INVESTIGATION OF NOVEL SCHIZOPHRENIA CANDIDATE GENES THROUGH BIOCHEMICAL AND COMPUTATIONAL METHODS

by

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Abstract

Schizophrenia is a complex highly heritable psychiatric disorder affecting ~1% of the human population. Complex disease research must consider the wide variety of confounding factors that contribute to disease pathology. Underlying genetic contributions to disease are often heterogeneous among the disease population and individual gene linkage and association signals may be weak and inconsistent within affected populations. The disease phenotype may actually result from multiple defects within one or more related functional pathways. Understanding the physical interactions that known susceptibility genes engage in provides insight into the functions and pathways contributing to disease, and also implicates the interacting genes and proteins as potential schizophrenia candidate genes.

While many candidate schizophrenia genes have been proposed, findings for only a few genes have been sufficiently replicated for them to be considered schizophrenia susceptibility genes, including neuregulin-1 and dysbindin. The first aim of this thesis was to identify novel candidate schizophrenia genes through investigation of the interactions and pathways that known susceptibility genes neuregulin-1 and dysbindin participate in.

The second aim of this thesis was the generation of a novel method for whole genome linkage metaanalysis. Numerous genome-wide linkage studies have been performed on a wide variety of schizophrenia cohorts, however highly significant genome-wide linkage signals have not been prevalent and there has been little replication between studies. It is possible that individual studies contain weak linkage signals that are consistent across multiple studies, but due to their lack of significance in any one study, have not been identified. The Marker Footprint Linkage Meta-analysis method was developed to allow for refinement of candidate schizophrenia linkage regions from existing studies and identification of novel regions that show broadly consistent, but perhaps weak, linkage signals across multiple studies.

Through these analyses a common protein interaction network that encompasses three of the current best schizophrenia susceptibility genes (neuregulin-1, dysbindin, and disrupted-In-schizophrenia-1) was identified. These findings greatly expand current knowledge of interactions with these important schizophrenia susceptibility genes. A novel method for performing genome-wide linkage meta-analyses was developed that incorporates recombination to refine existing linkage regions and identify novel linkage regions that have not previously been identified.

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Abbreviations & Gene Definitions

Abbreviations

ADP	Adenosine diphosphate
AEBSF	4-(2-Aminoethyl) benzenesulfonyl fluoride hydrochloride
ATCC	American tissue culture collection
B&H	Benjamini and Hochberg
BIND	Biomolecule interaction network database
BioGRID	The general repository for interaction datasets
BP	Biological process
CC	Cellular component
cDNA	Complementary deoxyribose nucleic acid, synthesized from a mature mRNA template
ChIP	Chromatin immunoprecipitation
ChIP-seq	Chromatin immunoprecipitation followed by high throughput sequencing
сМ	Centimorgan (equivalent to a 1% chance that a marker at one genetic locus on a
	chromosome will be separated from a marker at a second locus due to crossing over in a
	single generation)
DAPI	4',6-diamidino-2-phenylindole
DAVID	Database for annotation, visualization, and integrated discovery
DIP	Database of interacting proteins
DLPFC	Dorsolateral prefrontal cortex
DNA	Deoxyribonucleic acid
DSM-IV	Diagnostic and statistical manual of mental disorders version 4
DsRed	Red fluorescent protein
ECD	Extracellular domain
EDTA	Ethylenediaminetetraacetic acid
ESI	Electrospray ionization
ESI-MS/MS	Electrospray ionization tandem mass spectrometry
FDR	False discovery rate
FLAG	A peptide tag with the octopeptide sequence N-DYKDDDDK-C
GABA	Gamma-aminobutyric acid
GAD	Genetic association database
GFP	Green fluorescent protein
GO	Gene ontology
GSMA	Genome scan meta-analysis
GST	Glutathione S-transferase
GWAS	Genome-wide associated study
HEK293	Human embryonic kidney 293 cell line
HGMD	Human gene mutation database

HGNC	Human genome organization (HUGO) gene nomenclature committee
HPLC	High performance liquid chromatography
HPRD	Human protein reference database
HPS	Hermansky-Pudlak syndrome
HUGO	Human genome organization
ICD	Intracellular domain
ID	Identification
IMAGE	Integrated molecular analysis of gene expression, a public collection of genes
IntAct	Protein interaction database and analysis system
IP	Immunoprecipitation
IP-MS/MS	Immunoprecipitation followed by tandem mass spectrometry
KEGG	Kyoto encyclopedia of genes and genomes
LOD	Logarithm of odds
M2	Anti-FLAG M2 antibody
MAGS	Meta-analysis procedure for genome-wide linkage study
MALDI	Matrix assisted laser desorption / ionization
MATCH	A tool for searching transcription factor binding sites in DNA sequences
Mb	Megabase, (1,000,000 bases)
MES	2-(N-morpholino)ethanesulfonic acid
MF	Molecular function
MFLM	Marker footprint linkage meta-analysis
MINT	Molecular interactions database
MIPS	Mammalian protein-protein interaction database
mRNA	Messenger ribonucleic acid
MS	Mass spectrometry
MSP	Multiple scan probability
NCBI	National Center for Biotechnology Information
NIH	National Institutes of Health
NMDA	N-methyl D-aspartatic acid
NP-40	Nonyl phenoxylpolyethoxylethanol (a substitute for Nonidet P-40)
NSB	Non specific binding
NPL	Non-parametric linkage
NSF	N-ethylmaleimide sensitive fusion protein
NuPAGE	A precast gel system for high performance polyacrylamide gel electrophoresis
PBS	Phosphate buffered saline
PCR	Polymerase chain reaction
PRIDE	Proteomics identifications database
qPCR	Quantitative polymerase chain reaction
RDist	Recombination distance
RI	Relative information

RNA	Ribonucleic acid
SDS	Sodium dodecyl sulfate
SDS-PAGE	Sodium dodecyl sulfate polyacrylamide gel electrophoresis
SNP	Single-nucleotide polymorphism
TFBS	Transcription factor binding site
TBS	Tris buffered saline
Tm	Melting temperature of an oligonucleotide; the temperature at which half of the molecules
	are dissociated
TRANSFAC	A public database of transcription factors, their experimentally-proven binding sites, and
	regulated genes.
UCSC	University of California, Santa Cruz
WRPC	Weighted rank pairwise correlation statistic for linkage
X57	Mouse corpus striatum hybrid cell line
Y2H	Yeast-2-hybrid

Gene Definitions

ABCA1	ATP-binding cassette sub-family A member 1
ACMSD	2-amino-3-carboxymuconate-6-semialdehyde
ACTG1	Actin, cytoplasmic 2
ACTR1A	Alpha-centractin
ADRA1A	Alpha-1A adrenergic receptor
AKAP	A-kinase anchor protein family
AKAP8L	A-kinase anchor protein 8-like
AKT	Protein kinase B family
ANK	Ankyrin-1
AP3	Adapter-related protein complex-3
AP3B1	Adapter-related protein complex-3 subunit beta-1
AP3B2	Adapter-related protein complex-3 subunit beta-2
AP3D1	Adapter-related protein complex-3 subunit delta-1
APOE	Apolipoprotein E
APOER2	Low-density lipoprotein receptor-related protein 8 (alias for LRP8)
APP	Amyloid beta A4 protein
ARF1	Adenosine diphosphate (ADP) ribosylation factor-1
ARFGAP1	Adenosine diphosphate (ADP) ribosylation factor guanosine triphosphate (GTP)ase-
	activating protein-1
ARIA	Acetylcholine receptor-inducing activity (alias for neuregulin-1)
ASAP1	Adenosine diphosphate ribosylation factor guanosine triphosphate-ase activating protein
	(ARFGAP) with proto-oncogene tyrosine-protein kinase Src (SRC) homology 3 (SH3)
	domain, ankyrin (ANK) repeat and pleckstrin homology (PH) domain-containing protein 1

BACE1	Beta-secretase 1
BLOC1	Biogenesis of lysosome-related organelles complex-1
BLOC1S3	Biogenesis of lysosome-related organelles complex-1 subunit 3
BLOC2	Biogenesis of lysosome-related organelles complex-2
BRN2	POU domain, class 3, transcription factor 2 (alias for POU3F2)
C2H2	The classical zinc finger domain containing a zinc ion co-ordinate within two conserved
	cysteines and histidines
CAPON	Carboxyl-terminal PDZ ligand of neuronal nitric oxide synthase protein
CAPZB	F-actin-capping protein subunit beta
CCDC60	Coiled-coil domain-containing protein 60
ССТ	Chaperonin containing T-complex protein 1 complex
CCT3	Chaperonin containing T-complex protein 1 complex subunit 3
CCT8	Chaperonin containing T-complex protein 1 complex subunit 8
CDH2	Cadherin-2
COG7	Conserved oligomeric Golgi complex subunit 7
COMT	Catechol-O-methyl transferase
DAAM2	Disheveled-associated activator of morphogenesis 2
DAB1	Disabled homolog 1
DAO	D-amino acid oxidase
DAOA	D-amino acid oxidase activator
DBZ	Disrupted in schizophrenia-1 (DISC1) binding zinc finger protein
DCTN1	Dynactin subunit 1
DCTN2	Dynactin subunit 2
DCTN5	Dynactin subunit 5
DDR1	Epithelial discoidin domain-containing receptor 1
DGC	Dystrophin-associated glycoprotein complex
DISC1	Disrupted-on-schizophrenia-1
DLG4	Disks large homolog 4
DMD	Dystrophin
DPC	Dystrophin associated protein complex
DSP	Desmoplakin
DTNBP1	Dysbindin-1
DYNLL1	Dynein light chain, cytoplasmic
EGFR	Epidermal growth factor receptor
ERBB	Epidermal growth factor receptor family
ERBB2	Receptor tyrosine-protein kinase ErbB-2
ERBB4	Receptor tyrosine-protein kinase ErbB-4
EXOC1	Exocyst complex component-1
EXOC3	Exocyst complex component-3
EXOC4	Exocyst complex component-4

EXOC7	Exocyst complex component-7
FLNA	Filamin-A
FEZ1	Fasciculation and elongation protein zeta-1
G72	D-amino acid oxidase activator
GAPDH	Glyceraldehyde-3-phosphate dehydrogenase
GGF	Glial growth factor (alias for neuregulin-1)
GRB2	Growth factor receptor-bound protein 2
GRIN3A	Glutamate [NMDA] receptor subunit 3A
GRM	Metabotropic glutamate receptor
GTF2B	Transcription initiation factor IIB
HMGN1	Non-histone chromosomal protein HMG-14
HRG	Heregulin (alias for neuregulin-1)
IGFBP2	Insulin-like growth factor-binding protein 2
IGFBP4	Insulin-like growth factor-binding protein 4
IKZF4	Zinc finger protein Eos
IL1B	Interleukin-1 beta
ILF2	Interleukin enhancer-binding factor 2
ILF3	Interleukin enhancer-binding factor 3
ITGAL	Integrin alpha-L
JAK	Janus kinase is a family of intracellular non-receptor tyrosine kinases
JARID2	Protein jumonji
JNK	c-Jun N-terminal kinase family
JUN	Transcription activator AP-1
KIR	Family of KIR proteins
KIR3	Family of G protein-gated inwardly rectifying K+ channels (GIRKs)
LIMK	LIM domain kinase 1
LMNA	Lamin-A/C
LRP8	Low-density lipoprotein receptor-related protein 8
MAP6	Microtubule-associated protein 6
MAPK	Mitogen activated protein kinase
MUTED	Protein MUTED homolog
MYO18B	Myosin-XVIIIb
NDEL1	Nuclear distribution protein nudE-like 1
NDF	Neu differentiation factor (alias for neuregulin-1)
NF45	Interleukin enhancer-binding factor 2 (also called ILF2)
NF90	Interleukin enhancer-binding factor 3 (also called ILF3)
NME2	Nucleoside diphosphate kinase B
NOS1	Nitric oxide synthase, brain
NOS1AP	Carboxyl-terminal PDZ ligand of neuronal nitric oxide synthase protein
NQO2	Ribosyldihydronicotinamide degydrogenase [quinine]

NRG1	Neuregulin-1
OCT7	POU domain, class 3, transcription factor 2
OTX2	Homeobox protein OTX2
PAFAH1B1	Platelet-activating factor acetylhydrolase 1B subunit alpha
PCBP1	Poly(rC) binding protein 1
PCNT	Pericentrin
PDE4B	cAMP-specific 3',5'-cyclic phosphodiesterase 4B
PDZ	A common structural domain of 80-90 amino acids
PGM5	Phosphoglucomutase-like protein 5
PH	Pleckstrin homology domain
PI3K	Phosphoinositide 3-kinase family
PKA	Protein kinase A
PKP2	Plankophilin-2
PLDN	Pallidin
PLEC1	Plectin-1
PLXNA2	Plexin-A2
PKP2	Plakophilin-2
POU	A bipartite DNA binding domain
POU3F2	POU domain, class 3, transcription factor 2
PPM1B	Protein phosphatase 1B
PRKDC	DNA-dependent protein kinase catalytic subunit
PRMT5	Protein arginine N-methyltransferase 5
PSD95	Disks large homolog 4
PTMA	Prothymosin A
RAB11A	Ras-related protein Rab-11A
RAB1B	Ras-related protein Rab-1B
RAF	RAF proto-oncogene serine/threonine protein kinase
RAS	A family of genes encoding small GTPases
RB1	Retinoblastoma-associated protein
RELA	Transcription factor p65
RELN	Reelin
RGS4	Regulator of G-protein signaling 4
SEMA3A	Semaphorin-3A
SGSM1	Small G protein signaling modulator 1
SH3	SRC homology 3 domain
SNAP25	Synaptosomal associated protein 25
SNAPIN	SNARE-associated protein snapin
SNARE	Soluble N-ethylmaleimide sensitive fusion protein (NSF) attachment protein receptors
SNX	Sorting nexin family of proteins
SNX27	Sorting nexin-27

SOX	Sex determining region Y-box family of proteins
SOX11	Transcription factor SOX-11
STAT	Signal transducers and activator of transcription protein family
STXBP1	Syntaxin-binding protein 1
SYN1	Synapsin-1
SYPL1	Synaptophysin-like protein 1
TMEM33	Transmembrane protein 33
TUBA1C	Tubulin alpha-1C chain
TUBB2A	Tubulin beta-2A chain
TUBB2B	Tubulin beta-2B chain
UTRN	Utrophin
VAMP2	Vesicle associated membrane protein 2
VLDLR	Very low-density lipoprotein receptor
YTHDC2	Probable ATP-dependant RNA helicase YTHDC2
YWHAE	14-3-3 protein epsilon

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Dedication

I would like to dedicate this thesis to my parents, Ian and Lynda Mead, for instilling in me from such a young age to follow my own path, as life is a journey, not a destination, with happiness being our highest reward.

"Twenty years from now you will be more disappointed by the things you didn't do than by the ones you did do. So throw off the bowlines. Sail away from the safe harbor. Catch the trade winds in your sails. Explore. Dream. Discover." *Mark Twain*

Co-Authorship Statement

Together with my supervisors Rob Holt and Gregg Morin, I was responsible for the identification and design of the research program described in this thesis. I was primarily responsible for performing the research, data analyses, and manuscript preparation. Each chapter of the thesis was prepared as a multi-author publication. I was primarily responsible for all the research performed in each of these publications, however, the co-authors on these publications did contribute analyses, text, figures, tables, editorial suggestions, funding and supervision. Their specific contributions are briefly summarized here. Rob Holt and Gregg Morin contributed to study design, concepts, text, figures, editorial suggestions, funding and supervision for all chapters. Michael Kuzyk and Annie Moradian performed the mass spectrometry analyses, advised on subsequent data analysis of that data, contributed to images and provided editorial suggestions for Chapters 2 and 3. Gary Wilson provided advice and guidance on laboratory analysis and provided editorial suggestions for Chapter 4. Mikhail Bilenky performed the findpeaks analysis and provided editorial suggestions for Chapter 4. Many others made minor contributions to the research described herein (see author lists and acknowledgements in the individual publications for details).

1 Introduction

Human genetic variants contribute to a vast multitude of diseases. Methods for investigating the genetic etiology of disease were initially focused on Mendelian disorders and have had great success within that realm [1]. These methods have been less successful with investigations of complex diseases, where multiple susceptibility genes may participate in a set of functional pathways and the impairment of one of more of these pathways or functions produces disease. Schizophrenia is a complex psychiatric disorder that is highly heritable with a strong genetic component [2,3]. While a multitude of linkage and association studies have been performed on numerous schizophrenia families and cohorts, there has been little consistency among results, and in many studies the results did not meet statistical significance. There is a need to move beyond traditional methods in order to discover the underlying genetics of disease. By combining multiple genome-wide linkage studies in a linkage meta-analysis it may be possible to refine existing linkage regions and identify novel linkage regions that have consistent, weak signals across multiple studies. This would provide better definition of linkage regions across multiple populations and potentially expand researchers focus to regions that may contain valid susceptibility genes that would otherwise potentially go undetected. There are a number of different terms used to describe how robustly a gene has been linked to schizophrenia. From the least robust to the most, these include: "potential candidate schizophrenia genes", which are genes that are proposed to be involved in schizophrenia due to some characteristic but which have not yet been directly investigated for disease involvement; "candidate schizophrenia genes", which are genes that have had some direct evidence of disease involvement (e.g. one positive association result), but for which the evidence is not yet considered sufficient to be considered a susceptibility gene; and "schizophrenia susceptibility gene", for those few genes that have had considerable evidence showing contribution to schizophrenia etiology, typically replication in independent cohorts plus functional data. A small number of schizophrenia susceptibility genes have been identified, including dysbindin (DTNBP1), neuregulin-1 (NRG1), disruptedin-schizophrenia-1 (DISC1), and Catechol-O-methyl transferase (COMT). Based on the concept that complex disease is the disruption of one or more biological functions rather than the result of perturbation in one or more genes, identification of common interaction partners, functions, or pathways that known susceptibility genes participate in is critical to the identification of the genetic underpinnings of schizophrenia. This introduction reviews the issues and tools available for investigating the genetics of complex disease, as well as provides background on schizophrenia, which was the focus of this thesis.

1.1 Thesis Overview

The central objective of this thesis is the identification of potential candidate genes contributing to schizophrenia etiology. The first part of this thesis focuses on two of the most promising schizophrenia susceptibility genes, DTNBP1 and NRG1, and investigates their protein-protein interactions using immunoprecipitation (IP) and mass spectrometry (MS) techniques. The ability to identify proteins in a high-throughput manner, without prior inference as to the identity of the protein, using MS in combination

with the human genome sequence and annotations has been developed fairly recently [4, 5]. The identified interacting proteins not only provide information on DTNBP1 and NRG1 function, but their underlying genes may also be considered potential schizophrenia candidate genes. The second part of this thesis focuses on leveraging available whole genome linkage data, one of the only data resources that allows direct assessment of the connection between genetics and disease without bias to specific genomic regions. A bioinformatics approach was developed and used to combine available whole genome linkage analyses for the purpose of refining and identifying genomic regions that have shown consistent linkage over multiple studies.

1.2 Complex Disease

Complex genetic disease refers to common familial illnesses that do not show a simple Mendelian pattern of inheritance [6-8]. Some examples of complex disease include: coronary heart disease, deafness, epilepsy, hypertension, rheumatoid arthritis, type I and II diabetes, asthma, many cancers, and most psychiatric disorders, including schizophrenia [6]. Unlike monogenic diseases where a single genetic mutation may cause the disease phenotype, complex diseases involve a wide variety of risk factors found in both our environment and genetics [1, 8].

Several attributes that distinguish complex diseases from Mendelian disorders include locus heterogeneity, allelic heterogeneity, threshold inheritance, variable penetrance, epigenetics, epistasis, gene-environment interactions, temporal gene expression, and senescence [9-16]. These differences make identification of the genetic etiology of complex disease much more difficult. The potential effects of these complexities need to be incorporated into the analysis of complex disease systems, or at the very least, considered when interpreting results. Genetic heterogeneity in particular (where variation at different genetic loci can give rise to the same phenotype) is a common denominator in complex traits and can be considered to be the most important obstacle to overcome [17].

Another critical barrier to complex disease research, and in particular schizophrenia research, is the underlying phenotypic heterogeneity of the affected population. In general, disease is investigated as a set of binary traits where people are considered to be with or without disease, but this simple binary system does not apply well to complex disease which can consist of a spectrum of phenotypes [1]. In addition, for most complex diseases the pathophysiology is poorly understood. The identification of biomarkers and biological measures (e.g. blood glucose in diabetes) that allow cases to be stratified into homogeneous classes is imperative to the successful interpretation of the complexities of multifactorial diseases [6, 17].

There is also debate as to the underlying genetic theory for many complex diseases. The common disease-common allele theory states that disease results from the chance accumulation of multiple common variants, each with a small effect on susceptibility [6]. The rare allele-common disease theory

states that disease is caused by multiple different highly penetrant, rare, and severe mutations [10]. These polarized views remain unresolved and, in actuality, complex diseases are likely to be some combination of both theories [6, 10].

The culmination of these complex disease attributes is that the investigation of individual genes in complex disease becomes much more difficult due to weak and inconsistent disease risk for each gene within affected populations. The combined effect of multiple genetic perturbations within one or more pathways may result in the disease phenotype, or the underlying genetic susceptibility may stem from one or more possible mutations in many different members of a pathway. Therefore, taken in the context of one or more related functional pathways, subsets of genes involved in disease susceptibility provide an increased ability to infer a role in disease mechanisms when analyzed as a group, and are therefore more tractable for researchers to investigate [18]. Further, while simple loss of gene function may underlie a specific subset of the phenotypic defects, more subtle gene mutations that affect protein interactions, gene expression and translation, or protein stability without loss of gene function may be important. Even if a confirmed susceptibility gene for a disease is of minor effect, the biochemical pathways and molecular mechanisms it is involved in may prove relevant to the disorder in general [19]. It is informative to view complex diseases as a disruption of one or more biological functions rather than as a result of perturbations in single or small groups of genes [20]. There are potentially many pathways contributing to the optimal performance of a specific biological function, and therefore there are potentially many different pathways that may lead to disease [20].

1.3 Schizophrenia

Some of the most heritable complex diseases are the psychiatric disorders, including schizophrenia. Heritability is the proportion of phenotypic variation in the population due to genetic variation [21]. In a broad sense, the heritability of a trait is the degree to which it is genetically determined and is expressed as a ratio of the total genetic variance to phenotypic variance [21]. Schizophrenia has a high heritability of 80-87% [22-25], similar to that of bipolar disorder (79-93%) [22, 26, 27], in contrast to other complex diseases such as Alzheimer's disease (29-79%) [28-32], asthma (48-79%) [33] and breast cancer (25-50%) [34-36]. Schizophrenia is a psychiatric disorder identified 100 years ago by Kraeplin that affects approximately 1% of the population [37]. Psychiatric disorders, including schizophrenia, have added complexity in that they rely on non-biological descriptive measures (for example the Diagnostic and Statistical Manual of Mental Disorders fourth edition (DSM-IV) [38]) for the purposes of diagnosis, which has shown limited effectiveness for segregating individuals into phenotypically or genotypically homogeneous disease populations [6]. In addition, no conclusive consistent physiological markers have yet been defined for schizophrenia [39]. These factors increase the complexity of investigating schizophrenia, as the underlying affected populations may be widely heterogeneous.

While no conclusive physiological markers have been identified for schizophrenia, there has been a great deal of research focused on their identification. Alterations in the cytoarchitecture of various brain areas (hippocampus, prefrontal cortex, dorsal thalamus) have been a long term focus of schizophrenia research and evidence supports the existence of these alterations as a potential physiological representation of schizophrenia [40]. Neuropathology research has focused on the extended limbic system (hippocampus, dorsolateral prefrontal cortex (DLPFC) and cingulate gyrus) [37] and evidence that the prefrontal cortex is a site of abnormal brain function in schizophrenia is overwhelming [41]. One of many models for schizophrenia development is that it is a neurodevelopmental disorder where dysconnectivity or misconnectivity of neurons affect the precise organization of the neural circuitry and perhaps its plasticity [37], leading to abnormal synaptic connectivity [19]. Dysconnectivity refers to the abnormal functional integration of brain processes either due to aberrant neuronal wiring, or aberrant synaptic plasticity or both [42]. Synapses are specialized junctions between neurons, or neurons and adjacent cells that mediate transmission of signals. Signals are transduced by the release of neurotransmitters from the presynapse of one cell that is received through specialized neurotransmitter receptors on the postsynapse of adjacent cells. The human brain is thought to contain tens of billions of neurons, each having approximately 7,000 synapses, resulting in hundreds of trillions of synapses [43]. Synaptic plasticity occurs throughout life and refers to changes in the strength of the synapse (defined as the change in transmembrane potential resulting from activation) and its ability to process signal information. There are many mechanisms involved in affecting synaptic plasticity, one of which is change in the quantity of neurotransmitter released.

Alterations in neurotransmitter systems (dopamine, glutamine, gamma-aminobutyric acid (GABA)-ergic, serotonergic, cholinergic, and opioid) provide evidence of synaptic involvement in pathophysiological processes leading to symptoms of schizophrenia [39, 44, 45]. Dopamine, glutamate, and GABA are the systems that have received the most attention. Hyperactivation of the dopamine system was the first established hypothesis once it was established that traditional antipsychotics are principally dopamine D_2 receptor antagonists [46]. Subsequently, the glutamatergic system has received attention [19]. The hypofunction of the glutamate system in schizophrenia was first inferred from observations that N-methyl-D-aspartate (NMDA) receptor antagonists (ketamine, phencyclidine, and MK-801) induce schizophrenialike symptoms in normal individuals [46]. Glutamate has been described as the major excitatory neurotransmitter in the mammalian brain and is thought to be utilized by 40% of all synapses [47]. There is a variety of evidence that further supports impaired glutamatergic transmission involvement in Pyramidal cells, which use glutamate as their neurotransmitter, contribute to the schizophrenia. interconnectivity between the cerebral cortex and limbic system, brain regions that have been implicated in the pathophysiology of schizophrenia [47]. Many of the genes with the strongest associations with schizophrenia (COMT, D-amino acid oxidase activator (DAOA or G72), DISC1, DTNBP1, metabotropic glutamate receptor 3 (GRM3), NRG1, and regulator of G-protein signaling 4 (RGS4)) are involved in the glutamatergic signaling pathway [48]. COMT acts directly on monoaminergic neurotransmission and likely affects other synaptic populations, including glutamatergic synapses [19]. DAOA functions as an activator for D-amino acid oxidation [49]. Impaired DAOA activity is thought to reduce the availability of D-serine (an NMDA receptor co-agonist) and thereby reduce glutamatergic transmission. DISC1 has several interaction partners in common with glutamate receptors [48]. DTNBP1 regulates glutamate storage and release [48]. GRM3 is a receptor agonist and inhibits glutamate release. NRG1 is present in glutamatergic synaptic vesicles, affects NMDA receptors [19], and also interacts indirectly with the postsynaptic density proteins associated with ionotropic glutamate receptors through ErbB4 to alter synaptic plasticity [19]. RGS4 is a negative regulator of G-protein coupled receptors including the metabotropic glutamate receptors [19]. Finally, hypofunction of the GABA system, one of the most reproducible neuroanatomic alterations in schizophrenia, was shown to be caused by reduced NMDA receptors, for example any gene product that affects the quantity of neurotransmitters in the cell, their transportation, storage, and time and location of their release, or the location or number of their receptors may be considered a potential schizophrenia candidate gene. Researchers continue to investigate the physical attributes of the schizophrenic brain in an attempt to identify the elusive physiological marker for schizophrenia that would allow more definitive segregation of the affected population.

The heritability of schizophrenia indicates a strong genetic component, however the specific genetic risk factors remain largely unknown [50-52]. In addition to a strong genetic component, environmental risk factors contribute to schizophrenia etiology. Although far from conclusive, studies indicate environmental risk factors may include obstetric complications, stress, drug use, immigration, season of birth, urban upbringing, head injury, viral infection, and history of trauma [53]. Although environmental factors do play a role in the development of this disorder, the specific factors involved and how they contribute to disease is uncertain. Individual environmental risk factors are thought to contribute a minor component of risk for development of schizophrenia [54]. For the purpose of this thesis, I have focused on the underlying genetics of schizophrenia etiology, but it cannot be discounted that there are many more factors contributing to disease than can be attributed to a purely genetic origin.

Normal brain development and function is complex and involves a large number of exquisitely timed steps [55]. It has therefore been suggested that alterations at various developmental stages could contribute to the development of schizophrenia [55] and that the genetic defects contributing to the disease may affect the timing of gene expression rather than gene coding mutations. The result of more than 20 genome-wide linkage scans in more than 1,200 families with schizophrenia found evidence confirming that schizophrenia is a complex disease where multiple genes modify susceptibility, but any single gene is neither necessary nor sufficient to cause the disorder [15, 56]. There is accumulated evidence of involvement of a small subset of genes such as DTNBP1, DISC1, and NRG1 [50] in schizophrenia such that they are now considered schizophrenia susceptibility genes, however the picture is incomplete, and it is still uncertain how these genes contribute to the development of the disease.

1.4 Schizophrenia Susceptibility Genes

1.4.1 Dysbindin (DTNBP1)

A more detailed introduction to DTNBP1 will be provided in Chapter 2, which focuses on DTNBP1 protein-protein interactions. This section will provide a brief introduction as to why DTNBP1 was chosen as one of the genes of focus for the investigation of novel schizophrenia susceptibility genes, pathways, and function. DTNBP1 is located within one of the most consistently replicated schizophrenia linkage regions (6p22.3) [57-64] and has one of the most replicated schizophrenia association findings [65-74]. DTNBP1 is a widely expressed cytoplasmic protein involved in vesicle trafficking, and the specific biological functions it is associated with are expected to vary with cell and tissue types and the vesicle populations therein. Involvement of a protein at any part of the vesicle lifecycle is of interest from a schizophrenia standpoint. Vesicles store and transport material within the cell. In neurons, vesicles store and transport neurotransmitters for release at the synapse, a function which is known to be impaired in schizophrenic brain. The DTNBP1 knockout mouse model (sandy) shows increased dopamine turnover in specific brain regions [75]. Defects in neurosecretion and vesicular morphology in neuroendocrine cells and hippocampal synapses have also been identified at the single vesicle level in sandy mice, which implicate DTNBP1 in the regulation of exocytosis and vesicle biogenesis in endocrine cells and neurons [76]. These findings are consistent with the hypothesis that defective synaptic transmission and neurotransmitter release is a pathogenic mechanism in schizophrenia [50, 77]. In addition, schizophrenia patients have been found to have decreased expression of DTNBP1 at presynaptic glutamatergic terminals in the hippocampus [78, 79] and DLPFC [80]. This evidence culminates in DTNBP1 currently being considered one of the most promising schizophrenia susceptibility genes, and thus it was chosen as a focus within this thesis.

1.4.2 Neuregulin-1 (NRG1)

A more detailed introduction to NRG1 will be provided in Chapter 3, which focuses on NRG1 proteinprotein and protein-DNA interactions. This section will provide a brief introduction as to why NRG1 was chosen as a gene of focus for the investigation of novel schizophrenia susceptibility genes, pathways, and function. Our knowledge of NRG1 implicates it in many fundamental neuronal functions. In particular, NRG1 is known to be involved in neural development [81], neuronal differentiation, migration and survival [82-84], synaptic maturation and plasticity [85, 86], and myelination [87]. NRG1 is also one of the best replicated schizophrenia susceptibility genes [88-102]. Pharmacogenetics studies indicate that schizophrenia antipsychotics haloperidol, risperidone and clozapine increase expression of NRG1, and the ErbB receptors it is known to interact with, in rat hippocampus [103]. Schizophrenia NRG1 at-risk haplotypes have been shown to have decreased efficacy of glutamatergic and GABAergic neurotransmission [86, 104]. Finally, altered NRG1 signaling has been implicated in abnormal oligodendrocyte development and myelination as well as reduced oligodendrocyte numbers, which are all thought to play a role in the pathophysiology of schizophrenia [105]. This combination of factors makes NRG1 one of the most convincing schizophrenia susceptibility genes identified to date, and for that reason it was chosen for investigation in this thesis.

NRG1 is a widely expressed transmembrane protein with both extracellular and intracellular domains that is involved in cell-cell communication (among other functions). There has been a great deal of research in a variety of arenas focused on NRG1, including schizophrenia, heart disease, stroke, Hirschsprung's disease, and cancer. However, the majority of this research has focused on the extracellular domain (ECD) and its interaction with its receptor, another candidate schizophrenia gene, ErbB4 [106-108]. Very little research has focused on the intracellular domain (ICD), however there is evidence that once cleaved, the ICD is transported to the nucleus and affects transcription [109, 110]. For the investigations described in this thesis, I chose to focus on the protein and DNA interactions of the NRG1 ICD. The findings described in this thesis for NRG1 ICD may be informative not only in the context of schizophrenia etiology, but also for other complex diseases.

1.4.3 Disrupted-In-Schizophrenia-1 (DISC1)

DISC1 is also considered a promising schizophrenia susceptibility gene and although it was not investigated directly, it was found to have several common protein interacting partners with DTNBP1 and NRG1 based on the findings described in Chapters 2 and 3. The DISC1 gene was named Disrupted-in-Schizophrenia-1 because it was identified at a site for a balanced translocation (1:11) (q42.1;q14.3) that co-segregates with schizophrenia and other psychiatric disorders in a large Scottish pedigree [111, 112]. Several subsequent studies also found evidence of DISC1 association with schizophrenia [113-118]. A number of DISC1 interacting proteins have been identified, including PDE4B and FEZ1, which have also had positive schizophrenia association results [119, 120]. The biochemical investigation of DISC1 is still early and it is not yet understood how DISC1 contributes to schizophrenia etiology. However, there is evidence that DISC1 is involved in brain development, including neuronal migration, neurite outgrowth and neural maturation through interaction with several cytoskeletal proteins [121].

1.5 Traditional Disease Gene Finding Methods

Linkage and association studies are two main types of traditional molecular-genetic techniques that have been used to investigate candidate disease genes [15]. These techniques determine if a genetic locus or variant segregates with a given disease in the study population.

A linkage study attempts to detect genomic regions that harbor genes contributing to disease by identifying sites in the genome that show evidence of segregating with illness in families that have more than one affected member [122]. The major strength of linkage analysis is in mapping rare disorders through large families with many affected individuals [1]. Over 1,000 human monogenic disease genes

have been identified through this type of analysis [123, 124]. While linkage studies can be quite powerful and have had excellent success with some Mendelian disorders, they also have a number of weaknesses. They need to assume a mode of inheritance [125], are costly, require a large investment in recruiting families that contain affected members, and have low resolution. At best, linkage studies may restrict regions for disease to between 10-15 Mb and require further fine mapping and hunting to determine the causal variant. Genetic heterogeneity is also a major problem for linkage, and is one reason why studies in different populations produce different results. At the same time, linkage studies benefit from being performed within large families, where disease is likely to segregate with the same genetic (or epigenetic) aberration.

While linkage studies can identify large regions of the genome that co-segregate with disease in large families, association studies allow specific alleles to be tested for association with disease in the population. Association studies determine if a gene is involved in disease through genetic testing of variants in diseased (case) compared to non-diseased (control) individuals [1]. Recent advances in technology now allow the typing of over 1 million markers for only a few hundred dollars per person [125], allowing for whole genome association studies (GWAS). GWAS is a type of association study where regularly spaced genetic markers across the entire genome are tested for association with a specific disease or trait. GWAS has the benefit of being able to test variants across the entire genome rather than focusing on specific regions indicated from linkage studies or other information. However, the large number of tests performed by GWAS (one test per variant) means that multiple testing correction must be performed to accommodate increased potential for false discovery.

The underlying rationale of GWAS is that of common disease-common allele, and there was an expectation that many more loci associated with disease would be identified through GWAS. Unfortunately, for many complex traits and diseases (including schizophrenia), even after analysis by GWAS, only a small portion of estimated heritability has been explained [126], leading to a new concept called missing heritability. A number of risk haplotypes have been identified for NRG1 with odds ratios varying from 1.22 to 3.1 [93, 97, 99, 127]. Odds ratios (OR) from some of the best schizophrenia candidate / susceptibility genes include DTNBP1 (OR, 1.76) [70], BLOC1S3 (OR, 1.45) [128], DAO (OR, 1.71) [129], and GRM3 (OR 1.94 to 2.18) [130]. Rare variants in DISC1 are thought to contribute up to 2% of risk for schizophrenia, however common variants have an odds ratio of only 1.3 [131]. Epistatic effects between COMT and DISC1 produce an odds ratio of 2.46 [130]. There are many possible explanations for missing heritability, including the involvement of a large number of variants of small effect that have yet to be found, the involvement of variants that are not tested by GWAS (including structural variants and rare variants with possibly large effects), gene-gene interactions, epigenetic effects, and the influence of shared environment on the calculation of heritability. With the exception of epigenetic effects and environmental influence, the effects potentially contributing to the missing heritability in schizophrenia would benefit from improved knowledge of the protein interactions, functions, and pathways of known schizophrenia susceptibility genes, as the gene products involved likely represent some of the missing heritability.

There are a number of issues that must be considered when interpreting association studies. Isolation of a genetic variant which has a large difference in frequency between cases and controls provides insufficient evidence to assume a disease susceptibility role because the variant could simply be in linkage disequilibrium with the true causative variant. Careful construction of matched case and control sets is very important, since drawing sets from inherently different genetic populations may generate false positives. The replication studies that are required to validate initial findings are expensive, difficult and often conflicting. Association studies may fail to identify associations between genetic markers and disease phenotype when multiple, independent disease mutations are present (genetic heterogeneity) [125]. Genetic heterogeneity is a major confounding factor for association studies and disease variants identified in one population may not be present in other populations, resulting in lack of reproducibility of Association studies may not have sufficient power to identify rare causation variants. findinas. Association between genetic markers and disease phenotype can be present for reasons other than involvement in the disease, including population stratification and chance, leading to false positive associations [125], although use of the transmission disequilibrium test, which relies on genotyping trios (the proband, mother, and father), mitigates this risk [132].

Unfortunately, for the investigation of schizophrenia genes, linkage and association results have not been entirely consistent, which is not unusual for complex disorders [15]. Genetic heterogeneity, an important confounding factor in both linkage and association studies is a known characteristic of schizophrenia, and may perhaps exist at a greater level than previously thought [133]. In situations where there are complicating factors like those common to complex diseases (multiple potential disease pre-disposing variants of modest individual effect, gene-gene interactions, gene-environment interactions, or interpopulation (allelic or locus) heterogeneity), linkage and association methods require very large sample sizes to have a chance for successful outcome [125, 134]. In fact, schizophrenia provides a striking example of the limitations in the ability of traditional methods to identify the genetic etiology of a highly heritable complex disorder. Existing linkage studies have resulted in claims of linkage for 21 of the 23 pairs of chromosomes; however, the majority of genome scans have failed to replicate these findings [122]. No strong linkage signal appears to be emerging for schizophrenia and more importantly, there is no obvious criterion for distinguishing signal from noise [122]. This leads to several possible conclusions, including that many genes of small effect are relevant, that there is significant heterogeneity across populations or that samples much larger than those currently available will be required to detect reliable linkage. Some researchers have attempted to address these issues by using quantitative phenotypes to subdivide schizophrenia patients based on the theory that the genetic underpinnings of these phenotypes are a subset of those contributing to schizophrenia etiology.

There is concern about using linkage and association to determine candidate genes in complex disease as even those few regions that do show strong results will not necessarily account for the majority of genetic liability and may not segregate in many affected individuals [41]. However, even if a confirmed susceptibility gene for schizophrenia proved to be of minor effect, the biochemical pathways and molecular mechanisms it implicates may prove relevant to the disorder in general [19]. Conversely, candidate regions defined by linkage studies alone are not sufficient as determinants of potential genes. Proof of this is the discovery of D-amino acid oxidase (DAO), found at locus 12q24 [135], as a candidate schizophrenia susceptibility gene. Based solely on the schizophrenia candidate regions from linkage studies, DAO was not previously considered to be a schizophrenia susceptibility gene. Chumakov *et al.* [135] revealed DAO as a susceptibility gene while investigating the protein DAOA, a potential candidate gene for schizophrenia. DAOA was found to have positive association within schizophrenia populations and was therefore subject to a yeast two-hybrid analysis to determine potential interacting proteins. One of the interacting proteins identified was found to be DAO. Upon repeating their association analysis with DAO they found positive association with schizophrenia. This not only supports the need to further refine existing and identify novel schizophrenia linkage regions, but supports the idea that identification of interactions and pathways may be of great importance in finding candidate susceptibility genes.

1.6 Recombination

Genetic recombination occurs during mitosis and meiosis and is the process by which genetic material is broken and then joined (recombined) at a location different than its origin. In meiosis, recombination facilitates chromosomal crossover which leads to offspring having different combinations of genes than their parents. This is the predominant source of genetic variation between parents and offspring. Recombination can theoretically occur at any location along the chromosome and the frequency of recombination between two locations generally depends on distance [136]. However, recombination occurs with different frequencies at different locations along the genome. Recombination is an important aspect to consider when investigating linkage or association with disease. The higher the recombination rate in a region of interest, the more likely recombination has occurred between any two points within that region.

One resource for information on the actual rates of recombination in the human genome is the HapMap project, which is an international project focused on the identification and cataloging of genetic patterns, similarities, and differences in human beings [136]. They have determined the frequencies of millions of sequence variants as well as the degree of association between them for individuals from various populations, including Africa, Asia, and Europe [136]. In Chapter 4, one of the key unique aspects of the whole genome linkage meta-analysis method that I developed is the incorporation of recombination, as defined by the HapMap project, to determine how non-overlapping markers from different studies can be combined. By using HapMap recombination rates, the probability of recombination between 2 points can be estimated, reducing the possibility of incorrectly combining markers from different studies when they have a low probability of representing the same linkage signal.

1.7 Non-Traditional Disease Gene Finding Tools

There is a need to supplement traditional genetic methods for investigating complex diseases. Advances in genomic, proteomic, and metabolomic technologies have provided researchers with new tools to investigate complex disease, resulting in an explosion of data [137] and allowing for a more detailed investigation into the underlying genetic mechanics of complex disorders. Sophisticated molecular studies, including microarrays and proteomics, as well as appropriate transgenic and in-vitro characterizations of genes, their functions, and their interactions are required for the evaluation of the speculative integration of genetics and neurobiology [19]. While proteomic techniques including mass spectrometry, yeast-2-hybrid (Y2H), and protein microarrays provide information on protein interactions and expression, genomic techniques such as massively parallel sequencing, single nucleotide polymorphism (SNP) microarrays, and expression microarrays allow identification of disease-associated mutations and mRNA expression patterns. In addition, gene co-expression and differential expression data help inform the generation of biological system maps. Large-scale open-access projects also have a huge potential to impact genetic disease research (e.g. the human genome project, HapMap, etc.) [1, 17, 20]. Extensions of methodologies designed for monogenic inheritance will, when applied to complex disease, have much greater impact if they leverage knowledge of protein interaction pathways and networks. Repositories are being developed to house a variety of types of information including pathway information (e.g. Kyoto encyclopedia of genes and genomes (KEGG) [138]), protein interaction data (e.g. Human protein reference database (HPRD) [139], and many other more focused repositories [140]), disease association data (e.g. genetic association database (GAD http://geneticassociationdb.nih.gov/) [141]), and human genetic mutation data (e.g. Human gene mutation database (HGMD) [124]) so that it is more easily accessible to researchers. Protein interaction networks have been built from high throughput datasets for model organisms [142-145] and visualization tools are being developed so that pathways can more easily be generated, visualized, and manipulated (e.g. Cytoscape; [146]). Researchers need to consider all available evidence in the search for candidate genes in complex disease rather than discarding genes simply because they do not appear in candidate regions. An improved understanding of the specific relationships or pathways connecting genes and gene products would help provide context for future schizophrenia research.

1.7.1 Protein-protein interactions

Genetic mutations can affect the protein product of the gene in a number of ways, including protein abundance, posttranslational modifications, and the ability of proteins to interact with other molecules in the cell [147]. Changes in the properties of one protein can affect not only the protein itself, but also properties of other proteins [147]. Proteins can participate in multiple protein complexes, each of which may have different cellular roles [148-150]. In this way, a single protein can have multiple different functions according to its interaction partners and localization [151]. Identification of protein-protein interactions is an important way to understand a protein's function [151]. Therefore, a targeted investigation into the protein-protein interactions of a disease susceptibility gene product provides insight

into the underlying functions impaired in disease, and also provides a list of other proteins that may be impacted by mutations in the disease susceptibility gene, or conversely, a list of other proteins that may impact the disease susceptibility gene should their parent gene contain genetic mutations.

There are a large number of public protein interaction databases that collect data from various types of protein-protein interaction experiments, including biomolecule interaction network database (BIND) [152], database of interacting proteins (DIP) [153], protein interaction database and analysis system (IntAct) [154], molecular interactions database (MINT) [155], mammalian protein-protein interaction database (MIPS) [156], the general repository for interaction datasets (BioGRID) [157], and HPRD [139]. The information contained in these databases can be leveraged in complex disease investigations as a central location for protein interaction information that may provide context for disease genes where possible. Databases of the human protein interactome, however, are largely incomplete and contain false interaction data, therefore these databases may only provide a starting point for information gathering.

1.7.1.1 High-throughput protein-protein interaction detection methods

There are several methods for investigating protein-protein interactions for a gene product of interest. The high-throughput techniques that are most commonly used include Y2H and immunoprecipitation coupled to tandem mass spectrometry (IP-MS/MS) [156]. The Y2H assay capitalizes on the premise that transcription factors have a DNA binding domain and an activation domain [151]. For Y2H assay, the DNA binding domain and the activation domain are separated and each fused to one of two potentially interacting proteins [159]. If the proteins interact, they bring together the two domains of the transcription factor that then transactivates an easily detectable reporter gene. Some benefits of using Y2H are that it is highly scalable, large numbers of proteins can be processed at the same time, and only binary interactions are identified. The main criticism of this technique is that it can have high false-positive and false-negative rates [160]. The high false positive and negative rates are due to the fundamental nature of the screen. Y2H investigates interactions between overexpressed fusion proteins in the yeast nucleus. This environment is fundamentally different than that of proteins expressed at endogenous levels, *in vivo*, in human cells, at their natural subcellular localization, and all of these differences can contribute to false positive and negative interactions. Overexpression can result in non-specific interactions; the fused domains may interfere with true interacting partner binding, and promote spurious interactions; mammalian proteins are sometimes not correctly modified in yeast (e.g. post-translational modifications); and proteins may interact in the yeast nucleus that are normally never physically co-localized or temporally co-expressed in the cell.

Immunoprecipitation is one of the most commonly used methods for examining protein–protein interactions [161]. IP-MS/MS methods have been shown to allow the efficient and sensitive detection of protein binding partners [148, 162]. For the IP, protein complexes are purified using antibodies that either

recognize the endogenously expressed protein (or its mutant form) or recognize an affinity tag that is fused to the protein of interest. Affinity tags are generally made of short hydrophilic peptides (e.g. FLAG, hemagglutinin, or poly-His) or small proteins (e.g. Glutathione S-transferase (GST), thioredoxin, or Green Fluorescent Protein (GFP)) [151]. Sample preparation greatly affects the quality and coverage of results; therefore, after IP a second fractionation step is generally required. There are many methods to accommodate a second fractionation step, including one- or two-dimensional sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE), protein chromatography, peptide fractionation, isoelectric focusing (IEF), and strong cation exchange (SCX). The type of fractionation generally depends on the type of sample being analyzed, availability of instrumentation, cost, and desired level of coverage. After a second level of fractionation, the protein samples are digested into small peptides that are then identified using MS based analysis. Protein and peptide molecules have only been able to be routinely analyzed by MS for the past couple decades due to the advent of electrospray ionization (ESI) [4] and matrix-assisted laser desorption / ionization (MALDI) [5] that allow the ionization of the large molecules. Identification of proteins via MS analysis is another recent development made feasible due to available sequencing and annotation of complete genomes, resulting in the availability of a wealth of sequence databases that are the foundation of the high-throughput bioinformatics protein and peptide analysis methods [151].

Access to technology and expertise, reduced potential for false positives, and the ability for investigation within a human context using cell lines resulted in the decision to use IP via 3XFLAG affinity tags followed by one-dimensional SDS-PAGE, trypsin digestion, high performance liquid chromatography (HPLC), and MS analysis as the primary technique for protein-protein interaction investigation within this thesis. The 3XFLAG affinity tag was chosen as the primary tag for IP due to its efficiency, robustness, and ease of elution. Similar to Y2H, however, the use of a tagged protein results in protein expression levels that are not at physiological levels, potentially producing spurious interactions, and there is potential for the epitope tag to interfere with true interactions. The 3XFLAG affinity tag used here has the advantage of being a small hydrophilic peptide of only ~3 kDa [151], reducing the probability of physically impeding an interaction. Both N- and C- terminally tagged proteins were analyzed to improve the odds of identifying interaction partners that bind at the ends of the proteins and to avoid false positive and negative interactions due to the potentially altered protein structure. One-dimensional SDS-PAGE was performed to reduce the complexity of samples for MS analysis. The entire gel lane was excised and tryptic peptides extracted from the gel slices. Further fractionation was performed using HPLC separation. The combination of SDS-PAGE and HPLC fractionation of the protein and peptide samples generally provides sufficient fractionation that good coverage of abundant peptides is possible by MS analysis for most protein complexes. The fractionated peptide samples were introduced to the MS using electrospray ionization (ESI), which is a technique that allows for ionization of macromolecules. MS in this thesis actually represents a number of steps that allow for peptide sequence determination. After ionization, in the first stage of MS a spectrum of the mass/charge and abundance of ionized peptides is determined. In the second stage of MS, specific peptide ion mass/charge windows are selected for fragmentation and analysis. Collision induced fragmentation of the peptide ion allows a peptide to be fragmented into many of its possible composite ions, called b- and y-ions for those ions generated from a charged N- and Cterminal fragment, respectively. The mass/charge values of the b- and y-ions are then analyzed in the second MS stage. The combination of the peptide mass/charge values and the spectrum of b- and y-ion mass/charge values generated are then submitted to proteomics programs like Mascot [163] and X!Tandem [164] which use annotated genome sequences to predict peptide and protein identity. To reduce the false discovery rate, multiple replicate experiments and controls were performed and only those proteins that met specific criteria were considered possible protein interacting partners. Criteria to be considered a possible interacting partner included being identified in a minimum of two experiments, and not in more than one negative control, and having at least one of the experimental identifications with an X!Tandem log(E) score of less than -3.

1.7.1.2 Protein-protein interaction validation

While high-throughput methods allow the researcher the potential of discovering multiple protein-protein interactions within a small number of experiments, they can often produce results that contain false positives even after processing for non-specific interactions; therefore it is important to perform some level of verification to increase confidence that two proteins are true interacting partners. While there are a variety of methods that can be used for verification of protein interactions, the primary method used in this thesis was IP followed by western blot analysis (IP-western).

For IP-westerns, protein complexes were purified using antibodies that either recognized the endogenously expressed protein or an affinity tag fused to the protein of interest. The purified sample was then separated by 1D SDS-PAGE, transferred to a nitrocellulose membrane and probed using antibodies that specifically recognize the protein of interest. In this way, identification of potential protein interaction partners was performed by IP of the protein of interest and identification of interacting proteins through comparative MS analysis, while verification of interaction partners was performed by IP of the protein of interaction partners was performed by IP of the interaction partners was performed by IP of the protein of interaction partners was performed by IP of the protein of interaction partners was performed by IP of the inte

1.7.2 Protein-DNA interactions

As mentioned previously, protein abundance may also play an important role in disease etiology. There are many ways in which the abundance of the functional form of a protein can be altered including the accessibility of the gene to transcriptional machinery, targeting of transcriptional machinery to the genomic region, competitive expression between isoforms, modifications to the transcriptional, transportation, and translational machinery that participates in producing the protein, correct folding of the protein, transportation of the protein to its proper destination, post-translational modifications, and its degradation. Most of these functions are accommodated through protein-protein interactions; however protein-DNA interactions also play an important role in the recruitment or blocking of transcriptional

machinery at specific locations. Due to recent technology advances we now have the ability to investigate protein-DNA interactions in a high-throughput manner.

Broadly defined, a transcription factor is a protein that interacts with specific DNA sequences to effect transcriptional change. Transcription factors can effect gene transcription alone or in complexes. Transcription factors are generally composed of at least two types of domains: a DNA binding domain that targets a specific genomic site and a transcriptional regulation domain that recruits or blocks RNA polymerase from initiating transcription [165]. Other proteins in transcription factor complexes may perform other roles including, for example, coactivation, repression, chromatin remodeling, histone acetylation, and deacetylation, but do not require DNA binding domains. Transcription factors bind a variety of types of DNA sequences, including promoters, enhancers, and silencers, which in higher eukaryotes can be located as close as a few hundred base pairs from a gene's transcriptional start site in the case of promoters, to a great genomic distance away in the case of enhancers and silencers and can also be found upstream, downstream, or within the introns of genes [165].

To identify protein-DNA interactions there are two general strategies. Either one identifies the genomic locations or DNA sequences that a specific transcription factor binds to (transcription factor centric), or you can identify all the transcription factors that may bind to a specific DNA sequence (gene centric) [165]. For the purposes of the investigation described within this thesis, the focus was on identifying all the genes whose expression may be affected by the NRG1 ICD, for which there is evidence of being involved in transcription factor complexes. A transcription factor centric approach was taken using chromatin-immunoprecipitation (ChIP) followed by high-throughput sequencing (ChIP-seq). For ChIP, an antibody for the transcription factor of interest, or in this case a member of a transcription factor complex, is typically used to precipitate and purify DNA bound to the transcription factor (complex). These small DNA fragments may then be identified using a variety of methods, including polymerase chain reaction (PCR), microarrays, serial analysis of gene expression, or high throughput DNA sequencing [165]. For the research within this thesis, high-throughput sequencing was used to identify the genomic regions bound by the transcription factor complex containing the protein of interest. This was only possible due to the recent development of next generation massively parallel sequencing systems that has recently revolutionalized the sequencing field. In the case of ChIP-seq, it has not only decreased the cost and facilitated replicate experiments, but has also allowed for greater sensitivity and resolution in the identification of genome-wide binding sites than ever before [166].

Our knowledge of transcription factors and their binding sites in humans is largely incomplete [165]. There are databases available, however, that compile information on transcription factors, including a public database of transcription factors, their experimentally-proven binding sites, and regulated genes (TRANSFAC) [167]. There are a variety of tools built to interface with TRANSFAC that enable users to easily perform a variety of different types of queries. One such tool, called MATCH, can be used to identify transcription factor binding sites (TFBS) within a set of DNA sequences. For the research in this

thesis, I used MATCH and information within the TRANSFAC database to analyze the ChIP-seq results and identify known TFBS found within the ChIP-seq sequences.

To determine the genes likely to be affected by the binding of transcription factor complexes to genomic sites, genes most proximal to the protein-DNA binding sites were identified. Available data on gene expression pattern changes that result from mutations or changes in abundance of a candidate transcription factor protein can be used to increase confidence in specific protein-DNA binding events. Methods available to test expression changes include quantitative real time polymerase chain reaction (qPCR) and differential expression by microarray analysis. qPCR uses short oligonucleotide primers that span exon boundaries of genes whose expression pattern is being tested and quantitatively compares the rate of amplification between the reverse transcribed mRNA of different sample conditions for the protein of interest. Differential expression analysis by the simultaneous evaluation of quantitative measurements of the expression between different sample conditions for the candidate transcription factor protein of interest.

1.7.3 Gene function

Determining the function of a susceptibility gene can contribute to our understanding of disease etiology and pathology and therefore is of great interest. As discussed above, proteins can have multiple functions, and our knowledge of protein function is largely incomplete. However, most proteins perform functions by interacting with other proteins and interacting proteins are more likely to share a common function than non-interacting proteins [168]. Therefore, we can increase our understanding of the function of a protein of interest by identifying their its interacting partners.

We have seen an explosion in the accumulation of biological data in the past few decades. The gene ontology (GO) has emerged as a core repository for the functional annotation of gene products. GO provides structured datasets describing gene product attributes in three non-overlapping molecular biology domains (molecular function (MF), biological process (BP), and cellular component (CC)) [169]. Several tools have been developed that allow researchers to perform statistical analyses on GO data. One set of tools that was used in this thesis was the Database for Annotation, Visualization and Integrated Discovery (DAVID) bioinformatics resources, which provides a gene functional classification tool allowing statistical functional analyses of large gene lists [168].

1.7.4 Visualization of biological information using networks

Traditionally, researchers have operated at the individual gene or protein level. However, with the explosion of biological information and the development of high-throughput methodologies that allow

interrogation of whole genome attributes within individual experiments (e.g. genome-wide association studies, microarray technology), there is a need to be able to visualize results and relationships in a way that encompasses as much of the information as possible. Visualizing protein-protein and protein-DNA interactions as networks provides context for researchers to analyze how genes and gene products relate to each other. A network is typically represented as a set of points or nodes that are connected by lines or edges and can comprise one or more types of relationships. In the case of protein-protein and protein-DNA interactions, networks are displayed such that the nodes are specific genes or their gene products and the edges are their physical interactions. Networks pervade all aspects of human health [20], and have shown us that most gene products are highly interconnected with other gene products. The greater number of functional links associated with a gene containing a defect, the higher the probability for potential impact on a larger portion of the network. In this way, a defect in one gene can affect the activity of genes that otherwise carry no defects, but instead have a functional relationship with the defective gene [20]. To better understand the various disease mechanisms involved in complex disease in particular, it is not sufficient to know the precise list of disease genes; rather, we require a detailed understanding of the pathways that are influenced by the genes [20]. By extension, identifying potential disease mechanisms, or subsets of disease genes in the context of a network, can highlight molecular pathways for potential disease involvement.

1.8 Statistical Analyses

The explosion of biological data and the use of large scale analyses necessitate the use of computational and statistical techniques to determine result significance. Various computational re-sampling methods have emerged as common bioinformatic tools for the estimation of result significance, including random permutation analysis. For the purposes of the work done in this thesis, statistical significance was determined through random permutation-based analyses. Random permutation analysis is a statistical method used to determine how likely the result of the original analysis was due to random chance. To statistically analyze this, the raw inputs that produced the result are randomized and the analysis is re-run multiple times. The more randomized inputs that produce a result similar to the original result, the less significant the original result. Another statistical test, the Chi-squared test for independence, was also used in Chapters 2 and 3 to determine if the ratio of genes in schizophrenia linkage regions whose gene products were found to interact with my protein of interest was significant when compared to the background of all linkage regions identified in the genome. When multiple hypotheses are being tested at the same time, for example in GWAS, where each SNP is being tested for association with a specific trait or disease, there is a need to adjust the threshold for significance as there is a greater chance of false discovery than in individual tests. Traditionally, a Bonferroni correction would be used to determine a threshold of significance that would accommodate for multiple tests [170, 171]. The Bonferroni correction attempts to maintain the family-wise error rate by testing each hypothesis at a statistical significance level of [1 / the number of experiments] times what it would be if only one hypothesis was tested. However, in cases where thousands or more tests are being performed, the Bonferroni correction is so highly

stringent that in some cases there is no possibility of finding significance for truly positive results. A variety of other methods have been developed that are much less stringent while still adjusting for multiple tests and are therefore more amenable to situations with large numbers of tests. These multiple test correction methods include those which estimate false discovery rate (FDR), for example using the Benjamini and Hochberg method [172]. FDR methods are less conservative and control the expected proportion of incorrectly rejected null hypotheses (type I errors, false positives). The Benjamini and Hochberg method involves a sequential p-value procedure where the p-values of each test are ranked from smallest to largest, the largest value remains as it is and each subsequent value is adjusted by the total number of tests divided by its rank. Within this thesis, where multiple testing was an issue in determining statistical significance, the Benjamini and Hochberg method was used to adjust for multiple tests [172].

1.9 Thesis Chapters Summary

The objective of this thesis was to identify novel potential schizophrenia candidate genes using nontraditional methods of disease gene investigation. Two main approaches were taken. The first approach is based on the idea that the combined effect of multiple genetic perturbations within specific functional pathways may result in the disease phenotype, or that the underlying genetic susceptibility for disease may stem from mutations in one or more members of specific functional pathways. Therefore, any protein that interacts with a promising schizophrenia susceptibility gene product should be considered a potential schizophrenia candidate gene. The second approach takes advantage of whole genome linkage analysis, a method that directly investigates the relationship between disease and genetics across the entire genome in an unbiased way. Information from multiple whole genome linkage analyses can be combined to estimate schizophrenia linkage signals across the genome. To overcome the lack of reproduction between linkage studies and attempt to refine existing linkage regions through identification of consistent linkage signals across multiple studies, a new method of whole genome linkage metaanalysis was developed.

Chapter 2 focuses on an investigation of protein-protein interactions for the schizophrenia susceptibility gene DTNBP1. A set of 83 high confidence potential interacting proteins was identified for the DTNBP1 protein using IP-MS/MS. A subset of these interacting partners was chosen for verification using IP-western analysis. Novel interactions with members of the dynactin and exocyst complexes were identified and verified in this way. These interactions are of particular interest as both dynactin and exocyst complex members were previously identified as interacting partners of the schizophrenia susceptibility gene DISC1 through a Y2H investigation [173]. To further expand the protein interaction network, IP-MS/MS analyses of members of the dynactin and exocyst complexes were performed. To determine whether the resulting DTNBP1, dynactin complex, and exocyst complex protein interaction sets were overrepresented with proteins linked to schizophrenia, a statistical analysis was performed based on linkage data found in the psychiatric genetics evidence project linkage database. A gene

ontology analysis was also performed on the resulting protein interaction sets to identify potential functional themes. The resulting DTNBP1, dynactin complex, and exocyst complex interaction network links two of the best schizophrenia susceptibility genes currently identified, DTNBP1 and DISC1, encompasses many aspects of the vesicle life cycle, and involves many cytoskeletal proteins.

Chapter 3 focuses on the intracellular domain (ICD) of the schizophrenia susceptibility gene NRG1 to identify its protein-protein and protein-DNA interactions. A set of 22 novel high confidence potential interacting proteins were identified for NRG1 ICD using IP-MS/MS. A subset of these interactions was chosen for verification using IP-western analyses, including utrophin (UTRN), a known interacting partner of DTNBP1. To determine whether the resulting protein interaction sets were overrepresented with proteins found in genomic regions known to be linked to schizophrenia, a statistical analysis was performed based on linkage data found in the psychiatric genetics evidence project linkage database. A gene ontology analysis was also performed on the resulting protein interaction sets to identify potential functional themes. The resulting protein interaction network links two of the best schizophrenia susceptibility genes currently identified, NRG1 and DTNBP1, and includes cytoskeletal and transport related proteins as well as many nuclear and transcription factor proteins, supporting a role for NRG1 ICD in the nucleus and its involvement in transcription factor complexes.

There is evidence that the NRG1 ICD is translocated to the nucleus and affects transcription [109, 110, 174]. To investigate NRG1 as a potential transcription factor, a ChIP-seq analysis was performed, producing a set of 5,674 potential genomic binding sites. The ChIP-seq analysis identified genomic binding sites proximal to genes whose expression patterns are known to be influenced by NRG1 ICD nuclear localization, including DLG4 and ERBB2 [110]. These 5,674 regions were investigated to identify transcription factors with known TFBS within the ChIP-seq sequences using MATCH. The MATCH analysis identified the IK1 binding site as one of 164 TFBS overrepresented in the ChIP-seq peak sequences. The IK1 TFBS has previously been shown to be a binding sites were investigated to determine: a) if there was existing literature evidence of NRG1 impacting their expression, and b) if there was an overrepresentation of genes with a known association to schizophrenia based on the annotations contained within GAD. The implication of these results is that, once cleaved, the NRG1 ICD translocates to the nucleus where it binds with transcription factors to form transcription factor complexes that affect transcriptional change.

Chapter 4 describes a novel whole genome linkage meta-analysis method called Marker Footprint Linkage Meta-analysis (MFLM) that allows multiple linkage studies to be combined in a way that incorporates the use of recombination rates determined by the HapMap project. Linkage meta-analysis methods have many problems that must be overcome. First and foremost, it is difficult to gain access to linkage data from existing studies, including published datasets. For most linkage studies it is not possible to procure detailed results that include complete family trees along with all individual marker results for each individual such that the raw data can be pooled to perform a meta-analysis. In my

experience, even requests for summary statistics of marker ID and their associated linkage scores could not be met. Secondly, there are many different types of linkage scores resulting from different studies, including p-values, logarithm of odds (LOD) scores, and non-parametric linkage (NPL) scores which complicate the comparison of scores between studies. Thirdly, different linkage studies do not always use identical marker sets and therefore the meta-analysis method must have a way of determining how to combine signals from markers in similar regions but different studies that do not overlap. Finally, issues inherent in complex disease are often difficult to address, including underlying genetic heterogeneity and multiple genes of low penetrance. The MFLM method attempts to overcome some of these issues by: a) only requiring the summary statistics of marker ID and linkage score, b) converting the linkage score into a genomic probability score based on the relationship between the different types of linkage scores and their significance threshold as described in Schulze and McMahon [175], and c) using the recombination rates determined by the HapMap project to determine how to combine non-overlapping markers between Eight schizophrenia whole genome linkage study summary statistics were procured and studies. combined using the MFLM method. The results identified 24 nominally significant regions including one novel region, 9q31.1.
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2 Cytosolic Protein Interactions of the Schizophrenia Susceptibility Gene Dysbindin¹

2.1 Introduction

Schizophrenia is a complex psychiatric disorder with a strong genetic component and unknown etiology [1, 2]. A number of genes have been identified as schizophrenia susceptibility genes including DTNBP1 (DTNBP1), neuregulin (NRG1), catechol-O-methyltransferase (COMT), and disrupted-in-schizophrenia-1 (DISC1), among others [3]. DTNBP1 is one of the most robust schizophrenia susceptibility genes identified to date, located within one of the most consistently replicated schizophrenia linkage regions (6p22.3) [4-11] and having one of the most replicated schizophrenia association findings [12-21]. The DTNBP1 knockout mouse (*sandy*) shows increased dopamine turnover in specific brain regions [22], and schizophrenia patients have been found to have decreased expression of DTNBP1 at presynaptic glutamatergic terminals in the hippocampus [23, 24] and dorsolateral prefrontal cortex [25]. Defects in neurosecretion and vesicular morphology in neuroendocrine cells and hippocampal synapses have been identified at the single vesicle level in *sandy* mice and implicate DTNBP1 functions in the regulation of exocytosis and vesicle biogenesis in endocrine cells and neurons [26].

DTNBP1 was initially discovered as an interacting protein of dystrobrevin proteins (DTNA, DTNB) [27]. Mutations in the DTNBP1 gene have been shown to cause Hermansky-Pudlak Syndrome (HPS) type 7, one of eight known human HPS types caused by defects in intracellular protein trafficking resulting from the dysfunction of lysosome-related organelles. DTNBP1 is a member of the biogenesis of lysosomal related complex-1 (BLOC1) [28], which is known to interact with the biogenesis of lysosomal related complex-2 (BLOC2) and adapter-related protein complex-3 (AP3) complexes [29], and functions in organelle biogenesis and the protein transport pathway [30]. BLOC1 subunits are implicated in synaptic mechanisms [31]; Pallidin (PLDN) is involved in mediating vesicle docking and fusion [32] and disruption of soluble NSF-attachment receptor (SNARE)-associated protein (SNAPIN) causes defective secretion of neurotransmitters in mice [33]. Recently, Hikita *et al.* (2009) identified syntaxin binding partner-1 (STXBP1 or Munc18-1) as a DTNBP1 interacting protein in an analysis of DTNBP1 membrane interactions. STXBP1 has been implicated in the exocytosis of synaptic vesicles [34-36].

DISC1 was initially identified at a site for a balanced translocation (1:11) (q42.1;q14.3) that co-segregates with schizophrenia and other psychiatric disorders in a large Scottish pedigree [37, 38]. Several studies provide evidence of DISC1 association with schizophrenia [39-44]. DISC1 has been shown to interact with multiple proteins including nuclear protein distribution nudE-like 1 (NDEL1) [45, 46], platelet-activating factor acetylhydrolase IB subunit alpha (PAFAH1B1, also called LIS1) [47], cAMP-specific 3',5'-cyclic phosphodiesterase 4B (PDE4B) [48], growth factor receptor-bound protein 2 (GRB2) [49, 50],

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fasciculation and elongation protein zeta-1 (FEZ1) [51], DISC1-binding zinc-finger protein (DBZ) [52], and pericentrin (PCNT or kendrin) [53]. PDE4B and FEZ1 have also had positive schizophrenia association results [54, 55]. Through these interactions it is postulated that DISC1 is involved in brain development including neuronal migration, neurite outgrowth and neural maturation through interaction with several cytoskeletal proteins [56].

Defective synaptic transmission and neurotransmitter release is hypothesized to be a pathogenic mechanism in schizophrenia [3, 57]. Defects in presynaptic vesicle proteins have been associated with schizophrenia [58-60] and the schizophrenic brain has been shown to possess reduced levels of mRNA and/or proteins involved in synaptic vesicle fusion [61-64]. Our understanding of the vesicle life cycle involved in neurotransmitter release remains incomplete. For example, the disruption of DTNBP1 in *sandy* mice causes defects in neurosecretion and vesicle morphology in neuroendocrine cells and hippocampal synapses at the single vesicle level, including larger vesicle size, slower quantal vesicle release, lower release probability, and smaller total population of the readily releasable vesicle pool [26]. However, the detailed mechanisms for how these DTNBP1-associated phenomena may contribute to neurotransmitter release or schizophrenia pathogenesis are unknown.

We reasoned that a better understanding of DTNBP1 interacting proteins would facilitate the investigation of DTNBP1 pathways and functions and potentially provide insight into schizophrenia etiology. Using proteomic techniques we have identified DTNBP1 interacting proteins with vesicle trafficking components. Intriguingly, these data also identify potential common links for two of the best schizophrenia susceptibility genes, DTNBP1 and DISC1, to portions of the vesicle trafficking system.

2.2 Materials and Methods

2.2.1 Cloning

cDNAs for two isoforms of DTNBP1: version 1 (NM_032122) and version 3 (NM_183041), and exocyst component 4 (EXOC4), exocyst component 3 (EXOC3), AP3 subunit beta-1 (AP3B1), AP3 subunit beta-2 (AP3B2), dynactin subunit 2 (DCTN2), and alpha-centractin (ACTR1A, a member of the dynactin complex) were procured (IMAGE clones 4139934, 6183004, 5590332, 3914400, 7939584, and 3347881 respectively, (*American Type Culture Collection*,(ATCC), Manassas, VA, USA). The open reading frames were amplified (see Table 2.11 for PCR primer sets) and ligated into the V954 donor vector of the Creator Splice system [65]. The cDNA containing cassettes were transferred into mammalian expression acceptor vectors for fusion to both N- and C-terminal 3xFLAG tags (V180 and V181) by Cre-lox recombination. DTNBP1 version 1 was also transferred to GFP-fusion vectors (V4 and V6). Completed constructs were sequence verified prior to use.

2.2.2 Antibodies

Antibodies were anti-DTNBP1 (goat, sc-46931, Santa Cruz Biotechnology, Santa Cruz, CA, USA), anti-GFP (rabbit, sc-8334, Santa Cruz Biotechnology), anti-FLAG (mouse, M2, Sigma-Aldrich), anti-DISC1 (goat, ab41985, Abcam Inc, Cambridge, MA, USA), and fluorescent secondary antibodies (IR-700, Roche, Basel, Switzerland).

2.2.3 Cell culture

HEK293 (human embryonic kidney, ATCC) and X57 (mouse striatal, obtained from Marian DiFiglia at Massachusetts General Hospital, Boston, MA, USA) cells were maintained at 37°C and 5% CO₂ atmosphere in Dulbecco's modified eagle's medium with glutamax (Invitrogen, Carlsbad, CA, USA) supplemented with 10% added fetal bovine serum (Invitrogen).

2.2.4 Immunoprecipitation, protein complex preparation, and mass spectrometry

The 3XFLAG-tagged cDNA expression vectors were transfected into HEK293 (for DTNBP1) or X57 (for exocyst and dynactin complex proteins) cells using lipofectamine 2000 reagent (Invitrogen) in Optimem reduced serum media (Invitrogen). Cells were separately transfected with the parent acceptor vector for the negative control sample. Approximately 48 hours after transfection, confluent cells were harvested using chilled (4°C) phosphate buffered solution (1 mM NaH₂PO₄, 155 mM NaCl, 3 mM Na₂HPO₄, pH 7.4) and the pellets were stored at -80°C. Cell pellets were resuspended in lysis/wash buffer with protease inhibitors (Tris buffered saline (20mM Tris-base, 100mM NaCl, pH 7.4), 1mM EDTA, 1% NP-40, 10 μ g/ml Leupeptin, 10 μ g/ml Aprotinin, 10 μ g/ml Pepstatin, 1mM AEBSF, 2mM Na3VO4, 10mM β -Glycerophosphate) and forced through a 20 gauge syringe 3 times, and rocked for 30 minutes at 4°C. The cell debris was removed by centrifugation (15 min at 12,000 rpm) and the supernatant filtered through a 0.45 μ m membrane. The extracts were immunoprecipitated with anti-FLAG M2 agarose resin (Sigma-Aldrich, St. Louis, MO, USA) and proteins released with FLAG peptide, as described previously [66].

The immunoprecipitate eluates, from the 3XFLAG-tagged cDNA and empty vector control transfections, were lyophilized and rehydrated in loading buffer (Tris-Cl/SDS (58mM Tris-Cl, 0.05% SDS, pH 6.8), 5% glycerol, 1.7% SDS, 0.1M dithiothreitol, 0.03 μ M bromophenol blue) and heated at 85°C for 10 minutes. The eluates were separated by 1-dimensional SDS-PAGE using a 4-12% gradient NuPAGE gel (Invitrogen) with NuPAGE MES running buffer (Invitrogen) for ~1.5 hr at 150V. The gel was then stained in colloidal Coomassie (20% ethanol, 1.6% phosphoric acid, 8% ammonium sulfate, 0.08% Coomassie Brilliant Blue G-250) and de-stained with distilled H2O. The entirety of each lane was excised and

divided into 16 pieces; each slice was finely diced and transferred to a 96-well plate. Automated in-gel dehydration, alkylation, trypsin digestion, and extraction were performed (Progest; Genomic Solutions, Ann Arbor, MI, USA). The extracts were lyophilized and re-suspended in 3% acetonitrile, 1.5% formic acid.

High performance liquid chromatography-electrospray-tandem mass spectroscopy (HPLC-ESI-MS/MS) was performed on a 4,000 QTrap mass spectrometer (Applied Biosystems/Sciex, Foster City, CA), except for three DTNBP1 immunoprecipitations which were performed on a LCQ Deca (Thermo-Fisher). Both instruments were coupled to a Agilent 1,100 Nano-HPLC (Agilent, SantaClara, CA, USA) using a nano-ESI interface. For the 4,000 QTrap, samples were desalted using an on-line trap column (Agilent, Zorbax, 300SB-C18, 5µm, 5x0.3 mm) and chromatography coupled to electrospray was performed on a 75 μm x 150 mm reverse phase column (Jupiter 4μ Proteo 90 A, Phenomenex, Torrance, CA, USA) using Buffer A (5% HPLC grade acetonitrile (Fisher, Ottawa, Canada), 0.1% formic acid (Fluka, Sigma-Aldrich) and Buffer B (90% acetonitrile, 0.1% formic acid) in a linear gradient of 0-20% B for 37 minutes, 20-39% B for 16 minutes, and 39-90% B for 8 minutes at a flow rate of 300 nl/min. ESI-MS/MS was performed with ESI at 1,850 V, interface heater at 150 °C, at 4.7x10⁵ torr with nitrogen (99.999%, Praxair, Danbury, CT, USA) for nebulizer gas (0.5 ml/min) and curtain gas (2 L/min). Data were collected using a 400-1,600 m/z Enhanced MS scan followed by an Enhanced Resolution scan to select the top five +2 and +3 ions for collisional-induced dissociation and a final Enhanced Product Ion MS scan. For the LCQ Deca, the chromatography was performed with flow splitting to produce a 0.2 µl/min rate. The samples were washed on a trap column (Jupiter 4µ, Proteo 90 A, Phenomenex) using buffer A (5% HPLC grade acetonitrile, 0.1% formic acid and 0.02% TFA) for 5 minutes. Chromatography was then performed (column: 75 µm x 100 mm; Jupiter 4µ, Proteo 90 A, Phenomenex) using buffer B (90% acetonitrile, 0.1% formic acid, 0.02% TFA) in a linear gradient of 0-35% B for 37 minutes, 35-65% for 8 minutes and 65-100% for 2 minutes. The capillary was at 160°C and ESI at 1,800 V. The MS was operated at 1-1.9x10⁻⁵ torr in data-dependent acquisition mode with a full scan MS (400-1,400 m/z) followed by MS/MS of the three most intense precursor ions using collisional-induced dissociation (helium). The MS/MS spectra emanating from the gel slices for each lane were concatenated and searched against the Ensembl human or mouse databases, as appropriate, using the Mascot (Matrix Science, Boston, MA, USA) and X!Tandem (http://www.thegpm.org/TANDEM/) search engines. Search parameters were 0.3 Da and 0.4 Da for precursor and product ion mass tolerance, respectively; trypsin digestion; one missed cleavage; oxidation (methionine); deamidation (asparagine, glutamine); phosphorylation (serine, threonine, and tyrosine), and carbamidomethylation of cysteine. The raw data are available through the PRIDE database (http://www.ebi.ac.uk/pride/).

2.2.5 Identification of candidate interacting proteins

Using in house SpecterWeb software we processed the identified proteins from the MS/MS analyses by subtracting: 1) proteins found in more than one negative empty vector control sample; 2) common non-

specific binding proteins (heat shock, transcriptional and translational machinery, keratins, and protein arginine N-methyltransferase (PRMT5)); 3) proteins found in only 1 experimental sample; and 4) proteins without 2 observations each having X!Tandem log(E) scores \leq -3. The candidate interacting proteins were then subdivided into two tiers, where first tier proteins were those having a minimum of 2 unique peptides in each of at least 2 replicates, as identified by X!Tandem. The average X!Tandem log(E) score was calculated for each candidate protein across the experiments where it was observed. The list of candidate interacting proteins and the analysis data for the DTNBP1, dynactin and exocyst experiments are reported in Tables 2.2A, 2.3A, 2.4A, and Figures 2.9, 2.10, and 2.11, respectively.

2.2.6 Validation of protein interactions through immunoprecipitationwestern analysis

The 3XFLAG-tagged constructs were co-transfected with GFP-tagged DTNBP1 (N-tagged for X57 experiments, C-tagged for HEK293 experiments) into HEK293 or X57 cells as described above. Anti-FLAG immunoprecipitation and separation by one-dimensional SDS-PAGE is described above. The negative controls were cells transfected with the parent acceptor vectors. An aliquot of the input lysate without immunoprecipitation was used as a positive control. The proteins were electro-transferred to nitrocellulose for ~16 hrs at 100mA in towbin buffer (0.25M Tris-base, 2M glycine, pH 8.5, 20% methanol). The nitrocellulose was blocked using NuPAGE Odyssey blocking buffer (Invitrogen) before being probed using the appropriate antibody (1:200 anti-GFP antibody, or 1:500 anti-DISC1 antibody) for ~ 16 hrs at 4°C in blocking buffer. The filter was washed (three times, 5 minutes each) with TBS-Tween buffer (Tris buffered saline, 0.01%Tween-20) and then probed with the appropriate secondary antibody for 30 minutes at 22°C. The nitrocellulose was then washed with TBS-Tween buffer (three times, 5 minutes each) and imaged using an Odyssey system (LI-COR Biosciences, Lincoln, NE, USA).

2.2.7 Linkage and association with schizophrenia analysis

The genetic association database (GAD, http://geneticassociationdb.nih.gov/) and the psychiatric genetics evidence project linkage database (https://slep.unc.edu/evidence/) were used to determine whether any of the protein interaction sets were overrepresented with proteins having previous linkage or association evidence of involvement with schizophrenia. A query of the GAD database using the HGNC names showed few of the proteins have been investigated in schizophrenia association studies, thus GAD association data did not contribute to the schizophrenia over-representation analysis. Therefore, only the linkage database was queried with the cytogenetic location associated with each protein in order to perform the overrepresentation analysis. For AP3, BLOC1, CCT, dynactin, and exocyst all complex members were included in the analysis if any members of the complex had been identified in the protein interaction set. A Chi-squared test was used to determine the significance of finding the number of schizophrenia linked cytogenetic regions observed for each protein interaction set, given the number of cytogenetic regions across the entire human genome with evidence of schizophrenia linkage.

2.3 Results

2.3.1 DTNBP1 protein interactions

DTNBP1 interacts with vesicle trafficking complexes: exocyst, dynactin, AP3, CCT and cytoskeletal components. To obtain high confidence protein interaction partners for DTNBP1 we used a co-immunoprecipitation comparative mass spectrometry (MS) analysis procedure where peptides from immunoprecipitated DTNBP1 protein complexes were compared to peptides found in protein complexes from control immunoprecipitates. HEK293 cells were transfected with FLAG epitope-tagged versions of DTNBP1 isoform 1 and isoform 3 or an empty vector control. Protein complexes from cytosolic fractions of the experimental and control cells were immunoprecipitated by an anti-FLAG antibody and size fractionated using one dimensional SDS-PAGE. Rather than excise only individual visually observable bands and to obtain high sensitivity, accuracy and coverage we processed the entire lanes and compared the peptide (protein) composition between the experimental and control samples using the MS data. Seven independent experiments were performed; two experiments each for N- and C-tagged DTNBP1 isoform 1 and N-tagged isoform 3, and one experiment for C-tagged isoform 3, which were compared to six empty vector control experiments. In Figure 2.5, a representative gel image of a control and experimental sample is shown and in Figure 2.6 representative ion chromatograms, MS spectra and MS/MS fragment assignments of two peptides for each of six candidate interacting proteins between the experimental gel slice and the cognate control gel slice. This demonstrates the observation of an assigned peptide in the experimental sample and its absence in the control sample. From these experiments we identified 83 unique candidate DTNBP1-interacting proteins that met score quality thresholds (see Methods) and were observed in at least two independent experiments (Table 2.1, Figure 2.1, Table 2.2). Fourteen of the proteins were previously identified as DTNBP1 interacting proteins, including all seven members of BLOC1 [28], all six members of the AP3 complex, and DNA-dependent protein kinase catalytic subunit (PRKDC) [67] that previously had been shown to interact with either BLOC1 [29] or DTNBP1 itself [68]. The remaining 68 novel DTNBP1 interacting proteins include several members of the exocyst and dynactin complexes, and components of the cytoskeleton, including actin and tubulin and the CCT complex. These interactions support a role for DTNBP1 in vesicle trafficking.

Six DTNBP1 interactions were chosen for validation, including interactions with two members each of the dynactin (ACTR1A, DCTN2), exocyst (EXOC3, EXOC4), and AP3 (AP3B1, AP3B2) complexes (Table 2.1). Epitope-tagged versions of these proteins and DTNBP1 were co-expressed in HEK293 and X57 cells. Immunoprecipitation and western blotting confirmed the interaction of DTNBP1 with the six proteins in all 12 experiments with both HEK293 and X57 cells (Figure 2.2). Until recently (Hikita et al 2009), the interaction of DTNBP1 with individual members of the AP3 complex had not been shown. A Y2H experiment identified a candidate interaction between DTNBP1 and EXOC4 [58]; however, this interaction had not previously been validated in mammalian cells. The average log(E) scores for most of

the 68 novel DTNBP1 interactors were within the range of scores for the 18 known and/or validated DTNBP1 interacting proteins (Figure 2.9, and Table 2.2). This indicates that most of the proteins identified are likely to be true DTNBP1 interaction partners.

2.3.2 Exocyst and dynactin protein interactions

The exocyst and dynactin complexes interact with the CCT complex and vesicular transport, trafficking, and transporter associated proteins. In order to extend the DTNBP1-associated protein interaction network co-immunoprecipitation comparative mass spectrometry experiments were performed in X57 cells for two exocyst complex proteins (EXOC3, EXOC4) and two dynactin complex proteins (ACTR1A, DCTN2). Two experiments were performed for each of these four 'bait' proteins and compared to two empty vector controls; Figure 2.7 shows a representative gel image. The results identified 56 and 31 unique protein identifications for the exocyst and dynactin complexes, respectively, after processing for background, quality, and experimental replication (see Methods). Of these, 48 and 23 are novel interactions, respectively (Table 2.1, 2.3, and 2.4). Similar to the DTNBP1 data, the average log(E) scores for the novel exocyst and dynactin interacting proteins overlapped with the scores for their known interactors (Figures 2.10 and 2.11). In addition, 47 and 15 of the interactions in the exocyst and dynactin data were identified by both bait proteins, respectively (Table 2.1, 2.3, and 2.4), and thus represent independent corroboration of these candidate protein-protein interactions.

2.3.3 Verification of DISC1 interactions with exocyst and dynactin complexes

DISC1 interacts with the exocyst and dynactin complexes. Interactions between DISC1 and DCTN2 of the dynactin complex, and DISC1 with both EXOC1 and EXOC7 of the exocyst complex were previously shown by Y2H experiments [58]. To verify that these interactions occur in mammalian cells, we expressed epitope-tagged ACTR1A of the dynactin complex and EXOC3 of the exocyst complex in HEK293 cells, immunoprecipitated the tagged ACTR1A and EXOC3 complexes and then confirmed the presence of the DISC1 protein by western blot with an anti-DISC1 antibody (Figure 2.3). With this result we have shown that both DTNBP1 and DISC1 interact with the exocyst and dynactin complexes in human cells (Figure 2.1).

2.3.4 Gene ontology analysis of interacting proteins

Gene ontology (GO) analysis shows that exocyst and DTNBP1 interacting proteins share vesicle mediated transport and localization terms. The online DAVID Bioinformatics Resource (http://david.abcc.ncifcrf.gov/) was used to identify significant GO terms for the DTNBP1, dynactin, and exocyst interacting proteins. DAVID recognized 76 of the 83 proteins in the DTNBP1 interacting protein

list and produced significant GO terms for all 3 ontological categories (biological process (BP), cellular component (CC), molecular function (MF)) (Table 2.5). DAVID recognized 31 of the 31 proteins in the dynactin interacting protein list but only produced significant GO terms for the CC and MF categories; no significant GO terms were found for the BP category (Table 2.6). DAVID found 50 of the 56 proteins in the exocyst protein interacting protein list and produced significant GO terms for the BP and CC categories (Table 2.7). The biological process GO terms significantly overrepresented by DTNBP1 and exocyst interacting proteins are shown as an ontological tree in Figure 2.4. The 13/15 BP terms for the DTNBP1 interacting proteins were also identified as significant BP terms for the exocyst dataset; these include several localization and transport terms including vesicle-mediated transport and secretion by cell, confirming with this extended dataset that not only is DTNBP1 involved in vesicle trafficking, but it interacts with many other proteins that play a role in vesicle trafficking.

