str(round(dfmerge_607[dfmerge_607.Type == 'Site']['Best Probability'].mean()*100, 1)) + '%')
plt.gcf().text(0.5, 0.1, local_prob_607, fontsize=24, ha='center')
plt.savefig('607Sites_PieChart.svg')
plt.show()
```

Part 3

```
#Preprocess the msms file

#copy the previous df
dfmq = dfm.copy()

#remove the 601/607 identifier
dfmq.replace(['GlcNAc601', 'GlcNAc607'], 'GlcNAc', inplace=True)

#remove psms where the number of mods is not equal to the number of mods used for the ratio calculation
#this will remove all sites without ratios
dfmqf = dfmq[(dfmq.GlcNAc601 == dfmq['Pyl Count']) | (dfmq.GlcNAc607 == dfmq['Pyl Count'])]

#set new mod name
MOD_NAME = "GlcNAc"
pepProbPatt = re.compile(r'[A-Z][(]?\d?[.]?\d*[)]?')

PepInfo = namedtuple("PepInfo",["Protein","StartPos"])
peptideInfo = {}

# Get peptide start positions
pepDF = pd.read_csv("{}peptides.txt".format(sfolder), sep='\t')
for peptide in pepDF[["id","Leading razor protein","Start position"]].itertuples():
    if math.isnan(peptide[3]):
        peptideInfo[peptide.id] = PepInfo(peptide[2],-1)
    else:
        peptideInfo[peptide.id] = PepInfo(peptide[2],int(peptide[3]))

msmsDF = dfmqf
msmsDF = msmsDF[msmsDF.Modifications.str.contains("GlcNAc")]
msmsDF["Protein"] = msmsDF["Peptide ID"].apply(lambda x: peptideInfo[x].Protein)
msmsDF["StartPos"] = msmsDF["Peptide ID"].apply(lambda x: peptideInfo[x].StartPos)
msmsDF = msmsDF[msmsDF["StartPos"]>=0]
msmsDF.rename(columns={"Raw file":"RawFile","Scan number":"ScanNumber", "Ratio H/L":"Ratio"},
              inplace=True)
msmsDF['NumMods'] = msmsDF[["GlcNAc601","GlcNAc607"]].sum(axis=1)

#enumerate separately for 601 and 607 (there should be no overlapping sites)
#convert site prob columns to string
msmsDF[["GlcNAc601 Probabilities","GlcNAc607 Probabilities"]] = \
msmsDF[["GlcNAc601 Probabilities","GlcNAc607 Probabilities"]].astype(str)
msmsDF.loc[msmsDF.GlcNAc601 > 0, "Probabilities"] = msmsDF.apply(
    lambda x: ";".join([aa[2:-1] for pp,aa in enumerate(pepProbPatt.findall(
        x["GlcNAc601 Probabilities"])) if len(aa) > 1]),axis=1)
msmsDF.loc[msmsDF.GlcNAc607 > 0, "Probabilities"] = msmsDF.apply(
    lambda x: ";".join([aa[2:-1] for pp,aa in enumerate(pepProbPatt.findall(
        x["GlcNAc607 Probabilities"])) if len(aa) > 1]),axis=1)
msmsDF.loc[msmsDF.GlcNAc601 > 0, "Positions"] = msmsDF.apply(
    lambda x: ";".join([str(pp+x["StartPos"]) for pp,aa in enumerate(pepProbPatt.findall(
        x["GlcNAc601 Probabilities"])) if len(aa) > 1]),axis=1)
msmsDF.loc[msmsDF.GlcNAc607 > 0, "Positions"] = msmsDF.apply(
    lambda x: ";".join([str(pp+x["StartPos"]) for pp,aa in enumerate(pepProbPatt.findall(
        x["GlcNAc607 Probabilities"])) if len(aa) > 1]),axis=1)

df1_table = msmsDF[["RawFile","Protein","ScanNumber","NumMods","Positions","Probabilities","Ratio"]]
#Set localization probabilities to equal and export for sites and regions script

#set columns to keep in final df
cols_to_keep = ["RawFile","Protein","ScanNumber","NumMods","Positions","Probabilities","Ratio"]

#copy the df
df2_table = df1_table.copy()

#keeping the for loop structure from 20D09
i = 2
#count the number of S/Ts
locals()['df{}_table'.format(i)]['NumSites'] = locals()['df{}_table'.format(i)].Probabilities.str.count(';') + 1
#calculate the probability at each site based on the number of S/Ts (round to 3 decimals as in MQ)
locals()['df{}_table'.format(i)]['Prob'] = round(1/locals()['df{}_table'.format(i)].NumSites, 3)
#define a function to make a repeating list of probability values based on the number of S/Ts
def repeat(row):
    return [row.Prob]*row.NumSites
#apply this function to each df
locals()['df{}_table'.format(i)]['ProbList'] = locals()['df{}_table'.format(i)].apply(repeat, axis=1)
#transform the list into a semi-colon separated string for the sites and regions script
locals()['df{}_table'.format(i)]['ProbListFinal'] = locals()['df{}_table'.format(i)].ProbList.apply(
    lambda s: ';'.join(map(str, s)))
#replace all probability values
locals()['df{}_table'.format(i)]['Probabilities'] = locals()['df{}_table'.format(i)].ProbListFinal
#remake the original table with the columns required for the sites and regions script
locals()['df{}_tableF'.format(i)] = locals()['df{}_table'.format(i)][cols_to_keep]

#make a new column to denote the experiment

#set lists for experiment identifiers
list_mouse = ['A', 'B', 'C', 'D']
list_replicate = ['20171218', '20180223']

#rename the raw files for easier parsing
df2_tableF.RawFile.replace('Smpl-','', regex=True, inplace=True)

#add the experiment identifier column
```

```
for i in range(4):
    for j in range(2):
        df2_tableF.loc[(df2_tableF.RawFile.str.contains('_{}'.format(list_mouse[i])) &
                        df2_tableF.RawFile.str.contains(
                            '{}'.format(list_replicate[j]))), 'Experiment'] = '{}_{}'.format(list_mouse[i],j+1)

#export final table to txt file for sites and regions multi-experiment script
df2_tableF.to_csv('QuantSitesAndRegions_Preprocessed.txt'.format(i), sep='\t', index=False)
%%capture
#supresses the output of the cell

#Run the sites and regions script
%run -i SitesAndRegionsMultiExperiment.py QuantSitesAndRegions_Preprocessed.txt maxparcon_Quant.txt \
bestms2_Quant.txt
#Import the output and as in the 20D09 script
dfallsitesq = pd.read_csv('bestms2_Quant.txt', sep='\t')
dfregionsq = pd.read_csv('maxparcon_Quant.txt', sep='\t')
dfallsitesq = dfallsitesq[~dfallsitesq.Protein.str.contains(';')]
dfregionsq = dfregionsq[~dfregionsq.Protein.str.contains(';')]
dfregionsq.loc[dfregionsq['Site ID Constraints'].str.contains('of'), 'Type'] = 'Region'
dfregionsq.loc[~dfregionsq['Site ID Constraints'].str.contains('of'), 'Type'] = 'Site'
dfmergeq = dfallsitesq.merge(dfregionsq, how='left', on='Region ID')

#make two new experiment columns for replicate and mouse (facilitates making Venn diagrams)

for i in list_mouse:
    dfmergeq.loc[dfmergeq.Experiment.str.contains(i), 'Mouse'] = i

for i in range(2):
    dfmergeq.loc[dfmergeq.Experiment.str.contains(str(i+1)), 'Replicate'] = str(i+1)

#clean up this df
dfmergeq.rename(columns={'Protein_x': 'Protein'}, inplace=True)
dfmergeq.drop(columns={'Protein_y'}, inplace=True)
#Make Venn diagrams of the overlap between experiments and technical replicates

mouse_dict ={}

for i in list_mouse:
    mouse_dict['Pair {}'.format(i)] = set(dfmergeq[dfmergeq.Mouse == i]['Region ID'])

for i in range(2):
    locals()['set_{}'.format(i+1)] = set(dfmergeq[dfmergeq.Replicate == str(i+1)]['Region ID'])

plt.figure(figsize=(7,7))
venn.venn(mouse_dict, fontsize=18, legend_loc=None)
plt.title('Biological Replicate Overlap', fontsize=36)
plt.gcf().text(0.05, 0.5, 'Pair A', fontsize=24, ha='left')
plt.gcf().text(0.2, 0.7, 'Pair B', fontsize=24, ha='left')
plt.gcf().text(0.82, 0.7, 'Pair C', fontsize=24, ha='right')
plt.gcf().text(0.97, 0.5, 'Pair D', fontsize=24, ha='right')
plt.savefig('MouseRegionOverlap_Venn.svg')

plt.figure(figsize=(7,7))
fig = venn2([set_1, set_2], ('Replicate 1', 'Replicate 2'))
plt.title('Technical Replicate Overlap', fontsize=36)
for text in fig.set_labels:
    text.set_fontsize(32)
for text in fig.subset_labels:
    text.set_fontsize(24)
plt.savefig('ReplicateRegionOverlap_Venn.svg')


#Merge with the preprocssed dataframe to get the ratios

#first normalize the ratios in df_tableF by median sweeping

#copy the df
dfratios = df2_tableF.copy()

#merge with previous table on raw file, scan number, and protein
#note that all proteins that don't match will be discarded (decided based on score by the sites and regions script)
    #these may be real sites, but they will be ignored for the quantification, if there are really 2 peptides matching
    #to the same precursor, there is no way to quantify them seperately anyway
dfmergeqf = dfmergeq.rename(columns={'Best Scan Number':'ScanNumber', 'Best Raw File':'RawFile'})
dfq = dfmergeqf.merge(dfratios, on=['RawFile', 'ScanNumber', 'Protein', 'Experiment'])

#log 2 transform the ratios
dfq['LogRatio'] = np.log2(dfq.Ratio)

#subtract the median by experiment
for i in dfq.Experiment.unique():
    dfq.loc[dfq.Experiment == i, 'RatioNorm'] = dfq.loc[dfq.Experiment == i, 'LogRatio'].sub(
        dfq[dfq.Experiment ==  i]['LogRatio'].median())

#group the data by mouse (averagign the technical replicates together) and merge with the original regions df
dfrf = dfregionsq.merge(dfq.groupby(['Region ID', 'Mouse']).RatioNorm.mean().unstack(), on='Region ID', how='left')

#export for limma
dfrf.to_csv('Regions_Limma.csv')
%%R

#Perform limma on regions to find differentially expressed sites

#load limma
```

```
library(limma)

#read in the values
df = read.table('Regions_Limma.csv', sep=',', header=TRUE, row.names=1) #read in the file
df1 = df[c('A', 'B', 'C', 'D')] #take only relevant columns

#run limma
f1 = eBayes(lmFit(df1))

#write the output
write.table(topTable(f1,n=Inf,confint=.95),'RegionsRatios_limmaOut.csv', sep=',', col.names=NA)
#Read in the limma output and merge it back with the original df

#read in limma output and concatenate
dflimma = pd.read_csv('RegionsRatios_limmaOut.csv', index_col=0)
dfde = pd.concat([dfrf.loc[:,dfrf.columns[0:3]], dflimma], axis=1)
#Query uniprot to get list of gene names

#define input
uniprot_input = dfde.Protein

#define variables
url = 'https://www.uniprot.org/uploadlists/'
user_agent = 'Mozilla/5.0 (Windows NT 10.0; Win64; x64)'

#make a dictionary for the requests
params = {
    "from":"ACC+ID",
    "to":"ACC",
    "format":"tab",
    "columns": "genes(PREFERRED)",
    "query":" ".join(uniprot_input)
}

#query uniprot
data = urllib.parse.urlencode(params, doseq=False)
data = data.encode('ascii')
headers = {"User-Agent": user_agent}
request = urllib.request.Request(url, data, headers)
response = urllib.request.urlopen(request)
with urllib.request.urlopen(request) as f:
   response = f.read().decode()

#make a dataframe from the output
df_res = pd.read_csv(StringIO(response), sep='\t')
df_res #inspect


#Add the gene names to the ratios table from above based on the uniprot output
#Then, normalize the ratios based on the protein expression ratios