2.3.5 DTNBP1 and dynactin interacting proteins linked to schizophrenia

Genes encoding DTNBP1 and dynactin interaction networks are significantly overrepresented within chromosomal regions linked to schizophrenia. We used whole genome linkage data to determine if the genes that encode members of our DTNBP1, exocyst complex, and dynactin complex protein interaction sets tend to be located in cytogenetic regions linked to schizophrenia. Genetic linkage data were obtained from the Psychiatric Genetics Evidence Project Linkage Database (https://slep.unc.edu/evidence/) (Tables 2.8, 2.9, and 2.10). This database compiles findings from manual reviews of 144 papers in psychiatric genetics across a variety of disorders and includes studies on genome wide linkage and association, copy number variation, and gene expression. It shows that 366 of a total of 826 cytogenetic regions have been found to have strong or suggestive linkage to schizophrenia in whole genome scans. The DTNBP1 and the dynactin protein interaction networks (including all core complex members) comprise 96 and 34 total proteins, respectively, with 55 and 24 of these in schizophrenia linked cytogenetic regions (Chi-squared test; p = 0.017 and 0.006, respectively). In the 71 member exocyst network 34 genes were in schizophrenia linked cytogenetic regions, but this result was not significant (Chi-squared test; p=0.619).

2.4 Discussion

It has been suggested that compromised neurotransmission due to aberrations in synaptic trafficking of endosomal vesicles and their neurotransmitter related cargoes may contribute to the etiology of schizophrenia [69]. DTNBP1 is linked genetically to schizophrenia and has an essential role in synaptic vesicle trafficking and homeostatic modulation of neurotransmission [70]. Here, we investigate DTNBP1 protein interactions to identify additional proteins, pathways, and functions of possible relevance to schizophrenia. Our data significantly expand the overall protein interaction network for DTNBP1 and show that it is involved throughout the vesicle life cycle and vesicle trafficking system, from vesicle

biogenesis and cargo sorting (BLOC1, DTNBP1, AP3) to vesicle trafficking (dynactin, tubulin/actin proteins), to membrane targeting and vesicle tethering (exocyst).

Our results include human cytosolic protein interactions for DTNBP1 obtained from endogenous cellular complexes and complement a recent study that focused on membrane-associated protein interactions of DTNBP1 [68]. Our results are consistent with previous studies that show interactions between DTNBP1 and members of the AP3 complex [29, 68]. Since we focused on cytosolic interactions of DTNBP1 while Hikita *et al.* 2009 investigated membrane interactions of DTNBP1, there were a number of membrane or membrane associated proteins they observed that were not replicated in our analysis, including STXBP1, glyceraldehyde-3-phosphate dehydrogenase (GAPDH), ADP-ribosylation factor 1 (ARF1), ADP-ribosylation factor GTPase-activating protein 1 (ARFGAP), and Arf-GAP with SH3 domain, ANK repeat and PH domain-containing protein 1 (ASAP1). Conversely, most of the proteins found in our study were not found in the Hikita *et al.* 2009 study, including any members of BLOC1, of which DTNBP1 is known to be a member of [28], nor members of the exocyst and dynactin complexes. These differences are not surprising given the different experimental approaches, but further highlight that DTNBP1 plays a role in many aspects of the vesicle lifecycle, both within the cytoplasm as well as at the membrane surface. In this way, our results complement the findings in Hikita *et al.* 2009 and implicate DTNBP1 in vesicle associated protein trafficking processes throughout the cell [68].

Our data indicate DTNBP1 interacts with several actin and tubulin proteins and with members of the CCT and dynactin complexes, which are fundamental components of the cytoskeleton and microtubule matrix. The CCT complex is a large multi-subunit complex that mediates protein folding for a variety of proteins, including several actin, tubulin and cell cycle regulator proteins [71] and plays an important role in the assembly of the cytoskeleton and in cell division [72]. The 11 subunit dynactin complex [73] recruits and links the dynein motor protein to vesicles and to microtubules to facilitate cargo transport along the cytoskeletal matrix [74]. In neuronal axons, dynactin is involved in retrograde as well as anterograde transport [75, 76]. Mutations in dynactin subunits can cause defects in axonal transport; for instance, individuals with mutations in the DCTN1 subunit suffer from motor neuron disease [77]. The function of the dynactin complex may vary based on location, but in all cases it is thought to facilitate or regulate dynein or kinesin II targeting and recruitment. Our data also show the exocyst complex contacts the cytoskeletal transport system. In fact, the three proteins in common between DTNBP1 and the exocyst and dynactin complexes are CCT proteins (CCT3 and CCT8) and CAPZB, an actin-capping protein and a member of the dynactin complex (see Table 2.8). We have also verified a DISC1 interaction with dynactin. DISC1 has been shown to play an important role in microtubule dynamics through its interactions with pericentrin (PCNT) [78], and its interaction with the dynactin-dynein accessory components PAFAH1B1 and NDEL1 are thought to stabilize the motor assembly on the nuclear surface, the centrosome, and the cell cortex [45-47, 79]. Taken together, our data indicate that cytoskeletal interactions may be important for the vesicle transport functions of DTNBP1, DISC1 and exocyst.

Our data indicate DTNBP1 makes contact with several members of the exocyst complex. We also verified in mammalian cells an interaction of DISC1 with the exocyst complex. The exocyst complex is composed of 8 subunits, and through SNARE protein recruitment, is thought to integrate signals from several different signaling pathways to determine the location, timing and number of secretory vesicles docked with the plasma membrane [80]. In animal neurons, the exocyst complex is required for neurite branching and synaptogenesis, but not synaptic vesicle release at mature synapses [81, 82]. We also reproduced the interaction of DTNBP1 with the AP3 complex. AP3 is one of four adaptor protein complexes (AP1-4) that act as scaffolds, coordinating membrane lipids, membrane protein sorting signals, components of the vesicle fusion machinery, and additional components of the vesicle formation apparatus [83-85]. The AP3 complex is involved in the generation of synaptic vesicles in neurons. Mutations in the AP3 complex δ subunit AP3D1 result in the *mocha* mouse, affect spontaneous and evoked release at hippocampal mossy fiber synapses [86], and show a selective increase in the content of synaptic vesicle cargoes. Our data potentially extend the involvement of DTNBP1 and DISC1 into vesicle tethering through the exocyst complex and the regulation of active vesicle transport through the dynactin complex. While our data show both DTNBP1 and DISC1 interact with components of the dynactin and exocyst complexes, it is not known if DTNBP1 and DISC1 reside simultaneously in common protein complexes. Overall, our data indicate that DTNBP1 is involved throughout the vesicle transport process in vesicle generation, transport and membrane tethering through interactions with the BLOC1, AP3, exocyst and dynactin complexes and that DISC1 is also involved in the vesicle lifecycle at the transport and membrane tethering stages.

Defects in any of the many factors that coordinately regulate neurotransmitter vesicle cycling could contribute to the etiology of schizophrenia [69]. DTNBP1 over-expression induces expression of the SNARE protein synaptosomal-associated protein 25 (SNAP25) which is involved in mediating vesicle docking and fusion at the cellular membrane, and synapsin1 (SYN1) which is involved in regulating neurotransmitter release as well as increasing glutamatergic release [19]. Defects in BLOC1 indirectly cause redistribution of cargo to the cell surface [30]. AP3 and BLOC1 are linked to the fusion machinery involved in synaptic vesicle secretion that is hypothesized to be involved in schizophrenia; brain tissue from schizophrenia patients has reduced levels of DTNBP1 in hippocampal mossy fibers [23], a phenotype that is also found in the AP3 deficient mocha brain [31]. Ablation of DTNBP1 expression in mouse and rat model systems results in the diversion of dopamine and glutamate receptors from lysosomes to the cell surface [87-89]. Our data are consistent with the possibility that disruption of a DTNBP1-exocyst interaction may contribute to the diversion of glutamate and dopamine receptor containing vesicles from lysosomes to the plasma membrane. Overall, our results show DTNBP1 and DISC1 make multiple contacts with vesicle trafficking machinery. Thus, the aberrant function of DTNBP1 or DISC1, or the proteins in their interaction networks provide multiple sites for impairment of synaptic vesicle biogenesis. Our finding that genes for the proteins in our DTNBP1 and dynactin protein interaction networks are overrepresented in schizophrenia linked cytogenetic regions implies that the interaction networks of DTNBP1 and DISC1 as a whole should be considered in the pathology of schizophrenia.

Defining the protein interaction networks for schizophrenia susceptibility genes like DTNBP1 will help understand their function, but may also illuminate pathways where individual components may make small contributions to disease etiology, but a large contribution when taken together. An example of this is the epistatic genetic effect in schizophrenia of the non-DTNBP1 BLOC1 subunits BLOC1S3 and MUTED [90]. While members of the dynactin and exocyst complexes have not been considered potential candidate schizophrenia genes in the past, their functions and their interaction with two of the best schizophrenia susceptibility genes strongly supports future genetic investigation of these and other members of the DTNBP1, exocyst, dynactin, and DISC1 interaction networks.

2.5 Chapter 2 Tables

Table 2.1 - Protein Interactions Identified Through IP-MS

This table is a summary of the DTNBP1, exocyst, and dynactin protein interaction partners. These candidate interacting proteins were identified from the immunoprecipitation comparative mass spectrometry data using a number of filtering and quality criteria (see Methods and Tables 2.2, 2.3, and 2.4). Results are grouped by complex or interest. Proteins shown in bold were used in validation experiments.

DTNBP1 Interac	tors	Exocyst Intera	ictors	Dynactin Interactors		
HEK293 cells		X57 cells		X57 cells		
83 interacting p	roteins	56 interacting	proteins	31 interacting	g proteins	
BLOC1 Complex	x					
CNO BLOC1S1 BLOC1S2 BLOC1S3	DTNBP1 MUTED PLDN SNAPIN					
Dynactin Comp	lex					
ACTR1A CAPZA1 CAPZB DNDH1L	DCTN1 DCTN2 DCTN3	CAPZB		ACTR1A CAPZB DCTN1 DCTN2	DCTN3 DCTN4 DCTN5 DCTN6	
Exocyst Comple	ex					
EXOC3 EXOC4 EXOC6B		EXOC1 EXOC2 EXOC3 EXOC4	EXOC5 EXOC6 EXOC6B EXOC7			
Chaperonin Cor	ntaining TCP1 Co	omplex (CCT)				
CCT1 CCT3 CCT4	CCT5 CCT8	CCT3 CCT8		CCT2 CCT3 CCT6A	CCT7 CCT8	
Tubulin / Actin /	Associated Prote	ins				
ACTA1 ACTA2 ACTG1 CFL1 KIF2A MAPT MYO1D	MYO6 MYH10 SPTBN1 TUBA1B TUBA1C TUBB2B TUBB4	ACTBL2 MTAP1A TTN TUBA1A	TUBB2C TUBB3 TUBB6	ACTR10 ACTR1B KLHL2 PDCL3	TUBA1A TUBB2B TUBB3 TWF1	
AP3 Complex						
AP3B1 AP3B2 AP3D1	AP3M1 AP3S1 AP3S2					
Brain / Neuron A	Associated					
		ENO1 GDF7	PRPH1 PHGDH	CDH15		

DTNBP1 Int	DTNBP1 Interactors			Exocyst Interactors D			Dynactin Interactors	
Vesicular T	ransp	oort / Traffic	king A	ssociated /	Transporter			
AP2A1 COG5 COG7 KCNMA1		KCTD17 SCYL2 SLC1A5 SLC27A4	AE AF G/ HE KC	BCF2 RF3 RF4 APDH ERC1 CTD2	LRP1 RAB1B SEC61A1 SLC16A1 SLC16A3 UNC80		CLCN1 KCTD2	
Other Prote	eins		· ·				•	
AFG3L2 BCAS4 BTBD7 C11orf48 C17orf59 CDIPT CSNK1A11 CSNK1A1L CYP4F8 FASN HERC5	IFIT1 IGF2E MTDH NT5C PCBP PGAM PHGE PKM2 PRM1 PRKD PTPL	QPCT 3P3 SDCC 4 STAT1 2 TMCO 2 TMCO 2 TMEM 45 TOP1 0H UPF04 2 YTHO 8 YWHA 0C ZNF28 AD1	AG3 CA CA DE 33 DF 33 CA 33 CA 33 CA 33 CA 34 34 35 35 36 36 36 37 36 37 36 37 36 37 36 37 36 37 36 37 36 37 37 37 37 37 37 37 37 37 37 37 37 37	RID1B AD AND1 DOST HCR7 ALK1 APDHS SD17B12 DHA AGEE2 EST	PDIA3 PFKP PKM2 PPM1B PRPSAP1 PRPSAP2 RPN2 SSR1 TPI1 YWHAQ YWHAZ		CAD FEM1A GAPDHS MSH5	PFKP SSR1 TPI1

Table 2.2 - DTNBP1 Immunoprecipitation-Mass Spectrometry Data

Table 2.2A:

This table shows a summary of the number of unique protein hits resulting from the seven DTNBP1 experiments performed. The columns from left to right show the number of hits (unique protein assignments) after each successive subtraction to remove background proteins and to apply filtering and quality criteria (see Methods, NSB = non-specific background).

# total hits	# hits after vector HEK293 NSB removal	# hits after common NSB removal	# hits observed in at least 2 replicates	# hits remaining that meet minimal quality requirements
1,238	938	765	103	83

Table 2.2B:

This table shows a summary of the 83 candidate DTNBP1 protein interactors in HEK293 cells. Results are grouped by complex or interest. The 36 second tier interacting proteins are shaded in grey, leaving 47 first tier interacting proteins.

Interacting	DTNBP1	Epitope Tag	# Times	Mascot		X!Tandem		Tier
Protein ^a HGNC (Uniprot ID)	lsoform		Observed Per # Experiments	Score [⊳]	log(E) ^c	# Unique Peptides ^d	Average log(E)	
BLOC1 Con	nplex							
DTNBP1	Isoform 1	C-term 3XFLAG	2/2	3,256	-208.9	22	-106.1	1
(Q96EV8)				1,449	-129.3	10		
		N-term 3XFLAG	2/2	2,702	-140.2	15		
				3,183	-138.0	14		
	Isoform 3	N-term 3XFLAG	2/2	210	-52.2	7		
				312	-26.9	3		
		C-term 3XFLAG	1/1	647	-47.3	6		
SNAPIN	Isoform 1	N-term 3XFLAG	2/2	-	-88.6	9	-62.5	1
(O95295)				-	-86.6	10		
		C-term 3XFLAG	1/2	-	-59.9	6		
	Isoform 3	C-term 3XFLAG	1/1	-	-14.8	2		
CNO	Isoform 1	C-term 3XFLAG	2/2	156	-58.0	7	-41.1	1
(Q9NUP1)				125	-39.4	5		
		N-term 3XFLAG	2/2	110	-43.3	5		
				63	-23.7	3		
BLOC1S2	Isoform 1	N-term 3XFLAG	2/2	353	-44.6	5	-26.9	1
(Q6QNY1)				251	-38.8	5		
		C-term 3XFLAG	2/2	268	-21.4	3		
				58	-2.8	1		
MUTED	Isoform 1	C-term 3XFLAG	2/2	204	-37.5	5	-27.8	1
(Q8TDH9)				174	-25.2	4		
		N-term 3XFLAG	2/2	254	-29.9	4		
				102	-18.6	3		

Interacting	DTNBP1	Epitope Tag	# Times	Mascot		X!Tandem		Tier
Protein ^a HGNC (Uniprot ID)	lsoform		Observed Per # Experiments	Score [♭]	log(E) ^c	# Unique Peptides ^d	Average log(E)	
BLOC1S3	Isoform 1	C-term 3XFLAG	2/2	112	-36.8	5	-25.1	1
(Q6QNY0)				130	-29.0	4		
		N-term 3XFLAG	2/2	80	-20.4	3		
				120	-14.1	2		
BLOC1S1	Isoform 1	N-term 3XFLAG	2/2	190	-35.9	5	-23.5	1
(P78537)				141	-29.1	4		
		C-term 3XFLAG	2/2	51	-19.0	3		
				108	-10.0	2		
PLDN	Isoform 1	N-term 3XFLAG	2/2	77	-32.3	4	-15.4	1
(Q9UL45)				216	-24.2	3		
		C-term 3XFLAG	2/2	91	-4.1	1		
				91	-1.0	1		
AP3 Comple	ex							
AP3B1	Isoform 3	C-term 3XFLAG	1/1	460	-86.9	11	-35.1	1
(O00203)		N-term 3XFLAG	1/2	48	-2.2	1		
	Isoform 1	C-term 3XFLAG	2/2	217	-60.9	8		
				168	-47.4	6		
		N-term 3XFLAG	2/2	112	-10.3	2		
				49	-2.9	1		
AP3S1	Isoform 3	C-term 3XFLAG	1/1	144	-52.6	7	-17.9	1
(Q92572)		N-term 3XFLAG	2/2	130	-3.1	1		
				76	-3.0	1		
	Isoform 1	C-term 3XFLAG	2/2	77	-18.8	3		
				146	-12.0	2		
		N-term 3XFLAG	1/2	78	-	1		
AP3D1	Isoform 1	N-term 3XFLAG	2/2	677	-194.2	22	-99.1	1
(O14617)				544	-154.2	18		
		C-term 3XFLAG	2/2	420	-18.4	3		
				203	-57.6	7		
	Isoform 3	C-term 3XFLAG	1/1	330	-71.3	9		
AP3M1	Isoform 1	N-term 3XFLAG	2/2	-	-55.1	7	-19.3	1
(Q9Y212)				-	-1.8	1		
		C-term 3XFLAG	1/2	-	-18.9	3		
	Isoform 3	N-term 3XFLAG	1/2	-	-1.5	1		
AP3S2	Isoform 1	N-term 3XFLAG	2/2	-	-9.2	2	-3.7	2
(P59780)				65	-2.9	1		
		C-term 3XFLAG	1/2	-	-1.6	1		
	Isoform 3	C-term 3XFLAG	1/1	-	-1.1	1		
AP3B2	Isoform 3	C-term 3XFLAG	1/1	144	-24.9	3	-21.7	2
(Q13307)	Isoform 1	C-term 3XFLAG	1/2	79	-18.4	1		
Dynactin Co	omplex							
DCTN2	Isoform 1	C-term 3XFLAG	2/2	110	-21.6	3	-11.5	1
(Q13561)				191	-19.0	3		
	Isoform 3	N-term 3XFLAG	2/2	76	-2.7	1		
				136	-	9		
		C-term 3XFLAG	1/1	86	-2.7	1		

Interacting	DTNBP1	Epitope Tag	# Times	Mascot		X!Tandem		Tier
Protein ^a HGNC (Uniprot ID)	lsoform		Observed Per # Experiments	Score [₽]	log(E) ^c	# Unique Peptides ^d	Average log(E)	
DCTN1	Isoform 3	C-term 3XFLAG	1/1	217	-72.6	9	-48.6	1
(Q14203)	Isoform 1	C-term 3XFLAG	2/2	172	-51.8	7		
				182	-21.4	3		
ACTR1A	Isoform 3	N-term 3XFLAG	1/2	-	-19.6	3	-10.8	1
(P61163)	Isoform 1	C-term 3XFLAG	1/2	-	-1.9	1		
DCTN3	Isoform 1	C-term 3XFLAG	1/2	57	-9.5	2	-5.8	1
(075935)	Isoform 3	C-term 3XFLAG	1/1	67	-2.1	1		
CAPZA1	Isoform 3	C-term 3XFLAG	1/1	82	-10.9	1	-6.4	2
(F52907)	Isoform 1	N-term 3XFLAG	1/2	-	-1.9	1		
DNHD1L	Isoform 1	N-term 3XFLAG	2/2	-	-9.2	2	-5.4	2
(QOTEEO)				-	-1.6	1		
CAPZB (P47756)	Isoform 3	C-term 3XFLAG	1/2	57	-9.4	2	-5.25	2
(1 47730)	Isoform 1	C-term 3XFLAG	1/2	43	-1.1	1		
Exocyst Co	mplex							
EXOC4	Isoform 1	N-term 3XFLAG	1/2	247	-87.4	10	-41.3	1
(Q96A65)		C-term 3XFLAG	1/2	134	-26.7	4		
	Isoform 3	C-term 3XFLAG	1/1	48	-9.8	2		
EXOC3	Isoform 1	N-term 3XFLAG	2/2	80	-17.1	3	-13.3	1
(O60645)				79	-9.4	2		
EXOC6B	Isoform 3	C-term 3XFLAG	1/2	48	-10.9	2	-6.7	2
(Q9Y2D4)	Isoform 1	C-term 3XFLAG	1/2	57	-2.4	1		
Chaperonin	Containing	TCP1 Comple	ex (CCT)					
CCT1	Isoform 3	C-term 3XFLAG	1/1	-	-12.2	2	-10.4	1
(P17987)	Isoform 1	C-term 3XFLAG	1/2	-	-10.7	2		
		N-term 3XFLAG	2/2	-	-9.4	2		
				-	-9.2	2		
CCT5	Isoform 3	C-term 3XFLAG	1/1	114	-44.7	6	-16.3	1
(P48643)	Isoform 1	C-term 3XFLAG	1/2	39	-2.2	1		
		N-term 3XFLAG	1/2	70	-2.0	1		
CCT4	Isoform 3	C-term 3XFLAG	1/1	52	-11.3	2	-5.6	1
(P50991)	Isoform 1	C-term 3XFLAG	1/2	76	-4.0	1		
		N-term 3XFLAG	1/2	43	-1.4	1		
CCT8	Isoform 3	C-term 3XFLAG	1/1	242	-69.0	3	-36.1	2
(F50990)	Isoform 1	N-term 3XFLAG	1/2	-	-3.1	1		
CCT3	Isoform 3	C-term 3XFLAG	1/1	70	-21.8	3	-12.1	2
(P49308)	Isoform 1	N-term 3XFLAG	1/2	-	-2.3	1		
Tubulin / Ac	ctin Associa	ted Proteins						
TUBA1B	Isoform 1	C-term 3XFLAG	2/2	676	-120.3	13	-60.8	1
(P68363)				138	-27.7	4		
		N-term 3XFLAG	2/2	258	-80.7	9		
				319	-73.9	8		
	Isoform 3	N-term 3XFLAG	2/2	122	-	0		
				66	-	1		

Interacting	DTNBP1	Epitope Tag	# Times	Mascot		X!Tandem		Tier
Protein ^ª HGNC (Uniprot ID)	lsoform		Observed Per # Experiments	Score [®]	log(E) ^c	# Unique Peptides ^d	Average log(E)	
ACTG1	Isoform 3	C-term 3XFLAG	1/1	634	-66.2	8	-44.5	1
(P63261)		N-term 3XFLAG	1/2	106	-	1		
	Isoform 1	C-term 3XFLAG	2/2	251	-22.7	2		
				140	-	1		
		N-term 3XFLAG	1/2	210	-	4		
CFL1	Isoform 3	C-term 3XFLAG	1/1	236	-31.3	2	-15.6	1
(P23528)	Isoform 1	N-term 3XFLAG	2/2	67	-13.5	2		
				-	-2.1	1		
		C-term 3XFLAG	1/2	53	-	4		
SPTBN1	Isoform 3	C-term 3XFLAG	1/1	359	-126.6	16	-43.8	1
(Q01082)	Isoform 1	C-term 3XFLAG	1/2	115	-3.1	1		
		N-term 3XFLAG	1/2	52	-1.7	1		
MYH10	Isoform 3	C-term 3XFLAG	1/2	863	-303.3	23	-177.7	1
(P35580)	Isoform 1	N-term 3XFLAG	1/2	148	-52.0	3		
MYO6	Isoform 3	C-term 3XFLAG	1/1	-	-10.1	2	-9.0	1
(Q9UM54)	Isoform 1	N-term 3XFLAG	1/2	-	-7.9	2		
TUBB4	Isoform 3	C-term 3XFLAG	1/1	211	-72.5	1	-47.5	2
(P04350)	Isoform 1	C-term 3XFLAG	2/2	105	-22.5	1		
				508	-	2		
		N-term 3XFLAG	2/2	341	-	0		
				324	-	2		
TUBB2B	Isoform 1	C-term 3XFLAG	2/2	660	-160.5	2	-112.3	2
(Q9BVA1)				217 ^e	-	1		
		N-term 3XFLAG	1/2	408 ^e	-	0		
	Isoform 3	C-term 3XFLAG	1/1	226	-64.1	1		
TUBA1C	Isoform 1	N-term 3XFLAG	1/2	263	-79.0	1	-58.9	2
(Q9BQE3)		C-term 3XFLAG	1/2	608	-	0		
	Isoform 3	C-term 3XFLAG	1/1	225	-38.8	5		
ACTA1	Isoform 3	C-term 3XFLAG	1/1	439	-47.7	1	-24.8	2
(P68133)		N-term 3XFLAG	1/2	-	-1.9	1		
ACTA2	Isoform 1	N-term 3XFLAG	1/2	-	-41.2	1	-35.3	2
(P62736)		C-term 3XFLAG	1/2	-	-29.4	4		
MYO1D	Isoform 3	C-term 3XFLAG	1/1	102	-11.6	2	-6.5	2
(094832)	Isoform 1	N-term 3XFLAG	1/2	-	-1.4	1		
MAPT	Isoform 1	C-term 3XFLAG	2/2	-	-9.4	2	-5.8	2
(P10636)				-	-2.1	1		
KIF2A	Isoform 1	N-term 3XFLAG	2/2	45	-3.6	1	-2.4	2
(O00139)				51	-1.3	1		

Interacting	teracting DTNBP1 Epitope		# Times	Mascot		X!Tandem		Tier
Protein ^a HGNC (Uniprot ID)	lsoform		Observed Per # Experiments	Score [₽]	log(E) ^c	# Unique Peptides ^d	Average log(E)	
Vesicular T	ransport / T	rafficking Asso	ociated / Trans	sporter Pro	oteins			
KCTD17	Isoform 1	N-term 3XFLAG	2/2	1,123	-111.6	12	-55.5	1
(Q8N5Z5)				805	-85.5	8		
		C-term 3XFLAG	2/2	589	-60.9	6		
				177	-26.3	4		
	Isoform 3	C-term 3XFLAG	1/1	390	-75.2	8		
		N-term 3XFLAG	2/2	128	-10.4	1		
01.0074.4			2/2	131	-18.5	3		
SLC27A4 (Q6P1M0)	Isoform 1	N-term 3XFLAG	2/2	66	-70.0	9	-33.73	1
(000		C torm 2VELAC	1/1	43	-19.3	3		
0.01/1.0	la afarra d	C-term 3XFLAG	1/1	-	-11.9	2	04.0	4
(Q6P3W7)	Isoform 1	C-term 3XFLAG	1/2	709	-123.3	15	-84.0	1
	Isoform 3	C-term 3XFLAG	1/1	253	-45.9	6	40.0	4
(Q12791)	Isoform 1	N-term 3XFLAG	1/2	-	-18.9	3	-13.8	1
	la afa ma 0	C-term SXFLAG	1/2	-	-0.7	2	00.7	
(O95782)	Isoform 3	C-term 3XFLAG	1/1	186	-54.5	1	-28.7	2
(00007	Isoform 1	N-term 3XFLAG	1/2	-	-2.8	1		
(P83436)	Isoform 1	N-term 3XFLAG	2/2	57 66	-10.2 -3.3	1	-6.8	2
COG5	Isoform 1	N-term 3XFLAG	2/2	67	-10.0	2	-5.8	2
(Q9UP83)				-	-1.5	1		
SLC1A5	Isoform 3	C-term 3XFLAG	1/1	84	-3.2	1	-2.3	2
(Q15758)	Isoform 1	N-term 3XFLAG	1/2	42	-1.3	1		
Other Prote	ins							
PKM2	Isoform 1	N-term 3XFLAG	2/2	124	-44.4	5	-30.6	1
(P14618)				-	-33.4	5		
		C-term 3XFLAG	2/2	66	-19.9	3		
				-	-13.2	2		
	Isoform 3	C-term 3XFLAG	1/1	184	-42.0	5		
CSNK1A1	Isoform 1	C-term 3XFLAG	2/2	158	-54.4	7	-22.1	1
(P48729)				-	-11.6	2		
		N-term 3XFLAG	2/2	90	-25.7	4		
				71	-17.2	3		
	Isoform 3	N-term 3XFLAG	1/2	57	-1.5	1		
PPM1B	Isoform 1	C-term 3XFLAG	2/2	900	-125.5	13	-81.8	1
(O75688)				649	-70.3	9		
		N-term 3XFLAG	1/2	64	-9.0	2		
	Isoform 3	C-term 3XFLAG	1/1	418	-122.2	13		
C17orf59	Isoform 1	N-term 3XFLAG	2/2	378	-112.7	12	-49.4	1
(496654)				472	-71.5	8		
		C-term 3XFLAG	2/2	46	-9.2	2		
				134	-4.2	1		

Protein* HGNC (Uniput)Isoform Pr main sectorCeam 3XFLAGObserved Per # ExperimentsScore* per # per # main sector# Unique per # per # main sector# Unique per # main sector# Unique main	Interacting	DTNBP1	Epitope Tag # Times Mascot X!Tandem			Tier			
PRKDC (P78627) Isoform 1 C-term 3XFLAG 1/2 366 -75.9 9 -49.7 1 Isoform 3 C-term 3XFLAG 2/2 307 -68.8 9 -	Protein ^ª HGNC (Uniprot ID)	lsoform		Observed Per # Experiments	Score [₽]	log(E) ^c	# Unique Peptides ^d	Average log(E)	
(P78527) N-term 3XFLAG 2/2 307 468.8 9 Isoform 3 C-term 3XFLAG 1/1 83<-13.4	PRKDC	Isoform 1	C-term 3XFLAG	1/2	358	-75.9	9	-49.7	1
$ \begin{array}{ c c c c c c c c c c c c c c c c c c c$	(P78527)		N-term 3XFLAG	2/2	307	-68.8	9		
Isofom 3 C-lem 3XFLAG 1/1 83 -13.4 2 PC8P1 (015365) Isoform 1 N-lem 3XFLAG 2/2 119 -27.7 2 -13.4 1 C15365) Isoform 3 C-lem 3XFLAG 1/2 466 -11.3 2 -12.7 1					122	-40.5	6		
PCBP1 (Q15365) Isofom 1 		Isoform 3	C-term 3XFLAG	1/1	83	-13.4	2		
$ \left \begin{array}{c c c c c c c c c c c c c c c c c c c $	PCBP1	Isoform 1	N-term 3XFLAG	2/2	119	-27.7	2	-13.4	1
Isoform 3 C-term 3XFLAG 1/2 46 -11.3 2 BCA34 (Q8TDM0) Isoform 1 C-term 3XFLAG 2/2	(Q15365)				56	-	1		
Isoform 3 C-term 3XFLAG 1/1			C-term 3XFLAG	1/2	46	-11.3	2		
BCASA (QBTDM) Isoform 1 N-term 3XFLAG 2/2		Isoform 3	C-term 3XFLAG	1/1	-	-1.3	1		
(Q3TDM0) r C-tern 3XFLAG 2/2 67 2.9 1 FASN (P49327) Isoform 1 C-tern 3XFLAG 1/1 -444.4 6 -29.5 1 KG3L2 Isoform 1 C-tern 3XFLAG 1/2 -144.5 2 AFG3L2 Isoform 3 C-tern 3XFLAG 1/2 -144.5 2 (Q9Y4W6) Isoform 1 C-tern 3XFLAG 1/2 -144.5 2 Isoform 1 C-tern 3XFLAG 1/2 -144.5 2 1 (Q9Y4W6) Isoform 1 C-tern 3XFLAG 1/2 85 - 0 1 STAT1 (P4224) Isoform 1 C-tern 3XFLAG 2/2 90 -19.4 3 -13.2 1 Isoform 3 C-tern 3XFLAG 1/1 41 -2.3 1 - - 1 - - - 1 - - 1 - - - 1 - - 1 - - - - - <td>BCAS4</td> <td>Isoform 1</td> <td>N-term 3XFLAG</td> <td>2/2</td> <td>-</td> <td>-22.5</td> <td>3</td> <td>-12.7</td> <td>1</td>	BCAS4	Isoform 1	N-term 3XFLAG	2/2	-	-22.5	3	-12.7	1
$ \begin{array}{ $	(Q8TDM0)				88	-12.8	2		
$ \begin{array}{ c c c c c c c } \hline \begin{tabular}{ c c c c c c c c c c c c c c c c c c c$			C-term 3XFLAG	2/2	57	-2.9	1		
$ \begin{array}{ c c c c c c c c c c c c c c c c c c c$					58	-	0		
$ \begin{array}{ c c c c c c c c c c c c c c c c c c c$	FASN	Isoform 3	C-term 3XFLAG	1/1	-	-44.4	6	-29.5	1
$ \begin{array}{ $	(P49327)	Isoform 1	C-term 3XFLAG	1/2	-	-14.5	2		
$ \begin{array}{ c c c c c c c c c c c c c c c c c c c$			N-term 3XFLAG	1/2	85	-	0		
(Q9Y4W6) Isoform 1 C-term 3XFLAG 2/2 104 -34.2 5 STAT1 (P4224) Isoform 1 C-term 3XFLAG 2/2 90 -19.4 3 -13.2 1 Isoform 3 C-term 3XFLAG 1/1 41 -2.3 1 -13.2 1 -14.2 -14.2	AFG3L2	Isoform 3	C-term 3XFLAG	1/1	142	-46.8	6	-28.0	1
STAT1 (P42224) Isoform 1 C-term 3XFLAG Isoform 3 C-term 3XFLAG C-term 3XFLAG 2/2 1/1 90 -19.4 198 3.1 -13.2 1 PGAM5 (096H51) Isoform 1 C-term 3XFLAG 1/1 44 -2.3 1 -13.2 1 PGAM5 (096H51) Isoform 1 N-term 3XFLAG 1/1 44 -2.3 1 -13.6 1 Q90 -11.6 -18.6 3 -13.6 1	(Q9Y4W6)	Isoform 1	C-term 3XFLAG	2/2	104	-34.2	5		
STAT1 (P42224) Isoform 1 C-term 3XFLAG 2/2 90 -19.4 3 -13.2 1 Isoform 3 C-term 3XFLAG 1/1 41 -2.3 1 -13.2 1 PGAM5 (Q96HS1) Isoform 1 N-term 3XFLAG 1/1 41 -2.3 1 -13.2 1 PGAM5 (Q96HS1) Isoform 1 N-term 3XFLAG 2/2 116 -18.6 3 -13.6 1 (Q96HS1) Isoform 1 C-term 3XFLAG 1/2 81 -10.7 2 -13.6 1 (Q9P203) Isoform 1 C-term 3XFLAG 1/2 -51.0 7 -49.2 1 YWHAE (P62258) Isoform 3 C-term 3XFLAG 1/1 178 -52.9 7 -32.50 1 YTHDC2 (Q9HS0) Isoform 1 N-term 3XFLAG 1/2 80 -12.1 2 -27.7 1 IGF2BP3 (Q90425) Isoform 1 N-term 3XFLAG 2/2 113 -28.8 2 -27.6 1 <td></td> <td></td> <td></td> <td></td> <td>-</td> <td>-3.0</td> <td>1</td> <td></td> <td></td>					-	-3.0	1		
(P42224) Isoform 3 C-term 3XFLAG 1/1 41 -2.3 1 PGAM5 (Q96HS1) Isoform 1 N-term 3XFLAG 2/2 116 18.6 3 13.6 1 PGAM5 (Q96HS1) Isoform 1 C-term 3XFLAG 1/2 81 10.7 2 13.6 1 1 BTBD7 (Q92923) Isoform 1 C-term 3XFLAG 1/2 81 0.7 2 49.2 1 VWHAE (P62258) Isoform 1 C-term 3XFLAG 1/2 47.4 7 49.2 1 YWHAE (P62589) Isoform 1 N-term 3XFLAG 1/1 178 -52.9 7 -32.50 1 YTHDC2 (Q9H6S0) Isoform 1 N-term 3XFLAG 1/2 80 -12.1 2 1 IGF2BP3 (Q90425) Isoform 1 N-term 3XFLAG 2/2 113 -28.8 2 -27.6 1 QPCTL (Q91XS2) Isoform 1 N-term 3XFLAG 2/2 -44.0 4 -20.3 1	STAT1	Isoform 1	C-term 3XFLAG	2/2	90	-19.4	3	-13.2	1
Isoform 3 C-term 3XFLAG 1/1 41 -2.3 1 PGAM5 (Q96HS1) Isoform 1 N-term 3XFLAG 2/2 116 -18.6 3 -13.6 1 BTBD7 (Q9P203) Isoform 1 C-term 3XFLAG 1/2 81 -10.7 2 1 BTBD7 (Q9P203) Isoform 1 C-term 3XFLAG 1/2 - -551.0 7 -49.2 1 YWHAE Isoform 3 N-term 3XFLAG 1/2 - -47.4 7 - -32.50 1 YWHAE Isoform 1 N-term 3XFLAG 1/1 178 -52.9 7 -32.50 1 YTHDC2 (Q9H6S0) Isoform 1 N-term 3XFLAG 2/2 166 -36.4 5 -27.7 1 IGF2BP3 (000425) Isoform 1 N-term 3XFLAG 2/2 113 -28.8 2 -27.6 1 QPCTL (Q9XS2) Isoform 1 N-term 3XFLAG 2/2 113 -26.4 2 -27.6 1 QPCTL	(P42224)				198	-17.9	3		
$ \begin{array}{ c c c c c c c } \hline \mbox{PGAM5} (Q96HS1) \\ \hline \mbox{(Q96HS1)} \\ \hline \mbox{(Q96HS1)} \\ \hline \mbox{(Q97203)} \\ \hline \mbox{Isoform 1} \\ \hline \mbox{Isoform 3} \\ \hline \mbox{Isoform 1} \\ \hline \mbox{Isoform 3} \\ \hline \mbox{Isoform 3} \\ \hline \mbox{Isoform 1} \\ \hline \mbox{Isoform 3} \\ \hline \mbox{Isoform 1} \\ \hline \mbo$		Isoform 3	C-term 3XFLAG	1/1	41	-2.3	1		
(Q96HS1) Image: Figure Fi	PGAM5	Isoform 1	N-term 3XFLAG	2/2	116	-18.6	3	-13.6	1
$ \begin{array}{ c c c c c c c c c c c c c c c c c c c$	(Q96HS1)				105	-11.5	2		
$ \begin{array}{ c c c c c c c } \hline \mbox{BTBD7} \\ (Q9P203) \hline \mbox{Isoform 1} & C-term 3XFLAG & 1/2 & - & -51.0 & 7 & -49.2 & 1 \\ \hline \mbox{Isoform 3} & N-term 3XFLAG & 1/2 & - & -47.4 & 7 & -49.2 & 1 \\ \hline \mbox{Isoform 3} & C-term 3XFLAG & 1/2 & - & -47.4 & 7 & -49.2 & 1 \\ \hline \mbox{Isoform 1} & N-term 3XFLAG & 1/1 & 178 & -52.9 & 7 & -32.50 & 1 \\ \hline \mbox{Isoform 1} & N-term 3XFLAG & 1/2 & 80 & -12.1 & 2 & -27.7 & 1 \\ \hline \mbox{Isoform 1} & N-term 3XFLAG & 1/2 & 80 & -12.1 & 2 & -27.7 & 1 \\ \hline \mbox{IGF2BP3} & Isoform 1 & N-term 3XFLAG & 2/2 & 113 & -28.8 & 2 & -27.6 & 1 \\ \hline \mbox{IGF2BP3} & Isoform 1 & N-term 3XFLAG & 2/2 & 113 & -28.8 & 2 & -27.6 & 1 \\ \hline \mbox{IGF2BP3} & Isoform 1 & N-term 3XFLAG & 2/2 & - & -24.0 & 4 & -20.3 & 1 \\ \hline \mbox{IGF2BP3} & Isoform 1 & C-term 3XFLAG & 2/2 & - & -24.0 & 4 & -20.3 & 1 \\ \hline \mbox{IGP2V2X9} & - & Isoform 1 & N-term 3XFLAG & 2/2 & - & -24.0 & 4 & -20.3 & 1 \\ \hline \mbox{IGP2CL} & Isoform 1 & N-term 3XFLAG & 1/2 & - & -3.7 & 1 & -2.4 & 2 \\ \hline \mbox{IGPCAG3} & Isoform 1 & N-term 3XFLAG & 1/2 & - & -3.7 & 1 & -2.4 & 1 & -2.4 & 1 \\ \hline \mbox{IGPCAG3} & Isoform 1 & C-term 3XFLAG & 1/2 & - & -2.4 & 1 & -2.4 & 1 \\ \hline \mbox{IGPCAG3} & Isoform 1 & C-term 3XFLAG & 1/2 & - & -2.4 & 1 & -2.4 & 1 \\ \hline \mbox{IGPCAG3} & Isoform 1 & C-term 3XFLAG & 1/2 & - & -2.4 & 1 & -2.4 & 1 \\ \hline \mbox{IGPCAG3} & Isoform 1 & C-term 3XFLAG & 1/2 & - & -2.4 & 1 & -2.4 & 1 \\ \hline \mbox{IGPCAG3} & Isoform 1 & C-term 3XFLAG & 1/2 & - & -2.4 & 1 & -2.4 & -2.4 & 1 \\ \hline \mbox{IGPCAG3} & Isoform 1 & C-term 3XFLAG & 1/2 & - & -2.4 & 1 & -2.4 & -1.4 & -2.4 & -2.4 & -1.4 & -2.4$			C-term 3XFLAG	1/2	81	-10.7	2		
$ \begin{array}{ c c c c c c } \hline (Q9P203) & Isoform 3 & N-term 3XFLAG & 1/2 & - & -47.4 & 7 & & & & & & & & & & & & & & & & & $	BTBD7	Isoform 1	C-term 3XFLAG	1/2	-	-51.0	7	-49.2	1
$ \begin{array}{ c c c c c c c c c c c c c c c c c c c$	(Q9P203)	Isoform 3	N-term 3XFLAG	1/2	-	-47.4	7		
$ \begin{array}{ c c c c c c c } \hline $	YWHAE	Isoform 3	C-term 3XFLAG	1/1	178	-52.9	7	-32.50	1
YTHDC2 (Q9H6S0) Isoform 1 N-term 3XFLAG 2/2 166 -36.4 5 -27.7 1 IGF2BP3 (000425) Isoform 1 N-term 3XFLAG 2/2 113 -28.8 2 -27.6 1 ZNF281 (Q9Y2X9) Isoform 1 N-term 3XFLAG 2/2 113 -28.8 2 -27.6 1 QPCTL (Q9NXS2) Isoform 1 C-term 3XFLAG 2/2 - -24.0 4 -20.3 1 QPCTL (Q9NXS2) Isoform 1 N-term 3XFLAG 2/2 64 -11.7 2 -6.2 2 QPCTL (Q9NXS2) Isoform 1 N-term 3XFLAG 1/2 - -3.7 1 - - - - - - - - - 2 -	(P62258)	Isoform 1	N-term 3XFLAG	1/2	80	-12.1	2		
(Q9H6S0) Isoform 1 N-term 3XFLAG 2/2 113 28.8 2 27.6 1 (O00425) Isoform 1 N-term 3XFLAG 2/2 113 28.8 2 -27.6 1 (O00425) Isoform 1 C-term 3XFLAG 2/2 113 28.8 2 -27.6 1 (Q9Y2X9) Isoform 1 C-term 3XFLAG 2/2 - -24.0 4 -20.3 1 (Q9Y2X9) Isoform 1 C-term 3XFLAG 2/2 64 -11.7 2 -6.2 2 QPCTL (Q9NXS2) Isoform 1 N-term 3XFLAG 1/2 46 -3.2 1 SDCCAG3 (Q96C92) Isoform 1 C-term 3XFLAG 1/2 89 -3.5 1 -2.4 2 SDCCAG3 (Q96C92) Isoform 1 C-term 3XFLAG 2/2 - -2.4 1 -30.5 2 CSNK1A1L (Q8N752) Isoform 1 C-term 3XFLAG 1/2 - -44.2 1 -30.5 2	YTHDC2	Isoform 1	N-term 3XFLAG	2/2	166	-36.4	5	-27.7	1
$ \begin{array}{ c c c c c c c } \hline \mbox{IGF2BP3} (000425) & \mbox{Isoform 1} & \mbox{N-term 3XFLAG} & 2/2 & \mbox{113} & -28.8 & 2 & \mbox{-24.0} & 4 & 2 & \mbox{-24.0} & 4 & \mbox{-20.3} & $	(Q9H6S0)				103	-19.0	3		
$ \begin{array}{ c c c c c c c } \hline (000425) & & & & & & & & & & & & & & & & & & &$	IGF2BP3	Isoform 1	N-term 3XFLAG	2/2	113	-28.8	2	-27.6	1
$ \begin{array}{c c c c c c c } \hline ZNF281 \\ (Q9Y2X9) \\ \hline \\ (Q9Y2X9) \\ \hline \\ (Q9Y2X9) \\ \hline \\ \\ PCTL \\ (Q9NXS2) \\ \hline \\ \\ PCTL \\ (Q9NXS2) \\ \hline \\ \\ PCTL \\ (Q9NXS2) \\ \hline \\ \\ PCTH \\ \\ PCTH \\ \hline \\ \\ PCTH \\ \\ PCTH \\ \hline \\ \\ \\ PCTH \\ \hline \\ \\ PCTH \\ \\ \\ PCTH \\ \\ \\ PCTH \\ \\ \\ \\ \\ \\ PCTH \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\$	(000425)				121	-26.4	2		
(Q9Y2X9) Isoform 1 N-term 3XFLAG 2/2 64 16.5 3 QPCTL (Q9NXS2) Isoform 1 N-term 3XFLAG 2/2 64 11.7 2 -6.2 2 Main 2000	ZNF281	Isoform 1	C-term 3XFLAG	2/2	-	-24.0	4	-20.3	1
$ \begin{array}{c c c c c c c c c c c c c c c c c c c $	(Q9Y2X9)				-	-16.5	3		
$ \begin{array}{ c c c c c c c } (Q9NXS2) & & & & & & & & & & & & & & & & & & &$	QPCTL	Isoform 1	N-term 3XFLAG	2/2	64	-11.7	2	-6.2	2
C-term 3XFLAG 1/2 -3.7 1 SDCCAG3 (Q96C92) Isoform 1 C-term 3XFLAG 1/2 89 -3.5 1 -2.4 2 N-term 3XFLAG 2/2 - -2.4 1 -2.4 1 CSNK1A1L (Q8N752) Isoform 1 C-term 3XFLAG 1/2 - -44.2 1 -30.5 2 TOP1 (P11387) Isoform 1 N-term 3XFLAG 1/2 122 -27.4 4 -14.2 2	(Q9NXS2)				46	-3.2	1		
SDCCAG3 (Q96C92) Isoform 1 C-term 3XFLAG 1/2 89 -3.5 1 -2.4 2 N-term 3XFLAG 2/2 - -2.4 1 - - - - - - 2 - - 2.4 1 2 - - - - 2 - - - 2 - - - 1 - - - 1 - - - 2 - - - 2 - - - 1 - - - 1 - - - - 2 - - - 1 - - - - 3 - - 3 - - 3 - - 3 - - 3 - - 3 - - 3 - - 3 - - 1 - 1 - 1 - 1 </td <td></td> <td></td> <td>C-term 3XFLAG</td> <td>1/2</td> <td>-</td> <td>-3.7</td> <td>1</td> <td></td> <td></td>			C-term 3XFLAG	1/2	-	-3.7	1		
(Q96C92) N-term 3XFLAG 2/2 2.4 1 CSNK1A1L (Q8N752) Isoform 1 C-term 3XFLAG 1/2 - -44.2 1 -30.5 2 TOP1 (P11387) Isoform 1 N-term 3XFLAG 1/1 - 16.7 3 - - - - - - - 2 -	SDCCAG3	Isoform 1	C-term 3XFLAG	1/2	89	-3.5	1	-2.4	2
Isoform 1 C-term 3XFLAG 1/2 -	(Q96C92)		N-term 3XFLAG	2/2	-	-2.4	1		
CSNK1A1L (Q8N752) Isoform 1 C-term 3XFLAG 1/2 -44.2 1 -30.5 2 Isoform 3 C-term 3XFLAG 1/1 -16.7 3 -30.5 2 TOP1 (P11387) Isoform 1 N-term 3XFLAG 1/2 122 -27.4 4 -14.2 2					-	-1.3	1		
(Q8N752) Isoform 3 C-term 3XFLAG 1/1 16.7 3 TOP1 (P11387) Isoform 1 N-term 3XFLAG 1/2 122 -27.4 4 -14.2 2	CSNK1A1L	Isoform 1	C-term 3XFLAG	1/2	-	-44.2	1	-30.5	2
TOP1 (P11387) Isoform 1 N-term 3XFLAG 1/2 122 -27.4 4 -14.2 2 Isoform 3 C-term 3XFLAG 1/1 -10 1 <t< td=""><td>(Q8N752)</td><td>Isoform 3</td><td>C-term 3XFLAG</td><td>1/1</td><td>-</td><td>-16.7</td><td>3</td><td></td><td></td></t<>	(Q8N752)	Isoform 3	C-term 3XFLAG	1/1	-	-16.7	3		
(P11387) Isoform 3 C-term 3XELAG 1/1 -10 1	TOP1	Isoform 1	N-term 3XFLAG	1/2	122	-27.4	4	-14.2	2
	(P11387)	Isoform 3	C-term 3XFLAG	1/1	-	-1.0	1		

Interacting	DTNBP1	Epitope Tag	# Times	Mascot		X!Tandem		Tier
Protein ^a HGNC (Uniprot ID)	lsoform		Observed Per # Experiments	Score [®]	log(E) ^c	# Unique Peptides ^d	Average log(E)	
TMCO1 (Q9UM00)	Isoform 1	N-term 3XFLAG	2/2	-	-24.2 -2.9	3 1	-13.6	2
PHGDH	Isoform 3	C-term 3XFLAG	1/1	105	-20.8	3	-11.2	2
(O43175)	Isoform 1	C-term 3XFLAG	1/2	-	-1.5	1		
NT5C2	Isoform 1	C-term 3XFLAG	1/2	227	-19.8	3	-11.1	2
(P49902)	Isoform 3	C-term 3XFLAG	1/1	-	-2.4	1		
TMEM33	Isoform 1	N-term 3XFLAG	1/2	116	-11.5	2	-6.4	2
(P57088)	Isoform 3	C-term 3XFLAG	1/1	-	-1.3	1		
MTDH	Isoform 1	N-term 3XFLAG	2/2	98	-11.0	2	-8.1	2
(Q86UE4)				78	-5.2	1		
HERC5	Isoform 1	N-term 3XFLAG	2/2	91	-10.9	2	-6.2	2
(Q9UII4)				41	-1.4	1		
UPF0402	Isoform 1	N-term 3XFLAG	2/2	-	-9.9	2	-5.7	2
(Q96FH0)				-	-1.5	1		
CDIPT	Isoform 3	C-term 3XFLAG	1/1	41	-9.5	2	-5.7	2
(O14735)	Isoform 1	N-term 3XFLAG	1/2	51	-1.9	1		
IFIT1	Isoform 1	N-term 3XFLAG	1/2	-	-8.7	2	-5.6	2
(P09914)		C-term 3XFLAG	1/2	-	-2.4	1		
CYP4F8	Isoform 1	C-term 3XFLAG	1/2	-	-8.0	2	-4.7	2
(P98187)		N-term 3XFLAG	1/2	-	-1.3	1		
C11orf48	Isoform 1	N-term 3XFLAG	2/2	-	-3.9	1	-3.6	2
(Q9BQE6)				-	-3.3	1		
PTPLAD1	Isoform 1	N-term 3XFLAG	1/2	106	-3.9	1	-2.5	2
(Q9P035)		C-term 3XFLAG	1/2	49	-1.1	1		

^a – Interacting proteins are those meeting score quality thresholds (see Methods).

^b – Mascot score as calculated by the Matrix Science Mascot software algorithm against the Ensembl human protein database.

 $^{\circ}$ – The log (E) value is an estimate of the probability that the protein assignment happened randomly as calculated by the X!Tandem algorithm against the Ensembl human protein database.

^d - Number of uniquely assigned peptides assigned to an individual accession that contribute to the log(E) score as calculated by the X!Tandem algorithm unless no X!Tandem score was found, in which case the number of unique peptides contributing to the Mascot score is shown in italics. Additional non-unique peptides which map to multiple proteins within the Ensembl human protein database may contribute to individual X!Tandem or Mascot scores and are not reported here.

^e – This protein identification is likely a result of Mascot assigning ion scores from non-unique peptides to multiple proteins.

Table 2.3 - Dynactin Immunoprecipitation-Mass Spectrometry Data

Table 2.3A:

This table shows a summary of the number of unique protein hits resulting from the four dynactin complex experiments performed. The columns from left to right show the number of hits (unique protein assignments) after each successive subtraction to remove background proteins and to apply filtering and quality criteria (see Methods, NSB = non-specific background).

# hits total	# hits after vector X57 NSB removal	# hits after common NSB removal	# hits observed in at least 2 replicates	# hits remaining that meet minimal quality requirements
556	538	463	37	31

Table 2.3B:

This table shows a summary of the 31 candidate ACTR1A and DCTN2 interacting proteins in X57 cells. Bait protein = the tagged immunoprecipitated protein, either ACTR1A or DCTN2. The 9 second tier interacting proteins are shaded in grey, leaving 22 first tier interacting proteins.

Interacting	Bait Protein	# Times	Mascot		X!Tandem		Tier
Protein ^ª HGNC (Uniprot ID)		Observed Per # Experiments	Score "	log(E) ^c	# Unique Peptides ^d	Average log(E)	
Dynactin Co	omplex						
DCTN1	ACTR1A N-term	2/2	3,263	-476.4	47	-384.8	1
(O08788)	3XFLAG		1,480	-316.9	36		
	DCTN2 N-term	2/2	3,162	-438.1	43		
	3XFLAG		1,815	-307.9	35		
ACTR1A	ACTR1A N-term	2/2	2,795	-226.4	22	-170.4	1
(P61164)	3XFLAG		1,684	-135.7	15		
	DCTN2 N-term	2/2	1,489	-196.0	21		
	3XFLAG		1,002	-123.3	3		
DCTN2	ACTR1A N-term	2/2	2,208	-215.6	21	-158.2	1
(Q99KJ8)	3XFLAG		578	-128.6	14		
	DCTN2 N-term	2/2	3,650	-177.4	19		
	3XFLAG		3,087	-111.3	12		
CAPZB	DCTN2 N-term	2/2	745	-134.5	16	-119.8	1
(P47757)	3XFLAG		591	-104.3	13		
	ACTR1A N-term	2/2	902	-124.7	13		
	3XFLAG		305	-115.8	14		
DCTN4	DCTN2 N-term	2/2	1,515	-161.7	18	-97.8	1
(Q8CBY8)	3XFLAG		540	-78.7	9		
	ACTR1A N-term	2/2	862	-98.3	11		
	3XFLAG		211	-52.5	7		

Interacting	Bait Protein	# Times	Mascot	X!Tandem			Tier
Protein Observed HGNC Per # (Uniprot Experimen ID)	Observed Per # Experiments	Score "	log(E) ^c	# Unique Peptides ^d	Average log(E)		
DCTN3	ACTR1A N-term	2/2	585	-81.4	9	-54.6	1
(Q9Z0Y1)	3XFLAG		275	-53.1	7		
	DCTN2 N-term	2/2	600	-45.9	6		
	JAFLAG		627	-37.9	5		
DCTN5	DCTN2 N-term	2/2	151	-21.7	3	-11.2	1
(Q9QZB9)	JAFLAG		105	-6.0	1		
	ACTR1A N-term	2/2	105	-13.9	2		
	371 240		149	-3.1	1		
	ACTR1A N-term	2/2	100	-21.5	3	-12.6	1
(090004)	JAI LAG		74	-4.1	1		
	DCTN2 N-term 3XFLAG	1/2	80	-12.2	2		
Chaperonin	Containing TCP	I Complex (CC	T)				
CCT2	ACTR1A N-term 3XFLAG	2/2	1,109	-162.5	16	-138.9	1
(P80314)			724	-115.3	12		
CCT8	ACTR1A N-term 3XFLAG	2/2	1,130	-158.8	17	-133.9	1
(P42932)			510	-109.0	14		
CCT3	ACTR1A N-term 3XFLAG	2/2	1,124	-149.0	16	-111.9	1
(P80318)			688	-74.7	9		
CCT7	ACTR1A N-term	2/2	874	-111.5	11	-102.8	1
(P80313)	3XFLAG		252	-94.1	11		
CCT6A	ACTR1A N-term	2/2	557	-72.9	9	-64.9	1
(P80317)	3XFLAG		184	-56.9	7		
Tubulin / Ac	tin Associated P	roteins					
ACTR10	DCTN2 N-term	2/2	1,255	-196.0	21	-106.4	1
(Q9QZB7)	3XFLAG		434	-84.7	11		
	ACTR1A N-term	2/2	453	-103.1	12		
	JXFLAG		177	-41.6	6		
ACTR1B	DCTN2 N-term 3XFLAG	2/2	1,530	-180.7	7	-144.9	1
(Q8R5C5)			914	-134.8	16		
	ACTR1A N-term	2/2	2,069	-174.2	4		
	3XFLAG		1,244	-89.7	2		
TWF1	ACTR1A N-term	2/2	292	-50.6	6	-27.6	1
(Q91YR1)	3XFLAG		280	-36.9	4		
	DCTN2 N-term	2/2	141	-13.1	2		
	JAFLAG		83	-9.9	2		
PDCL3	ACTR1A N-term	2/2	204	-24.8	4	-15.4	1
(Q8BVF2)	JAFLAG		233	-10.5	2		
	DCTN2 N-term 3XFLAG	1/2	80	-10.9	2		

Interacting	Bait Protein	# Times	Mascot	X!Tandem			Tier
Protein HGNC (Uniprot ID)		Observed Per # Experiments	Score "	log(E) ^c	# Unique Peptides ^d	Average log(E)	
TUBB3	ACTR1A N-term	2/2	941	-180.3	6	-154.9	1
(Q9ERD7)	3XFLAG		753	-129.4	4		
KLHL2	DCTN2 N-term	2/2	231	-43.9	5	-40.85	1
(Q0JZF3)	JAFLAG		120	-37.8	5		
TUBB2B	ACTR1A N-term	2/2	819	-165.1	2	-157.8	2
(0000012)	SAI LAG		823	-150.5	1		
TUBA1A (P68369)	ACTR1A N-term 3XFLAG	2/2	1,264 780	-138.2 -114.4	1	-126.3	2
Brain / Neur	on Associated P	roteins	<u>L</u>	<u> </u>		L	<u>.</u>
CDH15 (P33146)	DCTN2 N-term 3XFLAG	1/2	-	-8.0	2	-4.6	2
	ACTR1A N-term 3XFLAG	1/2	-	-1.1	1		
Vesicular Tr	ansport / Trafficl	king Associate	d / Transp	oort Protei	ns		
CLCN1 (P35523)	ACTR1A N-term 3XFLAG	1/2	-	-16.0	3	-12.1	1
	DCTN2 N-term 3XFLAG	1/2	-	-8.1	2		
KCTD2	ACTR1A N-term	2/2	-	-50.4	3	-26.0	2
(Q14001)	3AFLAG		-	-1.5	1		
Other Protei	ns		T	1			I
CAD (076014)	ACTR1A N-term	2/2	128	-71.8	10	-52.1	1
			113	-32.3	5		
PFKP (Q9WUA3)	ACTR1A N-term 3XFLAG	2/2	132	-48.7	7	-33.6	1
(20110110)		2/2	92	-18.4	3		
FEM1A (Q9Z2G1)	3XFLAG	2/2	41	-4.0	1	-2.7	2
		2/2	41	-2.1	1		
	3XFLAG	212	42 52	-2.7	1		
MSH5	DCTN2 N-term 3XFLAG	1/2	-	-10.0	2	-4.8	2
(,	ACTR1A N-term	2/2	-	-3.2	1		
	3XFLAG		-	-1.3	1		
GAPDHS (Q64467)	ACTR1A N-term 3XFLAG	1/2	85	-40.5	3	-31.8	2
	DCTN2 N-term 3XFLAG	1/2	73	-23.1	1		
TPI1 (P17751)	DCTN2 N-term 3XFLAG	1/2	40	-8.3	2	-5.4	2
	ACTR1A N-term 3XFLAG	1/2	91	-2.5	1		
SSR1	ACTR1A N-term	2/2	44	-4.4	1	-3.6	2
(Q9CY50)	3XFLAG		49	-2.8	1		

^a – Interacting proteins are those meeting score quality thresholds (see Methods).

^b – Mascot score as calculated by the Matrix Science Mascot software algorithm against the Ensembl mouse protein database.

 c – The log (E) value is an estimate of the probability that the protein assignment happened randomly as calculated by the X!Tandem algorithm against the Ensembl mouse protein database.

^d - Number of uniquely assigned peptides assigned to an individual accession that contribute to the log(E) score as calculated by the X!Tandem algorithm unless no X!Tandem score was found, in which case the number of unique peptides contributing to the Mascot score is shown in italics. Additional non-unique peptides which map to multiple proteins within the Ensembl mouse protein database may contribute to individual X!Tandem or Mascot scores and are not reported here.

Table 2.4 - Exocyst Immunoprecipitation-Mass Spectrometry Data

Table 2.4A:

This table shows a summary of the number of unique protein hits resulting from the four exocyst complex experiments performed. The columns from left to right show the number of hits (unique protein assignments) after each successive subtraction to remove background proteins and to apply filtering and quality criteria (see Methods, NSB = non-specific background).

# hits total	# hits after vector X57 NSB removal	# hits after common NSB removal	# hits observed in at least 2 replicates	# hits remaining that meet minimal quality requirements
631	574	479	73	56

Table 2.4B:

This table shows a summary of the 56 candidate EXOC3 and EXOC4 interacting proteins in X57 cells. Bait protein = the tagged immunoprecipitated protein, either EXOC3 or EXOC4. The 24 second tier interacting proteins are shaded in grey, leaving 32 first tier interacting proteins.

Interacting	Bait Protein	# Times Observed Per # Experiments	Mascot	X!Tandem			Tier	
Protein ^a HGNC (Uniprot ID)			Score	log(E) ^c	# Unique Peptides ^d	Average log(E)		
Exocyst Co	mplex							
EXOC4	EXOC4 N-term	2/2	2,733	-461.1	38	-275.8	1	
(O35382)	3XFLAG		2,764	-425.6	34			
	EXOC3 N-term	2/2	305	-134.9	15			
	3XFLAG		414	-81.5	9			
EXOC3	EXOC3 N-term 3XFLAG	2/2	4,158	-327.8	32	-186.8	1	
(Q6KAR6)			3,192	-295.1	28			
	EXOC4 N-term 3XFLAG	2/2	311	-78.1	9			
			193	-46.3	6			
EXOC2 (Q9D4H1)	EXOC3 N-term 3XFLAG	2/2	378	-99.4	11	-50.9	1	
			242	-68.2	9			
	EXOC4 N-term 3XFLAG	2/2	94	-18.1	3			
			42	-17.9	3			
EXOC1 (Q8R3S6)	EXOC3 N-term 3XFLAG	COC1 EXOC3 N-term	2/2	110	-50.1	7	-28.8	1
			312	-49.9	6			
	EXOC4 N-term 3XFLAG	2/2	-	-18.7	3			
			55	-1.2	1			
EXOC7	EXOC4 N-term 3XFLAG	2/2	831	-182.4	18	-162.3	1	
(035250)			469	-142.2	16			
EXOC5	EXOC4 N-term	2/2	472	-117.9	13	-115.9	1	
(Q3TPX4)	3XFLAG		372	-113.8	13			

Interacting	Bait Protein	# Times	Mascot	X!Tandem			Tier	
Protein ^ª HGNC (Uniprot ID)		Observed Per # Experiments	Score	log(E) ^c	# Unique Peptides ^d	Average log(E)		
EXOC6	EXOC4 N-term	2/2	184	-34.7	5	-33.7	1	
(QOR313)	SAFLAG		86	-32.7	5			
EXOC6B	EXOC4 N-term	2/2	65	-19.6	3	-12.2	2	
	SAFLAG		54	-8.6	1			
Dynactin Co	omplex							
CAPZB (P47757)	EXOC4 N-term 3XFLAG	1/2	154	-18.9	3	-17.2	1	
	EXOC3 N-term 3XFLAG	1/2	75	-15.4	3			
Chaperonin	Containing T	CP1 Complex	(CCT)					
CCT3	EXOC4 N-term	2/2	103	-39.8	5	-18.8	1	
(P80318)	3XFLAG		113	-11.1	2			
	EXOC3 N-term	2/2	133	-12.8	2			
	3XFLAG		137	-11.6	2			
CCT8	EXOC4 N-term	2/2	280	-37.6	5	-19.7	1	
(P42932)	3XFLAG		81	-27.1	4			
	EXOC3 N-term	2/2	170	-11.3	2			
	3XFLAG		57	-2.8	1			
Tubulin / Ad	ctin Associate	d Proteins						
TUBA1A	EXOC4 N-term	2/2	931	-147.4	16	-104.5	1	
(P68369)	3XFLAG		505	-80.3	10			
	EXOC3 N-term	2/2	708	-104.7	11			
	3XFLAG		494	-85.4	10			
TUBB2C	EXOC4 N-term	2/2	600	-128.1	1	-106.1	1	
(P68372)	3XFLAG		412	-100.7	1			
	EXOC3 N-term	2/2	388	-104.8	13			
	0/11/2/10		656	-90.7	2			
TUBB3	EXOC4 N-term	2/2	321	-111.4	11	-91.4	1	
(Q9ERD7)	3AFLAG		531	-109.1	2			
	EXOC3 N-term	2/2	363	-80.3	3			
	371 270		643	-64.8	2			
TTN (A2ASS6)	EXOC4 N-term 3XFLAG	1/2	-	-64.6	9	-48.7	1	
	EXOC3 N-term 3XFLAG	1/2	-	-61.7	9			
TUBB6	EXOC4 N-term	2/2	210	-69.0	1	-59.2	2	
(Q922F4)	3XFLAG		130 ^e	-	1			
	EXOC3 N-term	2/2	246	-49.4	1			
	JAFLAG		282 ^e	-	2			
Interacting	Bait Protein	# Times	Mascot	X!Tandem			Tier	
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Protein [®] HGNC (Uniprot ID)		Observed Per # Experiments	Score	log(E) ^c	# Unique Peptides ^d	Average log(E)		
ACTBL2	EXOC3 N-term	2/2	91	-11.6	1	-11.5	2	
(Q8BFZ3)	3XFLAG		127	-11.3	1			
	EXOC4 N-term	2/2	240 ^e	-	1			
	3XFLAG		211 ^e	-	2			
MTAP1A (Q9QYR6)	EXOC3 N-term 3XFLAG	1/2	59	-28.2	4	-18.7	2	
	EXOC4 N-term 3XFLAG	1/2	44	-9.2	1			
Brain / Neu	ron Associate	d Proteins			•	-	-	
ENO1	EXOC4 N-term	2/2	64	-19.3	3	-11.4	1	
(P17182)	3XFLAG		65	-10.0	2			
	EXOC3 N-term	2/2	71	-13.3	2			
	3XFLAG		-	-3.1	1			
PRPH1 (P15331)	EXOC3 N-term 3XFLAG	1/2	157	-36.6	5	-24.0	1	
, , , , , , , , , , , , , , , , , , ,	EXOC4 N-term	EXOC4 N-term	2/2	107	-26.4	4		
	3XFLAG		65	-	4			
GDF7 (P43029)	EXOC4 N-term 3XFLAG	1/2	-	-25.5	4	-17.1	1	
	EXOC3 N-term	2/2	-	-15.8	3			
	3XFLAG		-	-10.1	2			
PHGDH (Q61753)	EXOC4 N-term 3XFLAG	1/2	57	-3.1	1	-2.3	2	
	EXOC3 N-term 3XFLAG	1/2	45	-1.4	1			
Vesicular T	ransport / Tra	fficking Assoc	iated / Tra	ansporter P	roteins			
ARF3	EXOC3 N-term	2/2	149	-29.2	4	-17.3	1	
(P61205)	3XFLAG		58	-	2			
	EXOC4 N-term	2/2	56	-18.8	3			
	3XFLAG		58	-3.9	1			
ARF4	EXOC4 N-term	2/2	79	-18.2	2	-14.4	1	
(P61750)	3XFLAG		58	-	0			
	EXOC3 N-term	2/2	102	-10.5	2			
	3XFLAG		77	-	1			
SEC61A1	EXOC4 N-term	2/2	75	-11.0	2	-7.4	1	
(P61620)	3XFLAG		64	-3.3	1			
	EXOC3 N-term	2/2	126	-10.2	2			
	3XFLAG		85	-5.0	1			
HERC1	EXOC4 N-term	2/2	270	-90.1	11	-45.0	1	
(Q99KS8)	3XFLAG		256	-43.9	6			
	EXOC3 N-term 3XFLAG	1/2	-	-1.1	1			

Interacting	Bait Protein	# Times	Mascot	X!Tandem			Tier
Protein [®] HGNC (Uniprot ID)		Observed Per # Experiments	Score	log(E) ^c	# Unique Peptides ^d	Average log(E)	
KCTD2 (Q8CEZ0)	EXOC4 N-term 3XFLAG	2/2	345	-51.9	3	-45.5	1
	EXOC3 N-term 3XFLAG	1/2	294	-39.0	3		
UNC80 (Q8BLN6)	EXOC4 N-term 3XFLAG	1/2	-	-51.1	7	-45.3	1
	EXOC3 N-term	2/2	-	-46.6	7		
	0/11/2/10		-	-38.1	6		
SLC16A3 (P57787)	EXOC3 N-term 3XFLAG	2/2	128	-20.2	3	-14.2	1
	EXOC4 N-term 3XFLAG	1/2	45	-8.2	2		
SLC16A1	EXOC4 N-term	2/2	104	-7.9	1	-4.6	2
(P53986)	3XFLAG		73	-3.5	1		
	EXOC3 N-term	2/2	90	-4.9	1		
	3XFLAG		44	-2.2	1		
GAPDH (P16858)	EXOC3 N-term 3XFLAG	1/2	-	-24.1	1	-20.9	2
	EXOC4 N-term	2/2	614	-17.7	1		
	3XFLAG		151	-	0		
RAB1B	EXOC3 N-term	2/2	102	-9.1	1	-7.6	2
(030101)	371 270		82	-6.1	1		
	EXOC4 N-term 3XFLAG	1/2	74	-	1		
LRP1	EXOC4 N-term	2/2	-	-9.5	2	-5.3	2
(Q912X7)	SAFLAG		-	-1.1	1		
ABCF2 (Q99LE6)	EXOC4 N-term 3XFLAG	1/2	93	-5.0	1	-4.5	2
	EXOC3 N-term 3XFLAG	1/2	48	-4.0	1		
Other Prote	ins						
PPM1B	EXOC4 N-term	2/2	324	-53.2	6	-27.0	1
(P36993)	3XFLAG		100	-50.1	7		
	EXOC3 N-term	2/2	-	-3.0	1		
	3XFLAG		71	-1.5	1		
CAD (076014)	EXOC3 N-term	2/2	64	-33.8	5	-23.0	1
	3XFLAG		64	-9.0	2		
	EXOC4 N-term	2/2	140	-31.0	4		
	3XFLAG		90	-18.2	3		
DDOST	EXOC3 N-term	2/2	104	-11.9	2	-10.6	1
(054734)	3XFLAG		100	-9.8	2		
	EXOC4 N-term	2/2	79	-10.2	2		
	3XFLAG		53	-	3		

Interacting	Bait Protein	# Times	Mascot	X!Tandem			Tier
Protein [®] HGNC (Uniprot ID)		Observed Per # Experiments	Score ^b	log(E) ^c	# Unique Peptides ^d	Average log(E)	
YWHAZ	EXOC3 N-term	2/2	95	-21.8	3	-16.6	1
(P63101)	3XFLAG		52	-	2		
	EXOC4 N-term 3XFLAG	1/2	94	-11.4	2		
ARID1B (Q8NFD5)	EXOC4 N-term 3XFLAG	1/2	-	-61.4	9	-56.8	1
	EXOC3 N-term 3XFLAG	1/2	-	-52.2	8		
PDIA3 (P27773)	EXOC4 N-term 3XFLAG	1/2	173	-48.9	6	-46.6	1
	EXOC3 N-term 3XFLAG	1/2	174	-44.3	6		
PRPSAP1 (Q9D0M1)	EXOC3 N-term 3XFLAG	1/2	131	-28.3	4	-22.3	1
	EXOC4 N-term 3XFLAG	1/2	172	-16.2	3		
PKM2 (P52480)	EXOC4 N-term 3XFLAG	1/2	61	-18.8	3	-14.5	1
	EXOC3 N-term 3XFLAG	1/2	65	-10.2	2		
GAPDHS	EXOC3 N-term	2/2	129	-26.4	1	-24.0	2
(Q64467)	3XFLAG		189	-	1		
	EXOC4 N-term	2/2	92	-21.6	2		
	3XFLAG		102	-	0		
HSD17B12	EXOC3 N-term	2/2	96	-10.7	2	-6.5	2
(070503)	JAFLAG		-	-1.0	1		
	EXOC4 N-term	2/2	53	-2.8	1		
	SAFLAG		83	-2.5	1		
LDHA	EXOC4 N-term	2/2	77	-19.2	3	-8.0	2
(F00336)	JAFLAG		48	-2.7	1		
	EXOC3 N-term	2/2	49	-2.1	1		
	SAFLAG		61	-	2		
YWHAQ	EXOC3 N-term	2/2	79	-11.8	2	-11.0	2
(P68254)	3XFLAG		81	-10.2	1		
	EXOC4 N-term 3XFLAG	1/2	59	-	1		
SSR1	EXOC3 N-term	2/2	47	-11.4	2	-5.1	2
(Q9CY50)	3XFLAG		60	-1.8	1		
	EXOC4 N-term 3XFLAG	1/2	53	-2.0	1		

Interacting	Bait Protein	# Times	Mascot		X!Tandem	X!Tandem		
Protein ^ª HGNC (Uniprot ID)		Observed Per # Experiments	Score	log(E) ^c	# Unique Peptides ^d	Average log(E)		
MAGEE2	EXOC3 N-term	2/2	_	-9.3	2	-4.3	2	
(Q52KG3)	3XFLAG		_	-1.1	1	1		
	EXOC4 N-term 3XFLAG	1/2	-	-2.5	1			
PFKP	EXOC4 N-term	2/2	49	-9.1	2	-5.3	2	
(Q9WUA3)	3XFLAG		68	-	3			
	EXOC3 N-term 3XFLAG	1/2	-	-1.4	1			
GALK1	EXOC3 N-term	2/2	46	-8.5	2	-4.9	2	
(Q9R0N0)	3XFLAG		75	-2.3	1			
	EXOC4 N-term 3XFLAG	1/2	-	-3.8	1			
MEST (Q07646)	EXOC4 N-term 3XFLAG	2/2	70	-5.9	1	-3.6	2	
			98	-2.8	1			
	EXOC3 N-term 3XFLAG	1/2	43	-2.1	1			
PRPSAP2 (Q8R574)	EXOC4 N-term 3XFLAG	1/2	94	-18.9	3	-14.9	2	
	EXOC3 N-term 3XFLAG	1/2	59	-10.9	1			
CAND1	EXOC3 N-term	2/2	79	-11.4	2	-6.2	2	
(Q6ZQ38)	3XFLAG		-	-1.0	1			
TPI1 (P17751)	EXOC4 N-term 3XFLAG	1/2	79	-9.6	2	-6.9	2	
	EXOC3 N-term 3XFLAG	1/2	64	-4.2	1			
RPN2 (Q9DBG6)	EXOC3 N-term 3XFLAG	1/2	-	-9.1	2	-7.0	2	
	EXOC4 N-term 3XFLAG	1/2	46	-4.8	1			
DHCR7	EXOC4 N-term	1/2	_	-3.1	1	-3.0	2	
(088455)	3XFLAG	1/2	-	-2.8	1			

^a – Interacting proteins are those meeting score quality thresholds (see Methods).

^b – Mascot score as calculated by the Matrix Science Mascot software algorithm against the Ensembl mouse protein database.

 $^{\circ}$ – The log (E) value is an estimate of the probability that the protein assignment happened randomly as calculated by the X!Tandem algorithm against the Ensembl mouse protein database.

^d - Number of uniquely assigned peptides assigned to an individual accession that contribute to the log(E) score as calculated by the X!Tandem algorithm unless no X!Tandem score was found, in which case the number of unique peptides contributing to the Mascot score is shown in italics. Additional non-unique

peptides which map to multiple proteins within the Ensembl mouse protein database may contribute to individual X!Tandem or Mascot scores and are not reported here.

^e – This protein identification is likely a result of Mascot assigning ion scores from non-unique peptides to multiple proteins.

Table 2.5 - Results of GO Analysis for DTNBP1 Interacting Proteins

This table displays the results of the DAVID Gene Ontology analysis of DTNBP1 immunoprecipitation results (76/83 identifications found by DAVID with *Homo sapiens* background).

Gene Ontology Term	# Contributing Genes	% of Genes Annotated to this Term	Multiple Test Corrected P-Value (Beniamini)
Biological Process			(,,
cellular localization	19	25	2.6x10-5
establishment of cellular localization	19	25	3.4x10-5
vesicle-mediated transport	14	18.4	1.6x10-4
cellular component organization and biogenesis	29	38.2	6.9x10-4
protein transport	14	18.4	3.4x10-3
intracellular transport	14	18.4	3.7x10-3
cytoskeleton organization and biogenesis	12	15.8	4.7x10-3
establishment of protein localization	14	18.4	5.1x10-3
protein localization	14	18.4	7.4x10-3
macromolecule localization	14	18.4	1.3x10-2
transport	25	32.9	2.8x10-2
establishment of localization	25	32.9	4.1x10-2
localization	27	35.5	4.2x10-2
secretion	9	11.8	4.4x10-2
secretion by cell	8	10.5	4.8x10-2
Cellular Component			
cytoplasm	57	75	8.2x10-11
cytoplasmic part	40	52.6	4.5x10-7
cytoskeletal part	17	22.4	1.0x10-5
vesicle	13	17.1	2.1x10-5
intracellular part	62	81.6	2.3x10-5
cytoplasmic vesicle	13	17.1	2.4x10-5
protein complex	27	35.5	2.4x10-5
coated membrane	7	9.2	3.6x10-5
membrane coat	7	9.2	3.6x10-5
macromolecular complex	29	38.2	6.0x10-5
cytoskeleton	19	25	6.4x10-5
actin cytoskeleton	10	13.2	1.1x10-4
cytoplasmic membrane-bound vesicle	11	14.5	1.2x10-4
membrane-bound vesicle	11	14.5	1.2x10-4
intracellular	62	81.6	1.5x10-4
intracellular organelle part	33	43.4	1.6x10-4
organelle part	33	43.4	1.6x10-4
Golgi apparatus	13	17.1	7.2x10-4
microtubule cytoskeleton	10	13.2	2.3x10-3
cell cortex	5	6.6	5.8x10-3
microtubule associated complex	6	7.9	7.0x10-3
chaperonin-containing T-complex	3	3.9	1.0x10-2
coated vesicle	6	7.9	1.1x10-2
intracellular non-membrane-bound organelle	20	26.3	1.2x10-2
non-membrane-bound organelle	20	26.3	1.2x10-2
dynactin complex	3	3.9	1.2x10-2
microtubule	7	9.2	1.3x10-2

Gene Ontology Term	# Contributing Genes	% of Genes Annotated to this Term	Multiple Test Corrected P-Value (Benjamini)
pigment granule	5	6.6	1.4x10-2
melanosome	5	6.6	1.4x10-2
coated pit	4	5.3	3.9x10-2
cytosol	9	11.8	4.3x10-2
coated vesicle membrane	4	5.3	5.0x10-2
Molecular Function			
protein binding	54	71.1	2.8x10-6
binding	67	88.2	6.9x10-4
nucleotide binding	24	31.6	1.3x10-2

Table 2.6 - Results of GO Analysis for Dynactin Interacting Proteins

This table displays the results of the DAVID Gene Ontology analysis of dynactin immunoprecipitation results (31/31 identifications found by DAVID with *Mus musculus* background). Only cellular component and molecular function GO terms were found significant.

Gene Ontology Term	# Contributing Genes	% of Genes Annotated to this Term	Multiple Test Corrected P-Value (Benjamini)
Cellular Component			
dynactin complex	7	22.6	8.7x10-14
cytoskeletal part	14	45.2	1.3x10-9
protein complex	20	64.5	1.5x10-9
microtubule cytoskeleton	12	38.7	1.5x10-9
microtubule associated complex	9	29	3.9x10-9
actin cytoskeleton	10	32.3	1.2x10-8
cytoskeleton	15	48.4	1.6x10-8
macromolecular complex	20	64.5	1.6x10-8
intracellular non-membrane-bound organelle	16	51.6	1.1x10-6
non-membrane-bound organelle	16	51.6	1.1x10-6
chaperonin-containing T-complex	4	12.9	2.0x10-5
cytoplasm	24	77.4	4.2x10-5
cytosolic part	5	16.1	2.1x10-3
organelle part	15	48.4	2.3x10-3
intracellular organelle part	15	48.4	2.3x10-3
intracellular part	26	83.9	9.4x10-3
microtubule	5	16.1	2.0x10-2
intracellular	26	83.9	2.9x10-2
Molecular Function			
purine nucleotide binding	13	41.9	2.0x10-2
unfolded protein binding	5	16.1	2.5x10-2
purine ribonucleotide binding	13	41.9	2.7x10-2
ribonucleotide binding	13	41.9	2.7x10-2

Table 2.7 - Results of GO Analysis for Exocyst Interacting Proteins

This table displays the results of the DAVID Gene Ontology analysis of exocyst immunoprecipitation results (50/56 identifications found by DAVID with *Mus musculus* background). Only biological process and cellular component GO terms were found.

Gene Ontology Term	# Contributing Genes	% of Genes Annotated to this Term	Multiple Test Corrected P-Value (Benjamini)
Biological Process			
cellular localization	18	36	1.6x10-6
establishment of cellular localization	18	36	2.3x10-6
exocytosis	8	16	2.3x10-5
secretion by cell	11	22	2.3x10-5
secretion	11	22	6.2x10-5
protein transport	13	26	6.5x10-4
vesicle-mediated transport	11	22	6.6x10-4
localization	25	50	8.1x10-4
establishment of protein localization	13	26	9.5x10-4
transport	23	46	9.5x10-4
establishment of localization	23	46	1.4x10-3
protein localization	13	26	1.7x10-3
macromolecule localization	13	26	2.3x10-3
cellular component organization and biogenesis	22	44	4.6x10-3
membrane docking	4	8	6.5x10-3
vesicle docking	4	8	6.5x10-3
glycolysis	5	10	6.8x10-3
alcohol catabolic process	5	10	1.1x10-2
glucose catabolic process	5	10	1.1x10-2
hexose catabolic process	5	10	1.1x10-2
monosaccharide catabolic process	5	10	1.1x10-2
hexose metabolic process	6	12	2.0x10-2
monosaccharide metabolic process	6	12	2.0x10-2
cellular carbohydrate catabolic process	5	10	2.0x10-2
carbohydrate catabolic process	5	10	2.5x10-2
alcohol metabolic process	7	14	4.0x10-2
Cellular Component			
exocyst	5	10	5.0x10-7
cytoplasm	32	64	2.2x10-4
cell cortex part	5	10	7.7x10-4
protein complex	17	34	1.7x10-3
cell cortex	5	10	2.2x10-3
cytoplasmic part	21	42	1.5x10-2
macromolecular complex	17	34	1.6x10-2

Table 2.8- Schizophrenia Linkage and Association Studies for DTNBP1 InteractingProteins

This table provides a summary of schizophrenia linkage and association studies for the 83 DTNBP1 candidate interacting proteins. The analysis also included all additional members of the CCT, exocyst, and dynactin core complexes not observed in the comparative MS analysis. The schizophrenia linkage analysis determined that 55 out of 96 proteins reside in cytogenetic regions linked with schizophrenia. A Chi-squared analysis against the full linkage database (826 cytogenetic regions with 366 linked to schizophrenia) showed that the DTNBP1 protein interaction network is significantly overrepresented with proteins in schizophrenia linked cytogenetic regions (p-value = 0.017).