#copy the df
dfde1 = dfrf.copy()

dfde1.insert(1, 'Gene', dfde.Protein)

#rename the uniprot output columns
df_res.rename(columns={df_res.columns[0]: "Gene", df_res.columns[1]: "UniprotID"}, inplace=True)

#set up the dictionary for mapping
di = df_res.set_index('UniprotID')['Gene'].to_dict()

#replace the gene name column in the ratios df with the gene name based on the above dictionary
dfde1['Gene'].replace(di, inplace=True)

#import the protein expression output
dfpe = pd.read_csv('PE_corrections.csv')

#average the fold change for duplicate genes and fill na with 0s
dfpec = dfpe.groupby('Gene').mean()

#rename the columns
dfde1.rename(columns={'A':'ASite', 'B':'BSite', 'C':'CSite', 'D':'DSite'}, inplace=True)

#merge the two dataframes (validating that there are not duplicate gene names in the proteins file)
dfcpe = dfde1.merge(dfpec, on='Gene', how='left', validate='m:1')

#export this to csv
dfcpe.to_csv('RegionsAndProteins_Ratios.csv')

#copy the df and fill nans in protein ratios with 0s
dfcpe1 = dfcpe.copy()
dfcpe1[['A', 'B', 'C', 'D']] = dfcpe1[['A', 'B', 'C', 'D']].fillna(0)

#subtract the protein expression column (taking the ratio of ratios)
for i in list_mouse:
    dfcpe1['{}Corrected'.format(i)] = dfcpe1['{}Site'.format(i)] - dfcpe1['{}'.format(i)]

#make a new column to indicate if it was corrected or not (there are no missing values in protein expression df)
dfcpe1.loc[dfcpe1.A == 0, 'Corrected'] = 'No'
dfcpe1.loc[dfcpe1.A != 0, 'Corrected'] = 'Yes'

#output relevant columns for limma
dfcpe1.iloc[:,np.r_[0:6,14:18]].to_csv('CorrectedRatios_Limma.csv')
%%R
```

```
#Perform limma on corrected regions to find differentially expressed sites

#load limma
library(limma)

#read in the values
df = read.table('CorrectedRatios_Limma.csv', sep=',', header=TRUE, row.names=1) #read in the file
df1 = df[c('ACorrected', 'BCorrected', 'CCorrected', 'DCorrected')] #take only relevant columns

#run limma
f1 = eBayes(lmFit(df1))

#write the output
write.table(topTable(f1,n=Inf,confint=.95),'CorrectedRatios_limmaOut.csv', sep=',', col.names=NA)
#Import the limma output, clean up, export up and downregulated sites, and export a new df with final ratios
#Export a df for cytoscape with genes and changing sites for cytoscape

df_limma_c = pd.read_csv('CorrectedRatios_limmaOut.csv', index_col=0)
df_limma_c.rename(columns={'adj.P.Val':'P-Val_Corrected', 'B':'B_Corrected', 'logFC':'logFC_Corrected'}, inplace=True)

#make a copy of the previous final ratios df and add the protein expression corrected columns in
dfde_c = dfde.copy()
dfde_c[['logFC_Corrected', 'P-Val_Corrected', 'B_Corrected']] = df_limma_c[['logFC_Corrected', 'P-Val_Corrected',
                                                                           'B_Corrected']]

#drop other limma data, rename columns to be consistent, add corrected and gene columns back in, and export
dfde_c.drop(columns={'CI.R', 'CI.L', 'AveExpr', 't', 'P.Value'}, inplace=True)
dfde_c.rename(columns={'adj.P.Val':'P-Val'}, inplace=True)
dfde_c['Corrected for Protein Expression'] = dfcpe1.Corrected
dfde_cf = dfde_c.copy()
dfde_cf.insert(1, 'Gene', dfcpe1.Gene)
dfde_cf.insert(3, 'Site ID Constraints', dfregionsq['Site ID Constraints'])
dfde_cf.to_csv('CorrectedRatios_Regions.csv', index=False)

#now make a table for importing into cytoscape

#take the relevant columns
df_ForCytoscape = dfde_cf[['Gene', 'Protein', 'Site ID Constraints', 'logFC_Corrected', 'P-Val_Corrected',
                           'Corrected for Protein Expression']]

#add an additional column for cytoscape splicing, and combine rows with the same gene
df_ForCytoscape.loc[dfde_cf['P-Val_Corrected'] < 0.05, 'Significantly Changing Site'] = 1

#concatentate sites/regions together with their position and fold change in a new column
df_ForCytoscape['Sites_Regions'] = (df_ForCytoscape['Protein'] + '@' +
                                               df_ForCytoscape['Site ID Constraints'] + ' (FC: ' +
                                               df_ForCytoscape['logFC_Corrected'].round(2).astype(str) +')')

#import the output of all protein logFC and protein logFC (grouped by gene) to df
dfpfc = pd.read_csv('Proteins_All.csv')
dfpfc = dfpfc[['Gene', 'logFC']]
dfpfc.rename(columns={'logFC':'ProteinLogFC'}, inplace=True)
dfpfc_g = dfpfc.groupby('Gene').mean()
df_ForCytoscape1 = df_ForCytoscape.merge(dfpfc_g, on='Gene', how='left')

#calculate the average fold change per gene and save in a separate df
dfavgFC = df_ForCytoscape1.groupby(['Gene'])['logFC_Corrected'].mean().reset_index()
dfavgFC.rename(columns={'logFC_Corrected':'AvgLogFC'}, inplace=True)

#store the concatenated sites/regions for each gene as a separate df
dfsrconcat = df_ForCytoscape1.groupby(['Gene'])['Sites_Regions'].apply('; '.join).reset_index()
dfsrconcat.rename(columns={'Sites_Regions':'O-GlcNAc Sites and Regions'}, inplace=True)

#store the concatenated significant sites/regions for each gene as a separate df
dfsigsrconcat = df_ForCytoscape1[df_ForCytoscape1['Significantly Changing Site'] == 1].groupby(
    ['Gene'])['Sites_Regions'].apply('; '.join).reset_index()
dfsigsrconcat.rename(columns={'Sites_Regions':'Significant Sites and Regions'}, inplace=True)

#combine everything together in the same df
df_ForCytoscape1 = df_ForCytoscape1.merge(dfavgFC, how='left', on='Gene')
df_ForCytoscape1 = df_ForCytoscape1.merge(dfsrconcat, how='left', on='Gene')
df_ForCytoscape1 = df_ForCytoscape1.merge(dfsigsrconcat, how='left', on='Gene')
df_ForCytoscape1.Gene = df_ForCytoscape1.Gene.str.upper()

#export for loading into cytoscape
df_ForCytoscape1[['Gene', 'AvgLogFC', 'ProteinLogFC', 'Corrected for Protein Expression', 'O-GlcNAc Sites and Regions',
                  'Significant Sites and Regions']].to_csv('RegionsAndProteinExpression_ForCytoscape.csv', index=False)
#Make a Venn diagram of significant regions before and after protein expression

set_uncorrected = set(dfde[dfde['adj.P.Val'] < 0.05]['Region ID'])
set_corrected = set(dfde_c[dfde_c['P-Val_Corrected'] < 0.05]['Region ID'])

plt.figure(figsize=(7,7))
fig = venn2([set_uncorrected, set_corrected], ('Uncorrected', ''))
plt.title('Significant Regions Overlap', fontsize=36)
for text in fig.set_labels:
    text.set_fontsize(32)
for text in fig.subset_labels:
    text.set_fontsize(24)
plt.gcf().text(0.9, 0.125, 'Corrected for\nProtein Expression', fontsize=32, ha='center')
plt.savefig('ReplicateRegionOverlap_Venn.svg')

#Export upregulated and downregulated sites for pathway analysis
```

```
#slice out the signficantly changing genes
dfup = dfde_cf[(dfde_cf.logFC_Corrected > 0) & (dfde_cf['P-Val_Corrected'] < 0.05)]
dfdown = dfde_cf[(dfde_cf.logFC_Corrected < 0) & (dfde_cf['P-Val_Corrected'] < 0.05)]

#group by gene
dfupgene = dfup.groupby('Gene').mean().reset_index()[['Gene', 'logFC_Corrected']]
dfdowngene = dfdown.groupby('Gene').mean().reset_index()[['Gene', 'logFC_Corrected']]

#rename the columns
dfupgene.rename({'logFC_Corrected':'logFC'}, axis=1, inplace=True)
dfdowngene.rename({'logFC_Corrected':'logFC'}, axis=1, inplace=True)

#export gene lists for pathway analysis
dfupgene[['Gene', 'logFC']].to_csv('Regions_Upregulated.csv', index=False)
dfdowngene[['Gene', 'logFC']].to_csv('Regions_Downregulated.csv', index=False)
#Output the number of upregulated and downregulated sites as well as how many were corrected for protein expression
print('In total, there were {} upregated regions on {} proteins.'.format(len(dfup), len(dfup.Protein.unique())))
print('Corrected for protein expression, there were {} upregated regions on {} proteins.'.format(
    len(dfup[dfup['Corrected for Protein Expression'] == 'Yes']),
    len(dfup[dfup['Corrected for Protein Expression'] == 'Yes'].Protein.unique())))
print('\n')
print('In total, there were {} downregulated regions on {} proteins.'.format(len(dfdown), len(dfdown.Protein.unique())))
print('Corrected for protein expression, there were {} downregulated regions on {} proteins.'.format(
    len(dfdown[dfdown['Corrected for Protein Expression'] == 'Yes']),
    len(dfdown[dfdown['Corrected for Protein Expression'] == 'Yes'].Protein.unique())))
print('\n')
print('In total, there were {} sites over {} regions on {} proteins.'.format(
    dfde['Min Sites'].sum(), len(dfde), len(dfde.Protein.unique())))
print('Corrected for protein expression, there were {} sites over {} regions on {} proteins.'.format(
    dfde_cf[dfde_cf['Corrected for Protein Expression'] == 'Yes']['Min Sites'].sum(),
    len(dfde_cf[dfde_cf['Corrected for Protein Expression'] == 'Yes']),
    len(dfde_cf[dfde_cf['Corrected for Protein Expression'] == 'Yes'].Protein.unique())))

#Make the volcano plot for the regions

#copy the df
dfvolcano = dfde_cf.copy()

#set seaborn style
sns.set_style('ticks')
sns.set_context('poster')

#take tke the -log10 of the p value
dfvolcano['NegLogP'] = -np.log10(dfvolcano['P-Val_Corrected'])

#plot the figure
plt.figure(figsize=(7,7))
g = sns.scatterplot(x='logFC_Corrected', y='NegLogP',
                    data=dfvolcano[(dfvolcano['Corrected for Protein Expression'] == 'Yes') &
                                   (dfvolcano['P-Val_Corrected'] < 0.05) & (dfvolcano['logFC_Corrected'] > 0)],
                    edgecolor=(1,0,0,1), facecolor=(1,0,0,0.25), marker='o', s=25)
g = sns.scatterplot(x='logFC_Corrected', y='NegLogP',
                    data=dfvolcano[(dfvolcano['Corrected for Protein Expression'] == 'No') &
                                   (dfvolcano['P-Val_Corrected'] < 0.05) & (dfvolcano['logFC_Corrected'] > 0)],
                    edgecolor=(1,0,0,1), facecolor='none', marker='o', s=25)

g = sns.scatterplot(x='logFC_Corrected', y='NegLogP',
                    data=dfvolcano[(dfvolcano['Corrected for Protein Expression'] == 'Yes') &
                                   (dfvolcano['P-Val_Corrected'] < 0.05) & (dfvolcano['logFC_Corrected'] < 0)],
                    edgecolor=(0,0,1,1), facecolor=(0,0,1,0.25), marker='o', s=25)
g = sns.scatterplot(x='logFC_Corrected', y='NegLogP',
                    data=dfvolcano[(dfvolcano['Corrected for Protein Expression'] == 'No') &
                                   (dfvolcano['P-Val_Corrected'] < 0.05) & (dfvolcano['logFC_Corrected'] < 0)],
                    edgecolor=(0,0,1,1), facecolor='none', marker='o', s=25)

g = sns.scatterplot(x='logFC_Corrected', y='NegLogP',
                    data=dfvolcano[(dfvolcano['Corrected for Protein Expression'] == 'Yes') &
                                   (dfvolcano['P-Val_Corrected'] > 0.05)],
                    edgecolor=(0.5,0.5,0.5,1), facecolor=(0.5,0.5,0.5,1), marker='o', s=25)
g = sns.scatterplot(x='logFC_Corrected', y='NegLogP',
                    data=dfvolcano[(dfvolcano['Corrected for Protein Expression'] == 'No') &
                                   (dfvolcano['P-Val_Corrected'] > 0.05)],
                    edgecolor=(0.5,0.5,0.5,1), facecolor='none', marker='o', s=25)

ax1 = g.axes
ax1.axhline(-np.log10(0.05), ls='--', color=(0.5,0.5,0.5,1), zorder=0, linewidth=1)
plt.xlabel('Log2 F.C.')
plt.ylabel('-Log10 P-Value')
plt.xlim([-6,6])