Protein	Cytogenic Location	Schizophrenia association study performed ^a (result)	Schizophrenia Linkage within the cytogenetic region ^b	Representative Linkage reference	PubMed ID
BLOC1 Cor	nplex	•	-	•	
BLOC1S1	12q13-q14	Yes (no association [90])	No		
BLOC1S2	10q24.31	Yes (no association [90])	No		
BLOC1S3	19q13.32	Yes (association found [90])	No		
CNO	4p16.1	Yes (no association [90])	Yes	Lerer et al. 2003	12808429
DTNBP1	6p22.3	Yes (association found [90])	Yes	Schwab et al. 2000	11126394
MUTED	6p25.1-	Yes (association found [90])	Yes	Straub et al. 1995	7581452
	p24.3			Straub et al. 2002	12098102
				Wang <i>et al.</i> 1995	7647789
PLDN	15q21.1	Yes (no association [90])	Yes	Faraone et al. 2006	17012687
SNAPIN	1q21.3	Yes (no association [90])	Yes	Brzustowicz et al. 2000	10784452
AP3 Compl	ex	•			
AP3B1	5q14.1	No	No		
AP3B2	15q25.2	No	No		
AP3D1	19p13.3	No	Yes	Wijsman et al. 2003	12874606
				Faraone et al. 1998	9674973
AP3M1	10q22.2	No	Yes	Faraone et al. 2006	17012687
				Fallin et al. 2003	12929083
AP3M2	8p11.21	No	Yes	Kaufmann et al. 1998	9674972
				Stefansson <i>et al.</i> 1998	12145742
AP3S1	5q23.1	No	Yes	Straub et al. 2002	12098102
AP3S2	15q26.1	No	No		
Dynactin C	omplex	•			
ACTR1A	10q24.32	No	Yes	Levinson et al. 1998	9619145
CAPZA1	1p13.2	No	Yes	Arinami et al. 2005	16380906
CAPZB	1p36.13	No	Yes	Escamilla et al. 2007	17044102
				Sklar et al. 2004	14699422
DCTN1	2p13	No	Yes	Coon et al. 1998	9857978
				Faraone et al. 1998	9674973
				Straub et al. 2002	12098102
DCTN2	12q13.2- q13.3	No	No		
DCTN3	9p13	No	No		
DCTN4	5q31-q32	No	Yes	Sklar et al. 2004	14699422
				Paunio <i>et al.</i> 2001	11751686

Protein	Cytogenic Location	Schizophrenia association study performed ^a (result)	Schizophrenia Linkage within the cytogenetic region ^b	Representative Linkage reference	PubMed ID
DCTN5	16p12.1	No	Yes	Williams et al. 2003	14628288
DCTN6	8p12-p11	No	Yes	Kaufmann et al. 1998	9674972
				Blouin et al. 1998	9731535
				Stefansson <i>et al.</i> 2002	12145742
DNHD1L ^d	11p15.4	No	No		
Exocyst Co	mplex		T	Γ	
EXOC1	4q12	No	Yes	Coon <i>et al.</i> 1994	7909992
EXOC2	6p25.3	No	Yes	Wang <i>et al.</i> 1995	7647789
				Straub et al. 2002	12098102
EXOC3	5p15.33	No	Yes	Shaw <i>et al.</i> 1998	9754621
EXOC4	7q31	No	Yes	Faraone et al. 2006	1/012687
EXOC5	14q23.1	NO	Yes		9674973
EXOCO	10q23.33	NO	Yes	Fallin et al. 2003	12929083
EVOCED	2-12.2	No	Vaa	Shaw et al. 1996	9734021
EXUCOD	13.2	INO	res	Earaono et al. 1996	900/9/0
				Straub et al. 2002	12008102
EXOC7 [°]	17a25.1	No	No		12090102
EXOC8	1042.2	No	Ves	Hamshere <i>et al.</i> 2005	16203053
LXCCC	1972.2		103	Fkelund et al. 2000	10767329
Chaperonin	Containing	TCP1 Complex (CCT)	1		10101020
CCT1	6q25.3	Yes (association found [91])	Yes	Straub et al. 2002	12098102
	- 1			Lindholm <i>et al.</i> 2001	11389481
CCT2	12q15	No	Yes	Gurling et al. 2001	11179014
CCT3	1q22	No	Yes	Brzustowicz <i>et al.</i> 2000	10784452
CCT4	2p15	No	Yes	Coon <i>et al.</i> 1998	9857978
				Faraone et al. 1998	9674973
CCT5	5p15.2	No	No		
CCT6A	7p11.2	No	No		
CCT7	2p13.2	No	Yes	Coon <i>et al.</i> 1998	9857978
				Faraone et al. 1998	9674973
				Straub et al. 2002	12098102
CCT8	21q21.3	No	Yes	Fallin <i>et al.</i> 2003	12929083
Tubulin / Ad	ctin Associat	ted Proteins			
ACTA1	1q42.13	No	Yes	Hamshere et al. 2005	16203953
ACTA2	10q23.31	No	Yes	Faraone et al. 2006	1/01268/
40704	7-00 4	A1-		Fallin et al. 2003	12929083
ACIGI	7p22.1	No	Yes	Lerer et al. 2003	12808429
	Fa10.1	No	No		
	17a21 21	No	No		
	17a11 2	No	No		
	12a13 12	No	No		
TURA1C	12g13.12	No	No		
TUBR2R	6p25 2	No	Yes	Straub et al. 2002	12098102
TUBB4	19p13.3	No	Yes	Faraone et al 1998	9674973
10007	10010.0			Wijsman <i>et al</i> 2003	12874606
Other Prote	ins		l		
AFG3L2	18p11.21	No	Yes	Escamilla et al. 2007	17044102

Protein	Cytogenic Location	Schizophrenia association study performed ^a (result)	Schizophrenia Linkage within the cytogenetic region ^b	Representative Linkage reference	PubMed ID
AP2A1	19q13.33	No	No		
BCAS4	20q13.13	No	Yes	Garver et al. 2001	11705708
BTBD7	14q32.13	No	No		
C11orf48	11q12.3	No	No		
C17orf59	17p13.1	No	No		
CDIPT	16p11.2	No	No		
COG5	7g22.3	No	Yes	Faraone <i>et al.</i> 1998	9674973
COG7	16p12.1	No	No		
CSNK1A1	5q33.1	No	Yes	Lewis <i>et al.</i> 2003	12802786
	- 1			Sklar et al. 2004	14699422
CSNK1A1 L	13q13.3	No	No		
CYP4F8	19p13.12	Νο	Yes	Faraone <i>et al</i> . 1998	9674973
FASN	17a25.3	No	No		
HFRC5	4g22 1	No	Yes	Moises et al 1995	7581457
	.4==			Faraone et al. 2006	17012687
IFIT1	10a23.31	No	Yes	Faraone et al. 2006	17012687
	10420.01		100	Fallin et al. 2003	12020083
IGE2BP3	7n15 3	No	No		12020000
	10022.3	No	Ves	Faraone et al 2006	17012687
KUNIVIA I	10422.5		165		12020092
KCTD17	22012.2	No	Voo		12929003
KCIDII	22412.5		Tes	Lewis et al. 2003	0724525
				Biouin et al. 1996	9731333
MTDU	000.4	A1-	N1-	Faraone et al. 2006	1/012687
MIDH	8q22.1	NO	NO		
MYH10	1/p13.1	NO	NO		
MYO6	6q14.1	No	No		
NT5C2	10q24.33	No	No		
PCBP1	2p14	No	Yes	Coon et al. 1998	9857978
				Faraone et al. 1998	9674973
PGAM5	12q24.33	No	No		
PHGDH	1p12	No	Yes	Arinami et al. 2005	16380906
				Lewis et al. 2003	12802786
PKM2	15q23	No	No		
PPM1B	2p21	No	No		
PRKDC	8q11.21	No	Yes	Kaufmann et al. 1998	9674972
				Moises et al. 1995	7581457
PTPLAD1	15q22.31	No	No		
QPCTL	19q13.32	No	No		
SCYL2	12q23.1	No	Yes	Faraone et al. 2006	17012687
SDCCAG3	9q34.3	No	Yes	Kaufmann et al. 1998	9674972
SLC1A5	19q13.32	No	No		
SLC27A4	9q34.11	No	Yes	Kaufmann <i>et al.</i> 1998	9674972
SPTBN1	2p16.2	No	Yes	Coon <i>et al.</i> 1998	9857978
STAT1	2q32.2	No	No		
TMCO1	1q24.1	No	Yes	Lewis et al. 2003	12802786
				Brzustowicz <i>et al.</i> 2000	10784452
				Gurling et al. 2001	11179014
TMEM33	4p13	No	Yes	Moises et al. 1995	7581457
				Coon <i>et al.</i> 1994	7909992

Protein	Cytogenic Location	Schizophrenia association study performed ^a (result)	Schizophrenia Linkage within the cytogenetic region ^b	Representative Linkage reference	PubMed ID
TOP1	20q12	No	Yes	Arinami et al. 2005	16380906
UPF0402	19p13.11	No	Yes	Faraone et al. 1998	9674973
YTHDC2	5q22.2	No	No		
YWHAE	17p13.3	Yes (associated with suicide) link to schizophrenia [92]	No		
ZNF281	1q32.1	No	No		

- ^a according to the NIH Genetic Association Database http://geneticassociationdb.nih.gov/
- ^b whether the genomic location overlaps with a region shown to have suggestive or significant linkage with schizophrenia in at least 1 study.
- ^c found adjacent to schizophrenia rare inherited copy number mutations [93].
- ^d found in copy number aberration in schizophrenic patients [94].

Table 2.9- Schizophrenia Linkage and Association Studies for Dynactin InteractingProteins

This table provides a summary of schizophrenia linkage and association studies for the 31 dynactin interacting proteins. The analysis also included all additional members of the dynactin and CCT core complexes not observed in the comparative MS analysis. The schizophrenia linkage analysis determined that 24 out of 34 proteins reside in cytogenetic regions linked with schizophrenia. A Chi-squared analysis against the full linkage database (826 cytogenetic regions with 366 linked to schizophrenia) showed that the dynactin protein interaction network is significantly overrepresented with proteins in schizophrenia linked cytogenetic regions (p-value = 0.006).

Gene	Cytogenic Location	Schizophrenia association study performed ^a (result)	Schizophrenia Linkage within the cytogenetic region ^b	Representative Linkage reference	PubMed ID		
Dynactin Complex							
ACTR1A	10q24.32	No	Yes	Levinson et al. 1998	9619145		
CAPZA1	1p13.2	No	Yes	Arinami et al. 2005	16380906		
CAPZB	1p36.13	No	Yes	Escamilla et al. 2007	17044102		
				Sklar et al. 2004	14699422		
DCTN1	2p13	No	Yes	Coon et al. 1998	9857978		
				Faraone et al. 1998	9674973		
				Straub et al. 2002	12098102		
DCTN2	12q13.2-q13.3	No	No				
DCTN3	9p13	No	No				
DCTN4	5q31-q32	No	Yes	Sklar et al. 2004	14699422		
				Paunio et al. 2001	11751686		
DCTN5	16p12.1	No	Yes	Williams et al. 2003	14628288		
DCTN6	8p12-p11	No	Yes	Kaufmann et al. 1998	9674972		
				Blouin et al. 1998	9731535		
				Stefansson et al. 2002	12145742		
Chaperoni	n Containing TCI	P1 Complex (CCT)	•	•			
CCT1	6q25.3	Yes (association found [91])	Yes	Straub et al. 2002	12098102		
				Lindholm et al. 2001	11389481		
CCT2	12q15	No	Yes	Gurling et al. 2001	11179014		
CCT3	1q22	No	Yes	Brzustowicz et al. 2000	10784452		
CCT4	2p15	No	Yes	Coon <i>et al.</i> 1998	9857978		
				Faraone et al. 1998	9674973		
CCT5	5p15.2	No	No				
CCT6A	7p11.2	No	No				
CCT7	2p13.2	No	Yes	Coon <i>et al.</i> 1998	9857978		
				Faraone et al. 1998	9674973		
				Straub et al. 2002	12098102		
CCT8	21q21.3	No	Yes	Fallin et al. 2003	12929083		
Tubulin / Actin Associated Proteins							
ACTR10	14q23.1	No	Yes	Faraone et al. 1998	9674973		
ACTR1B	2q11.2	No	Yes	Moises et al. 1995	7581457		
				Faraone et al. 1998	9674973		
KLHL2	4q32.3	No	Yes	Straub et al. 2002	12098102		
PDCL3	2q11.2	No	Yes	Moises et al. 1995	7581457		
				Faraone et al. 1998	9674973		
				Paunio et al. 2001	11751686		

Gene	Cytogenic Location	Schizophrenia association study performed ^a (result)	Schizophrenia Linkage within the cytogenetic region ^b	Representative Linkage reference	PubMed ID
TUBA1A	12q13.12	No	No		
TUBB2B	6p25.2	No	Yes	Wang et al. 1995	7647789
				Straub et al. 2002	12098102
TUBB3	16q24.3	No	No		
TWF1	12q12	No	No		
Other Prote	eins				
CAD	2p23.3	No	No		
CDH15	16q24.3	No	No		
CLCN1	7q34	No	Yes	Faraone et al. 2006	17012687
FEM1A	19p13.3	No	Yes	Wijsman et al. 2003	12874606
				Faraone et al. 1998	9674973
GAPDHS	19q13.12	No	Yes	Faraone et al. 1998	9674973
KCTD2	17q25.1	No	No		
MSH5	6p21.33	No	Yes	Fallin et al. 2003	12929083
PFKP	10p15.2	No	Yes	Faraone et al. 1998	9674973
				Straub et al. 2002	12098102
SSR1	6p24.3	No	Yes	Straub et al. 1995	7581452
				Wang et al. 1995	7647789
				Straub et al. 2002	12098102
TPI1	12p13.31	No	No		

^a - according to the NIH Genetic Association Database http://geneticassociationdb.nih.gov/

^b - whether the genomic location overlaps with a region shown to have suggestive or significant linkage with schizophrenia in at least 1 study.

Table 2.10 - Schizophrenia Linkage and Association Studies for Exocyst Interacting Proteins

This table provides a summary of schizophrenia linkage and association studies for the 56 exocyst interacting proteins. The analysis also included all additional members of the exocyst, dynactin and CCT core complexes not observed in the comparative MS analysis. The schizophrenia linkage analysis determined that 34 out of 71 proteins reside in cytogenetic regions linked with schizophrenia. A Chi-squared analysis against the full linkage database (826 cytogenetic regions with 366 linked to schizophrenia) showed that the exocyst protein interaction network does not contain a significant overrepresentation of proteins whose genes reside in schizophrenia linked cytogenetic regions (p-value = 0.619). While the exocyst complex alone has 7/8 proteins within cytogenetic regions that have been linked to schizophrenia, the remaining protein interaction set contains many proteins that reside in cytogenetic regions that have not be linked to schizophrenia.

Gene	Cytogenic Location	Schizophrenia association study performed ^a (result)	Schizophrenia Linkage within the cytogenetic region ^b	Representative Linkage reference	PubMed ID
Exocyst Com	nplex				
EXOC1	4q12	No	Yes	Coon <i>et al.</i> 1994	7909992
EXOC2	6p25.3	No	Yes	Wang <i>et al.</i> 1995	7647789
				Straub et al. 2002	12098102
EXOC3	5p15.33	No	Yes	Shaw <i>et al.</i> 1998	9754621
EXOC4	7q31	No	Yes	Faraone et al. 2006	17012687
EXOC5	14q23.1	No	Yes	Faraone et al. 1998	9674973
EXOC6	10q23.33	No	Yes	Fallin et al. 2003	12929083
				Shaw et al. 1998	9754621
EXOC6B	2p13.2	No	Yes	Coon et al. 1998	9857978
				Faraone et al. 1998	9674973
				Straub et al. 2002	12098102
EXOC7 °	17q25.1	No	No		
EXOC8	1q42.2	No	Yes	Hamshere et al. 2005	16203953
				Ekelund et al. 2000	10767329
Dynactin Cor	mplex				
ACTR1A	10q24.32	No	Yes	Levinson et al. 1998	9619145
CAPZA1	1p13.2	No	Yes	Arinami et al. 2005	16380906
CAPZB	1p36.13	No	Yes	Escamilla et al. 2007	17044102
				Sklar et al. 2004	14699422
DCTN1	2p13	No	Yes	Coon <i>et al.</i> 1998	9857978
				Faraone et al. 1998	9674973
				Straub et al. 2002	12098102
DCTN2	12q13.2-q13.3	No	No		
DCTN3	9p13	No	No		
DCTN4	5q31-q32	No	Yes	Sklar <i>et al.</i> 2004	14699422
				Paunio et al. 2001	11751686
DCTN5	16p12.1	No	Yes	Williams et al. 2003	14628288
DCTN6	8p12-p11	No	Yes	Kaufmann et al. 1998	9674972
				Blouin <i>et al.</i> 1998	9731535
				Stefansson et al. 2002	12145742

Gene	Cytogenic Location	Schizophrenia association study performed ^a (result)	Schizophrenia Linkage within the cytogenetic region ^b	Representative Linkage reference	PubMed ID	
Chaperonin Containing TCP1 Complex (CCT)						
CCT1	6g25.3	Yes (association	Yes	Straub et al. 2002	12098102	
		found [91])		Lindholm et al. 2001	11389481	
CCT2	12g15	No	Yes Gurling et al. 2001		11179014	
CCT3	1g22	No	Yes	Brzustowicz et al. 2000	10784452	
CCT4	2p15	No	Yes	Coon <i>et al.</i> 1998	9857978	
				Faraone et al. 1998	9674973	
CCT5	5p15.2	No	No			
CCT6A	7p11.2	No	No			
CCT7	2p13.2	No	Yes	Coon <i>et al.</i> 1998	9857978	
				Faraone <i>et al.</i> 1998	9674973	
				Straub et al. 2002	12098102	
CCT8	21a21.3	No	Yes	Fallin <i>et al.</i> 2003	12929083	
Tubulin / Actin A	ssociated Protein	s	<u> </u>			
ACTBL2	5a11.2	No	No			
MTAP1A	15g15 3	No	No			
TTN	2n31 2	No	No			
TUBA1A	12g13 12	No	No			
TUBB2C	9n34.3	No	Yes	Kaufmann et al. 1998	9674972	
TUBB3	16g24 3	No	No		0014012	
TUBB6	18n11 21	No	Yes	Schwab et al. 1998	9758604	
10000	10011.21	110	100	Escamilla et al. 2007	17044102	
Brain / Neuron A	ssociated Protein	e		Escarrinia et al. 2007	17044102	
	1p36 23	No	Ves	Escamilla et al. 2007	17044102	
GDF7	2n24 1	No	No		11044102	
PRPH1	12n13 12	No	No			
Vesicular Transı	ort / Trafficking A	ssociated / Transport	er Proteins			
ARE3	12n13 12	No	No			
ARF4	3n14 3	No	No			
GAPDH	12n13 31	No	No			
HERC1	15022 31	No	No			
I RP1	12013 3	No	No			
RAB1B	11013 1	No	No			
SEC61A1	3021 3	No	No			
SLC01A1	1n13 2	No	Yes	Arinami et al. 2005	16380906	
SLC16A3	17025.3	No	No		10000000	
	2034	No	No			
Other Proteins	2434					
	7036 1	No	No			
	6q25 3	No	Ves	Lindholm et al. 2001	11380/81	
ARIDID	0420.0	NO	103	Straub at al. 2007	12008102	
CAD	2023.3	No	No		12090102	
	2µ23.3	No	NO	Curling at al. 2001	11170014	
	12414.0	No	100		17044400	
16000	100.12	UNU	165		17044102	
	11-12 1	Na	Na	Skiar et al. 2004	14699422	
	17025.4	NO No				
GALKI	1/925.1	NU No	NU Maa	Ferrers et al. 4000	0074070	
GAPUHS	19013.12	NU No	Tes	Faraone et al. 1998	9674973	
	17-05-4	NO No	NO			
KCTD2	1/q25.1	NO	NO			

Gene	Cytogenic Location	Schizophrenia association study performed ^a (result)	Schizophrenia Linkage within the cytogenetic region ^b	Representative Linkage reference	PubMed ID
LDHA	11p15.1	No	No		
MAGEE2	Xq13.3	No	No		
MEST	7q32.2	No	Yes	Faraone et al. 2006	17012687
PDIA3	15q15.3	No	No		
PFKP	10p15.2	No	Yes	Faraone et al. 1998	9674973
				Straub et al. 2002	12098102
PHGDH	1p12	No	Yes	Arinami et al. 2005	16380906
				Lewis et al. 2003	12802786
PKM2	15q23	No	No		
PPM1B	2p21	No	No		
PRPSAP1	17q25.1	No	No		
PRPSAP2	17p11.2	No	No		
RPN2	20q11.23	No	Yes	Arinami et al. 2005	16380906
SSR1	6p24.3	No	Yes	Straub et al. 1995	7581452
				Wang et al. 1995	7647789
				Straub et al. 2002	12098102
TPI1	12p13.31	No	No		
YWHAQ	2p25.1	No	No		
YWHAZ	8q22.3	No	No		

^a - according to the NIH Genetic Association Database http://geneticassociationdb.nih.gov/

^b - whether the genomic location overlaps with a region shown to have suggestive or significant linkage with schizophrenia in at least 1 study.

^c - found adjacent to schizophrenia rare inherited copy number mutations [93].

Table 2.11 - Chart of PCR Primers Used for Cloning

This table provides all PCR primers used for cloning.

Gene	IMAGE ID	Primer type	Primer sequence	Length	Tm all (°C)	Tm overlap (oC)
DTNBP1v1	4139934	N5'	ATCGGGCGCGCCCTGGAGACCCTTCGCGAG	30	74.1	57.8
		N3'	ATCGTTAATTAATTAAGAGTCGCTGTCCTCACC	33	59.5	56.4
		C5'	ATCGGGCGCGCCATGCTGGAGACCCTTCGC	30	73.1	57.6
		C3'	ATCGTTAATTAAAGAGTCGCTGTCCTCACC	30	59.8	56.5
DTNBP1v3	4139934	N5'	ATCGGGCGCGCCCTTTCTGCGCACTGGGAG	30	73.2	56.4
		N3'	ATCGTTAATTAATTAAGAGTCGCTGTCCTCACC	33	59.5	56.4
		C5'	ATCGGGCGCGCCATGCTTTCTGCGCACTGG	30	72.3	56.4
		C5'	ATCGTTAATTAAAGAGTCGCTGTCCTCACC	30	59.8	56.5
EXOC4	6183004	N5'	ATCGGGCGCGCCGCGGCAGAAGCAGCTGGTGGG	33	77.3	66.1
		N3'	ATCGTTAATTAATTAAACGGTAGTTATCTTCTTG	34	54.5	47.9
		C5'	ATCGGGCGCGCCATGGCGGCAGAAGCAGCTGGTGGG	36	76.9	68.1
		C5'	ATCGTTAATTAAAACGGTAGTTATCTTCTTGTCCT	35	57.8	53.3
EXOC3	5590332	N5'	ATCGGGCGCGCCAAGGAGACAGACCGGGAG	30	72.3	56.1
		N3'	ATCGTTAATTAATTACTTGAGCAGCTTGGCCAC	33	60.5	58.0
		C5'	ATCGGGCGCGCCATGAAGGAGACAGACCGGG	31	72.0	56.4
		C5'	ATCGTTAATTAACTTGAGCAGCTTGGCCAC	30	60.9	57.0
AP3B1	3914400	N5'	ATCGGGCGCGCCTCCAGCAATAGTTTTCCTTACA	34	67.9	51.8
		N3'	ATCGTTAATTAATTACCCCTGAGACAGGAC	30	57.9	53.1
		C5'	ATCGGGCGCGCCATGTCCAGCAATAGTTTT	30	67.0	46.1
		C5'	ATCGTTAATTAACCCCTGAGACAGGACAGGCTTC	34	63.4	61.5
AP3B2	7939584	N5'	ATCGGGCGCGCCTCGGCCGCCCCGCCTACAGCGAA	36	79.6	72.8
		N3'	ATCGTTAATTAATTACTGGGTCAGAGCCTGTAT	33	58.9	55.1
		C5'	ATCGGGCGCGCCATGTCGGCCGCCCCCGCCT	31	80.0	70.5
		C5'	ATCGTTAATTAACTGGGTCAGAGCCTGTAT	30	59.1	53.5
DCTN2	3613836	N5'	ATCGGGCGCGCCGCGGACCCTAAATACGCCGAC	33	73.8	60.3
		N3'	ATCGTTAATTAATTACTTTCCCAGCTTCTT	30	55.3	48.0
		C5'	ATCGGGCGCGCCATGGCGGACCCTAAATAC	30	69.9	51.6
		C5'	ATCGTTAATTAACTTTCCCAGCTTCTTCATC	31	57.3	50.7
ACTR1A	3347881	N5'	ATCGGGCGCGCCGAGTCCTACGATGTGATCGCCA	34	72.5	58.5
		N3'	ATCGTTAATTAATTAGAAGGTTTTTCTGTG	30	52.9	44.1
		C5'	ATCGGGCGCGCCATGGAGTCCTACGATGTG	30	69.3	50.9
		C5'	ATCGTTAATTAAGAAGGTTTTTCTGTGGATGGATCGG	37	61.1	58.0

2.6 Chapter 2 Figures



Figure 2.1 - Overall Protein Interaction Network of the DTNBP1, Exocyst and Dynactin Complexes Identified through Immunoprecipitation-Mass Spectrometry

This protein interaction network shows the complete set of protein interactions (described in Tables 2.2, 2.3, and 2.4) for each of the five tagged immunoprecipitated 'bait' proteins (DTNBP1, ACTR1A, DCTN2, EXOC3, and EXOC4) identified in our immunoprecipitation comparative mass spectrometry data. Each circle denotes a protein. Proteins are clustered into complexes where applicable (grey circles represent proteins that are not clustered into a complex). Blue circles designate bait proteins, pink circles denote proteins clustered by complex. Orange lines are interactions which were validated in immunoprecipitation–western blot experiments (Figures 2.2 & 2.3). The number of proteins in the actin and tubulin associated cluster may be misleading: the mass spectrometry data strongly support

interactions with actin and tubulin proteins but it is unclear which paralogs are the predominant partners as some of the assigned peptides are common to multiple tubulin or actin proteins. The inset figure in the top left shows a high level view of the protein interaction network and extends the network to include DISC1. Asterisks denote novel interactions, dark blue circles indicate schizophrenia susceptibility genes.



Figure 2.2 - Validation of Protein Interactions between DTNBP1 and the Exocyst, Dynactin, and AP3 Complexes

Validation of protein interactions between DTNBP1 and the exocyst, dynactin, and AP3 complexes were performed in X57 and HEK293 cells through immunoprecipitation of 3XFLAG-tagged AP3B1, AP3B2, ACTR1A, DCTN2, EXOC3, and EXOC4 with an anti-FLAG antibody followed by western blot for GFP-tagged DTNBP1 using a GFP antibody. **A)** DTNBP1 – AP3 interaction validations in X57 and HEK293 cells; **B)** DTNBP1 – dynactin interaction validations in X57 and HEK293 cells; **C)** DTNBP1 – exocyst interaction validations in X57 and HEK293 cells. Arrows and boxes indicate the DTNBP1-GFP band, which is the expected size according to the positive control. The positive controls are the cell lysates without anti-FLAG immunoprecipitation and indicate the expected size of DTNBP1-GFP (68 kDa); positive control lysate amounts were not matched with experimental lanes. Additional bands are believed to be unspecific recognition of the GFP antibody or due to proteolytic cleavage and/or protein modifications.



Figure 2.3 - Validation of the DISC1 Interaction with the Dynactin and Exocyst Complexes

The DISC1 interaction with members of the dynactin and exocyst complexes were validated in HEK293 cells through immunoprecipitation of 3XFLAG-tagged ACTR1A (**A**) and of 3XFLAG-tagged EXOC3 (**B**) followed by western blot for DISC1 using a native polyclonal antibody; the major DISC1 isoform is a 75-85 kDa protein (arrow) [95].



Figure 2.4 - Ontological Classification of DTNBP1 and Exocyst Interacting Proteins

Significant biological process GO terms from the DTNBP1 and exocyst complex interacting proteins are displayed as a tree. Terms in blue boxes are those significantly overrepresented with exocyst interacting proteins while those in purple are those which are significantly overrepresented with DTNBP1 interacting proteins. Terms in red boxes are those which are significantly overrepresented with both DTNBP1 and exocyst interacting proteins. Multiple test corrected p-values are shown below the term for the DTNBP1 and exocyst complex analyses.



Figure 2.5 - Representative Gel of Immunoprecipitated DTNBP1 Protein Complexes

DTNBP1-3XFLAG (C-terminal tag) protein complexes were immunoprecipitated from transfected HEK293 cells using an anti-FLAG antibody and fractionated by one dimensional SDS-PAGE. The gel was imaged using colloidal Coomassie blue. A control anti-FLAG immunoprecipitation of cells expressing the empty vector control plasmid (V181) was also prepared and analyzed. The arrow indicates the position of the DTNBP1-3XFLAG protein (~43 kDa: 40 kDa DNTBP1 + 3 kDa 3XFLAG). The entire control and experimental lanes were excised in 16 slices for each lane. The control and experimental gel slices were analyzed by comparative MS analysis (see Methods). Results of the MS/MS analysis are shown in Figure 2.1 and detailed results are provided in Table 2.2. A total of seven DTNBP1 and six empty vector control experiments were processed in this manner.







Figure 2.6 - Peptide Ion Chromatograms for Representative DTNBP1 Interacting Proteins

Extracted ion chromatograms, MS/MS spectra and peptide fragment assignments are shown for two peptides each of six DTNBP1 interacting proteins identified through comparative MS analysis, including AP3D1, SNAPIN, EXOC3, EXOC4, DCTN1, and DCTN2. In practice, two peptide assignments are generally sufficient to unambiguously identify a protein. For most of the identified proteins more than two supporting peptides were assigned, see Tables 2.2, 2.3, and 2.4.

Left Panel: Extracted ion chromatograms (signal intensity in counts per second (cps)) for a 0.5 Da window encompassing the indicated mass/charge (m/z) value for each peptide (indicated by the arrow) are provided from the experimental gel slice (black line) and the cognate control empty vector gel slice (orange line). Individual peptides reproducibly elute at a characteristic elution time in the chromatographic gradient in repeat runs using the same column. The other peaks are ions with a similar m/z value that have different retention times and different MS/MS spectra that emanate from peptides with different primary sequences. The name of the assigned protein, the peptide ion mass m/z value, the charge state of the peptide ion, and in parentheses the Mascot score (first value) and the X!Tandem expectation score (second value) are provided in the upper right corner.

Right Panel: The MS/MS fragmentation spectrum used to identify the protein by the Mascot and X!Tandem algorithms. The assignment of the ion fragments to the indicated peptide sequence is shown in the rightmost cartoon. The "b" series ions emanate from a charged N-terminal fragment, while the "y" series ions emanate from a charged C-terminal ion. The mass differences between adjacent assigned ions are characteristic for the intervening amino acid residue.



Figure 2.7 - Representative Gel of Immunoprecipitated EXOC and DCTN Protein Complexes

N-terminal 3XFLAG tagged cDNAs for EXOC3, EXOC4, DCTN2 and ACTR1A were transfected into X57 cells. Protein complexes were immunoprecipitated using an anti-FLAG antibody and fractionated by onedimensional SDS-PAGE. The gel was imaged using colloidal Coomassie blue. A control anti-FLAG immunoprecipitation of cells expressing the empty vector control plasmid (V180) was also prepared and analyzed. The arrows indicate the position of the tagged proteins (113 kDa EXOC4; 90 kDa EXOC3; 48 kDa DCTN2; and 46 kDa ACTR1A, values include 3 kDa for the 3XFLAG tag). The entire control and experimental lanes were excised in 16 slices for each lane. The control and experimental gel slices were analyzed by comparative MS analysis (see Methods). Results of the MS/MS analysis are shown in Figure 2.1, and detailed results are provided in Tables 2.3, and 2.4. In total, two experiments were performed for each protein and compared to two empty vector control experiments.



Figure 2.8 - Venn Diagram of Overlap between Protein Interaction Datasets

The Venn diagram shows the overlap among candidate interacting proteins for the DTNBP1, dynactin, and exocyst complexes.



Figure 2.9 - Graph of Average Log(E) Scores for DTNBP1 Interacting Proteins

The graph shows the X!Tandem expectation scores (log(E), grey dots) for each observation of the candidate DTNBP1 interacting proteins in the seven DTNBP1 immunoprecipitation experiments. The squares are the average log(E) values of the observed values for each protein; red squares are tier 1 proteins, orange squares are tier 2 proteins, see Methods. The proteins are ordered left to right (protein rank) by increasing average log(E) value. Known DTNBP1 interacting proteins are indicated by a black arrow, DTNBP1 interactions validated by IP-western analysis (Figure 2.2) are indicated by the red arrows.



Figure 2.10 - Graph of Average Log(E) Scores for Dynactin Interacting Proteins

The graph shows the X!Tandem expectation scores (log(E), grey dots) for each observation of the candidate interacting proteins for the two DCTN2 and two ACTR1A immunoprecipitation experiments. The squares are the average log(E) values of the observed values for each protein; red squares are tier 1 proteins, orange squares are tier 2 proteins, see Methods. The proteins are ordered left to right (protein rank) by increasing average log(E) value. Known dynactin complex interactions are indicated by a black arrow.



Figure 2.11 - Graph of Average Log(E) Scores for Exocyst Interacting Proteins

The graph shows the X!Tandem expectation scores (log(E), grey dots) for each observation of the candidate interacting proteins in the two EXOC4 and two EXOC3 immunoprecipitation experiments. The squares are the average log(E) values of the observed values for each protein; red squares are tier 1 proteins, orange squares are tier 2 proteins, see Methods. The proteins are ordered left to right (protein rank) by increasing average log(E) value. Known exocyst complex interactions are indicated by a black arrow.

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3 Protein and DNA Interactions of the Intracellular Domain of Neuregulin-1¹

3.1 Introduction

Neuregulin-1 (NRG1), also known as heregulin (HRG), neu differentiation factor (NDF), glial growth factor (GGF), and acetylcholine receptor-inducing activity (ARIA) [1, 2], is a member of the neuregulin gene family, which consists of four epidermal growth factor receptor (EGFR)-like growth factors. NRG1 has diverse functions, and has been implicated in neural development [3], neuronal differentiation, migration and survival [4-6], synaptic maturation and plasticity [7, 8], and myelination [9]. NRG1 is a well replicated schizophrenia susceptibility gene [10-26]. While there are many candidate schizophrenia genes, findings for only a few genes have been sufficiently replicated in independent cohorts for them to be considered schizophrenia susceptibility genes. In addition to NRG1, these include, for example, DTNBP1 [27], COMT [28], and DISC1 [29]. While the specific mechanism for NRG1 involvement in schizophrenia remains unknown, there is evidence of its involvement in the disease beyond genetic association. Schizophrenia antipsychotics haloperidol, risperidone and clozapine have been shown to increase expression of NRG1 and epidermal growth factor receptors (ErbB) in rat hippocampus [30], schizophrenia NRG1 at-risk haplotypes decrease the efficacy of glutamatergic and GABAergic neurotransmission [8, 31], and altered NRG1 signaling has been implicated in abnormal oligodendrocyte development and myelination as well as reduced oligodendrocyte numbers [32].

NRG1 is a transmembrane protein with multiple isoforms. The predominant focus of research on NRG1 has been on the proteolytic release of the N-terminal extracellular domain (ECD), often referred to as HRG, which acts as a ligand for several members of the ErbB family of receptor tyrosine kinases [33]. Binding of NRG1 ECD to heterodimers or homodimers of ErbB proteins activates the intracellular tyrosine kinase domain of receptor tyrosine-protein kinase ErbB-2 (ErbB2) or ErbB4 and induces signaling cascades including the phosphoinositide 3-kinase (PI3K) / protein kinase B family (AKT), small GTPase gene family (RAS) / proto-oncogene serine/threonine protein kinase (RAF) / mitogen activated protein kinase family (JAK) / signal transducers and activator of transcription activator AP-1 (JUN), and janus kinase family (JAK) / signal transducers and activator of transcription protein family (STAT) pathways, which in turn regulate various cellular proliferative, migration, and differentiation processes [34]. ErbB4 is highly expressed at glutamatergic synapses where it interacts with disks large homolog 4 (DLG4, or PSD95) and colocalizes with N-methyl-D-aspartic acid (NMDA) [glutamate] receptors at synaptic sites [35]. NRG1 activated ErbB4 modulates expression of other receptors in the nervous system including gamma-aminobutyric acid receptor subunit beta 2 (GABRB2 or GABA_Aβ2), alpha-amino-3-hydroxyl-5-methyl-4-isoxazole-propionate (AMPA), and NMDA receptor subunits [36], and NRG/ErbB signaling has

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been implicated in regulating plasticity of glutamatergic synapses [35]. NRG1 has also been shown to play a role in regulation of the actin cytoskeleton, through which it affects cell shape, structure, and motility [37]. Recently, it has been determined that the NRG1 ICD undergoes proteolytic cleavage, which was shown to occur in coordination with cleavage of the ECD through activation with soluble ErbB2/4 ectodomain heterodimers [38]. This led to different functional mechanisms being revealed for NRG1 signaling where the ICD is translocated to the nucleus in an apparent nuclear signaling process that was shown to impact gene expression [39]. This type of signaling mechanism is well established for other transmembrane receptors (e.g. Notch) [40].

The present study examines the protein-protein and protein-DNA interactions of the NRG1 ICD. Nuclear localization of the NRG1 ICD has been observed in numerous cell types including primary human spiral ganglion neurons, HEK293 kidney cells, and endothelial cells [41]. Nuclear located NRG1 ICD in spiral ganglion neurons has already been shown to regulate the expression of several genes [39], including DLG4, a protein with important functions in signal transduction and modulating post-synaptic plasticity and adhesion [42, 43]. Bao *et al* 2004 showed that regulation of the DLG4 gene could occur through the interaction of the NRG1 ICD with IKZF4 (also called Eos), a C2H2 zinc finger transcription factor for DLG4 [39].

Here, using immunoprecipitation followed by tandem mass spectrometry (IP-MS/MS) we have identified a protein interaction network that links NRG1 to other schizophrenia susceptibility genes and also to nuclear and DNA binding proteins. Further, using chromatin-immunoprecipitation we found evidence that the NRG1 ICD interacts with genomic DNA at locations proximal to schizophrenia associated genes. Our results build on evidence that the NRG1 ICD acts as a transcriptional regulator and implicates the NRG1 ICD's participation in transcriptional feedback loops for members of its protein interaction network.

3.2 Materials and Methods

3.2.1 Cloning

The following cDNAs were purchased: NRG1 ICD-a, -c (AK097005, NITE Biological Resource Centre, Kisarazu-shi, Japan); and NRG1 ICD-b (BM819389, Genome Research Center and the Center for Functional Analysis of Human Genome, Korea Research Institute of Bioscience and Biotechnology, Daejeon, Korea); DTNBP1 isoform 1 (IMAGE clone 4139934, ATCC, Manassas, VA, USA), AKAP8L (IMAGE 3504388, ATCC); SNX27 (IMAGE 8069328, ATCC). The open reading frames of these cDNAs were amplified (PCR primers: Table 3.1) to allow for N-terminal and C-terminal fusions to an epitope tag. These were ligated into the V954 donor vector of the Creator Splice system [44]. The cDNA containing cassettes were transferred into mammalian expression acceptor vectors for fusion to both N- and C-terminal 3xFLAG tags (V180 and V181) by Cre-lox recombination. NRG1 ICD-a was also transferred to

GFP-fusion vectors (V4 and V6) and DSRed vectors (V1662 and V1663). Completed constructs were sequence verified prior to use.

3.2.2 Cell culture

HEK293 (human embryonic kidney, ATCC) and X57 (mouse striatal, obtained from Marian DiFiglia at Massachusetts General Hospital, Boston, MA, USA) cells were maintained at 37° C and 5% CO₂ atmosphere in Dulbecco's modified eagle's medium with glutamax (Invitrogen, Carlsbad, CA, USA) supplemented with 10% added fetal bovine serum (Invitrogen).

3.2.3 Immunoprecipitation

For mass spectrometry experiments, the 3XFLAG-tagged cDNA expression vectors were transfected into HEK293 cells using lipofectamine 2000 reagent (Invitrogen) with Optimem reduced serum media (Invitrogen); cells were transfected with the parent (empty) acceptor vector for negative controls. For western blot experiments, the 3XFLAG-tagged constructs were co-transfected with GFP-tagged NRG1 (N-tagged for X57 experiments, C-tagged for HEK293 experiments) into HEK293 or X57 cells as above; cells were transfected with the parent acceptor vectors for negative controls. After transfection, confluent cells (~48 hours) were harvested using 4°C phosphate buffered solution (1 mM phosphate, 155 mM NaCl, 3 mM Na₂HPO₄, pH 7.4) and the pellets were stored at -80°C. Cell pellets were resuspended in lysis/wash buffer with protease inhibitors (Tris buffered saline (20mM Tris-base, 100mM NaCl, pH 7.4), 1mM EDTA, 1% NP-40, 10 ug/ml Leupeptin, 10 ug/ml Aprotinin, 10ug/ml Pepstatin, 1mM AEBSF, 2mM Na₃VO₄, 10mM β -Glycerophosphate), forced through a 20 gauge syringe 3 times, and rocked for 30 minutes at 4°C. The cell debris removed by centrifugation (15 min at 12,000 rpm) and the supernatant filtered through a 0.45 μ m membrane. The extract was immunoprecipitated with anti-FLAG M2 agarose (Sigma-Aldrich, St. Louis, MO, USA) and proteins were released with FLAG peptide, as described previously [45].

3.2.4 Protein separation and mass spectrometry

The immunoprecipitate eluate was lyophilized and rehydrated in loading buffer (Tris-Cl/SDS (58mM Tris-Cl, 0.05% SDS, pH 6.8), 5% glycerol, 1.7% SDS, 0.1M dithiothreitol, 0.03µM bromophenol blue) and heated at 85°C for 10 min. The eluate was separated by 1-dimensional SDS-PAGE using a 4-12% gradient NuPAGE gel (Invitrogen) with NuPAGE MES running buffer (Invitrogen) for ~1.5 hr at 150V. The gel was then stained in colloidal Coomassie (20% ethanol, 1.6% phosphoric acid, 8% ammonium sulfate, 0.08% Coomassie Brilliant Blue G-250) and de-stained with distilled H₂O. The entirety of lanes containing the experimental and control samples were excised and divided into 16 pieces; each slice was finely diced and transferred to a 96-well plate. Automated in-gel dehydration, alkylation, trypsin digestion, and extraction were performed (Progest; Genomic Solutions, Ann Arbor, MI, USA). The extracts were lyophilized and resuspended in 3% acetonitrile, 1.5% formic acid. High performance liquid chromatography-electrospray-tandem mass spectroscopy (HPLC-ESI-MS/MS) was performed on an

Agilent 1100 nano-HPLC (Agilent, SantaClara, CA, USA) coupled to a 4000 QTrap mass spectrometer (Applied Biosystems/Sciex, Foster City, CA) using a nano-ESI interface. Samples were desalted using an on-line trap column (Agilent, Zorbax, 300SB-C18, 5µm, 5x0.3 mm) and chromatography coupled to electrospray was performed on a 75 µm x 150 mm reverse phase column (Jupiter 4µ Proteo 90 A, Phenomenex, Torrance, CA, USA) using Buffer A (5% HPLC grade acetonitrile (Fisher, Ottawa, Canada), 0.1% formic acid (Fluka, Sigma-Aldrich)) and Buffer B (90% acetonitrile, 0.1% formic acid) in a linear gradient of 0-20% B for 37 min, 20-39% B for 16 min, and 39-90% B for 8 min at a flow rate of 300 nl/min. ESI-MS/MS was performed with 1850 V, interface heater at 150°C at 4.7x10⁻⁵ torr with nitrogen (99.999%, Praxair, Danbury, CT, USA) for nebulizer gas (0.5 ml/min) and curtain gas (2 L/min). Data were collected using a 400-1600 m/z enhanced MS scan followed by an enhanced resolution scan to select the top five +2 and +3 ions for collisional-induced dissociation and a final enhanced product ion MS scan. The spectra were searched against the Ensembl human or mouse databases, as appropriate, using the Mascot (Matrix Science, Boston, MA, USA) and X!Tandem (http://www.thegpm.org/TANDEM/) search engines. Search parameters were 0.3 Da and 0.4 Da for precursor and product ion mass tolerance, respectively; trypsin digestion; one missed cleavage; oxidation (methionine); deamidation (asparagine, glutamine); phosphorylation (serine, threonine, and tyrosine), and carbamidomethylation of cysteine. In house SpecterWeb software was used to assemble datasets. The raw data are available through the PRIDE database (http://www.ebi.ac.uk/pride/).

3.2.5 Identification of candidate protein interacting proteins

Candidate protein interacting protein lists were defined by successive subtraction of: 1) proteins found in more than one negative empty vector control sample (out of 6 negative control immunoprecipitation experiments); 2) common non-specific binding proteins (heat shock, transcriptional and translational machinery, keratins, and protein arginine N-methyltransferase 5 (PRMT5)); 3) proteins found in only 1 experimental sample; and 4) proteins without two observations each having X!Tandem log(E) scores \leq -3 and \geq 2 unique peptides. Table 3.2 describes the results of this processing across all the NRG1 ICD experiments. The average X!Tandem log(E) score was calculated for each candidate protein across the experiments where it was observed (see Table 3.3; Figure 3.1).

3.2.6 Antibodies

Antibodies were anti-NRG1 (rabbit, sc-348, Santa Cruz Biotechnology, Santa Cruz, CA, USA), anti-DTNBP1 (goat, sc-46931, Santa Cruz Biotechnology), anti-GFP (rabbit, sc-8334, Santa Cruz Biotechnology), anti-FLAG (mouse, M2, Sigma-Aldrich), anti-UTRN (rabbit, sc-15377, Santa Cruz Biotechnology), and a fluorescent secondary antibody (IR-700, Roche (Basel, Switzerland)).

3.2.7 Validation of protein interactions through immunoprecipitationwestern analysis

The immunoprecipitate eluate was lyophilized, rehydrated in loading buffer, and separated by SDS-PAGE as above. An aliquot of the input lysate was used as a positive control for size determination. The proteins were electro-transferred to nitrocellulose for ~16 hrs at 100mA in towbin buffer (0.25M Tris-base, 2M glycine, pH 8.5, 20% methanol). The nitrocellulose was blocked using NuPAGE Odyssey blocking buffer (Invitrogen) and then probed with the appropriate antibody (1:5000 anti-FLAG, or 1:200 anti-GFP) for ~16 hrs at 4°C in blocking buffer. The filter was washed (three times, 5 min each) with TBS-Tween buffer (Tris buffered saline, 0.01%Tween-20) and then probed with the appropriate fluorescent secondary antibody for 30 min at 22°C. The nitrocellulose was then washed with TBS-Tween buffer (three times, 5 min each) and imaged with an Odyssey scanner (LI-COR Biosciences, Lincoln, NE, USA).

3.2.8 Immunofluorescence

Approximately 36 hours after transfection of GFP-tagged NRG1-a or sorting nexin-27 (SNX27) cDNAs or co-transfection of DSRed-tagged NRG1-a and GFP-tagged SNX27 cDNAs into HEK293 cells, the cells were passaged into 4 well chamber slides (Labtek). After 24 hours to allow cells to adhere to the slide, the cells were washed with room temperature phosphate buffered saline (PBS) and the media and chambers removed. Cells were mounted with antifade reagent with 4',6-diamidino-2-phenylindole (DAPI) at room temperature (SlowFade Gold; Invitrogen). Images were obtained using a 63X objective on a microscope (Axioplan2; Carl Zeiss, Inc.) and captured with a cooled mono 12-bit camera (QImaging) and Northern Eclipse image analysis software (Empix Imaging, Inc.).

3.2.9 Chromatin immunoprecipitation-sequencing (ChIP-seq) analysis

HEK293 cells were transfected with N-terminal 3XFLAG NRG1-a as described above. After 48 hours the cells were crosslinked with 1% formaldehyde for 10 min at room temperature. Cross-linking was stopped by the addition of glycine to 125 mM final concentration, and cells were washed twice in cold PBS, harvested, and stored at -80°C. ChIP-seq protocols were followed as in Robertson *et al.* (2007) with the following exceptions: The protein-G-sepharose beads were prepared by 5 washes in lysis/wash buffer and resuspended 1:1 in lysis/wash buffer [46]. The immunoprecipitation was carried out for 1 h at 4°C with 100 µg of pre-cleared chromatin and 4ug of anti-NRG1 antibody (SantaCruz Biotechnologies, SC-348). ChIP-seq libraries were constructed as described [46] using 9.85 ng of immunoprecipitated DNA. They were then sequenced and yielded ~15 million 36 base reads. The sequencing results were aligned to the NCBI reference human (hg18) genomes using Eland (Illumina). We used FindPeaks v2.0 to generate overlap profiles, or 'peaks' for immunoprecipitated DNA fragments [46, 47]. False discovery rate analysis determined that peaks with a height of at least 9 were significant, resulting in 6,623 peaks. Using the UCSC table browser (hg18, NCBI build 36.1, http://genome.ucsc.edu/) [48, 49], we then eliminated any peaks overlapping more than 50% with simple repeat regions, resulting in 5,674 peaks. Sequences for the 5,674 peaks were run using the MATCH algorithm (http://www.gene-regulation.

com/cgibin/pub/programs/match/ bin/match.cgi) [50] against the Transfac database [51] to identify known transcription factors whose binding sites were represented within the ChIP-seq peaks. To determine significance, the peak sequences were randomized and then re-analyzed by MATCH 1,000 times. Using the UCSC Table browser (hg18, NCBI build 36.1, http://genome.ucsc.edu/) [48, 49], we identified genes that overlapped peak regions as well as the closest non-overlapping gene (if any) within 50,000 base pairs up and downstream of the peak.

3.2.10 Linkage and association with schizophrenia analysis for the NRG1 ICD protein interacting proteins

The genetic association database (GAD, http://geneticassociationdb.nih.gov/) [52] and the psychiatric genetics evidence project linkage database (https://slep.unc.edu/evidence/) [53] were used to determine whether any of the protein interaction sets were overrepresented with proteins having previous linkage or association evidence of involvement with schizophrenia. A query of the GAD database using the HGNC names of the 22 NRG1 ICD interacting proteins showed none of the proteins have been investigated in schizophrenia association studies, thus GAD association data did not contribute to the schizophrenia over-representation analysis. Therefore, only the psychiatric genetics linkage database was queried with the cytogenetic location associated with each protein in order to perform the overrepresentation analysis (Table 3.4). A Chi-squared test was used to determine the significance of finding the number of schizophrenia linked cytogenetic regions observed for each protein interaction set, given the number of cytogenetic regions across the entire human genome with evidence of schizophrenia linkage.

3.2.11 Schizophrenia association within ChIP-seq proximal genes

To determine if there is an overrepresentation of schizophrenia associated ChIP-seq proximal genes, the GAD database [52] was used to identify any ChIP-seq proximal genes that had had at least one positive association with schizophrenia. Schizophrenia had 143 genes associated with disease. The Ensembl database was used to generate a list of 33,046 unique human associated gene names (Ensembl 54, NCBI36, June 2009). A random sampling of 143 genes was selected from Ensembl full human gene list and the number of these selected genes represented in the ChIP-seq proximal gene list was determined. The random re-sampling was performed 1,000 times and a maximum of 11 ChIP-seq genes were identified in any one iteration for a p-value < 0.001.

3.3 Results

3.3.1 NRG1 ICD interacting proteins

NRG1 has multiple interacting partners in common with DTNBP1, forming a protein interaction network that connects schizophrenia susceptibility genes. The NRG1 ICD has 3 isoforms: a (ICD-a), b (ICD-b), and c (ICD-c) (Figure 3.2). While they share a common 3-exon N-terminal portion, ICD-a

and ICD-b each have a different fourth exon at their C-terminus, whereas ICD-c is truncated immediately after the third exon. Epitope-tagged versions of these isoforms were immunoprecipitated from HEK293 cells and analyzed by mass spectrometry. Six independent experiments were performed, including two of N-terminal epitope tagged ICD-a, one each for N-terminal epitope tagged ICD-b and ICD-c, and one each of C-terminal epitope tagged ICD-a and ICD-b, these were compared to six negative control experiments with parent (empty) vector transfected cells. We identified 1,152 proteins in total, representing 671 non-redundant proteins (Table 3.2). After removing proteins found in the vector controls, common non-specific binding proteins, those observed in only 1 experiment, and those that did not meet minimal quality criteria, there were 22 non-redundant proteins remaining (see Methods) (Tables 3.2, 3.3, and 3.5). The filter requiring observation in 2 or more experiments was notably the most effective filter, particularly for proteins identified by only 1 peptide. However, all 3 filters were required to effectively remove background proteins, as shown when the filters were individually applied to the overall 1,152 or 671 protein datasets (Table 3.2). All 22 remaining proteins represent novel NRG1 interacting proteins and include many transcription factors, nuclear, cytoskeletal, and / or transport proteins. There were six common interacting proteins found between NRG1 and the schizophrenia susceptibility gene DTNBP1 including alpha-centractin (ACTG1), poly(rC) binding protein 1 (PCBP1), protein phosphatase 1B (PPM1B), tubulin alpha 1C chain (TUBA1C), ATP-dependent RNA helicase (YTHDC2), and utrophin (UTRN) (Table 3.5) [54].

Three putative NRG1 ICD interactions were chosen for validation; a-kinase anchor protein 8-like (AKAP8L), sorting nexin 27 (SNX27), and UTRN. These interactions were chosen based on their biological function and the fact that they spanned a wide range of confidence values. AKAP8L was selected because of its nuclear localization and the involvement of a-kinase anchor protein (AKAP) family proteins in initiating signaling pathways through protein kinase A (PKA). AKAP8L, was identified in three immunoprecipitation experiments, but with weaker scores (average log(E) = -13.8, Table 3.3, Figure 3.1). Thus, validation of the NRG1 ICD-AKAP8L interaction would increase confidence in the other candidate interacting proteins with similar or smaller average log(E) values. SNX27 is known to be involved in endocytic recycling of vesicles [55] and, therefore, potentially informative regarding the involvement of the NRG1 ICD in protein transport and vesicle trafficking. SNX27 was identified in four experiments and was one of the stronger interactions with an average log(E) in the top 10 interacting proteins (average log(E) =-64.0, Table 3.3, Figure 3.1). UTRN is a scaffolding protein for the dystrophin associated protein complex (DPC or DGC) and tethers the cytoskeleton to the cell membrane [56]. UTRN is a known interacting protein of the schizophrenia susceptibility gene DTNBP1 [57] and it was, therefore, pertinent to validate our observed interaction between two of the best established schizophrenia susceptibility genes. UTRN was the second strongest identified interacting protein with an average log(E) of -110.0 (Table 3.3, Figure 3.1).

Validations were performed in HEK293 and X57 cells. AKAP8L was epitope tagged with 3XFLAG and co-expressed with GFP tagged NRG1 ICD-a in HEK293 and X57 cells. Immunoprecipitation of AKAP8L with an anti-FLAG antibody and western blotting for the NRG1 ICD with an anti-GFP antibody confirmed

the presence of NRG1 in AKAP8L complexes (Figure 3.3). For the SNX27-NRG1 ICD interaction, we first characterized the localization of SNX27 and the NRG1 ICD. GFP-tagged SNX27 showed punctate cytoplasmic staining (Figure 3.4A), while GFP-tagged-NRG1 ICD-a showed a diffuse cytoplasmic and an intense nuclear staining pattern (Figure 3.4B), further demonstrating that the NRG1 ICD localizes to the nucleus. When GFP-tagged SNX27 and dsRed-tagged NRG1 ICD-a were co-transfected the NRG1 ICD nuclear staining diminished and a punctate cytoplasmic staining was observed that directly overlapped the characteristic pattern of SNX27 (Figure 3.4C-D). This shift in the localization of the NRG1 ICD implies that there is an interaction between the NRG1 ICD and SNX27 that alters the localization of the NRG1 ICD protein. For the NRG1-UTRN interaction, HEK293 and X57 cells were transfected with epitope tagged NRG1 ICD-a and UTRN complexes were immunoprecipitated with a UTRN polyclonal antibody. Western blot analysis of the resulting immunoprecipitate confirmed the presence of NRG1 (Figure 3.5A).

The IP-MS/MS interaction data predict that some proteins interact with specific NRG1 ICD isoforms (Table 3.3). For instance, UTRN is strongly observed only in the N-tagged ICD-a experiments, suggesting it binds to the C-terminal portion of ICD-a. Conversely, the interactions of SNX27 and AKAP8L with N- and C-tagged versions of isoforms ICD-a and ICD-c suggest these proteins interact with the common N-terminal portion of the ICD (Figure 3.2).

The remaining 19 putative NRG1 ICD interactions have not been independently validated by immunoprecipitation-western, however, the average log(E) scores for most (13) of the 19 unvalidated NRG1 ICD interacting proteins were within the range of scores for the 3 validated NRG1 ICD protein interacting proteins (Figure 3.1). This, along with finding the proteins in replicate experiments, and the observation that the proteins identified have consistent biological functions (Tables 3.3 and 3.5), indicates that most of the proteins identified are likely to be true NRG1 ICD interacting proteins.

3.3.2 NRG1 ICD protein-DNA interactions

NRG1 ICD-a immunoprecipitates genomic DNA. We performed ChIP-seq to identify genomic DNA regions associated with NRG1 ICD complexes. ChIP-seq was performed on a lysate from NRG1 ICD-a transfected HEK293 cells. The NRG1 ICD linked DNA complexes were immunoprecipitated with a native NRG1 ICD antibody and sequenced on an Illumina GAII Analyzer to yield approximately 15 million 36 base reads. The reads were aligned to the genome and analyzed using the Findpeaks program [46] to determine chromosomal regions containing a significant enrichment of sequence reads (called peaks). There were 6,623 peaks that exceeded the estimated false discovery rate (FDR) threshold (height of 9, FDR \leq 0.01; for FDR method see [47]). Peaks containing more than 50% simple repeats were removed, leaving 5,674 peaks (Table 6.1 in Appendix 1). The remaining peaks had an average width of 576 base pairs (with a range of 201-3,985 base pairs). All subsequent analyses refer to this 5,674 peak set. Examples of ChIP-seq peaks proximal to DTNBP1, DISC1, and DLG4 are provided in Figures 3.6 and 3.7.

The NRG1 ICD-a immunoprecipitates genomic regions proximal to NRG1-regulated genes. We examined if genes proximal to the NRG1 ICD-a ChIP-seq peaks were previously known to be regulated by the NRG1 ICD. Proximal genes were defined as any gene directly overlapping the peak, the first gene within 50,000 bp upstream of the peak, and the first gene within 50,000 bp downstream of the peak (Table 5.1 in Appendix 1). This definition captures most regions expected to affect transcription as proximal promoter elements, or as distal enhancers/repressors. Bao et al. 2004 found 32 genes to be significantly differentially expressed in response to NRG1 ICD nuclear localization in mouse spiral ganglion neurons, and we found ten of these 32 genes in our HEK293 ChIP-seg peak proximal gene set [39]. These ten genes include DLG4 (Figure 3.6), ERBB2, cadherin-2 (CDH2), cytoplasmic dynein light chain (DYNLL1), insulin-like growth factor-binding protein 2 (IGFBP2), insulin-like growth factor-binding protein 4 (IGFBP4), integrin alpha-L (ITGAL), nucleoside diphosphate kinase B (NME2), prothymosin A (PTMA), and non-histone chromosomal protein HMG-14 (HMGN1). To determine significance, 1,000 random resampling iterations were performed, whereby 32 genes were randomly chosen from the set of all human genes (defined as 33,046 unique associated gene names gueried from ensmart – NCBI36) and the number overlapping our ChIP-seq peak proximal gene set were determined. No more than four matches were found in any iteration (p<0.001).

3.3.3 Investigation of known TFBSs within ChIP-seq peak sequences

164 known transcription factor binding sites (TFBSs) are over-represented in the NRG1 ICD-a ChIP-seq peak sequences. The ChIP-seq peak sequences were analyzed by the MATCH algorithm [50] against the Transfac database [51] to identify known TFBSs within the sequences. There were 339 unique TFBSs found within the ChIP-seq peak sequences. Of the 5,674 peaks, 5557 peaks contained at least one of these 339 TFBSs. To determine if any TFBSs were overrepresented within our ChIP-seq peak sequences the sequence underlying each peak was randomized and the MATCH analysis repeated 1,000 times. A nominal p-value for each TFBS was approximated based on the number of times the randomized sequences produced the same or greater number of matches for the TFBS as the actual sequences. Multiple test correction was performed on the nominal p-values using the Benjamini and Hochberg method [58]. A total of 164 TFBSs were significantly over-represented (Table 3.8), including IK1, which was previously identified as a transcription motif for the NRG1 ICD / IKZF4 transcription factor complex [39]. While none of the transcription factors known to bind to these significantly overrepresented TFBSs were identified as NRG1 ICD interacting proteins, four of the NRG1 ICD interacting proteins identified from our IP-MS/MS analysis have known interactions with these transcription factors, including AKAP8L, lamin-A/C (LMNA), plakophilin-2 (PKP2), and transcription factor SOX-11 (SOX11) (Table 3.6).

3.3.4 NRG1 ICD ChIP-seq regions and schizophrenia associated genes

NRG1 ICD-a ChIP-seq peaks are proximal to schizophrenia susceptibility genes. ChIP-seq peaks were found proximal to DTNBP1 and DISC1 (Figure 3.7), both of which are well established schizophrenia susceptibility genes. To more fully explore schizophrenia genes in relation to our ChIP-seq peaks we used GAD, an archive of human genetic association studies of complex diseases and disorders (http://geneticassociationdb.nih.gov/) [52]. In GAD, as of this writing, a total of 143 unique genes from 318 schizophrenia genetic association studies showed evidence of positive genetic association. We observed 37 of these 143 genes proximal to ChIP-seq peaks by the above criteria (Table 3.7). To determine significance, 1,000 random resampling iterations were performed whereby 143 human genes were randomly chosen from a set of all human genes (defined as 33,046 unique associated gene names queried from ensmart – NCBI36) and the number overlapping our ChIP-seq peak proximal genes set was determined. The random resampling analysis did not find overlap with more than 11 of 143 genes in any iteration, resulting in a p-value of p < 0.001.

3.4 Discussion

Three major schizophrenia susceptibility genes, NRG1, DTNBP1, and DISC1 participate in a common protein interaction network. We investigated protein interactions of the schizophrenia susceptibility gene NRG1's intracellular domain to identify new proteins, pathways, or functions potentially involved in schizophrenia. The only interacting proteins identified for the NRG1 ICD prior to our analysis was LIM domain kinase 1 (LIMK) [59] and Zinc finger protein Eos (IKZF4) [39]. Our analysis identified a number of novel proteins as potential interacting proteins of the NRG1 ICD, including five proteins that provide a common link between NRG1 and DTNBP1 and one protein (UTRN) that provides a common link between NRG1, DTNBP1, and DISC1. We have previously shown that DTNBP1 also has common links to DISC1 through interactions with the exocyst and dynactin complexes [54]. Combined, these results define a protein interaction network that incorporates three of the best schizophrenia susceptibility genes identified to date (Figure 3.8, Table 3.5). Additionally, our results show that the NRG1 ICD immunoprecipitates genomic DNA upstream of or overlapping with DTNBP1 and DISC1 genes, respectively. This is of particular interest in the context of recent evidence by Bray et al. 2008, which showed a trans-acting effect on DTNBP1 expression from a region of chromosome 8p that directly overlaps the NRG1 gene [60]. This implies that these schizophrenia susceptibility genes may be participating in common (or interdependent) pathway(s), and further, that these pathways and the protein interaction network they represent may provide insight into the mechanisms contributing to schizophrenia pathology and therefore warrant further investigation.

The NRG1 ICD interacts with cytoskeletal proteins. The NRG1 ICD interacting protein with the best average log(E) score was UTRN. UTRN is a known interaction partner of both DTNBP1 [57] and DISC1 [61]. UTRN is a paralog of dystrophin (DMD) [62-64], and has also been shown to be functionally homologous to DMD [65]. UTRN and DMD are involved in anchoring the cytoskeleton to the plasma

membrane [66] and act as scaffolds upon which the DPC is assembled [67]. DTNBP1 interacts with several members of the DPC including DMD [57]. A potential link between the DPC and neuropsychiatric disorders has been established: impairment in the function and assembly of the DPC are causative for several muscular dystrophies [68] and many patients with muscular dystrophies have also been found to have cognitive impairment, learning disability, and an increased incidence of some neuropsychiatric disorders [67]. The NRG1 ICD-UTRN interaction suggests NRG1 could impact these DPC-related disorders.

The NRG1 ICD and DTNBP1 share interactions with other cytoskeletal proteins, including the tubulin and actin proteins TUBA1C and ACTG1 (Figure 3.8). DISC1 is also known to interact with cytoskeletal proteins including tubulin and actin. Tubulin is the major constituent of microtubules and impairment of microtubule associated genes (e.g. microtubule-associated protein 6 (MAP6)) have been shown to result in behavioral alterations and neurotransmission defects similar to those of schizophrenia disorders [69]. Actins also play an important role in neuronal function and therefore are potentially of interest for schizophrenia pathology. Actins are highly conserved proteins involved in various functions in neurons including cell motility, membrane integrity, short distance cargo transport, axonal morphogenesis, and axonal pathfinding to synaptic targets [70]. In fact, disheveled-associated activator of morphogenesis 2 (DAAM2), an actin assembly factor, was recently identified as a potential biomarker for schizophrenia and its expression changes were found to be correlated with psychotic episodes [71].

There is evidence that NRG1 plays a role in the regulation of the actin cytoskeleton and of cell shape and motility [37]. We also identified other NRG1 ICD interactions with cytoskeletal related proteins that are not shared with DTNBP1, including actin related filamin-a (FLNA) and desmosome associated proteins (desmoplakin (DSP), plectin-1 (PLEC1), plankophilin-2 (PKP2)) (Table 3.5, Figure 3.8). These interactions, as well as those shared with DTNBP1, provide a potential mechanism through which NRG1 may influence cell shape and motility functions and suggest a direct means for the NRG1 ICD to contribute to schizophrenia pathogenesis.

The NRG1 ICD interacts with transport proteins. Our results also demonstrate an interaction between the NRG1 ICD and SNX27, a member of the sorting nexin family. Sorting nexins comprise a family of peripheral membrane proteins, which all contain a SNX-Phox-homology domain that is involved in endocytic trafficking of proteins [55] and the regulation of cargo sorting [72]. SNX27 was recently found to interact with and regulate the surface expression of KIR3 [73, 74], a member of the KIR family of ion channels, which effect resting membrane potential. Regulation of KIR3 channel activity would be expected to change the firing properties of neurons [73]. Regulation of neuronal membrane excitability is an essential process for proper signaling in the brain. These interactions provide a potential mechanism whereby the NRG1 ICD could effect signaling in the brain, and are therefore of interest to schizophrenia pathology.

Cytoskeletal and transport proteins have both been implicated in schizophrenia pathology prior to this work [75, 76] and several other schizophrenia susceptibility genes, including DTNBP1 and DISC1, have been shown to have cytoskeletal and transport related functions [77-84]. Therefore, the NRG1 ICD interactions with cytoskeletal and transport related proteins not only contribute to our understanding of the NRG1 ICD function, but also provide functional and physical ties to other schizophrenia susceptibility genes and further implicate a potential role for cytoskeletal and transport proteins in schizophrenia setiology.

The NRG1 ICD interacts with transcription related genes. Previous work has shown that the NRG1 ICD can act as a transcriptional transactivator [38], effect significant differential expression of a subset of genes [39], and act as a transcriptional repressor in yeast [85]. We identified several novel NRG1 ICD protein interactions with known nuclear and transcription factor proteins, including ZNF503, FOXA1, and SOX11. Both AKAP8L and ZNF503 contain C2H2 zinc finger motifs, motifs that are also found in the NRG1 ICD interacting proteins previously identified [39, 86]. ZNF503 and FOXA1 affect growth and patterning during development [87, 88], including neural cell differentiation for FOXA1 [89]. SOX11 is thought to play a central role in the development of the nervous system, regulating events that promote neurite growth and neuron survival [90, 91]. SOX11 also binds the POU domain, class 3 transcription factor 2 protein (POU3F2/BRN2/OCT7) [90], for which there was an overrepresentation of binding sites found within the NRG1 ICD ChIP-seq results. POU3F2 was identified as significant in a genome wide association study of schizophrenia using brain activation as a quantitative phenotype [92].

Through ChIP-seq we showed that the NRG1 ICD immunoprecipitates numerous genomic DNA regions that contain known TFBS, including the IK1 TFBS which was previously identified as a binding site for the NRG1 ICD / IKZF4 transcription factor complex [39]. Additionally, 10 out of the 32 significantly differentially expressed genes from the Bao *et al.* 2004 experiment are proximal to peaks in our ChIP-seq data. While the transcription factors that interact with the NRG1 ICD did not have binding sites within our ChIP-seq peaks, the literature supports various interactions between other NRG1 ICD interacting proteins and transcription factors with binding sites within our ChIP-seq peaks (Table 3.6). Taken together, our data suggest the NRG1 ICD is regulating transcription by forming complexes, for example with SOX11/POU3F2 or other transcription factor proteins, to effect transcriptional changes, some of which may relate to neuron structure or function.

The protein and DNA interactions of the NRG1 ICD contribute to our understanding of NRG1 functionality. While we have focused our investigation on implications for schizophrenia pathology, NRG1 has also been implicated in heart disease [93], Hirschsprung's disease [94] and cancer [95] as well as a wide variety of functions, including cardiac and neuronal development [93], induction of acetylcholine receptors [96, 97], and cellular proliferation, migration, differentiation, and survival or apoptosis [9, 98-104]. NRG1 has been a focus of cancer research in particular and has been implicated in angiogenesis [105], tumorigenesis and metastasis [106], and apoptosis [107]. NRG1 is a major tumorigenic force in a variety of cancer types [33] and over-expression of NRG1 is sufficient for tumor

development and metastasis [37, 106] and occurs in approximately 30% of breast cancer cases [108-111]. Most of these functions have traditionally been ascribed to the NRG1 ECD and its interaction with the ErbB family of proteins. However, our IP-MS/MS data indicate that the NRG1 ICD interacts with a diverse set of proteins and implicate the NRG1 ICD in multiple intracellular functions. These interactions also provide further evidence that the NRG1 ICD has a function within the nucleus, interacting with nuclear localized proteins, including many transcription factor proteins; this transcriptional role is also supported by the identification of NRG1 ICD - DNA interactions in our ChIP-seq analysis. The NRG1 protein interaction network also identifies new potential functions outside the nucleus related to cytoskeletal organization and transport. Overall, our results greatly expand the overall protein interaction network for the NRG1 ICD, underscore the importance of investigating NRG1 from an intracellular perspective, and show that the NRG1 ICD may play a significant role in the diverse functions ascribed to NRG1.

3.5 Chapter 3 Tables

Table 3.1 - PCR Primers

This table provides all PCR primers used for cloning. $Tm \ all$ – the melting temperature of the entire sequence in degrees Celsius; $Tm \ overlap$ – the melting temperature of the sequence that overlaps with the cDNA of the gene to be amplified.

Gene	IMAGE / clone ID	Primer type	Primer sequence	Length	Tm all (°C)	Tm overlap (°C)
DTNBP1	4139934	N5'	ATCGGGCGCGCCCTGGAGACCCTTCGCGAG	30	74.1	57.8
Isoform 1		N3'	ATCGTTAATTAATTAAGAGTCGCTGTCCTCACC	33	59.5	56.4
		C5'	ATCGGGCGCGCCATGCTGGAGACCCTTCGC	30	73.1	57.6
		C3'	ATCGTTAATTAAAGAGTCGCTGTCCTCACC	30	59.8	56.5
NRG1	AK097005	N5'	ATCGGGCGCGCCAAACAGCGGAAAAAGCTG	30	69.5	51.4
ICD-a		N3'	ATCGTTAATTAATTATACAGCAATAGGGTCTTG	33	55.6	49.5
		C5'	ATCGGGCGCGCCATGAAACAGCGGAAAAAGCTG	33	69.9	51.4
		C5'	ATCGTTAATTAATACAGCAATAGGGTCTTG	30	55.4	48.5
NRG1	BM819389	N5'	CTGTAATCGTGATGTCATCCG	21	53.1	53.1
ICD-b		N3'	ATCGTTAATTAATTAGAGAATGAAGCTTAAATGGGG	36	57.4	52.9
		C5'	CTGTAATCGTGATGTCATCCG	21	53.1	53.1
		C5'	ATCGTTAATTAAGAGAATGAAGCTTAAATGGGG	33	57.3	51.4
NRG1c	AK097005	N5'	ATCGGGCGCGCCAAACAGCGGAAAAAGCTG	30	69.5	51.4
ICD-c		N3'	ATCGTTAATTAATTACCTTTCACTATGAGGAGA	33	56.0	50.0
		C5'	ATCGGGCGCGCCATGAAACAGCGGAAAAAGCTG	33	69.9	51.4
		C5'	ATCGTTAATTAACCTTTCACTATGAGGAGA	30	55.8	47.6
AKAP8L	3504388	N5'	ATCGGGCGCGCCAGCTACACAGGCTTTGTC	30	70.1	52.2
		N3'	ATCGTTAATTAATTACGGGGCGCCCCCGCCGCCCCC	36	71.3	77.7
		C5'	ATCGGGCGCGCCATGAGCTACACAGGCTTT	30	69.7	51.1
		C5'	ATCGTTAATTAACGGGGCGCCCCCGCCGCCCTCC	34	73.6	78.8
SNX27	8069328	N5'	ATCGGGCGCGCGCGGGACGAGGACGGGGAAGGG	33	77.8	66.8
		N3'	ATCGTTAATTAATTAATATTCCTCTTTTCT	30	50.3	39.0
		C5'	ATCGGGCGCGCCATGGCGGACGAGGACGGG	30	75.9	62.8
		C5'	ATCGTTAATTAAATATTCCTCTTTTCTCCACT	32	55.0	47.9

Table 3.2 - Summary of NRG1 ICD IP-MS/MS Hit Counts by Experiment

This table shows a summary of the number of protein hits (protein assignments) resulting from the six NRG1 ICD experiments performed, as compared to six negative control empty vector immunoprecipitations. The table shows the results of the successive or individual processing steps (see Methods). *Experiment* - the NRG1 ICD isoform, tag position (N or C), and replicate number (where appropriate) for each IP-MS/MS experiment; *NSB* - non-specific background; *vector NSB* - NSB proteins found in the empty vector control experiments; *common NSB* - commonly observed NSB proteins; *minimal quality criteria* - having at least two observations each having X!Tandem log(E) scores \leq -3 and \geq 2 unique peptides.

	S	uccessive proce	Successive processing results (# hits)					Individual processing results (# hits) ^b			
Experiment	# total hits	after vector NSB removal	after common NSB removal	observed in at least 2 replicates	that meet minimal quality criteria	after vector NSB removal	after common NSB removal		observed in at least 2 replicates		
NRG1 ICD-a N - 1	256	160	97	29	16	-	-		_		
NRG1 ICD-a N - 2	349	226	150	36	19	-	-		_		
NRG1 ICD-a C	111	78	49	15	5	-	-		-		
NRG1 ICD-b N	129	89	60	17	6	-	-		-		
NRG1 ICD-b C	134	92	57	15	5	-	-		-		
NRG1 ICD-c N	173	125	81	24	11	-	-		-		
Total hits ^a	1,152	770 (0.33)	494 (0.36)	136 (0.72)	62 (0.54)	770 (0.33)	592 (0.49)		714 (0.38)		
Total hits with 1 peptide ^a	585	484 (0.17)	355 (0.27)	72 (0.80)	7 (0.90)	484 (0.17)	369 (0.37)		246 (0.58)		
Total hits with \geq 2 peptides ^a	567	286 (0.50)	139 (0.51)	64 (0.54)	55 (0.14)	286 (0.50)	223 (0.61)		468 (0.17)		
Total non-redundant hits ^a	671	544 (0.19)	413 (0.24)	55 (0.87)	22 (0.60)	544 (0.19)	447 (0.33)		233 (0.65)		
Total non-redundant hits with ≥ 2 peptides ^a	280	177 (0.37)	106 (0.40)	31 ^c (0.71)	22 ^c (0.29)	177 (0.37)	134 (0.52)		181 (0.35)		

^a - in parentheses: fraction removed by processing step.

^b - The number of original hits remaining after the single indicated processing step.

^c - The proteins removed in the last filter (resulting in the drop from 31 to 22 proteins) were hits that had one observation with two or more peptides while the other observation had only one peptide.

Table 3.3 - NRG1 ICD IP-MS/MS Interacting Partner Details

This table shows a summary of the candidate NRG1 ICD protein interacting proteins in HEK293 cells. Results are grouped by complex or interest. There were 22 interacting proteins that met the minimum threshold criteria (see Methods). *# Times Observed Per # Expts* - the number of times the protein was observed across all experiments for the isoform listed in the NRG1 isoform-column; *X*!*Tandem # Unique Peptides* - The number of unique peptides contributing to the protein identification; *X*!*Tandem Average log(E)* - The average X!Tandem log(E) score for the interacting protein across all experiments.

Interacting	Name	NRG1	Epitope Tag	# Times	Mascot		X!Tandem	
Protein" HGNC (Uniprot ID)		Isoform		Observed Per # Expts	Score *	log(E) ^c	# Unique Peptides ^d	Avg log(E)
DNA binding	g / Transcripti	ion Factor	Related Protei	ns				
NRG1	Neuregulin-1	ICD-a	N-term 3XFLAG	2/2	392	-192.2	22	-106.8
(Q15491)					1,581	-151.8	17	
			C-term 3XFLAG	1/1	1,688	-118.6	14	
		ICD-c	N-term 3XFLAG	1/1	890	-91.4	11	
		ICD-b	N-term 3XFLAG	1/1	261	-58.6	7	
			C-term 3XFLAG	1/1	139	-28.1	4	
ILF2	Interleukin	ICD-a	N-term 3XFLAG	1/2	317	-46.2	6	-20.3
(Q12905)	binding factor 2	ICD-c	N-term 3XFLAG	1/1	106	-19.1	3	
		ICD-b	C-term 3XFLAG	1/1	55	-8.4	2	
			N-term 3XFLAG	1/1	94	-7.5	1	
FLNA	Filamin-A	ICD-a	N-term 3XFLAG	1/2	686	-227.6	24	-113.1
(P21333)		ICD-c	N-term 3XFLAG	1/1	243	-108.8	13	
		ICD-b	C-term 3XFLAG	1/1	51	-3.0	1	
AKAP8L	A-kinase anchor	ICD-a	N-term 3XFLAG	2/2	102	-27.4	4	-13.8
(Q9ULX6)	protein 8-like				72	-3.3	1	
		ICD-c	N-term 3XFLAG	1/1	41	-10.6	2	
PCBP1	Poly(rC)-binding	ICD-a	N-term 3XFLAG	2/2	72	-9.5	2	-9.2
(Q15365)	protein 1				59	-8.6	2	
		ICD-c	N-term 3XFLAG	1/1	88	-9.4	2	
ILF3	Interleukin	ICD-a	N-term 3XFLAG	2/2	236	-95.3	12	-88.9
(Q12906)	enhancer- binding factor 3				354	-82.4	10	
ZNF503	Zinc finger	ICD-b	C-term 3XFLAG	1/1	-	-29.8	5	-27.3
(Q96F45)	protein 503	ICD-a	N-term 3XFLAG	1/2	-	-24.7	4	
SOX11	Transcription	ICD-a	N-term 3XFLAG	1/2	-	-29.9	5	-19.2
(P35716)	factor SOX-11	ICD-c	N-term 3XFLAG	1/1	-	-8.4	2	
FOXA1	Hepatocyte	ICD-a	N-term 3XFLAG	2/2	-	-16.4	3	-12.5
(P55317)	nuclear factor 3- alpha				-	-8.6	2	
Other Nucle	ar Annotated	Proteins						
TTN	Titin	ICD-a	N-term 3XFLAG	1/2	-	-31.2	5	-20.8
(Q8WZ42)			C-term 3XFLAG	1/1	-	-23.2	4	
		ICD-b	N-term 3XFLAG	1/1	-	-8.1	2	
SERBP1	Plasminogen	ICD-a	N-term 3XFLAG	2/2	76	-15.8	2	-11.0
(Q8NC51)	activator inhibitor 1 RNA-				75	-7.7	1	1
	binding protein	ICD-b	N-term 3XFLAG	1/1	53	-9.4	2	

Interacting	Name NRG1 Epitope Tag # Times		# Times	Mascot	X!Tandem			
Protein ^a HGNC (Uniprot ID)		Isoform		Observed Per # Expts	Score [®]	log(E) ^c	# Unique Peptides ^d	Avg log(E)
LMNA	Lamin-A/C	ICD-a	N-term 3XFLAG	2/2	230	-35.4	5	-26.6
(P02545)					87	-17.8	3	
PKP2	Plakophilin-2	ICD-a	N-term 3XFLAG	2/2	156	-27.8	4	-19.9
(Q99959)					113	-12.0	2	
Cytoskeleto	n / Transport	Related P	roteins					
ACTG1	Actin,	ICD-a	N-term 3XFLAG	1/2	285	-66.5	8	-44.0
(P63261)	cytoplasmic 2		C-term 3XFLAG	1/1	143	-54.8	7	
		ICD-c	N-term 3XFLAG	1/1	280	-60.4	7	
		ICD-b	N-term 3XFLAG	1/1	154	-28.6	4	
			C-term 3XFLAG	1/1	76	-9.5	2	
TUBA1C	Tubulin alpha-	ICD-c	N-term 3XFLAG	1/1	650	-133.1	15	-84.4
(Q9BQE3)	1C chain	ICD-a	N-term 3XFLAG	2/2	427	-89.7	10	
					374 ^e	-83.1	1	
			C-term 3XFLAG	1/1	-	-31.6	5	
SNX27	Sorting nexin-27	ICD-c	N-term 3XFLAG	1/1	483	-90.1	11	-64.0
(Q96L92)		ICD-a	N-term 3XFLAG	2/2	271	-86.5	10	
					216	-78.1	10	
			C-term 3XFLAG	1/1	39	-1.2	1	
DSP (P15924)	Desmoplakin	ICD-c	N-term 3XFLAG	1/1	-	-16.8	3	-13.9
		ICD-a	N-term 3XFLAG	2/2	74	-16.0	3	
					75	-8.9	2	
PLEC1	Plectin-1	ICD-a	N-term 3XFLAG	2/2	74	-10.8	2	-7.8
(Q15149)					80	-10.5	2	
		ICD-c	N-term 3XFLAG	1/1	47	-2.1	1	
UTRN	Utrophin	ICD-a	N-term 3XFLAG	2/2	578	-152.8	18	-110.0
(P46939)					324	-67.1	8	
COL19A1	Collagen alpha-	ICD-b	N-term 3XFLAG	1/1	-	-8.7	2	-8.4
(Q14993)	1(XIX) chain	ICD-a	N-term 3XFLAG	1/2	-	-8.0	2	
Other Protei	ins							
PPM1B	Protein	ICD-b	C-term 3XFLAG	1/1	375	-72.4	8	-60.4
(075688)	phosphatase 1B		N-term 3XFLAG	1/1	492	-69.0	8	
		ICD-a	C-term 3XFLAG	1/1	334	-69.0	8	
		ICD-c	N-term 3XFLAG	1/1	290	-31.2	4	
PGK1	Phosphoglycerat	ICD-a	N-term 3XFLAG	2/2	-	-29.5	4	-24.3
(P00558)	e kinase 1				-	-19.1	3	
YTHDC2	Probable ATP-	ICD-a	N-term 3XFLAG	2/2	78	-18.0	3	-13.7
(Q9H6S0)	dependent RNA helicase YTHDC2				-	-9.3	2	

^a – Interacting proteins were not observed in empty vector control immunoprecipitations.

^b – Mascot score as calculated by the Matrix Science Mascot software algorithm against the Ensembl human protein database.

^c – The log (E) value is an estimate of the probability that the protein assignment happened randomly as calculated by the X!Tandem algorithm against the Ensembl human protein database.

^d - Number of uniquely assigned peptides assigned to an individual accession that contribute to the log(E) score as calculated by the X!Tandem algorithm unless no X!Tandem score was found, in which case the

number of unique peptides contributing to the Mascot score is shown in italics. Additional non-unique peptides which map to multiple proteins within the Ensembl human protein database may contribute to individual X!Tandem or Mascot scores are not reported here.

^e – The protein identification score is likely a result of Mascot and X!Tandem assigning ion scores from non-unique peptides to multiple proteins.

This table provides a summary of schizophrenia linkage and association studies for the 22 NRG1 ICD candidate interacting proteins. The schizophrenia linkage analysis determined that 14 out of 22 proteins reside in cytogenetic regions linked with schizophrenia. A Chi-squared analysis against the full linkage database (826 cytogenetic regions with 366 linked to schizophrenia) showed no overrepresentation. *Schizophrenia association study performed (result)* – shows whether a schizophrenia association study has been performed on the interacting protein's gene based on the GAD [52].

Interacting Protein (HGNC)	Cytogenetic Location	Schizophrenia association study performed ^a (result)	Schizophrenia linkage within the cytogenetic region ^b	Representative linkage reference	PubMed ID
DNA bind	ing / Transci	ription Relate	d Proteins		
NRG1	8p12	Yes	Yes	Kaufmann et al. 1998	9674972
		(Association		Blouin et al. 1998	9731535
		iouria)		Stefansson et al. 2002	12145742
FLNA	Xq28	No	No		
ILF2	1q21.3	No	Yes	Arinami et al. 2005	16380906
AKAP8L	19p13.12	No	Yes	Faraone et al. 1998	9674973
ILF3	19p13.2	No	Yes	Faraone et al. 1998	9674973
PCBP1	2p14	No	Yes	Coon et al. 1998	9857978
				Faraone et al. 1998	9674973
				Straub et al. 2002	12098102
SOX11	2p25.2	No	No		
ZNF503	10q22.2	No	Yes	Faraone et al. 2006	17012687
				Fallin et al. 2003	12929083
FOXA1	14q21.1	No	Yes	Arinami et al. 2005	16380906
				Lerer et al. 2003	12808429
				Blouin et al. 1998	9731535
Other Nuc	lear Annota	ted Proteins			
SERBP1	1p31.3	No	Yes	Garver et al. 2001	11705708
LMNA	1q22	No	Yes	Brzustowicz et al. 2000	10784452
TTN	2q31.2	No	No		
PKP2	12p11.21	No	No		
Cytoskele	ton / Transp	ort Related P	roteins		
SNX27	1q21.3	No	Yes	Brzustowicz et al. 2000	10784452
ACTG1	7p22.1	No	Yes	Lerer et al. 2003	12808429
TUBA1C	12q13.12	No	No		
DSP	6p24.3	No	Yes	Kaufmann et al. 1998	9674972
				Lerer et al. 2003	12808429
				Straub et al. 2002	12098102
PLEC1	8q24.3	No	No		
UTRN	6q24.2	No	Yes	Lerer et al. 2003	12808429
				Kaufmann et al. 1998	9674972
				Straub et al. 2002	12098102
COL19A1	6q13	No	Yes	Straub et al. 2002	12098102

Interacting Protein (HGNC)	Cytogenetic Location	Schizophrenia association study performed ^a (result)	Schizophrenia linkage within the cytogenetic region ^b	Representative linkage reference	PubMed ID
Other Prot					
PPM1B	2p21	No	No		
PGK1	Xq21.1	No	No		
YTHDC2	5q22.2	No	Yes	Straub et al. 2002	12098102

^a - according to the NIH Genetic Association Database http://geneticassociationdb.nih.gov/

^b - whether the genomic location overlaps with a region shown to have suggestive or significant linkage with schizophrenia in at least 1 study.

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Table 3.5 - Novel NRG1 ICD Interacting Proteins

This table is a summary of the NRG1 ICD interacting proteins identified from the IP-MS/MS data using a number of filtering and quality criteria (see Methods and Table 3.2). Results are grouped by function. Protein HGNC names shown in bold were used in validation experiments and those shown in italics have evidence of being DTNBP1 interacting proteins [54].

Interacting Protein HGNC Name (Uniprot ID)	Name
DNA binding / Transcription Factor Related	d Proteins
AKAP8L (Q9ULX6)	A-kinase anchor protein 8-like
FLNA (P21333)	Filamin-A
FOXA1 (P55317)	Hepatocyte nuclear factor 3-alpha
ILF2 (Q12905)	Interleukin enhancer-binding factor 2
ILF3 (Q12906)	Interleukin enhancer-binding factor 3
NRG1 (Q15491)	Neuregulin-1
<i>PCBP1</i> (Q15365)	Poly(rC)-binding protein 1
SOX11 (P35716)	Transcription factor SOX-11
ZNF503 (Q96F45)	Zinc finger protein 503
Other Nuclear Annotated Proteins	
LMNA (P02545)	Lamin-A/C
PKP2 (Q99959)	Plakophilin-2
SERBP1 (Q8NC51)	Plasminogen activator inhibitor 1 RNA-binding protein
TTN (Q8WZ42)	Titin
Cytoskeleton / Transport Related Proteins	
ACTG1 (P63261)	Actin, cytoplasmic 2
COL19A1 (Q14993)	Collagen alpha-1(XIX) chain
DSP (P15924)	Desmoplakin
PLEC1 (Q15149)	Plectin-1
SNX27 (Q96L92)	Sorting nexin-27
TUBA1C (Q9BQE3)	Tubulin alpha-1C chain
UTRN (P46939)	Utrophin
Other Proteins	
PGK1 (P00558)	Phosphoglycerate kinase 1
PPM1B (O75688)	Protein phosphatase 1B
YTHDC2 (Q9H6S0)	Probable ATP-dependent RNA helicase YTHDC2

Table 3.6 - The NRG1 ICD Interacting Proteins that have Known Interactions with ChIP-

Seq Associated Transcription Factors

This table lists known interactions connecting the list of the NRG1 ICD interacting proteins to the transcription factors found significantly overrepresented in the ChIP-seq results.

Interacting Protein	ChIP-seq associated transcription factor
AKAP8L	RELA
LMNA	RB1
PKP2	GTF2B
SOX11	BRN2 / POU3F2

Table 3.7 - Schizophrenia Related NRG1 ICD-a ChIP-Seq Peak Proximal Genes

The following table contains the list of 37 / 143 genes proximal to the NRG1 ICD-a ChIP-seq peaks that have a minimum of one positive schizophrenia association in GAD [52] (p< 0.001). The columns are as follows, from the left: *Gene* – the HGNC name of the schizophrenia related ChIP-seq peak proximal gene; *Location* – the cytogenetic location of the gene; *Chr* – the chromosomal location of the gene; *Start* – the start coordinates of the gene (base pairs); *End* – the end coordinates of the gene (base pairs); *Chr* – the chromosomal location of the ChIP-seq peak; *Start* – the start coordinates of the ChIP-seq peak; *Start* – the start coordinates of the ChIP-seq peak (base pairs); *End* – the end coordinates of the ChIP-seq peak (base pairs); *Height* – the height of the ChIP-seq peak; *Distance from closest peak* (*bp*) – the smallest distance in base pairs from the gene to the ChIP-seq peak; *Gene-Peak Context* – the orientation of the peak with respect to the gene: "overlaps peak" means the peak and gene have a minimum of one base pair overlap, "peak downstream" means that the peak is downstream of the gene but not overlapping, "peak upstream" means the peak is upstream of the gene but not overlapping. The NRG1 ICD was previously shown to interact with IKZF4 to form a transcription factor complex and bind to the IK1 TFBS [39]. There is one schizophrenia associated gene (RXRB) proximal to a ChIP-seq peak containing IK1 TFBS.

	Gen	e Info	ormation		Peak Information					Distance	Gene –
Gene	Location	Chr	Start	End	Chr	Start	End	Width	Height	closest peak (bp)	Context
ALK	2p23	2	29,269,143	29,997,936	2	29,314,729	29,314,940	211	15		Overlaps Peak
ATN1	12p13.31	12	6,903,886	6,924,076	12	6,903,664	6,904,160	496	11		Overlaps Peak
					12	6,917,263	6,917,675	412	18		Overlaps Peak
CHL1	3p26.1	3	213,649	426,097	3	214,824	215,300	476	10		Overlaps Peak
CYP1A2	15q24	15	72,828,236	72,835,994	15	72,866,798	72,867,642	844	10	30,804	Peak Downstream
DDR1	6p21.3	6	30,959,839	30,975,912	6	30,953,466	30,953,943	477	9	2,841	Peak Upstream
					6	30,960,475	30,960,808	333	9		Overlaps Peak
					6	30,962,010	30,962,951	941	11		Overlaps Peak
DISC1	1q42.1	1	229,829,183	230,243,641	1	229,828,723	229,830,420	1,697	14		Overlaps Peak
					1	230,058,490	230,059,040	550	9		Overlaps Peak
					1	230,167,686	230,168,122	436	10		Overlaps Peak
DTNBP1	6p22.3	6	15,631,017	15,771,250	6	15,599,439	15,599,890	451	9	31,130	Peak Downstream
					6	15,771,150	15,771,848	698	9		Overlaps Peak
					6	15,799,296	15,800,036	740	9	28,046	Peak Upstream
ERBB4	2q33.3- q34	2	211,948,686	213,111,597	2	212,318,301	212,318,609	308	9		Overlaps Peak

	Gene	e Info	ormation		Peak Information				Distance	Gene –	
Gene	Location	Chr	Start	End	Chr	Start	End	Width	Height	closest peak (bp)	Context
FOXP2	7q31	7	113,513,617	114,117,391	7	114,080,481	114,080,978	497	9		Overlaps Peak
GABBR1	6p21.31	6	29,631,386	29,708,839	6	29,702,298	29,702,644	346	11		Overlaps Peak
GDNF	5p13.1- p12	5	37,851,509	37,875,539	5	37,852,715	37,853,229	514	9		Overlaps Peak
					5	37,883,748	37,884,229	481	10	8,209	Peak Upstream
GRIK3	1p34-p33	1	37,039,200	37,272,431	1	37,118,034	37,118,668	634	9		Overlaps Peak
GRIN1	9q34.3	9	139,153,429	139,183,029	9	139,183,665	139,184,026	361	10	637	Peak Upstream
GRM5	11q14.3	11	87,880,625	88,438,761	11	87,917,125	87,917,469	344	9		Overlaps Peak
HLA-DRB1	6p21.3	6	32,593,131	32,665,559	6	32,628,272	32,628,921	649	9		Overlaps Peak
JARID2	6p24-p23	6	15,354,505	15,630,232	6	15,356,054	15,356,442	388	10		Overlaps Peak
					6	15,356,690	15,356,992	302	9		Overlaps Peak
					6	15,357,113	15,357,580	467	11		Overlaps Peak
					6	15,388,881	15,389,522	641	9		Overlaps Peak
					6	15,599,439	15,599,890	451	9		Overlaps Peak
MED12	Xq13	Х	70,255,130	70,279,029	Х	70,265,290	70,266,689	1,399	9		Overlaps Peak
					Х	70,288,339	70,288,829	490	9	9,311	Peak Downstream
MICB	6p21.3	6	31,573,944	31,586,880	6	31,569,585	31,570,235	650	9	3,607	Peak Upstream
MPZL1	1q24.2	1	165,957,831	166,026,684	1	165,950,373	165,951,136	763	13	6,690	Peak Upstream
NEUROG1	5q23-q31	5	134,897,870	134,899,538	5	134,851,767	134,852,147	380	9	45,724	Peak Downstream
					5	134,915,307	134,916,004	697	9	15,769	Peak Upstream
NOTCH4	6p21.3	6	31,238,539	31,784,329	6	32,271,496	32,272,611	1,115	9		Overlaps Peak
NPY	7p15.1	7	24,290,333	24,298,002	7	24,290,366	24,290,745	379	9		Overlaps Peak
NQO2	6pter-q12	6	2,933,199	2,964,993	6	2,933,566	2,934,628	1,062	10		Overlaps Peak
					6	2,935,641	2,936,056	415	10		Overlaps Peak
					6	2,936,273	2,936,601	328	9		Overlaps Peak
					6	2,968,450	2,969,574	1,124	9	3,455	Peak Downstream
NRG3	10q22- q23	10	83,625,076	84,735,341	10	83,900,001	83,900,647	646	9		Overlaps Peak
PDE4B	1p31	1	66,030,780	66,612,850	1	66,151,653	66,152,000	347	9		Overlaps Peak
					1	66,509,435	66,509,874	439	9		Overlaps Peak

	Gene	Info	rmation			Pea	k Informatio		Distance	Gene –	
Gene	Location	Chr	Start	End	Chr	Start	End	Width	Height	closest peak (bp)	Context
PIP5K2A	10p12.32	10	22,865,827	23,043,490	10	22,881,856	22,882,276	420	9		Overlaps Peak
					10	22,893,671	22,894,027	356	9		Overlaps Peak
					10	22,902,855	22,903,200	345	9		Overlaps Peak
PLA2G1B	12q23- q24.1	12	119,244,296	119,249,975	12	119,247,670	119,248,007	337	10		Overlaps Peak
PRODH	22q11.21	22	17,280,294	17,304,066	22	17,258,302	17,258,709	407	20		Overlaps Peak
					22	17,260,459	17,260,703	244	12		Overlaps Peak
RXRB	6p21.3	6	33,269,342	33,276,410	6	33,276,091	33,277,089	998	11		Overlaps Peak
S100B	21q22.3	21	46,842,958	46,849,463	21	46,879,632	46,880,400	768	9	30,083	Peak Upstream
SLC25A27	6p11.2-q12	6	46,728,637	46,753,886	6	46,727,919	46,728,381	462	10	257	Peak Upstream
					6	46,731,477	46,731,843	366	9		Overlaps Peak
SLC6A3	5p15.3	5	1,445,908	1,498,543	5	1,433,578	1,434,125	547	9	11,789	Peak Downstream
SNAP29	22q11.21	22	19,543,291	19,574,109	22	19,569,773	19,570,548	775	11		Overlaps Peak
					22	19,601,179	19,602,148	969	11	27,070	Peak Downstream
SOX10	22q13.1	22	36,698,264	36,713,375	22	36,725,469	36,726,252	783	9	12,094	Peak Upstream
SYN3	22q12.3	22	31,238,539	31,784,329	22	31,573,113	31,573,584	471	9		Overlaps Peak
ZNF74	22q11.2	22	19,078,450	19,092,752	22	19,077,857	19,078,562	705	9		Overlaps Peak

Table 3.8 - Known Transcription Factor Binding Sites in the ChIP-Seq Data

This table shows 164 known transcription factors from the Transfac database whose binding sites are over-represented within the ChIP-seq peaks. *Transfac Matrix* – the specific matrix from the Transfac database that has a binding sequence overrepresented within the ChIP-seq peaks; *Actual Count* – the number of times the Transfac Matrix matched sequences in the ChIP-seq peaks; *# Bootstraps* \geq *Actual (out of 100)* – this is the number of times the Transfac Matrix sequence was seen more frequently in the randomized peak sequences than in the actual sequences.

Transfac Matrix	Associated Transcription Factor Gene	Actual Count	# Bootstraps ≥ Actual (out of 100)	P-value	Benjamini & Hochberg Corrected
V\$GATA4_Q3	GATA-4	2,296	0	<0.001	<0.002
V\$FOXP3_Q4	FOXP3	1,363	0	<0.001	<0.002
V\$EVI1_04	EVI-1	1,270	0	<0.001	<0.002
V\$NFKB_Q6_01	NF-kappaB, NFkappaB(-like), NF-kappaB2 (p49), NF-kappaB2 precursor, p105, p50, p52, ReIA	1,250	0	<0.001	<0.002
V\$HNF1_C	HNF-1 alpha-A	1,071	0	<0.001	<0.002
V\$MAZ_Q6	MAZ	1,071	0	<0.001	<0.002
V\$MYOGNF1_01	myogenin / NF1	979	0	<0.001	<0.002
V\$E2F_Q6	DP-1, E2F, E2F+E4, E2F1, E2F1:DP1, E2F3a, E2F4, E2F7	964	0	<0.001	<0.002
V\$HNF4_DR1_Q3	HNF-4	929	0	<0.001	<0.002
V\$PAX_Q6	PAX2, PAX5, PAX8	927	0	<0.001	<0.002
V\$PBX_Q3	PBX	923	0	<0.001	<0.002
V\$EFC_Q6	RFX1, RFX5:RFXAP:RFXANK	922	0	<0.001	<0.002
V\$MYC_Q2	c-Myc, MAX1	912	0	<0.001	<0.002
V\$CDPCR1_01	CUTL1	826	0	<0.001	<0.002
V\$HNF4_Q6_01	HNF4, HNF-4alpha, HNF-4alpha1, HNF- 4alpha2, HNF-4alpha3, HNF-4alpha4	784	0	<0.001	<0.002
V\$PAX6_01	PAX-6	771	0	<0.001	<0.002
V\$PPARG_03	PPAR-gamma1, PPAR-gamma2	764	0	<0.001	<0.002
V\$ELK1_02	ELK-1	738	0	<0.001	<0.002
V\$HNF1_Q6	HNF1alpha, HNF1beta	646	0	<0.001	<0.002
V\$PAX3_B	PAX3	608	0	<0.001	<0.002
V\$COUPTF_Q6	COUP-TF1, COUP-TF2	602	0	<0.001	<0.002
V\$COMP1_01	COMP1	596	0	<0.001	<0.002
V\$TFIIA_Q6	TFIIA, TFIIA-alpha/beta precursor, TFIIA- gamma	554	0	<0.001	<0.002
V\$USF_Q6	USF2, USF2b	488	0	<0.001	<0.002
V\$BACH2_01	BACH2	467	0	<0.001	<0.002
V\$NKX25_01	NKX2-5	437	0	<0.001	<0.002
V\$CREL_01	C-REL	430	0	<0.001	<0.002
V\$VMYB_01	V-MYB	381	0	<0.001	<0.002
V\$CDX2_Q5	CDX2	367	0	<0.001	<0.002
V\$CREB_Q2_01	CREB, CREMalpha, deltaCREB	339	0	<0.001	<0.002
V\$CREB_Q4_01	CREB, CREMalpha, deltaCREB	321	0	<0.001	<0.002
V\$E2F_Q4	E2F	303	0	<0.001	<0.002
V\$CAAT_01	cellular and viral CCAAT box	294	0	<0.001	<0.002
V\$E2F1_Q6_01	E2F-1	293	0	<0.001	< 0.002
V\$IRF7_01	IRF-7	288	0	<0.001	< 0.002
V\$CREBP1CJUN_01	ATF2, c-Jun	287	0	<0.001	<0.002

Transfac Matrix	Associated Transcription Factor Gene	Actual Count	# Bootstraps ≥ Actual (out of 100)	P-value	Benjamini & Hochberg Corrected
V\$CEBPGAMMA_Q6	C/EBPgamma	262	0	<0.001	<0.002
V\$CREBATF_Q6	ATF, ATF1, ATF2, ATF3, ATF4, ATF5, ATF6, ATF-a, ATF-Adelta, CREB, CREMalpha, deltaCREB	257	0	<0.001	<0.002
V\$CREB_01	CREB, deltaCREB	256	0	<0.001	<0.002
V\$FOX_Q2	FOXF2, FOXJ2 (long isoform), FOXK2a, FOXM1a, FOXM1b, FOXN2, FOX01a, FOX03a, FOX04	251	0	<0.001	<0.002
V\$E2F1_Q3_01	E2F-1	249	0	<0.001	<0.002
V\$HAND1E47_01	HAND1:E47 heterodimer	232	0	<0.001	<0.002
V\$LDSPOLYA_B	Lentiviral Poly A downstream element	217	0	<0.001	<0.002
V\$HES1_Q2	HES1	216	0	<0.001	<0.002
V\$NFY_Q6_01	CP1C, NF-Y, NF-YA, NF-YB	204	0	<0.001	<0.002
V\$ATF3_Q6	ATF3	184	0	<0.001	<0.002
V\$E2F4DP2_01	E2F4:DP2 heterodimer	184	0	<0.001	<0.002
V\$CEBPDELTA_Q6	C/EBPdelta	182	0	<0.001	<0.002
V\$MEF2_Q6_01	aMEF2, MEF2A, MEF2DAB	182	0	<0.001	<0.002
V\$CP2_01	CP2	177	0	<0.001	<0.002
V\$AP1_Q2	AP1	172	0	<0.001	<0.002
V\$SF1_Q6	SF-1	170	0	<0.001	<0.002
V\$KROX_Q6	EGR1, EGR2, EGR3, EGR4	168	0	<0.001	<0.002
V\$VMAF_01	V-MAF	168	0	<0.001	<0.002
V\$DEC_Q1	DEC1, DEC2	161	0	<0.001	<0.002
V\$ELK1_01	ELK-1	155	0	<0.001	< 0.002
V\$ATF4_Q2	ATF-4	149	0	<0.001	<0.002
V\$PIT1_Q6	POU1F1	149	0	<0.001	<0.002
V\$SRF_Q5_01	SRF	143	0	<0.001	< 0.002
V\$HNF3B_01	HNF-3beta	140	0	<0.001	<0.002
V\$TCF4_Q5	TCF-4	131	0	<0.001	< 0.002
V\$MYCMAX_02	c-Myc, MAX1	128	0	<0.001	<0.002
V\$HLF_01	HLF	125	0	<0.001	< 0.002
V\$MRF2_01	MRF-2	120	0	<0.001	< 0.002
	NRF2	120	0	<0.001	< 0.002
V\$E2F1DP1RB_01	RB:E2F1:DP1 trimeric complex	119	0	<0.001	< 0.002
V\$ER_Q6	ER-alpha, ER-alpha:ER-beta, ER-beta	119	0	<0.001	< 0.002
V\$CREB 02	CREB, deltaCREB	118	0	<0.001	<0.002
V\$DEAF1 01	DEAF1	118	0	<0.001	<0.002
V\$AP2ALPHA_02	AP-2alphaA	111	0	<0.001	< 0.002
V\$CDPCR3HD_01	CUTL1	110	0	<0.001	< 0.002
V\$SMAD3_Q6	SMAD3	110	0	<0.001	<0.002
V\$E2F_Q3_01	DP-1, E2F, E2F+E4, E2F1, E2F1:DP1, E2F3a, E2F4	106	0	<0.001	<0.002
V\$E2F1_Q4_01	DP-1, E2F, E2F+E4, E2F-1, E2F-3a, E2F-4	106	0	<0.001	< 0.002
V\$MTATA_B	muscle TATA box	105	0	<0.001	<0.002
V\$E2F_Q6_01	DP-1, E2F, E2F+E4, E2F1, E2F1:DP1, E2F3a, E2F4, E2F7	103	0	<0.001	<0.002
V\$SMAD4_Q6	SMAD4	102	0	<0.001	< 0.002
V\$TITF1_Q3	NKX2-1	98	0	<0.001	<0.002
V\$STAF_02	STAF	95	0	<0.001	<0.002
V\$CREB_Q4	CREB	94	0	<0.001	<0.002
V\$GATA1_02	GATA1	92	0	<0.001	<0.002
V\$AP1_C	AP1	86	0	<0.001	<0.002
V\$NRF2_Q4	NRF2	84	0	<0.001	<0.002

Transfac Matrix	Associated Transcription Factor Gene	Actual Count	# Bootstraps ≥ Actual (out of 100)	P-value	Benjamini & Hochberg Corrected
V\$NFY_Q6	NF-Y, NF-YA, NF-YB	75	0	<0.001	<0.002
V\$LPOLYA_B	Lentiviral Poly A	74	0	<0.001	<0.002
V\$MAZR_01	MAZR	74	0	<0.001	<0.002
V\$HFH3_01	FOXI1	73	0	<0.001	<0.002
V\$NFY_01	NF-Y	70	0	<0.001	<0.002
V\$GABP_B	GABP-alpha, GABP-beta (1, 2)	68	0	<0.001	<0.002
V\$NFKB_Q6	NF-kappaB, NFkappaB2, p105, p50, p52, RelA	68	0	<0.001	<0.002
V\$NRF1_Q6	NRF-1	68	0	<0.001	<0.002
V\$ATF6_01	ATF6	66	0	<0.001	<0.002
V\$IRF_Q6_01	IRF-1, IRF-2, IRF-3, IRF-4, IRF-5, IRF-7A, IRF-7H, IRF-8, IRF-9, ISGF-3	66	0	<0.001	<0.002
V\$OCT1_06	POU2F1	65	0	<0.001	<0.002
V\$BARBIE_01	barbiturate-inducible element	59	0	<0.001	<0.002
V\$IRF_Q6	IRF-1, IRF-2, IRF-3, IRF-4, IRF-5, IRF-6, IRF-7A, IRF-7H, IRF-8	59	0	<0.001	<0.002
V\$E12_Q6	E12	58	0	<0.001	<0.002
V\$SRF_Q5_02	SRF	57	0	<0.001	<0.002
V\$VMYB_02	v-Myb	57	0	<0.001	<0.002
V\$GATA1_03	GATA-1	56	0	<0.001	<0.002
V\$NFE2_01	NF-E2, NF-E2 p45	56	0	<0.001	<0.002
V\$AML_Q6	AML1, AML1a, AML1b, AML1c, AML2, AML3, AML3a, AML3b	55	0	<0.001	<0.002
V\$DR3_Q4	CAR, CAR:RXR-alpha, PXR-1, PXR-1:RXR- alpha, PXR-1:RXR-beta, RXR-alpha, VDR	55	0	<0.001	<0.002
V\$NMYC_01	N-MYC	55	0	<0.001	<0.002
V\$ATF1_Q6	ATF-1	54	0	<0.001	<0.002
V\$NFKAPPAB_01	NF-kappaB, p50, RelA	54	0	<0.001	<0.002
V\$IK1_01	IK1	53	0	<0.001	<0.002
V\$BRN2_01	POU3F2	50	0	<0.001	<0.002
V\$E2F_Q3	E2F	47	0	<0.001	<0.002
V\$GCM_Q2	GCMa	47	0	<0.001	<0.002
V\$YY1_02	YY1	45	0	<0.001	<0.002
V\$NKX25_02	NKX2-5	44	0	<0.001	<0.002
V\$CREB_Q2	CREB	42	0	<0.001	<0.002
V\$TATA_C	TBP, TFIID	42	0	<0.001	<0.002
V\$USF_01	USF1	42	0	<0.001	<0.002
V\$SREBP_Q3	SREBP1a, SREBP1b, SREBP1c, SREBP-2	40	0	<0.001	<0.002
V\$GLI_Q2	GLI1, GLI2alpha, GLI3	39	0	<0.001	<0.002
V\$ETS2_B	c-Ets-2	37	0	<0.001	<0.002
V\$LEF1TCF1_Q4	LEF-1, TCF-1, TCF-1A, TCF-1B, TCF-1C, TCF-1E, TCF-F, TCF-1G	37	0	<0.001	<0.002
V\$TEF_Q6	TEF	35	0	<0.001	<0.002
V\$ARNT_01	ARNT	34	0	<0.001	<0.002
V\$MMEF2_Q6	aMEF2	34	0	<0.001	<0.002
V\$PITX2_Q2	PITX2	33	0	<0.001	<0.002
V\$STAT5A_02	STAT5A	33	0	<0.001	<0.002
V\$MEIS1_01	MEIS-1	31	0	<0.001	<0.002
V\$ACAAT_B	Avian C-type CCAAT box	28	0	<0.001	<0.002
V\$HIF1_Q5	HIF-1, HIF-1alpha	28	0	<0.001	<0.002
V\$AHRARNT_01	AHR, ARNT	27	0	<0.001	<0.002
V\$ATF_B	ATF	27	0	<0.001	<0.002
V\$TEL2_Q6	TEL-2a, TEL-2b, TEL-2c	25	0	<0.001	<0.002

Transfac Matrix	Associated Transcription Factor Gene	Actual Count	# Bootstraps ≥ Actual (out of 100)	P-value	Benjamini & Hochberg Corrected
V\$ZID_01	ZID	25	0	<0.001	<0.002
V\$ARNT_02	ARNT	24	0	<0.001	<0.002
V\$EVI1_06	EVI1	24	0	<0.001	<0.002
V\$SREBP1_01	SREBP1a, SREBP1b, SREBP1c	23	0	<0.001	<0.002
V\$CACCCBINDING FACTOR_Q6	CACCC-binding factor	22	0	<0.001	<0.002
V\$E2_Q6	papilloma virus regulator E2	21	0	<0.001	<0.002
V\$E47_02	E47	21	0	<0.001	<0.002
V\$STAF_01	STAF	21	0	<0.001	<0.002
V\$MEF2_02	MEF-2A	20	0	<0.001	<0.002
V\$OLF1_01	OLF-1	17	0	<0.001	<0.002
V\$STRA13_01	STRA13	17	0	<0.001	<0.002
V\$TCF11MAFG_01	LCR-F1	16	0	<0.001	<0.002
V\$SRF_Q6	SRF	15	0	<0.001	<0.002
V\$AMEF2_Q6	aMEF-2	14	0	<0.001	<0.002
V\$E2F_01	E2F	14	0	<0.001	<0.002
V\$TBX5_Q5	TBX5 (long isoform)	14	0	<0.001	<0.002
V\$HFH4_01	FOXJ1A, FOXJ1B	9	0	<0.001	<0.002
V\$STAT5B_01	STAT5B	9	0	<0.001	<0.002
V\$AP2ALPHA_03	AP-2alphaA	8	0	<0.001	<0.002
V\$OCT1_05	POU2F1	6	0	<0.001	<0.002
V\$HNF4_01_B	HNF-4alpha1	3	0	<0.001	<0.002
V\$HIF1_Q3	HIF-1, HIF-1alpha	20	1	0.001	0.002
V\$ALPHACP1_01	NF-Y	12	1	0.001	0.002
V\$NKX25_Q5	NKX2-5	11	2	0.002	0.004
V\$NFY_C	NF-Y, NF-YA, NF-YB	7	2	0.002	0.004
V\$E2_01	papilloma virus regulator E2	8	4	0.004	0.009
V\$FOXJ2_01	FOXJ2 (long isoform)	44	8	0.008	0.017
V\$FOXJ2_02	FOXJ2 (long isoform)	61	9	0.009	0.019
V\$VJUN_01	V-JUN	2	10	0.010	0.021
V\$USF_C	USF1	132	11	0.011	0.023
V\$SRF_Q4	SRF	40	13	0.013	0.027
V\$DEAF1_02	DEAF1	11	14	0.014	0.029
V\$POU6F1_01	POU6F1	18	16	0.016	0.033
V\$TAL1ALPHAE47_01	TAL-1alpha:E47 heterodimer	17	22	0.022	0.045

3.6 Chapter 3 Figures

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This graph shows the X!Tandem expectation scores (log(E), grey dots) for each observation of the candidate interacting proteins in the six NRG1 ICD immunoprecipitation experiments. The squares are the average log(E) values of the observed values for each protein; red squares are interactions validated by immunoprecipitation-western analysis (Figures 3.3 and 3.5) or co-localization (Figure 3.4), blue squares are non-validated interactions. The proteins are ordered left to right (protein rank) by increasing average log(E) value.



Figure 3.2 - NRG1 ICD Isoforms

Shown are the exon structure, length (in amino acids) and the calculated molecular weight of the three different NRG1 ICD isoforms.



Figure 3.3 - Validation of the AKAP8L Interaction with the NRG1 ICD

This figure shows the validation of protein interactions between NRG1 ICD-a and AKAP8L in both HEK293 and X57 cells through immunoprecipitation of 3XFLAG-tagged AKAP8L followed by western blot for GFP tagged NRG1 ICD-a using an anti-GFP antibody. Arrows indicate an NRG1 ICD-a-GFP band, which is the expected size (~70 kD including GFP tag) according to the positive control. Positive controls represent aliquots taken from the lysate prior to immunoprecipitation. The amount of protein in the positive control lanes were not matched with the experimental samples. Negative controls are the immunoprecipitation performed on cells co-transfected with both parent (empty) vectors for the 3XFLAG (V180) and GFP (V4) tagged constructs. The occurrence of multiple bands smaller than the expected size is thought to be due to proteolytic cleavage and or protein modifications.


Co-immunofluorescence of NRG1 ICD-a (red) and SNX27 (green)



Figure 3.4 - Validation of the Interaction of the NRG1 ICD with SNX27

Indirect immunofluorescence of the NRG1 ICD-a and SNX27 was used to show their cellular locations and co-localization. A) N-terminal GFP-tagged NRG1 ICD-a immunofluorescence showing cytoplasmic and nuclear staining. B) N-terminal GFP-tagged SNX27 immunofluorescence showing punctate cytoplasmic staining. C), D), and E) HEK293 cells were co-transfected with N-terminal dsRed-tagged NRG1 ICD-a and N-terminal GFP-tagged SNX27. C) and D) show the green and red channels, respectively; E) shows the merged channels and the co-localization of the NRG1 ICD-a and SNX27.



Figure 3.5 - Validation of the UTRN Interactions with the NRG1 ICD and DTNBP1

Validation of protein interactions: A) between UTRN and the NRG1 ICD-a in both X57 and HEK293 cells; B) between UTRN and DTNBP1 performed in HEK293 cells. Immunoprecipitation was achieved using UTRN native antibody (goat for NRG1 (A), rabbit for DTNBP1 (B)) conjugated to protein G beads followed by western blot for 3XFLAG tagged NRG1 or 3XFLAG tagged DTNBP1 using an anti-FLAG antibody. Arrows indicate the band of the expected size in comparison to the positive control. Positive controls represent aliquots taken from the lysate prior to immunoprecipitation. The amount of protein in the positive control lanes were not matched with the experimental samples. Negative controls were the immunoprecipitation performed on cells transfected with the parent (empty) vector (V180) for the 3XFLAG tagged construct.



Figure 3.6 - The NRG1 ICD ChIP-Seq Peaks Upstream of the DLG4 Gene

Shown is an example of an NRG1 ICD ChIP-seq peak; the ChIP-seq peaks at the 5' end of DLG4 in the UCSC browser (hg18, NCBI build 36.1, http://genome.ucsc.edu/) [48, 49].



Figure 3.7 - The NRG1 ICD ChIP-Seq Peaks Proximal to Schizophrenia Susceptibility Genes DTNBP1 and DISC1

Shown are the NRG1 ICD ChIP-seq peaks around the schizophrenia susceptibility genes DTNBP1 and DISC1. A) ChIP-seq peaks at the 5' end of DTNBP1 in the UCSC browser; B) ChIP-seq peaks across the DISC1 gene in the UCSC browser (hg18, NCBI build 36.1, http://genome.ucsc.edu/) [48, 49].



Figure 3.8 - The NRG1 ICD Protein Interaction Network

This protein interaction network shows interacting proteins identified for the NRG1 ICD by IP-MS/MS analysis (Tables 3.3 and 3.5). The BioGRID database was used to add previously published interactions between for NRG1. The DTNBP1 and DISC1 data are from Mead *et al.* 2010 [54].



Figure 3.9 - Representative Gel of Immunoprecipitated NRG1 Protein Complexes

NRG1-3XFLAG (C-terminal tag) protein complexes were immunoprecipitated from transfected HEK293 cells using an anti-FLAG antibody and fractionated by one dimensional SDS-PAGE. The gel was imaged using colloidal Coomassie blue. A control anti-FLAG immunoprecipitation of cells expressing the empty vector control plasmid (V181) was also prepared and analyzed. The arrow indicates the position of the NRG1-3XFLAG protein (~47 kDa: 44 kDa DNTBP1 + 3 kDa 3XFLAG). The entire control and experimental lanes were excised in 16 slices for each lane. The control and experimental gel slices were analyzed by comparative MS analysis (see Methods). Results of the MS/MS analysis are shown in Figure 3.8 and detailed results are provided in Table 3.2. A total of five NRG1 and six empty vector control experiments were processed in this manner

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4 A Meta-Analysis of Schizophrenia Linkage Data that Utilizes Recombination Distance¹

4.1 Introduction

Schizophrenia is a severe psychiatric disorder, affecting approximately 1% of the population [1]. It is highly heritable [2, 3], indicating a strong genetic component, but the specific genetic risk factors remain largely unknown [4, 5]. In complex diseases such as schizophrenia, it is possible that there are many genes contributing to overall disease risk at low levels. While individual studies may identify regions significantly linked to schizophrenia in particular families, findings are only considered robust if they are replicated in other studies. In schizophrenia in particular, linkage studies have been confounded by small sample sizes in combination with heterogeneity between populations and low risk alleles. Existing studies have identified linkage regions on 21 of the 23 chromosomes, however many regions did not meet genome-wide significance and most failed to be replicated [6-8]. Regions that have been replicated multiple times include the regions around 6p22.3 (DTNBP1) [9, 10], 8p21 (NRG1) [11-13], 13q32 (DAOA) [12, 14, 15], and 10p12.2 (PIP4K2A) [16-18]. A meta-analysis is an analytical technique that combines results from several studies in an attempt to overcome limitations from individual studies. An effective meta-analysis should identify new loci with modest but consistent signals and discriminate between loci that have shown linkage over a number of studies versus those that have had only a single linkage result.

Most published schizophrenia linkage studies have a small subset of markers in common, but the majority of markers across all studies are unique to one or a small number of studies. This is typical for linkage studies, regardless of the disease of interest. Therefore, a central issue for meta-analyses of linkage data is determining how to group or compare linkage signals from different studies. More specifically, the challenge is in determining how linkage signals from non-overlapping markers in different studies should be combined across the genome. Other linkage meta-analyses have employed different strategies to achieve this: The Genome Scan Meta-Analysis (GSMA) method [19] bins markers in 20-30 cM bins [20, 21] and then within each study bins are ranked based on maximum evidence for linkage. The ranks across all studies in each bin are then summed and the bin with the smallest summed rank has the strongest result. The GSMA method overcomes issues with non-identical marker use and disparate scoring types between studies by binning markers and ranking scores; however ranking scores eliminates the relative relationship between different studies. For example, the 4th ranked score in one study could meet significant requirements, but not meet even suggestive linkage requirements in another study. Using the GSMA method, when the studies are combined the two scores have the same rank and are therefore given the same weight when combining the studies. In this way, weak scores from one study could be treated as equal to significant scores in another study and consistent but weakly scoring regions have less ability to accumulate in the GSMA method, especially where individual studies within

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the meta-analysis have other high scoring regions unique to that study, that reduce the rank of the weak scoring region. In addition, grouping markers within large bins of 20-30cM means that linkage signals may not represent a common underlying signal and could result in erroneous conclusions. In an attempt to overcome this, the analysis is redone by re-binning the markers in different ways to see if the same regions remain significant; while this may help discover errors due to inappropriate marker binning it does not address the other underlying issues.

The Multiple Scan Probability (MSP) meta-analysis method described by Badner and Gershon [22] combines P-value statistics using a modified Fisher meta-analysis method [23] and determines genomic regions of interest where the combined p-value allows rejection of the null hypothesis. They extrapolate point-wise p-values to regions of the genome using the Feingold *et al.* estimate [24] that incorporates a different recombination rate based on the analysis method and family structure for each linkage study. This analysis was able to combine scores from non-overlapping markers and used an estimate of recombination rate to determine the regions that the scores applied to. However, the information required to estimate recombination rate is not always readily available from articles or authors. Badner had previous involvement with linkage studies performed on bipolar disorder [25, 26], including a genome scan for the NIMH genetics initiative for bipolar disorder [25]. The assumption is that this involvement allowed for procuring raw datasets, as it is our experience that procuring even a minimal dataset of marker and score from individual linkage studies is often quite difficult. Raw and underlying data, which would be needed to estimate family recombination rates in MSP analyses, is generally unavailable.

Other genome wide linkage meta-analysis methods have been described, but have not been applied to schizophrenia studies. For example, Etzel *et al.* 2005 created the Meta-Analysis procedure for Genome wide linkage Studies (MAGS) method which requires that the marker maps, sample size, information content at each marker, and linkage summary statistics are available [27]. A weighted average is used to determine the final score [27].

When implemented for schizophrenia, the GSMA method showed significant linkage in 2q with several regions having nominal significance including 1q, 3p, 5q, 6p, 6q, 8p, 10p, 11q, 14p, 15q, 16q, 17q, 18q, 20q, and 22q [20]. Badner and Gershon's implementation of MSP for schizophrenia found 3 regions of significance including 8p, 13q and 22q. While a large number of linkage studies have been performed for schizophrenia, the varied results suggest that new approaches to meta-analysis could uncover new candidate loci.

Here, we present a meta-analysis approach called the Marker Footprint Linkage Meta-analysis (MFLM) method that leverages the HapMap recombination rate [28] to allow marker linkage signals to be combined across studies in a rational manner. The HapMap recombination rates are estimated by comparing the genotypes of 1.6 million SNPs in three samples: 24 European Americans, 23 African Americans, and 24 Han Chinese from Los Angeles [29]. A recent study by Serre *et al.* investigated recombination rate patterns among different human populations and found that they are, in general,

conserved across the genome [30]. This further substantiates the validity of the HapMap recombination rate data for use in the context of a meta-analysis. The underlying principle behind using recombination rate is that the smaller the recombination distance between two markers, the more likely those markers are to be transmissible on the same, unrecombined genomic segment, and therefore the more likely the linkage signals are to be comparable across studies. The MFLM method allows markers from disparate marker maps to be combined based on recombination distance, allows inclusion of studies using different scoring methods, and does not require information content or more detailed raw or underlying data from the original studies. The purpose of the MFLM performed here is to discover regions of the genome that have shown consistent linkage results over numerous whole-genome linkage studies for schizophrenia regardless of whether they met significance criteria in individual studies.

4.2 Materials and Methods

4.2.1 Selection of genome scans

We requested data from seventeen previously published genome-wide linkage studies. Eight of 17 schizophrenia datasets were provided, encompassing 477 pedigrees and 1187 affected individuals (Brzustowicz et al. 2000 [31]; DeLisi et al. 2002 [32]; Klei et al. 2005 [33]; Levinson et al. 1998 [34]; Lindholm et al. 2001 [35]; Moises et al. 1995 [36]; Paunio et al. 2001 [37]; Schwab et al. 2000 [38]). Information on the studies is shown in Table 4.1. Inclusion of a larger number of studies would increase the power to detect loci with small effects.

4.2.2 Recombination rate footprint meta-analysis method

Data from all available genome scans were loaded into a local mySQL database. Markers were mapped to chromosomal coordinates on the (NCBI Build human genome 35) using UniSTS (www.ncbi.nlm.nih.gov/genome/unists) and manual searches. 97.8% of markers were successfully mapped to unique chromosomal coordinates. There were some unsuccessfully mapped markers due to datasets using ambiguous marker names, or markers with names that were unidentifiable, which were not included in the study. The coordinates for mapped markers were then used to determine the HapMap region associated with each marker based on the "recombination rates and hotspots for HapMap Phase I" dataset download, released in September 28, 2005 [39]. A HapMap region is the region between a pair of adjacent SNPs with HapMap defined genotypes and recombination frequency. There are 1,025,767 HapMap regions with an average length of 2,768 bp +/- standard deviation 4,563 bp. It is important to note that HapMap regions, as indicated here, are not linkage disequilibrium blocks, although proximal HapMap regions may be in linkage disequilibrium.

To incorporate studies using different linkage methods, we converted linkage scores to representative genomic probability scores using the relationship between linkage score and significance levels shown by Schulze and McMahon [40] (Figure 4.1) and described by Nyholt 2000 for LOD and MLS scores, and by Kruglyak *et al.* 1996 for NPL scores [41, 42]. This allowed us to retain the relative significance levels of scores within and between studies. For subsequent analysis the log of the genomic probability score (log-genomic probability score) was used. For studies with multiple analyses utilizing disparate models (parametric, non-parametric, dominant, recessive, etc), we used results from the model that produced the most significant scores.

The meta-analysis was then performed as follows:

1) A footprint for each marker within each study was determined. Each marker location and score provides a measure of linkage at specific locations for the study population. There is no information about whether the linkage signal at the marker location is maximal for the region. There is a need, however, to estimate the linkage signal in the regions intervening markers so that studies with non-identical marker sets can be combined. For the purposes of the MFLM, the signal at the location of the marker is considered to be maximal and a 'footprint' is defined around each marker to estimate what the linkage score might be for the adjacent regions based on the signal from that marker. The footprint is defined as the decaying log-genomic probability score distribution around each marker based on the HapMap recombination rates in those regions such that each footprint distribution tail reaches a score of 0 after 50 cM. One cM is equivalent to a 1% chance that a marker at one genetic locus on a chromosome will be separated from a marker at a second locus due to crossing over in a single generation. Therefore, at a distance of 50cM from the linkage marker, there is a 50% chance that recombination has occurred in the intervening region which is equal to the chance that the markers are on separate chromosomes (ie. unlinked) and therefore linkage is uninformative beyond 50 cM.

For each HapMap region within each footprint distribution, the relative informativeness (RI) of the score is also calculated. The RI is a value from 1 to 0 that decays from 1 at the marker location to 0 at 50cM from the marker location based on the recombination rate and distance. This value is later used to determine the genomic distribution when footprint distributions overlap. The RI is a measure of how much linkage information is retained from the original linkage marker at any point along its footprint, regardless of the score that the footprint represents at that same location.

To calculate the footprint distribution of scores for each marker:

a. The HapMap region overlapping a marker location is identified. The footprint score assigned to this HapMap region is the marker's log-genomic probability score (defined as the log of the genomic probability score, which is calculated based on the Shulze and McMahon [40] conversion of the actual study linkage score type to a genomic probability score). The RI value for this HapMap region is assigned a value of 1, meaning that the footprint score within this

region is close enough to the original marker that all of the original linkage information from the marker is likely to be retained.

b. The adjacent HapMap region (both upstream and downstream directions) are identified. The footprint score and relative informativeness for these regions are defined by the relative recombination distance from the original marker that the footprint is based upon. First the relative recombination rate (RecombRate) across the HapMap region is determined based on the size of the region

RecombRate = (Recombination Rate (cM/Mb) / 1,000,000) * (|EndCoord – StartCoord| + 1)

Then the footprint score for these regions is defined by adjusting the original log-genomic probability score from the marker with this recombination rate:

FootprintScore_{region} = MarkerScore * (1-(RecombRate/50))

A relative informativeness score for these regions is similarly defined:

c. This is repeated for each subsequent HapMap region, moving outward from the original marker location. The intervening recombination distance (RDist) is the sum of the recombination rates for the intervening regions:

RDist is used to adjust the footprint score and relative informativeness:

FootprintScore_{region} = MarkerScore * (1-(RDist/50)) RI_{region} = (1-(RDist/50))

Step (c) is repeated until either the RDist is \geq 50 cM or the end of the chromosome is found. This creates a decaying score distribution (footprint) around each marker along the genome. The score and relative informativeness decrease linearly as the recombination distance increases. By using the recombination rate to determine how the linkage scores decay we ensure that the score decreases more quickly in regions with higher recombination.

2) Genome-wide linkage distribution defined for each study:

Within each study, the tails of the footprints created in step 1) may overlap with each other. Therefore to create a single representative genome-wide linkage distribution for each study all the footprints are merged into a single continuous distribution. Within each study, since there is considerable overlap between footprints, the footprint score with the greatest relative informativeness is used. An example of this is shown in Figure 4.2.

3) Genome distributions for each study are combined:

The genome distributions from each individual study are combined by summing the scores from each study within each HapMap region, resulting in a final linkage meta-analysis score assigned to each HapMap region. An examples of this is shown in Figure 4.3.

4) Assign final linkage meta-analysis scores to gene and non-gene regions across the genome:

There are over 1 million HapMap regions across the genome. While using these regions facilitated incorporating HapMap recombination rates to generate final linkage meta-analysis scores across the genome, this results in unnecessary granularity as the average HapMap region is 2,768 bp wide. The general goal of linkage studies is the identification of genomic regions and genes that segregate with disease. Therefore, the human genome was separated into 54,779 gene and non-gene regions. Ensembl (NCBI35) was used to identify gene regions – defined as 1,000 bp upstream of the transcription start site to 1,000 bp downstream of the transcription stop site. Any intervening regions of the genome that were not represented by a gene region were defined as non-genic regions, and numbered starting in chromosome 1. Each gene and non-gene region was assigned the maximum final meta-analysis score from the overlapping HapMap regions.

5) Determine significance of gene and non-gene region scores

To determine the nominal significance of each gene and non-gene region a re-sampling method is employed. The original log-probability linkage scores are randomly re-assigned to marker locations, across all studies without replacement and the entire linkage meta-analysis performed on the randomized scores. The randomization analysis was performed 1,000 times, allowing nominal p-values to be assigned to each gene and non-gene region.

6) Identification of significant genomic regions

Gene and non-gene regions with a p-value of ≤ 0.05 were determined to be nominally significant. Adjacent nominally significant gene / non-gene regions were grouped to delineate extended genomic regions containing nominally significant gene and non-gene regions.

4.2.3 Schizophrenia associated genes in significant regions

To determine if there were any known schizophrenia associated genes in the significant regions, the genetic association database (GAD, http://geneticassociationdb.nih.gov/) [43] was used. A list of 143

genes having a minimum of one positive schizophrenia association was generated. Schizophrenia associated genes represented within the MFLM meta-analysis significant regions were identified. To determine if the number of schizophrenia associated genes within MFLM regions was significant, a random re-sampling analysis was performed. There were 574 unique genes within the nominally significant MFLM regions. The Ensembl database was used to generate a list of 33,046 unique human associated gene names (Ensembl 54, NCB136, June 2009). A total of 10,000 random resampling iterations were performed where 574 genes were chosen at random from a list of all human genes and the number of schizophrenia associated genes within the list was determined.

4.3 Results

4.3.1 Schizophrenia meta-analysis significant regions

Twenty-four nominally significant regions were identified. We performed a novel linkage metaanalysis using the MFLM method described above to identify genomic regions with consistent, but perhaps weaker linkage signals over numerous genome-wide linkage studies. Our analysis combined the results from 8 previous genome-wide linkage analyses with 929 families, 1,187 affected individuals, and 3,151 linkage markers (Figure 4.4 shows final meta-analysis scores across the genome), and identified 24 nominally significant regions (p <= 0.05) including 20p12.1-p11.23, 2q11.2-q14.1, 1q23.1q23.3, 6p25.3-p25.2, 9q21.13-q21.31, 3q28-q29, 4q21.1-q21.3, 16p21.1, 6p21.33, 12q24.13-q24.22, 8p21.3-p21.2, 10p15.1-p14, 9q31.2-q31.3, 2q21.2-q21.3, 4p14-p13, 14q21.3-q22.3, 3p24.3, 9q31.1, 20p12.1, 3p25.3, and 8p23.1 (Table 4.2). (There were 4 distinct significant regions found within 3q28.) Several of these regions were not found to be within or adjacent to suggestive or significant regions in the original studies (4p14-13, 8p21.3-p21.2, 8p23.1, 12q24.13-q24.22, 14q21.3-q22.3, 16p21.1). While a number of the strongest linked regions in the underlying studies were represented in the meta-analysis results, there were also a number of regions that achieved significant or suggestive linkage in the underlying studies that did not come through the meta-analysis including the 5g [37], 13g32-32 [31], 10g23 [34], 11g21 [34], 17g32.2 [33], 22g12 [16], and Xp [37]. One novel region (9g31.1) found in this meta-analysis has not been previously identified in individual studies or meta-analyses, according to the psychiatric genetics evidence project linkage database (https://slep.unc.edu/evidence/) [44] and manual literature search. There were also several regions identified in this meta-analysis that other metaanalyses did not identify, but which have been found previously in other linkage studies including 4g21.1q21.3, 4p14-p13, 9q21.13-q21.31, 9q31.2-31.3, 12q24.13-q24.22, and 14q21.3-q22.3.

4.3.2 Schizophrenia associated genes in significant regions

Regions identified by the MFLM meta-analysis are over-represented with schizophrenia associated genes. Within the 24 nominally significant regions, there are 574 genes (Table 3). Seven of these genes (IL1B, RGS4, NOS1AP (also called CAPON), NQO2, DDR1, NOS1, and ADRA1A) have at minimum one positive schizophrenia association result (from GAD, out of 143 genes with a minimum of one positive schizophrenia association [43]). This finding was determined to be significant through a random sampling analysis where 574 genes were selected from a list of all human genes (33,046 genes total based on Ensembl 54, NCB136, June 2009) 10,000 times and the number of schizophrenia associated genes determined each time, resulting in a p-value of 0.0108 for this finding.

4.4 Discussion

Massive research effort has been put towards identifying schizophrenia susceptibility genes. Traditional linkage and association studies in general have failed to consistently identify genes of interest. There are many possible reasons related to the nature of complex diseases that could explain why disease genes remain elusive, including locus heterogeneity, allelic heterogeneity, variable penetrance, epigenetics, epistasis, gene-environment interactions, and temporal gene expression, to name a few. Study size is also a factor, as increasingly larger affected populations are required to allow for the power to identify the many small risk alleles that are now thought to be contributing to disease. These previous whole genome linkage studies, however, should not be discarded, as they contain valuable family based linkage information. In individual linkage studies, regions of interest can only be determined by those that meet traditional suggestive or significant linkage criteria. However, as we now expect many genes to be of small effect size, we should take advantage of these previous linkage studies and attempt to identify linkage signals based on consistency over multiple studies while not requiring the individual linkage signals to be significant. Thus, development and implementation of a linkage meta-analysis method that takes advantage of existing linkage studies to identify new schizophrenia linkage regions and refine existing schizophrenia linkage regions based on consistency over multiple studies while not requiring the individual linkage signals to be significant. Thus, development and implementation of a linkage meta-analysis method that takes advantage of existing linkage studies to identify new schizophrenia linkage regions and refine existing schizophrenia linkage regions based on consistency over multiple studies is necessary.

One major issue for linkage meta-analyses is that available whole-genome linkage studies do not use identical linkage marker sets. To best understand how to combine markers in a way that is meaningful to the underlying genetics, the representative region for each marker must be carefully determined. Combining markers based purely on physical distance does not take into consideration spatially different recombination effects, and therefore may combine markers that do not represent linkage from the same region, which is counter-productive in that it obscures true linkage signals. Ideally, we would be able to determine the exact region of the genome an individual marker represents.

To address this, the MFLM method uses the best available recombination information to determine the region the marker is most likely to represent. Currently, this is the HapMap Recombination Rate Frequency data. The HapMap Project [28] generated a high-resolution genetic map based on millions of SNPs across the entire human genome and on sampling many individuals from multiple populations. The result is a far more comprehensive and finely-scaled estimation of positional recombination rates than previous estimates. The HapMap recombination rates represent those from the populations sampled in their study, rather than the recombination events specific to the families tested in the linkage studies, but

it allows a conservative or stringent approximation of the representative region surrounding each linkage marker. While it is possible that using the recombination rates from the HapMap project is too stringent an approximation of the recombination occurring in individual families, access to the original family data is scarce, and therefore the benefits of using the HapMap data far outweighs the alternative. This also means that the estimated marker representative regions are conservative, and therefore it is highly unlikely that linkage signals from markers will be combined between studies if they do not represent linkage from truly overlapping regions. The MFLM meta-analysis method uses the HapMap recombination rate data to determine the representative region around each marker.

The MFLM meta-analysis method uses a minimal information set (marker location and linkage summary statistic) from multiple whole-genome studies to investigate regions of the genome that show consistent, but potentially weaker linkage results over multiple studies. The studies are not required to use the same summary statistic (LOD score, p-value); the MFLM method converts each summary statistic into a genomic p-value so that they are comparable between studies in the meta-analysis. The genomic region that each linkage marker is likely to represent is determined using the HapMap recombination rates for the regions surrounding the marker. This allows overlapping marker signals to be summed across studies, and therefore regions with consistent linkage can accumulate. The MFLM method of determining the representative genomic region for each marker greatly reduces the possibility that markers not representing the same genomic region will be combined and may thereby obscure the true linkage signal for that region.

The MFLM meta-analysis method, with the incorporation of HapMap recombination rates is an attempt to improve upon existing methods. The GSMA method arbitrarily bins markers into 20-30 cM regions, and then ranks markers within each region, taking the highest rank from each study as the representative for each region. Therefore, it is highly probable that, with the GSMA method, markers are being combined that do not represent the same genomic region. In addition, the GSMA method ranks markers in relation to each other within each study in an effort to deal with studies with different summary statistics. This is useful if the expectation is that the gene or genes of interest will always be highly ranked compared to the rest of the genome; unfortunately, with a complex disease, this not always true. Ranking the markers rather than using their actual summary statistic scores obscures underlying strong results as they would not always be highly ranked with respect to other markers within each study.

The Badner and Gershon method (MSP) uses multiple different summary statistic types from different linkage studies, similarly to the MFLM method. To determine how markers from different studies can be combined, they use information from the family structure and assume that linkage evidence would be seen over 20–30 cM distances. In addition, they only combine markers across regions of this size that contain at least one score with pointwise significance (p-value < 0.01) in the original study. Unfortunately, underlying and raw data is not always available, so calculating the true recombination rate from within the family is not always possible. Also, by requiring a region to have achieved pointwise significance in at

least one study, the method ignores all regions that may have shown consistent weak linkage over all studies.

The MFLM method identified several novel regions of interest (24% of regions were novel to the underlying studies, 4% of regions were entirely novel and had not had linkage reported previously) as well as confirming a number of regions found in previous studies (71% of regions) (Table 4). Each of the existing meta-analyses used a different set of linkage studies as a starting point, and therefore it is difficult to attribute differences in the results specifically to an aspect of the methods employed. This analysis had an overlap of 7/17 studies with the 2003 GSMA study, 7/32 with the 2009 GSMA study, and 5/18 with the Badner and Gershon study. The Klei et al. 2005 study was the only study incorporated in these results that was not represented in other meta-analyses.

It is therefore encouraging to see some consistency between the results of the different meta-analysis methods. There were three regions (1q, 2q, 8p) in common between the MSP, two GSMA, and MFLM studies. Three of the corresponding four regions of nominal significance from the MFLM studies contain genes that have had at least one positive schizophrenia association study according to GAD (RGS4 and NOS1AP, IL1B, and ADR1A for 1q23.1-q23.3, 2q11.2-q14.1, 8p21.3-p21.2 regions, respectively). The remaining region that does not contain a known schizophrenia associated gene from GAD (2g21.2-g21.3) contains the 2-amino-3-carboxymuconate-6-semialdehyde decarboxylase (ACMSD) gene which is potentially of interest for schizophrenia. ACMS can be converted non-enzymatically to guinolate, a potent endogenous excitotoxin of neuronal cells which has been implicated in the pathogenesis of various neurodegenerative disorders [45]. While these genes may not have had sufficient replication of linkage and association with schizophrenia to warrant definition as schizophrenia susceptibility genes, their finding in each of the meta-analyses suggests they exhibited fairly consistent, but perhaps not significant linkage over multiple studies. There is some overlap between the underlying studies of the different metaanalyses (Table 5), and therefore it is possible that these consistent results are based on the common underlying studies. The one novel region (9g31.1) found by our analysis that has not been found in any other linkage or linkage meta-analysis contains the glutamate [NMDA] receptor subunit 3A (GRIN3A) gene. While there has been one negative and no positive association findings for GRIN3A, it is consistent with the glutamate hypothesis for schizophrenia.

Seven genes with positive association schizophrenia findings were found in the 24 nominally significant regions (p = 0.0108). Before genome wide association studies (GWAS), traditional association analyses focused on specific regions of interest. In this way, only a subset of regions that have been deemed of interest, for example from schizophrenia linkage results, have had association studies performed on them. Therefore it may seem a circular argument that we found a prevalence of associated genes in linkage regions based on meta-analysis results from existing linkage studies. This finding still has merit as seven of the 24 regions identified by the meta-analysis were not identified in the original underlying studies so would not have been the basis for fine scale mapping and positional cloning. Absent from the identified nominally significant linkage regions are regions overlapping NRG1 (8p12), DTNBP1 (6p22.3),

and DISC1 (1q42.2). There were regions identified in 8p, 6p, and 1q, respectively, however these regions were several Mb from the annotated transcriptional start and stop sites of our genes of interest. However, for the meta-analysis to identify regions of interest, they must show consistent linkage across multiple studies. While it is unknown whether the studies contain underlying low levels of linkage with these regions, consistent strong linkage signals were not shown. Across the eight studies, 8p12 (NRG1) was not identified, although there were suggestive linkage signals in two studies elsewhere on 8p. No linkage signals specific to the 1q42.2 (DISC1) region were found across the 8 studies, but one study found suggestive linkage across 1q and a second study found regions elsewhere on 1q that met significant and suggestive linkage. Similarly, for DTNBP1, the 6p22.3 region was not specifically found in any one study; however two studies found suggestive linkage across 6p and a third study found suggestive linkage elsewhere on 6p.

One of the biggest limitations for the current study or any meta-analysis is the availability of data. Generally, the more information contributing to the meta-analysis, the better the results will be. A larger number of studies with diverse sets of markers would improve results using the MFLM method.

There is some speculation that linkage studies are no longer useful with the advent of GWAS methodology. However, while GWAS methods have greater power to detect weak associations to single common DNA sequence variants, linkage analysis can detect diverse genetic effects that segregate in families, including multiple rare variants within one locus or several weakly associated loci in the same region that may be specific to that pedigree [21]. Genetic heterogeneity is a confounding factor for complex disease gene investigation for both linkage and association studies, however in linkage studies, the prevalence of genetic heterogeneity is much reduced through the use of family studies. GWAS, on the other hand, require large affected populations, and in many cases combine data from multiple different populations, which increases the probability of incurring issues related to genetic heterogeneity. The MFLM meta-analysis method is a novel whole-genome meta-analysis method that uses spatially specific recombination rate information to determine how to combine data from multiple linkage studies. By incorporating the local HapMap recombination frequency to determine how to combine scores from non-overlapping markers we are able to capitalize on the locally refined recombination data the HapMap project has accumulated. By sampling the recombination rate over smaller regions, a more detailed picture is given of recombination in the human population. The availability of the recombination rate data allows us to determine how likely two markers are to represent linkage over the same region. We used the MFLM method with existing schizophrenia linkage studies and identified regions of interest. These results can be used to formulate hypotheses and potentially perform more directed association studies for these regions, and this method could be applied to other complex disorders to identify regions of interest.

4.5 Chapter 4 Tables

Table 4.1 - Schizophrenia Whole-Genome Linkage Studies Included in Meta-analysis

Results from eight whole-genome linkage studies were included in this meta-analysis. *Publication* –the first author and year of the publication reference; # *Affected* – The number of affected individuals in each study; # *Pedigrees* – the number of pedigrees included in each study; *Output* – the type of output for each study; # *Loci Tested* – The number of markers (loci) included in each study; *Significant Regions* – identified regions that met significance criteria; Suggestive Regions – identified regions that met suggestive criteria; *Model* – the type of model used in each analysis.

Publication	# Affected	# Pedigrees	Output	# Loci Tested	Significant Regions	Suggestive Regions	Model
Brzustowicz [31]	79	22	HLOD	381	1q21-q22	1p21-13 2p23-p22 3p13 8p22 8p21 12q22-q24 13q31-q32	Dominant-Recessive (Single Point)
DeLisi [32]	132	60	LOD	407			non-parametric (Multipoint)
Klei [33]	33	30	NPL	391		3q28 17q23.2	non-parametric (Multipoint)
Levinson [34]	126	43	NPL	310	10q23 2q12-13	4q22-23 9q22 11q21	non-parametric (Multipoint)
Lindholm [35]	43	1	LOD	371		2p15 3p26.1-25.1 3p25 6p24 6q25 8p23.1 20p11.2 20q13.33	Dominant (Single Point)
Moises [36]	213	65	P values	413		6p 9 20	non-parametric (WRPC)
Paunio [37]	390	185	LOD	415	1q 2q 5q	4q 9q Xp	Dominant-Recessive (Single Point)
Schwab [38]	171	71	MLS	463		6p 10p	non-parametric (Multipoint)

Table 4.2 - Nominally Significant Regions Resulting from the MFLM

Twenty-four nominally significant regions were identified by the MFLM (ordered by their nominal significance). *Chr* – the chromosome where the region is located; *Start* – the start coordinates of the region; *End* – the end coordinates of the region; *Size* – the size of the region in base pairs; *Min Score* – the lowest final meta-analysis score within the region; *Max Score* – the highest final meta-analysis score within the region; *Max Score* – the highest final meta-analysis score within the region; *Max p-value* – the highest p-value in the region; *Cytogenic regions* – the cytogenic regions associated with the nominally significant regions; *Schizophrenia Associated Genes* – genes having a minimum of one positive association in GAD [43].

Chr	Stort	End	Size (hp)	Min	Мах	Min	Мах	Cytogenic	Schizophrenia
CIII	Start	Ella	Size (bp)	Score	Score	p-value	p-value	Regions	Associated Genes
2	101,965,870	114,915,586	12,949,716	11.00	13.56	0.001	0.026	2q11.2-q14.1	IL1B
20	15,914,710	19,862,743	3,948,033	10.48	14.42	0.001	0.048	20p12.1-p11.23	
1	155,328,991	161,259,718	5,930,727	10.05	13.72	0.002	0.048	1q23.1-q23.3	RGS4, NOS1AP
6	2,191,845	3,797,546	1,605,701	10.82	11.20	0.003	0.008	6p25.3-p25.2	NQO2
9	74,340,818	80,410,496	6,069,678	10.47	13.12	0.006	0.035	9q21.13-q21.31	
3	192,412,024	194,756,398	2,344,374	11.59	12.33	0.007	0.009	3q28-q29	
4	78,172,800	87,326,575	9,153,775	9.39	12.11	0.012	0.050	4q21.1-q21.3	
16	22,985,868	24,319,940	1,334,072	10.48	11.87	0.015	0.017	16p12.1	
6	30,907,415	31,348,834	441,419	11.19	11.99	0.019	0.042	6p21.33	DDR1
12	111,957,382	116,369,183	4,411,801	9.33	11.29	0.021	0.050	12q24.13-q24.22	NOS1
8	22,607,760	26,926,580	4,318,820	9.55	11.50	0.022	0.029	8p21.3-p21.2	ADRA1A
10	5,712,434	8,158,170	2,445,736	10.15	11.49	0.022	0.049	10p15.1-p14	
9	107,503,976	110,040,403	2,536,427	10.03	10.61	0.023	0.034	9q31.2-q31.3	
2	133,707,309	136,708,241	3,000,932	11.47	14.42	0.025	0.032	2q21.2-q21.3	
4	38,449,595	42,500,830	4,051,235	10.04	10.80	0.027	0.049	4p14-p13	
14	49,088,101	56,362,563	7,274,462	9.13	11.00	0.028	0.050	14q21.3-q22.3	OTX2*
3	16,531,226	19,553,137	3,021,911	9.85	10.03	0.030	0.034	3p24.3	
9	101,230,804	102,848,515	1,617,711	10.06	10.11	0.039	0.041	9q31.1	
3	189,605,611	190,371,465	765,854	9.83	10.34	0.041	0.050	3q28	
3	191,098,757	191,651,367	552,610	10.64	11.05	0.042	0.047	3q28	
3	191,841,654	192,024,297	182,643	10.38	10.55	0.043	0.043	3q28	
20	15,157,588	15,210,513	52,925	10.22	10.23	0.047	0.047	20p12.1	
3	9,364,127	10,341,745	977,618	9.94	10.19	0.049	0.050	3p25.3	
8	12,585,149	12,622,790	37,641	9.85	9.86	0.050	0.050	8p23.1	

*OTX2 has a positive association with bipolar disorder but has not been tested for association with schizophrenia according to GAD [43].

Table 4.3 - Genes in Significant Regions

There were 574 genes found within the significant regions. *Region* – the cytogenic representation of the nominally significant region, with the coordinates in parenthesis to differentiate between regions within the same cytogenic region; *Gene Name* – the genes found within the region.

Region	Gene Name							
1q23.1-q23.3	ADAMTS4 AIM2 APCS APOA2 ARHGAP30 ATF6 ATP1A2 ATP1A4 B4GALT3 C1orf110 C1orf111 C1orf192 C1orf204 CADM3 CASQ1 CCDC19	CD244 CD48 CD84 COPA CRP DARC DDR2 DEDD DUSP12 DUSP23 F11R FCER1A FCER1A FCER1G FCGR2A FCGR2B FCGR2C FCGR3A	FCRL6 FCRLA FCRLB FLJ42075 FP14381 HSD17B7 HSPA6 IFI16 IGSF8 IGSF9 ITLN1 ITLN2 KAT KCNJ10 KCNJ9 KLHDC9	LY9 MNDA MPZ NCSTN NDUFS2 NHLH1 NIT1 NOS1AP NR113 NUF2 OLFML2B OR10J3 OR10J5 OR10J8P OR10X1 OR10Z1	OR6K2 OR6K3 OR6K6 OR6N1 OR6N2 OR6Y1 PEA15 PEX19 PFDN2 PIGM PPOX PVRL4 PYHIN1 RGS4 RGS5 SDHC	SH2D1B SLAMF1 SLAMF6 SLAMF7 SLAMF8 SPTA1 TAGLN2 TOMM40L UAP1 UFC1 UHMK1 USF1 USP21 VANGL2 WDR42A		
2q11.2-q14.1	AC005035.2 AC007271.4 AC012360.7-2 AC108463.3 AC108938.4 AC109344.4 ACOXL ACTR3 ANAPC1 ANKRD57 BCL2L11 BUB1 C2orf40 C2orf49	CBWD1 CBWD2 CBWD3 CBWD6 CCDC138 CHCHD5 CKAP2L DKFZp686E10196 DKFZp6866K04236 EDAR FAM138A FBLN7 FHL2 FLJ38359	FOXD4L1 GCC2 GPR45 IL18R1 IL18RAP IL1A IL1F10 IL1F10 IL1F5 IL1F6 IL1F7 IL1F8 IL1F9 IL1R1	IL1R2 IL1RL1 IL1RL2 IL1RN LIMS1 LOC205251 MALL MAP4K4 MERTK MFSD9 MRPS9 NCK2 NPHP1	PAX8 POLR1B POU3F3 PSD4 RABL2A RANBP2 RGPD4 RGPD5 SEPT10 SLC20A1 SLC35F5 SLC5A7 SLC9A2 SLC9A4	ST6GAL2 SULT1C2 SULT1C3 SULT1C4 TGFBRAP1 TMEM182 TMEM87B TTL UXS1 WASH1 XXyac- YRM2039.2 ZC3H6 ZC3H8		
2q21.2-q21.3	AC010974.1 AC011755.7 AC016725.4 ACMSD	CCNT2 CXCR4 DARS	FLJ27338 FLJ43018 LCT	MCM6 MGAT5 R3HDM1	RAB3GAP1 TMEM163 UBXD2	UBXN4 YSK4 ZR/ANB3		
3p25.3	AC018506.5 AC105287.5-2 ARPC4 BRPF1 C3orf10	C3orf24 C3orf42 CAMK1 CIDEC CPNE9	CRELD1 FANCD2 FLJ35033 GHRL IL17RC	IL17RE IRAK2 JAGN1 LHFPL4 MTMR14	OGG1 PRRT3 RPUSD3 SEC13L1 SETD5	TADA3L TATDN2 THUMPD3 TMEM111 VHL		
3p24.3	DAZL	KCNH8	PLCL2	SATB1	TBC1D5			
3q28 (189.6-190.4 Mb)	AC104669.6	LPP						
3q28 (191.0-191.7 Mb)	CLDN1	CLDN16	LEPREL1	TMEM207				
3q28 (191.8-192.0 Mb)	IL1RAP							
3q28-q29	ATP13A4 ATP13A5	C3orf59 CCDC50	FGF12	HRASLS	OSTN	UTS2D		
4p14-p13	AC021860.6-1 AC021860.6-2 AC098591.4-2 APBB2 ATP8A1 BEND4	C4orf34 CHRNA9 FAM114A1 KLB KLF3 KLHL5	LIAS LIMCH1 N4BP2 NSUN7 PDS5A PHOX2B	RBM47 RFC1 RHOH RPL9 SLC30A9 TLR1	TLR10 TLR6 TMEM156 TMEM33 UBE2K UCHL1	UGDH WDR19		

Region	Gene Name						
4q21.1-q21.3	AC007163.3-1 AC021192.7-1 AGPAT9 ANTXR2 ANXA3 ARHGAP24 BMP2K BMP3	C4orf11 C4orf12 C4orf22 CCNG2 CCNI CDS1 CNOT6L COPS4	COQ2 CXCL13 ENOPH1 FAM175A FGF5 FRAS1 GDEP GK2	HELQ HNRNPD HNRPDL HPSE LIN54 MAPK10 MOP-1 MRPL1	MRPS18C NKX6-1 PAQR3 PLAC8 PRDM8 PRKG2 RASGEF1B SCD5	SEC31A SEPT11 THAP9 UNQ3028 WDFY3	
6p25.3-p25.2	BPHL C6orf145 C6orf195	DKFZp686I15217 FAM50B FLJ30534	MGC39372 MYLK4 NQO2	RIPK1 SERPINB1 SERPINB6	SERPINB9 SLC22A23 TUBB2A	TUBB2B WRNIP1	
6p21.33	C6orf15 C6orf205 CCHCR1	CDSN DDR1 DPCR1	GTF2H4 HCG27 HLA-C	POU5F1 PSORS1C1 PSORS1C2	PSORS1C3 SFTA2 TCF19	VARSL	
8p21.3-p21.2	AC051642.5-1 AC051642.5-3 AC105046.10 ADAM28 ADAM7	ADAMDEC1 ADRA1A BNIP3L CDCA2 CHMP7	DOCK5 DPYSL2 EBF2 ENTPD4 FLJ26613	GNRH1 KCTD9 LOXL2 NEF3 NKX3-1	PNMA2 PPP2R2A PRO1584 RHOBTB2 SLC25A37	STC1 TNFRSF10A TNFRSF10B TNFRSF10C TNFRSF10D	
9q21.13-q21.31	C9orf40 C9orf41 C9orf95 CEP78	CHCHD9 FOXB2 GCNT1	GNA14 GNAQ LOC642947	OSTF1 PCSK5 PRUNE2	PSAT1 RFK RORB	TLE4 TRPM6 VPS13A	
9q31.1	ALDOB C9orf125	CYLC2 GRIN3A	MRPL50	PPP3R2	RNF20	ZNF189	
9q31.2-q31.3	AC009060.7-1 ACTL7A	ACTL7B C9orf5	C9orf6 CTNNAL1	EPB41L4B IKBKAP	PALM2	PTPN3	
10p15.1-p14	AL137145.13-1 ANKRD16 ASB13 ATP5C1	C10orf18 FBXO18 FLJ16284	FLJ45983 GATA3 GDI2	IL15RA IL2RA ITIH2	ITIH5 KIN PFKFB3	PRKCQ RBM17 SFMBT2	
12q24.13-q24.22	C12orf49 C12orf52 DDX54 DTX1	FBXO21 FBXW8 HRK IQCD	LHX5 MED13L NCRNA00173 NOS1	PLBD2 RASAL1 RBM19 RNFT2	SDS SDSL SLC24A6 TBX3	TBX5 TESC TPCN1 UNQ514	
14q21.3-q22.3	AL109758.3-1 AL139099.3 AL355773.4-1 AL627171.1-1 ARF6 ATP5S BMP4 C14orf101 C14orf104 C14orf138	C14orf166 C14orf29 CDKL1 CDKN3 CGMFLM1 CHMP4B CNIH DDHD1 DLGAP5 ERO1L	FBXO34 FRMD6 GCH1 GMFB GNG2 GNPNAT1 KIAA0831 KLHDC1 KLHDC2 KTN1	L2HGDH LGALS3 MAP4K5 MAPK1IP1L MGAT2 NID2 NIN OTX2 PELI2 PLEKHC1	POLE2 PPIL5 PRO2425 PSMC6 PTGDR PTGER2 PYGL RPL36AL RPS29 SAMD4A	SAV1 SDCCAG1 SOCS4 SPG3A STYX TBPL2 TMX1 TRIM9 TXNDC16 WDHD1	
16p12.1	CACNG3 CHP2 COG7	DCTN5 EARS2 ERN2	FLJ27242 GGA2 NDUFAB1	PALB2 PLK1 PRKCB	SCNN1B SCNN1G UBFD1	USP31	
20p12.1	C20orf133						
20p12.1-p11.23	AL050321.11 BFSP1 C20orf12 C20orf179 C20orf23	C20orf72 C20orf78 C20orf79 CSRP2BP DSTN	FLJ40178 HARS2 HCG2019237 MGC44328 OTOR	OVOL2 PCSK2 POLR3F RBBP9 RIN2	RRBP1 SEC23B SLC24A3 SNRPB2 SNX5	ZNF133	

Table 4.4 - Summary of Regions of Interest from Various Schizophrenia Meta-Analyses

Twelve of the 24 regions of interest identified by this MFLM study were also found in the MSP [46], GSMA 2003 [20], and/or GSMA 2009 [21] study. Regions identified in a previous study are indicated by grey boxes with the specific region indicated in bold.

Chr	MSP Result	GSMA Result 2003	GSMA Result 2009 ("All")	MFLM Result
1	1q°	1p13.3-q23.3*, 1q23.3-q31.1 °	1p13.2-q23.3, 1p32.2-p31.1	1q23.1-q23.3
2	2q°	2p12-q22.1**, 2q22.1-q23.3*	2q12.1-q21.2, 2q21.2-q31.1, 2q33.3-q36.3	2q11.2-q14.1, 2q21.2-q21.3
3		3p25.3-p22.1*	3p14.1-q13.32	3q28-q29, 3p24.3, 3p25.3
4				4q21.1-q21.3 4p14-p13
5		5q23.2-q34*	5q31.3-q35.1, 5q35.1-q35.3	
6	6q°	6pter-p22.3*, 6p22.3-p21.1*, 6q15-q23.2°		6p25.3-p25.2, 6p21.33
7	7q°			
8	8p*	8p22-p21.1*	8p22-p12	8p21.3-p21.2, 8p23.1
9				9q21.13-q21.31, 9q31.2-q31.3 9q31.1
10		10pter-p14°	10q26.12-q26.3	10p15.1-p14
11		11q22.3-q24.1*		
12				12q24.13-q24.22
13	13q*			
14		14pter-q13.1*		14q21.3-q22.3
15	15q°	15q21.3-q26.1 °		
16		16p13-q12.2 °		16p12.1
17		17q21.33-q24.3°		
18		18q22.1-qter ^o		
19				
20		20p12.3-p11*		20p12.1-p11.23
21				
22	22q*	22pter-q12.3*		
Х				

** Most significant

* Significant

° Suggestive

Table 4.5 - Overlap between Studies

Each of the schizophrenia meta-analyses compared here used a different set of schizophrenia studies. Shown here is the number of studies that each of the meta-analyses have in common, with the percentage of overlap in parentheses.

Study	GSMA [20]	GSMA [21]	MSP [46]	MFLM
GSMA [20]		14 (44%)	9 (50%)	7 (88%)
GSMA [21]	14 (82%)		5 (28%)	7 (88%)
MSP [46]	9 (53%)	5 (16%)		5 (63%)
MFLM	7 (41%)	7 (22%)	5 (28%)	
Total Number of Studies	17	32	18	8
in Meta-analysis		52	10	5

4.6 Chapter 4 Figures



Figure 4.1 - Relationship between Linkage Score and Significance Level

Image courtesy of Schulze and McMahon 2003 [40]. The figure displays the relationship between commonly used linkage score statistics and significance level. P values for LOD scores and MLS are calculated as detailed in Nyholt [41]. P values for NPL scores are estimated using the normal approximation [42].



Figure 4.2 - An Example of Footprint and Genomic Distributions

An example of the footprint and genome distributions is shown based on data from the DeLisi *et al.* 2002 [32] study for chromosome 1. The blue lines show the footprint distributions generated by the linkage markers on chromosome 1. The red line shows the resulting genomic distribution resulting from the most informative footprint for each HapMap region.



Figure 4.3 - Schizophrenia Genomic Distributions and Final Meta-Analysis Score for All Studies on Chromosome 1

Shown are genomic distributions for chromosome 1 (black: DeLisi, purple: Paunio, dark blue: Moises, light blue: Schwab, cyan: Levinson, dark green: Brzustowicz, yellow: Lindholm, orange: Klei) and the resulting final meta-analysis scores (shown in red).



Figure 4.4 - Final Meta-Analysis P-Value Results Across the Genome

This graph plots the p-values for each genomic region across the entire genome by genomic location. Regions reaching nominal significance are shown with red diamonds. Nonsignificant regions are shown with grey circles.

4.7 References

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5 Conclusion

5.1 Summary of Major Findings

The focus of my thesis had two objectives, one was to identify potential schizophrenia candidate genes through identification of protein interactions with known schizophrenia susceptibility genes; and the second was the refinement of schizophrenia linkage regions and estimation of schizophrenia linkage across the genome by combining information from multiple whole genome linkage studies. The first objective resulted in the identification of protein interactions that form a network linking three of the best known schizophrenia susceptibility genes to proteins with cytoskeletal, transport, and transcription related functions as well as many aspects of the vesicle lifecycle. The second objective resulted in the identification rate information to combine linkage signals between linkage studies and estimate linkage across the genome, and in the refinement of existing schizophrenia linkage regions as well as the identification of a novel schizophrenia linkage regions as well as the identification of a novel schizophrenia linkage regions as well as the identification of a novel schizophrenia linkage regions as well as the identification of a novel schizophrenia linkage regions as well as the identification of a novel schizophrenia linkage regions as well as the identification of a novel schizophrenia linkage regions.

Chapters 2 and 3 described the results of investigations into the physical interactions of the schizophrenia susceptibility genes DTNBP1 and NRG1. Protein-protein interactions were investigated using IP-MS/MS. My investigation identified 83 high quality interactions with DTNBP1, including 68 novel interactions and 14 previously identified interactions involving all members of BLOC-1 and several members of the AP3 complex. Novel interactions with DTNBP1 included many interactions with the exocyst, dynactin, and CCT complexes and cytoskeletal components. Members of the exocyst and dynactin complexes have previously been identified as interacting with another schizophrenia susceptibility gene, DISC1, by Y2H. As part of the investigations described in this thesis I verified the exocyst-DISC1 and dynactin-DISC1 interactions in mammalian cells by IP-western. IP-MS/MS was used to expand the exocyst complex and dynactin complex protein-protein interaction sets, identifying 48 and 23 novel interactions for the exocyst and dynactin complex proteins, respectively. For neuregulin, 22 novel high quality interactions were identified, including 5 proteins also found as novel high quality DTNBP1 protein interacting partners, and UTRN, a protein with prior evidence of interaction with both DTNBP1 [1] and DISC1 [2]. Recently, a meta-analysis of 32 schizophrenia linkage studies confirmed linkage to the NRG1 locus [3], and a GWAS study showed association to SNPs for both NRG1 and ErbB4 [4]. Combined, these results indicate that three of the best known schizophrenia susceptibility genes participate in a common protein interaction network together with other schizophrenia associated genes including MUTED, BLOC1S3, CCT1, ERBB4, and FEZ1, producing a schizophrenia relevant network that contains highly confident connections between more schizophrenia implicated genes than others in current literature.

Chapter 3 also focused on an investigation of protein-DNA interactions for the NRG1 ICD using ChIPseq. A total of 5,674 peaks were identified with confidence, having an average width of 576 base pairs. Genes proximal to these peaks are those expected to be influenced by DNA binding at peak locations. A previous study by Bao *et al.* 2004 investigated differential gene expression due to NRG1 ICD nuclear localization and found 32 genes to be significantly differentially expressed in mouse spiral ganglion neurons. Of these genes, a significant number of genes (10 of the 32, p < 0.001) were proximal to my ChIP-seq peaks found in HEK293 cells, including DLG4, ERBB2, CDH2, DYNLL1, IGFBP2, IGFBP4, ITGAL, NME2, PTMA, and HGMN1. MATCH was used to identify TFBS within the 5,674 peak sequences and identified 164 TFBS that were significantly overrepresented. While none of the transcription factors associated with these TFBS were found as interacting proteins with the NRG1 ICD, several of the transcription factors are known to interact with NRG1 ICD interacting proteins, including AKAP8L, LMNA, PKP2, and SOX11, which were known to interact with RELA, RB1, GTF2B, and POU3F2, respectively. Of the 143 genes with at least one schizophrenia genetic association, 37 were found proximal to ChIP-seq peaks (p < 0.001), including DISC1, DTBNP1, and ERBB4.

In Chapter 4, a novel meta-analysis method called marker footprint linkage meta-analysis (MFLM) was described that incorporates the use of recombination rates as determined by the HapMap project. The MFLM method was used to combine eight whole genome schizophrenia linkage studies and resulted in the identification of 24 nominally significant regions, including 20p12.1-p11.23, 2q11.2-q14.1, 1q23.1-q23.3, 6p25.3-p25.2, 9q21.13-q21.31, 3q28-q29, 4q21.1-q21.3, 16p21.1, 6p21.33, 12q24.13-q24.22, 8p21.3-p21.2, 10p15.1-p14, 9q31.2-q31.3, 2q21.2-q21.3, 4p14-p13, 14q21.3-q22.3, 3p24.3, 9q31.1, 20p12.1, 3p25.3, and 8p23.1. Of these, 5 regions were identified that were novel to the underlying studies but have been found in other analyses, these were 4p14-13, 8p21.3-p21.2, 12q24.13-q24.22, 14q21.3-q22.3, and 16p21.1. In addition, one novel region (9q31.1) was identified that has not been identified in any other whole genome linkage study or meta-analysis to date. Within the 24 regions of nominal significance identified by the meta-analysis, there were 574 genes, five of which exist in the NRG1-DTNBP1-DISC1 protein interaction network generated based on protein interactions from the literature in combination with the results in Chapters 2 and 3 (conserved oligomeric Golgi complex subunit 7 (COG7), dynactin subunit 5 (DCTN5), transmembrane protein 33 (TMEM33), tubulin beta-2A chain (TUBB2A), tubulin beta-2B chain (TUBB2B)) (see Figure 5.1).

5.2 Providing a Protein Interaction Context for Schizophrenia

There are many hypotheses about the underlying etiology of schizophrenia, most of which can be grouped as either neurochemical related or neurodevelopmental related [5]. Neurochemical hypotheses focus on the neurotransmitter systems (dopamine, glutamate, GABAergic). Neurochemical hypotheses are substantiated by a) abnormalities found in schizophrenic brain known to be involved in neurotransmission; and b) by the mechanism of action of pharmaceutical agents used for treatment of disease and mimicking schizophrenia phenotypes [5]. Neurodevelopmental hypotheses focus on structural alterations in schizophrenia [6] that have been shown to emerge early in development [5], in particular at adolescence. A loss of approximately 30% of synapses developed during childhood in the DLPFC has been shown to be a natural part of neurodevelopment in normal adolescence. In schizophrenia, this synapse loss has been shown to be increased, up to 60% [7].

Alterations in neurotransmitter systems can include the production and metabolism, trafficking, storage, localization, compartmentalization, and availability of neurotransmitters and their receptors. Schizophrenia has been described as a disease of the synapse [8-11] and changes in neurotransmitter systems can affect synaptic plasticity and loss. The strength of synapses are reinforced through stimulation and weakened through lack of stimulation by neurotransmitters. A 281 protein NRG1-DTNBP1-DISC1 protein interaction network was generated from the interaction demonstrated within this thesis, BioGRID, String, and other literature sources (Figure 5.1). Of this 281 protein interaction network, there were 15 proteins annotated with a synapse cellular component localization in GO (CDH15, DLG4, DMD, DTNA, GRIN2B, ITSN1, LZTS1, NBEA, SNAPIN, SNTA1, SNTB1, SNTB2, SYNE1, UTRN and VAMP2, p = 0.00024 as determined by DAVID [12]) and five proteins annotated as being involved in the regulation of neurotransmitter levels biological process (GRIN2B, KCNMA1, PLDN, SNAPIN, and VAMP2 p=0.69).

The vesicle lifecycle plays an important role in the accumulation, transportation, release, endocytic recycling, compartmentalization, and storage of neurotransmitters. The overall NRG1-DTNBP1-DISC1 protein interaction network includes 24 proteins annotated as part of the vesicle cellular component ($p = 3.5 \times 10^{-6}$) and 36 proteins annotated as participating in vesicle mediated transport ($p = 1.1 \times 10^{-11}$). The BLOC1 proteins are involved in vesicle biogenesis and cargo sorting; the AP3 complex is involved in vesicle cargo sorting; the dynactin complex is involved in vesicle transportation; the exocyst complex is involved in endocytic recycling; MYO6 is involved in uncoated vesicle transportation after endocytic recycling [13] (See Figure 5.2). Disruption at any point of the vesicle lifecycle associated with neurotransmitters and their receptors could result in alterations in synapse formation, potentially leading to misconnectivity or dysconnectivity of neurons and inappropriate neuronal response to stimuli.

Neuronal physiology requires the maintenance of a highly asymmetrical shape and polarity to allow for proper neuronal function [14]. The cytoskeleton plays a key role in maintaining neuronal shape and structure. Neuronal development involves the formation of projections from the cell body (soma) outward towards other cells. These projections are called neurites and are the precursors of axons and dendrites. Dendrites can have hundreds or thousands of small membraneous protrusions called dendritic spines which transmit electric signals to the soma. In the developing brain, neurites are also formed on the leading edges of migrating neurons and operate as guides for migration [15, 16]. Cytoskeletal reorganization plays a key role in neuritogenesis [14] and is of particular importance in the synaptic plasticity of dendritic spines. Decreased dendritic spine density found in cerebral cortical pyramidal neurons in schizophrenia [17, 18]. Small, but significant reductions have been found in somal volume of neurons in the prefrontal cortex in schizophrenia patients [19, 20]. A dynamic cytoskeleton allows dendritic spines to rapidly change their volumes or shapes in response to stimuli. Cytoarchitectural abnormalities have been described in schizophrenic brain [21] including neuronal shape, loss of dendrites and spines, as well as irregular distribution of neuronal elongations [14]. Gene expression studies in

schizophrenia have implicated impairments of cytoskeletal assembly [22-24]. Differential regulation of cytoskeletal proteins has been observed in schizophrenia, including interacting proteins described in this thesis, such as TUBB2B, PLEC1, and DISC1 interacting proteins KIF21A and MAP1A [25, 26]. Each of NRG1, DTNBP1, and DISC1 has evidence of protein interactions with multiple cytoskeletal (actin and tubulin) proteins, including ACTG1 and TUBA1C for both NRG1 and DTNBP1 identified from the IP-MS/MS experiments described here and ACTA1 for both DTNBP1 and DISC1, among many others. In the 281 proteins in the overall protein interaction network 70 genes were annotated as part of the cytoskeleton cellular component ($p = 4.1 \times 10^{-22}$) and 34 genes annotated as participating in cytoskeletal organization and biogenesis ($p = 4.1 \times 10^{-10}$).

One cytoskeletal protein that is of particular interest based on my results is UTRN. UTRN is the only protein identified that has evidence of protein interactions with each of NRG1, DTNBP1 [1], and DISC1 [2]. UTRN is an autosomal homologue of DMD, either of which act as a scaffolding protein for the DPC, which is comprised of 5 classes of proteins including dystroglycans, syntrophins, dystrobrevins, sarcoglycans, and sarcospan [27]. The DPC has mainly been studied in the context of muscular dystrophies and cardiomyopathies and is critical for muscle fiber integrity by linking the actin cytoskeleton to the extracellular matrix [27, 28]. It has also been shown to have roles as a signaling complex and as a scaffold for membrane proteins. In non-muscle tissues the DPC is concentrated at membranes, suggesting involvement in signaling function, and its components have binding domains for membrane channels or transporters [27]. The DPC in the brain has evidence of involvement in synapse formation and plasticity and in neurons is located post-synaptically at inhibitory synapses, co-localizing with GABAA receptors and in excitatory neurons at the post-synaptic densities. Evidence is accumulating for involvement of neuronal cytoskeletal alterations resulting in loss of synaptic connectivity and the ability to transmit information in schizophrenia patients [14].

The various schizophrenia hypotheses cover a wide spectrum of possible insults to neuronal function including defects within neurotransmitter systems, vesicle trafficking, synapse formation, plasticity, and strength, and connectivity. The underlying functions associated with these hypotheses are not distinct from each other and impacts to one of these functions have implication for others. Changes to vesicle trafficking impacts neurotransmitter systems, which affects synapses, and in they in turn affect neuronal connectivity. All of these neuronal functions rely on the cytoskeleton. The overall NRG1-DTNBP1-DISC1 protein interaction network described here involves numerous proteins that are involved throughout the vesicle lifecycle, in neurotransmitter and synapse associated functions, and many cytoskeletal proteins. Nineteen of the proteins have had schizophrenia association studies performed on them, 10 of which have had at least one positive association found (APOE, BLOC1S3, DISC1, DTNBP1, ERBB4, FEZ1, GRIN2B, MUTED, NRG1, PRNP; according to GAD [29] and selected literature [30]). All of the 281 genes involved in the network are within a few interactions of one the three most robust schizophrenia susceptibility genes identified to date and are therefore of particular interest for involvement in future association studies.

5.3 In the Context of Recent GWAS Results

GWAS for schizophrenia are still in their early stages. Of the available GWAS, few are large enough to detect risk alleles of small effect (odds ratio < 1.5) and most are based on pooled DNA samples, which reduces detection sensitivity [31]. A few of the available GWAS results are described here in the context of my thesis.

A 2006 GWAS study of 25,000 SNPs across 14,000 genes using a 3-stage DNA pooling method on 320 European schizophrenia patients and 325 matched controls found significant association for 62 SNPs [32]. As the false positive rate was expected to be high, the 62 SNPs were then genotyped in an additional case-control sample and the most consistent effect was found associated with the PLXNA2 gene on chromosome 1q32 [32]. PLXNA2 is a member of the semaphorin receptor family, implicated in the development of axonal projections and neural regeneration [32]. The PLXNA2 ligand semaphorin-3A (SEMA3A) has been found to be increased in the cerebellum in individuals with schizophrenia [33]. PLXNA2 is necessary for signaling by class 3 semaphorins for remodeling of the cytoskeleton in neurons. Although there are no direct physical interactions that have been identified that link PLXNA2 to the NRG1-DTNBP1-DISC1 protein interaction network, it is of interest that PLXNA2 is tightly linked with the cytoskeleton.