#define points to label
ptup = ['Elovl6', 'Plin2', 'Plin3', 'Plin4', 'Plin5', 'Ugt1a5']
ptdown = ['Elovl3', 'Creld2', 'Manba', 'Ces3b', 'Ppt2', 'Ctsf']

for i in ptup:
    g.text((dfvolcano['logFC_Corrected'][dfvolcano.Gene == i].max() + 0.15),
           (dfvolcano['NegLogP'][dfvolcano.Gene == i].max() - 0.15),
           i, color='black', fontsize=14, weight='bold', zorder=1)

g.text((dfvolcano['logFC_Corrected'][dfvolcano.Gene == 'Bhmt'].max() - 1.25),
       (dfvolcano['NegLogP'][dfvolcano.Gene == 'Bhmt'].max() + 0.05),
       'Bhmt', color='black', fontsize=14, weight='bold', zorder=1)

for i in ptdown:
    g.text((dfvolcano['logFC_Corrected'][dfvolcano.Gene == i].max() - 0),
```

```
            (dfvolcano['NegLogP'][dfvolcano.Gene == i].max() - 0.2),
            i, color='black', fontsize=14, weight='bold', zorder=1, ha='right')

g.text((dfvolcano['logFC_Corrected'][dfvolcano.Gene == 'Egfr'].max() - 0),
    (dfvolcano['NegLogP'][dfvolcano.Gene == 'Egfr'].max() - 0.25),
    'Egfr', color='black', fontsize=14, weight='bold', zorder=1, ha='center')

#Export a list of all O-GlcNAc substrates for making the network
#First, get the gene names from uniprot

#make a set of all proteins in sites and regions table
proteinset = set(pd.concat([dfregions_601.Protein, dfregions_607.Protein]))

#define input
uniprot_input = proteinset

#define variables
url = 'https://www.uniprot.org/uploadlists/'
user_agent = 'Mozilla/5.0 (Windows NT 10.0; Win64; x64)'

#make a dictionary for the requests
params = {
    "from":"ACC+ID",
    "to":"ACC",
    "format":"tab",
    "columns": "genes(PREFERRED)",
    "query":" ".join(uniprot_input)
}

#query uniprot
data = urllib.parse.urlencode(params, doseq=False)
data = data.encode('ascii')
headers = {"User-Agent": user_agent}
request = urllib.request.Request(url, data, headers)
response = urllib.request.urlopen(request)
with urllib.request.urlopen(request) as f:
   response = f.read().decode()

#make a dataframe from the output
df_res = pd.read_csv(StringIO(response), sep='\t')
df_res #inspect

Make a df of substrates and export for cytoscape

#copy the df
dfde1 = dfrf.copy()

dfde1.insert(1, 'Gene', dfde.Protein)

#rename the uniprot output columns and prepare for export like with previous script for OGT substrates
df_res.rename(columns={df_res.columns[0]: "Gene", df_res.columns[1]: "UniprotID"}, inplace=True)
df_res.UniprotID = 1
df_res.rename(columns={'UniprotID':'OGT_Substrate'}, inplace=True)
df_res.drop_duplicates(subset='Gene', inplace=True)

#export
df_res.to_csv('OGTSubstrates.csv', index=False)
#Count the total number of proteins identified
print('Total number of O-GlcNAcylated proteins: ', len(proteinset))
```

Part 4

```
#Preprocess the data and output for sites and regions script

#copy the previous df
dfmover = dfm.copy()

#remove the 601/607 identifier
dfmoverf = dfmover.replace(['GlcNAc601', 'GlcNAc607'], 'GlcNAc')

#Add an experiment columns based on the GlcNAc601 and GlcNAc607 columns
dfmoverf.loc[dfmoverf.GlcNAc601 == 1, 'Experiment'] = 'WT'
dfmoverf.loc[dfmoverf.GlcNAc607 == 1, 'Experiment'] = 'db/db'

#set new mod name
MOD_NAME = "GlcNAc"
pepProbPatt = re.compile(r'[A-Z][()?\d?[.]?\d*[)]?')

PepInfo = namedtuple("PepInfo",["Protein","StartPos"])
peptideInfo = {}

# Get peptide start positions
pepDF = pd.read_csv("{}peptides.txt".format(sfolder), sep='\t')
for peptide in pepDF[["id","Leading razor protein","Start position"]].itertuples():
    if math.isnan(peptide[3]):
        peptideInfo[peptide.id] = PepInfo(peptide[2],-1)
    else:
        peptideInfo[peptide.id] = PepInfo(peptide[2],int(peptide[3]))

msmsDFover = dfmoverf
msmsDFover = msmsDFover[msmsDFover.Modifications.str.contains("GlcNAc")]
msmsDFover["Protein"] = msmsDFover["Peptide ID"].apply(lambda x: peptideInfo[x].Protein)
msmsDFover["StartPos"] = msmsDFover["Peptide ID"].apply(lambda x: peptideInfo[x].StartPos)
```

```
msmsDFover = msmsDFover[msmsDFover["StartPos"]>=0]
msmsDFover.rename(columns={"Raw file":"RawFile","Scan number":"ScanNumber", "Ratio H/L":"Ratio"},
             inplace=True)
msmsDFover['NumMods'] = msmsDFover[["GlcNAc601","GlcNAc607"]].sum(axis=1)