In a 2008 GWAS study of sex specific pooled DNA for 660 cases and 2,771 controls from Ashkenazi Jewish decent using Affymetrix 500K SNP microarrays, the most significant finding was in an intron of the reelin (RELN) gene in females, which was replicated in European and Chinese populations [34]. RELN is a serine protease [35] that acts via a number of receptor-mediated pathways in neurons [36]. Loss of function mutants in both RELN and lissencephaly-1 (PAFAH1B1 or LIS1) cause lissencephaly in humans and PAFAH1B1 and disabled homolog-1 (DAB1) interact in a RELN-dependent manner [37]. PAFAH1B1 was identified as an interacting partner with the dynactin complex and has prior evidence of interaction with DISC1. RELN also shares a common biological pathway with apolipoprotein E (APOE) in that both compete to bind APOE receptors very low-density lipoprotein receptor (VLDLR) and low-density lipoprotein receptor-related protein 8 (LRP8, also called APOER2) [38]. The BACE1 protein is required for the cleavage of the APOE binding protein amyloid beta A4 protein (APP); interestingly, beta-secretase 1 (BACE1) is also involved in the proteolytic processing of transmembrane NRG1 [39].

The 2009 Kirov GWAS study used DNA pooling to analyze 574 schizophrenia patients, their parents, and 605 controls using Illumina HumanHap550 arrays and identified 40 significant SNPs, the most significant being within the coiled-coil domain-containing protein 60 (CCDC60) gene [40] of which little is known. Other significant SNPs were found in phosphoglucomutase-like protein-5 (PGM5), known to interact with UTRN and DMD, synaptophysin-like protein-1 (SYPL1), known to interact with vesicle associated membrane protein 2 (VAMP2) which interacts with the BLOC-1 complex through SNAPIN, and small G protein signaling modulator-1 (SGSM1), known to interact with ras-related protein 1B (RAB1B) and ras-

related protein 11A (RAB11A) which our data show interact with the exocyst complex and DTNBP1, respectively.

The 2009 Liu GWAS used DNA pooling to analyze 400 microsatellite markers for 119 schizophrenia patients and 119 controls from the Shandong province in China and found three significant SNPs including one within the protein jumonji (JARID2) gene located directly upstream of the DTNBP1 gene [41] (Figure 3.8A).

Overall, while no GWAS finding directly implicates any of the overall NRG1-DTNBP1-DISC1 protein interaction network members, there were a number of findings that have known connections to the overall network.

5.4 Mechanisms

While the mechanisms of action for many of the genes in the overall NRG1-DTNBP1-DISC1 protein interaction network have yet to be discovered, there are a number of hypotheses one can derive from the existing information. The protein interactions identified for the NRG1 ICD could implicate NRG1 in a number of functions. Based on the data I would hypothesize that the NRG1 ICD likely interacts with UTRN at the membrane prior to cleavage. UTRN is a scaffolding protein and member of the DPC complex that links the actin cytoskeleton to the extracellular matrix and may be involved in signaling processes. While the DPC has traditionally been discussed as a post-synaptic density protein, it is possible that it has presynaptic functions as well. Proteolytic release of the NRG1 ICD would then potentially affect its interaction with UTRN and in theory could initiate signaling, potentially to initiate NRG1 has been implicated in neural development [42], neuronal cytoskeletal rearrangement. differentiation, migration and survival [43-45], synaptic maturation and plasticity [46, 47], and myelination [48]. Many of these functions rely on cytoskeletal changes and since NRG1 has also been shown to play a role in regulation of the actin cytoskeleton [49] the novel demonstration of a NRG1-UTRN interaction provides mechanism for its affect on the cytoskeleton. It is possible that NRG1-UTRN signaling modulates cytoskeletal rearrangement and therefore could potentially play an important role in neuronal migration, synapse formation, and neurodevelopment.

The NRG1 ICD - SNX27 interaction is high confidence interation and of particular interest as SNX27 has recently been found to interact with and regulate the surface expression of Kir3 ion channels [50]. SNX27 promotes endosomal movement of Kir3 ion channels and leads to reduced surface expression, increased degradation, and smaller potassium currents [50]. Thus it is highly probable that the interaction between NRG1 ICD and SNX27 regulates a signaling cascade that directly affects neuron potentiation. This in conjunction with NRG1 activation of ErbB4, which has been shown to modulate expression of neurotransmitter receptors, could have a direct effects on synaptic plasticity and connectivity. Cleavage of the NRG1 ICD occurs in coordination with cleavage of the NRG1 ECD and thus signals from the cleavage event are translated both pre- and post-synaptically and could act to regulate synaptic plasticity.

It is highly likely that cleavage of the NRG1 ICD that leads to its nuclear localization and involvement in transcriptional regulation is part of a feedback loop, as many NRG1 ICD interaction partners and other schizophrenia associated genes, including ERBB4, were identified as proximal to ChIP-seq peaks.

DTNBP1 is well established as a member of the BLOC1 complex, and direct interaction between DTNBP1 and AP3M1 has been shown [51]. An association study of most of the AP3 complex genes (AP3M1, AP3M2, AP3D1, AP3B1, and AP3B2) was performed in a Japanese cohort. While one allele within the AP3M1 gene was found to be nominally significant and one allele in AP3B1 showed weak association, neither met multiple test correction significance after Bonferroni adjustment [51]. Unfortunately, there was no attempt to investigate potential epistatic effects between the AP3 alleles and DTNBP1 alleles. DTNBP1 is known to play a role in the vesicle lifecycle due to the AP3 and BLOC1 interactions and other evidence of DTNBP1's influence on vesicle size and number [51]. Therefore it was not surprising to find novel interactions with other complexes involved in the vesicle lifecycle. As a member of BLOC1, DTNBP1 is involved in the biogenesis of vesicles. Both BLOC1 and AP3 are involved in cargo sorting and therefore many of the weaker interactions identified for DTNBP1 may represent the proximity of DTNBP1, as a part of BLOC1, with vesicle cargo rather than an otherwise functional interaction.

DTNBP1 and the NRG1 ICD were both found to interact with several CCT complex proteins. The CCT complex is a molecular chaperone that plays an important role in the folding of proteins in the cytosol. An estimated 15% of proteins are folded with the assistance of the CCT complex, including actin and tubulin [53]. It is possible that these interactions are opportunistic as the CCT complex has binding interfaces for many proteins, however, both tubulin and actin are dependant on CCT for folding and as such, any demand for cytoskeletal changes would likely require CCT complex involvement. This dependency of the actin cytoskeleton makes interactions between the CCT complex and both DTNBP1 and the NRG1 ICD more compelling. The interaction with the NRG1 ICD is of particular interest, with its implications for synaptic plasticity and neuronal migration, as the interaction with the CCT complex could be part of a potential signaling cascade potentially initiated when the NRG1 ICD is cleaved.

These possible mechanistic implications are intriguing, but it remains to be seen if any of these hypotheses will be supported. However, my data provide new testable hypotheses about the mechanisms underlying important observations about schizophrenia pathology. Based on this, the main objective of my thesis was met and it will be interesting to observe how my results are incorporated into schizophrenia research in the future.

5.5 Implications Beyond Schizophrenia

The NRG1/DNTPBP1/DISC1 protein interaction network and the MFLM method have implications outside of schizophrenia. The majority of members of the overall protein interaction network identified in this thesis have widespread expression in many tissues. As stated previously, NRG1 has been investigated with respect to numerous different complex diseases, particularly cancer. Also included in the overall protein interaction network are APOE, APP, and BACE1, which have all shown genetic association with Alzheimer's disease. A number of proteins in the overall network have ties with the Wnt signaling pathway (DISC1 [54], SCYL2 [55]) which is known to be involved in cancer. The cellular processes associated with proteins in the overall network are fundamental to any cell (vesicle trafficking / transport, cytoskeletal regulation, and gene transcription) and therefore could contribute to other diseases in different ways dependent on the specific cellular context of the protein interaction network.

5.6 Strengths, Weaknesses, and Contributions to the Field of Study

There are a variety of strengths and weaknesses inherent in the investigations comprising this thesis. For the protein interaction investigations, the assumption was made that NRG1 and DTNBP1 are involved in schizophrenia etiology. While they are currently considered two of the best schizophrenia susceptibility genes, they have each had both a positive and association results. Regardless of their involvement in disease, the protein interactions identified contribute to our understanding of their broader function in many cell types and to the overall body of human protein interactions.

The protein interaction investigations were performed in cell lines which have had some degree of genetic modification in order to allow for maintained growth in culture. Tagged constructs were introduced to the cells so that immunoprecipitation could be performed using antibodies against the epitope tag and therefore protein levels of the gene product of interest would have been at non-physiological levels. The interactions identified from the IP-MS/MS experiments are not limited to binary interactions and may include indirect interactions. Further experimentation would be required to determine true binary The high quality protein interaction sets, however, were found in multiple replicate interactions. experiments and passed high stringency requirements. In addition, of a subset of the high quality interactions were verified using IP-western methods; therefore this set of proteins is expected to contain a majority of true interactions that have functional significance. At the outset of the IP-MS/MS experiment, members of BLOC1 were considered to be positive controls for the DTNBP1 protein interaction investigation. Not only were all members of the BLOC1 complex identified as high quality interacting proteins, multiple members of the AP3 complex were also identified, supporting evidence from the 2006 DiPietro et al. paper of an interaction between the AP3 and BLOC1 complexes [56]. Investigations of the identified interactions to validate functional relationships would be useful to support these results.

In Chapter 3, the NRG1 ICD ChIP-seq investigation identified regions of the genome that immunoprecipitate with the NRG1 ICD. The implication is that the NRG1 ICD is participating in

transcription factor complexes which bind to specific genomic locations to affect transcriptional changes. The ChIP-seq results were performed in HEK293 cells and included a significant portion of the genes whose expression was affected due to increased NRG1 ICD nuclear localization in mouse spiral ganglion neurons [57]. The overlap of these datasets is likely more significant than the data suggests as these experiments found such a degree of overlap even though the experiments were performed in different organisms. Further validation is needed to determine that NRG1 does participate in transcription factor complexes that bind DNA and affect transcriptional change as well as to determine the gene sets whose expression is modulated by NRG1.

The protein-protein and protein-DNA investigations were performed in cell lines including HEK293 cells and X57 cells. HEK293 cells are derived from human kidney and therefore it is unknown as to whether the interactions identified within this work represent true interactions that occur *in vivo* in human neurons. Interestingly, there is evidence that HEK293 cells are of neuronal origin [57]. Shaw *et al.* 2003 shows that cell lines generated through transformation with sheared adenovirus all express neuronal markers, such as neuronal filament subunits [57]. The hypothesis is that adenovirus preferentially transforms human neuronal lineage cells and it is possible that the HEK293 cell line is the result of adenovirus selectively transforming into a neuronal progenitor cell located in the kidney. X57 cells are immortalized mouse striatal cells and as such, any interactions of the transfected proteins are with mouse proteins. Thus, they may not represent interactions that occur *in vivo* in human neurons. Also, neurons grow in a specific environment with a high degree of cell-cell contact. It is unknown how the change in the external environment affects the context of protein-protein interactions within the cell. Previously, I discussed that an integral property of neurons is their ability to establish polarity to cultivate synapses with pre- and post-synaptic contexts; however, in cell lines there is no context of polarity and therefore protein interactions are potentially being compartmentalized differently within the cell and spurious interactions could result.

For the meta-analysis investigation described in Chapter 4, the MFLM method developed is the first that incorporates the use of recombination rates to determine how to combine linkage information from studies using disparate marker sets. The meta-analysis itself, however, includes only 8 whole genome schizophrenia linkage studies. Access to more linkage information, or potentially meta-analyses performed based on multiple genome linkage studies within specific population sets, would strengthen the results.

A primary aim of my thesis was to identify potential candidate schizophrenia genes. Potential candidate genes can be identified in many different ways, but the most promising candidates are those that have known functions that relate to processes previously implicated in schizophrenia. Previous studies have shown that interaction partners of known schizophrenia susceptibility genes have an increased probability of being associated with disease (e.g. ERBB4 interaction with NRG1; MUTED, BLOC1S3 interactions with DTNBP1; FEZ1 interaction with DISC1). In total, 68 and 22 novel interacting partners for DTNBP1 and NRG1 were identified, respectively. While few of these genes have been tested for association with schizophrenia, many are cytoskeletal, vesicle and transport related, or synapse associated proteins and

therefore have multiple lines of evidence implicating them in schizophrenia etiology. Similarly, the MFLM results identified a novel schizophrenia linkage region that had previously not been identified (9q31.1). This region contains GRIN3A, an NMDA receptor subtype of glutamate-gated ion channels that may play a role in the development of dendritic spines. While a recent association study showed no association for schizophrenia with common mutations in GRIN3A in a Chinese population, several rare mutations were identified that may contribute to schizophrenia pathogenesis [58]. While the MFLM method was developed for investigation of schizophrenia, the method could be applied to any complex disease providing multiple available genome wide linkage association studies are available to identify consistent regions of interest.

5.7 Future Directions

The protein interactions identified within this thesis generates pathways and networks of interest for schizophrenia. All the interactions identified can be considered new potential candidate schizophrenia genes and therefore are of interest for investigation through association studies. As was shown for BLOC1S3 in the context of DTNBP1, while the individual association with disease may not prove to be significant, there may be epistatic effects where the combined contribution to disease is more than the sum of its parts [30].

It would also be interesting to investigate the protein-DNA interactions of the NRG1 ICD in more depth and determine the transcription factor complexes that the NRG1 ICD may participate in through the investigation of protein interactions from nuclear lysate preparations, which may reveal its nuclear interactome in more depth. Further investigations into the specific genes whose expression patterns are influenced by the NRG1 ICD could be performed using qPCR and gene expression analyses and through gel shift assays to study binding to specific genomic sequences.

There is an abundance of information available that could contribute to an investigation of potential schizophrenia candidate genes and pathways. There is a need to be able to combine all available information to aid in the identification of genes and pathways of interest. The results of the meta-analysis and the protein interaction investigation described within this thesis could directly contribute to this type of analysis. The meta-analysis score results could be used to rank genes on their likelihood for involvement in disease etiology in combination with association study results. Once ranked, the genes could be put in the context of a protein interaction network to identify pathways that have accumulated low ranking genes, thus identifying pathways of interest in disease pathology.

5.8 Conclusions

After decades of linkage and association studies and even with the recent application of multiple GWAS, only a small number of robust schizophrenia susceptibility genes have been identified. While theories

and models for potential mechanisms contributing to schizophrenia abound, there has yet to emerge one unifying theme that explains this complex disorder. It fact, it is possible that schizophrenia actually represents a spectrum of disorders that each result in a similar phenotype, allowing them to be categorized by descriptive measures into what we call schizophrenia. Or perhaps we will eventually determine that schizophrenia is the result of the accumulation of multiple combinations of tens or even hundreds of risk alleles along multiple pathways and that those risk alleles can be a combination of common alleles that contribute small margins of risk, rare alleles of various risk contribution, and structural variations.

In terms of reducing the incidence of schizophrenia in the population, the application of basic research is still far off. Identification of the pathways and mechanisms involved in schizophrenia susceptibility in the future will allow for drug development to target those pathways and improve treatment and outcomes for patients. Should the model of schizophrenia as a neurodevelopmental disorder prove true, it is even possible that treatments could be designed to accommodate for the defects in neurodevelopmental pathways that contribute to disease and could thereby reduce the incidence of schizophrenia in the future. The protein interactions identified within this thesis and the network of pathways they represent bring us closer to this goal. These findings highlight a multitude of new potential schizophrenia candidate genes both through identification of novel linkage regions through schizophrenia linkage meta-analysis and identification of interacting partners of known schizophrenia candidate genes. They also provide insight into the potential functions and pathways involved in disease etiology by forming a protein interaction network that links three of the best known schizophrenia susceptibility genes.

5.9 Chapter 5 Figures



Figure 5.1 - The Overall NRG1-DTNBP1-DISC1 Protein Interaction Network

Protein interactions from Chapters 2 and 3 are expanded with select protein interactions from BioGRID, String, and other literature to generate a 281 protein interaction network. Proteins are shown as nodes and edges represent evidence of protein-protein interaction.



Figure 5.2 - Proteins of Interest Involved in the Vesicle Lifecycle from a Presynaptic Perspective

This image depicts several of the DTNBP1 and NRG1 ICD interactions (shown with grey arrows) in the context of vesicle trafficking of neurotransmitters in the presynapse. Movement is indicated by black arrows.

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6 Appendix 1 – Additional Tables

6.1 ChIP-Seq Peak Regions and Associated Genes

Table 6.1 - ChIP-Seq Peak Regions and Associated Genes

This table provides a complete list of the 5,674 ChIP-seq peak regions after the FDR threshold and simple repeat analysis. The list contains genes that overlap the ChIP-seq peak as well as the closest gene up and downstream of the peak within 50,000 bp. There are 1,035 peaks (out of 5,674 total) where there are no genes that overlap or are within 50,000 bp of the peak. The gene list was generated through the Ensembl biomart interface using the Ensembl 54, Homo sapiens genes NCBI36 database and contains 6312 unique associated gene names.

The columns are as follows, from the left: *Chr* – the chromosome location of the peak; *Start* – the start location of the peak; *End* – the end location of the peak; *Width* – the nucleotide width of the peak; *Height* – the maximum height of the peak; *Overlapping Genes Gene Name* – the names of genes found overlapping by a minimum of one basepair with the peak; *Closest Non-Overlapping Gene Downstream of Peak Gene Name* – the name of the closest gene downstream of the peak within 50,000 basepairs that has no overlap with the peak; *Closest Non-Overlapping Gene Downstream of Peak Distance* – the minimum distance between the Closest Non-Overlapping Gene Downstream of Peak and the start of the peak; *Closest Non-Overlapping Gene Upstream of Peak Gene Name* – the name of the closest gene upstream of the peak and the start of the peak; *Closest Non-Overlapping Gene Upstream of Peak Distance* – the name of the peak within 50,000 basepairs that has no overlap of the peak within 50,000 basepairs that has no overlapping Gene Upstream of Peak Distance – the name of the closest gene upstream of the peak within 50,000 basepairs that has no overlap with the peak; *Closest Non-Overlapping Gene Upstream of Peak Distance* – the name of the closest gene upstream of Peak within 50,000 basepairs that has no overlap with the peak; *Closest Non-Overlapping Gene Upstream of Peak Distance* – the minimum distance between the Closest Non-Overlapping Gene Upstream of Peak Distance – the minimum distance between the Closest Non-Overlapping Gene Upstream of Peak and the end of the peak.

	Pe	ak Information	1		Overlapping	Closest Non-overlapping Gene to Peak Region				
					Genes	Downstream	of Peak	Upstream o	f Peak	
Chr	Start	End	Width	Height	Gene Name	Gene Name	Distance	Gene Name	Distance	
1	559,565	559,981	416	20	RP5-857K21.10, RP5-857K21.11,	AC114498.2-7	1,635	RP5-857K21.14	581	
1	923,665	924,020	355	9				HES4	188	
1	988,970	989,363	393	15	AL390719.47-1,			AGRN	7,615	
1	1,229,723	1,230,504	781	9	ACAP3,	PUSL1	3,353	CPSF3L	6,324	
1	1,300,321	1,301,058	737	9	AURKAIP1,	RP5-890O3.3	2,849			
1	1,437,022	1,437,379	357	9		ATAD3A	15			
1	1,499,995	1,501,085	1,090	9	SSU72,	AL645728.31	10,857	ATAD3A	40,067	
1	1,698,946	1,699,453	507	9	NADK,			GNB1	7,137	
1	1,816,712	1,817,043	331	9		GNB1	4,357			
1	1,865,112	1,865,630	518	9				KIAA1751	8,982	
1	3,256,362	3,256,679	317	10	PRDM16,	No non-overlappi	ng genes wit	hin 50,000bp		
1	3,259,503	3,259,800	297	10	PRDM16,	No non-overlappi	ng genes wit	hin 50,000bp		
1	6,175,983	6,176,389	406	9	RPL22,	C1orf188	12,088	ICMT	27,451	
1	6,181,736	6,182,604	868	9	RPL22,	C1orf188	5,873			
1	6,326,086	6,326,555	469	9	ACOT7,	No non-overlappi	ng genes wit	hin 50,000bp		
1	8,685,957	8,686,329	372	20	RERE,	RP4-633I8.1	46,747			
1	8,805,267	8,805,737	470	9		RERE	4,981			
1	9,124,836	9,125,191	355	9				hsa-mir-34a	9,123	
1	9,164,540	9,165,204	664	9		hsa-mir-34a	30,117			
1	9,477,887	9,478,527	640	9		SLC25A33	43,588			
1	10,381,492	10,381,855	363	12	PGD,	APITD1	30,891	KIF1B	17,244	

1	11,245,105	11,245,736	631	10	FRAP1,	UBIAD1	10,130	RP4-796F18.2	15,524
1	11,320,207	11,320,625	418	9				UBIAD1	42,508
1	12,110,514	12,110,803	289	9	TNFRSF8,	TNFRSF1B	38,844		
1	12,126,117	12,126,733	616	9	TNFRSF8,	TNFRSF1B	22,914		
1	12,460,628	12,461,243	615	9	VPS13D,	No non-overlappi	ng genes wit	hin 50,000bp	
1	12,532,290	12,532,876	586	9		AL031296.1	19,228	DHRS3	17,650
1	12,600,745	12,601,201	456	12		DHRS3	364		-
1	12,602,393	12,602,739	346	11		DHRS3	2,012		
1	16.048.323	16.049.097	774	10	SPEN.	AL450998.19	1.094		
1	16.639.373	16.639.945	572	14	NECAP2.	SPATA21	2.867		
1	16 712 939	16 713 342	403	15	U1	CROCCI 2	21 248	AI 355149 13-1	33 405
1	16 744 829	16 745 213	384	14	,	AI 355149 13-2	7 331	AI 355149 13-1	1 534
1	16 758 715	16 759 088	373	14		RP5-875013.6	7 102	NBPF1	3,911
1	16,759,585	16 759 930	345	9		RP5-875013.6	7,102	NBPF1	3 069
1	16,811,020	16 812 308	1 288	9	NRPF1		1,012	CROCCI 1	5 032
1	16,812,427	16 813 156	720	16	NBPE1				4 184
1	16 813 350	16 814 245	886	10			700		3 005
1	16 815 700	16,816,754	1 045	12			3 140		5,095
1	16,015,709	16 921 192	1,045	9			7 472		7 570
1	16,020,041	10,021,102	1,141	10		INDELI	7,472	AL 137790.0-2	7,370
1	10,023,915	10,024,332	417	9	CRUCCLI,	AL 107700 0 1	401	AL13//90.0-2	4,420
1	10,043,153	10,043,300	207	9	AL 137790.0-2,	AL 137790.0-1	401	1.14	21 907
I	10,043,453	10,043,970	517	22	AL 137709 9 1	CRUCCLI	13,410	01	21,097
1	16 977 077	16 977 517	440	17	AL137730.0-1,			AL 137708 8 3	1 1 9 3
1	16,009,775	16,000,428	653	0	ESDND	AL 021020 1 2	15 220	AL 137790.0-3	23 606
1	16,900,775	16,909,420	704	10	LOFINE,	ALUZ 1920. 1-2	6 006	AL021920.1-3	23,000
1	17,005,001	17,005,609	607	10	111	ESFINE	0,900	ALUZ 1920.1-2	6 407
1	17,095,091	17,095,096	5007	10	01,			RF11-1001019.5	0,407
1	17,103,030	17,104,440	200	10	KIA A 0000		41 140		0,033
1	19,450,475	19,450,769	510	10	MRTO4.	UDR4	41,140		14,270
1	20.895.798	20.896.287	489	10	KIF17.	RP5-930J4.5	2.705		
1	21,469,258	21,469,642	384	11	ECE1.	No non-overlappi	na aenes wit	hin 50.000bp	
1	21 544 659	21 545 599	940	10	,	FCF1	75		
1	21 982 664	21 982 975	311	10		USP48	389		
1	22 138 129	22 139 002	873	.0		HSPG2	1 832		
1	22 224 388	22 224 680	292	10		AL 031281 6	5 056	FLA3A	150
1	22,903,467	22 903 988	521	10		FPHB2	5,000		100
1	23 218 212	23 218 722	510	11	AOF2	No non-overlanni	na aenes wit	hin 50 000hn	
1	23,376,717	23 377 100	383	10	, (01 2,	LUZP1	8 820		
1	23 696 228	23 696 645	417	10		AL 021154 1-1	4 215	F2F2	8 864
1	23 833 810	23 834 429	619	9	MDS2	RP11-223.115.2	34 942		0,001
1	24 269 900	24 270 185	285	10			01,012	II 22RA1	48 663
1	25 141 047	25 141 362	315	9	RUNX3	No non-overlanni	na aenes wit	hin 50 000hn	40,000
1	25,141,047	25,141,302	511	10	11011710,	SVE2	7 215	C1orf63	2 002
1	25,400,013	25,405,020	755	11	C1orf63	SVE2	14 594	AL 028711 18	46 203
1	25,440,134	25,770,349	7/2	0	MAN1C1	No non-overlappi	na aenes wit	hin 50 000hn	40,293
1	25,007,990	25,000,743	600	9	MAN1C1	SEPN1	25 577	iiii 30,000p	
1	26 107 091	26 107 691	600	9	ΡΔΕΔΗ2	SCARNA17	20,077		
1	26 107 902	20,197,001	164	14	1 /1 /1 /2,		1,403		
1	26 210 204	26 211 100	-10 1	9	וואוח		12 676		
1	20,310,304	20,011,100	1 200	9	ZNE502		40,070	CPPP1	6 000
1	20,300,095	20,303,035	1,200	10	CCDC24	AL 255977 25	11 240		20,990
1	20,434,075	20,434,492	417	13		AL300077.20	11,340	CAISFER4	32,455
1	20,737,370	20,730,347	977	9	RESONAL,	RF11-49210119.1	10,242		10.011
1	20,019,774	20,020,444	1 250	10			20,150	RP11-4921019.5	19,011
1	20,091,354	20,092,013	1,209	12		ARIDIA No pop overlanni	2,490	hin EQ QQQhn	
1	20,090,994	20,097,075	100	9		No non-overlappi	ng genes wit	hin 50,000bp	
1	21,298,222	21,298,620	398	9	SLUGAI,	No non-overlappi	ng genes wit	hin 50,000bp	
1	27,298,740	27,299,092	352	9	SLUYAT,	No non-overlappi	ng genes wit	qauuu,uc niin	
1	27,521,003	27,521,550	547	9	INENI222,	Ub	2,747	AL 000 (00 / 0	4 000
1	27,565,596	27,566,281	685	9	MAP3K6,	14/4 0 5 0		AL663123.1-3	1,320
1	27,689,438	27,690,050	612	9		WASE2	182		1
1	27,717,315	27,717,674	359	9	411504	WASE2	28,059	AHDC1	15,459
1	27,774,206	27,774,712	506	9	AHDC1,	0045111	• ·= ·	FGR	36,678
1	28,029,661	28,030,021	360	13	PPP1R8,	SCARNA1	3,478	U6	5,920
1	28,113,448	28,114,214	766	9	RPA2,	SMPDL3B	19,877	C1orf38	27,665

1	28,304,225	28,304,576	351	9		RP5-1053E7.2	4,261		
1	28,447,124	28,447,482	358	9			, -	ATPIF1	9,928
1	28 780 824	28 781 133	309	12	SNHG12	SNORA16	671	TRNAU1AP	3 181
1	28 847 740	28 848 358	618	12	U111	TAF12	5 568		0,101
1	29,380,762	29 381 341	579	15	SFRS4	174 12	0,000	MECR	10 631
1	29,401,939	29 402 463	524	10	MECR	SFRS4	20 991	MEOR	10,001
1	30 100 825	30 101 731	906	9	MEOR,	AI 645944 11	28,605		
1	30 964 528	30,965,007	470	11	ΜΔΤΝ1	/ LOHOOHH. 11	20,000		12 896
	00,004,020	50,505,007	475		AI 137857 29				12,000
1	31 836 183	31 836 499	316	9		HCRTR1	19 389	TINAGI 1	10.311
1	32 485 205	32 485 774	569	9	FAM167B	ICK	3 653		,
1	33 275 014	33 275 378	364	10	AK2	AL 020995 14	7 250		
1	33 710 486	33 711 341	855	9	7.5CAN20	AL 138837 12	30 187	CSMD2	40 855
1	35,806,835	35 807 798	963	a	200, 1120,	TEAP2E	3 760		1 872
1	36 387 680	36 388 187	507	11			5,766	NODI	1,072
1	36 624 264	36 625 089	825	a	11011100,	STK40	180	LSM10	6 529
1	36 702 347	36 702 752	405	12	MRPS15	011040	100	CSF3R	1 479
1	37 118 034	37 118 668	634	9	GRIK3	No non-overlanni	na aenes wit	bin 50 000bn	1,475
1	38 098 246	38 008 722	476	9	Ortino,	MTE1	367		234
1	38 228 203	38 228 702	580	1/	SE3A3		020	FHI 3	6 230
1	30,220,203	30,220,792	380	14		00	8 4 4 0	TTILS	0,209
1	40.083.812	40.084.400	678	12		DD1 118 121 24	40,557		35 335
1	40,003,012	40,004,490	010	12			49,007		40.000
1	40,139,950	40,140,763	210	12	IVITCLI,		10,100		42,300
1	40,105,329	40,105,041	029	9		MITCLI	25,055		17,506
1	40,495,974	40,496,902	920	10	ZIMPSTE24,		E 056	RP 1-39G22.4	4,029
1	40,576,873	40,577,413	540	9	AL 024200 4 2	RP1-228H13.1	5,056		
1	40,929,512	40,930,180	608	1.1	ALU31289.1-2,	RINS3	25,597		
1	41 625 451	41 626 547	1 006	0	NETO,			EOYO6	3 602
1	41,020,401	41,020,347	1,090	9			1 201	FUAU0	3,002
1	42,100,100	42,100,002	410	9		HIVEF3	1,201		10.051
1	42,037,339	42,037,005	440 500	9	RIIVINLA,	DDCC	1 420	RP11-157D16.2	12,001
1	42,092,437	42,092,945	400	9			1,430		
1	42,094,307	42,094,900	421	10	PPCS,		42		
1	43,005,430	43,005,692	262	10			117		45.000
I	43,410,022	43,410,091	009	10	EDINA IBPZ,	55_IRNA	23,904	FAIVITOSA	15,300
1	13 528 058	13 520 503	545	0	WDIX05,	C1orf210	5 121		
1	43,320,330	40,020,000	853	13		01011210	5,121	EDI3	6 083
1	44,431,434	44 643 700	614	10	DNE220	EDI3	10 560		14 013
1	44,045,095	44,043,703	473	10	C1orf228 115		43,503	115	9.036
1	44,959,605	44,900,278	473	10	01011220, 03,	115	2 167	00 C1orf228	9,030
1	44,971,090	44,972,000	686	9	KIE2C	115	2,107	01011220	7,740
1	45,024,363	45,024,650	206	10	RI 20, RESTA	DD11 260E10 4	5 3 90	DDS9	7 3 25
1	45,024,303	45,024,059	290	10		RF11-2091 19.4	9,309	NF 30	7,525
1	45,759,022	45,700,407	704	13			28 441	DD4 607E16 1	18 220
1	45 822 012	45 822 105	104	11	NASP		20,441	ΔKR1A1	1/ 605
1	47 412 504	40,020,400	201	11	1101,	DD1 19D14 2	0.205		7 060
1	47,410,004	47,410,000	301	40	FOYD2	INF 1-10D14.2	9,323		1903
1	47 745 227	47 7/5 701	440	10	1 0/102,	RP4-666022 1	8 600	AL 356/58 12	10,000
1	51 171 150	51 /7/ 201	+94 70F	9	DNE11	ΔΙ 162/20 15 2	0,009	ALJJU4J0.1J	4,009
1	52 271 144	52 272 246	1 175	9	TYNDC12	AL 102430.10-2	4,040	SPD out arch	36 011
I	52,271,141	52,212,310	1,175	9	KTI12	DTFJL4	22,009		30,044
1	52 203 675	52 204 181	506	10	1X1114,	TXNDC12	10		
1	53 080 010	53 081 831	012	10	770114		37 447	7VG11B	17 006
1	53 150 582	53 160 212	620	10		SCP2	5 210	RP4-631H13.6	726
1	54 076 226	54 077 000	770	12	TMEM/8	RP4_65/H10.2	2,310	N 4 -031113.0	120
1	54 052 055	54 054 220	112	12		111	2,101	C1orf175	5 100
1	55 102 196	55 102 520	224	10	· · · · · · · · · · · · · · · · · · ·		26 533	0101173	0,420
1	50,192,100	50,192,520	254	10			20,000	AL 136005 44 0	22 005
1	50,020,324	59,020,003	359	11	JUN,		24 044	AL 130903.11-2	<i>აა,905</i>
1	50,054,398	59,055,003	600	9	FCCV	JUN No pop overlars:	31,811	hin EO OOOhn	
1	50 007 600	50 000 010	207	9	FCCV	No non-overlappi	ng genes wit	hin 50,000bp	
1	09,997,092	59,998,019	321	11	FGG1,	No non-overlappi	ng genes wit		40.400
1	61,002,000	61 000 404	404	9			10 400	INFIA	48,430
1	01,982,089	01,982,431	342	12	INAUL,		18,406		
1	03,555,179	v3,555,540	361	9		LOYD3	5,778		

1	63,761,350	63,761,739	389	17	ITGB3BP,	DLEU2L	25,484		
1	62 092 270	62 092 766	406	0	EFCAB7,	POP1	20 515	AL 161742 7 1	12 200
1	64 592 607	03,963,700	490	9		No non overlenni	20,010	AL101742.7-1	43,200
1	04,363,097	04,564,200	503	9		No non-overlappi	ng genes wit	hin 50,000bp	
1	00,101,000	66,152,000	347	9	PDE4B,	No non-overlappi	ng genes wit	hin 50,000bp	
1	66,509,435	00,509,874	439	9	PDE4B,	No non-ovenappi	ng genes wit	nin 50,000p	
1	67,163,660	67,164,054	394	10	MIER1,	WDR78	502		
1	67,168,172	67,168,664	492	12	MIER1,	WDR78	5,014	04 444	07.504
1	67,292,609	67,292,946	337	11	SLC35D1,	41 4000 40 05 4	4.040	C10ff141	37,501
1	67,432,206	67,432,566	360	9	IL23R,	AL109843.25-1	1,849		
1	67,669,166	67,669,578	412	10		SERBP1	455		
1	67,670,029	67,670,369	340	9		SERBP1	1,318		
1	67,938,834	67,939,622	788	10				GNG12	115
1	68,070,111	68,070,786	675	9	GNG12,	No non-overlappi	ng genes wit	hin 50,000bp	
1	68,468,574	68,468,974	400	9	GPR177,	hsa-mir-1262	46,693	RP11-518D3.4	11,771
1	68,470,199	68,470,530	331	10	GPR177,	hsa-mir-1262	48,318	RP11-518D3.4	10,215
1	68,735,272	68,735,584	312	14	DEPDC1,	RPE65	47,042	RP4-694A7.3	17,062
1	70,592,819	70,593,367	548	13	ANKRD13C,	No non-overlappi	ng genes wit	hin 50,000bp	
					HHLA3,		ľ		
1	71,047,441	71,047,687	246	10				PTGER3	42,937
1	74,971,109	74,971,867	758	9	CRYZ, TYW3,	AC091611.5	10,305		
1	81,629,356	81,629,733	377	9	LPHN2,	RP11-159J16.1	34,996		
1	82,039,213	82,039,974	761	9	LPHN2,	No non-overlappi	ng genes wit	hin 50,000bp	
1	85,514,566	85,515,482	916	9	BCL10,	C1orf52	16,623	Y_RNA	11,893
1	85,819,350	85,819,854	504	9	CYR61,	SNORD81	10,697		
1	87,152,027	87,152,464	437	11	RP4-604K5.1,	HS2ST1	455		
1	87,152,477	87,152,732	255	9	RP4-604K5.1,	HS2ST1	187		
1	87,153,366	87,154,241	875	9	HS2ST1,	RP4-604K5.1	671		
1	87,369,928	87,370,612	684	9	HS2ST1,	AL139139.9-2	18,957		
					AL139139.9-1,				
1	89,763,450	89,763,863	413	11	LRRC8B,	No non-overlappi	ng genes wit	hin 50,000bp	
1	91,260,111	91,260,874	763	9	ZNF644,	RPL5P6	1,190		
1	91,625,229	91,625,769	540	235	HFM1,	No non-overlappi	ng genes wit	hin 50,000bp	
					AC098691.2,				
1	92,536,635	92,537,026	391	11	GLMN,	RPAP2	167		
1	93,022,886	93,023,873	987	12	EVI5,	RP11-330C7.4	35,411	RP11-330C7.1	27,789
1	93,069,950	93,070,571	621	11	RPL5,	SNORD21	4,863	FAM69A	9,772
1	93,086,356	93,086,710	354	9	FAM69A,			SNORA51	2,029
1	93,317,043	93,317,669	626	13	MTF2,	No non-overlappi	ng genes wit	hin 50,000bp	
1	93,583,850	93,584,404	554	10	DR1,	Y_RNA	39,452	RP4-713B5.2	38,228
1	93,845,578	93,846,092	514	9	BCAR3,	No non-overlappi	ng genes wit	hin 50,000bp	
1	94,085,546	94,086,018	472	12		BCAR3	252	hsa-mir-760	491
1	94,117,160	94,117,662	502	9	DNTTIP2,			GCLM	7,516
1	95.061.253	95.061.647	394	9	SLC44A3.	No non-overlappi	na aenes wit	hin 50.000bp	
1	99.883.816	99.884.768	952	9	PALMD.	No non-overlappi	na aenes wit	hin 50.000bp	
1	100.087.803	100.088.419	616	9	AGL.			RP4-58106.1	6.898
1	100.370.859	100.371.570	711	11	SASS6.			LRRC39	15.427
-		,,			CCDC76,				· - , · - ·
1	100,487.233	100,488.327	1,094	9	DBT, RP11-	RTCD1	16.024	RP11-305E17.5	35.419
	, _ ,	,	,		305E17.4,		.,		,
1	107,914,411	107,914,820	409	17				AC114491.1	164
1	107,914,835	107,915,234	399	13	AC114491.1,			VAV3	73
1	109,090,458	109,091,009	551	10	STXBP3,			FNDC7	3,570
1	109,419,978	109,420,534	556	10	TAF13,	TMEM167B	11.872	RP5-1065J22.7	26,723
1	109,444,030	109,444,543	513	10			,	RP5-1065J22.7	2,714
1	109,621,466	109,621.828	362	10				CELSR2	1.565
1	109,770.563	109,771.061	498	11	PSMA5.	SORT1	28.477		,
1	109,837.950	109,838.821	871	11	CYB561D1.		.,	ATXN7L2	1.001
1	109.892 523	109.893.030	507	9	GNAI3.			GPR61	2 545
. 1	109 960 852	109 961 152	300	9		AMPD2	2 830		_,010
1	109 965 145	109 965 498	353	a	AMPD2	GNAT2	7 917		
1	110 328 501	110 329 101	510	a 3	AHCYL1	FAM40A	46 621		
1	110 656 696	110 657 010	323	10		RBM15	21 020	SNORA25	30 04/
1	112 001 468	112 001 764	206	10		C1orf183	7 020		00,044
1	113 018 359	113 018 050	502	12	MOV10	0101100	1,523		2 504
1	110,010,000	110,010,000	332	9	1110 110,	1			2,004

1	114,690,658	114,691,029	371	11				TRIM33	45,893
1	114,855,299	114,855,703	404	10	TRIM33,	RP11-343L14.2	24,436	Y RNA	20,322
1	115.101.934	115.102.342	408	14	CSDE1.	NRAS	40.896		11.281
1	115 994 037	115 994 323	286	11	VANGI 1	SNORA42	27 888	SRP euk arch	43 121
1	117 466 124	117 466 623	499	10		TRIM45	115		,
1	118 098 137	118 098 578	441					AL 390877 1	23 654
1	118 272 966	118 273 537	571	9	GDAP2	WDR3	377	1200001111	20,001
1	141 831 981	141 832 690	709	14	00/11/2,	No non-overlanni	na aenes wit	hin 50 000hn	
1	1/1 838 886	1/1 830 732	846	11		No non-overlappi	ng genes wit	hin 50,000bp	
1	141,030,000	141,033,732	404	11		No non-overlappi	ng genes wit	hin 50,000bp	
1	141,040,700	141,047,234	494	11		No non-overlappi	ng genes wit	hin 50,000bp	
1	141,047,409	141,040,070	209	10		No non-ovenappi	ng genes wit	nin 50,000bp	
1	141,851,038	141,851,377	339	12		No non-overlappi	ng genes wit		
1	141,861,065	141,861,460	395	11		No non-overlappi	ng genes wit	hin 50,000bp	
1	142,120,105	142,120,934	829	22		BX5/16/2.6	33,723	BX5/16/2.8	32,372
1	142,124,001	142,124,458	457	23		BX5/16/2.6	37,619	BX5/16/2.8	36,268
1	142,124,703	142,125,480	777	10		BX571672.6	38,321	BX571672.8	36,970
1	142,375,717	142,376,010	293	11		No non-overlappi	ng genes wit	hin 50,000bp	
1	142,720,807	142,721,396	589	12	SRGAP2P2,	No non-overlappi	ng genes wit	hin 50,000bp	
1	142,721,400	142,721,695	295	9	SRGAP2P2,	No non-overlappi	ng genes wit	hin 50,000bp	
1	142,721,816	142,722,308	492	10	SRGAP2P2,	No non-overlappi	ng genes wit	hin 50,000bp	
1	142,723,399	142,724,477	1,078	12	SRGAP2P2,	No non-overlappi	ng genes wit	hin 50,000bp	
1	143,240,493	143,240,953	460	9		U1	4,442		
1	143,597,535	143,598,243	708	9	PDE4DIP,	No non-overlappi	ng genes wit	hin 50,000bp	
1	143,634,996	143,635,400	404	10	PDE4DIP,	U2	20,629		
1	143,642,713	143,643,092	379	12	PDE4DIP,	U2	12,937		
1	143.643.170	143.643.679	509	18	PDE4DIP.	U2	12.350		
1	143.644.206	143.644.513	307	9	PDE4DIP.	U2	11,516		
1	143 710 062	143 710 489	427	9	PDF4DIP	No non-overlappi	na aenes wit	hin 50 000bp	
1	143 734 263	143 735 227	964	9	PDF4DIP	No non-overlappi	na aenes wit	hin 50 000hp	
1	143 739 607	143 740 421	814	9		No non-overlappi	ng genee wit	hin 50,000bp	
1	143 750 257	143 750 560	303	10		No non-overlappi	ng genes wit	hin 50,000bp	
1	143 750 651	143 752 102	1 4 5 1	10		No non-overlappi	ng genes wit	hin 50,000bp	
1	143 752 167	143,752,102	420	10		No non-overlappi	ng genes wit	hin 50,000bp	
1	143,752,107	143,732,507	420	10			27 215	nin 30,000p	
1	143,709,049	143,770,009	1,040	10		SEC22B	37,213		
1	143,765,907	143,700,720	701	11		SECZZB	21,170		
1	143,767,012	143,767,720	708	12	PDE4DIP,		20,164		
1	143,788,902	143,789,504	602	9			1,350		
1	143,799,102	143,800,192	1,090	9		SEC22B	7,712		
1	143,802,388	143,802,800	412	9		SEC22B	5,104		
1	143,803,370	143,804,143	773	13		SEC22B	3,761		
1	143,807,612	143,808,140	528	12	SEC22B,	PDE4DIP	20,060	AL359758.15-1	42,242
1	143,813,871	143,814,597	726	9	SEC22B,	PDE4DIP	26,319	AL359758.15-1	35,785
1	143,821,938	143,822,411	473	9	SEC22B,	PDE4DIP	34,386	AL359758.15-1	27,971
1	143,823,594	143,823,902	308	10	SEC22B,	PDE4DIP	36,042	AL359758.15-1	26,480
1	143,826,736	143,827,598	862	11	SEC22B,	PDE4DIP	39,184	AL359758.15-1	22,784
1	143,997,294	143,997,579	285	10	NOTCH2NL,	NBPF8	3,550	AL592307.36-1	8,436
1	144,106,564	144,107,128	564	9		HFE2	17,500	U1	12,287
1	144,107,810	144,109,413	1,603	9		HFE2	15,215	U1	13,533
1	144,110,443	144,110,857	414	16		HFE2	13,771	U1	16,166
1	144,166,656	144,167,126	470	9				POLR3GL	467
1	144,286,918	144,287,506	588	9	PIAS3,			ANKRD35	7,035
1	145,022,338	145,022,971	633	10	RP11-325P15.3,	RP11-325P15.2	586	U1	4,253
					U1,				
1	145,110,234	145,111,192	958	11	PRKAB2,	AL356378.17-1	5,116		
1	145,183,468	145,183,843	375	9	CHD1L,	FMO5	19,899	RP11-337C18.7	20,904
1	146,203,801	146,204,352	551	9			, -	U1	1,270
1	146,273,107	146,273.836	729	9	U1,	RP11-495P10.4	16.354	AL592207.9-4	15.565
1	146.292 153	146.292 530	377	9	AL592207.9-5		,	U1	8 596
1	146 608 131	146 608 604	473	12	U1			NBPF10	8 269
1	147 117 680	147 118 054	374	12	- ',	RP11-14N7 3	2 708	RP11-763R22 7	2 373
1	147 104 512	147 10/ 072	450	0	AL 663102 4	5S rRNA	1/ 507	DRD5P2	2/ 202
1	147 / 20 06/	147 /00 0/7	202	9	111	AL 356057 27 F	11 210	AL 356057 27 /	10 250
1	147 404 04 4	147 404 200	270	10	01,	111	11,319	ALJJUJJ1.21-4	49,009
1	147 564 405	147 561 404	3/0	9		AL 256057 07 7	109		
I	147,001,125	147,001,484	228	13		ALJJU931.21-1	1,071		

1	148,123,718	148,124,161	443	9	HIST2H2BE,	BOLA1	949	HIST2H2AB	1,537
1	148,936,114	148,936,447	333	10	GOLPH3L,	U6	4,519	HORMAD1	713
1	149,218,512	149,218,898	386	10		ANXA9	2,280		
1	149,234,762	149,235,123	361	9	FAM63A,			ANXA9	31
1	149,286,567	149,287,063	496	10	BNIPL, C1orf56,			CDC42SE1	3,010
1	149,309,345	149,310,429	1,084	10	GABPB2,			MLLT11	1,752
1	149,404,941	149,405,334	393	14	LYSMD1,			TMOD4	3,753
					SCNM1,				
1	149,429,017	149,429,429	412	9	VPS72,	PIP5K1A	8,223		
1	149,493,351	149,493,830	479	11	PSMD4,			PIP5K1A	4,722
1	149,520,392	149,521,332	940	9		ZNF687	80	PI4KB	9,705
1	149,610,948	149,611,393	445	9	SELENBP1,	RFX5	24,522	POGZ	30,431
1	150,148,360	150,148,898	538	10	THEM4,			AL450992.4	38,127
1	150,183,705	150,184,449	744	9				AL450992.4	2,576
1	151,910,204	151,910,648	444	14		ILF2	101	SNAPIN	9,275
1	152,202,234	152,202,772	538	9	SLC39A1,	CREB3L4	4,231		
1	152,229,732	152,230,307	575	10	RPS27,	RAB13	4,302	NUP210L	1,483
1	152,511,117	152,512,079	962	9	HAX1,			UBAP2L	1,098
1	152,797,740	152,799,094	1,354	10	UBE2Q1,	CHRNB2	7,787		
1	153,289,599	153,290,150	551	9	DCST1,	ADAM15	236		
1	153,317,856	153,318,336	480	9	EFNA3,			EFNA4	9,205
1	153,406,015	153,406,506	491	9		TRIM46	6,464	KRTCAP2	2,003
1	153,429,847	153,430,350	503	10		MUC1	517	THBS3	1,655
1	153,497,993	153,499,501	1,508	9	SCAMP3, CLK2,	C1orf2	6,095		
1	154,333,021	154,333,378	357	11	LMNA,	MEX3A	14,608	AL355388.30	19,152
1	154,449,648	154,450,139	491	10	PMF1,			SLC25A44	438
1	154,452,728	154,453,364	636	159	PMF1,			AL135927.14-2	1,549
1	154,518,155	154,518,873	718	11	SMG5, C1orf85,	TMEM79	490		
1	154,520,978	154,521,290	312	10	C1orf85,	SMG5	1,738		
4	454 574 005	454 574 000	004	0	TMEM79,	DUDO	00 700	TN/51/70	45.077
1	154,574,235	154,574,899	664	9	CCI3, Clorf192	RHBG	30,728	IMEM/9	45,377
1	154 740 473	154 740 072	400	0	01011102,	MEE2D	3 3 2 0		
1	154,740,475	154,838,241	552	10	СРАТСНИ		5,520		6 974
1	154 896 264	154 896 686	422	9				BCAN	325
1	154 897 651	154 898 108	457	9				BCAN	1 712
1	154 965 132	154 965 694	562	9	ISG20L2			AL 590666 8	3 911
•	101,000,102	10 1,000,00 1	002	Ū	C1orf66,			/ 2000000.0	0,011
1	155,003,247	155,004,013	766	13	PRCC,	HDGF	14,383	C1orf66	29,882
1	155,465,948	155,466,257	309	9		No non-overlappi	ng genes wit	hin 50,000bp	
1	157,377,874	157,378,278	404	10		CADM3	29,762		
1	158,152,730	158,153,047	317	9				TAGLN2	1,474
1	158,159,337	158,160,534	1,197	9	TAGLN2,			IGSF9	2,919
1	158,162,058	158,162,494	436	13		TAGLN2	150	IGSF9	959
1	158,247,375	158,247,757	382	9		RP11-226L15.1	8,957		
1	158,268,765	158,269,375	610	9		PIGM	360	KCNJ10	5,282
1	158,314,987	158,315,309	322	11		KCNJ9	2,675		
1	158,442,272	158,442,591	319	9	PEA15,			CASQ1	3,974
1	158,447,702	158,448,043	341	11	PEA15,			WDR42A	4,086
1	158,579,168	158,580,236	1,068	9	COPA, NCSTN,	Y_RNA	16,538	RP11-179G5.4	25,048
1	159,390,152	159,390,616	464	9	UFC1,	USP21	5,262		
1	159,438,530	159,438,909	379	12	NDUFS2,	ADAMTS4	3,061		
1	159,550,331	159,550,787	456	11		SDHC	3		
1	159,635,650	159,636,309	659	10		U6	1,394		
1	159,658,257	159,658,679	422	11				AL592295.25-2	900
1	159,664,285	159,664,858	573	11				AL592295.25-2	6,928
1	159,767,321	159,767,711	390	9				HSPA6	4,016
1	159,776,519	159,776,958	439	9		RP11-5K23.3	1,945	FCGR3A	1,221
1	159,857,781	159,858,191	410	10		RP11-25K21.5	1,782	FCGR3B	1,419
1	160,002,462	160,003,251	789	11	ATF6,			DUSP12	8,889
1	161,083,366	161,083,676	310	11	RP11-331H2.4,			C1orf110	4,054
1	161,558,029	161,558,508	479	15	NUF2,	No non-overlappi	ng genes wit	hin 50,000bp	
1	163,493,752	163,494,123	371	11	LMX1A,	No non-overlappi	ng genes wit	hin 50,000bp	
1	163,867,644	163,868,012	368	9	MGST3,	RP11-466F5.3	39,105	ALDH9A1	30,061
	400 000 000	163 934 307	719	11		AI 451074 13-1	304	1	

1	164.505.633	164.505.843	210	9				AL596087.11	5.810
1	165 111 858	165 112 290	432	11	TADA1I			RP1-9F21 5	6 787
1	165 455 660	165 456 583	014	0	TABATE,		161		0,101
1	165 509 900	165 500 402	504	3		No pop ovorloppi	ng gapaa wit	hin 50 000hn	
1	105,506,699	105,509,403	304	9	FUUZF1,		ng genes wit		6.966
1	105,769,501	165,770,011	450	9			0.000	CREGI	0,800
1	165,950,373	165,951,136	763	13		MPZL1	6,690	RCSD1	8,264
1	165,951,264	165,951,624	360	13		MPZL1	6,202	RCSD1	9,155
1	166,461,557	166,462,029	472	12	SFT2D2,			RP1-69E11.3	10,043
1	168,029,876	168,031,241	1,365	9	C1orf156,	No non-overlappi	ng genes wit	hin 50,000bp	
					C1orf112,		1		
1	168,129,105	168,130,095	990	10	SCYL3,			AL031297.4-2	15,221
1	168,437,461	168,437,777	316	11				RP11-297H3.2	8,998
1	173,235,125	173,236,395	1,270	9	CACYBP,			Z99127.2	2,737
1	173,265,492	173,265,796	304	10		MRPS14	6,308		
1	175,184,676	175,185,022	346	9	ASTN1.	No non-overlappi	na aenes wit	hin 50.000bp	
1	176 288 787	176 289 097	310	12	,	AL 359075 15	15 079		
1	176 778 222	176 778 815	503	. <u> </u>	RP5-000P15 2	5S rRNA	17 856	C1orf49	10 906
	110,110,222	170,770,010	000	5	C1orf220		17,000	0101143	10,000
1	177 464 419	177 464 876	457	Q	ARI 2			RP11-345118 4	6 536
1	170 110 205	170 110 701	506	14			4 669	1111-040110.4	0,000
1	170,110,223	170,110,731	500	14	TURTAIFT,		4,000	him 50 000hm	
1	179,546,334	179,546,684	350	9		No non-overlappi	ng genes wit	nin 50,000p	
1	181,024,795	181,025,646	851	9	NPL,	DHX9	49,428		
1	181,278,353	181,278,748	395	10	LAMC1,	No non-overlappi	ng genes wit	hin 50,000bp	
1	181,706,926	181,707,274	348	12		SMG7	983		
1	181,707,538	181,708,002	464	20		SMG7	255		
1	181,708,314	181,708,732	418	9	SMG7,	No non-overlappi	ng genes wit	hin 50,000bp	
1	182,384,146	182,384,451	305	10				Y_RNA	23,020
1	182.771.811	182.772.384	573	9	C1orf21.	GS1-115G20.2	29.884	_	
1	184 366 247	184 366 587	340	9	HMCN1	No non-overlappi	na aenes wit	hin 50 000bp	
1	191 348 971	191 349 648	677	9		GLRX2	7 104		
1	101 357 331	101 358 132	801	10	CDC73	hsa-mir-1278	14 124		29 801
1	101,007,001	101,050,102	300	10		No non ovorlanni		hin 50 000hn	20,001
1	194,959,009	194,959,479	390	9	orn,		ng genes wit		0 404
1	195,722,091	195,723,077	300	9		110	44.470	CKBI	0,404
1	198,264,719	198,265,277	558	14	NR5A2,	U6	14,173		
1	198,274,859	198,275,243	384	9	NR5A2,	AC096633.2-1	14,569		
1	199,597,332	199,597,734	402	10	TNNT2,			LAD1	18,859
1	200,354,692	200,355,063	371	10		GPR37L1	3,589		
1	200,428,565	200,429,341	776	9		LGR6	220	PTPRV	3,518
1	200,472,155	200,472,554	399	10	LGR6,			AL356953.17-2	4,643
1	200,584,287	200,584,833	546	9	PPP1R12B,	UBE2T	6,580		
1	201,275,455	201,275,896	441	9	PPFIA4,			TMEM183A	15,635
1	201,280,685	201.281.003	318	9	PPFIA4.	ADORA1	45,402	TMEM183A	20.865
1	201 558 795	201 559 195	400	9	,	U6	3 945		
1	202 634 211	202 634 633	422	a a		00	0,010	RP11-730N20 3	3 686
1	202,004,211	202,004,000	375	10		DDD1D15B	3/ 127	111-7001120.0	3,000
1	202,001,009	202,002,044	J10 AAG	10	1 11/3020,		0.662		
1	202,142,020	202,142,412	440	12			9,002		
1	202,742,628	202,743,080	452	12			9,054		
1	202,801,487	202,801,925	438	10		DS_IRNA	3,215		
1	203,063,863	203,064,633	770	11	NFASC,	No non-overlappi	ng genes wit	nin 50,000bp	
1	203,985,797	203,986,452	655	9	NUCKS1,	SNORA72	18,694	RAB7L1	17,849
1	204,476,740	204,477,242	502	9		CTSE	6,840		
1	204,852,109	204,852,588	479	10	LGTN,	DYRK3	14,143	RASSF5	22,871
1	205,324,592	205,324,885	293	10		C4BPB	3,950	PFKFB2	3,601
1	206,068,501	206,068,793	292	9	C1orf132,	hsa-mir-29b-2	26,010	CD46	33,020
1	206,483.614	206,484,263	649	9	PLXNA2.			RP11-2P2.1	10.995
1	206,484,849	206,485,379	530	11	-,	PLXNA2	561	RP11-2P2 1	9 879
1	206 892 352	206 802 736	38/	۰. ۵				RP11_450K23 1	44 601
1	200,032,032	200,032,730	202	10	C1orf74				2 1 <i>1 1</i>
1	200,024,432	200,024,734	302	10	0101174,		0.077	INAFOITO	۷,144
1	208,534,862	208,535,275	413	12	KONILIA	RP4-00/H12.4	8,3//		
1	209,374,055	209,374,418	363	12	KCNH1,	KP11-543B16.1	39,035	D0052	
1	209,585,261	209,585,964	703	9	IRAF5,	C1ort97	36,804	RCOR3	29,061
1	209,754,000	209,754,535	535	9		RD3	21,118		
1	209,817,679	209,818,051	372	11	SLC30A1,	No non-overlappi	ng genes wit	hin 50,000bp	
1	210,274,979	210,275,420	441	13	INTS7,	DTL	334	SNORA26	9,332
1	210,525,239	210,525,750	511	9	PPP2R5A,			RP11-384C4.3	23,266

1	210,835,785	210,836,230	445	9	ATF3,	FAM71A	28,209		
1	211,031,371	211,031,983	612	12	NSL1, TATDN3,	RP11-348H3.2	32,009	C1orf227	38,131
1	212,501,415	212,501,799	384	10		SMYD2	19,400		
1	218,286,395	218,286,859	464	11	EPRS.	IARS2	47.208	BPNT1	10.588
1	218.329.660	218.330.012	352	11	BPNT1.	IARS2	4.055		- ,
1	218,512,386	218,512,814	428	10	RAB3GAP2.	AL445435.11	4,505		
1	218 929 998	218 930 536	538	10	C1orf115		.,	MARK1	25 577
1	219 131 097	219 131 485	388		0.000.000			ніх	6 079
1	219 454 974	219 455 362	388	g		No non-overlanni	na aenes wit	hin 50 000hn	0,010
1	210,404,074	210,400,002	366	0		No non-overlappi	ng genes wit	hin 50,000bp	
1	210,407,227	219,407,090	445	9			ing genes wit		14 043
1	219,090,001	219,090,440	335	9		DD11 1/0 119 1	2.646		44,343
1	220,303,407	220,303,742	1 6 4 5	9	MIA2	DD11 270 110 C	2,040		
1	220,003,234	220,004,079	1,045	9	IVIIAJ,	RP11-370J10.0	1,411	him 50 000hm	
1	221,000,201	221,000,760	202	10			ng genes wit		
1	221,161,830	221,162,154	324	9	DISP1,	AC093152.2	9,919	TI D5	0.074
1	221,343,071	221,343,533	462	9				TLR5	6,674
1	221,363,503	221,363,966	463	13	TLR5,	No non-overlappi	ng genes wit	hin 50,000bp	
1	221,373,510	221,374,046	536	9	TLR5,	No non-overlappi	ng genes wit	hin 50,000bp	
1	221,382,611	221,383,916	1,305	9	TLR5,	No non-overlappi	ng genes wit	hin 50,000bp	
1	221,539,526	221,539,824	298	9	SUSD4,	No non-overlappi	ng genes wit	hin 50,000bp	
1	221,764,649	221,765,008	359	10				CAPN8	16,600
1	221,882,367	221,883,014	647	13	CAPN8,			RP11-105I12.1	15,420
1	221,952,443	221,953,085	642	13				U6	7,960
1	221,969,115	221,969,650	535	11	CAPN2,	CAPN8	49,099	U6	24,632
1	221,987,292	221,987,677	385	9	CAPN2,			U6	42,809
1	222,069,765	222,070,491	726	9	TP53BP2,			CAPN2	39,597
1	222,099,652	222,100,778	1,126	13	TP53BP2,			RP11-332L18.3	10,126
1	222,368,233	222,368,911	678	10	FBXO28,	No non-overlappi	ng genes wit	hin 50,000bp	
1	222,431,105	222,431,384	279	9		AC092809.2-1	1,074		
1	222,437,039	222,438,512	1.473	9	DEGS1.	AC092809.2-1	7.008	SNORA72	2.947
1	222,458,902	222,459,600	698	9	1	AC092809.2-1	28.871	DEGS1	11,139
1	222 584 600	222 585 027	427	10		NVI	93		,
1	222 610 933	222 611 372	439	12	CNIH4	NVI	26 4 26	AC092809 2-2	19 721
1	222,010,000	222,011,012	718	10	011114,	No non-overlanni	20,720	hin 50 000hn	10,721
1	222,757,077	222,756,004	1 130	10		No non-overlappi	ng genes wit	hin 50,000bp	
1	222,704,904	222,700,094	308	10		No non overlappi	ng genes wit	hin 50,000bp	
1	222,700,037	222,700,303	1 167	10			ng genes wit	DD11 100E13 2	40.280
1	222,070,003	222,071,170	1,107	10				RF11-100E13.2	40,209
1	222,071,200	222,071,473	200	10	Сіліпэ,			CNILL2	41,494
1	223,034,213	223,034,592	3/9	9					39,324
1	223,088,304	223,088,552	248	9	DNIALIAA	No non-overlappi	ng genes wit	nin 50,000bp	
1	223,183,014	223,184,096	482	10	DNAH 14,	No non-overlappi	ng genes wit	nin 50,000bp	
1	223,504,842	223,505,206	364	9	AC092811.2,	No non-overlappi	ng genes wit		10.071
1	223,680,934	223,683,296	2,362	9	LBR,				12,2/1
1	223,735,296	223,735,634	338	9					5,523
1	223,779,551	223,779,934	383	9	ENAH,	No non-overlappi	ng genes wit	nin 50,000bp	
1	223,909,259	223,909,655	396	9		ENAH	1,791		
1	223,911,796	223,912,321	525	10		ENAH	4,328		
1	223,950,372	223,950,946	574	9		ENAH	42,904		
1	223,971,895	223,972,357	462	10		U6	23,243		
1	224,017,943	224,019,021	1,078	9		SRP9	13,133	U6	22,236
1	224,021,022	224,022,066	1,044	9		SRP9	10,088	U6	25,315
1	224,031,657	224,032,019	362	11		SRP9	135		
1	224,163,203	224,163,511	308	10		LEFTY1	19,734	PYCR2	10,690
1	224,177,705	224,178,743	1,038	11	PYCR2,	LEFTY1	34,236	LEFTY2	12,184
1	224,216,638	224,217,035	397	10		AL117348.26	1,469		
1	224,253,182	224,254,166	984	11	C1orf55,			AL117348.26	34,425
1	224,256,339	224,257,508	1,169	9		C1orf55	2,650		· · ·
1	224,318,595	224,318,904	309	13	H3F3A,	No non-overlappi	ng genes wit	hin 50,000bp	
1	224,336.931	224,338.089	1,158	9				H3F3A	10.606
1	224.376.760	224.377.569	809	11				ACBD3	21.436
1	224,416,662	224,417,018	356	.9	ACBD3.			RP11-275I14.2	26.179
1	224 440 919	224 441 274	355	11	ACBD3			RP11-275I14 2	1.923
1	224,441 411	224,441 697	286	 	,	ACBD3	365	RP11-275I14 2	1 500
1	224 471 632	224 471 945	313	10		MIXI 1	5 907		.,000
			515	10	1		5,557		

1	224,562,709	224,563,636	927	9	LIN9,			AL359742.15-1	4,023
1	224,587,640	224,588,091	451	9		RP11-125A15.1	14,623	PARP1	27,693
1	224.627.971	224.628.755	784	9	PARP1.	No non-overlappi	na aenes wit	hin 50.000bp	,
1	224.660.613	224.661.103	490	9	PARP1.	RP11-118H4.1	31.785	AL359704.9-2	18.648
1	224.661.742	224,662,199	457	10	PARP1.	RP11-118H4.1	30.689	AL359704.9-2	17.552
1	224.803.933	224.804.517	584	10	C1orf95.	No non-overlappi	na aenes wit	hin 50.000bp	,
1	224.858.601	224,859,166	565	9				C1orf95	2.237
1	224,909,755	224,910,513	758	9	ITPKB.	No non-overlappi	na aenes wit	hin 50.000bp	_,
1	224 965 503	224 966 193	690	9	ITPKB	No non-overlappi	na aenes wit	hin 50 000bp	
1	224 978 361	224 978 699	338	11	ITPKB	No non-overlappi	na aenes wit	hin 50 000hp	
1	225 130 160	225 130 710	550	10	PSEN2	AI 391628 18	20 502	iiii 00,0000p	
1	225,100,100	225,100,710	508	a		712001020.10	20,002	RP5-1087E8 2	17 874
1	225,134,011	225,134,313	867	9		No non-overlanni	na aenes wit	hin 50 000hn	17,074
1	225,371,000	225,372,030	638	9			302	IIII 30,000bp	
1	225,735,007	225,750,275	3/18	15	SNAD47	1111-27504.4	502	AL 136378 1/	1 1 3 5
'	223,303,400	223,303,010	540	15	JMJD4			AL 130370.14	1,100
1	226 201 436	226 201 789	353	Q	ΜΝΤΩΔ			RP11-10213 2	27 880
1	226,201,400	226,201,700	452	10				C1orf35	17,000
1	226,337,797	226,338,389	592	11	ARE1			C1orf35	16 663
1	220,337,737	220,350,309	595	16	C1orf35			MDDI 55	3 044
1	220,337,374	220,337,333	303	10	0101135,	CUK1	8 576		3,044
1	220,303,333	220,305,710	1 744	10			0,370	KF11-5201114.1	3,400
1	220,080,072	220,393,410	1,744	10		C1orf145	4,000		
1	220,409,021	220,409,451	430	9	OBSON,	C1011145	1,033		
1	220,470,074	220,477,081	407	10			8,686	AL 120000 45 4	A 77 4
1	220,711,423	220,711,763	340	9	HIST3HZA,	HIST3H2BB	008	AL139288.15-1	6,774
1	226,711,903	226,712,353	450	10	HIST3H2A,	HIST3H2BB	/8	AL139288.15-1	6,184
1	226,717,853	226,718,613	760	9	AL139288.15-1,	HIST 3H2A	5,656	HIST3H2BB	4,971
1	226,740,735	226,741,673	938	15		RNF187	44	DUE 407	E 074
1	226,755,163	226,755,535	372	9				RNF187	5,871
1	226,769,585	226,769,948	363	9		AL139288.15-2	2,958		
1	226,937,204	226,937,739	535	9	RHOU,			RP4-646B12.2	47,014
1	226,983,485	226,984,971	1,486	13				RHOU	34,453
1	227,033,392	227,033,760	368	9		No non-overlappi	ng genes wit	hin 50,000bp	
1	227,052,995	227,053,371	376	9		No non-overlappi	ng genes wit	hin 50,000bp	
1	227,272,485	227,272,999	514	11				RP5-1065P14.1	27,530
1	227,409,301	227,409,800	499	9		AL162595.17-1	25,277		
1	227,412,508	227,412,925	417	9		AL162595.17-1	28,484		
1	227,427,633	227,428,315	682	9		TMEM78	23,691	AL162595.17-2	44,979
1	227,429,430	227,430,145	715	9		TMEM78	21,861	AL162595.17-2	43,149
1	227,455,608	227,456,006	398	10				TMEM78	1,428
1	227,545,050	227,545,932	882	10	C1orf96,	AL160004.18-1	39,566	RAB4A	36,789
1	227,582,498	227,583,382	884	9		AL160004.18-1	2,116		
1	227,601,525	227,601,951	426	9		RP5-1068B5.1	25,439	AL160004.18-2	11,003
1	227,612,967	227,613,395	428	9	AL160004.18-2,	RP5-1068B5.1	13,995	ACTA1	20,220
1	227,710,487	227,711,414	927	11	NUP133,			ABCB10	7,539
1	227,716,831	227,717,388	557	9		NUP133	6,120	ABCB10	1,565
1	227,752,058	227,752,790	732	9	ABCB10,	U4	14,499	TAF5L	42,691
					5S_rRNA,				
1	227,760,752	227,761,496	744	10	ABCB10,			5S_rRNA	8,360
1	227,828,983	227.829.282	299	10	URB2,	TAF5L	566		
1		1							
1	228,096,658	228,097,005	347	11		No non-overlappi	ng genes wit	hin 50,000bp	
	228,096,658 228,347,728	228,097,005 228,348,130	347 402	11 10	GALNT2,	No non-overlappi No non-overlappi	ng genes wit ng genes wit	hin 50,000bp hin 50,000bp	
1	228,096,658 228,347,728 228,398,151	228,097,005 228,348,130 228,398,638	347 402 487	11 10 9	GALNT2, GALNT2,	No non-overlappi No non-overlappi No non-overlappi	ng genes wit ng genes wit ng genes wit	hin 50,000bp hin 50,000bp hin 50,000bp	
1	228,096,658 228,347,728 228,398,151 228,471,026	228,097,005 228,348,130 228,398,638 228,471,485	347 402 487 459	11 10 9 10	GALNT2, GALNT2, GALNT2,	No non-overlappi No non-overlappi No non-overlappi	ng genes wit ng genes wit ng genes wit	hin 50,000bp hin 50,000bp hin 50,000bp AL691479.15	46,576
1 1 1	228,096,658 228,347,728 228,398,151 228,471,026 228,473,430	228,097,005 228,348,130 228,398,638 228,471,485 228,473,944	347 402 487 459 514	11 10 9 10 10	GALNT2, GALNT2, GALNT2, GALNT2,	No non-overlappi No non-overlappi No non-overlappi	ng genes wit ng genes wit ng genes wit	hin 50,000bp hin 50,000bp hin 50,000bp AL691479.15 AL691479.15	46,576
1 1 1 1	228,096,658 228,347,728 228,398,151 228,471,026 228,473,430 228,844,497	228,097,005 228,348,130 228,398,638 228,471,485 228,473,944 228,845,074	347 402 487 459 514 577	11 10 9 10 10 10	GALNT2, GALNT2, GALNT2, GALNT2, COG2,	No non-overlappi No non-overlappi No non-overlappi RP11-543E8.2	ng genes wit ng genes wit ng genes wit 29,716	hin 50,000bp hin 50,000bp hin 50,000bp AL691479.15 AL691479.15	46,576 44,117
1 1 1 1 1	228,096,658 228,347,728 228,398,151 228,471,026 228,473,430 228,844,497 228,845,163	228,097,005 228,348,130 228,398,638 228,471,485 228,473,944 228,845,074 228,845,074	347 402 487 459 514 577 277	11 10 9 10 10 10 9	GALNT2, GALNT2, GALNT2, GALNT2, COG2, COG2,	No non-overlappi No non-overlappi No non-overlappi RP11-543E8.2 RP11-543E8.2	ng genes wit ng genes wit ng genes wit 29,716 30.382	hin 50,000bp hin 50,000bp hin 50,000bp AL691479.15 AL691479.15	46,576 44,117
1 1 1 1 1 1	228,096,658 228,347,728 228,398,151 228,471,026 228,473,430 228,844,497 228,845,163 228,951,299	228,097,005 228,348,130 228,398,638 228,471,485 228,473,944 228,845,074 228,845,074 228,845,440 228,951,660	347 402 487 459 514 577 277 361	11 10 9 10 10 10 9 11	GALNT2, GALNT2, GALNT2, GALNT2, COG2, COG2, CAPN9.	No non-overlappi No non-overlappi No non-overlappi RP11-543E8.2 RP11-543E8.2 AGT	ng genes wit ng genes wit ng genes wit 29,716 30,382 34,735	hin 50,000bp hin 50,000bp hin 50,000bp AL691479.15 AL691479.15	46,576 44,117
1 1 1 1 1 1 1 1	228,096,658 228,347,728 228,398,151 228,471,026 228,473,430 228,844,497 228,845,163 228,951,299 229,074,244	228,097,005 228,348,130 228,398,638 228,471,485 228,473,944 228,845,074 228,845,440 228,951,660 229,074,456	347 402 487 459 514 577 277 361 212	11 10 9 10 10 10 10 9 11	GALNT2, GALNT2, GALNT2, GALNT2, COG2, COG2, CAPN9,	No non-overlappi No non-overlappi No non-overlappi RP11-543E8.2 RP11-543E8.2 AGT C1orf198	ng genes wit ng genes wit 29,716 30,382 34,735 3.331	hin 50,000bp hin 50,000bp hin 50,000bp AL691479.15 AL691479.15	46,576 44,117
1 1 1 1 1 1 1 1 1	228,096,658 228,347,728 228,398,151 228,471,026 228,473,430 228,844,497 228,845,163 228,951,299 229,074,244 229,180,008	228,097,005 228,348,130 228,398,638 228,471,485 228,473,944 228,845,074 228,845,440 228,951,660 229,074,456 229,180,476	347 402 487 459 514 577 277 361 212 468	11 10 9 10 10 10 10 9 11 11 11	GALNT2, GALNT2, GALNT2, GALNT2, COG2, COG2, CAPN9, TTC13.	No non-overlappi No non-overlappi No non-overlappi RP11-543E8.2 RP11-543E8.2 AGT C1orf198 ARV1	ng genes wit ng genes wit 29,716 30,382 34,735 3,331 970	hin 50,000bp hin 50,000bp hin 50,000bp AL691479.15 AL691479.15	46,576 44,117
1 1 1 1 1 1 1 1 1 1 1	228,096,658 228,347,728 228,398,151 228,471,026 228,473,430 228,844,497 228,845,163 228,951,299 229,074,244 229,180,008 229,180,862	228,097,005 228,348,130 228,398,638 228,471,485 228,473,944 228,845,074 228,845,440 228,951,660 229,074,456 229,180,476 229,181,739	347 402 487 459 514 577 277 361 212 468 877	111 10 9 10 10 10 10 9 11 11 11 11 12 13	GALNT2, GALNT2, GALNT2, GALNT2, COG2, COG2, CAPN9, TTC13, TTC13, ARV1	No non-overlappi No non-overlappi No non-overlappi RP11-543E8.2 RP11-543E8.2 AGT C1orf198 ARV1 RP11-423F24 3	ng genes wit ng genes wit 29,716 30,382 34,735 3,331 970 42 241	hin 50,000bp hin 50,000bp AL691479.15 AL691479.15 FAM89A	46,576 44,117 39,819
1 1 1 1 1 1 1 1 1 1 1 1 1	228,096,658 228,347,728 228,398,151 228,471,026 228,473,430 228,844,497 228,845,163 228,951,299 229,074,244 229,180,008 229,180,862 229,235,032	228,097,005 228,348,130 228,398,638 228,471,485 228,473,944 228,845,074 228,845,074 228,951,660 229,074,456 229,180,476 229,181,739 229,235,784	347 402 487 459 514 577 277 361 212 468 877 752	111 10 9 10 10 10 10 9 11 11 11 11 12 13 9	GALNT2, GALNT2, GALNT2, GALNT2, COG2, COG2, CAPN9, TTC13, TTC13, ARV1, FAM89A.	No non-overlappi No non-overlappi No non-overlappi RP11-543E8.2 RP11-543E8.2 AGT C1orf198 ARV1 RP11-423F24.3 hsa-mir-1182	ng genes wit ng genes wit 29,716 30,382 34,735 3,331 970 42,241 12,739	hin 50,000bp hin 50,000bp AL691479.15 AL691479.15 FAM89A RP11-423F24 3	46,576 44,117 39,819 10,480
1 1 1 1 1 1 1 1 1 1 1 1 1	228,096,658 228,347,728 228,398,151 228,471,026 228,4473,430 228,844,497 228,845,163 228,951,299 229,074,244 229,180,008 229,180,862 229,235,032 229,241,259	228,097,005 228,348,130 228,398,638 228,471,485 228,473,944 228,845,074 228,845,440 228,951,660 229,074,456 229,180,476 229,181,739 229,235,784 229,241,743	347 402 487 514 577 277 361 212 468 877 752 484	111 10 9 10 10 10 10 10 9 11 11 11 12 13 9 9	GALNT2, GALNT2, GALNT2, GALNT2, COG2, COG2, CAPN9, TTC13, TTC13, ARV1, FAM89A, FAM89A	No non-overlappi No non-overlappi No non-overlappi RP11-543E8.2 RP11-543E8.2 AGT C1orf198 ARV1 RP11-423F24.3 hsa-mir-1182 hsa-mir-1182	ng genes wit ng genes wit 29,716 30,382 34,735 3,331 970 42,241 12,739 18,966	hin 50,000bp hin 50,000bp AL691479.15 AL691479.15 FAM89A RP11-423F24.3 RP11-423F24.3	46,576 44,117 39,819 10,480 16 707
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	228,096,658 228,347,728 228,398,151 228,471,026 228,4473,430 228,844,497 228,845,163 228,951,299 229,074,244 229,180,008 229,180,862 229,235,032 229,241,259 229,29,242,66	228,097,005 228,348,130 228,398,638 228,471,485 228,473,944 228,845,074 228,845,074 228,951,660 229,074,456 229,180,476 229,181,739 229,235,784 229,241,743 229,29,245,85	347 402 487 514 577 277 361 212 468 877 752 484 319	111 10 9 10 10 10 10 10 9 11 11 11 12 13 9 9 9	GALNT2, GALNT2, GALNT2, GALNT2, COG2, COG2, CAPN9, TTC13, TTC13, ARV1, FAM89A, FAM89A,	No non-overlappi No non-overlappi No non-overlappi RP11-543E8.2 RP11-543E8.2 AGT C1orf198 ARV1 RP11-423F24.3 hsa-mir-1182 hsa-mir-1182	ng genes wit ng genes wit 29,716 30,382 34,735 3,331 970 42,241 12,739 18,966	hin 50,000bp hin 50,000bp AL691479.15 AL691479.15 AL691479.15 FAM89A RP11-423F24.3 RP11-423F24.3 RP5-1097F14 1	46,576 44,117 39,819 10,480 16,707 25,615
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	228,096,658 228,347,728 228,398,151 228,471,026 228,473,430 228,844,497 228,845,163 228,951,299 229,074,244 229,180,008 229,180,862 229,235,032 229,241,259 229,294,266 229,443,396	228,097,005 228,348,130 228,398,638 228,471,485 228,473,944 228,845,074 228,845,074 228,845,440 228,951,660 229,074,456 229,180,476 229,181,739 229,235,784 229,241,743 229,294,585 229,444 522	347 402 487 514 577 277 361 212 468 877 752 484 319	111 10 9 10 10 10 10 10 9 11 11 11 12 13 9 9 9 10	GALNT2, GALNT2, GALNT2, GALNT2, COG2, COG2, CAPN9, TTC13, TTC13, ARV1, FAM89A, FAM89A, C1orf131	No non-overlappi No non-overlappi No non-overlappi RP11-543E8.2 RP11-543E8.2 AGT C1orf198 ARV1 RP11-423F24.3 hsa-mir-1182 hsa-mir-1182	ng genes wit ng genes wit 29,716 30,382 34,735 3,331 970 42,241 12,739 18,966	hin 50,000bp hin 50,000bp AL691479.15 AL691479.15 AL691479.15 FAM89A RP11-423F24.3 RP11-423F24.3 RP11-423F24.3 RP5-1097F14.1 TRIM67	46,576 44,117 39,819 10,480 16,707 25,615 19,459

					GNPAT,				
1	229,540,012	229,541,137	1,125	14	EXOC8,			EGLN1	26,917
	, ,	, ,			C1orf124,				,
1	229,624,775	229,625,189	414	11	EGLN1,	AL117352.12-1	47,894		
1	229,678,305	229,678,653	348	9	RP11-295G20.1,	No non-overlappi	ng genes wit	hin 50,000bp	
1	229,828,723	229,830,420	1,697	14	DISC1,	U5	42,584		
1	230,058,490	230,059,040	550	9	DISC1,	No non-overlappi	ng genes wit	hin 50,000bp	
1	230,167,686	230,168,122	436	10	DISC1,	No non-overlappi	ng genes wit	hin 50,000bp	
1	230,476,148	230,477,005	857	9		No non-overlappi	ng genes wit	hin 50,000bp	
1	230,488,409	230,488,739	330	9		No non-overlappi	ng genes wit	hin 50,000bp	
1	230,638,960	230,639,259	299	9	SIPA1L2,	No non-overlappi	ng genes wit	hin 50,000bp	
1	230,796,289	230,796,893	604	10		SIPA1L2	32,362		
1	230.831.395	230.832.014	619	10		No non-overlappi	na aenes wit	hin 50.000bp	
1	230 864 213	230 864 551	338	9		AI 355274 22	38 040		
1	230.872.934	230.873.517	583	9		AL355274.22	29.074		
1	230 886 192	230 886 691	499	9		AI 355274 22	15 900		
1	230 886 854	230 887 664	810	9		AL 355274 22	14 927		
1	231 071 176	231 071 659	483	10		111	36 620		
1	231 152 473	231 153 031	558	q	C1orf57		00,020	RP4-659119 1	32 086
1	231 227 507	231 227 856	340	10	PCNXI 2			C1orf57	46 665
1	231,227,307	231 243 120	364	13		No non-overlanni	na aenes wit	bin 50 000bn	+0,000
1	231,242,703	231,245,125	782	10	PCNYL2,	No non-overlappi	ng genes wit	hin 50,000bp	
1	231,313,139	231 260 526	102	10	DONNEZ,	No non overlappi	ng genes wit	hin 50,000bp	
1	231,309,032	231 / 13 230	404	9	DONALZ,	non-ovenappi	ng genes wit		17 110
1	231,443,419	231,443,627	400	14	PUNALZ,		22.204	RP9-002P0.1	47,410
1	231,530,376	231,530,920	044 450	12	MAPSK 19,		32,294		
1	231,790,433	231,790,665	452	9			20,400	him 50 000hm	
1	231,037,112	231,037,790	004	9		No non-overlappi	ng genes wit	hin 50,000bp	
1	232,120,470	232,120,815	345	9 0	SLU35F3,	No non-overlappi	ng genes wit	nin 50,000bp	
1	232,327,440	232,328,437	991	9	SLU35F3,	No non-overlappi	ng genes wit	nin 50,000bp	
1	232,389,143	232,389,596	453	9	SLC35F3,	No non-overlappi	ng genes wit		
1	232,504,287	232,505,127	840	y Q	SLC35F3,	No non-overlappi	ng genes wit	nin 50,000bp	10.001
1	232,512,394	232,512,782	388	9	SLC35F3,	DD5 007004 4	45.044	RP5-827C21.1	46,291
-	232,575,321	232.575.924	603	14	C10ff31,	RP5-827021.1	15,811	TARBPT	17,758
1	000 000 700	000 040 504	700	40		No			,
1	232,639,732	232,640,501	769	10	TARBP1,	No non-overlappi	ng genes wit	hin 50,000bp	
1 1 1	232,639,732 232,680,939	232,640,501 232,681,730	769 791	10 17	TARBP1, TARBP1,	No non-overlappi No non-overlappi	ng genes wit ng genes wit	hin 50,000bp hin 50,000bp	
1 1 1 1	232,639,732 232,680,939 232,701,509	232,640,501 232,681,730 232,701,860	769 791 351	10 17 11	TARBP1, TARBP1,	No non-overlappi No non-overlappi TARBP1	ng genes wit ng genes wit 20,037	hin 50,000bp hin 50,000bp	
1 1 1 1 1	232,639,732 232,680,939 232,701,509 232,718,797	232,640,501 232,681,730 232,701,860 232,719,078	769 791 351 281	10 17 11 9	TARBP1, TARBP1,	No non-overlappi No non-overlappi TARBP1 TARBP1	ng genes wit ng genes wit 20,037 37,325	hin 50,000bp hin 50,000bp	
1 1 1 1 1 1	232,639,732 232,680,939 232,701,509 232,718,797 232,745,646	232,640,501 232,681,730 232,701,860 232,719,078 232,746,314	769 791 351 281 668	10 17 11 9 10	TARBP1, TARBP1,	No non-overlappi No non-overlappi TARBP1 TARBP1 U8	ng genes wit ng genes wit 20,037 37,325 49,330	hin 50,000bp hin 50,000bp	
1 1 1 1 1 1 1 1	232,639,732 232,680,939 232,701,509 232,718,797 232,745,646 232,746,453	232,640,501 232,681,730 232,701,860 232,719,078 232,746,314 232,746,987	769 791 351 281 668 534	10 17 11 9 10 9	TARBP1, TARBP1,	No non-overlappi No non-overlappi TARBP1 TARBP1 U8 U8	ng genes wit ng genes wit 20,037 37,325 49,330 48,657	hin 50,000bp hin 50,000bp	
1 1 1 1 1 1 1 1 1 1	232,639,732 232,680,939 232,701,509 232,718,797 232,745,646 232,746,453 232,801,966	232,640,501 232,681,730 232,701,860 232,719,078 232,746,314 232,746,987 232,802,531	769 791 351 281 668 534 565	10 17 11 9 10 9 12	TARBP1, TARBP1,	No non-overlappi No non-overlappi TARBP1 TARBP1 U8 U8	ng genes wit ng genes wit 20,037 37,325 49,330 48,657	hin 50,000bp hin 50,000bp IRF2BP2	4,107
1 1 1 1 1 1 1 1 1 1 1	232,639,732 232,680,939 232,701,509 232,718,797 232,745,646 232,746,453 232,801,966 232,809,471	232,640,501 232,681,730 232,701,860 232,719,078 232,746,314 232,746,987 232,802,531 232,810,070	769 791 351 281 668 534 565 599	10 17 11 9 10 9 12 9	TARBP1, TARBP1, IRF2BP2,	No non-overlappi No non-overlappi TARBP1 TARBP1 U8 U8	ng genes wit ng genes wit 20,037 37,325 49,330 48,657	hin 50,000bp hin 50,000bp IRF2BP2 U8	4,107 13,700
1 1 1 1 1 1 1 1 1 1 1 1 1	232,639,732 232,680,939 232,701,509 232,718,797 232,745,646 232,746,453 232,801,966 232,809,471 232,810,335	232,640,501 232,681,730 232,701,860 232,719,078 232,746,314 232,746,987 232,802,531 232,810,070 232,811,317	769 791 351 281 668 534 565 599 982	10 17 11 9 10 9 10 9 12 9 12	TARBP1, TARBP1, IRF2BP2, IRF2BP2,	No non-overlappi No non-overlappi TARBP1 TARBP1 U8 U8	ng genes wit ng genes wit 20,037 37,325 49,330 48,657	hin 50,000bp hin 50,000bp IRF2BP2 U8 U8	4,107 13,700 14,564
1 1 1 1 1 1 1 1 1 1 1 1 1	232,639,732 232,680,939 232,701,509 232,718,797 232,745,646 232,746,453 232,801,966 232,809,471 232,810,335 232,813,017	232,640,501 232,681,730 232,701,860 232,719,078 232,746,314 232,746,987 232,802,531 232,810,070 232,811,317 232,813,335	769 791 351 281 668 534 565 599 982 318	10 17 11 9 10 9 12 9 12 10	TARBP1, TARBP1, IRF2BP2, IRF2BP2,	No non-overlappi No non-overlappi TARBP1 TARBP1 U8 U8 IRF2BP2	ng genes wit ng genes wit 20,037 37,325 49,330 48,657 1,123	hin 50,000bp hin 50,000bp IRF2BP2 U8 U8	4,107 13,700 14,564
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	232,639,732 232,680,939 232,701,509 232,745,646 232,745,646 232,801,966 232,809,471 232,810,335 232,813,017 232,813,353	232,640,501 232,681,730 232,701,860 232,719,078 232,746,314 232,746,987 232,802,531 232,810,070 232,811,317 232,813,335 232,813,335	769 791 351 281 668 534 565 599 982 318 594	10 17 11 9 10 9 12 9 12 10 9 9	TARBP1, TARBP1, IRF2BP2, IRF2BP2,	No non-overlappi No non-overlappi TARBP1 TARBP1 U8 U8 IRF2BP2 IRF2BP2 IRF2BP2	ng genes wit ng genes wit 20,037 37,325 49,330 48,657 1,123 1,459	hin 50,000bp hin 50,000bp IRF2BP2 U8 U8	4,107 13,700 14,564
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	232,639,732 232,680,939 232,701,509 232,745,646 232,745,646 232,801,966 232,809,471 232,810,335 232,813,017 232,813,353 232,814,751	232,640,501 232,681,730 232,701,860 232,719,078 232,746,314 232,746,987 232,802,531 232,810,070 232,811,317 232,813,335 232,813,347 232,813,380	769 791 351 281 668 534 565 599 982 318 594 629	10 17 11 9 10 9 12 9 12 10 9 12	TARBP1, TARBP1, IRF2BP2, IRF2BP2,	No non-overlappi No non-overlappi TARBP1 TARBP1 U8 U8 IRF2BP2 IRF2BP2 IRF2BP2 IRF2BP2	ng genes wit ng genes wit 20,037 37,325 49,330 48,657 1,123 1,459 2,857	hin 50,000bp hin 50,000bp IRF2BP2 U8 U8	4,107 13,700 14,564
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	232,639,732 232,680,939 232,701,509 232,745,646 232,745,646 232,801,966 232,809,471 232,810,335 232,813,017 232,813,353 232,814,751 232,831,401	232,640,501 232,681,730 232,701,860 232,719,078 232,746,314 232,746,987 232,802,531 232,810,070 232,811,317 232,813,335 232,813,947 232,815,380 232,831,927	769 791 351 281 668 534 565 599 982 318 594 629 526	10 17 11 9 10 9 12 9 12 10 9 15 9 9	TARBP1, TARBP1, IRF2BP2, IRF2BP2,	No non-overlappi No non-overlappi TARBP1 TARBP1 U8 U8 IRF2BP2 IRF2BP2 IRF2BP2 IRF2BP2 IRF2BP2	ng genes wit ng genes wit 20,037 37,325 49,330 48,657 1,123 1,459 2,857 19,507	hin 50,000bp hin 50,000bp IRF2BP2 U8 U8 U8	4,107 13,700 14,564 35,630
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	232,639,732 232,680,939 232,701,509 232,718,797 232,745,646 232,746,453 232,801,966 232,809,471 232,810,335 232,813,017 232,813,353 232,814,751 232,831,401 232,902,112	232,640,501 232,681,730 232,701,860 232,719,078 232,746,987 232,802,531 232,810,070 232,811,317 232,813,335 232,813,947 232,815,380 232,831,927 232,802,657	769 791 351 281 668 534 565 599 982 318 594 629 526 526 545	10 17 11 9 10 9 12 9 12 10 9 15 9 11	TARBP1, TARBP1, IRF2BP2, IRF2BP2,	No non-overlappi No non-overlappi TARBP1 TARBP1 U8 U8 U8 IRF2BP2 IRF2BP2 IRF2BP2 IRF2BP2 IRF2BP2 IRF2BP2 No non-overlappi	ng genes wit ng genes wit 20,037 37,325 49,330 48,657 1,123 1,459 2,857 19,507 ng genes wit	hin 50,000bp hin 50,000bp IRF2BP2 U8 U8 U8 U8 hin 50,000bp	4,107 13,700 14,564 35,630
1 1	232,639,732 232,680,939 232,701,509 232,745,646 232,745,646 232,746,453 232,801,966 232,809,471 232,810,335 232,813,017 232,813,353 232,814,751 232,831,401 232,902,112 232,902,663	232,640,501 232,681,730 232,701,860 232,719,078 232,746,314 232,746,987 232,802,531 232,810,070 232,811,317 232,813,335 232,813,947 232,815,380 232,831,927 232,902,657 232,903,118	769 791 351 281 668 534 565 599 982 318 599 82 318 594 629 526 545 455	10 17 11 9 10 9 12 9 12 10 9 15 9 15 9 11	TARBP1, TARBP1, IRF2BP2, IRF2BP2,	No non-overlappi No non-overlappi TARBP1 TARBP1 U8 U8 IRF2BP2 IRF2BP2 IRF2BP2 IRF2BP2 IRF2BP2 IRF2BP2 No non-overlappi	ng genes wit ng genes wit 20,037 37,325 49,330 48,657 1,123 1,459 2,857 19,507 ng genes wit ng genes wit	hin 50,000bp hin 50,000bp IRF2BP2 U8 U8 U8 U8 hin 50,000bp hin 50,000bp	4,107 13,700 14,564 35,630
	232,639,732 232,680,939 232,701,509 232,718,797 232,745,646 232,746,453 232,801,966 232,809,471 232,810,335 232,813,017 232,813,353 232,814,751 232,831,401 232,902,112 232,902,663 232,926,260	232,640,501 232,681,730 232,701,860 232,719,078 232,746,987 232,802,531 232,810,070 232,811,317 232,813,335 232,813,947 232,815,380 232,831,927 232,902,657 232,903,118 232,926,863	769 791 351 281 668 534 565 599 982 318 594 629 526 545 455 603	10 17 11 9 10 9 12 9 12 10 9 15 9 15 9 11 19 10	TARBP1, TARBP1, IRF2BP2, IRF2BP2,	No non-overlappi No non-overlappi TARBP1 TARBP1 U8 U8 IRF2BP2 IRF2BP2 IRF2BP2 IRF2BP2 IRF2BP2 IRF2BP2 No non-overlappi No non-overlappi No non-overlappi	ng genes wit ng genes wit 20,037 37,325 49,330 48,657 1,123 1,459 2,857 19,507 ng genes wit ng genes wit ng genes wit	hin 50,000bp hin 50,000bp IRF2BP2 U8 U8 U8 hin 50,000bp hin 50,000bp hin 50,000bp	4,107 13,700 14,564 35,630
I 1	232,639,732 232,680,939 232,701,509 232,718,797 232,745,646 232,746,453 232,801,966 232,809,471 232,810,335 232,813,017 232,813,353 232,814,751 232,831,401 232,902,112 232,902,663 232,926,260 232,957,621	232,640,501 232,681,730 232,701,860 232,719,078 232,746,314 232,746,987 232,802,531 232,810,070 232,811,317 232,813,335 232,813,947 232,815,380 232,831,927 232,902,657 232,903,118 232,926,863 232,958,350	769 791 351 281 668 534 565 599 982 318 594 629 526 545 455 603 729	10 17 11 9 10 9 12 12 10 9 12 10 9 15 9 11 11 9 10 9	TARBP1, TARBP1, IRF2BP2, IRF2BP2,	No non-overlappi No non-overlappi TARBP1 TARBP1 U8 U8 U8 IRF2BP2 IRF2BP2 IRF2BP2 IRF2BP2 IRF2BP2 IRF2BP2 No non-overlappi No non-overlappi No non-overlappi	ng genes wit ng genes wit 20,037 37,325 49,330 48,657 1,123 1,459 2,857 19,507 ng genes wit ng genes wit ng genes wit ng genes wit	hin 50,000bp hin 50,000bp IRF2BP2 U8 U8 U8 hin 50,000bp hin 50,000bp hin 50,000bp hin 50,000bp	4,107 13,700 14,564 35,630
	232,639,732 232,680,939 232,701,509 232,745,646 232,745,646 232,746,453 232,801,966 232,809,471 232,810,335 232,813,017 232,813,353 232,814,751 232,831,401 232,902,112 232,902,663 232,926,260 232,957,621 232,974,372	232,640,501 232,681,730 232,701,860 232,719,078 232,746,987 232,802,531 232,810,070 232,811,317 232,813,335 232,813,947 232,815,380 232,831,927 232,902,657 232,903,118 232,926,863 232,958,350 232,975,154	769 791 351 281 668 534 565 599 982 318 594 629 526 545 455 603 729 782	10 17 11 9 10 9 12 12 10 9 12 10 9 15 9 11 11 9 10 9 12	TARBP1, TARBP1, IRF2BP2, IRF2BP2,	No non-overlappi No non-overlappi TARBP1 TARBP1 U8 U8 U8 IRF2BP2 IRF2BP2 IRF2BP2 IRF2BP2 IRF2BP2 IRF2BP2 No non-overlappi No non-overlappi No non-overlappi No non-overlappi	ng genes wit ng genes wit 20,037 37,325 49,330 48,657 1,123 1,459 2,857 19,507 ng genes wit ng genes wit ng genes wit ng genes wit ng genes wit ng genes wit	hin 50,000bp hin 50,000bp IRF2BP2 U8 U8 U8 hin 50,000bp hin 50,000bp hin 50,000bp hin 50,000bp hin 50,000bp	4,107 13,700 14,564 35,630
1 1	232,639,732 232,680,939 232,701,509 232,718,797 232,745,646 232,746,453 232,801,966 232,809,471 232,810,335 232,813,017 232,813,353 232,814,751 232,831,401 232,902,112 232,902,663 232,926,260 232,957,621 232,974,372 232,978,639	232,640,501 232,681,730 232,701,860 232,719,078 232,746,987 232,802,531 232,810,070 232,811,317 232,813,335 232,813,947 232,815,380 232,831,927 232,902,657 232,903,118 232,926,863 232,958,350 232,975,154 232,979,708	769 791 351 281 668 534 565 599 982 318 594 629 526 545 455 603 729 782 1,069	10 17 11 9 10 9 12 12 10 9 12 10 9 15 9 11 11 9 10 9 12 10	TARBP1, TARBP1, IRF2BP2, IRF2BP2,	No non-overlappi No non-overlappi TARBP1 TARBP1 U8 U8 U8 IRF2BP2 IRF2BP2 IRF2BP2 IRF2BP2 IRF2BP2 IRF2BP2 No non-overlappi No non-overlappi No non-overlappi No non-overlappi No non-overlappi	ng genes wit ng genes wit 20,037 37,325 49,330 48,657 1,123 1,459 2,857 19,507 ng genes wit ng genes wit	hin 50,000bp hin 50,000bp IRF2BP2 U8 U8 U8 hin 50,000bp hin 50,000bp hin 50,000bp hin 50,000bp hin 50,000bp hin 50,000bp	4,107 13,700 14,564 35,630
$ \begin{array}{c} 1 \\ $	232,639,732 232,680,939 232,701,509 232,718,797 232,745,646 232,746,453 232,801,966 232,809,471 232,810,335 232,813,017 232,813,353 232,814,751 232,902,112 232,902,663 232,926,260 232,957,621 232,974,372 232,978,639 232,979,868	232,640,501 232,681,730 232,701,860 232,719,078 232,746,314 232,746,987 232,802,531 232,810,070 232,811,317 232,813,335 232,813,947 232,815,380 232,831,927 232,902,657 232,903,118 232,926,863 232,958,350 232,975,154 232,980,563	769 791 351 281 668 534 565 599 982 318 594 629 526 545 455 603 729 782 1,069 695	10 17 11 9 10 9 12 10 9 12 10 9 15 9 11 15 9 11 10 9 10 9 12 10 9 9	TARBP1, TARBP1, IRF2BP2, IRF2BP2, IRF2BP2,	No non-overlappi No non-overlappi TARBP1 TARBP1 U8 U8 IRF2BP2 IRF2BP2 IRF2BP2 IRF2BP2 IRF2BP2 No non-overlappi No non-overlappi No non-overlappi No non-overlappi No non-overlappi No non-overlappi No non-overlappi No non-overlappi	ng genes wit ng genes wit 20,037 37,325 49,330 48,657 1,123 1,459 2,857 19,507 ng genes wit ng genes wit	hin 50,000bp hin 50,000bp IRF2BP2 U8 U8 U8 U8 hin 50,000bp hin 50,000bp hin 50,000bp hin 50,000bp hin 50,000bp hin 50,000bp hin 50,000bp hin 50,000bp hin 50,000bp	4,107 13,700 14,564 35,630
1 1	232,639,732 232,680,939 232,701,509 232,718,797 232,745,646 232,746,453 232,801,966 232,809,471 232,810,335 232,813,017 232,813,353 232,814,751 232,902,112 232,902,663 232,926,260 232,957,621 232,974,372 232,979,868 232,981,466	232,640,501 232,681,730 232,701,860 232,719,078 232,746,987 232,802,531 232,810,070 232,811,317 232,813,335 232,813,947 232,815,380 232,831,927 232,902,657 232,903,118 232,926,863 232,958,350 232,975,154 232,979,708 232,980,563 232,982,138	769 791 351 281 668 534 565 599 982 318 594 629 526 545 455 603 729 782 1,069 695 672	10 17 11 9 10 9 12 12 10 9 12 10 9 115 9 111 9 10 9 12 10 9 9 12 10 9 9	TARBP1, TARBP1, IRF2BP2, IRF2BP2, IRF2BP2,	No non-overlappi No non-overlappi TARBP1 TARBP1 U8 U8 IRF2BP2 IRF2BP2 IRF2BP2 IRF2BP2 IRF2BP2 No non-overlappi No non-overlappi No non-overlappi No non-overlappi No non-overlappi No non-overlappi No non-overlappi No non-overlappi No non-overlappi No non-overlappi	ng genes wit ng genes wit 20,037 37,325 49,330 48,657 1,123 1,459 2,857 19,507 ng genes wit ng genes wit	hin 50,000bp hin 50,000bp IRF2BP2 U8 U8 U8 U8 hin 50,000bp hin 50,000bp hin 50,000bp hin 50,000bp hin 50,000bp hin 50,000bp hin 50,000bp hin 50,000bp hin 50,000bp hin 50,000bp	4,107 13,700 14,564 35,630
1 1	232,639,732 232,680,939 232,701,509 232,718,797 232,745,646 232,746,453 232,801,966 232,809,471 232,810,335 232,813,017 232,813,353 232,814,751 232,902,112 232,902,663 232,926,260 232,957,621 232,974,372 232,974,372 232,979,868 232,981,466 232,983,810	232,640,501 232,681,730 232,701,860 232,719,078 232,746,987 232,802,531 232,810,070 232,811,317 232,813,335 232,813,947 232,815,380 232,831,927 232,902,657 232,903,118 232,926,863 232,958,350 232,975,154 232,979,708 232,980,563 232,984,132	769 791 351 281 668 534 565 599 982 318 594 629 526 545 455 603 729 782 1,069 695 672 322	10 17 11 9 10 9 12 10 9 12 10 9 115 9 115 9 110 9 112 100 9 9 12 10 9 9	TARBP1, TARBP1, IRF2BP2, IRF2BP2, IRF2BP2,	No non-overlappi No non-overlappi TARBP1 TARBP1 U8 U8 IRF2BP2 IRF2BP2 IRF2BP2 IRF2BP2 IRF2BP2 No non-overlappi No non-overlappi	ng genes wit ng genes wit 20,037 37,325 49,330 48,657 1,123 1,459 2,857 19,507 ng genes wit ng genes wit	hin 50,000bp hin 50,000bp IRF2BP2 U8 U8 U8 hin 50,000bp hin 50,000bp	4,107 13,700 14,564 35,630
$ \frac{1}{1} \frac$	232,639,732 232,680,939 232,701,509 232,718,797 232,745,646 232,746,453 232,801,966 232,809,471 232,810,335 232,813,017 232,813,353 232,814,751 232,902,112 232,902,663 232,926,260 232,957,621 232,974,372 232,974,372 232,979,868 232,981,466 232,983,810 233,067,763	232,640,501 232,681,730 232,701,860 232,719,078 232,746,987 232,802,531 232,810,070 232,811,317 232,813,335 232,813,947 232,815,380 232,831,927 232,902,657 232,903,118 232,926,863 232,958,350 232,975,154 232,979,708 232,980,563 232,984,132 233,068,314	769 791 351 281 668 534 565 599 982 318 594 629 526 545 455 603 729 782 1,069 695 672 322 551	10 17 11 9 10 9 12 10 9 12 10 9 115 9 115 9 110 9 112 100 9 9 12 100 9 9 10 9 9	TARBP1, TARBP1, IRF2BP2, IRF2BP2, IRF2BP2,	No non-overlappi No non-overlappi TARBP1 TARBP1 U8 U8 IRF2BP2 IRF2BP2 IRF2BP2 IRF2BP2 IRF2BP2 No non-overlappi No non-overlappi	ng genes wit ng genes wit 20,037 37,325 49,330 48,657 1,123 1,459 2,857 19,507 ng genes wit ng genes wit	hin 50,000bp hin 50,000bp IRF2BP2 U8 U8 U8 U8 hin 50,000bp hin 50,000bp	4,107 13,700 14,564 35,630 27,320
1 1	232,639,732 232,680,939 232,701,509 232,718,797 232,745,646 232,746,453 232,801,966 232,809,471 232,810,335 232,813,017 232,813,3017 232,813,3017 232,813,3017 232,813,401 232,902,112 232,902,663 232,926,260 232,957,621 232,974,372 232,974,372 232,979,868 232,979,868 232,981,466 232,983,810 233,067,763 233,172,915	232,640,501 232,681,730 232,701,860 232,719,078 232,746,987 232,802,531 232,810,070 232,811,317 232,813,335 232,813,947 232,815,380 232,831,927 232,902,657 232,902,657 232,903,118 232,926,863 232,958,350 232,975,154 232,979,708 232,980,563 232,984,132 233,068,314 233,173,495	769 791 351 281 668 534 565 599 982 318 594 629 526 545 455 603 729 782 1,069 695 672 322 551 580	10 17 11 9 10 9 12 10 9 12 10 9 12 10 9 11 10 9 12 10 9 9 12 10 9 9 12 10 9 9 12 10 9 11	TARBP1, TARBP1, IRF2BP2, IRF2BP2, IRF2BP2,	No non-overlappi No non-overlappi TARBP1 TARBP1 U8 U8 IRF2BP2 IRF2BP2 IRF2BP2 IRF2BP2 IRF2BP2 No non-overlappi No non-overlappi SRP_euk_arch No non-overlappi	ng genes wit ng genes wit 20,037 37,325 49,330 48,657 1,123 1,459 2,857 19,507 ng genes wit ng genes wit	hin 50,000bp hin 50,000bp IRF2BP2 U8 U8 U8 hin 50,000bp hin 50,000bp	4,107 13,700 14,564 35,630 27,320
I 1	232,639,732 232,680,939 232,701,509 232,745,646 232,746,453 232,801,966 232,809,471 232,810,335 232,813,017 232,813,017 232,813,017 232,813,017 232,813,017 232,814,751 232,902,112 232,902,663 232,926,260 232,957,621 232,974,372 232,974,372 232,979,868 232,979,868 232,981,466 232,983,810 233,067,763 233,172,915 233,177,360	232,640,501 232,681,730 232,701,860 232,719,078 232,746,987 232,802,531 232,810,070 232,811,317 232,813,335 232,813,947 232,815,380 232,831,927 232,902,657 232,902,657 232,902,657 232,903,118 232,926,863 232,958,350 232,975,154 232,979,708 232,980,563 232,984,132 233,068,314 233,173,495 233,177,973	769 791 351 281 668 534 565 599 982 318 594 629 526 545 672 782 1,069 695 672 322 551 580 613	10 17 11 9 10 9 12 10 9 12 10 9 12 10 9 11 10 9 12 10 9 9 10 9 9 10 9 9 10 9 9 10	TARBP1, TARBP1, IRF2BP2, IRF2BP2, IRF2BP2,	No non-overlappi No non-overlappi TARBP1 TARBP1 U8 U8 IRF2BP2 IRF2BP2 IRF2BP2 IRF2BP2 IRF2BP2 No non-overlappi No non-overlappi	ng genes wit ng genes wit 20,037 37,325 49,330 48,657 1,123 1,459 2,857 19,507 ng genes wit ng genes wit	hin 50,000bp hin 50,000bp IRF2BP2 U8 U8 U8 bin 50,000bp hin 50,000bp	4,107 13,700 14,564 35,630 27,320
$ \frac{1}{1} \frac$	232,639,732 232,680,939 232,701,509 232,745,646 232,746,453 232,801,966 232,809,471 232,810,335 232,813,017 232,813,313 232,814,751 232,902,112 232,902,663 232,926,260 232,957,621 232,974,372 232,974,372 232,979,868 232,979,868 232,979,868 232,979,868 232,979,868 232,979,868 232,979,868 232,979,868 232,979,868 232,979,868 232,974,372 233,067,763 233,177,360 233,313,466	232,640,501 232,681,730 232,701,860 232,719,078 232,746,987 232,802,531 232,810,070 232,811,317 232,813,335 232,813,947 232,815,380 232,831,927 232,902,657 232,902,657 232,902,657 232,903,118 232,926,863 232,958,350 232,975,154 232,979,708 232,980,563 232,984,132 232,984,132 233,068,314 233,173,495 233,17,973 233,314,003	769 791 351 281 668 534 565 599 982 318 594 629 526 545 603 729 782 1,069 695 672 322 551 580 613 537	10 17 11 9 10 9 12 10 9 12 10 9 12 10 9 11 10 9 9 10 9 9 10 9 9 10 9 9 10 9 9 10 9 9 10 9 9 10 10 9 9 12 12 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 9 112 10 9 9 9 112 10 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	TARBP1, TARBP1, IRF2BP2, IRF2BP2, IRF2BP2,	No non-overlappi No non-overlappi TARBP1 TARBP1 U8 U8 IRF2BP2 IRF2BP2 IRF2BP2 IRF2BP2 IRF2BP2 No non-overlappi No non-overlappi No non-overlappi No non-overlappi No non-overlappi No non-overlappi No non-overlappi No non-overlappi No non-overlappi SRP_euk_arch No non-overlappi	ng genes wit ng genes wit 20,037 37,325 49,330 48,657 1,123 1,459 2,857 19,507 ng genes wit ng genes wit	hin 50,000bp hin 50,000bp IRF2BP2 U8 U8 U8 hin 50,000bp hin 50,000bp	4,107 13,700 14,564 35,630 27,320 13,122
1 1	232,639,732 232,680,939 232,701,509 232,745,646 232,746,453 232,801,966 232,809,471 232,810,335 232,813,017 232,813,353 232,814,751 232,831,401 232,902,112 232,902,663 232,926,260 232,957,621 232,974,372 232,979,868 232,974,372 232,979,868 232,979,868 232,979,868 232,979,868 232,979,868 232,979,868 232,979,868 232,979,868 232,974,372 233,067,763 233,177,360 233,313,466 233,358,301	232,640,501 232,681,730 232,701,860 232,719,078 232,746,987 232,802,531 232,810,070 232,811,317 232,813,335 232,813,947 232,815,380 232,831,927 232,902,657 232,902,657 232,903,118 232,926,863 232,958,350 232,975,154 232,979,708 232,980,563 232,984,132 232,984,132 233,068,314 233,173,495 233,17,973 233,314,003 233,359,104	769 791 351 281 668 534 565 599 982 318 594 629 526 545 603 729 782 1,069 695 672 322 551 580 613 537 803	10 17 11 9 10 9 12 10 9 12 10 9 115 9 115 9 110 9 110 9 9 10 9 9 10 9 9 10 9 9 10 9 9 10 9 9 10 10 9 9 12 12 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 110 9 9 112 10 9 9 110 9 9 110 9 9 110 9 9 110 9 9 10 9 9 10 10 9 9 9 10 10 9 9 9 10 10 9 9 9 10 10 9 9 9 10 10 9 9 9 10 10 9 9 9 10 10 9 9 9 10 10 9 9 9 10 10 9 9 9 10 10 9 9 9 10 10 9 9 9 10 10 9 9 9 10 10 9 9 10 10 9 9 10 10 9 9 9 10 10 9 9 9 10 10 9 9 10 10 9 9 10 10 9 9 10 10 9 9 10 10 9 9 10 10 9 9 10 10 9 9 10 10 9 9 10 10 10 9 9 10 10 10 9 9 10 10 10 10 10 10 10 10 10 10 10 10 10	TARBP1, TARBP1, IRF2BP2, IRF2B	No non-overlappi No non-overlappi TARBP1 TARBP1 U8 U8 IRF2BP2 IRF2BP2 IRF2BP2 IRF2BP2 IRF2BP2 No non-overlappi No non-overlappi No non-overlappi No non-overlappi No non-overlappi No non-overlappi No non-overlappi No non-overlappi No non-overlappi No non-overlappi SRP_euk_arch No non-overlappi SRP_euk_arch No non-overlappi SNORA14	ng genes wit ng genes wit 20,037 37,325 49,330 48,657 1,123 1,459 2,857 19,507 ng genes wit ng genes wit	hin 50,000bp hin 50,000bp IRF2BP2 U8 U8 U8 bin 50,000bp hin 50,000bp RP4-597N16.1 RBM34	4,107 13,700 14,564 35,630 27,320 27,320 13,122 2,469
1 1	232,639,732 232,680,939 232,701,509 232,745,646 232,746,453 232,801,966 232,809,471 232,810,335 232,813,017 232,813,017 232,813,353 232,814,751 232,902,112 232,902,663 232,926,260 232,957,621 232,974,372 232,974,372 232,979,868 232,979,868 232,979,868 232,979,868 232,979,868 232,979,868 232,979,868 232,979,868 232,979,868 232,979,868 232,979,868 232,979,868 232,979,868 232,979,868 232,979,868 233,067,763 233,177,360 233,313,466 233,358,301 233,390,762	232,640,501 232,681,730 232,701,860 232,719,078 232,746,987 232,802,531 232,810,070 232,811,317 232,813,335 232,813,947 232,815,380 232,831,927 232,902,657 232,902,657 232,902,657 232,902,657 232,903,118 232,926,863 232,958,350 232,975,154 232,979,708 232,980,563 232,984,132 232,984,132 233,068,314 233,173,495 233,17,973 233,314,003 233,359,104 233,391,613	769 791 351 281 668 534 565 599 982 318 594 629 526 545 603 729 782 1,069 695 672 322 551 580 613 537 803 851	10 17 11 9 10 9 12 10 9 12 10 9 115 9 115 9 110 9 112 100 9 9 102 10 9 9 100 9 9 100 9 9 100 9 9 100 9 100 9 12 12 100 9 9 12 12 100 9 9 12 12 100 9 9 12 12 100 9 9 12 12 100 9 9 12 12 100 9 9 12 12 100 9 9 12 12 100 9 9 12 12 100 9 9 12 12 100 9 9 12 12 100 9 9 12 12 100 9 9 12 12 100 9 9 12 12 10 9 12 10 9 9 12 12 10 9 9 12 12 10 9 9 12 12 10 9 9 12 12 10 9 9 12 12 10 9 9 12 12 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 110 9 9 110 9 9 110 9 9 10 10 9 9 10 10 9 9 10 10 9 9 10 10 9 9 10 10 9 9 10 10 9 9 10 10 9 9 10 10 9 9 10 10 9 9 10 10 9 9 10 10 9 9 10 10 9 9 10 10 9 9 10 10 10 9 9 10 10 10 9 9 10 10 10 9 9 10 10 10 9 9 10 10 10 10 9 9 10 10 10 10 9 10 10 10 10 10 10 10 10 10 10 10 10 10	TARBP1, TARBP1, IRF2BP2, IRF2B	No non-overlappi No non-overlappi TARBP1 TARBP1 U8 U8 IRF2BP2 IRF2BP2 IRF2BP2 IRF2BP2 IRF2BP2 No non-overlappi No non-overlappi No non-overlappi No non-overlappi No non-overlappi No non-overlappi No non-overlappi No non-overlappi SRP_euk_arch No non-overlappi SRP_euk_arch No non-overlappi SRP_euk_arch	ng genes wit ng genes wit 20,037 37,325 49,330 48,657 1,123 1,459 2,857 19,507 ng genes wit ng genes wit a8,242 ng genes wit	hin 50,000bp hin 50,000bp IRF2BP2 U8 U8 U8 U8 hin 50,000bp hin 50,000bp KP4-597N16.1 RBM34 ARID4B	4,107 13,700 14,564 35,630 27,320 13,122 2,469 5,220
$ \frac{1}{1} \frac$	232,639,732 232,680,939 232,701,509 232,718,797 232,745,646 232,746,453 232,801,966 232,809,471 232,810,335 232,813,017 232,813,353 232,814,751 232,831,401 232,902,112 232,902,663 232,926,260 232,957,621 232,974,372 232,978,639 232,979,868 232,981,466 232,983,810 233,067,763 233,177,360 233,313,466 233,358,301 233,390,762 233,557,341	232,640,501 232,681,730 232,701,860 232,719,078 232,746,987 232,802,531 232,810,070 232,811,317 232,813,335 232,813,947 232,815,380 232,831,927 232,902,657 232,902,657 232,902,657 232,902,657 232,903,118 232,926,863 232,958,350 232,975,154 232,979,708 232,980,563 232,984,132 232,984,132 233,068,314 233,177,973 233,314,003 233,359,104 233,359,580	769 791 351 281 668 534 565 599 982 318 594 629 526 545 603 729 782 1,069 695 672 322 551 580 613 537 803 851 2,239	10 17 11 9 10 9 12 10 9 12 10 9 15 9 11 10 9 12 10 9 10 9 9 10 9 9 10 9 9 10 9 9 10 9 9 10 9 9 10 9 9 12 12 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 110 9 9 10 9 9 10 10 9 9 9 10 10 9 9 9 10 9 9 9 10 10 9 9 9 10 9 9 9 10 9 9 9 10 9 9 9 10 9 9 9 10 9 9 9 10 9 9 9 10 9 9 9 10 9 9 9 10 9 9 9 10 9 9 9 10 9 9 9 10 9 9 9 10 9 9 9 10 9 9 9 10 9 9 9 10 9 9 9 10 9 9 9 10 9 9 9 9	TARBP1, TARBP1, TARBP1, IRF2BP2, IRF2BP	No non-overlappi No non-overlappi TARBP1 TARBP1 U8 U8 IRF2BP2 IRF2BP2 IRF2BP2 IRF2BP2 IRF2BP2 No non-overlappi No non-overlappi No non-overlappi No non-overlappi No non-overlappi No non-overlappi No non-overlappi No non-overlappi SRP_euk_arch No non-overlappi SRP_euk_arch No non-overlappi SRP_euk_arch No non-overlappi SRP_euk_arch No non-overlappi SRDRA14 RP11-382D8.3	ng genes wit ng genes wit 20,037 37,325 49,330 48,657 1,123 1,459 2,857 19,507 ng genes wit ng genes wit	hin 50,000bp hin 50,000bp IRF2BP2 U8 U8 U8 bin 50,000bp hin 50,000bp KP4-597N16.1 RBM34 ARID4B	4,107 13,700 14,564 35,630 27,320 13,122 2,469 5,220
1 1	232,639,732 232,680,939 232,701,509 232,718,797 232,745,646 232,746,453 232,801,966 232,809,471 232,810,335 232,813,017 232,813,353 232,814,751 232,831,401 232,902,112 232,902,663 232,926,260 232,957,621 232,974,372 232,974,372 232,979,868 232,979,868 232,979,868 232,979,868 232,979,868 232,979,868 232,979,868 232,979,868 232,979,868 232,979,868 232,979,868 232,979,868 232,979,868 233,067,763 233,177,360 233,313,466 233,357,341	232,640,501 232,681,730 232,701,860 232,719,078 232,746,987 232,802,531 232,810,070 232,811,317 232,813,335 232,813,947 232,815,380 232,831,927 232,902,657 232,902,657 232,902,657 232,903,118 232,926,863 232,958,350 232,975,154 232,979,708 232,980,563 232,984,132 232,984,132 233,068,314 233,173,495 233,177,973 233,314,003 233,359,104 233,359,580	769 791 351 281 668 534 565 599 982 318 594 629 526 545 455 603 729 782 1,069 695 672 322 551 580 613 537 803 851 2,239	10 17 11 9 10 9 12 10 9 12 10 9 11 10 9 12 10 9 11 10 9 9 10 9 9 10 9 9 10 9 9 10 9 9 10 9 9 10 9 9 10 9 9 12 12 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 112 10 9 9 110 9 9 10 10 9 9 10 10 9 9 10 10 9 9 10 10 9 9 9 10 10 9 9 9 10 9 9 9 10 9 9 9 10 9 9 9 10 9 9 9 10 9 9 9 10 9 9 9 10 9 9 9 10 9 9 9 10 9 9 9 10 9 9 9 10 9 9 9 10 9 9 9 10 9 9 9 10 9 9 9 10 9 9 9 10 9 9 9 9	TARBP1, TARBP1, TARBP1, IRF2BP2, IRF2BP2, IRF2BP2, IRF2BP2, TOMM20, RBM34, ARID4B, GGPS1,	No non-overlappi No non-overlappi TARBP1 TARBP1 U8 U8 IRF2BP2 IRF2BP2 IRF2BP2 IRF2BP2 IRF2BP2 No non-overlappi No non-overlappi No non-overlappi No non-overlappi No non-overlappi No non-overlappi No non-overlappi No non-overlappi No non-overlappi SRP_euk_arch No non-overlappi SRP_euk_arch No non-overlappi SRP_euk_arch No non-overlappi SNORA14 RP11-382D8.3	ng genes wit ng genes wit 20,037 37,325 49,330 48,657 1,123 1,459 2,857 19,507 ng genes wit ng genes wit	hin 50,000bp hin 50,000bp IRF2BP2 U8 U8 U8 bin 50,000bp hin 50,000bp KP4-597N16.1 RBM34 ARID4B	4,107 13,700 14,564 35,630 27,320 13,122 2,469 5,220
1 1	232,639,732 232,680,939 232,701,509 232,745,646 232,746,453 232,801,966 232,809,471 232,810,335 232,813,017 232,813,017 232,813,353 232,814,751 232,902,112 232,902,663 232,926,260 232,957,621 232,974,372 232,974,372 232,979,868 232,974,372 232,979,868 232,979,868 232,974,372 232,979,868 232,979,868 232,974,372 232,979,868 232,974,372 233,177,360 233,177,360 233,313,466 233,358,301 233,390,762 233,557,341 233,597,045	232,640,501 232,681,730 232,701,860 232,719,078 232,746,987 232,802,531 232,810,070 232,811,317 232,813,335 232,813,947 232,815,380 232,831,927 232,902,657 232,902,657 232,902,657 232,902,657 232,903,118 232,926,863 232,958,350 232,975,154 232,979,708 232,980,563 232,984,132 232,984,132 233,068,314 233,173,495 233,177,973 233,314,003 233,359,104 233,359,580 233,597,667	769 791 351 281 668 534 565 599 982 318 594 629 526 545 603 729 782 1,069 695 672 322 551 580 613 537 803 851 2,239 622	10 17 11 9 10 9 12 10 9 12 10 9 11 10 9 11 10 9 10 9	TARBP1, TARBP1, TARBP1, IRF2BP2, IRF2BP	No non-overlappi No non-overlappi TARBP1 TARBP1 U8 U8 IRF2BP2 IRF2BP2 IRF2BP2 IRF2BP2 IRF2BP2 No non-overlappi No non-overlappi No non-overlappi No non-overlappi No non-overlappi No non-overlappi No non-overlappi No non-overlappi SRP_euk_arch No non-overlappi SRP_euk_arch No non-overlappi SRP_euk_arch No non-overlappi SNORA14 RP11-382D8.3	ng genes wit ng genes wit 20,037 37,325 49,330 48,657 1,123 1,459 2,857 19,507 ng genes wit ng genes wit 38,242 ng genes wit 37,164	hin 50,000bp hin 50,000bp IRF2BP2 U8 U8 U8 hin 50,000bp hin 50,000bp KP4-597N16.1 RBM34 ARID4B RP11-382D8.5	4,107 13,700 14,564 35,630 27,320 13,122 2,469 5,220 4,847

1	233,644,908	233,645,569	661	9	TBCE,			B3GALNT2	34,321
1	233,733,530	233,733,814	284	10	B3GALNT2,	RP4-534P7.2	16,078	RP11-	34,158
								293G6B.6	
1	233,734,001	233,735,136	1,135	13	B3GALNT2,	RP4-534P7.2	14,756	RP11-	32,836
								293G6B.6	
1	233,870,370	233,870,875	505	9	GNG4,			LYST	20,089
1	234,064,343	234,064,835	492	11	LYST,			hsa-mir-1537	18,088
1	234,071,537	234,072,081	544	10	LYST,			hsa-mir-1537	10,842
1	234,095,838	234,096,385	547	10	LYST,	hsa-mir-1537	12,855		
1	234,130,646	234,131,792	1,146	9		U6	13,546		
1	234,135,386	234,135,877	491	9		U6	9,461		
1	234,147,201	234,147,692	491	12				U6	1,757
1	234,150,152	234,150,650	498	10				U6	4,708
1	234,150,941	234,151,386	445	9				U6	5,497
1	234,201,522	234,202,112	590	10				NID1	3,652
1	234,250,286	234,250,786	500	9	NID1,	No non-overlappi	ng genes wit	hin 50,000bp	
1	234,288,008	234,288,487	479	10	NID1,	No non-overlappi	ng genes wit	hin 50,000bp	
1	234,296,504	234,297,118	614	11		NID1	1,400		
1	234,326,862	234,327,477	615	15		AL122018.37	12,492		
1	234,371,492	234,372,176	684	9	000/000	GPR137B	321		
1	234,372,445	234,373,580	1,135	9	GPR137B,			AL122018.37	32,210
1	234,511,509	234,512,477	968	9	ERO1LB,			RP11-478H16.1	3,422
1	234,624,803	234,625,649	846	10	EDARADD,	No non-overlappi	ng genes wit	nin 50,000bp	
1	224 606 925	224 607 105	270	0	AL 130 103.9,	No non overlanni	na aonoo wit	hin 50 000hn	
1	234,090,025	234,097,195	370	9	EDARADD, AI 136105.9	No non-ovenappi	ng genes wit	nin 50,000bp	
1	234 753 800	234 754 109	309	11	I GALS8			HFATR1	26 485
1	234 754 279	234 754 732	453	9	LGALS8			HEATR1	25 862
1	234 834 127	234 835 298	1 171	10	HEATR1	No non-overlappi	na aenes wit	hin 50 000hp	20,002
1	234 972 785	234 973 129	344	10	ACTN2	No non-overlappi	ng genes wit	hin 50,000bp	
1	235 024 734	235 025 651	917	14	MTR	RP11-182B22 2	23 906	ACTN2	30 871
1	235 077 581	235 077 961	380		MTR		20,000	RP11-182B22 2	27 145
1	235,102,060	235,102,442	382	9	MTR.	AL359259.18	28.442		
1	235,193,395	235,193,699	304	9		RP11-182B22.4	17.563	MT1P2	40.411
1	235.242.753	235,243,164	411	12		MT1P2	8.458		- ,
1	235,832,804	235,833,383	579	9	RYR2,	AL442065.11	47,716		
	, ,	, ,			AL365332.9,				
1	236,103,361	236,103,915	554	15				ZP4	8,418
1	236,127,726	236,128,118	392	9		ZP4	7,168		
1	236,661,174	236,661,541	367	9				AL359551.13-2	48,782
1	237,940,820	237,941,323	503	9	CHRM3,	No non-overlappi	ng genes wit	hin 50,000bp	
1	238,321,294	238,322,104	810	9	FMN2,	No non-overlappi	ng genes wit	hin 50,000bp	
1	238,518,598	238,518,893	295	10	FMN2,	No non-overlappi	ng genes wit	hin 50,000bp	
1	238,827,044	238,827,605	561	9	GREM2,	RP11-467l20.4	46,743	RP11-467I20.3	38,917
1	239,620,771	239,621,708	937	9		RGS7	33,618		
1	239,653,628	239,653,947	319	16		No non-overlappi	ng genes wit	hin 50,000bp	
1	240,077,753	240,078,617	864	12	EXU1,			RP11-553N16.1	15,041
1	240,124,110	240,124,463	353	9				EXU1	4,440
1	240,312,972	240,313,386	414	9		No. margare de la		PLD5	4,926
1	240,697,264	240,697,786	522	9	PLD5,	No non-overlappi	ng genes wit	nin 50,000bp	
1	241,485,438	241,486,460	1,022	13	SDCCAG8,	CEP1/U	107		
1	241,603,221	241,603,669	448	y Q	SDCCAG8,	No non-overlappi	ng genes wit	hin 50,000bp	
1	241,727,729	241,728,308	579	9	SDCCAG8,	No non-overlappi	ng genes wit	nin 50,000bp	
1	241 060 425	241 060 937	112	0	ΔKT3	No non-ovorlanni	na aenec wit	hin 50 000bn	
1	241,909,423	241,909,037	359	9	ARTS,	No non-overlappi	ng genes wit	hin 50,000bp	
1	242 276 869	242,100,300	1 366	9		7NE238	ווש שפוופס שונ 2 מבח	iiii 30,000p	
1	242 281 082	242 282 506	1,300 524	9	7NF238	No non-overlanni	2,900	hin 50 000bp	
1	242,201,902	242,202,000	324	9	ZINI 200,		ng genes wit	7NE238	7 125
1	242 411 302	242 4/5 070	677	9		No non-overlanni	na aenes wit	hin 50 000hn	7,100
1	242 555 376	242 556 076	700	9		C1orf100	26 484	iiii 30,000p	
1	242 595 528	242 595 850	322	10	C1orf100	0101100	20,704	RP11-518I 10.3	29 050
1	242 882 518	242 883 230	712	12	PPPDF1			C1orf101	12 237
1	242 883 797	242 884 219	422	۲. ۹	PPPDF1			C1orf101	13 516
1	242 897 471	242 897 885	414	Q	PPPDF1			RP11-173A6 2	26 470
•	,007,471	,007,000		5	··· ·· ·· ·· ·· ·· ·· ·· ·· ·· ·· ·· ··	1	1		20,470

1	242,922,672	242,923,080	408	9	PPPDE1,			RP11-173A6.2	1,275
1	243,063,698	243,065,526	1,828	9	BX323046.3-2,	FAM36A	61	BX323046.3-1	7,435
1	243,094,156	243,094,851	695	10	HNRNPU,	C1orf199	17,380	FAM36A	20,937
1	243,185,370	243,185,682	312	9		EFCAB2	14,112	7SK	11,229
2	3,600,444	3,600,915	471	12	RPS7,	RNASEH1	16,629	AC010907.10	42,098
2	9,827,642	9,828,434	792	9		U4	29,279		
2	10,008,440	10,009,552	1,112	9	GRHL1,			TAF1B	16,446
2	10,874,893	10,875,242	349	10	PDIA6,			ATP6V1C2	32,214
2	11,475,501	11,475,850	349	9				E2F6	26,102
2	11,502,215	11,502,640	425	9	E2F6,	No non-overlappi	ng genes wit	hin 50,000bp	
2	11,801,532	11,801,850	318	11	LPIN1,	No non-overlappi	ng genes wit	hin 50,000bp	
2	12,772,682	12,773,315	633	9		TRIB2	1,151		
2	15,618,618	15,619,106	488	11	NAG,	DDX1	29,647		
2	17,211,087	17,211,586	499	9		AC096556.1-1	43,199		
2	17,798,979	17,799,368	389	11	SMC6, GEN1,	No non-overlappi	ng genes wit	hin 50,000bp	
2	17,875,244	17,876,067	823	9		SMC6	30,301	MSGN1	13,396
2	18,604,986	18,605,303	317	10	RDH14,			U6	22,811
2	19,426,012	19,426,602	590	9		OSR1	4,147		
2	19,964,942	19,965,696	754	9	TTC32,			WDR35	7,816
2	20,510,964	20,511,539	575	9	RHOB,	Y_RNA	32,547		
2	23,427,878	23,428,176	298	12		AC012506.9	46,809		
2	24,152,570	24,152,995	425	11	AC008073.5,			TP53I3	814
2	24,160,146	24,161,426	1,280	9	TP53I3,	AC008073.5	7,328		
2	24,436,420	24,437,214	794	9	ITSN2,	AC009228.4-2	3,830		
2	25,048,334	25,048,843	509	13	DNAJC27,	SNORD14	2,484		
2	25,118,858	25,119,883	1,025	9	EFR3B,	SRP_euk_arch	14,522	AC013267.4	36,391
2	25,740,847	25,741,553	706	9	DTNB,			Y_RNA	31,896
2	25,954,284	25,955,543	1,259	9	ASXL2,			AC064847.4	7,794
2	26,350,677	26,351,045	368	9	HADHB,	HADHA	29,579	GPR113	33,500
2	26,681,650	26,682,153	503	10	CIB4,	OTOF	46,580	C2orf70	25,746
2	27,078,892	27,079,211	319	9	AC011740.7,	TMEM214	30,138		
					MAPRE3,				
2	27,126,995	27,127,640	645	21		AGBL5	355	TMEM214	8,930
2	27,144,809	27,145,255	446	10	AGBL5,	EMILIN1	9,779		
2	27,157,570	27,158,140	570	12	EMILIN1,	КНК	4,975		
2	27,446,183	27,447,108	925	9	EIF2B4, SNX17,			ZNF513	6,498
2	27,740,024	27,740,654	630	12	SLC4A1AP,	SUPT7L	13		
2	27,966,462	27,967,260	798	9	RBKS, BRE,	No non-overlappi	ng genes wit	hin 50,000bp	
2	28,432,350	28,432,878	528	9		FOSL2	36,295	BRE	17,078
2	28,696,945	28,698,018	1,073	9	PLB1,	No non-overlappi	ng genes wit	hin 50,000bp	
2	28,946,385	28,946,941	556	13	TRMT61B,	SNORD92	43,091	SPDYA	19,404
•	00.044.700	00.044.040	044	45	WDR43,				10 701
2	29,314,729	29,314,940	211	15	ALN,	A CO10007 0 4	04.000		48,721
2	30,166,945	30,167,602	05/	10		ACU10907.6-1	24,362	ACU16907.2	12,303
2	32,350,339	32,357,014	6/5	9	TIPF4,	NLRG4	11,912		
2	34,356,636	34,357,179	543	9	EIEOAKO		ng genes wit		10.001
2	37,190,872	37,191,430	1 000	9	EIFZAKZ,		25,883		10,981
2	37,404,385	37,405,407	1,022	9	EIFZAKZ,	PRKUJ	5,844		7,010
2	37,470,498	37,470,780	282	10		No non cuertare			22,530
2	31,152,518	31,153,002	424	10		No non-overlappi	ng genes wit	hin 50,000bp	
2	30,450,939	30,457,440	501	9	ATLZ,	No non-overlappi	ng genes wit	hin 50,000bp	
2	30,521,400	30,521,990	504	9		No non-overlappi	ng genes wit	hin 50,000bp	
2	39 542 055	39 542 274	240	9		No non-overlappi	ng genes wit	hin 50,000bp	
2	30,543,055	30,343,374	319	9		No non-overlappi	ng genes wit	hin 50,000bp	
2	30,003,340	30,003,102	442	9		No non-overlappi	ng genes wit	hin 50,000bp	
2	20,140,000	30,141,330	444	9	GALIVI,		ang genes wit		00.457
2	30,001,390	30,001,790	592	9	GALINI,	GEIVIIINO	30,390	SFRS/	22,437
2	38,831,684	38,832,201	517	15	SFKSI, GEMINA			GALIN	16,655
2	39 517 859	39 518 211	323	10		ΜΑΡ4Κ3	61		
2	41 495 180	41 495 590	<u>4</u> 01	10		No non-overlappi	na aenes wit	hin 50.000bp	
2	41 986 168	41 986 602	43/	10		Y RNA	48 152	AC104654 3	11 485
2	42 223 434	42 223 800	375	10		FMI 4	26 188		11,405
2	42 371 124	42 371 462	338	9 0	FMI 4	No non-overlappi	na aenes wit	hin 50 000hn	
2	42 890 459	42 891 508	1 049	11	,	AC098824 5	11 103	AC098824 6	15 461
-	12,000,400	12,001,000	1,540		1		. 1, 100		10,401

2	42,987,197	42,988,245	1,048	9		No non-overlappi			
2	43,697,018	43,697,401	383	9				Y RNA	4,120
2	44,124,922	44.125.251	329	12		LRPPRC	48.274		21.286
2	44,167,815	44,168,311	496	9		AC019129.1	21.018		,
2	44,441,590	44,442,731	1,141	9	PREPL.		,	SLC3A1	40,126
	, ,	, , -	,		C2orf34,				-, -
2	45,280,724	45,281,001	277	9	AC009236.4,	No non-overlappi	ng genes wit	hin 50,000bp	
2	45,731,547	45,731,922	375	14		PRKCE	625		
2	46,115,086	46,115,507	421	11	PRKCE.	AC017078.1	30,134		
2	46.202.007	46.202.328	321	9	PRKCE.	No non-overlappi	na aenes wit	hin 50.000bp	
2	47 257 002	47 257 776	774	10	CALM2	C2orf61	21 072		
2	47 438 136	47 438 450	314	9	FPCAM			7SK	1 655
2	47 484 017	47 484 359	342	9	MSH2	7SK	43 589	FPCAM	16,356
2	48 188 236	48 188 624	388	9		No non-overlanni	na aenes wit	hin 50 000hn	10,000
2	54 410 912	54 411 549	637	9	C2orf73		ing gonoo mi	ACYP2	24 975
2	54 978 621	54 978 944	323	9	EMI 6	AC013414 7	30 178	7.0112	24,070
2	55 500 420	55 500 909	480	28		A0010414.7	30,170	BTE3L2	14 885
2	55 607 035	55 608 077	1 042	10	SMEK2	AC015082 0-1	37 805	DNDT1	16 00/
2	55 774 103	55,030,377	1,042	10		No non ovorlanni	57,005	hin 50 000hn	10,334
2	59 126 017	59 127 516	42Z	9		No non overlappi	ng genes wit	hin 50,000bp	
2	60 625 102	50,127,510	507	9	vrnz,			1111 30,000bp	
2	60,035,105	60 755 512	327	10		AC012409 10 2	26 611	AC012409 10 1	22 455
2	60,755,096	60,755,512	410	9		ACU12490.10-2	30,011	ACU12496.10-1	33,435
2	61,097,323	61,098,385	1,062	11	PUSIU, PEXIS,	KIAA 1841	48,187	55_IRINA	17,816
2	62,296,020	62,296,384	364	10	B3GNT1,	AC093401.4-2	49,250	SRP_euk_arch	46,645
2	63,669,036	63,669,589	553	10	C20ff86,	MDH1	/	DELLA	10.000
2	64,130,388	64,130,679	291	10		VPS54	30,670	PELI1	42,820
2	64,738,476	64,738,842	366	y Q		SERTAD2	3,926		
2	64,810,951	64,811,583	632	9		No non-overlappi	ng genes wit	nin 50,000bp	
2	65,513,183	65,513,670	487	13		SPRED2	368		
2	66,515,504	66,515,914	410	11		MEIS1	122		
2	68,400,346	68,400,696	350	10	CNRIP1,	PLEK	45,130	AC017083.7-1	46,504
2	68,547,865	68,548,485	620	9	FBXO48, APLF,	No non-overlappi	ng genes wit	hin 50,000bp	
2	69,909,838	69,910,336	498	13	GMCL1,			ANXA4	2,743
2	70,166,496	70,167,294	798	9		PCBP1	812		
2	70,223,269	70,223,569	300	11				C2orf42	6,954
2	70,329,223	70,329,758	535	10	TIA1,	PCYOX1	9,002	hsa-mir-1285-2	3,796
2	70,373,836	70,374,543	707	9	SNRPG,			FAM136A	2,070
2	70,698,140	70,698,494	354	9				ADD2	44,279
2	70,848,578	70,848,927	349	9	ADD2, FIGLA,	AC007395.3	34,870	CLEC4F	40,363
2	71,210,347	71,210,878	531	9	MCEE,	MPHOSPH10	74		
2	71,237,945	71,238,369	424	9				MPHOSPH10	7,207
2	71,357,070	71,357,398	328	12	ZNF638,	PAIP2B	49,361		
2	72,943,207	72,943,484	277	11		SPR	24,572		
2	73,370,906	73,371,491	585	10		AC069404.5	7,829	EGR4	75
2	74,472,373	74,472,814	441	9	DCTN1,	AC005041.2	16,047	C2orf81	22,150
2	74,535,308	74,535,884	576	18	INO80B,	WBP1	3,151	GCS1	5,809
2	74,538,344	74,539,080	736	9	INO80B, WBP1,			GCS1	2,613
2	74,563,658	74,564,243	585	10	TTC31,	CCDC142	27		
2	80,536,368	80,536,745	377	9	CTNNA2,	No non-overlappi	ng genes wit	hin 50,000bp	
2	84,487,193	84,487,577	384	9				SUCLG1	16,588
2	84,539,903	84,540,563	660	9	SUCLG1,	No non-overlappi	ng genes wit	hin 50,000bp	
2	85,006,240	85,006,888	648	13				AC022210.8	8,940
2	85,007,646	85,007,916	270	10		KCMF1	43,811	AC022210.8	10,346
2	85,052,466	85,052,878	412	11	KCMF1,	No non-overlappi	ng genes wit	hin 50,000bp	
2	85,619,220	85,620,046	826	11	MAT2A,			GGCX	9,672
2	85,969,604	85,970,266	662	10	ST3GAL5,	No non-overlappi	ng genes wit	hin 50,000bp	
2	86,275,913	86,276,282	369	11	IMMT,	MRPL35	3,809		
2	88,082,427	88,082,895	468	11		AC108479.5-1	12,338	U2	14,093
2	91,041,163	91,041,619	456	9		AC027612.6-2	1,195		
2	91,125,975	91,126,608	633	13	AC027612.6-2.	AC018696.4	27,798		
2	91,127,417	91,127,917	500	9	AC027612.6-2.	AC018696.4	29,240		
2	91,136,196	91,136,495	299	10	AC027612.6-2.	AC018696.4	38.019		
2	91,145,044	91,145,493	449	11	AC027612.6-2,	AC018696.4	46,867		
2	91,145,782	91,146,298	516	9	AC027612.6-2.	AC018696.4	47,605		
·					. ,				

2	91 150 525	91 151 192	667	12	AC027612 6-2			AC027612 6-3	45 967
2	01 157 258	01 157 087	720	14	AC027612.6.2			AC027612.6.3	30 172
2	91,157,250	91,157,907	129	14	AC027012.0-2,			AC027012.0-3	39,172
2	91,159,032	91,159,446	414	11	AC027612.6-2,			AC027612.6-3	37,713
2	91,160,729	91,161,248	519	10	AC027612.6-2,			AC027612.6-3	35,911
2	91,169,237	91,169,811	574	9	AC027612.6-2,			AC027612.6-3	27,348
2	91.170.820	91.171.313	493	11	AC027612.6-2.			AC027612.6-3	25.846
2	91 175 775	91 176 662	887	9	AC027612 6-2	5S_rRNA	49 948	AC027612 6-3	20 497
2	01,170,170	01,170,002	007	12	AC027612.6 2,		47,572	AC027612.6 2	10 100
2	91,170,130	91,179,037	099	13	AC027012.0-2,	JJ_IRNA	47,573	AC027012.0-3	10,122
2	91,179,113	91,179,461	348	11	AC027612.6-2,	55_rrna	47,149	AC027612.6-3	17,698
2	91,180,058	91,180,953	895	15	AC027612.6-2,	5S_rRNA	45,657	AC027612.6-3	16,206
2	91,181,596	91,181,913	317	11	AC027612.6-2,	5S_rRNA	44,697	AC027612.6-3	15,246
2	91.182.018	91.183.055	1.037	12	AC027612.6-2.	5S rRNA	43.555	AC027612.6-3	14.104
2	95 194 799	95 195 242	443	13	7NF2	ZNE514	5 809		, -
2	09 500 620	09 501 702	1 1 5 4	10	C2 or f G 4	2111 314	5,005		10 209
2	90,090,009	90,591,795	1,134	9	UNC50			WGA14A	10,200
~	00 740 070	00 740 004	000	10		N			
2	98,712,972	98,713,364	392	12	MGAT4A,	No non-overlappi	ng genes wit	nin 50,000bp	
2	99,163,951	99,164,449	498	11	MRPL30,	MITD1	6		
2	101,128,224	101,128,637	413	9	TBC1D8,	No non-overlappi	ng genes wit	hin 50,000bp	
2	101,291,457	101,291,937	480	11	RNF149,	SNORD89	35,514	C2orf29	38,249
2	104 827 938	104 828 461	523	9	,	POU3E3	9 940		,
2	109 701 004	109 702 592	599	11		1 0 0 0 1 0	0,010		31 860
2	100,701,994	100,702,502	040	11	NANDEZ,	NI			51,000
2	109,118,621	109,119,237	616	y		No non-overlappi	ng genes wit	nin 50,000bp	
2	111,642,539	111,642,969	430	9				BCL2L11	46
2	113,016,302	113,016,808	506	10	POLR1B,			TTL	9,613
2	113.058.080	113.059.025	945	10	CHCHD5.	Y RNA	4,448	POLR1B	6.201
2	113 238 044	113 239 077	1 033	9	CKAP2I		, -	II 1A	8 889
2	114.057.502	114 057 970	276	11		EAM20D	202		4 5 4 7
2	114,007,003	114,007,079	370	11		FAIVIJ9D	202	FAIVI 130D	4,047
2	114,363,505	114,364,026	521	11	ACTR3,	AC104653.5	41,222		
2	119,480,376	119,480,644	268	10				MARCO	11,670
2	119,905,405	119,905,891	486	11	TMEM37,			SCTR	8,000
2	120.233.440	120.234.168	728	10	PTPN4.	No non-overlappi	na aenes wit	hin 50.000bp	
2	121 026 786	121 027 383	597	9	,	No non-overlappi	na aenes wit	hin 50 000hn	
		121,021,000	001	0		non oronappi	ng gonoo ma		
2	121 030 244	121 020 973	620	0		No non ovorlanni	na aonos wit	hin 50 000hn	
2	121,039,244	121,039,873	629	9		No non-overlappi	ng genes wit	hin 50,000bp	04.000
2 2	121,039,244 121,149,680	121,039,873 121,150,021	629 341	9		No non-overlappi	ng genes wit	hin 50,000bp Y_RNA	24,260
2 2 2 2	121,039,244 121,149,680 121,154,344	121,039,873 121,150,021 121,154,657	629 341 313	9 9 10		No non-overlappi	ng genes wit	hin 50,000bp Y_RNA Y_RNA	24,260 28,924
2 2 2 2 2	121,039,244 121,149,680 121,154,344 121,541,673	121,039,873 121,150,021 121,154,657 121,542,017	629 341 313 344	9 9 10 9		No non-overlappi Y_RNA	ng genes wit 26,917	hin 50,000bp Y_RNA Y_RNA AC016764.8-2	24,260 28,924 32,409
2 2 2 2 2 2	121,039,244 121,149,680 121,154,344 121,541,673 121,554,020	121,039,873 121,150,021 121,154,657 121,542,017 121,554,494	629 341 313 344 474	9 9 10 9 9		No non-overlappi Y_RNA Y_RNA	ng genes wit 26,917 39,264	hin 50,000bp Y_RNA Y_RNA AC016764.8-2 AC016764.8-2	24,260 28,924 32,409 44,756
2 2 2 2 2 2 2 2 2 2	121,039,244 121,149,680 121,154,344 121,541,673 121,554,020 121,602,766	121,039,873 121,150,021 121,154,657 121,542,017 121,554,494 121,603,122	629 341 313 344 474 356	9 9 10 9 9 9		No non-overlappi Y_RNA Y_RNA No non-overlappi	26,917 39,264	hin 50,000bp Y_RNA Y_RNA AC016764.8-2 AC016764.8-2 hin 50 000bp	24,260 28,924 32,409 44,756
2 2 2 2 2 2 2 2 2 2 2 2	121,039,244 121,149,680 121,154,344 121,541,673 121,554,020 121,602,766 122,004,778	121,039,873 121,150,021 121,154,657 121,542,017 121,554,494 121,603,122 122,005,235	629 341 313 344 474 356 457	9 9 10 9 9 10 12		No non-overlappi Y_RNA Y_RNA No non-overlappi No non-overlappi	26,917 39,264 ng genes wit	hin 50,000bp Y_RNA Y_RNA AC016764.8-2 AC016764.8-2 hin 50,000bp bin 50,000bp	24,260 28,924 32,409 44,756
2 2 2 2 2 2 2 2 2 2 2 2 2	121,039,244 121,149,680 121,154,344 121,541,673 121,554,020 121,602,766 122,004,778	121,039,873 121,150,021 121,154,657 121,542,017 121,554,494 121,603,122 122,005,235	629 341 313 344 474 356 457	9 9 10 9 9 10 12	CLASP1, Il/atac	No non-overlappi Y_RNA Y_RNA No non-overlappi No non-overlappi	26,917 39,264 ng genes wit	hin 50,000bp Y_RNA Y_RNA AC016764.8-2 AC016764.8-2 hin 50,000bp hin 50,000bp	24,260 28,924 32,409 44,756
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	121,039,244 121,149,680 121,154,344 121,541,673 121,554,020 121,602,766 122,004,778	121,039,873 121,150,021 121,154,657 121,542,017 121,554,494 121,603,122 122,005,235	629 341 313 344 474 356 457 307	9 9 10 9 9 9 10 12	CLASP1, U4atac,	No non-overlappi Y_RNA Y_RNA No non-overlappi No non-overlappi	26,917 39,264 ng genes wit ng genes wit	hin 50,000bp Y_RNA Y_RNA AC016764.8-2 AC016764.8-2 hin 50,000bp hin 50,000bp	24,260 28,924 32,409 44,756
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	121,039,244 121,149,680 121,154,344 121,541,673 121,554,020 121,602,766 122,004,778 127,002,195	121,039,873 121,150,021 121,154,657 121,542,017 121,554,494 121,603,122 122,005,235 127,002,502	629 341 313 344 474 356 457 307	9 9 10 9 9 9 10 12 9 9	CLASP1, U4atac,	No non-overlappi Y_RNA Y_RNA No non-overlappi No non-overlappi	26,917 39,264 ng genes wit ng genes wit	hin 50,000bp Y_RNA Y_RNA AC016764.8-2 AC016764.8-2 hin 50,000bp hin 50,000bp AC013474.10-1	24,260 28,924 32,409 44,756 28,975
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	121,039,244 121,149,680 121,154,344 121,541,673 121,554,020 121,602,766 122,004,778 127,002,195 127,607,792	121,039,873 121,150,021 121,154,657 121,542,017 121,554,494 121,603,122 122,005,235 127,002,502 127,608,174	629 341 313 344 474 356 457 307 382	9 9 10 9 9 10 12 9 9	CLASP1, U4atac,	No non-overlappi Y_RNA Y_RNA No non-overlappi No non-overlappi BIN1	26,917 39,264 ng genes wit ng genes wit 26,458	hin 50,000bp Y_RNA Y_RNA AC016764.8-2 AC016764.8-2 hin 50,000bp hin 50,000bp AC013474.10-1 CYP27C1	24,260 28,924 32,409 44,756 28,975 49,714
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	121,039,244 121,149,680 121,154,344 121,541,673 121,554,020 121,602,766 122,004,778 127,002,195 127,607,792 127,861,051	121,039,873 121,150,021 121,154,657 121,542,017 121,554,494 121,603,122 122,005,235 127,002,502 127,608,174 127,861,502	629 341 313 344 474 356 457 307 382 451	9 9 10 9 9 10 12 9 9 9 9	CLASP1, U4atac, MAP3K2,	No non-overlappi Y_RNA Y_RNA No non-overlappi No non-overlappi BIN1 PROC	26,917 39,264 ng genes wit ng genes wit 26,458 30,985	hin 50,000bp Y_RNA Y_RNA AC016764.8-2 AC016764.8-2 hin 50,000bp hin 50,000bp AC013474.10-1 CYP27C1	24,260 28,924 32,409 44,756 28,975 49,714
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	121,039,244 121,149,680 121,154,344 121,541,673 121,554,020 121,602,766 122,004,778 127,002,195 127,607,792 127,861,051 127,882,633	121,039,873 121,150,021 121,154,657 121,554,494 121,603,122 122,005,235 127,002,502 127,608,174 127,861,502 127,883,153	629 341 313 344 474 356 457 307 382 451 520	9 9 10 9 10 12 9 9 9 9 11	CLASP1, U4atac, MAP3K2,	No non-overlappi Y_RNA Y_RNA No non-overlappi No non-overlappi BIN1 PROC PROC	26,917 39,264 ng genes wit genes wit 26,458 30,985 9,334	hin 50,000bp Y_RNA Y_RNA AC016764.8-2 AC016764.8-2 hin 50,000bp hin 50,000bp AC013474.10-1 CYP27C1	24,260 28,924 32,409 44,756 28,975 49,714
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	121,039,244 121,149,680 121,154,344 121,541,673 121,554,020 121,602,766 122,004,778 127,002,195 127,607,792 127,861,051 127,882,633 128,294,130	121,039,873 121,150,021 121,154,657 121,542,017 121,554,494 121,603,122 122,005,235 127,002,502 127,608,174 127,861,502 127,883,153 128,294,594	629 341 313 344 474 356 457 307 382 451 520 464	9 9 10 9 9 10 12 9 9 9 9 11 9 9 9 9	CLASP1, U4atac, MAP3K2,	No non-overlappi Y_RNA Y_RNA No non-overlappi No non-overlappi BIN1 PROC PROC WDR33	26,917 39,264 ng genes wit 26,458 30,985 9,334 8,915	hin 50,000bp Y_RNA Y_RNA AC016764.8-2 AC016764.8-2 hin 50,000bp hin 50,000bp AC013474.10-1 CYP27C1 Y_RNA	24,260 28,924 32,409 44,756 28,975 49,714 9,197
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	121,039,244 121,149,680 121,154,344 121,541,673 121,554,020 121,602,766 122,004,778 127,002,195 127,607,792 127,861,051 127,882,633 128,294,130 132,728,389	121,039,873 121,150,021 121,154,657 121,542,017 121,554,494 121,603,122 122,005,235 127,002,502 127,608,174 127,861,502 127,883,153 128,294,594 132,728,668	629 341 313 344 474 356 457 307 382 451 520 464 279	9 9 10 9 9 10 12 9 9 9 11 11 9 9 63	CLASP1, U4atac, MAP3K2,	No non-overlappi Y_RNA Y_RNA No non-overlappi No non-overlappi BIN1 PROC PROC WDR33 5 8S rRNA	26,917 39,264 ng genes wit 26,458 30,985 9,334 8,915 1.041	hin 50,000bp Y_RNA Y_RNA AC016764.8-2 AC016764.8-2 hin 50,000bp hin 50,000bp AC013474.10-1 CYP27C1 Y_RNA SSU rRNA 5	24,260 28,924 32,409 44,756 28,975 49,714 9,197 9,197
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	121,039,244 121,149,680 121,154,344 121,541,673 121,554,020 121,602,766 122,004,778 127,002,195 127,607,792 127,861,051 127,882,633 128,294,130 132,728,389 132,728,823	121,039,873 121,150,021 121,154,657 121,542,017 121,554,494 121,603,122 122,005,235 127,002,502 127,608,174 127,861,502 127,883,153 128,294,594 132,728,668 132,729,920	629 341 313 344 474 356 457 307 382 451 520 464 279 1 097	9 9 9 9 9 10 12 9 9 9 11 9 9 9 63 121	CLASP1, U4atac, MAP3K2, SSU rRNA 5	No non-overlappi Y_RNA Y_RNA No non-overlappi No non-overlappi BIN1 PROC PROC WDR33 5_8S_rRNA 5_8S_rRNA	26,917 39,264 ng genes wit 26,458 30,985 9,334 8,915 1,041 1 475	hin 50,000bp Y_RNA Y_RNA AC016764.8-2 AC016764.8-2 hin 50,000bp hin 50,000bp AC013474.10-1 CYP27C1 Y_RNA SSU_rRNA_5 bsa-mir-663b	24,260 28,924 32,409 44,756 28,975 49,714 9,197 9,197 917
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	121,039,244 121,149,680 121,154,344 121,54,020 121,602,766 122,004,778 127,002,195 127,607,792 127,861,051 127,882,633 128,294,130 132,728,389 132,728,823	121,039,873 121,150,021 121,154,657 121,542,017 121,554,494 121,603,122 122,005,235 127,002,502 127,608,174 127,861,502 127,883,153 128,294,594 132,728,668 132,729,920	629 341 313 344 474 356 457 307 382 451 520 464 279 1,097	9 9 9 9 9 10 12 9 9 9 11 9 9 9 63 121	CLASP1, U4atac, MAP3K2, SSU_rRNA_5, bs2_mir_662b	No non-overlappi Y_RNA Y_RNA No non-overlappi No non-overlappi BIN1 PROC PROC PROC WDR33 5_8S_rRNA 5_8S_rRNA SSLI rRNA 5	26,917 39,264 ng genes wit 26,458 30,985 9,334 8,915 1,041 1,475	hin 50,000bp Y_RNA Y_RNA AC016764.8-2 AC016764.8-2 hin 50,000bp hin 50,000bp AC013474.10-1 CYP27C1 Y_RNA SSU_rRNA_5 hsa-mir-663b	24,260 28,924 32,409 44,756 28,975 49,714 9,197 9,197 917 1,089
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	121,039,244 121,149,680 121,154,344 121,54,020 121,602,766 122,004,778 127,002,195 127,607,792 127,861,051 127,882,633 128,294,130 132,728,389 132,728,389	121,039,873 121,150,021 121,154,657 121,542,017 121,554,494 121,603,122 122,005,235 127,002,502 127,608,174 127,861,502 127,883,153 128,294,594 132,728,668 132,729,920 132,731,213	629 341 313 344 474 356 457 307 382 451 520 464 279 1,097 402	9 9 9 9 9 10 12 9 9 9 11 9 9 9 63 121 18	CLASP1, U4atac, MAP3K2, SSU_rRNA_5, hsa-mir-663b,	No non-overlappi Y_RNA Y_RNA No non-overlappi No non-overlappi BIN1 PROC PROC WDR33 5_8S_rRNA 5_8S_rRNA SSU_rRNA_5	26,917 39,264 ng genes wit ng genes wit 26,458 30,985 9,334 8,915 1,041 1,475 593	hin 50,000bp Y_RNA Y_RNA AC016764.8-2 AC016764.8-2 hin 50,000bp AC013474.10-1 CYP27C1 Y_RNA SSU_rRNA_5 hsa-mir-663b	24,260 28,924 32,409 44,756 28,975 49,714 9,197 9,197 917 1,089
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	121,039,244 121,149,680 121,154,344 121,541,673 121,554,020 121,602,766 122,004,778 127,002,195 127,607,792 127,861,051 127,882,633 128,294,130 132,728,389 132,728,823 132,730,811 132,731,456	121,039,873 121,150,021 121,154,657 121,542,017 121,554,494 121,603,122 122,005,235 127,002,502 127,608,174 127,861,502 127,883,153 128,294,594 132,728,668 132,729,920 132,731,213 132,732,235	629 341 313 344 474 356 457 307 382 451 520 464 279 1,097 402 779	9 9 9 9 9 10 12 9 9 11 9 9 63 121 18 34	CLASP1, U4atac, MAP3K2, SSU_rRNA_5, hsa-mir-663b,	No non-overlappi Y_RNA Y_RNA No non-overlappi No non-overlappi BIN1 PROC PROC WDR33 5_8S_rRNA 5_8S_rRNA SSU_rRNA_5 hsa-mir-663b	26,917 39,264 ng genes wit ng genes wit 26,458 30,985 9,334 8,915 1,041 1,475 593 333	hin 50,000bp Y_RNA AC016764.8-2 AC016764.8-2 hin 50,000bp hin 50,000bp AC013474.10-1 CYP27C1 Y_RNA SSU_rRNA_5 hsa-mir-663b	24,260 28,924 32,409 44,756 28,975 49,714 9,197 9,197 9,197 1,089
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	121,039,244 121,149,680 121,154,344 121,541,673 121,554,020 121,602,766 122,004,778 127,002,195 127,607,792 127,861,051 127,882,633 128,294,130 132,728,389 132,728,823 132,730,811 132,731,456 132,732,874	121,039,873 121,150,021 121,154,657 121,542,017 121,554,494 121,603,122 122,005,235 127,002,502 127,608,174 127,861,502 127,883,153 128,294,594 132,728,668 132,729,920 132,731,213 132,732,235 132,733,906	629 341 313 344 474 356 457 307 382 451 520 464 279 1,097 402 779 1,032	9 9 9 9 9 10 12 9 9 9 11 9 9 63 121 18 34 33	CLASP1, U4atac, MAP3K2, SSU_rRNA_5, hsa-mir-663b,	No non-overlappi Y_RNA Y_RNA No non-overlappi No non-overlappi BIN1 PROC PROC WDR33 5_8S_rRNA 5_8S_rRNA SSU_rRNA_5 hsa-mir-663b hsa-mir-663b	26,917 39,264 ng genes wit ng genes wit 26,458 30,985 9,334 8,915 1,041 1,475 593 333 1,751	hin 50,000bp Y_RNA Y_RNA AC016764.8-2 AC016764.8-2 hin 50,000bp AC013474.10-1 CYP27C1 Y_RNA SSU_rRNA_5 hsa-mir-663b	24,260 28,924 32,409 44,756 28,975 49,714 9,197 9,197 917 1,089
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	121,039,244 121,149,680 121,154,344 121,541,673 121,554,020 121,602,766 122,004,778 127,002,195 127,607,792 127,861,051 127,882,633 128,294,130 132,728,389 132,728,823 132,730,811 132,731,456 132,732,874 132,735,116	121,039,873 121,150,021 121,154,657 121,542,017 121,554,494 121,603,122 122,005,235 127,002,502 127,608,174 127,861,502 127,883,153 128,294,594 132,728,668 132,729,920 132,731,213 132,732,235 132,733,906 132,736,101	629 341 313 344 474 356 457 307 382 451 520 464 279 1,097 402 779 1,032 985	9 9 9 9 9 10 12 9 9 9 9 9 11 9 9 9 63 121 18 34 33 39	CLASP1, U4atac, MAP3K2, SSU_rRNA_5, hsa-mir-663b,	No non-overlappi Y_RNA Y_RNA No non-overlappi No non-overlappi BIN1 PROC PROC WDR33 5_8S_rRNA 5_8S_rRNA 5_8S_rRNA SSU_rRNA_5 hsa-mir-663b hsa-mir-663b	26,917 39,264 ng genes wit 26,458 30,985 9,334 8,915 1,041 1,475 593 333 1,751 3,993	hin 50,000bp Y_RNA Y_RNA AC016764.8-2 AC016764.8-2 hin 50,000bp hin 50,000bp AC013474.10-1 CYP27C1 Y_RNA SSU_rRNA_5 hsa-mir-663b	24,260 28,924 32,409 44,756 28,975 49,714 9,197 9,197 917 1,089
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	121,039,244 121,149,680 121,154,344 121,541,673 121,554,020 121,602,766 122,004,778 127,002,195 127,607,792 127,861,051 127,882,633 128,294,130 132,728,889 132,728,889 132,728,823 132,730,811 132,731,456 132,735,116 132,736,103	121,039,873 121,150,021 121,154,657 121,542,017 121,554,494 121,603,122 122,005,235 127,002,502 127,608,174 127,861,502 127,883,153 128,294,594 132,728,668 132,729,920 132,731,213 132,732,235 132,733,906 132,736,101 132,736,305	629 341 313 344 474 356 457 307 382 451 520 464 279 1,097 402 779 1,032 985 202	9 9 9 9 9 10 12 9 9 9 11 9 9 63 121 18 34 33 39 14	CLASP1, U4atac, MAP3K2, SSU_rRNA_5, hsa-mir-663b,	No non-overlappi Y_RNA Y_RNA No non-overlappi No non-overlappi BIN1 PROC PROC WDR33 5_8S_rRNA 5_8S_rRNA 5_8S_rRNA SSU_rRNA_5 hsa-mir-663b hsa-mir-663b hsa-mir-663b	26,917 39,264 ng genes wit 26,458 30,985 9,334 8,915 1,041 1,475 593 333 1,751 3,993 4,980	hin 50,000bp Y_RNA AC016764.8-2 AC016764.8-2 hin 50,000bp hin 50,000bp AC013474.10-1 CYP27C1 Y_RNA SSU_rRNA_5 hsa-mir-663b	24,260 28,924 32,409 44,756 28,975 49,714 9,197 9,197 917 1,089
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	121,039,244 121,149,680 121,154,344 121,541,673 121,554,020 121,602,766 122,004,778 127,002,195 127,607,792 127,861,051 127,882,633 128,294,130 132,728,889 132,728,823 132,730,811 132,731,456 132,735,116 132,735,116 132,736,103 132,736,103	121,039,873 121,150,021 121,154,657 121,542,017 121,554,494 121,603,122 122,005,235 127,002,502 127,608,174 127,861,502 127,883,153 128,294,594 132,728,668 132,729,920 132,731,213 132,732,235 132,733,906 132,736,101 132,736,305 132,737,001	629 341 313 344 474 356 457 307 382 451 520 464 279 1,097 402 779 1,032 985 202 611	9 9 9 9 9 10 12 9 9 9 11 9 9 63 121 18 34 33 339 14	CLASP1, U4atac, MAP3K2, SSU_rRNA_5, hsa-mir-663b,	No non-overlappi Y_RNA Y_RNA No non-overlappi No non-overlappi BIN1 PROC PROC WDR33 5_8S_rRNA 5_8S_rRNA 5_8S_rRNA SSU_rRNA_5 hsa-mir-663b hsa-mir-663b hsa-mir-663b hsa-mir-663b	26,917 39,264 ng genes wit 26,458 30,985 9,334 8,915 1,041 1,475 593 333 1,751 3,993 4,980 5 267	hin 50,000bp Y_RNA Y_RNA AC016764.8-2 AC016764.8-2 hin 50,000bp hin 50,000bp AC013474.10-1 CYP27C1 Y_RNA SSU_rRNA_5 hsa-mir-663b	24,260 28,924 32,409 44,756 28,975 49,714 9,197 9,197 917 1,089
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	121,039,244 121,149,680 121,154,344 121,541,673 121,554,020 121,602,766 122,004,778 127,002,195 127,607,792 127,861,051 127,882,633 128,294,130 132,728,889 132,728,823 132,730,811 132,731,456 132,735,116 132,736,103 132,736,390 132,736,390	121,039,873 121,150,021 121,154,657 121,542,017 121,554,494 121,603,122 122,005,235 127,002,502 127,608,174 127,861,502 127,883,153 128,294,594 132,728,668 132,729,920 132,731,213 132,732,235 132,733,906 132,736,101 132,736,305 132,737,001	629 341 313 344 474 356 457 307 382 451 520 464 279 1,097 402 779 1,032 985 202 611 775	9 9 9 9 9 10 12 9 9 9 11 12 121 18 34 33 39 9 14 5 5 40	CLASP1, U4atac, MAP3K2, SSU_rRNA_5, hsa-mir-663b,	No non-overlappi Y_RNA Y_RNA No non-overlappi No non-overlappi BIN1 PROC PROC WDR33 5_8S_rRNA 5_8S_RRNA 5_	26,917 39,264 ng genes wit 26,458 30,985 9,334 8,915 1,041 1,475 593 333 1,751 3,993 4,980 5,267 8 222	hin 50,000bp Y_RNA Y_RNA AC016764.8-2 AC016764.8-2 hin 50,000bp hin 50,000bp AC013474.10-1 CYP27C1 Y_RNA SSU_rRNA_5 hsa-mir-663b	24,260 28,924 32,409 44,756 28,975 49,714 9,197 9,197 917 1,089
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	121,039,244 121,149,680 121,154,344 121,54,473 121,554,020 121,602,766 122,004,778 127,002,195 127,607,792 127,861,051 127,882,633 128,294,130 132,728,389 132,728,823 132,730,811 132,731,456 132,732,874 132,735,116 132,736,103 132,739,445	121,039,873 121,150,021 121,154,657 121,542,017 121,554,494 121,603,122 122,005,235 127,002,502 127,608,174 127,861,502 127,883,153 128,294,594 132,728,668 132,729,920 132,731,213 132,732,235 132,733,906 132,736,101 132,736,305 132,737,001 132,740,220	629 341 313 344 474 356 457 307 382 451 520 464 279 1,037 779 1,032 985 202 611 775	9 9 9 9 9 10 12 9 9 9 11 9 9 9 63 121 18 34 33 39 14 35 9 9	CLASP1, U4atac, MAP3K2, SSU_rRNA_5, hsa-mir-663b,	No non-overlappi Y_RNA Y_RNA No non-overlappi No non-overlappi BIN1 PROC PROC WDR33 5_8S_rRNA 5_8S_rRNA 5_8S_rRNA SSU_rRNA_5 hsa-mir-663b hsa-mir-663b hsa-mir-663b hsa-mir-663b	ng genes wit 26,917 39,264 ng genes wit 26,458 30,985 9,334 8,915 1,041 1,475 593 333 1,751 3,993 4,980 5,267	hin 50,000bp Y_RNA Y_RNA AC016764.8-2 AC016764.8-2 hin 50,000bp hin 50,000bp AC013474.10-1 CYP27C1 Y_RNA SSU_rRNA_5 hsa-mir-663b AC007522.2.4	24,260 28,924 32,409 44,756 28,975 49,714 9,197 9,197 1,089
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	121,039,244 121,149,680 121,154,344 121,54,020 121,602,766 122,004,778 127,002,195 127,607,792 127,861,051 127,882,633 128,294,130 132,728,389 132,728,823 132,730,811 132,732,874 132,735,116 132,736,103 132,739,445 132,739,445 132,739,445	121,039,873 121,150,021 121,154,657 121,542,017 121,554,494 121,603,122 122,005,235 127,002,502 127,608,174 127,861,502 127,883,153 128,294,594 132,728,668 132,729,920 132,731,213 132,732,235 132,733,906 132,736,101 132,736,305 132,737,001 132,740,220 132,742,341	629 341 313 344 474 356 457 307 382 451 520 464 279 1,097 402 779 1,032 985 202 611 775 768	9 9 9 9 9 10 12 9 9 9 9 11 19 9 9 63 121 18 34 33 39 14 35 9 9	CLASP1, U4atac, MAP3K2, SSU_rRNA_5, hsa-mir-663b,	No non-overlappi Y_RNA Y_RNA No non-overlappi No non-overlappi BIN1 PROC PROC WDR33 5_8S_rRNA 5_8S_rRNA 5_8S_rRNA SSU_rRNA_5 hsa-mir-663b hsa-mir-663b hsa-mir-663b hsa-mir-663b	ng genes wit 26,917 39,264 ng genes wit 26,458 30,985 9,334 8,915 1,041 1,475 5933 333 1,751 3,993 4,980 5,267 8,322 10,450	hin 50,000bp Y_RNA Y_RNA AC016764.8-2 AC016764.8-2 hin 50,000bp AC013474.10-1 CYP27C1 Y_RNA SSU_rRNA_5 hsa-mir-663b AC097532.3-1	24,260 28,924 32,409 44,756 28,975 49,714 9,197 9,197 1,089
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	121,039,244 121,149,680 121,154,344 121,54,020 121,602,766 122,004,778 127,002,195 127,607,792 127,861,051 127,882,633 128,294,130 132,728,823 132,730,811 132,730,811 132,735,116 132,735,116 132,736,103 132,736,390 132,739,445 132,741,573 132,742,419	121,039,873 121,150,021 121,154,657 121,542,017 121,554,494 121,603,122 122,005,235 127,002,502 127,608,174 127,861,502 127,883,153 128,294,594 132,728,668 132,729,920 132,731,213 132,732,235 132,733,906 132,736,101 132,736,305 132,737,001 132,742,341 132,742,896	629 341 313 344 474 356 457 307 382 451 520 464 279 1,097 402 779 1,032 985 202 611 775 768 477	9 9 9 9 9 10 12 9 9 9 9 11 9 9 9 63 121 18 34 33 39 14 4 35 49 66 25	CLASP1, U4atac, MAP3K2, SSU_rRNA_5, hsa-mir-663b,	No non-overlappi Y_RNA Y_RNA No non-overlappi No non-overlappi BIN1 PROC PROC WDR33 5_8S_rRNA 5_8S_rRNA 5_8S_rRNA SSU_rRNA_5 hsa-mir-663b hsa-mir-663b hsa-mir-663b hsa-mir-663b hsa-mir-663b hsa-mir-663b hsa-mir-663b	ng genes wit 26,917 39,264 ng genes wit genes wit 26,458 30,985 9,334 8,915 1,041 1,475 593 333 1,751 3,993 4,980 5,267 8,322 10,450 11,296	hin 50,000bp Y_RNA Y_RNA AC016764.8-2 AC016764.8-2 hin 50,000bp AC013474.10-1 CYP27C1 Y_RNA SSU_rRNA_5 hsa-mir-663b AC097532.3-1 AC097532.3-1	24,260 28,924 32,409 44,756 28,975 49,714 9,197 9,197 917 1,089
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	121,039,244 121,149,680 121,154,344 121,541,673 121,554,020 121,602,766 122,004,778 127,002,195 127,607,792 127,861,051 127,882,633 128,294,130 132,728,823 132,728,823 132,730,811 132,732,874 132,735,116 132,735,116 132,736,103 132,736,403 132,739,445 132,741,573 132,742,419 132,743,001	121,039,873 121,150,021 121,154,657 121,542,017 121,554,494 121,603,122 122,005,235 127,002,502 127,608,174 127,861,502 127,883,153 128,294,594 132,728,668 132,729,920 132,731,213 132,732,235 132,733,906 132,736,101 132,736,305 132,737,001 132,742,341 132,742,896 132,742,896	629 341 313 344 474 356 457 307 382 451 520 464 279 1,097 402 779 1,032 985 202 611 775 768 477 696	9 9 9 9 9 10 12 9 9 9 11 9 9 9 63 121 18 34 33 39 14 4 33 39 14 5 49 66 25 67	CLASP1, U4atac, MAP3K2, SSU_rRNA_5, hsa-mir-663b,	No non-overlappi Y_RNA Y_RNA No non-overlappi No non-overlappi BIN1 PROC PROC WDR33 5_8S_rRNA 5_8S_rRNA 5_8S_rRNA 5_8S_rRNA SSU_rRNA_5 hsa-mir-663b hsa-mir-663b hsa-mir-663b hsa-mir-663b hsa-mir-663b hsa-mir-663b hsa-mir-663b hsa-mir-663b	ng genes wit 26,917 39,264 ng genes wit ng genes wit 26,458 30,985 9,334 8,915 1,041 1,475 593 333 1,751 3,993 4,980 5,267 8,322 10,450 11,296 11,878	hin 50,000bp Y_RNA Y_RNA AC016764.8-2 AC016764.8-2 hin 50,000bp AC013474.10-1 CYP27C1 Y_RNA SSU_rRNA_5 hsa-mir-663b AC097532.3-1 AC097532.3-1 AC097532.3-1	24,260 28,924 32,409 44,756 28,975 49,714 9,197 9,197 9,197 917 1,089 12,776 12,221 11,420
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	121,039,244 121,149,680 121,154,344 121,541,673 121,554,020 121,602,766 122,004,778 127,002,195 127,607,792 127,861,051 127,882,633 128,294,130 132,728,889 132,728,889 132,728,889 132,730,811 132,730,811 132,735,116 132,735,116 132,736,103 132,736,103 132,736,103 132,736,103 132,739,445 132,741,573 132,742,419 132,745,201	121,039,873 121,150,021 121,154,657 121,542,017 121,554,494 121,603,122 122,005,235 127,002,502 127,608,174 127,861,502 127,883,153 128,294,594 132,728,668 132,729,920 132,731,213 132,732,235 132,733,906 132,736,101 132,736,305 132,737,001 132,740,220 132,742,341 132,742,896 132,743,697 132,748,385	629 341 313 344 474 356 457 307 382 451 520 464 279 1,097 402 779 1,032 985 202 611 775 768 477 696 3,184	9 9 9 9 9 10 12 9 9 9 9 11 9 9 9 63 121 18 34 33 339 141 35 49 66 25 54	CLASP1, U4atac, MAP3K2, SSU_rRNA_5, hsa-mir-663b,	No non-overlappi Y_RNA Y_RNA No non-overlappi No non-overlappi BIN1 PROC PROC WDR33 5_8S_rRNA 5_8S_rRNA 5_8S_rRNA 5_8S_rRNA SSU_rRNA_5 hsa-mir-663b hsa-mir-663b hsa-mir-663b hsa-mir-663b hsa-mir-663b	26,917 39,264 ng genes wit g genes wit 26,458 30,985 9,334 8,915 1,041 1,475 593 333 1,751 3,993 4,980 5,267 8,322 10,450 11,296 11,878	hin 50,000bp Y_RNA AC016764.8-2 AC016764.8-2 AC016764.8-2 hin 50,000bp AC013474.10-1 CYP27C1 Y_RNA SSU_rRNA_5 hsa-mir-663b AC097532.3-1 AC097532.3-1 AC097532.3-1 AC097532.3-1	24,260 28,924 32,409 44,756 28,975 49,714 9,197 9,197 917 1,089
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	121,039,244 121,149,680 121,154,344 121,541,673 121,554,020 121,602,766 122,004,778 127,002,195 127,607,792 127,861,051 127,882,633 128,294,130 132,728,889 132,728,823 132,730,811 132,731,456 132,732,874 132,735,116 132,736,103 132,736,103 132,736,403 132,736,403 132,736,403 132,736,403 132,736,403 132,742,419 132,745,201 132,745,201	121,039,873 121,150,021 121,154,657 121,542,017 121,554,494 121,603,122 122,005,235 127,002,502 127,608,174 127,861,502 127,883,153 128,294,594 132,728,668 132,729,920 132,731,213 132,732,235 132,733,906 132,736,101 132,736,305 132,737,001 132,742,341 132,742,896 132,742,896 132,742,896	629 341 313 344 474 356 457 307 382 451 520 464 279 1,097 402 779 1,032 985 202 611 775 768 477 696 3,184 689	9 9 9 9 9 10 12 9 9 9 11 9 9 9 63 121 18 34 33 339 121 18 34 5 66 25 67 54 22	CLASP1, U4atac, MAP3K2, SSU_rRNA_5, hsa-mir-663b,	No non-overlappi Y_RNA Y_RNA No non-overlappi No non-overlappi BIN1 PROC PROC WDR33 5_8S_rRNA 5_8S_rRNA 5_8S_rRNA 5_8S_rRNA SSU_rRNA_5 hsa-mir-663b hsa-mir-663b hsa-mir-663b hsa-mir-663b hsa-mir-663b	26,917 39,264 ng genes wit 26,458 30,985 9,334 8,915 1,041 1,475 593 333 1,751 3,993 4,980 5,267 8,322 10,450 11,296 11,878	hin 50,000bp Y_RNA AC016764.8-2 AC016764.8-2 AC016764.8-2 hin 50,000bp AC013474.10-1 CYP27C1 Y_RNA SSU_rRNA_5 hsa-mir-663b AC097532.3-1 AC097532.3-1 AC097532.3-1 AC097532.3-1 AC097532.3-1	24,260 28,924 32,409 44,756 28,975 49,714 9,197 9,197 9,197 917 1,089
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	121,039,244 121,149,680 121,154,344 121,541,673 121,554,020 121,602,766 122,004,778 127,002,195 127,607,792 127,861,051 127,882,633 128,294,130 132,728,823 132,730,811 132,735,874 132,735,116 132,735,116 132,735,116 132,735,116 132,736,103 132,736,403 132,739,445 132,744,573 132,744,501 132,745,201 132,745,201	121,039,873 121,150,021 121,154,657 121,542,017 121,554,494 121,603,122 122,005,235 127,002,502 127,608,174 127,861,502 127,883,153 128,294,594 132,728,668 132,729,920 132,731,213 132,732,235 132,733,906 132,736,101 132,736,305 132,736,001 132,742,341 132,742,896 132,743,697 132,743,697 132,748,385 132,749,614	629 341 313 344 474 356 457 307 382 451 520 464 279 1,097 402 779 1,032 985 202 611 775 202 611 775 768 477 696 3,184 689 565	9 9 9 10 9 9 9 9 9 9 11 9 9 9 63 121 18 34 33 33 9 14 35 49 66 25 67 54 22	CLASP1, U4atac, MAP3K2, SSU_rRNA_5, hsa-mir-663b,	No non-overlappi Y_RNA Y_RNA No non-overlappi No non-overlappi BIN1 PROC PROC WDR33 5_8S_rRNA 5_8S_rRNA 5_8S_rRNA 5_8S_rRNA SSU_rRNA_5 hsa-mir-663b hsa-mir-663b hsa-mir-663b hsa-mir-663b hsa-mir-663b hsa-mir-663b	26,917 39,264 ng genes wit 26,458 30,985 9,334 8,915 1,041 1,475 593 333 1,751 3,993 4,980 5,267 8,322 10,450 11,296 11,878	hin 50,000bp Y_RNA AC016764.8-2 AC016764.8-2 AC016764.8-2 hin 50,000bp hin 50,000bp AC013474.10-1 CYP27C1 Y_RNA SSU_rRNA_5 hsa-mir-663b AC097532.3-1 AC097532.3-1 AC097532.3-1 AC097532.3-1 AC097532.3-1 AC097532.3-1	24,260 28,924 32,409 44,756 28,975 49,714 9,197 9,197 9,197 1,089 12,776 12,221 11,420 6,732 5,503 4 921
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	121,039,244 121,149,680 121,154,344 121,541,673 121,554,020 121,602,766 122,004,778 127,002,195 127,607,792 127,861,051 127,882,633 128,294,130 132,728,389 132,728,389 132,728,823 132,730,811 132,735,116 132,735,116 132,736,103 132,736,390 132,739,445 132,741,573 132,742,419 132,745,201 132,748,925 132,749,631	121,039,873 121,150,021 121,154,657 121,542,017 121,554,494 121,603,122 122,005,235 127,002,502 127,608,174 127,861,502 127,883,153 128,294,594 132,728,668 132,729,920 132,731,213 132,732,235 132,733,906 132,736,101 132,736,305 132,736,001 132,740,220 132,742,341 132,742,896 132,742,896 132,742,896 132,743,697 132,748,385 132,749,614 132,750,196	629 341 313 344 474 356 457 307 382 451 520 464 279 1,097 402 779 1,032 985 202 611 775 768 477 696 3,184 689 555	9 9 9 10 9 9 9 9 9 9 11 12 9 9 9 6 3 121 18 34 33 39 9 14 35 66 255 67 54 222	CLASP1, U4atac, MAP3K2, SSU_rRNA_5, hsa-mir-663b,	No non-overlappi Y_RNA Y_RNA No non-overlappi No non-overlappi BIN1 PROC PROC WDR33 5_8S_rRNA 5_8S_rRNA 5_8S_rRNA SSU_rRNA_5 hsa-mir-663b hsa-mir-663b hsa-mir-663b hsa-mir-663b hsa-mir-663b hsa-mir-663b hsa-mir-663b	26,917 39,264 ng genes wit 26,458 30,985 9,334 8,915 1,041 1,475 593 333 1,751 3,993 4,980 5,267 8,322 10,450 11,296 11,878	hin 50,000bp Y_RNA Y_RNA AC016764.8-2 AC016764.8-2 AC016764.8-2 hin 50,000bp hin 50,000bp AC013474.10-1 CYP27C1 Y_RNA SSU_rRNA_5 hsa-mir-663b AC097532.3-1 AC097532.3-1 AC097532.3-1 AC097532.3-1 AC097532.3-1 AC097532.3-1	24,260 28,924 32,409 44,756 28,975 49,714 9,197 9,197 9,197 9,197 9,197 1,089 1,097 1,089 1,099
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	121,039,244 121,149,680 121,154,344 121,54,473 121,554,020 121,602,766 122,004,778 127,002,195 127,607,792 127,861,051 127,882,633 128,294,130 132,728,823 132,728,823 132,730,811 132,730,811 132,735,116 132,735,116 132,736,103 132,736,103 132,736,390 132,739,445 132,741,573 132,742,419 132,743,001 132,745,201 132,749,631 132,749,631	121,039,873 121,150,021 121,154,657 121,542,017 121,554,494 121,603,122 122,005,235 127,002,502 127,608,174 127,861,502 127,883,153 128,294,594 132,728,668 132,729,920 132,731,213 132,732,235 132,733,906 132,736,101 132,736,305 132,736,305 132,740,220 132,742,341 132,742,896 132,742,341 132,742,896 132,743,697 132,748,385 132,749,614 132,750,196 132,751,395	629 341 313 344 474 356 457 307 382 451 520 464 279 1,097 402 779 1,032 985 202 611 775 768 477 696 3,184 689 565 737	9 9 9 9 9 9 10 12 9 9 9 9 11 1 9 9 9 63 121 18 34 33 39 9 66 67 67 54 22 377 54	CLASP1, U4atac, MAP3K2, SSU_rRNA_5, hsa-mir-663b,	No non-overlappi Y_RNA Y_RNA No non-overlappi No non-overlappi BIN1 PROC PROC WDR33 5_8S_rRNA 5_8S_rRNA 5_8S_rRNA SSU_rRNA_5 hsa-mir-663b hsa-mir-663b hsa-mir-663b hsa-mir-663b hsa-mir-663b hsa-mir-663b hsa-mir-663b	ng genes wit 26,917 39,264 ng genes wit 26,458 30,985 9,334 8,915 1,041 1,475 593 333 1,751 3,993 4,980 5,267 8,322 10,450 11,296 11,878	hin 50,000bp Y_RNA Y_RNA AC016764.8-2 AC016764.8-2 AC016764.8-2 hin 50,000bp hin 50,000bp AC013474.10-1 CYP27C1 Y_RNA SSU_rRNA_5 hsa-mir-663b AC097532.3-1 AC097532.3-1 AC097532.3-1 AC097532.3-1 AC097532.3-1 AC097532.3-1 AC097532.3-1	24,260 28,924 32,409 44,756 28,975 49,714 9,197 9,197 9,197 9,197 1,089 1,099
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	121,039,244 121,149,680 121,154,344 121,54,673 121,554,020 121,602,766 122,004,778 127,002,195 127,607,792 127,861,051 127,882,633 128,294,130 132,728,389 132,728,389 132,728,389 132,730,811 132,730,811 132,730,811 132,736,103 132,736,103 132,736,103 132,736,103 132,736,103 132,736,103 132,741,573 132,741,573 132,742,419 132,745,201 132,749,631 132,749,631 132,750,658 132,752,109	121,039,873 121,150,021 121,154,657 121,542,017 121,554,494 121,603,122 122,005,235 127,002,502 127,608,174 127,861,502 127,883,153 128,294,594 132,728,668 132,729,920 132,731,213 132,732,235 132,733,906 132,736,101 132,736,305 132,736,305 132,740,220 132,742,341 132,742,896 132,742,341 132,742,896 132,742,341 132,742,896 132,742,341 132,742,896 132,743,697 132,748,385 132,749,614 132,750,196 132,751,395 132,752,681	629 341 313 344 474 356 457 307 382 451 520 464 279 1,037 709 1,032 985 202 611 775 768 477 696 3,184 689 565 737 572	9 9 9 10 9 9 9 9 9 9 9 11 9 9 9 63 121 18 34 33 39 14 33 39 14 35 66 25 67 54 22 37 48 18	CLASP1, U4atac, MAP3K2, SSU_rRNA_5, hsa-mir-663b,	No non-overlappi Y_RNA Y_RNA No non-overlappi No non-overlappi BIN1 PROC PROC WDR33 5_8S_rRNA 5_8S_rRNA 5_8S_rRNA SSU_rRNA_5 hsa-mir-663b hsa-mir-663b hsa-mir-663b hsa-mir-663b hsa-mir-663b hsa-mir-663b	ng genes wit 26,917 39,264 ng genes wit 26,458 30,985 9,334 8,915 1,041 1,475 593 333 1,751 3,993 4,980 5,267 8,322 10,450 11,296 11,878	hin 50,000bp Y_RNA AC016764.8-2 AC016764.8-2 AC016764.8-2 hin 50,000bp hin 50,000bp AC013474.10-1 CYP27C1 Y_RNA SSU_rRNA_5 hsa-mir-663b AC097532.3-1 AC097532.3-1 AC097532.3-1 AC097532.3-1 AC097532.3-1 AC097532.3-1 AC097532.3-1 AC097532.3-1 AC097532.3-1 AC097532.3-1	24,260 28,924 32,409 44,756 28,975 49,714 9,197 9,197 9,197 9,197 1,089 1,099
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	121,039,244 121,149,680 121,154,344 121,54,020 121,602,766 122,004,778 127,002,195 127,607,792 127,861,051 127,882,633 128,294,130 132,728,389 132,728,823 132,730,811 132,730,811 132,735,116 132,732,874 132,736,103 132,736,103 132,736,103 132,736,103 132,736,103 132,736,103 132,741,573 132,742,419 132,745,201 132,745,201 132,749,631 132,749,631 132,752,109 132,752,109	121,039,873 121,150,021 121,154,657 121,542,017 121,554,494 121,603,122 122,005,235 127,002,502 127,608,174 127,861,502 127,883,153 128,294,594 132,728,668 132,729,920 132,731,213 132,732,235 132,732,001 132,736,101 132,736,305 132,737,001 132,742,341 132,753,201	629 341 313 344 474 356 457 307 382 451 520 464 279 1,097 402 779 1,032 985 202 611 775 768 477 696 3,184 689 565 737 572 357	9 9 9 9 9 10 12 9 9 9 11 19 9 9 9 11 18 33 121 18 33 33 9 14 33 39 14 35 66 25 67 54 22 37 48 18	CLASP1, U4atac, MAP3K2, SSU_rRNA_5, hsa-mir-663b,	No non-overlappi Y_RNA Y_RNA No non-overlappi No non-overlappi BIN1 PROC PROC WDR33 5_8S_rRNA 5_8S_rRNA 5_8S_rRNA SSU_rRNA_5 hsa-mir-663b hsa-mir-663b hsa-mir-663b hsa-mir-663b hsa-mir-663b hsa-mir-663b	ng genes wit 26,917 39,264 ng genes wit 26,458 30,985 9,334 8,915 1,041 1,475 5933 1,751 3,993 4,980 5,267 8,322 10,450 11,296 11,878	hin 50,000bp Y_RNA AC016764.8-2 AC016764.8-2 AC016764.8-2 hin 50,000bp hin 50,000bp AC013474.10-1 CYP27C1 Y_RNA SSU_rRNA_5 hsa-mir-663b AC097532.3-1 AC097532.3-1 AC097532.3-1 AC097532.3-1 AC097532.3-1 AC097532.3-1 AC097532.3-1 AC097532.3-1 AC097532.3-1 AC097532.3-1 AC097532.3-1 AC097532.3-1 AC097532.3-1 AC097532.3-1	24,260 28,924 32,409 44,756 28,975 49,714 9,197 9,197 9,197 1,089 12,776 12,221 11,420 6,732 5,503 4,921 3,722 2,436 1,916
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	121,039,244 121,149,680 121,154,344 121,54,020 121,602,766 122,004,778 127,002,195 127,607,792 127,861,051 127,882,633 128,294,130 132,728,389 132,728,389 132,728,389 132,730,811 132,730,811 132,735,116 132,732,874 132,735,116 132,736,103 132,736,103 132,736,103 132,736,103 132,736,103 132,739,445 132,741,573 132,742,419 132,744,9631 132,749,631 132,752,109 132,752,109	121,039,873 121,150,021 121,154,657 121,542,017 121,554,494 121,603,122 122,005,235 127,002,502 127,608,174 127,861,502 127,883,153 128,294,594 132,728,668 132,729,920 132,731,213 132,732,235 132,733,906 132,736,101 132,736,305 132,736,001 132,742,341 132,744,3697	629 341 313 344 474 356 457 307 382 451 520 464 279 1,097 402 779 1,032 985 202 611 775 768 477 696 3,184 689 565 737 572 357 398	9 9 9 9 9 10 12 9 9 9 9 11 19 9 9 9 63 121 18 33 33 9 14 33 39 14 35 66 255 67 54 225 67 54 225 37 48 18	CLASP1, U4atac, MAP3K2, SSU_rRNA_5, hsa-mir-663b,	No non-overlappi Y_RNA Y_RNA No non-overlappi No non-overlappi BIN1 PROC PROC WDR33 5_8S_rRNA 5_8S_rRNA 5_8S_rRNA 5_8S_rRNA SSU_rRNA_5 hsa-mir-663b hsa-mir-663b hsa-mir-663b hsa-mir-663b hsa-mir-663b	26,917 39,264 ng genes wit 26,458 30,985 9,334 8,915 1,041 1,475 5933 333 1,751 3,993 4,980 5,267 8,322 10,450 11,296 11,878	hin 50,000bp Y_RNA Y_RNA AC016764.8-2 AC016764.8-2 AC016764.8-2 hin 50,000bp AC013474.10-1 CYP27C1 Y_RNA SSU_rRNA_5 hsa-mir-663b AC097532.3-1 AC097532.3-1 AC097532.3-1 AC097532.3-1 AC097532.3-1 AC097532.3-1 AC097532.3-1 AC097532.3-1 AC097532.3-1 AC097532.3-1 AC097532.3-1 AC097532.3-1 AC097532.3-1 AC097532.3-1 AC097532.3-1 AC097532.3-1	24,260 28,924 32,409 44,756 28,975 49,714 9,197 9,197 1,089 12,776 12,221 11,420 6,732 5,503 4,921 3,722 2,436 1,916 267