#enumerate separately for 601 and 607 (there should be no overlapping sites)
#convert site prob columns to string
msmsDFover[["GlcNAc601 Probabilities","GlcNAc607 Probabilities"]] = \
msmsDFover[["GlcNAc601 Probabilities","GlcNAc607 Probabilities"]].astype(str)
msmsDFover.loc[msmsDFover.GlcNAc601 > 0, "Probabilities"] = msmsDFover.apply(
    lambda x: ";".join([aa[2:-1] for pp,aa in enumerate(pepProbPatt.findall(
        x["GlcNAc601 Probabilities"])) if len(aa) > 1]),axis=1)
msmsDFover.loc[msmsDFover.GlcNAc607 > 0, "Probabilities"] = msmsDFover.apply(
    lambda x: ";".join([aa[2:-1] for pp,aa in enumerate(pepProbPatt.findall(
        x["GlcNAc607 Probabilities"])) if len(aa) > 1]),axis=1)
msmsDFover.loc[msmsDFover.GlcNAc601 > 0, "Positions"] = msmsDFover.apply(
    lambda x: ";".join([str(pp+x["StartPos"]) for pp,aa in enumerate(pepProbPatt.findall(
        x["GlcNAc601 Probabilities"])) if len(aa) > 1]),axis=1)
msmsDFover.loc[msmsDFover.GlcNAc607 > 0, "Positions"] = msmsDFover.apply(
    lambda x: ";".join([str(pp+x["StartPos"]) for pp,aa in enumerate(pepProbPatt.findall(
        x["GlcNAc607 Probabilities"])) if len(aa) > 1]),axis=1)

df1_tableo = msmsDFover[["RawFile","Protein","ScanNumber","NumMods","Positions","Probabilities","Ratio","Experiment"]]
df1_tableo.to_csv('RegionOverlap_Preprocessed.txt', sep='\t', index=False)
%%capture
#supresses the output of the cell

#Run the sites and regions script
%run -i SitesAndRegionsMultiExperiment.py RegionOverlap_Preprocessed.txt maxparcon_Overlap.txt \
bestms2_Overlap.txt
#Import the output and as in the 20D09 script
dfallsitesover = pd.read_csv('bestms2_Overlap.txt', sep='\t')
dfregionsover = pd.read_csv('maxparcon_Overlap.txt', sep='\t')
dfallsitesover = dfallsitesover[~dfallsitesover.Protein.str.contains(';')]
dfregionsover = dfregionsover[~dfregionsover.Protein.str.contains(';')]
dfregionsover.loc[dfregionsover['Site ID Constraints'].str.contains('of'), 'Type'] = 'Region'
dfregionsover.loc[~dfregionsover['Site ID Constraints'].str.contains('of'), 'Type'] = 'Site'
dfmergeover = dfallsitesover.merge(dfregionsover, how='left', on='Region ID')

#clean up this df
dfmergeover.rename(columns={'Protein_x': 'Protein'}, inplace=True)
dfmergeover.drop(columns={'Protein_y'}, inplace=True)

#make a new column in the regions df denoting where it was found

#define a function to collapse the data in the merged df
def experimentO(x):
    if x.Experiment.eq('WT').all():
        return 'WT'
    elif x.Experiment.eq('db/db').all():
        return 'db/db'
    else:
        return 'Both'

df_exp = dfmergeover.groupby(['Region ID']).apply(experimentO)

#add this back to the regions df
dfregionsover['Experiment'] = df_exp

series_sr = dfregionsover.groupby('Experiment')['Min Sites'].sum()
#Make the Venn diagram

plt.figure(figsize=(7,7))
fig = venn2([series_sr[2], series_sr[1], series_sr[0]], ('db/db', 'WT'))
#plt.title('Technical Replicate Overlap', fontsize=36)
for text in fig.set_labels:
    text.set_fontsize(32)
for text in fig.subset_labels:
    text.set_fontsize(24)
plt.savefig('ReplicateRegionOverlap_Venn.svg')
```

A7.5.4. Interactor Glycosylation Correlation Analysis.

```
#Import python packages
import re
import sys
import pandas as pd
import networkx as nx
import itertools as it
from collections import namedtuple
import numpy as np
import matplotlib
import matplotlib.pyplot as plt
from IPython.display import display
from functools import reduce
import seaborn as sns; sns.set()
from io import StringIO
from matplotlib_venn import venn2_unweighted
```

```
from matplotlib_venn import venn2
import venn
import pandas as pd
import numpy as np
from io import StringIO
import urllib.request, urllib.parse, urllib.error,urllib.request,urllib.error,urllib.parse
import math
import scipy.stats as stats

#set up R environment and import R packages
import rpy2
import rpy2.ipython
%load_ext rpy2.ipython

#require R packages
%R require(limma)
%R require(ibb)

#magic function to show plots inline
%matplotlib inline

#ignore warnings
import warnings
warnings.filterwarnings("ignore")


#Import the relevant data and clean up the dfs

#import data
dfppi = pd.read_csv('PPINetworkLiverF_ForCytoscape.csv')
dfpe = pd.read_csv('ProteinFC_ForCytoscape.csv')
dfgly = pd.read_csv('CorrectedRatios_Regions.csv')
dfint = pd.read_csv('OGTIntsLiverF_ForCytoscape.csv')
dfsub = pd.read_csv('OGTSubsLiverF_ForCytoscape.csv')

#take relevant columns and clean up (and remove self interaction from dfppi)
dfgly2 = dfgly[['Gene', 'logFC_Corrected', 'Corrected for Protein Expression']]
dfgly2.Gene = dfgly2.Gene.str.upper()
dfgly2.rename(columns={'Corrected for Protein Expression':'PE_Corr'}, inplace=True)
dfpe2 = dfpe[['Gene', 'ProteinLogFC']]
dfppi2 = dfppi[dfppi.Interactor_A != dfppi.Interactor_B]
dfppi2.rename(columns={'Interactor_A':'Gene'}, inplace=True)

#merge the subs and ints dfs with the ppi df
dfppi3 = dfppi2.merge(dfint, on='Gene', how='left').merge(dfsub, on='Gene', how='left')