2	132,755,382	132,755,668	286	13		AC097532.3-1	174		
2	132,821,419	132,821,801	382	9		No non-overlappi	ng genes wit	hin 50,000bp	
2	133,144,572	133,145,356	784	10	LYPD1,			AC010974.1	488
2	136,215,197	136,215,945	748	13	UBXD2,			R3HDM1	15,889
2	136,459,083	136,460,139	1,056	9	DARS,	No non-overlappi	ng genes wit	hin 50,000bp	
2	136,830,091	136,830,599	508	9		No non-overlappi	ng genes wit	hin 50,000bp	
2	138,666,729	138,667,166	437	9		No non-overlappi	ng genes wit	hin 50,000bp	
2	142,221,492	142,221,716	224	9	LRP1B,	No non-overlappi	ng genes wit	hin 50,000bp	
2	143,615,379	143,615,756	377	9	ARHGAP15,	AC013437.8-10	40,499	AC013437.8-4	47,108
2	149,118,468	149,118,845	377	9		EPC2	193		
2	150,152,260	150,152,790	530	11	MMADHC,			U6	22,638
2	151,854,043	151,854,653	610	9	NMI,	RBM43	27,420		
2	151,974,436	151,974,927	491	10	RIF1,			TNFAIP6	29,633
2	152,392,671	152,393,666	995	9	ARL5A,			CACNB4	8,723
2	156,964,905	156,966,094	1,189	9				AC092686.3-1	8,810
2	159,310,602	159,311,018	416	9		AC005042.2	10,842		
2	159,518,724	159,519,010	286	10		TANC1	14,382		
2	160,276,930	160,277,358	428	17	7-Mar,	No non-overlappi	ng genes wit	hin 50,000bp	
2	160,806,442	160,806,945	503	9		ITGB6	41,381	RBMS1	31,816
2	161,843,417	161,843,973	556	10		PSMD14	28,822	TANK	42,439
2	161,844,747	161,845,297	550	12		PSMD14	27,498	TANK	43,769
2	161,846,964	161,847,403	439	17		PSMD14	25,392	TANK	45,986
2	169,674,463	169,674,825	362	9			-	DHRS9	13,540
2	169,948,625	169,948,864	239	9		LRP2	21,257		
2	170,389,466	170,389,897	431	9	METTL5,	UBR3	2,317	AC009967.8-2	8,359
2	170,582,958	170,583,325	367	10	UBR3,	No non-overlappi	ng genes wit	hin 50,000bp	,
2	171,280,177	171,280,821	644	9	SP5,	AC007405.2	854	, ,	
2	172,094,716	172,094,995	279	13	CYBRD1,			C2orf37	44,910
2	172,105,917	172.106.501	584	11	CYBRD1.	No non-overlappi	na aenes wit	hin 50.000bp	,
2	172,668,213	172,668,543	330	10	- ,			DLX2	3,870
2	172.669.997	172.670.526	529	10				DLX2	1.887
2	173.103.566	173.103.881	315	9		PDK1	25.144	ITGA6	24,139
2	173.649.219	173.649.771	552	9	ZAK.		,	RAPGEF4	23.352
2	173.927.278	173.927.666	388	10	,	CDCA7	141		
2	174.022.143	174.022.449	306	11		AC073465.5-1	17.357	AC073465.5-2	36,390
2	174,909,146	174.909.912	766	9	SP9.		,	AC106900.1	11.214
	,, -	,,-			AC018470.11,				,
2	176,652,759	176,653,073	314	17	RPLP1P4,			EVX2	8
2	176,669,745	176,670,444	699	11	RPLP1P4,	HOXD12	2,260	HOXD13	833
2	176,670,584	176,670,902	318	9	RPLP1P4,	HOXD12	1,802	HOXD13	1,672
2	176,676,900	176,677,536	636	9	RPLP1P4,	HOXD11	2,794	HOXD12	2,733
2	176,704,207	176,704,553	346	10	RPLP1P4,	AC009336.13	1,468	HOXD9	6,437
					HOXD8,				
2	177,760,687	177,761,194	507	9		Y_RNA	6,763		
2	177,836,181	177,837,181	1,000	9	AC079305.6-2, N	FE2L2,		AC079305.6-3	19,303
2	179,051,925	179,052,340	415	13		FKBP7	357		
2	179,127,430	179,127,811	381	9	TTN,			PLEKHA3	49,404
2	188,889,741	188,890,421	680	9	GULP1,	5S_rRNA	39,925	hsa-mir-561	19,181
2	190,013,877	190,014,671	794	9	WDR75,	No non-overlappi	ng genes wit	hin 50,000bp	
2	190,233,940	190,234,711	771	11	ASNSD1,	ANKAR	14,964		
2	190,247,144	190,248,118	974	9		ANKAR	1,557	ASNSD1	3,344
2	190,335,419	190,335,795	376	14	OSGEPL1,			ORMDL1	7,500
2	191,110,695	191,111,160	465	12	AC108047.4,	TMEM194B	3,002		
2	191,584,414	191,584,709	295	9	STAT1,			STAT4	17,838
2	191,586,689	191,587,348	659	11	STAT1,			STAT4	15,199
2	191,593,065	191,593,560	495	13		STAT1	5,884	STAT4	8,987
2	191,603,490	191,604,024	534	10	STAT4,	STAT1	16,309		
2	191,739,030	191,739,327	297	10		STAT4	14,469	U6	44,003
2	192,768,377	192,769,094	717	10		TMEFF2	473		
2	197,372,482	197,372,871	389	11	GTF3C3,			C2orf66	5,343
2	198,072,781	198,073,839	1,058	9	HSPD1, HSPE1,	MOBKL3	14,711	COQ10B	24,685
2	198,088,208	198,089,181	973	9	MOBKL3,	HSPD1	14,965	HSPE1	11,857
2	200,036,377	200,036,706	329	9	SATB2,	No non-overlappi	ng genes wit	hin 50,000bp	
2	200,528,437	200,529,321	884	9	C2orf60,			C2orf69	28,161
					C2orf47,				

2	201,436,562	201,437,666	1,104	9	CLK1,			PPIL3	6,259
2	201.474.451	201.474.740	289	9	NIF3L1.	AC005037.2-2	2.406	AC005037.2-1	2.363
2	201 535 651	201 536 860	1 209	9	ORC2I		,	FAM126B	15 172
2	201 644 714	201 645 107	393	11	NDUER3	FAM126B	77	174011208	10,112
2	203 161 626	203 161 996	370	13		AC009960 10-2	25 757	BMPR2	20 907
2	203,101,020	203,101,000	305	10		AL \$20046	26,101		20,507
2	203,367,901	203,366,260	422	0		AL320K10	20,444	AL320R0	20,070
2	204,355,202	204,355,634	432	9		ACU10136.0-1	0,732	06	91
2	205,117,962	205,118,428	400	11		PARD3B	333	701/	0.005
2	206,802,988	206,803,858	870	9				7SK	8,385
2	208,198,635	208,199,387	752	9		FAM119A	359		
2	212,318,301	212,318,609	308	9	ERBB4,	AC105921.5-3	32,222	AC105921.5-1	29,882
2	213,724,735	213,725,181	446	13		IKZF2	157		
2	217,071,503	217,072,019	516	12	RPL37A,			SMARCAL1	15,482
2	217,265,100	217,265,503	403	9	IGFBP5,			IGFBP2	27,696
2	218.362.146	218.362.492	346	9				TNS1	10.265
2	218 790 278	218 790 755	477	9	ARPC2	AC097483 3	32 228	AAMP	46 344
2	218 859 794	218 860 387	503	9		ΔΔΜΡ	16 657	AC021016 5-1	12 147
2	210,000,704	210,000,007	555	5	AC021016 5-2		10,007	A0021010.0-1	12,147
2	218 874 217	218 874 572	355	10	PNKD	TMBIM1	8 603		
2	210,074,217	210,074,072	721	0		haa mir 26h	0,000	SI C11A1	2 201
2	210,972,131	210,972,072	121	9			2,741	SLUTIAT	2,291
2	219,141,319	219,141,746	427	9	USP37,	RQUDT	96	D0041	0.007
2	219,244,477	219,245,450	973	12	RNF25, STK36,		-	BCSIL	8,067
2	219,304,543	219,304,903	360	9	TTLL4,	CYP27A1	49,842	STK36	28,865
2	219,420,579	219,420,936	357	10		WNT6	11,847	CYP27A1	32,325
2	219,433,091	219,433,377	286	10	WNT6,	WNT10A	20,111	CYP27A1	44,837
2	219,481,972	219,482,232	260	10				U6	6,918
2	219,778,997	219,779,740	743	9		ZFAND2B	10	ABCB6	2,998
2	219.802.092	219.803.007	915	10	ATG9A.	AC068946.4	5.021	GLB1L	6.565
					ANKZF1,				,
2	219.817.752	219.818.694	942	9	GLB1L, STK16.			TUBA1	3,983
2	220 103 039	220 103 727	688	9	ACCN4			CHPF	8 195
2	220,170,047	220 171 227	1 180	a a	STK11IP	79K	6.097		0,100
2	220,170,047	2220,171,227	205	0	011(1111),		49.965		
	/// 5/0 /00		290	3			40,000		
2	207 400 400	222,020,000	202	10			140		
2	227,408,482	227,408,875	393	10		RHBDD1	142	hin 50 000h n	
2 2 2	227,408,482 229,753,549	227,408,875 229,754,004	393 455	10 68	PID1,	RHBDD1 No non-overlappi	142 ng genes wit	hin 50,000bp	
2 2 2	227,408,482 229,753,549	222,323,003 227,408,875 229,754,004	393 455	10 68	PID1, AC006368.2,	RHBDD1 No non-overlappi	142 ng genes wit	hin 50,000bp	14.004
2 2 2 2	227,408,482 229,753,549 230,494,899	227,408,875 229,754,004 230,496,069	393 455 1,170	10 68 9	PID1, AC006368.2, TRIP12, FRY026	RHBDD1 No non-overlappi	142 ng genes wit	hin 50,000bp AC009973.10-2	14,694
2 2 2 2	227,408,482 229,753,549 230,494,899	222,323,003 227,408,875 229,754,004 230,496,069	393 455 1,170	10 68 9	PID1, AC006368.2, TRIP12, FBXO36,	RHBDD1 No non-overlappi	142 ng genes wit	hin 50,000bp AC009973.10-2	14,694
2 2 2 2 2	227,408,482 229,753,549 230,494,899 230,639,921	227,408,875 229,754,004 230,496,069 230,640,310	393 455 1,170 389	10 68 9 11	PID1, AC006368.2, TRIP12, FBXO36, SLC16A14,	RHBDD1 No non-overlappi	142 ng genes wit 8,637	hin 50,000bp AC009973.10-2	14,694
2 2 2 2 2 2 2 2 2	227,408,482 229,753,549 230,494,899 230,639,921 230,984,599	227,408,875 229,754,004 230,496,069 230,640,310 230,985,049	393 455 1,170 389 450	10 68 9 11 9	PID1, AC006368.2, TRIP12, FBXO36, SLC16A14,	RHBDD1 No non-overlappi Y_RNA SP100	142 ng genes wit 8,637 4,150	hin 50,000bp AC009973.10-2 SP140L	14,694
2 2 2 2 2 2 2 2 2	227,408,482 229,753,549 230,494,899 230,639,921 230,984,599 231,629,453	227,408,875 229,754,004 230,496,069 230,640,310 230,985,049 231,629,720	393 455 1,170 389 450 267	10 68 9 11 9 10	PID1, AC006368.2, TRIP12, FBXO36, SLC16A14,	RHBDD1 No non-overlappi Y_RNA SP100 PSMD1	142 ng genes wit 8,637 4,150 132	hin 50,000bp AC009973.10-2 SP140L C2orf72	14,694 7,910 9,140
2 2 2 2 2 2 2 2 2 2 2	227,408,482 229,753,549 230,494,899 230,639,921 230,984,599 231,629,453 231,818,523	222,323,000 227,408,875 229,754,004 230,496,069 230,640,310 230,985,049 231,629,720 231,819,107	393 455 1,170 389 450 267 584	10 68 9 11 9 10 9	PID1, AC006368.2, TRIP12, FBXO36, SLC16A14, ARMC9,	RHBDD1 No non-overlappi Y_RNA SP100 PSMD1	142 ng genes wit 8,637 4,150 132	hin 50,000bp AC009973.10-2 SP140L C2orf72 AC018738.4	14,694 7,910 9,140 90
2 2 2 2 2 2 2 2 2 2 2 2	227,408,482 229,753,549 230,494,899 230,639,921 230,984,599 231,629,453 231,818,523 232,185,588	222,323,000 227,408,875 229,754,004 230,496,069 230,640,310 230,985,049 231,629,720 231,819,107 232,186,251	393 455 1,170 389 450 267 584 663	10 68 9 11 9 10 9 10 9 12	PID1, AC006368.2, TRIP12, FBXO36, SLC16A14, ARMC9,	RHBDD1 No non-overlappi Y_RNA SP100 PSMD1	142 ng genes wit 8,637 4,150 132	hin 50,000bp AC009973.10-2 SP140L C2orf72 AC018738.4 C2orf57	14,694 7,910 9,140 90 18,352
2 2 2 2 2 2 2 2 2 2 2 2 2 2	227,408,482 229,753,549 230,494,899 230,639,921 230,984,599 231,629,453 231,818,523 232,185,588 232,186,695	222,323,000 227,408,875 229,754,004 230,496,069 230,640,310 230,985,049 231,629,720 231,819,107 232,186,251 232,186,991	393 455 1,170 389 450 267 584 663 296	10 68 9 11 9 10 9 12 9	PID1, AC006368.2, TRIP12, FBXO36, SLC16A14, ARMC9,	Y_RNA SP100 PSMD1	142 ng genes wit 8,637 4,150 132	hin 50,000bp AC009973.10-2 SP140L C2orf72 AC018738.4 C2orf57 C2orf57	14,694 7,910 9,140 90 18,352 19,459
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	227,408,482 229,753,549 230,494,899 230,639,921 230,984,599 231,629,453 231,818,523 232,185,588 232,186,695 232,278,871	227,408,875 229,754,004 230,496,069 230,640,310 230,985,049 231,629,720 231,819,107 232,186,251 232,186,991 232,281,089	393 455 1,170 389 450 267 584 663 296 2,218	10 68 9 11 9 10 9 10 9 12 9 9 9	PID1, AC006368.2, TRIP12, FBXO36, SLC16A14, ARMC9, PTMA,	THBDD1 No non-overlappi Y_RNA SP100 PSMD1 U4	142 ng genes wit 8,637 4,150 132 3,390	hin 50,000bp AC009973.10-2 SP140L C2orf72 AC018738.4 C2orf57 C2orf57	14,694 7,910 9,140 90 18,352 19,459
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	227,408,482 229,753,549 230,494,899 230,639,921 230,984,599 231,629,453 231,818,523 232,185,588 232,186,695 232,278,871 232,286,483	222,323,496,069 230,640,310 230,985,049 231,629,720 231,819,107 232,186,251 232,186,991 232,281,089 232,287,189	393 455 1,170 389 450 267 584 663 296 2,218 706	10 68 9 11 9 10 9 10 9 12 9 9 9 13	PID1, AC006368.2, TRIP12, FBXO36, SLC16A14, ARMC9, PTMA, PTMA,	RHBDD1 No non-overlappi Y_RNA SP100 PSMD1 U4	142 ng genes wit 8,637 4,150 132 3,390	hin 50,000bp AC009973.10-2 SP140L C2orf72 AC018738.4 C2orf57 C2orf57 U4	14,694 7,910 9,140 90 18,352 19,459 1.857
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	227,408,482 229,753,549 230,494,899 230,639,921 230,984,599 231,629,453 231,818,523 232,185,588 232,186,695 232,278,871 232,286,483 232,287,255	227,408,875 229,754,004 230,496,069 230,640,310 230,985,049 231,629,720 231,819,107 232,186,251 232,186,991 232,281,089 232,287,189 232,287,563	393 455 1,170 389 450 267 584 663 296 2,218 706 308	10 68 9 11 9 10 9 10 9 9 12 9 9 9 13 9 9	PID1, AC006368.2, TRIP12, FBXO36, SLC16A14, ARMC9, PTMA, PTMA,	RHBDD1 No non-overlappi Y_RNA SP100 PSMD1 U4	142 ng genes wit 8,637 4,150 132 3,390	hin 50,000bp AC009973.10-2 SP140L C2orf72 AC018738.4 C2orf57 C2orf57 U4 PTMA	14,694 7,910 9,140 90 18,352 19,459 1,857 760
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	227,408,482 229,753,549 230,494,899 230,639,921 230,984,599 231,629,453 231,818,523 232,185,588 232,186,695 232,278,871 232,286,483 232,287,255 232,359,079	227,408,875 229,754,004 230,496,069 230,640,310 230,985,049 231,629,720 231,819,107 232,186,251 232,186,991 232,281,089 232,287,189 232,287,563 232,359,692	393 455 1,170 389 450 267 584 663 296 2,218 706 308 613	10 68 9 11 9 10 9 12 9 9 9 13 9 9 9 9	PID1, AC006368.2, TRIP12, FBXO36, SLC16A14, ARMC9, PTMA, PTMA, COPS7B.	RHBDD1 No non-overlappi Y_RNA SP100 PSMD1 U4 U4	142 ng genes wit 8,637 4,150 132 3,390 4,834	hin 50,000bp AC009973.10-2 SP140L C2orf72 AC018738.4 C2orf57 C2orf57 U4 PTMA	14,694 7,910 9,140 90 18,352 19,459 1,857 760
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	227,408,482 229,753,549 230,494,899 230,639,921 230,984,599 231,629,453 231,818,523 232,185,588 232,185,588 232,186,695 232,278,871 232,286,483 232,287,255 232,359,079 232,498,642	227,408,875 229,754,004 230,496,069 230,640,310 230,985,049 231,629,720 231,819,107 232,186,251 232,186,991 232,281,089 232,287,189 232,287,563 232,287,563 232,359,692 232,499,741	393 455 1,170 389 450 267 584 663 296 2,218 706 308 613 1 099	10 68 9 11 9 10 9 12 9 9 9 13 9 9 9 9 9 9 9	PID1, AC006368.2, TRIP12, FBXO36, SLC16A14, ARMC9, PTMA, PTMA, PTMA, COPS7B, NPPC	RHBDD1 No non-overlappi Y_RNA SP100 PSMD1 U4 U4 PDE6D bsa-mir-1471	142 ng genes wit 8,637 4,150 132 3,390 4,834 33 390	hin 50,000bp AC009973.10-2 SP140L C2orf72 AC018738.4 C2orf57 C2orf57 U4 PTMA	14,694 7,910 9,140 90 18,352 19,459 1,857 760
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	227,408,482 229,753,549 230,494,899 230,639,921 230,984,599 231,629,453 231,818,523 232,185,588 232,185,588 232,186,695 232,278,871 232,286,483 232,287,255 232,359,079 232,498,642 233,206,233	227,408,875 229,754,004 230,496,069 230,640,310 230,985,049 231,629,720 231,819,107 232,186,251 232,186,991 232,281,089 232,287,189 232,287,563 232,287,563 232,359,692 232,499,741 233,206,765	393 455 1,170 389 450 267 584 663 296 2,218 706 308 613 1,099 532	10 68 9 11 9 10 9 9 9 9 9 13 9 9 9 9 9 9 9	PID1, AC006368.2, TRIP12, FBXO36, SLC16A14, ARMC9, PTMA, PTMA, PTMA, COPS7B, NPPC, EEHD1	RHBDD1 No non-overlappi Y_RNA SP100 PSMD1 U4 U4 PDE6D hsa-mir-1471 AC073254 6	142 ng genes wit 8,637 4,150 132 3,390 4,834 33,390 16 039	hin 50,000bp AC009973.10-2 SP140L C2orf72 AC018738.4 C2orf57 C2orf57 U4 PTMA EIE4E2	14,694 7,910 9,140 90 18,352 19,459 1,857 760
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	227,408,482 229,753,549 230,494,899 230,639,921 230,984,599 231,629,453 231,818,523 232,185,588 232,185,588 232,185,588 232,186,695 232,278,871 232,286,483 232,287,255 232,359,079 232,498,642 233,206,235	227,408,875 229,754,004 230,496,069 230,640,310 230,985,049 231,629,720 231,819,107 232,186,251 232,186,991 232,281,089 232,287,189 232,287,563 232,287,563 232,359,692 232,499,741 233,206,765	393 455 1,170 389 450 267 584 663 296 2,218 706 308 613 1,099 532	10 68 9 11 9 10 9 12 9 9 9 9 13 9 9 9 9 9 9 9 9 0 10	PID1, AC006368.2, TRIP12, FBXO36, SLC16A14, ARMC9, PTMA, PTMA, PTMA, COPS7B, NPPC, EFHD1, ACAP1	RHBDD1 No non-overlappi Y_RNA SP100 PSMD1 U4 U4 PDE6D hsa-mir-1471 AC073254.6	142 ng genes wit 8,637 4,150 132 3,390 4,834 33,390 16,039	hin 50,000bp AC009973.10-2 SP140L C2orf72 AC018738.4 C2orf57 C2orf57 U4 PTMA EIF4E2 AC064974.4	14,694 7,910 9,140 90 18,352 19,459 1,857 760 49,635
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	227,408,482 229,753,549 230,494,899 230,639,921 230,984,599 231,629,453 231,818,523 232,185,588 232,185,588 232,186,695 232,278,871 232,286,483 232,287,255 232,359,079 232,498,642 233,206,233 236,290,259	227,408,875 229,754,004 230,496,069 230,640,310 230,985,049 231,629,720 231,819,107 232,186,251 232,186,991 232,287,189 232,287,189 232,287,563 232,359,692 232,499,741 233,206,765 236,290,789	393 455 1,170 389 450 267 584 663 2,218 706 308 613 1,099 532 530	10 68 9 11 9 10 9 10 9 9 13 9 9 9 9 10 9 9	PID1, AC006368.2, TRIP12, FBXO36, SLC16A14, ARMC9, PTMA, PTMA, PTMA, COPS7B, NPPC, EFHD1, AGAP1, COP2	RHBDD1 No non-overlappi Y_RNA SP100 PSMD1 U4 U4 PDE6D hsa-mir-1471 AC073254.6	142 ng genes wit 8,637 4,150 132 3,390 4,834 33,390 16,039	hin 50,000bp AC009973.10-2 SP140L C2orf72 AC018738.4 C2orf57 C2orf57 U4 PTMA EIF4E2 AC064874.4	14,694 7,910 9,140 90 18,352 19,459 1,857 760 49,635 47,038
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	227,408,482 229,753,549 230,494,899 230,639,921 230,984,599 231,629,453 231,818,523 232,185,588 232,185,588 232,186,695 232,278,871 232,286,483 232,287,255 232,359,079 232,498,642 233,206,233 236,290,259 237,658,898	227,408,875 229,754,004 230,496,069 230,640,310 230,985,049 231,629,720 231,819,107 232,186,251 232,186,991 232,287,189 232,287,189 232,287,189 232,287,563 232,359,692 232,499,741 233,206,765 236,290,789 237,659,465	393 455 1,170 389 450 267 584 663 2,218 706 308 613 1,099 532 530 530	10 68 9 11 9 10 9 9 12 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	PID1, AC006368.2, TRIP12, FBXO36, SLC16A14, ARMC9, PTMA, PTMA, PTMA, COPS7B, NPPC, EFHD1, AGAP1, COPS8, MTEDED2	RHBDD1 No non-overlappi Y_RNA SP100 PSMD1 U4 U4 PDE6D hsa-mir-1471 AC073254.6 AC105760.3	142 ng genes wit 8,637 4,150 132 3,390 4,834 33,390 16,039 29,349	hin 50,000bp AC009973.10-2 SP140L C2orf72 AC018738.4 C2orf57 C2orf57 U4 PTMA EIF4E2 AC064874.4	14,694 7,910 9,140 90 18,352 19,459 1,857 760 49,635 47,038
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	227,408,482 229,753,549 230,494,899 230,639,921 230,984,599 231,629,453 231,818,523 232,185,588 232,185,588 232,185,588 232,278,871 232,286,483 232,287,255 232,359,079 232,498,642 233,206,233 236,290,259 237,658,898 241,690,313	227,408,875 229,754,004 230,496,069 230,640,310 230,985,049 231,629,720 231,819,107 232,186,251 232,186,251 232,287,189 232,287,189 232,287,563 232,359,692 232,499,741 233,206,765 236,290,789 237,659,465 241,690,632	393 455 1,170 389 450 267 584 663 296 2,218 706 308 613 1,099 532 530 567 319	10 68 9 11 9 10 9 12 9 9 12 9 9 12 9 9 13 9 9 9 10 9 9 10 9 9 10	PID1, AC006368.2, TRIP12, FBXO36, SLC16A14, ARMC9, PTMA, PTMA, PTMA, COPS7B, NPPC, EFHD1, AGAP1, COPS8, MTERFD2,	RHBDD1 No non-overlappi Y_RNA SP100 PSMD1 U4 U4 PDE6D hsa-mir-1471 AC073254.6 AC105760.3	142 ng genes wit 8,637 4,150 132 3,390 4,834 33,390 16,039 29,349	hin 50,000bp AC009973.10-2 SP140L C2orf72 AC018738.4 C2orf57 C2orf57 U4 PTMA EIF4E2 AC064874.4 PASK	14,694 7,910 9,140 90 18,352 19,459 1,857 760 49,635 47,038 3,556
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	227,408,482 229,753,549 230,494,899 230,639,921 230,984,599 231,629,453 231,818,523 232,185,588 232,185,588 232,186,695 232,278,871 232,286,483 232,287,255 232,359,079 232,498,642 233,206,233 236,290,259 237,658,898 241,690,313 241,737,982	2227,408,875 229,754,004 230,496,069 230,640,310 230,985,049 231,629,720 231,819,107 232,186,251 232,186,991 232,287,189 232,287,189 232,287,563 232,359,692 232,499,741 233,206,765 236,290,789 237,659,465 241,690,632 241,738,348	393 455 1,170 389 450 267 584 663 2,218 706 308 613 1,099 532 530 567 319 366	10 68 9 11 9 10 9 12 9 9 13 9 9 9 13 9 9 9 10 9 9 10 9 9 12 12	PID1, AC006368.2, TRIP12, FBXO36, SLC16A14, ARMC9, PTMA, PTMA, PTMA, COPS7B, NPPC, EFHD1, AGAP1, COPS8, MTERFD2, PASK, PPP1R7,	RHBDD1 No non-overlappi Y_RNA SP100 PSMD1 U4 U4 PDE6D hsa-mir-1471 AC073254.6 AC105760.3 ANO7	142 ng genes wit 8,637 4,150 132 3,390 4,834 33,390 16,039 29,349 38,249	hin 50,000bp AC009973.10-2 SP140L C2orf72 AC018738.4 C2orf57 C2orf57 U4 PTMA EIF4E2 AC064874.4 PASK AC005237.2	14,694 7,910 9,140 90 18,352 19,459 1,857 760 49,635 47,038 3,556 30,951
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	227,408,482 229,753,549 230,494,899 230,639,921 230,984,599 231,629,453 231,818,523 232,185,588 232,185,588 232,185,588 232,278,871 232,286,483 232,287,255 232,359,079 232,498,642 233,206,233 236,290,259 237,658,898 241,690,313 241,737,982 214,824	227,408,875 229,754,004 230,496,069 230,640,310 230,985,049 231,629,720 231,819,107 232,186,251 232,186,251 232,287,189 232,287,189 232,287,563 232,359,692 232,499,741 233,206,765 236,290,789 237,659,465 241,690,632 241,738,348 215,300	393 455 1,170 389 450 267 584 663 2,218 706 308 613 1,099 532 530 567 319 366 476	10 68 9 11 9 10 9 12 9 9 12 9 9 13 9 9 9 10 9 9 10 9 9 12 11 11	PID1, AC006368.2, TRIP12, FBXO36, SLC16A14, ARMC9, PTMA, PTMA, PTMA, COPS7B, NPPC, EFHD1, AGAP1, COPS8, MTERFD2, PASK, PPP1R7, CHL1,	RHBDD1 No non-overlappi Y_RNA SP100 PSMD1 U4 U4 PDE6D hsa-mir-1471 AC073254.6 AC105760.3 ANO7 No non-overlappi	142 ng genes wit 8,637 4,150 132 3,390 4,834 33,390 16,039 29,349 38,249 ng genes wit	hin 50,000bp AC009973.10-2 SP140L C2orf72 AC018738.4 C2orf57 C2orf57 U4 PTMA EIF4E2 AC064874.4 PASK AC005237.2 hin 50,000bp	14,694 7,910 9,140 90 18,352 19,459 1,857 760 49,635 47,038 3,556 30,951
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	227,408,482 229,753,549 230,494,899 230,639,921 230,984,599 231,629,453 231,818,523 232,185,588 232,185,588 232,185,588 232,278,871 232,286,483 232,287,255 232,359,079 232,498,642 233,206,233 236,290,259 237,658,898 241,690,313 241,737,982 214,824 636,072	227,408,875 229,754,004 230,496,069 230,640,310 230,985,049 231,629,720 231,819,107 232,186,251 232,287,189 232,287,189 232,287,189 232,287,563 232,359,692 232,499,741 233,206,765 236,290,789 237,659,465 241,690,632 241,738,348 215,300 636,540	393 455 1,170 389 450 267 584 663 296 2,218 706 308 613 1,099 532 530 567 319 366 476 468	10 68 9 11 9 10 9 12 9 9 12 13 9 9 9 10 9 9 10 9 9 10 9 9 12 11 10 10	PID1, AC006368.2, TRIP12, FBXO36, SLC16A14, ARMC9, PTMA, PTMA, PTMA, COPS7B, NPPC, EFHD1, AGAP1, COPS8, MTERFD2, PASK, PPP1R7, CHL1,	RHBDD1 No non-overlappi Y_RNA SP100 PSMD1 U4 U4 PDE6D hsa-mir-1471 AC073254.6 AC105760.3 ANO7 No non-overlappi No non-overlappi	142 ng genes wit 8,637 4,150 132 3,390 4,834 33,390 16,039 29,349 38,249 ng genes wit ng genes wit	hin 50,000bp AC009973.10-2 SP140L C2orf72 AC018738.4 C2orf57 C2orf57 U4 PTMA EIF4E2 AC064874.4 PASK AC005237.2 hin 50,000bp	14,694 7,910 9,140 90 18,352 19,459 1,857 760 49,635 47,038 3,556 30,951
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	227,408,482 229,753,549 230,494,899 230,639,921 230,984,599 231,629,453 231,818,523 232,185,588 232,185,588 232,185,588 232,278,871 232,286,483 232,287,255 232,278,871 232,286,483 232,287,255 232,359,079 232,498,642 233,206,233 236,290,259 237,658,898 241,690,313 241,737,982 214,824 636,072 1,631,389	227,408,875 229,754,004 230,496,069 230,640,310 230,985,049 231,629,720 231,819,107 232,186,251 232,186,991 232,287,189 232,287,189 232,287,189 232,287,563 232,359,692 232,499,741 233,206,765 236,290,789 237,659,465 241,690,632 241,738,348 215,300 636,540 1,631,765	393 455 1,170 389 450 267 584 663 296 2,218 706 308 613 1,099 532 530 567 319 366 476 468 376	10 68 9 11 9 10 9 12 9 9 12 9 9 12 13 9 9 9 10 9 9 10 9 9 12 11 10 10 10	PID1, AC006368.2, TRIP12, FBXO36, SLC16A14, ARMC9, PTMA, PTMA, PTMA, COPS7B, NPPC, EFHD1, AGAP1, COPS8, MTERFD2, PASK, PPP1R7, CHL1,	RHBDD1 No non-overlappi Y_RNA SP100 PSMD1 U4 U4 PDE6D hsa-mir-1471 AC073254.6 AC105760.3 ANO7 No non-overlappi No non-overlappi RPL23AP38	142 ng genes wit 8,637 4,150 132 3,390 4,834 33,390 16,039 29,349 38,249 ng genes wit ng genes wit 18,460	hin 50,000bp AC009973.10-2 SP140L C2orf72 AC018738.4 C2orf57 C2orf57 U4 PTMA EIF4E2 AC064874.4 PASK AC005237.2 hin 50,000bp hin 50,000bp	14,694 7,910 9,140 90 18,352 19,459 1,857 760 49,635 47,038 3,556 30,951
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	227,408,482 229,753,549 230,494,899 230,639,921 230,984,599 231,629,453 231,818,523 232,185,588 232,185,588 232,185,588 232,278,871 232,286,483 232,287,255 232,278,871 232,286,483 232,287,255 232,359,079 232,498,642 233,206,233 236,290,259 237,658,898 241,690,313 241,737,982 214,824 636,072 1,631,389 3,196,309	227,408,875 229,754,004 230,496,069 230,640,310 230,985,049 231,629,720 231,819,107 232,186,251 232,186,991 232,287,189 232,287,189 232,287,189 232,287,563 232,359,692 232,499,741 233,206,765 236,290,789 237,659,465 241,690,632 241,738,348 215,300 636,540 1,631,765 3,196,671	393 3455 1,170 389 450 267 584 663 296 2,218 706 308 613 1,099 532 530 567 319 366 476 468 376 362	10 68 9 11 9 10 9 12 9 9 12 9 9 12 13 9 9 9 12 10 9 9 12 11 10 9 9 9 9 12 12 10 9 9 9 9 10 9 9 9 10 10 9 9 9 10 10 9 9 9 10 10 9 9 10 10 9 9 10 10 9 9 10 10 9 9 10 10 9 9 10 10 9 9 10 10 9 9 10 10 9 9 10 10 9 9 10 10 9 9 10 10 9 9 9 10 10 9 9 9 10 10 9 9 10 10 9 9 9 10 10 9 9 9 10 10 9 9 9 10 10 9 9 10 10 9 9 10 10 9 9 10 10 9 9 10 10 9 9 10 10 9 9 9 10 10 9 9 10 10 9 9 10 10 9 9 10 10 9 9 10 10 9 9 10 10 9 9 10 10 9 9 10 10 9 9 10 10 9 9 10 10 9 9 10 10 9 9 10 10 9 9 10 10 9 9 10 10 9 9 9 10 10 9 9 9 10 10 9 9 9 10 10 9 9 9 10 10 9 9 9 10 10 9 9 9 10 10 9 9 9 10 10 9 9 9 10 10 9 9 9 10 10 9 9 9 10 10 9 9 9 10 10 9 9 9 10 10 9 9 9 9	PID1, AC006368.2, TRIP12, FBXO36, SLC16A14, ARMC9, PTMA, PTMA, PTMA, COPS7B, NPPC, EFHD1, AGAP1, COPS8, MTERFD2, PASK, PPP1R7, CHL1, CRBN,	RHBDD1 No non-overlappi Y_RNA SP100 PSMD1 U4 U4 PDE6D hsa-mir-1471 AC073254.6 AC105760.3 ANO7 No non-overlappi No non-overlappi RPL23AP38	142 ng genes wit 8,637 4,150 132 3,390 4,834 33,390 16,039 29,349 38,249 ng genes wit 18,460	hin 50,000bp AC009973.10-2 SP140L C2orf72 AC018738.4 C2orf57 C2orf57 U4 PTMA EIF4E2 AC064874.4 PASK AC005237.2 hin 50,000bp hin 50,000bp	14,694 7,910 9,140 90 18,352 19,459 1,857 760 49,635 47,038 3,556 30,951
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	227,408,482 229,753,549 230,494,899 230,639,921 230,984,599 231,629,453 231,818,523 232,185,588 232,185,588 232,186,695 232,278,871 232,286,483 232,287,255 232,359,079 232,498,642 233,206,233 236,290,259 237,658,898 241,690,313 241,737,982 214,824 636,072 1,631,389 3,196,309 4,672,720	227,408,875 229,754,004 230,496,069 230,640,310 230,985,049 231,629,720 231,819,107 232,186,251 232,186,991 232,287,189 232,287,189 232,287,189 232,287,189 232,287,189 232,287,563 232,359,692 232,499,741 233,206,765 236,290,789 237,659,465 241,690,632 241,738,348 215,300 636,540 1,631,765 3,196,671 4,673,276	393 393 455 1,170 389 450 267 584 663 296 2,218 706 308 613 1,099 532 530 567 319 366 476 468 376 362 556	10 68 9 11 9 10 9 12 9 9 12 9 9 12 13 9 9 9 12 10 9 9 12 11 10 9 9 9 9 9 9 9 9 10 10 9 9 9 9 10 10 9 9 9 10 10 9 9 9 10 10 9 9 9 10 10 9 9 9 10 10 9 9 10 10 9 9 9 9	PID1, AC006368.2, TRIP12, FBXO36, SLC16A14, ARMC9, PTMA, PTMA, PTMA, COPS7B, NPPC, EFHD1, AGAP1, COPS8, MTERFD2, PASK, PPP1R7, CHL1, CRBN, ITPR1,	RHBDD1 No non-overlappi Y_RNA SP100 PSMD1 U4 U4 PDE6D hsa-mir-1471 AC073254.6 AC105760.3 ANO7 No non-overlappi No non-overlappi RPL23AP38 No non-overlappi	142 ng genes wit 8,637 4,150 132 3,390 4,834 33,390 16,039 29,349 38,249 ng genes wit 18,460 ng genes wit	hin 50,000bp AC009973.10-2 SP140L C2orf72 AC018738.4 C2orf57 C2orf57 U4 PTMA EIF4E2 AC064874.4 PASK AC005237.2 hin 50,000bp hin 50,000bp TRNT1 hin 50,000bp	14,694 7,910 9,140 90 18,352 19,459 1,857 760 49,635 47,038 3,556 30,951
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2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	227,408,482 229,753,549 230,639,921 230,984,599 231,629,453 231,818,523 232,185,588 232,185,588 232,186,695 232,278,871 232,286,483 232,287,255 232,287,255 232,359,079 232,498,642 233,206,233 236,290,259 237,658,898 241,690,313 241,737,982 214,824 636,072 1,631,389 3,196,309 4,672,720 4,705,063 5,138,774	227,408,875 229,754,004 230,496,069 230,640,310 230,985,049 231,629,720 231,819,107 232,186,251 232,186,991 232,287,189 232,287,189 232,287,189 232,287,189 232,287,563 232,359,692 232,499,741 233,206,765 236,290,789 237,659,465 241,690,632 241,738,348 215,300 636,540 1,631,765 3,196,671 4,673,276 4,705,369 5,139,324	393 393 455 1,170 389 450 267 584 663 296 2,218 706 308 613 1,099 532 530 567 319 366 476 468 376 362 556 306 5550	10 68 9 11 9 10 9 12 9 9 9 12 9 9 9 13 9 9 9 13 9 9 9 13 9 9 9 9 10 10 9 9 9 10 10 9 9 9 9 9 9 9	PID1, AC006368.2, TRIP12, FBXO36, SLC16A14, ARMC9, PTMA, PTMA, PTMA, COPS7B, NPPC, EFHD1, AGAP1, COPS8, MTERFD2, PASK, PPP1R7, CHL1, CRBN, ITPR1, ITPR1, ARL8B,	Y_RNA SP100 PSMD1 U4 U4 U4 PDE6D hsa-mir-1471 AC073254.6 AC105760.3 ANO7 No non-overlappi RPL23AP38 No non-overlappi No non-overlappi No non-overlappi No non-overlappi No non-overlappi Y RNA	142 ng genes wit 8,637 4,150 132 3,390 4,834 33,390 16,039 29,349 38,249 ng genes wit 18,460 ng genes wit 18,460 ng genes wit 35,810	hin 50,000bp AC009973.10-2 SP140L C2orf72 AC018738.4 C2orf57 C2orf57 U4 PTMA EIF4E2 AC064874.4 PASK AC005237.2 hin 50,000bp hin 50,000bp hin 50,000bp	14,694 7,910 9,140 90 18,352 19,459 1,857 760 49,635 47,038 3,556 30,951
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	227,408,482 229,753,549 230,494,899 230,639,921 230,984,599 231,629,453 231,818,523 232,185,588 232,185,588 232,185,588 232,185,588 232,278,871 232,286,483 232,287,255 232,359,079 232,498,642 233,206,233 236,290,259 237,658,898 241,690,313 241,737,982 214,824 636,072 1,631,389 3,196,309 4,672,720 4,705,063 5,138,774 9,266,193	227,408,875 229,754,004 230,496,069 230,640,310 230,985,049 231,629,720 231,819,107 232,186,251 232,186,991 232,287,189 232,287,189 232,287,189 232,287,189 232,287,563 232,359,692 232,499,741 233,206,765 236,290,789 237,659,465 241,690,632 241,738,348 215,300 636,540 1,631,765 3,196,671 4,673,276 4,705,369 5,139,324 9,266,768	393 393 455 1,170 389 450 267 584 663 296 2,218 706 308 613 1,099 532 530 567 319 366 476 468 376 366 476 468 376 362 556 306 550 550 575	10 68 9 11 9 10 9 12 9 9 9 12 12 9 9 9 9 9 12 10 9 9 9 9 12 11 10 10 10 10 9 9 9 9 9 9 9 9 9 9 9 9	PID1, AC006368.2, TRIP12, FBXO36, SLC16A14, ARMC9, PTMA, PTMA, PTMA, COPS7B, NPPC, EFHD1, AGAP1, COPS8, MTERFD2, PASK, PPP1R7, CHL1, CRBN, ITPR1, ITPR1, ARL8B, SRGAP3.	Y_RNA SP100 PSMD1 U4 U4 U4 PDE6D hsa-mir-1471 AC073254.6 AC105760.3 ANO7 No non-overlappi RPL23AP38 No non-overlappi No non-overlappi Y_RNA No non-overlappi	142 ng genes wit 8,637 4,150 132 3,390 4,834 33,390 16,039 29,349 38,249 ng genes wit 18,460 ng genes wit 18,460 ng genes wit 35,810 ng genes wit	hin 50,000bp AC009973.10-2 SP140L C2orf72 AC018738.4 C2orf57 C2orf57 U4 PTMA EIF4E2 AC064874.4 PASK AC005237.2 hin 50,000bp hin 50,000bp hin 50,000bp	14,694 7,910 9,140 90 18,352 19,459 1,857 760 49,635 47,038 3,556 30,951 30,607
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	227,408,482 229,753,549 230,494,899 230,639,921 230,984,599 231,629,453 231,818,523 232,185,588 232,185,588 232,185,588 232,185,588 232,278,871 232,286,483 232,287,255 232,359,079 232,498,642 233,206,233 236,290,259 237,658,898 241,690,313 241,737,982 214,824 636,072 1,631,389 3,196,309 4,672,720 4,705,063 5,138,774 9,266,193 9,416,448	227,408,875 229,754,004 230,496,069 230,640,310 230,985,049 231,629,720 231,819,107 232,186,251 232,186,991 232,287,189 232,287,189 232,287,189 232,287,189 232,287,563 232,359,692 232,499,741 233,206,765 236,290,789 237,659,465 241,690,632 241,738,348 215,300 636,540 1,631,765 3,196,671 4,673,276 4,705,369 5,139,324 9,266,768 9,416,807	393 393 455 1,170 389 450 267 584 663 296 2,218 706 308 613 1,099 532 530 567 319 366 476 468 376 366 476 468 376 362 556 306 550 555 359	10 68 9 11 9 10 9 12 9 9 12 9 9 9 9 13 9 9 9 9 10 10 9 9 9 12 11 10 10 10 10 9 9 9 9 9 9 9 9 9 9 9 9	PID1, AC006368.2, TRIP12, FBXO36, SLC16A14, ARMC9, PTMA, PTMA, PTMA, COPS7B, NPPC, EFHD1, AGAP1, COPS8, MTERFD2, PASK, PPP1R7, CHL1, CRBN, ITPR1, ITPR1, ARL8B, SRGAP3, SETD5,	Y_RNA SP100 PSMD1 U4 U4 U4 PDE6D hsa-mir-1471 AC073254.6 AC105760.3 ANO7 No non-overlappi RPL23AP38 No non-overlappi RPL23AP38 No non-overlappi Y_RNA No non-overlappi Y_RNA No non-overlappi AC018506.5	142 ng genes wit 8,637 4,150 132 3,390 4,834 33,390 16,039 29,349 38,249 ng genes wit 18,460 ng genes wit 35,810 ng genes wit 2,780	hin 50,000bp AC009973.10-2 SP140L C2orf72 AC018738.4 C2orf57 C2orf57 U4 PTMA EIF4E2 AC064874.4 PASK AC005237.2 hin 50,000bp hin 50,000bp hin 50,000bp hin 50,000bp	14,694 7,910 9,140 90 18,352 19,459 1,857 760 49,635 47,038 3,556 30,951 30,607
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	227,408,482 229,753,549 230,494,899 230,639,921 230,984,599 231,629,453 231,818,523 232,185,588 232,185,588 232,185,588 232,185,588 232,278,871 232,286,483 232,287,255 232,359,079 232,498,642 233,206,233 236,290,259 237,658,898 241,690,313 241,737,982 214,824 636,072 1,631,389 3,196,309 4,672,720 4,705,063 5,138,774 9,266,193 9,416,448 9,963,013	227,408,875 229,754,004 230,496,069 230,640,310 230,985,049 231,629,720 231,819,107 232,186,251 232,186,991 232,287,189 232,287,189 232,287,189 232,287,563 232,359,692 232,499,741 233,206,765 236,290,789 237,659,465 241,690,632 241,738,348 215,300 636,540 1,631,765 3,196,671 4,673,276 4,705,369 5,139,324 9,266,768 9,416,807 9,963,410	393 3455 1,170 389 450 267 584 663 296 2,218 706 308 613 1,099 532 530 567 319 366 476 468 376 366 550 556 550 557 5359 307	10 68 9 111 9 10 9 9 12 9 9 9 9 12 11 10 10 10 10 10 10 9 9 9 9 9 9 9 9 9	PID1, AC006368.2, TRIP12, FBXO36, SLC16A14, ARMC9, PTMA, PTMA, PTMA, COPS7B, NPPC, EFHD1, AGAP1, COPS8, MTERFD2, PASK, PPP1R7, CHL1, CRBN, ITPR1, ITPR1, ARL8B, SRGAP3, SETD5, CREID1	Y_RNA SP100 PSMD1 U4 U4 PDE6D hsa-mir-1471 AC073254.6 AC105760.3 ANO7 No non-overlappi RPL23AP38 No non-overlappi RPL23AP38 No non-overlappi Y_RNA No non-overlappi Y_RNA No non-overlappi J_C18506.5 U6	142 ng genes wit 8,637 4,150 132 3,390 4,834 33,390 16,039 29,349 38,249 ng genes wit 18,460 ng genes wit 18,460 ng genes wit 25,810 ng genes wit 2,780 27,176	hin 50,000bp AC009973.10-2 SP140L C2orf72 AC018738.4 C2orf57 C2orf57 U4 PTMA EIF4E2 AC064874.4 PASK AC005237.2 hin 50,000bp hin 50,000bp hin 50,000bp hin 50,000bp	14,694 7,910 9,140 90 18,352 19,459 1,857 760 49,635 47,038 3,556 30,951 30,607

3	10,131,958	10,132,297	339	12		C3orf10	80	AC034193.5-3	56
3	10,264,784	10,265,627	843	10	TATDN2,			IRAK2	4,357
3	12,468,796	12,469,209	413	9		TSEN2	31,733	PPARG	17,941
3	12,573,274	12,573,714	440	13	MKRN2,	5S_rRNA	45,562	TSEN2	23,463
3	12,680,443	12,681,099	656	13	RAF1,			AC026170.5	31,112
3	14,418,510	14,418,995	485	9		SLC6A6	115	5S_rRNA	7,249
3	14,667,757	14,668,792	1,035	9	C3orf19,	C3orf20	22,866		
3	15,114,990	15,116,068	1,078	9	ZFYVE20,	MRPS25	33,170	AC090954.3	34,826
3	29,351,953	29,352,255	302	10	RBMS3,			AC098650.2	33,577
3	32,702,190	32,702,579	389	9	CNOT10,			AC138972.8-1	8,082
3	38,148,073	38,148,441	368	9	ACAA1,	Y_RNA	6,184	DLEC1	8,840
3	45,404,825	45,405,355	530	10	LARS2,	No non-overlappi	ng genes wit	hin 50,000bp	
3	45,704,917	45,705,862	945	9		SACM1L	31	LIMD1	7,158
3	48,104,098	48,104,459	361	10	MAP4,			SRP_euk_arch	6,838
3	48,729,349	48,729,648	299	10	IP6K2,	NCKIPSD	31,011	PRKAR2A	33,449
3	49,145,204	49,145,712	508	9	CCDC36,	USP19	11,888	CCDC71	29,261
					LAMB2,			· · ·	
3	49,424,357	49,425,065	708	9	RHOA, TCTA,			AMT	4,151
3	50,340,737	50,341,387	650	9	D 4 D Z 4 A	TUSC2	65	RASSF1	834
3	51,646,989	51,647,322	333	9	RAD54L2,	U6atac	26,371	0510574	
3	52,891,376	52,891,960	584	9	MUSIN1,	0105500		SFMB11	21,708
3	53,356,336	53,356,879	543	9	DCP1A,	SNURD38	14,141	SNURA26	39,901
3	57,516,649	57,517,258	609	11	PDE12,			06	6,937
3	57,558,446	57,558,694	248	10		ARF4	328		
3	61,521,852	61,522,681	829	10	PTPRG,	No non-overlappi	ng genes wit	hin 50,000bp	
3	64,147,471	64,148,184	713	9	PRICKLE2,	No non-overlappi	ng genes wit	hin 50,000bp	
3	71,336,146	71,336,506	360	9	FOXP1,	No non-overlappi	ng genes wit		04.007
3	73,128,404	73,128,711	307	10	PPP4R2,	10100550.0.0	10.005	GL18D4	21,327
3	73,242,422	73,242,983	561	26	02,	AC103559.2-2	18,325	AC103559.2-1	28,492
3	75,773,836	75,774,237	401	9		AC108724.4-2	18,177	nsa-mir-1324	11,137
3	75,780,083	75,780,568	485	23		FRG2C	15,603	nsa-mir-1324	17,384
3	75,780,695	75,781,472	1 01 4	13		FRG2C	14,699	nsa-mir-1324	17,996
<u>ა</u>	75,000,000	75,001,022	1,014	9				FRG2C	1,334
3 2	75,010,039	75,619,013	679	9				FRG2C	19,565
2	75,019,301	75,620,039	50/0 50/	10			410	FRGZU	20,307
3 2	96,015,315	96,015,699	204	9			412		
3	101,009,009	100,010,018	503	9	KIAA1524	AC009222.23	2,311		14 701
3	109,790,930	109,791,529	595	9	DZIP3			SNORATU	14,701
3	116 985 467	116 985 800	333	10	BEIT 0,			I SAMP	26 053
3	121 619 104	121 619 402	298	10	ESTI 1	No non-overlappi	na aenes wit	hin 50 000bp	20,000
3	123 585 563	123 585 943	380	.0	FAM162A	CCDC58	799		
3	123 617 351	123 618 100	749	9		WDR5B	286	KPNA1	5 338
3	125,931,689	125 932 024	335	11	UMPS	TIDI (OB	200	KAI RN	8 963
3	127.866.617	127.866.948	331	9	C3orf46.	TXNRD3	9.982		-,
3	137,953.815	137,954,494	679	9	STAG1.	No non-overlappi	ng genes wit	hin 50,000bp	
3	138,004,187	138,004,559	372	9	,	TMEM22	15.992		
3	144,202,706	144,203,281	575	9	AC018450.26-2.	PAQR9	37.838		
3	156,945,425	156,945,815	390	12	,		,	C3orf33	17,280
3	172,070.537	172,071.020	483	12	RPL22L1,	AC117476.6-1	27.882	EIF5A2	17.878
3	178,558,760	178,559.071	311	9	,	No non-overlappi	ng genes wit	hin 50,000bp	1.
3	185,329,453	185,329,910	457	9		EIF2B5	5,594		
3	196,330,504	196,330,793	289	9	C3orf21,			AC106705.7-1	17,953
3	198,109,843	198,110,323	480	17	SENP5,			NCBP2	36,347
4	1	415	414	9		ZNF595	42,812		
4	1,700	2,438	738	10		ZNF595	40,789		
4	37,835	38,176	341	11		ZNF595	5,051		
4	41,624	42,319	695	9		ZNF595	908		
4	1,231,791	1,232,605	814	9	CTBP1,	C4orf42	1,572		
4	1,683,687	1,684,226	539	9	SLBP,	TACC3	8,828	TMEM129	3,252
4	1,781,398	1,781,675	277	10				FGFR3	1,002
4	1,980,559	1,980,891	332	10	WHSC2,	hsa-mir-943	22,557	WHSC1	26,827
4	4,594,565	4,594,839	274	11	STX18,	No non-overlappi	ng genes wit	hin 50,000bp	
4	6,692,980	6,693,374	394	10	MRFAP1,	AC093323.3	32,698	MAN2B2	17,891
4	6,762,376	6,762,758	382	11	MRFAP1L1,	CNO	5,985		

4	6,768,580	6,769,021	441	12	CNO,	MRFAP1L1	6,075		
4	12,251,008	12,251,615	607	14		No non-overlappi	ng genes wit	hin 50,000bp	
4	22,125,733	22,126,132	399	9	GPR125,	No non-overlappi	ng genes wit	hin 50,000bp	
4	24,083,472	24,084,120	648	12				hsa-mir-573	46,793
4	24,770,757	24,771,442	685	9	SEPSECS.	No non-overlappi	na aenes wit	hin 50.000bp	,
4	26,194,386	26,195,041	655	9	TBC1D19,	No non-overlappi	ng genes wit	hin 50,000bp	
4	39,136,667	39,137,380	713	10	RPL9. LIAS.		00	KLB	9.919
4	48.865.190	48.865.574	384	9	-, -,	AC118282.4-2	28.403		- ,
4	49.009.383	49.010.118	735	9		No non-overlappi	na aenes wit	hin 50.000bp	
4	49 010 755	49 011 153	398	13		No non-overlappi	na aenes wit	hin 50 000hp	
4	49 206 893	49 207 399	506	14		No non-overlappi	na aenes wit	hin 50 000hp	
4	49 208 207	49 209 199	992	q		No non-overlappi	ng genes wit	hin 50,000bp	
-	40,200,207	40,200,100	408	10		No non-overlappi	ng genes wit	hin 50,000bp	
4	70 331 058	70 331 500	400	37	AC108078 3 1		ng genes wit	AC108078.3.3	7 562
4	70,331,030	70,331,300	502	10		116	12 172	AC 100070.3-3	14 426
4	77,026,015	77,026,419	202	10	DEE2 AC1106	00	13,173		14,430
4	77,026,015	77,026,418	403	17	PPEFZ, ACTIUS	0.3-1,	04.004		24,415
4	77,414,769	77,415,209	440	9	FAM47E,	STBD1	31,624	AC034139.7-2	38,007
4	78,216,076	78,216,430	354	12	CCNI,			AC104771.4-2	6,146
4	78,296,858	78,297,301	443	9		CCNG2	250		
4	80,492,478	80,492,778	300	16		ARD1B	26,283		
4	83,514,412	83,514,768	356	10		HNRNPD	239		
4	86,967,606	86,968,235	629	9	ARHGAP24,	No non-overlappi	ng genes wit	hin 50,000bp	
4	88,075,847	88,076,688	841	11		C4orf36	43,248	AC093827.3	13,154
4	88,292,442	88,292,872	430	9				KLHL8	8,366
4	89,596,925	89,598,007	1,082	9	HERC5,			HERC6	13,654
4	103,900,441	103,901,485	1,044	9	MANBA,	AF224669.1-1	30,680	UBE2D3	34,732
4	106,849,058	106,849,433	375	10	INTS12,	No non-overlappi	ng genes wit	hin 50,000bp	
					GSTCD,		00		
4	108,860,099	108,861,476	1,377	9	PAPSS1,	No non-overlappi	ng genes wit	hin 50,000bp	
4	109,388,312	109,388,638	326	9		No non-overlappi	ng genes wit	hin 50,000bp	
4	109,903,159	109,903,600	441	9	AGXT2L1,	No non-overlappi	ng genes wit	hin 50,000bp	
4	113,777,324	113,777,886	562	9	C4orf21,	AC106864.5-1	17,415	hsa-mir-367	10,593
	-, ,-	-, ,		-	LARP7,		, -		-,
4	121,151,647	121,151,903	256	9				MAD2L1	48,137
4	141,664,493	141,664,872	379	10	ELMOD2,			UCP1	35,628
4	142.273.898	142.274.233	335	9	RNF150.	No non-overlappi	na aenes wit	hin 50.000bp	,
4	150,249,934	150,250,144	210	9	1	No non-overlappi	na aenes wit	hin 50.000bp	
4	156,899,255	156,899,646	391	9		GUCY1B3	15		
4	159 863 820	159 864 472	652	10	C4orf46 PPID	FNIP2	45 160	FTFDH	14 528
4	174 527 354	174 527 844	490	12		SAP30	824		,•=•
4	186 850 207	186 850 518	311	9	SORBS2	0,4 00	021	Y RNA	17 503
4	100,000,201	100,000,010	855	14	0011202,	No non-overlanni	na aenes wit	hin 50 000hn	11,000
-	100,715,505	100,716,202	607	14		No non overlappi	ng genes wit	hin 50,000bp	
4	100 717 845	100 718 366	521	1		No non overlappi	ng genes wit	hin 50,000bp	
4	100,717,040	100,710,000	166	9		No non overlappi	ng genes wit	hin 50,000bp	
4	190,737,330	100 744 200	400	10		No non-overlappi	ng genes wit	hin 50,000bp	
4	100 007 240	100 007 704	270	9			10 400		
4	190,007,348	100,007,721	5/3	9			19,480		
4	190,917,363	190,917,939	5/6	9	AC010440 7 0	01	49,501	SI COA 3	4.40
5	525,598	526,279	081	9	ACU10442.7-3,			SLUYAJ	146
5	/24,454	/25,057	603	9				CEP/2	17,790
5	1,063,305	1,064,550	1,245	9	NKD2,	01.001.15		AC116351.2-3	5,913
5	1,209,808	1,210,145	337	9		SLC6A19	44,565	21.221	
5	1,433,578	1,434,125	547	9		CLPTM1L	35,579	SLC6A3	11,789
5	1,647,571	1,648,075	504	9		AC091849.2	1,314		
5	1,845,974	1,846,284	310	11		NDUFS6	8,225	MRPL36	5,215
5	5,030,549	5,031,051	502	9		No non-overlappi	ng genes wit	hin 50,000bp	
5	5,303,421	5,303,755	334	10	ADAMTS16,	No non-overlappi	ng genes wit	hin 50,000bp	
5	6,911,793	6,912,338	545	9		7SK	10,218		
5	10,427,041	10,427,443	402	10	6-Mar, SSU_rRN	A_5,		Y_RNA	36,543
					AC012640.12-1,	1			
5	10,495,097	10,495,746	649	9	ROPN1L,			6-Mar	6,606
5	10,608,524	10,608,785	261	10		ANKRD33B	8,795		
5	11,041,002	11,041,540	538	9	CTNND2,	U6	38,772		
5	14,143,837	14,144,223	386	9		No non-overlappi	ng genes wit	hin 50,000bp	
5	14,185,220	14,185,899	679	10		TRIO	10,930		
5	14,265,264	14,265,741	477	9	TRIO,	No non-overlappi	ng genes wit	hin 50,000bp	
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5	14,284,902	14,285,463	561	9	TRIO,	No non-overlappi	ng genes wit	hin 50,000bp	
5	14,923,061	14,923,808	747	9	ANKH,	AC016575.7	39,859		
5	16,518,890	16,519,419	529	11	ZNF622,			FAM134B	6,729
5	16,947,360	16,948,014	654	10		MYO10	10,638	AC010310.5	40,164
5	17,269,135	17,269,988	853	11	AC026790.5-2,	BASP1	762		
5	34,043,899	34,044,474	575	10	AMACR,	SLC45A2	23,362		
5	34.623.326	34.623.632	306	10		No non-overlappi	na aenes wit	hin 50.000bp	
5	34,890,270	34,890,600	330	9	TTC23L.	AC026801.7-1	7.217		
5	34 951 159	34 951 764	605	10	RAD1 BXDC2	DNAJA5	13 691	TTC23I	34 629
5	35 739 272	35 739 701	429	.0	SPEF2	No non-overlappi	na aenes wit	hin 50 000hn	0.1,020
5	35 851 316	35 851 831	515	10	0,			SPEE2	847
5	36 642 278	36 642 860	582	9	SI C1A3	No non-overlanni	na aenes wit	hin 50 000hn	011
5	36 726 019	36 726 770	751	12	0201710,		ing genes wit	SI C143	1 828
5	36 780 367	36 780 789	422	10		No non-overlanni	na aenes wit	bin 50 000bn	1,020
5	36 780 867	36 781 183	316	10		No non-overlappi	ng genes wit	hin 50,000bp	
5	27 295 054	27 295 457	402	10			1 407	nin 50,000bp	
5	37,203,034	37,203,437	403	12		AC025449.0-5	1,497	116	21 474
5	37,704,395	37,704,710	521	9	NURIU,		40,440	00	31,474
5	37,852,715	37,853,229	514	9	GDNF,	AC008869.5	2,767		
5	37,883,748	37,884,229	481	10		GDNF	8,209	him 50.000hm	
5	38,451,924	38,452,551	627	9	EGFLAM,	No non-overlappi	ng genes wit		04.404
5	39,109,231	39,109,711	480	9	AC026713.5,			FYB	31,404
5	39,109,840	39,110,236	396	9	AC026713.5,			FYB	30,879
5	39,460,888	39,461,293	405	9	DAB2,	No non-overlappi	ng genes wit	hin 50,000bp	
5	40,715,734	40,716,523	789	9	PTGER4,			SNORA63	24,781
5	40,870,924	40,871,460	536	20	RPL37,	SNORD72	2,330		
5	40,888,112	40,888,416	304	9	CARD6,	RPL37	16,968		
5	41,939,314	41,940,367	1,053	9	C5orf51,	FBXO4	20,746		
5	41,960,831	41,961,439	608	9	FBXO4,			C5orf51	3,337
5	42,143,241	42,143,680	439	9		No non-overlappi	ng genes wit	hin 50,000bp	
5	42,459,798	42,460,440	642	9	GHR,			AC093225.2	42,309
5	43,044,289	43,044,621	332	11				AC008875.9	5,661
5	43,053,364	43,054,103	739	9	AC008875.9,	AC025171.8	23,849	C5orf39	21,155
5	43,055,313	43,056,324	1,011	9		AC008875.9	730		
5	43,075,280	43,075,860	580	10	C5orf39,	AC025171.8	2,092		
5	43,076,044	43,076,391	347	9	C5orf39,	AC025171.8	1,561		
5	43,077,754	43,078,119	365	9	C5orf39,	AC008875.9	23,171		
					AC025171.8,				
5	43,078,361	43,079,368	1,007	10	C5orf39,	AC008875.9	23,778		
					AC025171.8,				
5	43,100,432	43,101,051	619	15		C5orf39	21,403	AC025171.8	19,183
5	43,101,766	43,103,342	1,576	13		C5orf39	22,737	AC025171.8	20,517
5	43,515,923	43,516,297	374	9	C5orf28,			C5orf34	6,270
5	43,519,173	43,520,596	1,423	9	C5orf28,			C5orf34	1,971
5	43,591,951	43,592,532	581	9	PAIP1,	C5orf34	41,007	AC010435.6-1	30,257
5	43,662,936	43,663,301	365	10	NNT,	AC010435.6-1	38,854	AC010435.6-2	39,323
5	53,848,956	53,849,343	387	13		SNX18	7		
5	54,491,286	54,491,849	563	9	CDC20B, GPX8,			hsa-mir-449a	10,268
5	54,507,833	54,508,404	571	10		CDC20B	3,073	5S_rRNA	8,095
5	54,558,438	54,559,077	639	9				CCNO	3,663
5	54,639,129	54,639,728	599	13	DHX29,	No non-overlappi	ng genes wit	hin 50,000bp	
					SKIV2L2,				
5	54,786,622	54,787,237	615	9	PPAP2A,			SKIV2L2	29,459
5	55,444,649	55,444,906	257	10	ANKRD55,	AC016585.8	12,382	5S_rRNA	33,417
5	56,145,697	56,147,076	1,379	9	MAP3K1,	No non-overlappi	ng genes wit	hin 50,000bp	
5	56,459,132	56,459,438	306	10		GPBP1	46,263	Y_RNA	41,254
5	56,694,797	56,695,118	321	9		No non-overlappi	ng genes wit	hin 50,000bp	
5	56,826,156	56,826,492	336	10		ACTBL2	11.865		
5	57,791,790	57,792.236	446	10		PLK2	120		
5	57.913 710	57.914 201	491	10		RAB3C	495		
5	58.218 421	58.218 726	305	13				RAB3C	35 259
5	60 031 482	60 032 182	700	.0 Q	DEPDC1B	No non-overlappi	na aenes wit	hin 50.000hn	00,200
5	60 493 569	60 494 304	735	9	C5orf43			NDUFAF2	8 960
5	61 735 164	61 735 732	568	10	DIMT1I	IPO11	8 610		0,000
5	64 369 364	64 369 816	452	۰0 ۵			0,010	SDCCAG10	19 018
U	51,000,004	51,000,010	-102	3	1	1	1	2223/010	10,010

5	66,522,004	66,522,606	602	9	CD180,			MAST4	20,825
5	67,992,659	67,993,143	484	9		No non-overlappi	ng genes wit	hin 50,000bp	
5	68,339,396	68,339,727	331	10		7SK	37,061		
5	71,182,321	71,182,838	517	87	AC116340.3,	No non-overlappi	ng genes wit	hin 50,000bp	
5	71,497,685	71,498,646	961	9	MAP1B,	No non-overlappi	ng genes wit	hin 50,000bp	
5	71,639,925	71,640,396	471	11	MRPS27,			AC026406.5-1	5,584
5	72,148,528	72,149,293	765	9	TNPO1,			Y RNA	48,134
5	73,538,041	73,538,411	370	10		AC091899.2	30,803	-	
5	73,648,590	73,649,209	619	9		AC106732.2-1	358		
5	73.783.690	73,784,013	323	10		No non-overlappi	na aenes wit	hin 50.000bp	
5	73,963,701	73,964,154	453	10	ENC1.	No non-overlappi	na aenes wit	hin 50.000bp	
5	74.098.389	74.098.997	608	12	GFM2, TINP1.	U6	11.893	FAM169A	10.158
5	78,239,968	78.240.477	509	9	ARSB.	No non-overlappi	na aenes wit	hin 50.000bp	,
5	78.845.945	78.846.603	658	9	- ,	HOMER1	149	RPL29P15	3,469
5	79,224,739	79.225.203	464	10		No non-overlappi	na aenes wit	hin 50.000bp	- ,
5	79.820.007	79.820.304	297	12	FAM151B.		3.3	ZFYVE16	8.753
5	81 183 155	81 183 716	561	10		AC026726 7	40 350		0,100
5	82 243 155	82 243 524	369	9		No non-overlappi	na aenes wit	hin 50 000bp	
5	82 804 578	82 805 377	799	9	CSPG2	No non-overlappi	ng genes wit	hin 50,000bp	
5	86 187 014	86 187 500	486	9	001 02,		ng gonoo mit	AC008539.6	23 503
5	88 214 617	88 215 024	407	21	MEE2C	No non-overlappi	na aenes wit	hin 50 000bp	20,000
5	80,806,044	80,806,630	505	10	AC003510.2		ng genes wit		40 561
5	03,000,044	09,000,009	555	10	POI R3G				40,501
5	90 714 735	90 715 369	634	9	ARRDC3	No non-overlappi	na aenes wit	hin 50 000bp	
5	92,960,847	92,961,206	359	10		AC106818.2	613	NR2F1	5.313
5	93 038 859	93 039 198	339	11	FAM172A	No non-overlappi	na aenes wit	hin 50 000bp	-,
5	93 494 581	93 494 790	209	12	.,	FAM172A	21 485	AC104127 2	20.678
5	95 196 238	95 196 712	474	9		GLRX	12 040	RHOBTB3	38 411
5	95 319 612	95 320 161	549	9	FII2	OLIVY	12,010	AC008592.4	14 340
5	95 322 296	95 322 826	530	9	FII2			AC008592.4	11,675
5	96 107 364	96 107 782	418	9	CAST			ARTS-1	14 488
5	96 169 341	96 169 995	654	9	ARTS-1			CAST	33 198
5	96 295 920	96 296 846	926	9	/		8	0/101	00,100
5	96 296 872	96 297 274	402	10		AC008850 3	6 485		
5	99,899,088	00 800 422	334	9	ΕΝΠΕΓ, ΕΔΜ174Δ	No non-overlanni	na aenes wit	hin 50 000hn	
5	102 1/3 087	102 144 318	331	9	$1 \wedge 10 \cap 1 \rightarrow 1$	No non-overlappi	ng genes wit	hin 50,000bp	
5	102,140,007	102,144,010	308	9	DAM	No non-overlappi	ng genes wit	hin 50,000bp	
5	102,223,771	102,230,103	958	11	GIN1 HISPPD1	No non-overlappi	ng genes wit	hin 50,000bp	
5	102,405,221	102,404,173	580	9		No non-overlappi	ng genes wit	hin 50,000bp	
5	107 028 833	107 029 163	330	9	EENA5	No non-overlappi	ng genes wit	hin 50,000bp	
5	108,000,003	108 002 364	1 461	9	2110.00,	FED	10 058	1111 00,00000	
5	108 112 140	108 112 797	657	13	FER	No non-overlanni	na aenes wit	hin 50 000hn	
5	110 455 548	110 456 099	551	11	WDR36		ng genes wit		13 926
5	111 523 928	111 524 401	563	12	EPR41144	No non-overlanni	na aenes wit	hin 50 000hn	10,020
5	111 524 522	111 524 860	337	10	EPB411 44	No non-overlappi	ng genes wit	hin 50,000bp	
5	111 782 700	111 783 571	781	10	$EPB41I 4\Delta$	No non-overlappi	ng genes wit	hin 50,000bp	
5	114 989 876	114 990 233	357	12	LI DI ILT/1,	TICAM2	110	00,000bp	
5	115 448 486	115 440 186	700	9		AC034236 5-1	41 620		
5	115 038 270	115 038 769	100	11	SEMA6A	No non-overlappi	na aenes wit	hin 50 000hn	
5	115 030 500	115 030 020	320	10		SEMA6A	1 051	iiii 30,000bp	
5	121 0/0 502	121 0/0 792	200	10		No non-ovorlanni	na aenee wit	hin 50 000bp	
5	121,949,502	121,949,702	200	10			13 631	SNY24	27 212
5	122,400,000	122,400,907	307	9		No non ovorlanni	na aonos wit	511724	21,212
5	122,018,000	122,019,040	270	10		No non-ovenappi	ng genes wit		30 556
5	123,903,093	123,903,471	456	10		No non overlenni	na aonoo wit	ZNI 000	30,330
5	124,030,033	124,033,149	400	9	ZNI 000,		ng genes wit		
Э Е	124,112,0//	124,113,09/	02C	10		LINFOUS	3,8/3	hin 50 000km	
5 F	124,110,311	125,050,094	341	10			E 440		
ວ ೯	125,956,568	125,959,084	490	10			5,448	<u> </u>	
Э Е	120,904,203	120,904,773	2 200	9			5,274		
5 F	120,139,972	120,142,232	2,200	10	LIVIIND I,	MEGE10	20,904		
ວ ೯	120,002,944	120,003,332	<u></u>	10		No pop overlage:	1,182	hin EO OCOhn	
Э Е	120,260,620	120,260,000	250	10	CHEVS	No non-overlappi	ng genes wit	hin 50,000bp	
ວ 	129,209,030	120,000,309	309	9	01010,				E 500
Э	130,999,404	130,999,709	305	9		NAFGEF0	5/6		5,598