#merge in the protein expression fc for interactor A (rename the column back to interactor a)
dfppi4 = dfppi3.merge(dfpe2, how='left', on='Gene')
dfppi4.rename(columns={'Gene':'Interactor_A'}, inplace=True)

#merge in the glycosylation fc for interactor b
dfppi4.rename(columns={'Interactor_B':'Gene'}, inplace=True)
dfppi5 = dfppi4.merge(dfgly2, how='right', on='Gene')

#now slice out only the interactors with values for protein expression and that are attached to subs with O-GlcNAc FC
dfppi6 = dfppi5[dfppi5.OGT_Interactor == 1]
dfppi6.dropna(subset=['ProteinLogFC', 'logFC_Corrected'], inplace=True)
#Flip everything around

fdfppi = dfppi.reindex(columns={'Interactor_B', 'Interactor_A'}).rename(
    columns={'Interactor_B':'Interactor_A', 'Interactor_A':'Interactor_B'})

#import data
fdfpe = pd.read_csv('ProteinFC_ForCytoscape.csv')
fdfgly = pd.read_csv('CorrectedRatios_Regions.csv')
fdfint = pd.read_csv('OGTIntsLiverF_ForCytoscape.csv')
fdfsub = pd.read_csv('OGTSubsLiverF_ForCytoscape.csv')

#take relevant columns and clean up (and remove self interaction from fdfppi)
fdfgly2 = fdfgly[['Gene', 'logFC_Corrected', 'Corrected for Protein Expression']]
fdfgly2.Gene = fdfgly2.Gene.str.upper()
fdfgly2.rename(columns={'Corrected for Protein Expression':'PE_Corr'}, inplace=True)
fdfpe2 = fdfpe[['Gene', 'ProteinLogFC']]
fdfppi2 = fdfppi[fdfppi.Interactor_A != fdfppi.Interactor_B]
fdfppi2.rename(columns={'Interactor_A':'Gene'}, inplace=True)

#merge the subs and ints fdfs with the ppi fdf
fdfppi3 = fdfppi2.merge(fdfint, on='Gene', how='left').merge(fdfsub, on='Gene', how='left')

#merge in the protein expression fc for interactor A (rename the column back to interactor a)
fdfppi4 = fdfppi3.merge(fdfpe2, how='left', on='Gene')
fdfppi4.rename(columns={'Gene':'Interactor_A'}, inplace=True)

#merge in the glycosylation fc for interactor b
fdfppi4.rename(columns={'Interactor_B':'Gene'}, inplace=True)
fdfppi5 = fdfppi4.merge(fdfgly2, how='right', on='Gene')

#now slice out only the interactors with values for protein expression and that are attached to subs with O-GlcNAc FC
fdfppi6 = fdfppi5[fdfppi5.OGT_Interactor == 1]
fdfppi6.dropna(subset=['ProteinLogFC', 'logFC_Corrected'], inplace=True)
#merge the dfs back together
dff = pd.concat([dfppi6, fdfppi6]).drop_duplicates(subset=['Interactor_A', 'Gene', 'ProteinLogFC', 'logFC_Corrected'])
#Plot interactor fold change vs interacting substrate glycosylation change

sns.set_style('ticks')
```

```
sns.set_context('talk')

#scatterplot
plt.figure
sns.scatterplot(x='ProteinLogFC', y='logFC_Corrected', data=dff, s=15, alpha=0.5, edgecolor='none')
plt.xlabel('Interactor Log2 F.C.')
plt.ylabel('O-GlcNAc Region Log2 F.C.')
plt.xlim([-3,3])
plt.ylim([-7,7])
sns.despine()

#regplot
plt.figure()
plt.ylim([-7,7])
plt.xlim([-3,3])
ax = sns.regplot(x='ProteinLogFC', y='logFC_Corrected', data=dff, truncate=False, line_kws={'color':'k'},
            scatter_kws={"marker": "D", "s": 15, "color": "b", "alpha":0.25})
plt.xlabel('Interactor Log2 F.C.')
plt.ylabel('O-GlcNAc Region Log2 F.C.')
sns.despine()


#Calculate Spearman's correlation coefficient
spearmans = stats.spearmanr(dff.ProteinLogFC, dff.logFC_Corrected)
spearmans


#Perform the adapter rank script and repeat the above analysis with the top adpator candidates
#See 20E03 notebook, will keep the for loop structure

df1= dfppi
dfints1 = dfint.copy()
dfsubs1 = dfsub.copy()

i=1
locals()['df{}'.format(i)] = locals()['df{}'.format(i)].merge(
    locals()['dfints{}'.format(i)], how='left', left_on='Interactor_B', right_on='Gene').drop('Gene', axis=1)
locals()['df{}'.format(i)] = locals()['df{}'.format(i)].merge(
    locals()['dfsubs{}'.format(i)], how='left', left_on='Interactor_B', right_on='Gene').drop('Gene', axis=1)

#Interactions with substrates (regardless of if those substrates are also interactors) are given one point
#Interactors with interactors that are not substrates are given -0.5 points
def score(df):
    if df.OGT_Substrate == 1:
        return 1
    else:
        return -0.5

#calculate the score for each df and drop all of the instances of self interactions in the table
#group the df by interactor a to make an adapter rank df
locals()['df{}'.format(i)]['Score'] = locals()['df{}'.format(i)].apply(score, axis=1)
locals()['df{}'.format(i)] = locals()['df{}'.format(i)][locals()[
    'df{}'.format(i)].Interactor_A != locals()['df{}'.format(i)].Interactor_B]
locals()['dfar_{}'.format(i)] = locals()['df{}'.format(i)].groupby(
    'Interactor_A').Score.sum().reset_index().sort_values(by=['Score'], ascending=False)

#Remove genes that are only substrates to make the final adapter ranking list
#first merge the df with the interactor list and then drop all nan from the interactor column (and drop added columns)
locals()['dfarF_{}'.format(i)] = locals()['dfar_{}'.format(i)].merge(
    locals()['dfints{}'.format(i)], how='left', left_on='Interactor_A', right_on='Gene').dropna(
    subset=['OGT_Interactor']).drop(['OGT_Interactor', 'Gene'], axis=1)
#Flip adapter rank and make final list

df2 = dfppi.reindex(columns={'Interactor_B', 'Interactor_A'}).rename(
    columns={'Interactor_B':'Interactor_A', 'Interactor_A':'Interactor_B'})
dfints2 = dfint.copy()
dfsubs2 = dfsub.copy()

i=2
locals()['df{}'.format(i)] = locals()['df{}'.format(i)].merge(
    locals()['dfints{}'.format(i)], how='left', left_on='Interactor_B', right_on='Gene').drop('Gene', axis=1)
locals()['df{}'.format(i)] = locals()['df{}'.format(i)].merge(
    locals()['dfsubs{}'.format(i)], how='left', left_on='Interactor_B', right_on='Gene').drop('Gene', axis=1)

#Interactions with substrates (regardless of if those substrates are also interactors) are given one point
#Interactors with interactors that are not substrates are given -0.5 points
def score(df):
    if df.OGT_Substrate == 1:
        return 1
    else:
        return -0.5

#calculate the score for each df and drop all of the instances of self interactions in the table
#group the df by interactor a to make an adapter rank df
locals()['df{}'.format(i)]['Score'] = locals()['df{}'.format(i)].apply(score, axis=1)
locals()['df{}'.format(i)] = locals()['df{}'.format(i)][locals()[
    'df{}'.format(i)].Interactor_A != locals()['df{}'.format(i)].Interactor_B]
locals()['dfar_{}'.format(i)] = locals()['df{}'.format(i)].groupby(
    'Interactor_A').Score.sum().reset_index().sort_values(by=['Score'], ascending=False)

#Remove genes that are only substrates to make the final adapter ranking list
#first merge the df with the interactor list and then drop all nan from the interactor column (and drop added columns)
locals()['dfarF_{}'.format(i)] = locals()['dfar_{}'.format(i)].merge(
    locals()['dfints{}'.format(i)], how='left', left_on='Interactor_A', right_on='Gene').dropna(
    subset=['OGT_Interactor']).drop(['OGT_Interactor', 'Gene'], axis=1)
```

```
dfadran = pd.concat([dfarF_1, dfarF_2]).sort_values(by='Score', ascending=False).drop_duplicates(subset='Interactor_A')
#Export top adaptors
dfadran.to_csv('AdaptorRanking.csv', index=False)
topadaptorlist = dfadran[dfadran.Score > 2].Interactor_A.to_list()

#Remake the plots without Egfr

dfppi8 = dff[dff.Interactor_A.isin(topadaptorlist)]

#scatterplot
plt.figure
sns.scatterplot(x='ProteinLogFC', y='logFC_Corrected', data=dfppi8, s=15, alpha=0.5, edgecolor='none')
plt.xlabel('Interactor Log2 F.C.')
plt.ylabel('O-GlcNAc Region Log2 F.C.')
plt.xlim([-2,2])
plt.ylim([-7,7])
sns.despine()

#regplot
plt.figure()
plt.ylim([-7,7])
plt.xlim([-2,2])
ax = sns.regplot(x='ProteinLogFC', y='logFC_Corrected', data=dfppi8, truncate=False, line_kws={'color':'k'},
            scatter_kws={"marker": "D", "s": 15, "color": "b", "alpha":0.25})
plt.xlabel('Interactor Log2 F.C.')
plt.ylabel('O-GlcNAc Region Log2 F.C.')
sns.despine()


#Calculate Spearman's R
spearmans = stats.spearmanr(dfppi8.ProteinLogFC, dfppi8.logFC_Corrected)
spearmans


#Output potential adaptor interactions up/up
dfadaptup = dff[(dff.ProteinLogFC > 0.5) & (dff.logFC_Corrected > 0.75)]
dfadaptup = dfadaptup.merge(dfadran, on='Interactor_A', how='left')
dfadaptup.rename(columns={'Interactor_A':'Adaptor', 'Gene':'Target'}, inplace=True)
dfadaptup = dfadaptup[dfadaptup.PE_Corr == 'Yes']
dfadaptup.drop(columns={'OGT_Interactor', 'OGT_Substrate'}, inplace=True)
dfadaptup.to_csv('AdaptorInteraction_Up.csv', index=False)
#Output potential adaptor interactions down/down
dfadaptdown = dff[(dff.ProteinLogFC < -0.5) & (dff.logFC_Corrected < -0.75)]
dfadaptdown = dfadaptdown.merge(dfadran, on='Interactor_A', how='left')
dfadaptdown.rename(columns={'Interactor_A':'Adaptor', 'Gene':'Target'}, inplace=True)
dfadaptdown = dfadaptdown[dfadaptdown.PE_Corr == 'Yes']
dfadaptdown.drop(columns={'OGT_Interactor', 'OGT_Substrate'}, inplace=True)
dfadaptdown.to_csv('AdaptorInteraction_Down.csv', index=False)
#Output potential adaptor interactions up/down
dfadaptupopp = dff[(dff.ProteinLogFC > 0.5) & (dff.logFC_Corrected < -0.75)]
dfadaptupopp = dfadaptupopp.merge(dfadran, on='Interactor_A', how='left')
dfadaptupopp.rename(columns={'Interactor_A':'Adaptor', 'Gene':'Target'}, inplace=True)
dfadaptupopp = dfadaptupopp[dfadaptupopp.PE_Corr == 'Yes']
dfadaptupopp.drop(columns={'OGT_Interactor', 'OGT_Substrate'}, inplace=True)
dfadaptupopp.to_csv('AdaptorInteraction_Up_Opposite.csv', index=False)
#Output potential adaptor interactions down/up
dfadaptdownopp = dff[(dff.ProteinLogFC < -0.5) & (dff.logFC_Corrected > 0.75)]
dfadaptdownopp = dfadaptdownopp.merge(dfadran, on='Interactor_A', how='left')
dfadaptdownopp.rename(columns={'Interactor_A':'Adaptor', 'Gene':'Target'}, inplace=True)
dfadaptdownopp = dfadaptdownopp[dfadaptdownopp.PE_Corr == 'Yes']
dfadaptdownopp.drop(columns={'OGT_Interactor', 'OGT_Substrate'}, inplace=True)
dfadaptdownopp.to_csv('AdaptorInteraction_Down_Opposite.csv', index=False)
```