5	131,853,487	131,853,890	403	10	IRF1,			AC116366.4	13,852
5	132,177,188	132,177,632	444	9	ANKRD43,			SHROOM1	8,102
5	132,229,604	132,230,769	1,165	11	GDF9, UQCRQ,	LEAP2	5,144	AFF4	8,201
5	132,415,012	132,415,767	755	16	HSPA4.	ZCCHC10	24.873		-, -
5	132,474,314	132,475,070	756	9	,			HSPA4	5,706
5	133,366,821	133,367,102	281	10	VDAC1,	C5orf15	34,444		,
5	133,540,235	133,540,918	683	9	SKP1A,			PPP2CA	19,129
5	133,611,300	133,611,684	384	9		PPP2CA	21,451		
5	133,775,113	133,776,173	1,060	9	CDKN2AIPNL,	CDKL3	44,449	UBE2B	19,415
5	133,890,341	133,890,719	378	11	PHF15,			AC005355.1-1	8,714
5	133,950,694	133,951,016	322	9				PHF15	3,877
5	134,268,332	134,268,877	545	10	PCBD2,			C5orf14	3,110
5	134,287,578	134,288,364	786	19	PCBD2,			AC008670.6-2	1,685
					AC008670.6-1,				
5	134,289,318	134,289,757	439	16	PCBD2,			AC008670.6-2	292
5	134,290,438	134,290,840	402	13	PCBD2,	AC008670.6-4	191	AC008670.6-5	1,076
5	134,851,767	134,852,147	380	9		C5orf20	35,779	NEUROG1	45,724
5	134,915,307	134,916,004	697	9		NEUROG1	15,769	CXCL14	18,270
5	135,444,003	135,444,326	323	11	Vault,			TGFBI	16,600
5	135,599,379	135,599,712	333	10	TRPC7,	No non-overlappi	ng genes wit	hin 50,000bp	
5	137,117,788	137,118,345	557	10	HNRPA0,	KLHL3	18,340		
5	137,252,800	137,253,428	628	14	PKD2L2,			MYOT	1,362
5	137,474,822	137,475,202	380	9		U6	4,959	NME5	3,559
5	137,700,959	137,702,036	1,077	9	FAM53C,	CDC25C	5,544		
5	138,545,619	138,546,146	527	9	SIL1,	U6	39,177		
5	138,561,200	138,562,249	1,049	9	SIL1,	U6	23,074		
5	138,626,193	138,626,612	419	10		MATR3	11,079	U6	40,768
5	138,656,946	138,657,401	455	15	MATR3,	5S_rRNA	6,039		
5	138,657,830	138,658,609	779	9	MATR3,	5S_rRNA	4,831		
5	138,659,326	138,659,620	294	10	MATR3,	5S_rRNA	3,820		
5	138,704,818	138,705,052	234	9		PAIP2	366	MATR3	9,559
5	138,705,234	138,705,569	335	20	PAIP2,	AC011404.6-1	8,351	MATR3	9,975
5	138,756,167	138,756,779	612	12		AC135457.2-1	2,663	AC135457.2-2	3,374
5	138,803,063	138,803,476	413	9	DNAJC18,	U5	8,019		
5	138,877,881	138,878,258	377	9		IMEM173	35,405	Y_RNA	36,411
5	139,717,329	139,717,936	607	9		SLC4A9	2,035		
5	140,007,512	140,007,827	315	11	AC116353.2-2,	NDUFA2	88	TMC06	2,335
5	140,051,108	140,051,490	382	10	HARS, HARS2,	ZMAT2	8,726	7144 70	
5	140,070,867	140,071,315	448	13	Vault,	Vault	7,380		4,444
5	140,078,446	140,078,990	544	14	Vault,	vauit	6,938		7,310
5	140,085,643	140,086,205	562	16	Vault,			55_fRNA	5,621
5	140,286,173	140,286,516	343	9	PCDHA2, PCDHA4, PCDHA6, PCDHA9, PCDHA13, PCDHA11, PCDHA12,	No non-overlappi	ng genes wit	nin 50,000p	
5	140,835,395	140,835,967	572	10	PCDHGA2, PCDHGA3, PCDHGA6, PCDHGA8, PCDHGB7, PCDHGA11, PCDHGA12,	AC008781.7	3,100		
5	141,051,855	141,052,250	395	10		ARAP3	9,871		
5	141,208,842	141,209,197	355	9				PCDH1	3,670
5	145,194,627	145,195,945	1,318	9	PRELID2,			GRXCR2	23,544
5	145,335,036	145,335,316	280	11	SH3RF2,	No non-overlappi	ng genes wit	hin 50,000bp	
5	145,562,803	145,563,455	652	9	RBM27,	LARS	13,739		
5	145,806,675	145,806,963	288	11	000000	TCERG1	103		
5	146,325,872	146,326,244	372	10	PPP2R2B,	No non-overlappi	ng genes wit	nin 50,000bp	
5	148,741,581	148,742,159	578	9			2,550		
5	149,074,369	149,074,672	303	10		AC022100.7-2	7,154		
5 5	149,809,160	149,810,046	250	13	RF314,	AC011274 6 2	136		
Э	101,004,058	101,004,408	ა 50	10	i Sr.,	AUUI 13/4.0-2	0,921	1	

5	151,130,629	151,131,853	1,224	9	G3BP1,	AC091982.3-1	4,636		
5	157,534,351	157,534,960	609	9		No non-overlappi	ng genes wit	hin 50,000bp	
5	158,535,134	158,535,501	367	9	RNF145,	No non-overlappi	ng genes wit	hin 50,000bp	
5	159,368,554	159,369,154	600	11	TTC1,			Y_RNA	423
5	159,424,906	159,425,254	348	11	TTC1,	No non-overlappi	ng genes wit	hin 50,000bp	
					PWWP2A,				
5	167,082,763	167,083,224	461	9	ODZ2,	No non-overlappi	ng genes wit	hin 50,000bp	
5	167,553,659	167,553,966	307	10	ODZ2,	No non-overlappi	ng genes wit	hin 50,000bp	
5	167,650,980	167,651,351	371	9		WWC1	319		
5	167,661,872	167,662,276	404	9	WWC1,			ODZ2	38,133
5	167,939,141	167,939,553	412	9	PANK3,	hsa-mir-103-1-	18,581	FBLL1	49,055
						as			
5	167,959,951	167,960,256	305	12		PANK3	20,785		
5	168,374,758	168,375,311	553	9	SLIT3,	No non-overlappi	ng genes wit	hin 50,000bp	
5	171,366,113	171,367,188	1,075	9	FBXW11,			STK10	34,491
5	171,643,846	171,644,660	814	11		UBTD2	446	AC008671.6-2	4,922
5	171,714,155	171,715,046	891	9	SH3PXD2B,	No non-overlappi	ng genes wit	hin 50,000bp	
5	172,503,909	172,504,564	655	10	BNIP1,			C5orf41	7,342
5	173,405,059	173,405,405	346	10	AC093310.1,			C5orf47	39,311
5	173,730,803	173,731,584	781	9		No non-overlappi	ng genes wit	hin 50,000bp	
5	173,771,034	173,771,380	346	9		No non-overlappi	ng genes wit	hin 50,000bp	
5	174,474,181	174,474,592	411	14		No non-overlappi	ng genes wit	hin 50,000bp	
5	175,089,421	175,089,990	569	9				U6	25,808
5	176,145,969	176,146,601	632	9		UNC5A	23,565		
5	176,381,654	176,382,463	809	11	ZNF346,	UIMC1	15,296		
5	176,814,585	176,815,079	494	9	PRR7,			DBN1	1,141
5	176,860,440	176,860,759	319	9		PDLIM7	3,232	DOK3	1,893
5	176.876.544	176.876.870	326	13	DDX41.	DOK3	7.085	AC145098.2-2	2.527
5	177.563.678	177.564.140	462	9	HNRNPAB.		,	AGXT2L2	4.057
5	177.594.651	177.594.985	334	10	,	AGXT2L2	2.259	COL23A1	2.240
5	177.985.813	177,986,714	901	9	CLK4.	AC022096.7	6.214		, -
5	178,910,541	178,910,859	318	9	RUFY1.	No non-overlappi	na aenes wit	hin 50.000bp	
5	179,180,160	179,180,657	497	9	SQSTM1.	MGAT4B	13.613	C5orf45	16.216
5	179 431 446	179 432 000	554	10	RNF130		,	AC122713.2	13 323
5	179 568 071	179 568 389	318	.0	RASGEF1C			MAPK9	26,999
5	180 518 705	180 519 218	513	9				OR2V2	3 209
5	180 528 993	180 529 490	497	10		AC008620 12-4	4 742	0.1212	0,200
5	180 533 037	180 533 831	794	.0		AC008620 12-4	8 786		
5	180 547 092	180 547 705	613	12			0,100	TRIM7	5 826
5	180 547 967	180 548 634	667	14				TRIM7	4 897
5	180 550 785	180 551 623	838	9				TRIM7	1,007
5	180 566 238	180 566 723	485	12		TRIM7	1 455		1,000
5	180 566 921	180 567 842	921	9		TRIM7	2 138		
5	180 576 773	180 578 713	1 940	9		TRIM41	4 199		
5	180 581 347	180 582 176	820	20		TRIM41	736		
5	180 582 577	180 584 138	1 561	20	TRIM41	TRIM7	17 70/	GNB2L1	12 308
6	93 438	94 022	584	a 3		AI 353654 29	3 553	RP1-24022.3	3 370
6	241 116	241 644	528	10	DUSP22	No non-overlappi	na aenes wit	hin 50 000bp	0,019
6	266 643	267 415	772	10	DUSP22	No non-overlappi	ng genes wit	hin 50 000bp	
6	200,040	272 0/0	462	12	DUSP22	No non-overlappi	na aenes wit	hin 50,0005p	
6	272,470	272,340	402	11		No non-overlappi	ng genes wit	hin 50,000bp	
6	273,913	274,309	5/6	11	DUSP22	No non-overlappi	ng genes wit	hin 50,000bp	
6	280 600	213,402	711	9		No non-overlappi	ng genes wit	hin 50,000bp	
6	200,090	201,401	663	0		No non overlappi	ng genes wit	hin 50,000bp	
6	201,097	202,200	810	9	2001 22,		ng genes wit	DUSP22	5 575
6	310 946	312 102	277	11			23 567		16 162
6	1 000 416	1 001 201	965	· · · ·			20,007	AL 033391 2 2	10,403
6	1 116 150	1 116 420	000 275	10		AL035531.17	40,473	ALUJJJO 1.2-2	40,235
6	1,110,153	1,110,428	2/5	10	EOVO1	ALUSSSS1.17	15,326	hin 50 000hn	
0	1,257,396	1,257,708	312	11		No non-overlappi	ng genes wit	hin 50,000bp	
0	1,258,941	1,259,614	0/3	12	FUAQT,	FOXE2			
0 C	1,333,393	1,333,691	298	16		FUAF2	1,377		4 754
o c	1,342,585	1,342,979	394	9		DD11 457 104 4	0 754		1,754
0	1,469,274	1,469,973	699	10		KP11-15/J24.1	8,751	ALD12329.17-2	1,041
6	1,541,224	1,541,776	552	9	AL 00/01/07	ALU34344.24-1	/2	AL 004044 5 4 5	00.01-
6	1,541,914	1,542,507	593	9	AL034344.24-1,	FUXC1	13,173	ALU34344.24-2	20,017

6	1,712,672	1,713,385	713	9	GMDS,	No non-overlappi	ng genes wit	hin 50,000bp	
6	1,726,514	1,726,775	261	10	GMDS,	No non-overlappi	ng genes wit	hin 50,000bp	
6	1,778,071	1,778,472	401	11	GMDS,	No non-overlappi	ng genes wit	hin 50,000bp	
6	2,191,053	2,192,142	1,089	9		GMDS	208		
6	2.298.818	2.299.443	625	9				AL591120.3	9.972
6	2.394.328	2,394,688	360	10		AL031768.9-3	7.817		- / -
6	2 579 525	2 579 986	461	11	C6orf195		.,	MYI K4	28 885
6	2 712 405	2 713 021	616		WRNIP1	ΜΥΙ Κ4	16 252		
6	2 799 295	2 799 959	664	g	,	SERPINB1	12 200	SERPINB9	32 548
6	2,700,200	2,700,000	455	0			22 750		21 681
6	2,071,250	2,071,711	503	10			22,750		15 440
6	2,077,550	2,077,943	1 062	10	AL 100051 04 1		20,044	SERFINDO	15,449
0	2,933,300	2,934,020	1,002	10	AL 133351.34-1,	NQO2	4,003		
0	2,935,641	2,936,056	415	10	AL133351.34-1,	NQO2	3,175		
6	2,936,273	2,936,601	328	9	AL133351.34-1,	NQO2	2,630		0.455
6	2,968,450	2,969,574	1,124	9	AL133351.34-2,			NQU2	3,455
6	3,064,154	3,064,506	352	10	BPHL,			RIPK1	3,734
6	3,071,697	3,072,006	309	10	BPHL,	AL031963.40-6	27,871	RIPK1	11,277
6	3,154,235	3,154,556	321	10		AL445309.13-2	16,209	TUBB2B	14,960
6	3,154,563	3,155,022	459	9		AL445309.13-2	15,743	TUBB2B	14,494
6	3,172,096	3,172,580	484	10	TUBB2B,			AL445309.13-2	1,227
6	3,202,330	3,202,616	286	10	AL445309.13-1,	PSMG4	1,677		
6	3,214,624	3,214,967	343	10	PSMG4, SLC22A23.			AL445309.13-1	1,611
6	3 355 972	3 356 429	457	11	SI C22A23	No non-overlappi	na aenes wit	hin 50 000bp	
6	3 400 303	3 400 874	571	a	SI C22A23	No non-overlappi	ng genes wit	hin 50,000bp	
6	3 402 110	3 402 668	558	0	02022/120,		376	IIII 00,0000p	
6	3 402 919	3 403 351	533	12		SL C22A23	1 094		
0	3,402,010	3,403,331	200	12		SLUZZAZS	1,004	hin EO 000hn	
0	3,507,010	3,507,339	323	10		No non-overlappi	ng genes wit	nin 50,000bp	
6	3,557,737	3,558,305	568	11		No non-overlappi	ng genes wit	nin 50,000p	
6	3,687,355	3,687,937	582	9	C6orf145,	RP11-420L9.2	11,395		
6	3,695,110	3,696,098	988	9	C6orf145,	RP11-420L9.2	3,234		
6	3,873,165	3,874,234	1,069	9				RP1-140K8.3	5,836
6	3,966,142	3,967,433	1,291	9	AL033383.26, PRPF4B,	AL138831.12	6,557		
6	4,264,404	4,265,181	777	9		No non-overlappi	ng genes wit	hin 50,000bp	
6	4,284,337	4,284,781	444	9		No non-overlappi	ng genes wit	hin 50,000bp	
6	4.297.098	4.297.562	464	11		No non-overlappi	na aenes wit	hin 50.000bp	
6	4 360 579	4 361 319	740	9		5S_rRNA	11 877		
6	4 592 710	4 593 401	691	12			.,	AI 034376 10	35 559
6	4 721 013	4 721 359	346	18	CDYI	No non-overlanni	na aenes wit	hin 50 000hn	00,000
6	4 751 304	4,721,000	326	10		No non-overlappi	ng genes wit	hin 50,000bp	
6	4 753 073	4,753,000	3/9	10		No non overlappi	ng genes wit	hin 50,000bp	
6	4,755,075	4,755,421	440	10	ODTL,			AL 250642.27	14.000
0	4,975,694	4,976,306	412	12	FAD00	RPP40	20,024	AL339043.27	14,000
6	5,289,439	5,289,861	422	9	FARS2,	No non-overlappi	ng genes wit		
6	5,392,940	5,393,495	555	9	FAR52,	No non-overlappi	ng genes wit	nin 50,000bp	
6	5,992,008	5,992,343	335	9		NKN1	39,376		
6	6,632,504	6,632,816	312	10				LY86	32,289
6	6,837,383	6,837,842	459	10				SRP_euk_arch	45,992
6	6,996,967	6,997,617	650	9		No non-overlappi	ng genes wit	hin 50,000bp	
6	7,003,538	7,003,962	424	15		RREB1	48,867	AL355336.15-1	48,600
6	7,060,857	7,061,654	797	9	RREB1,	AL355336.15-1	7,639		
6	7,334,407	7,335,269	862	12	CAGE1, RIOK1,	RP11-69L16.6	47,119		
6	7,335,293	7,335,584	291	9	RIOK1,	CAGE1	352		
6	7.450.536	7.450.884	348	11	*	RP11-288G3.3	551		
6	7 485 588	7 486 135	547	9		DSP	734		
6	7 486 358	7 486 747	380	10		DSP	122		
6	7 670 007	7 671 601	71/	0		BMP6	300		
C C	7 956 404	7 956 750	7 14 EE0	9			309		26.000
0 C	7,000,194	1,000,103	209	10	TXNDCO,	AL 000004 4	44.00-		20,909
0	8,008,811	8,009,516	705	12	TANDUS,	ALU23094.1	11,937		15,122
6	8,009,594	8,009,896	302	10	TXNDC5,	ALU23694.1	12,720	EEF1E1	14,742
6	8,047,025	8,047,662	637	14	EEF1E1,	TXNDC5	37,379		
6	10,044,702	10,045,191	489	9	OFCC1,	No non-overlappi	ng genes wit	hin 50,000bp	
6	10,446,662	10,447,035	373	9				RP1-290I10.2	26,808
6	10,511,982	10,512,510	528	10	TFAP2A,	RP1-290I10.2	37,181	C6orf218	25,072
6	10,521,975	10,522,537	562	10	TFAP2A,	RP1-290I10.2	47,174	C6orf218	15,045

6	10,522,720	10,523,943	1,223	13	TFAP2A,	RP1-290I10.2	47,919	C6orf218	13,639
6	10,527,532	10,528,691	1,159	9	TFAP2A,			C6orf218	8,891
6	10,802,439	10,802,853	414	9	C6orf52,	PAK1IP1	321		
6	10.802.861	10.803.547	686	9	PAK1IP1.	C6orf52	33		
6	10.855.304	10.856.332	1.028	11	TMEM14B.			AL024498.13-1	4.676
6	10,946,223	10,946,963	740	10	MAK.	SYCP2L	48.087	GCM2	34,487
6	11 152 663	11 153 258	595	15		FLOVI 2	53		,
6	11 201 746	11 202 425	679	11				AI 136139.6	9 488
6	11 202 530	11 203 035	505	9				AL 136139.6	8 878
6	11,202,000	11,200,000	500	0					10,500
6	11,200,422	11 241 110	070	9		No non overlenni	na aonoo wit	hin 50 000hn	10,500
0	11,340,232	11,341,110	0/0	9	NEDD9,		ng genes wit		
6	11,357,692	11,358,184	492	10		NEDD9	16,015		
6	11,444,124	11,444,488	364	9		No non-overlappi	ng genes wit	hin 50,000bp	
6	11,500,896	11,501,477	581	9		No non-overlappi	ng genes wit	hin 50,000bp	
6	11,645,475	11,646,339	864	9	TMEM170B,	U1	33,585	RP11-716O23.3	20,790
6	12,115,661	12,116,088	427	10		HIVEP1	4,469		
6	12,121,153	12,121,798	645	12	HIVEP1,	No non-overlappi	ng genes wit	hin 50,000bp	
6	12,341,897	12,342,361	464	10		No non-overlappi	ng genes wit	hin 50,000bp	
6	12,398,016	12,398,824	808	11	EDN1,	RP3-451B15.3	28,847		
6	12,746,235	12,746,668	433	9		No non-overlappi	ng genes wit	hin 50,000bp	
6	13,122,091	13,123,786	1,695	9	PHACTR1,	No non-overlappi	ng genes wit	hin 50,000bp	
6	13.273.739	13,274,119	380	10	PHACTR1.	U1	48,148		
6	13 436 247	13 436 730	483	11	TBC1D7	AL008729 1-1	32 450	GFOD1	29 311
6	13 444 621	13 445 136	515	Q	TBC1D7	AL 008729 1-1	40 824	GEOD1	20,011
6	13 570 736	13 571 120	303	12		AL000723.1-1	40,024	Cforf114	6 363
6	12,570,730	12,571,129	442	12		AL 501060 4	20.004	0001114	0,505
0	13,369,076	13,369,519	443	9	GFODT, Ceorf114	AL591909.4	30,294		
6	12 504 074	12 505 279	204	0		Ceorf114	590		
0	13,594,974	13,395,276	304	9	GFODI,	00	000		
6	13,595,529	13,595,868	339	11	GFOD1,	C60ff114	1,135		
6	13,682,377	13,682,646	269	10		SIR15	166		
6	13,721,498	13,723,642	2,144	9	NOL7,			SIRT5	999
6	13,820,103	13,820,454	351	10		RANBP9	171		
6	13,921,689	13,922,263	574	9	CCDC90A,	No non-overlappi	ng genes wit	hin 50,000bp	
6	13,922,292	13,923,019	727	14	CCDC90A,	No non-overlappi	ng genes wit	hin 50,000bp	
6	13,981,598	13,982,352	754	9		No non-overlappi	ng genes wit	hin 50,000bp	
6	14,252,864	14,253,180	316	13				CD83	7,736
6	14,318,973	14,320,061	1,088	9		No non-overlappi	ng genes wit	hin 50,000bp	
6	14,766,168	14,766,617	449	9				U6	11,320
6	14,908,063	14,908,500	437	9		No non-overlappi	ng genes wit	hin 50,000bp	
6	14,918,174	14.918.779	605	9		No non-overlappi	na aenes wit	hin 50.000bp	
6	15 356 054	15 356 442	388	10	JARID2	No non-overlappi	na aenes wit	hin 50 000bp	
6	15 356 690	15 356 992	302	9	JARID2	No non-overlappi	na aenes wit	hin 50 000hp	
6	15 357 113	15 357 580	467	11	JARID2	No non-overlappi	ng genee wit	hin 50,000bp	
6	15 388 881	15 380 522	6/1	0			33 608		43.055
6	15 500 420	15 500 900	151	9		30	55,000		21 120
0	10,099,439	10,099,890	451	9		No non sustant			51,130
Ø	15,771,150	15,771,848	098	9	רין שאווט.	NU HUN-OVERIAPPI	ng genes wit	quou, uc min	
6	15,799,296	15,800,036	/40	9			28,046		
6	15,841,773	15,842,456	683	9		No non-overlappi	ng genes wit	nin 50,000bp	
6	15,844,546	15,845,126	580	9		No non-overlappi	ng genes wit	nin 50,000bp	
6	16,064,531	16,064,943	412	9				AL365265.23	21,004
6	16,439,464	16,439,979	515	11	ATXN1,			GMPR	35,705
6	16,440,400	16,440,869	469	9	ATXN1,			GMPR	36,641
6	16,444,697	16,445,023	326	9	ATXN1,			GMPR	40,938
6	16,866,782	16,867,311	529	9	ATXN1,	No non-overlappi	ng genes wit	hin 50,000bp	
					AL137003.12,				
6	16,869,128	16,869,718	590	9	ATXN1,	No non-overlappi	ng genes wit	hin 50,000bp	
					AL137003.12,				
6	16,869,780	16,871,151	1,371	9		AL137003.12	80		
6	16,879,092	16,879,407	315	11		AL137003.12	9,392		
6	17,072,815	17,073,538	723	10		No non-overlappi	ng genes wit	hin 50,000bp	
6	17,502,213	17,502,834	621	9	CAP2,			RP1-273P12.1	11.883
6	17.541 178	17.541 775	597	9	CAP2	No non-overlappi	na genes wit	hin 50.000bp	,
6	17 814 835	17 815 339	504	10	,	NUP153	38		
6	18 230 641	18 231 255	614	15	NHI RC1			TPMT	5 271
6	18 612 172	18 612 527	365	10				IBRDC2	25 2/5
U	10,012,172	10,012,007	000	10	I	1		1011002	55,545

6	19,490,768	19,491,113	345	9				RP11-686D16.2	33,495
6	19,580,177	19,580,669	492	9				5S_rRNA	33,576
6	19,959,823	19,960,384	561	11				ID4	10,930
6	20,399,875	20,400,204	329	10				AL158198.14	9,565
6	21,226,380	21,226,746	366	12	CDKAL1,			CXorf29	35,120
6	21,372,824	21,373,225	401	9				CDKAL1	32,210
6	21,509,251	21,509,730	479	9		No non-overlappi	ng genes wit	hin 50,000bp	
6	21,644,566	21,644,884	318	9		No non-overlappi	ng genes wit	hin 50,000bp	
6	21,695,400	21,696,814	1,414	9		SOX4	5,137		
6	21,701,600	21,702,289	689	12	SOX4,	RP3-322L4.2	8,049		
6	21,772,362	21,773,034	672	9		No non-overlappi	ng genes wit	hin 50,000bp	
6	22,061,982	22,062,854	872	13		No non-overlappi	ng genes wit	hin 50,000bp	
6	23,014,331	23,014,670	339	10				AL590231.8	41,503
6	23,631,156	23,631,503	347	9		No non-overlappi	ng genes wit	hin 50,000bp	
6	24,465,855	24,466,675	820	9	DCDC2,	U6	7,183		
					KAAG1,				
6	24,774,838	24,775,649	811	12	TTRAP, THEM2,	KIAA0319	20,476	C6orf62	37,497
6	24,803,697	24,804,126	429	9	THEM2,			C6orf62	9,020
6	24,828,358	24,829,279	921	9		C6orf62	250		
6	24,883,168	24,884,203	1,035	12	GMNN,	RP3-369A17.2	23,337	FAM65B	28,289
6	25,018,370	25,018,758	388	10	FAM65B,	RP1-245M18.2	37,329		
6	25,432,819	25,433,286	467	9	LRRC16A,	Y_RNA	37,079		
6	25,557,983	25,558,296	313	10	LRRC16A,			AL160037.17	14,420
6	25,598,223	25,598,741	518	9	LRRC16A,	No non-overlappi	ng genes wit	hin 50,000bp	
6	25,684,600	25,684,989	389	9	LRRC16A,	No non-overlappi	ng genes wit	hin 50,000bp	
6	25,751,509	25,752,011	502	9		SCGN	8,397		
6	26,011,999	26,012,397	398	10				SLC17A2	8,573
6	26,070,816	26,071,491	675	12	TRIM38,	SLC17A2	31,998		
6	26,128,740	26,129,142	402	13	HIST1H3A,	HIST1H4A	743	HIST1H1PS2	3,932
6	26,134,910	26,135,741	831	9	HIST1H4A,	HIST1H1A	8,971	HIST1H3B	4,116
-					HIST1H4B,				
6	26,139,883	26,140,345	462	15	HIST1H4A,	HIST1H4B	4,424	HIST1H2AB	1,038
<u> </u>	00 4 44 700	00 4 40 004	400	11	HIST TH3B,				0.000
6	26,141,799	26,142,201	402	11	HIST1H4A,	HISTTHZAB	24	HIST1H2BB	9,283
ю	20,162,956	20,105,096	2,140	9				HISTING	7,955
6	26 174 208	26 174 482	274	10	HISTIHIA	HIST1H1C	0.573		
6	26,174,200	26,174,402	810	10			3,575	ЫСТ1Н1Т	2 874
0	20,211,955	20,212,752	013	10	HIST1H4C.				2,074
6	26.232.168	26.232.645	477	10	HIST1H4A.	HIST1H2BC	35		
-	,,	,,			HIST1H2AC,				
6	26,265,299	26,265,971	672	10	HIST1H4A,	HIST1H2BD	357		
					HIST1H2AC,				
					HIST1H1E,				
6	26,296,800	26,297,506	706	12	HIST1H4A,	HIST1H1PS1	6,267	HIST1H2AC	4,366
-					HIST1H4D,				
6	26,312,245	26,313,500	1,255	10	HIST1H4A,	HIST1H3D	4,745	RPS10P1	1,385
e	26 202 244	26 202 002	640	4 -			10 407		11 640
0	20,393,244	20,393,893	400	15	11131 1∏4∏,		12,497		11,043
0 6	20,394,418	20,394,914	490	13			10 700		16 000
0	20,413,540	20,413,853	313	12			19,799		10,230
0 F	20,419,104	20,419,047	203	14			20,443		10,530
6	20,420,710	20,420,941	231	10					9,142 9 554
6	20,421,020	20,421,529	433	22			36 453		30 551
0 e	20,430,194	20,430,027	433	20	HJEJAFI,		30,403	ALUZ 1911.4-1	30,331
0	20,430,007	20,431,140	4/3	10		HISESAP I	108 E 400		
6	20,430,097	20,430,032	200	1/			5,190		
6	20,430,200	20,430,000	283	14			5,707		
0	20,430,348	20,430,710	302	12	BTN342	AL 021017 4 1	12 200		
0	20,413,528	20,473,936	408	9	ΔΙ 021917 4-2	ALUZ 1917.4-1	12,280		
6	26 491 085	26 491 574	480	12	RTN2A2			BTN3A2	4 558
6	26 641 025	26 641 405	380	16	5 11127C,	HMGN4	5 146		-,550
6	26 645 434	26 646 652	1 218	22	HMGN4	U6	17 760	AI 121936 17-1	14 033
6	26 662 173	26 662 673	500	12		AI 121936 17-1	1 417	HMGN4	7 0.34
6	26 664 704	26 665 024	320	11		AL121936 17-2	2 136	HMGN4	9.565
~	,	,,	225				_,		2,000

6 26,879,853 26,869,325 472 13 AL12193.17.1 19,077 AL12193.17.2 12,822 6 26,865,162 26,885,069 447 18 ABT1 19,560 AL12193.17.2 17,931 6 28,703,947 26,703,947 26,703,941 444 11 ABT1 768 6 28,703,947 26,703,941 444 11 ABT1 768 7 6 28,703,947 26,703,941 444 11 ABT1 768 6 27,707,408 27,107,737 329 18 11 AL51142AL NIRT142BJ NIRT142BJ AL51142AL 44,711 6 27,202,62 27,203,421 1,327 9 HIST1142AL HIST1142BJ 465 HIST144I 5,108 7 27,220,428 27,209,72 648 9 HIST1142AL HIST1142BJ 464 HIST1442BL 40,055 8 7,223,122 10,15 11,327 11,327 11,31742BJ 40,357 6 27,223,162 10,33 <t< th=""><th>6</th><th>26,676,859</th><th>26,677,254</th><th>395</th><th>23</th><th></th><th></th><th></th><th>AL121936.17-2</th><th>9,628</th></t<>	6	26,676,859	26,677,254	395	23				AL121936.17-2	9,628
6 26 26 26 26 26 26 26 26 26 26 26 26 26 27 27 17 27 17 27 17 28 27 27 17 27 17 17 28 27 </td <td>6</td> <td>26,679,853</td> <td>26,680,325</td> <td>472</td> <td>13</td> <td></td> <td>AL121936.17-1</td> <td>19,097</td> <td>AL121936.17-2</td> <td>12,622</td>	6	26,679,853	26,680,325	472	13		AL121936.17-1	19,097	AL121936.17-2	12,622
6 6 6868:162 26.868:069 447 18 ABT1 19.550 AL12'936.17.2 17.831 6 28.703,947 28.704,947 28.7	6	26,683,606	26,684,331	725	12		ABT1	20,828	AL121936.17-2	16,375
6 6 722.39 26.703.662 723 14 ABT1 1.497 6 26.703.597 26.705.541 944 110 ABT1 AL12196.17.1 43.841 VN1R6.5P 33.220 6 27.867.505 27.867.697 759 11 AL51044.11.3 5.240 6 27.167.607 72.967.502 250 9 HIST1H2AL HIST1H2AG 5.508 6 27.202.712 27.203.341 1.327 9 HIST1H2AG HIST1H2AG 5.508 6 27.208.014 27.209.372 544 9 HIST1H2AG HIST1H2AG 4.6080 6 27.221.527 27.221.395 455 9 HIST1H2AG HIST1H2AH B4ST1H44 5.139 7 27.225.343 384 11 HIST1H2AH HIST1H2AH B4ST1H44 5.139 6 27.223.159 27.224.355 415 10 RP11.209A2.1 22.717 HIST1H2AH 9.673 6 27.2305.17 27.244.28	6	26,685,162	26,685,609	447	18		ABT1	19,550	AL121936.17-2	17,931
6 6 703.847 26.704.381 444 11 ABT1 768 6 26.705.927 26.705.841 944 10 ABT1 43.841 VNIRE5P 33.220 6 26.705.827 26.705.841 11.98 9 VNIRT2P 12.845 6 27.707.737 229 18 VNIRT2P 75.900 6 27.207.72 27.209.201 12.264 VNIRT2P 75.900 6 27.209.428 27.209.341 1.327 9 HIST1H2AL HIST1H2AL HIST1H2AL HIST1H2AL 11511444 5.714 HIST1H2AK 4.900 6 27.223.542 27.223.543 344 11 HIST1H2AL HIST1H2AL HIST1H2AL HIST1H2AL 4.981 11.981 6.166 11.981 11.981 4.1671 4.723 11.981 6.7223.573 11.981 11.981 11.981 11.981 11.981 11.981 11.981 11.981 11.981 11.981 11.981 11.981 11.981	6	26,702,939	26,703,662	723	14		ABT1	1,497		
6 6 78,704.597 28,705.547 944 10 ABT1, AL 1298.17.1 41.3441 WHR6.597 33.220 6 28,965.050 27,006.548 1.198 9 WHR11P 7.503 6 27,167.6500 27,007.737 229 18 WHR11P 7.503 6 27,202,712 27,203.292 520 9 HIST1H2BL HIST1H2AG 5.508 - 6 27,208,014 27,203.292 544 9 HIST1H2AG 5.508 - 4,711 45,111 4,711 513 6 27,220,812 27,223,92 544 9 HIST1H2AG HIST1H2AH 514 513 6 27,222,502 27,223,33 344 11 HIST1H2AH 514 114 514 10 RP11.200A2.1 22,71 HIST1H2AH 40.375 6 27,228,327 27,224,285 415 10 RP11.200A2.1 22,71 HIST1H2AH 40.375 6 27,2306,717 27,242,425	6	26,703,947	26,704,391	444	11		ABT1	768		
6 6 72,08,05,02 22,08,06,01 77,09 11 AL50104.17.13 52,40 6 72,708,708 27,107,737 329 18 VNIR17P 72,00 6 72,702,708 27,107,737 329 18 VNIR17P 75,03 6 72,702,712 72,03,292 520 9 HIST1H2AL HIST1H2AL HIST1H2AL 41,011 5,714 HIST1H2AK 41,711 6 72,722,722 72,223,64 468 9 HIST1H2AL HIST1H2AL HIST1H2AK 448 HIST1H4H 5,714 HIST1H4H 5,714 HIST1H4H 5,130 6 27,223,159 72,223,64 384 11 HIST1H2AL HIST1H2AL HIST1H2AL 40,375 6 27,223,159 72,223,54 384 11 HIST1H2AL HIST1H2AL 40,375 7 72,64,285 61 11 RP11,200A2.1 1,067 1,207 12,217 HIST1H2AL 40,375 6 27,306,712 <	6	26,704,597	26,705,541	944	10	ABT1,	AL121936.17-1	43,841	VN1R6-5P	33,220
6 6 77.065.360 27.006.548 1.198 9 VINTR1P 12.646 6 27.167.040 27.102.772 27.203.292 520 9 HIST1H2BJ. HIST1H2BJ. HIST1H2BJ. HIST1H2BJ. FINT1H2BJ. FINT1H4I 6.100 6 27.223.62 27.223.015 453 9 HIST1H2BK. HIST1H2BJ. FINT1H4I 6.100 FINT1H4I 6.100 FINT1H4I 6.100 FINT1H4I 6.100 FINT1H4I 6.100 FINT1H4I 6.100 FINT1H2BJ.	6	26,865,922	26,866,691	769	11				AL591044.11-3	5,240
6 27,107,406 27,107,737 329 16 VNR112 VNR111P 7.508 6 27,202,722 250.09 HIST1H2AL, HIST1H2AC, HIST1H2AC, G HIST1H2AL, HIST1H2AC,	6	27,095,350	27,096,548	1,198	9				VN1R12P	12,645
6 27,202,772 27,202,202 500 9 HISTH2AG HISTH2AG 508 6 27,208,014 27,209,341 1.327 9 HISTH2AG, HISTH2AG, HISTH2AG, HISTH2AG, F14 9 HISTH2AG, HISTH2AG, HISTH2AG, HISTH2AB, HISTH2AG, HISTH2AB, HISTH2AB, 408 9 HISTH2AB, 9.821 HISTH2AB,	6	27,167,408	27.167.737	329	18				VN1R11P	7.503
6 27.208.014 27.209.341 1.327 9 HIST1H2AL HIST1H2AD, 57.14 HIST1H2BK 4.711 6 27.209.428 27.209.972 544 9 HIST1H2AD, HIST1H2AD, 908 HIST1H2BK 408 6 27.221.592 27.223.015 453 9 HIST1H2AK, HIST1H2AH, 904 HIST1H2BK 405 6 27.223.519 27.223.519 27.223.519 28.21 HIST1H2AH, HIST1H2AH, HIST1H2AH, 6.165 6 27.223.623 27.823.199 28.21 11.11 HIST1H2AH, HIST1H2AH, 9.821 6 27.283.671 27.243.425 614 11 RP11-209A.21 22.717 HIST1H2AH, 40.375 6 27.280.521 2.836 13 RP11-209A.21 2.846 1.971 RP11-209A.21 2.846 6 27.306.712 2.7306.716 344 13 PRSS16 16.971 <rp11-209a.21< td=""> 2.846 6 27.336.744 27.3206.97 633 9.979 1.4021808.2-3 8.692 1</rp11-209a.21<>	6	27.202.772	27.203.292	520	9	HIST1H2BJ.	HIST1H2AG	5.508		,
Image: Construct of the second seco	6	27.208.014	27.209.341	1.327	9	HIST1H2BJ.	HIST1H4I	5,714	HIST1H2BK	4,711
6 27.209.428 27.209.927 544 9HISTHI2AC, HISTH2AK, HIST	-			.,	-	HIST1H2AG,		-,		-,
6 27.221.527 27.221.996 468 9 HIST1H2RK HIST1H2AH 946 HIST1H4I 6.165 6 27.222.159 27.223.543 384 11 HIST1H2AH, HIST1H2AH, HIST1H2AH, HIST1H2AH 9.821 6 27.223.613 37.233.159 326 14 HIST1H2BK 30.235 HIST1H2AH 9.821 6 27.225.620 27.285.208 614 11 RP11-009A2.1 2.2171 HIST1H2AH 49.821 6 27.285.500 62 72.805.610 415 10 RP11-209A2.1 1.067 C 2.236.616 344 13 PRSS16 16.071 RP11-209A2.1 2.224 18.530 6 27.306.762 27.314.66 840 9 PRSS16 16.071 RP11-209A2.1 12.224 18.530 6 27.335.780 300 10 AL021808.2-2 8.592 - - - - - - - - - - - -	6	27,209,428	27,209,972	544	9	HIST1H2AG,	HIST1H2BJ	908	HIST1H2BK	4,080
6 27,222,562 27,223,015 453 9 HIST1H2BK, HIST1H2AH, HIST1H2AH, HIST1H2AH, HIST1H2AH, HIST1H2AH, HIST1H2AH, IST1H2AH, IST1H2AH, 9,821 6 27,223,159 27,223,159 326 14 HIST1H2BK, 30,235 HIST1H2AH, 9,821 6 27,253,050 326 14 HIST1H2BK, 30,235 HIST1H2AH, 29,821 6 27,263,051 326 14 11 RP11-209A,21 1,067 2,244 6 27,206,072 27,209,203 386 13 RP11-209A,21 1,067 6 27,306,0172 27,306,016 344 13 PRSS16 16,071 <rp11-209a,21< td=""> 12,284 6 27,314,066 300 10 AL021808,2-2 8,929 1 14,021808,2-3 8,780 6 27,314,073 27,315,063 300 10 AL021808,2-3 8,293 1 1 14,021808,2-3 3,667 6 27,376,076 27 9 AL021808,</rp11-209a,21<>	6	27,221,527	27,221,995	468	9	HIST1H2BK,	HIST1H2AH	845	HIST1H4I	5,130
$\begin{tabular}{ c c c c c c c c c c c c c c c c c c c$	6	27,222,562	27,223,015	453	9	HIST1H2BK,			HIST1H4I	6,165
6 27,223,159 27,223,43 384 11 HIST1H2AH, HIST1H2AH HIST1H2AH, HIST1H2AH HIST1H2AH HIST1H2AH 98,21 6 27,233,67 27,263,65 326 14 HIST1H2BH 30,236 HIST1H2AH 99,537 6 27,283,67 27,264,285 614 11 RP11-209A2.1 2,2717 HIST1H2AH 49,375 6 27,289,006 27,200,285 415 10 RP11-209A2.1 1,067 6 27,306,712 27,306,516 344 13 PRS516 16,071 RP11-209A2.1 12,02A.1 13,140 6 27,313,068 381 10 PRS516 9,079 145,500 6 27,350,078 27,331,050 288 10 AL021808.2-3 8,692 - 6 27,350,078 27,316,067 267 9 AL021808.2-3 8,670 - - 6 27,350,071 27,378,076 27,378,079 73,360 27,373,600 27,373,600 27,373,600 27,373,600		, ,				HIST1H2AH,				,
6 27,233,117 27,234,132 1015 14 HITH2RK 30,235 HISTHP2AH 9,821 6 27,285,330 27,285,356 36 14 HISTHP2AH 29,537 6 27,285,500 27,285,935 415 10 RP11-209A2.1 22,717 HISTHP2AH 40,375 6 27,289,500 27,289,506 344 13 PR5516 16,971 RP11-209A2.1 3,140 6 27,305,761 344 13 PR5516 16,971 RP11-209A2.1 12,284 6 27,313,127 27,313,608 381 10 PR5516 12,021 RP11-209A2.1 12,2984 6 27,350,763 27,351,750 28 10 AL021808.2-3 8,780 - 6 27,350,7763 27,351,750 28 11 AL021808.2-3 8,780 - - 2,939 AL021808.2-3 6,401 6 27,350,909 27,350,871 34 11 AL021808.2-3 3,667 - <td>6</td> <td>27,223,159</td> <td>27,223,543</td> <td>384</td> <td>11</td> <td>HIST1H2AH,</td> <td>HIST1H2BK</td> <td>561</td> <td>HIST1H4I</td> <td>6,762</td>	6	27,223,159	27,223,543	384	11	HIST1H2AH,	HIST1H2BK	561	HIST1H4I	6,762
6 27.252.833 27.253.156 326 14 HISTH2RK 50.235 HISTH2AH 29.577 6 27.285.520 27.285.935 415 10 RP11-209A2.1 22.717 HISTH2AH 40.375 6 27.289.906 27.290.242 386 13 RP11-209A2.1 3.140 6 27.290.762 27.291.097 315 10 RP11-209A2.1 3.140 6 27.306.712 27.305.516 344 13 PRSS16 16.971 RP11-209A2.1 18.500 6 27.315.062 27.311.466 40 9 PRSS16 19.207 18.500 6 27.351.622 27.315.063 300 10 AL021808.2-3 8.780 1.07 6 27.3551.762 27.616 27.79 9 AL021808.2-3 3.667 .0121808.2-3 3.667 6 27.350.476 27.379.459 481 13 AL021808.2-4 2.939 AL021808.2-3 6.401 6 27.370.826 27.371.459<	6	27,233,117	27,234,132	1,015	14				HIST1H2AH	9,821
6 27,265,671 27,265,20 27,285,21 22,294 27,285,20 27,285,21 22,294 22,294 22,284 22,294 22,294 22,294 22,294 22,294 22,294 22,294 22,294 22,294 22,294 22,294 22,294 22,294 22	6	27,252,833	27,253,159	326	14		HIST1H2BK	30,235	HIST1H2AH	29,537
6 27,285,520 27,285,935 415 10 RP11-209A2.1 1.067 6 27,289,0782 27,280,0782 27,280,0782 27,280,0782 27,280,0782 27,280,0782 27,280,0782 27,280,0782 27,280,0781 2,264 6 27,300,782 27,280,0781 315 10 RP11-209A2.1 18,503 6 27,306,26 27,311,466 840 9 PRSS16 16,971 RP11-209A2.1 12,2984 6 27,351,063 301 10 AL021808.2-2 8,592 - 6 27,351,076 27 9 AL021808.2-3 8,780 - 6 27,351,076 27 9 AL021808.2-3 8,693 - - 6 27,351,076 27 9 AL021808.2-4 2,934 AL021808.2-3 9,562 6 27,370,826 27,371,439 633 17 AL021808.2-4 1,030 6 27,370,826 27,371,439 633 17 AL021808.2-4 2,044 </td <td>6</td> <td>27,263,671</td> <td>27,264,285</td> <td>614</td> <td>11</td> <td></td> <td>RP11-209A2.1</td> <td>22,717</td> <td>HIST1H2AH</td> <td>40,375</td>	6	27,263,671	27,264,285	614	11		RP11-209A2.1	22,717	HIST1H2AH	40,375
	6	27,285,520	27,285,935	415	10		RP11-209A2.1	1,067		
6 27.290.782 27.291.097 315 10 RP11-209A2.1 3.140 6 27.306.172 27.306.516 344 13 PRSS16 16.971 RP11-209A2.1 18.50 6 27.310.622 27.311.466 840 9 PRSS16 9.979 22.984 6 27.311.466 840 9 PRSS16 9.979 22.984 6 27.351.742 27.351.063 30 10 AL021808.2-2 8.592 - 6 27.350.763 27.351.560 288 10 AL021808.2-3 8.760 - 6 27.350.90 27.356.716 267 9 AL021808.2-4 2.939 AL021808.2-3 6.401 6 27.360.27 27.366.71 27.4 9 AL021808.2-4 2.084 6 27.370.826 27.41.459 33 17 AL021808.2-4 2.084 6 27.436.320 27.37.3946 346 14 AL021808.2-4 2.084 6 27.	6	27,289,906	27,290,292	386	13				RP11-209A2.1	2,264
6 27.306.172 27.306.516 344 13 PRSS16 16.071 RP11-209A2.1 18.530 6 27.310.626 27.311.466 840 9 PRSS16 12.021 RP11-209A2.1 22.984 6 27.327.434 27.328.097 663 9 PRSS16 9.979 6 27.357.63 27.351.063 300 10 AL021808.2-3 8.293 6 27.357.62 27.351.550 288 10 AL021808.2-3 8.293 6 27.365.909 27.367.711 344 11 AL021808.2-4 AL021808.2-3 9.562 6 27.378.677 27.371.459 633 17 AL021808.2-4 2.039 AL021808.2-4 1.103 6 27.378.607 27.372.531 724 9 AL021808.2-4 3.867 6 27.464.632 27.464.991 628 14 AL021808.2-4 3.877 6 27.464.632 27.464.991 628 14 ZNF304 17.000 <	6	27,290,782	27,291,097	315	10				RP11-209A2.1	3,140
6 27.310.628 27.311.466 840 9 PRSS16 12.021 RP11-209A.1 22.984 6 27.327.343 27.335.08 381 10 PRSS16 4.021808.2-2 8.592 6 27.357.434 27.351.063 300 10 AL021808.2-3 8.780 6 27.351.262 27.351.063 27.351.676 267 9 AL021808.2-3 3.667 6 27.369.476 27.369.959 481 13 AL021808.2-4 AL021808.2-3 9.662 6 27.370.826 27.371.459 633 17 AL021808.2-4 1.103 6 27.370.826 27.371.459 633 17 AL021808.2-4 3.867 6 27.370.826 27.471.611 27.410.824 3.867 48.41 AL021808.2-4 3.867 6 27.470.611 27.410.71 460 14 AL021808.2 3.867 6 27.464.361	6	27,306,172	27,306,516	344	13		PRSS16	16,971	RP11-209A2.1	18,530
$ \begin{array}{c c c c c c c c c c c c c c c c c c c $	6	27,310,626	27,311,466	840	9		PRSS16	12,021	RP11-209A2.1	22,984
$ \begin{array}{c c c c c c c c c c c c c c c c c c c $	6	27.313.127	27.313.508	381	10		PRSS16	9,979		,
$ \begin{array}{c c c c c c c c c c c c c c c c c c c $	6	27.327.434	27.328.097	663	9	PRSS16.	AL021808.2-2	8,592		
$ \begin{array}{c c c c c c c c c c c c c c c c c c c $	6	27 350 763	27 351 063	300	10		AL 021808 2-3	8 780		
$ \begin{array}{c c c c c c c c c c c c c c c c c c c $	6	27 351 262	27 351 550	288	10		AL 021808 2-3	8 293		
6 27,366,317 27,366,711 394 11 AL021808.2-4 2,339 AL021808.2-3 6,401 6 27,370,826 27,371,459 633 17 AL021808.2-4 AL021808.2-4 1,003 6 27,371,807 27,371,459 633 17 AL021808.2-4 2,084 6 27,371,807 27,373,946 346 14 AL021808.2-4 2,084 6 27,408,526 27,409,029 503 16 AL021808.2-1 6,901 6 27,401,611 27,411,071 460 14 AL021808.2-1 6,901 6 27,404,363 27,464,991 628 14 ZNF391 ZNF204 17,080 40,021808.2-1 6,901 6 27,548,527 27,554,497 382 12 ZNF184 5,257 5 5 6 27,579,207 27,579,212 1,005 D XXbac- 19,622 5 5 6 27,579,207 27,579,212 1,005 D BPG3418.2 D </td <td>6</td> <td>27 355 909</td> <td>27 356 176</td> <td>267</td> <td></td> <td></td> <td>AL 021808 2-3</td> <td>3 667</td> <td></td> <td></td>	6	27 355 909	27 356 176	267			AL 021808 2-3	3 667		
$ \begin{array}{c c c c c c c c c c c c c c c c c c c $	6	27 366 317	27,366,711	394	11		AL 021808 2-4	2 939	AL 021808 2-3	6 401
$ \begin{array}{ c c c c c c c c c c c c c c c c c c c$	6	27 369 478	27 369 959	481	13	AL 021808 2-4		_,	AL 021808 2-3	9.562
$ \begin{array}{ c c c c c c c c c c c c c c c c c c c$	6	27,370,826	27 371 459	633	17	,			AL 021808 2-4	1 103
$ \begin{array}{ c c c c c c c c c c c c c c c c c c c$	6	27 371 807	27 372 531	724	9				AL 021808 2-4	2 084
$ \begin{array}{ c c c c c c c c c c c c c c c c c c c$	6	27 373 600	27 373 946	346	14				AL 021808 2-4	3 877
$ \begin{array}{c c c c c c c c c c c c c c c c c c c $	6	27 408 526	27 409 029	503	16				AL 021808 2-1	6 916
$ \begin{array}{c c c c c c c c c c c c c c c c c c c $	6	27 410 611	27 411 071	460	10				AL 021808 2-1	9 001
6 27,548,527 27,549,239 712 16 ZNF184, ZNF184, XXbac- BPG3418.2 49,555 6 27,554,115 27,554,497 382 12 ZNF184 5,257 6 27,554,115 27,554,497 382 12 ZNF184 5,257 6 27,554,528 27,575,646 1,118 16 ZNF184 22,530 6 27,577,8207 27,579,212 1,005 10 XXbac- BPG3418.2 19,173	6	27 464 363	27 464 991	628	14	ZNE391	ZNE204	17 080	7 (EO2 1000).E 1	0,001
6 27,63,632 27,63,625 112 13 13 13 13 13 13 14<	6	27 548 527	27 549 239	712	16	ZNF184	XXbac-	49 595		
$ \begin{array}{c c c c c c c c c c c c c c c c c c c $	Ũ			• •=		,	BPG3418.2	,		
$ \begin{array}{c c c c c c c c c c c c c c c c c c c $	6	27,554,115	27,554,497	382	12		ZNF184	5,257		
$ \begin{array}{c c c c c c c c c c c c c c c c c c c $	6	27,554,528	27,555,646	1,118	16		ZNF184	5,670		
$ \begin{array}{c c c c c c c c c c c c c c c c c c c $	6	27,571.388	27,571.917	529	22		ZNF184	22.530		
$ \begin{array}{ c c c c c c c c c c c c c c c c c c c$	6	27,578.207	27,579,212	1,005	10		XXbac-	19.622		
6 27,579,261 27,579,661 400 14 XXbac- BPG34l8.2 19,173 6 27,581,033 27,581,792 759 14 XXbac- BPG34l8.2 17,042 6 27,594,665 27,595,008 343 9 XXbac- BPG34l8.2 3,826 6 27,595,064 27,595,553 489 10 XXbac- BPG34l8.2 3,281 6 27,621,061 27,621,702 641 15 XXbac- BPG34l8.2 3,281 6 27,623,270 27,623,707 437 13 U6 48,463 XXbac- BPG34l8.3 6 27,628,837 27,629,498 661 14 XXbac- BPG34l8.3 7,083 6 27,667,359 27,667,821 462 12 U6 4,349 6 27,667,359 27,667,821 462 12 U6 3,396 6 27,677,707 27,678,788 1,081 11 U6 5,432 6 27,681,303 27,681,620 317 19 U6 5,432 6 27,684,962 27,685,378 416 10<		, ., .,	, -, -	,			BPG3418.2	-,		
6 27,581,033 27,581,792 759 14 XXbac- BPG34l8.2 17,042 BPG34l8.2 6 27,594,665 27,595,008 343 9 XXbac- BPG34l8.2 3,826 6 27,595,064 27,595,553 489 10 XXbac- BPG34l8.2 3,281 6 27,621,061 27,621,702 641 15 XXbac- BPG34l8.2 3,281 6 27,623,270 27,623,707 437 13 U6 48,463 XXbac- BPG34l8.3 12,874 BPG34l8.3 6 27,628,837 27,629,498 661 14 XXbac- BPG34l8.3 7,083 BPG34l8.3 6 27,667,359 27,667,821 462 12 U6 4,349 6 27,668,351 27,678,788 1,081 11 U6 3,396 6 27,681,303 27,681,620 317 19 U6 3,396 6 27,684,962 27,685,378 416 10 XXbac- BPG34l8.3 47,460 U6 9,028 <td>6</td> <td>27,579,261</td> <td>27,579,661</td> <td>400</td> <td>14</td> <td></td> <td>XXbac- BPG34I8.2</td> <td>19,173</td> <td></td> <td></td>	6	27,579,261	27,579,661	400	14		XXbac- BPG34I8.2	19,173		
Image: Constraint of the second sec	6	27,581,033	27,581,792	759	14		XXbac-	17,042		
6 27,594,665 27,595,008 343 9 XXbac- BPG34l8.2 3,826		-	-				BPG34I8.2			
Image: Constraint of the second sec	6	27,594,665	27,595,008	343	9		XXbac-	3,826		
6 27,595,064 27,595,553 489 10 XXbac- BPG34l8.2 3,281 11 6 27,621,061 27,621,702 641 15 XXbac- BPG34l8.2 14,879 6 27,623,270 27,623,707 437 13 U6 48,463 XXbac- BPG34l8.3 12,874 6 27,628,837 27,629,498 661 14 XXbac- BPG34l8.3 7,083 6 27,667,359 27,667,821 462 12 U6 4,349 6 27,667,351 27,668,774 423 19 U6 3,396 6 27,677,707 27,678,788 1,081 11 U6 3,396 6 27,681,303 27,681,620 317 19 U6 3,396 6 27,684,962 27,685,378 416 10 XXbac- BPG34l8.3 47,460 U6 9,028							BPG3418.2			
6 27,621,061 27,621,702 641 15 XXbac- BPG3418.2 XXbac- BPG3418.3 14,879 BPG3418.3 6 27,623,270 27,623,707 437 13 U6 48,463 XXbac- BPG3418.3 12,874 BPG3418.3 6 27,628,837 27,629,498 661 14 XXbac- BPG3418.3 7,083 BPG3418.3 6 27,667,359 27,667,821 462 12 U6 4,349 6 27,667,351 27,668,774 423 19 U6 3,396 6 27,677,707 27,678,788 1,081 11 U6 47,460 9,028 6 27,684,962 27,685,378 416 10 XXbac- BPG3418.3 47,460 U6 12,687	6	27,595,064	27,595,553	489	10		XXbac-	3,281		
6 27,621,061 27,621,02 641 15 XXbac- BPG3418.3 14,879 BPG3418.3 6 27,623,270 27,623,707 437 13 U6 48,463 XXbac- BPG3418.3 12,874 BPG3418.3 6 27,628,837 27,629,498 661 14 XXbac- BPG3418.3 7,083 BPG3418.3 6 27,667,359 27,667,821 462 12 U6 4,349 6 27,668,351 27,668,774 423 19 U6 3,396 6 27,677,707 27,678,788 1,081 11 U6 5,432 6 27,681,303 27,681,620 317 19 U6 9,028 6 27,684,962 27,685,378 416 10 XXbac- BPG3418.3 47,460 U6 12,687	-						BPG3418.2		200	
6 27,623,270 27,623,707 437 13 U6 48,463 XXbac- BPG34I8.3 12,874 6 27,628,837 27,629,498 661 14 XXbac- BPG34I8.3 7,083 6 27,667,359 27,667,821 462 12 U6 4,349 6 27,668,351 27,668,774 423 19 U6 3,396 6 27,677,707 27,678,788 1,081 11 U6 3,396 6 27,681,303 27,681,620 317 19 U6 9,028 6 27,684,962 27,685,378 416 10 XXbac- BPG34I8.3 47,460 U6 12,687	6	27,621,061	27,621,702	641	15				XXbac-	14,879
6 27,623,270 27,623,707 437 13 06 48,463 XA02C- BPG3418.3 12,874 6 27,628,837 27,629,498 661 14 XXbac- BPG3418.3 7,083 6 27,667,359 27,667,821 462 12 U6 4,349 6 27,668,351 27,668,774 423 19 U6 3,396 6 27,677,707 27,678,788 1,081 11 U6 5,432 6 27,681,303 27,681,620 317 19 U6 9,028 6 27,684,962 27,685,378 416 10 XXbac- BPG3418.3 47,460 U6 12,687	<u> </u>	07 000 070	07 000 707	407	10		110	40.400	BPG3418.3	10.074
6 27,628,837 27,629,498 661 14 Life XXbac- BPG3418.3 XXbac- BPG3418.3 7,083 BPG3418.3 6 27,667,359 27,667,821 462 12 U6 4,349 6 27,668,351 27,668,774 423 19 U6 3,396 6 27,677,707 27,678,788 1,081 11 U6 5,432 6 27,681,303 27,681,620 317 19 U6 9,028 6 27,684,962 27,685,378 416 10 XXbac- BPG3418.3 47,460 U6 12,687	ь	21,623,270	21,623,707	437	13		00	48,463	AADAC-	12,874
6 27,667,359 27,667,821 462 12 U6 4,349 6 27,668,351 27,668,774 423 19 U6 3,396 6 27,677,707 27,678,788 1,081 11 U6 5,432 6 27,681,303 27,681,620 317 19 U6 9,028 6 27,684,962 27,685,378 416 10 XXbac- BPG34l8.3 47,460 U6 12,687	6	27 628 837	27 620 /08	661	1/				YYbac-	7 083
6 27,667,359 27,667,821 462 12 U6 4,349 6 27,668,351 27,668,774 423 19 U6 3,396 6 27,677,707 27,678,788 1,081 11 U6 5,432 6 27,681,303 27,681,620 317 19 U6 9,028 6 27,684,962 27,685,378 416 10 XXbac- BPG34l8.3 47,460 U6 12,687	U	21,020,007	21,023,430	001	14				BPG34I8.3	1,005
6 27,668,351 27,668,774 423 19 U6 3,396 6 27,677,707 27,678,788 1,081 11 U6 5,432 6 27,681,303 27,681,620 317 19 U6 9,028 6 27,684,962 27,685,378 416 10 XXbac- BPG34l8.3 47,460 U6 12,687	6	27 667 359	27 667 821	462	12		116	4 340		
6 27,677,707 27,678,788 1,081 11 U6 5,432 6 27,681,303 27,681,620 317 19 U6 9,028 6 27,684,962 27,685,378 416 10 XXbac- BPG3418.3 47,460 U6 12,687	6	27 668 351	27 668 774	423	10		116	3 306		
6 27,681,303 27,681,620 317 19 U6 9,028 6 27,684,962 27,685,378 416 10 XXbac- BPG34l8.3 47,460 U6 12,687	6	27 677 707	27 678 788	1 081	11			0,000	U6	5 432
6 27,684,962 27,685,378 416 10 XXbac- BPG34l8.3 47,460 U6 12,687	6	27 681 303	27 681 620	317	19				U6	9 028
BPG34l8.3	6	27 684 962	27 685 378	416	10		XXbac-	47 460	U6	12 687
	~		,000,010		.0		BPG3418.3	,		,

6	27,692,205	27,692,467	262	9				U6	19,930
6	27,692,711	27,693,285	574	9				U6	20,436
6	27,693,409	27,694,391	982	11				U6	21,134
6	27,706,998	27.707.609	611	14				RP1-15D7.1	20.749
6	27,708,847	27,709,354	507	10				RP1-15D7.1	19.004
6	27,726,402	27.726.881	479	18				RP1-15D7.1	1.477
6	27,744,186	27.744.658	472	10		RP1-15D7.1	15.603	-	,
6	27,746,107	27,746,467	360	9		RP1-15D7.1	17.524		
6	27,747,897	27.748.391	494	18		RP1-15D7.1	19,314		
6	27 759 850	27 760 651	801	10		RP1-15D7 1	31 267		
6	27 762 944	27 763 364	420	.0		RP1-15D7 1	34 361	RP1-97D16 1	48 969
6	27,763,436	27,764,369	933	15		RP1-15D7.1	34,853	RP1-97D16.1	47,964
6	27 796 492	27 797 284	792	9			,	RP1-97D16 1	15 049
6	27 828 909	27 829 345	436	14		RP1-97D16 1	14 657	RP1-97D16 4	27 033
6	27 829 776	27 830 387	611	9		RP1-97D16 1	15 524	RP1-97D16 4	25,991
6	27 847 912	27 848 768	856	9				RP1-97D16 4	7 610
6	27 853 473	27 853 832	359	9				RP1-97D16.4	2 546
6	27,866,907	27 867 340	433	20		RP1-97D164	10 038	HIST1H2BI	15 861
6	27,867,912	27,868,341	429	16		RP1-97D16.4	11 043	HIST1H2BL	14 860
6	27 871 416	27,800,041	476	g		HIST1H4PS1	10 923	HIST1H2BL	11 309
6	27,885,701	27,886,412	711	13	НІСТ1Н3Н	HIST1H2BI	2 013	HIST1H2AL	1 203
6	27,003,701	27,000,412	824	10	HIST1H3H	HIST1H4K	6 652		1,200
0	27,913,930	27,314,700	024	5	HIST1H2AK		0,052		
					HIST1H2BN,				
6	27.940.655	27.941.560	905	14	HIST1H3H.	HIST1H2BPS2	497	HIST1H1B	1.046
-	,- ,	,. ,			HIST1H2AL,		_	-	,
6	27,941,826	27,942,157	331	9	HIST1H3H,	HIST1H2BPS2	1,668	HIST1H2AL	241
6	27,970,002	27,971,612	1,610	9		HIST1H2AM	1,096	HIST1H3H	358
6	27,978,088	27,978,812	724	17		HIST1H2AM	9,182	OR2B2	8,191
6	28,156,502	28,157,078	576	20	ZNF165,			OR1F12P	6,512
6	28,200,220	28,200,762	542	9	ZNF435,			RP1-265C24.5	7,912
6	28,212,408	28,213,075	667	13		ZNF192	4,620	ZNF435	6,575
6	28,217,275	28,218,033	758	9	ZNF192,	AL358933.15	1,218		-
6	28,237,127	28,237,768	641	9			-	ZNF192	3,912
6	28,288,689	28,289,084	395	14				AL022393.1	4,793
6	28,474,860	28,475,923	1,063	9	ZSCAN12,	ZNF323	44,909	ZKSCAN3	30,333
6	28,550,131	28,550,561	430	10		Z98745.1-2	5,921		
6	28,550,664	28,550,941	277	9		Z98745.1-2	5,541		
6	28,618,207	28,619,049	842	14		GPX6	6,533	GPX5	8,284
6	28,662,495	28,663,568	1,073	11	SCAND3,			AL121932.19	46,270
6	28,664,957	28,665,766	809	15		SCAND3	1,866		
6	28,672,956	28,673,479	523	12		SCAND3	9,865		
6	28,682,255	28,683,113	858	14		SCAND3	19,164	AL121932.19	26,725
6	28,710,393	28,710,707	314	10		AL121932.19	484		
6	28,710,807	28,711,393	586	10		AL121932.19	898		
6	28,719,117	28,719,492	375	16		AL121932.19	9,208		
6	28,723,771	28,724,749	978	11		AL121932.19	13,862	AL390196.17-1	44,217
6	28,733,632	28,734,229	597	13		AL121932.19	23,723	AL390196.17-1	34,737
6	28,749,420	28,749,936	516	19		AL121932.19	39,511	AL390196.17-1	19,030
6	28,786,155	28,786,829	674	14		AL390196.17-1	17,116	AL390196.17-2	16,005
6	28,801,553	28,802,053	500	9		RPSAP2	5,720	AL390196.17-2	781
6	28,804,851	28,805,247	396	12		AL390196.17-2	1,945		
6	28,818,603	28,818,882	279	11				RPSAP2	9,943
6	28,823,281	28,823,871	590	14		AL390196.17-2	20,375	RPSAP2	14,621
6	28,833,711	28,834,329	618	12		AL662890.3-2	17,343	RPSAP2	25,051
6	28,842,065	28,842,522	457	9		AL662890.3-2	9,150		· · ·
6	28,865,054	28,865,943	889	9		NOL5BP	5,294		
6	28,871,412	28,871,997	585	15		NOL5BP	11,652	AL662890.3-2	19,633
6	28,878,434	28,879,483	1,049	9		NOL5BP	18,674	AL662890.3-2	26,655
6	28,883,456	28,883,729	273	11		NOL5BP	23,696	AL662890.3-2	31,677
6	28,887,600	28,888,247	647	9		NOL5BP	27,840	AL662890.3-2	35,821
6	28,892,742	28,893,179	437	21		NOL5BP	32,982	AL662890.3-2	40,963
6	28,899,021	28,899,315	294	10		AL662890.3-1	37,857	AL662890.3-2	47,242
6	28,913,679	28,914,383	704	13		AL662890.3-1	22,789		
-	28 914 494	28,914,765	271	11		AI 662890 3-1	22 407	ZNF463P	49 823

6	28,939,239	28,940,328	1,089	14				AL662890.3-1	1,448
6	28,941,965	28,942,509	544	10				AL662890.3-1	4,174
6	28,956,665	28,957,386	721	15				ZNF463P	7,202
6	28.971.816	28.972.264	448	19		ZNF463P	6.154	TRIM27	6.494
6	28,972,391	28,972,808	417	13		ZNF463P	6.729	TRIM27	5,950
6	28,998,451	28,999,317	866	10	TRIM27.			U6	6.951
6	29 015 909	29 017 711	1 802	12	, ,	C6orf100	1 949		-,
6	29 019 283	29 020 522	1 239	12	C6orf100	TRIM27	19 536	KRT18P1	24 364
6	20,010,200	20,020,022	420	11	00011100,	11(11)/27	10,000	C6orf100	6 322
6	29,020,014	29,027,034	207	15				C6orf100	0,322
6	29,020,790	29,029,177	267	10				COULTOU CDD out orch	0,490
0	29,057,347	29,057,014	207	10				SRP_euk_arch	3,021
0	29,057,678	29,058,097	419	18				SRP_euk_arch	4,152
6	29,058,367	29,058,707	340	10				SRP_euk_arch	4,841
6	29,061,238	29,061,507	269	15				SRP_euk_arch	7,712
6	29,702,298	29,702,644	346	11	GABBR1,			SUMO2P	9,172
6	29,725,680	29,726,226	546	12		MOG	6,562		
6	29,813,750	29,814,284	534	10	AL645939.6-3,	HCG9P5	9,761	HLA-F	9,888
6	29,828,607	29,829,405	798	9		IFITM4P	1,703	Y_RNA	2,379
6	30,041,717	30,042,049	332	10		HCG9	8,799	MICD	4,508
6	30,061,401	30,061,782	381	9		BAT1P2	7,183	HCG9	7,226
6	30,136,386	30,137,315	929	10	C6orf12,	PPP1R11	5,150	RNF39	8,708
					C6orf12,				
~	20 4 40 4 4 4	20 4 40 000	1 400	~		CCortto	E 044		4 470
6	30,142,141	30,143,603	1,462	9	FFFIRTT,	Coon12	5,241		1,476
6	30,177,636	30,178,109	473	12				TRIM31	546
6	30,206,665	30,207,150	485	11		TRIM40	4,714		
6	30,265,872	30,266,369	497	9	TRIM26,	PAIP1P1	1,502		
6	30,339,529	30,339,801	272	10	HLA-L,			AL662795.5	20,303
6	30,401,353	30,401,773	420	11		TRIM39	827		
6	30,402,067	30,402,568	501	10		TRIM39	32		
6	30,402,832	30,403,344	512	9	TRIM39,	RPP21	17,579	HCG19P	31,690
6	30,420,859	30,421,193	334	10	RPP21,	HLA-N	5,979	TRIM39	1,374
6	30.433.277	30.433.832	555	9				HCG19P	1.202
6	30 559 400	30 560 071	671	9		AI 662873 3	1 603		, -
6	30,630,868	30,632,066	1 198	10	GNI 1	PRR3	669		
6	30 672 874	30 673 450	576	10	01121,	1 1 1 10	000	PPP1R10	2 712
6	30,688,401	30,688,726	325	10		MDDS18D	4 850	AL 662800 4	2,712
6	20,602,401	20,602,720	442	10		MIRE 310D	4,059	AL002000.4	5,259
0	30,092,310	30,092,756	442	9		AL002000.4	200		
0	30,692,767	30,693,145	3/8	12	PPP1R10,	MRPS18B	440		05
6	30,702,216	30,702,868	652	9	C60rf134,	PTMAP1	6,520	MRPS18B	65
6	30,722,972	30,723,742	770	10	C6orf136,			C6orf134	390
6	30,748,157	30,748,942	785	13	DHX16,			KIAA1949	3,203
6	30,754,344	30,755,263	919	9	KIAA1949,	DHX16	5,608	NRM	8,540
6	30,765,920	30,766,637	717	9	NRM,	KIAA1949	2,269	RPL7P4	5,925
6	30,792,484	30,793,661	1,177	9	MDC1,	TUBB	2,475	FLOT1	9,831
6	30,806,163	30,807,013	850	9	FLOT1,			TUBB	4,981
6	30,817,506	30,818,157	651	12	FLOT1,			IER3	798
6	30,818,881	30,819,718	837	13	IER3,	FLOT1	438		
6	30,828,164	30.828.516	352	11		IER3	7.858		
6	30,845,242	30,845,880	638	11		IER3	24 936	AL662797 7	42 742
6	30 933 315	30 933 644	329	13		7SK	6 362		,. /2
6	30 953 466	30 953 943	477	.0 Q			2 8/1		
6	30,000,400	30,060,808	333	9		GTE2H4	2,041	79K	20 167
6	20,900,475	20.062.051	041	9			23,140	751	20,107
6	30,902,010	30,902,931	941	11			21,005		21,702
0	30,983,294	30,984,071	111	14	GTF2H4,	VARSL	5,890	DDRI	7,382
b	31,018,244	31,018,886	642	10			7,993		
6	31,057,574	31,058,133	559	9		C6orf205	1,341		
6	31,148,044	31,149,135	1,091	9		U6	9,631		
6	31,233,900	31,234,388	488	9	CCHCR1,			POU5F1	5,706
6	21 442 405	21 442 452	004	40			0.704		
0 A	31,442,495	31,443,156	001	13			2,734		
6	31,478,711	31,479,477	766	9	MICA,	Y_RNA	705		
6	31,491,448	31,491,751	303	10	MICA,	Y_RNA	13,442	ZDHHC20P2	34,853
6	31,569,585	31,570,235	650	9		MICB	3,607	Y_RNA	2,210
6	31.617.366	31,618,306	940	12	BAT1,	SNORD83	432	ATP6V1G2	1,912

6	31,623,033	31,623,558	525	9	NFKBIL1,	ATP6V1G2	427		
6	31.660.970	31.661.629	659	9	,	LST1	306	NCR3	3.023
6	31 672 830	31 673 196	366	10		NCR3	4 089	LST1	8 165
6	31 674 189	31 674 756	567	12		NCR3	5 448	LST1	9 524
6	31 695 941	31 696 299	358	12		BAT2	130		3 164
6	31 728 324	31 728 964	640	10	BAT3 ADOM	DATZ	150	C6orf47	5,104
6	21 726 251	21 726 726	475	10	Charf47		2 2 1 0		3,030
6	21,730,231	31,730,720	473	12	COULTAT,	I_RNA	2,310		209
0	31,741,339	31,742,009	730	10	DATA, CONKZD,		4,011		2,102
6	31,778,543	31,779,314	771	11	BAI5,	LY6G6F	3,346	LY6G6E	8,213
6	31,813,583	31,814,174	591	11	CLIC1,	MSH5	1,579		
6	31,814,878	31,816,341	1,463	9	CLIC1, MSH5,	DDAH2	8,859		
					C6orf26,				
6	31,845,509	31,845,877	368	10	C6orf27,			C6orf26	4,902
6	31,852,079	31,853,343	1,264	9	C6orf27, VARS,			Y_RNA	1,230
6	31,871,540	31,872,003	463	10	VARS,			LSM2	1,152
6	31,882,027	31,882,994	967	11	LSM2,	HSPA1A	8,305	HSPA1L	2,382
6	31,902,555	31,903,293	738	10		HSPA1B	374	HSPA1A	8,853
6	31,910,106	31,910,893	787	10	C6orf48,	SNORD48	126	HSPA1B	4,096
6	31,938,959	31,939,760	801	9	SLC44A4.	NEU1	297		
6	31,977,806	31 978 436	630	10	,	ZBTB12	58		
6	31 997 618	31 998 014	396	 0		C2	5 450		
6	32 047 514	32 048 843	1 3 2 0	11	DOM37 STK10	AL 645022 11 1	9,400	SKIV/2I	2 005
0	32,047,314	32,040,043	1,329	11	EKDDI	AL045922.11-1	0,937	SKIVZL	2,005
6	32,205,805	32,206,427	622	11	FKBPL,	CREBLI	1,797		
6	32,228,651	32,229,018	367	11	PRRT1,	PP12	261		
6	32,229,414	32,230,722	1,308	10	PPT2,	PRRT1	576		
6	32,252,912	32,253,730	818	9	AGPAT1,	RNF5	379	AGER	2,993
6	32,271,496	32,272,611	1,115	9	NOTCH4,	GPSM3	218		
6	32,628,272	32,628,921	649	9		HLA-DRB5	22,250	HLA-DRB1	25,592
6	32,698,131	32,698,557	426	16		HLA-DQA1	14,555	AL662789.11	35,855
6	32,914,422	32,914,772	350	11	TAP2,	PSMB9	5,119	PSMB8	1,700
6	32.969.515	32.971.401	1.886	9		HLA-Z	770		
6	33 043 400	33 043 686	286	15		BRD2	729		
6	33 045 051	33 045 785	734	13	BRD2		16 188		34 152
6	33 047 188	33 048 272	1 08/	14	BRD2,		18 325		31 665
6	33,047,100	33 048 030	511	10			10,520		31,003
6	22 276 001	22 277 090	000	10			19,000		51,007
0	33,270,091	33,277,009	990	11		NSD1/B0	3,308	r_RNA	040
6	22 224 110	22 224 770	661	11	SLUJSKI,				1 240
0	33,324,110	33,324,779	4 074						1,249
6	33,325,414	33,326,685	1,271	9	VPS52,	22212		HIAISFIP	9,969
6	33,346,953	33,347,354	401	9	VPS52,	RPS18	476	WDR46	7,510
6	33,347,486	33,348,088	602	17	VPS52, RPS18,	B3GALT4	4 807	WDR46	6.776
6	33,352,239	33,353,656	1,417	0			4,001		-,
				9	RPS18,	VPS52	4,522	WDR46	1,208
6	33 390 595			9	B3GALT4,	VPS52	4,522	WDR46	1,208
6	00,000,000	33,391,179	584	9	RPS18, B3GALT4, ZBTB22,	VPS52 TAPBP	4,522	WDR46 DAXX	1,208 3,134
6	33,393,411	33,391,179 33,393,871	584 460	9	B3GALT4, ZBTB22, ZBTB22,	VPS52 TAPBP TAPBP	4,522 481 3,297	WDR46 DAXX DAXX	1,208 3,134 442
G	33,393,411 33,398,620	33,391,179 33,393,871 33,398,996	584 460 376	9 9 9 12	BIGALT4, ZBTB22, ZBTB22, DAXX,	VPS52 TAPBP TAPBP ZBTB22	4,522 4,522 481 3,297 5,132	WDR46 DAXX DAXX	1,208 3,134 442
0	33,393,411 33,398,620 33,399,082	33,391,179 33,393,871 33,398,996 33,399,998	584 460 376 916	9 9 9 9 12 9	B3GALT4, ZBTB22, ZBTB22, DAXX,	VPS52 TAPBP TAPBP ZBTB22 DAXX	4,522 4,522 481 3,297 5,132 317	WDR46 DAXX DAXX	1,208 3,134 442
6	33,393,411 33,398,620 33,399,082 33,466,889	33,391,179 33,393,871 33,398,996 33,399,998 33,467,363	584 460 376 916 474	9 9 9 12 9 16	BIGALT4, ZBTB22, ZBTB22, DAXX,	VPS52 TAPBP TAPBP ZBTB22 DAXX KIFC1	4,522 481 3,297 5,132 317 235	WDR46 DAXX DAXX AL662799.16-2	1,208 3,134 442
6 6	33,393,411 33,398,620 33,399,082 33,466,889 33,467,556	33,391,179 33,393,871 33,398,996 33,399,998 33,467,363 33,468,023	584 460 376 916 474 467	9 9 9 12 9 16 10	KPS18, B3GALT4, ZBTB22, ZBTB22, DAXX, KIFC1,	VPS52 TAPBP ZBTB22 DAXX KIFC1 RPL35AP4	4,522 481 3,297 5,132 317 235 2,326	WDR46 DAXX DAXX AL662799.16-2 AL662799.16-2	1,208 3,134 442 8,451 7,791
6 6 6	33,393,411 33,398,620 33,399,082 33,466,889 33,467,556 33,485,567	33,391,179 33,393,871 33,398,996 33,399,998 33,467,363 33,468,023 33,468,023	584 460 376 916 474 467 633	9 9 9 12 9 16 10 11	KPS18, B3GALT4, ZBTB22, ZBTB22, DAXX, KIFC1, KIFC1.	VPS52 TAPBP ZBTB22 DAXX KIFC1 RPL35AP4 PHF1	4,522 481 3,297 5,132 317 235 2,326 572	WDR46 DAXX DAXX AL662799.16-2 AL662799.16-2 CUTA	1,208 3,134 442 8,451 7,791 6,097
6 6 6 6	33,393,411 33,398,620 33,399,082 33,466,889 33,467,556 33,485,567 33,493,659	33,391,179 33,393,871 33,398,996 33,399,998 33,467,363 33,468,023 33,486,200 33,494,226	584 460 376 916 474 467 633 567	9 9 9 12 9 16 10 11 11	KPS18, B3GALT4, ZBTB22, ZBTB22, DAXX, KIFC1, KIFC1, CUTA	VPS52 TAPBP TAPBP ZBTB22 DAXX KIFC1 RPL35AP4 PHF1 SYNGAP1	4,507 4,522 481 3,297 5,132 317 235 2,326 572 1,693	WDR46 DAXX DAXX AL662799.16-2 AL662799.16-2 CUTA PHF1	1,208 3,134 442 8,451 7,791 6,097 1 465
6 6 6 6	33,393,411 33,398,620 33,399,082 33,466,889 33,467,556 33,485,567 33,493,659 33,505,119	33,391,179 33,393,871 33,398,996 33,399,998 33,467,363 33,468,023 33,468,023 33,486,200 33,494,226 33,505,593	584 460 376 916 474 467 633 567 474	9 9 9 12 9 16 10 11 11 13	KPS18, B3GALT4, ZBTB22, ZBTB22, DAXX, KIFC1, KIFC1, CUTA, SYNGAP1	VPS52 TAPBP TAPBP ZBTB22 DAXX KIFC1 RPL35AP4 PHF1 SYNGAP1 CUITA	4,537 4,522 481 3,297 5,132 317 2,355 2,326 572 1,693 11,076	WDR46 DAXX DAXX AL662799.16-2 AL662799.16-2 CUTA PHF1 PHF1 PHF1	1,208 3,134 442 8,451 7,791 6,097 1,465
6 6 6 6 6 6	33,393,411 33,398,620 33,399,082 33,466,889 33,467,556 33,485,567 33,493,659 33,505,119 33,500,5119	33,391,179 33,393,871 33,398,996 33,399,998 33,467,363 33,468,023 33,468,023 33,486,200 33,494,226 33,505,593 33,503,574	584 460 376 916 474 467 633 567 474 377	9 9 9 12 9 16 10 11 11 13 9	KPS18, B3GALT4, ZBTB22, ZBTB22, DAXX, KIFC1, KIFC1, CUTA, SYNGAP1, SYNGAP1	VPS52 TAPBP ZBTB22 DAXX KIFC1 RPL35AP4 PHF1 SYNGAP1 CUTA	4,537 4,522 481 3,297 5,132 317 235 2,326 572 1,693 11,076 35 954	WDR46 DAXX DAXX AL662799.16-2 AL662799.16-2 CUTA PHF1 PHF1 PHF1 PHF1	1,208 3,134 442 8,451 7,791 6,097 1,465 12,925 37,802
6 6 6 6 6 6	33,393,411 33,398,620 33,399,082 33,466,889 33,467,556 33,485,567 33,493,659 33,505,119 33,529,997	33,391,179 33,393,871 33,398,996 33,399,998 33,467,363 33,468,023 33,468,023 33,486,200 33,494,226 33,505,593 33,530,374	584 460 376 916 474 467 633 567 474 377	9 9 9 12 9 16 10 11 13 9 13	KPS18, B3GALT4, ZBTB22, ZBTB22, DAXX, KIFC1, KIFC1, CUTA, SYNGAP1, SYNGAP1, ZBTB9	VPS52 TAPBP TAPBP ZBTB22 DAXX KIFC1 RPL35AP4 PHF1 SYNGAP1 CUTA CUTA	4,522 481 3,297 5,132 317 235 2,326 572 1,693 11,076 35,954	WDR46 DAXX DAXX AL662799.16-2 AL662799.16-2 CUTA PHF1 PHF1 PHF1 PHF1	1,208 3,134 442 8,451 7,791 6,097 1,465 12,925 37,803
6 6 6 6 6 6	33,393,411 33,398,620 33,399,082 33,466,889 33,467,556 33,485,567 33,493,659 33,505,119 33,529,997	33,391,179 33,393,871 33,398,996 33,399,998 33,467,363 33,468,023 33,468,023 33,448,200 33,494,226 33,505,593 33,530,374 33,646,801	584 460 376 916 474 467 633 567 474 377	9 9 9 12 9 16 10 11 13 9 13	KPS18, B3GALT4, ZBTB22, ZBTB22, DAXX, KIFC1, KIFC1, CUTA, SYNGAP1, ZSYNGAP1, ZBTB9,	VPS52 TAPBP TAPBP ZBTB22 DAXX KIFC1 RPL35AP4 PHF1 SYNGAP1 CUTA CUTA	4,522 481 3,297 5,132 317 235 2,326 572 1,693 11,076 35,954	WDR46 DAXX DAXX AL662799.16-2 AL662799.16-2 CUTA PHF1 PHF1 PHF1 PHF1 PHF1	1,208 3,134 442 8,451 7,791 6,097 1,465 12,925 37,803
6 6 6 6 6 6 6 6	33,393,411 33,398,620 33,399,082 33,466,889 33,467,556 33,485,567 33,493,659 33,505,119 33,529,997 33,646,560	33,391,179 33,393,871 33,398,996 33,399,998 33,467,363 33,467,363 33,468,023 33,446,200 33,494,226 33,505,593 33,505,593 33,530,374 33,646,891	584 460 376 916 474 467 633 567 474 377 331	9 9 9 12 9 16 10 11 13 9 13 10	KPS18, B3GALT4, ZBTB22, ZBTB22, DAXX, KIFC1, KIFC1, CUTA, SYNGAP1, ZSTNGAP1, ZBTB9,	VPS52 TAPBP TAPBP ZBTB22 DAXX KIFC1 RPL35AP4 PHF1 SYNGAP1 CUTA CUTA	4,522 481 3,297 5,132 317 235 2,326 572 1,693 11,076 35,954	WDR46 DAXX DAXX AL662799.16-2 AL662799.16-2 CUTA PHF1 PHF1 PHF1 PHF1 BAK1	1,208 3,134 442 8,451 7,791 6,097 1,465 12,925 37,803 1,411
6 6 6 6 6 6 6 6	33,393,411 33,398,620 33,399,082 33,466,889 33,467,556 33,485,567 33,493,659 33,505,119 33,529,997 33,646,560 33,646,560	33,391,179 33,393,871 33,398,996 33,399,998 33,467,363 33,468,023 33,468,023 33,446,200 33,494,226 33,505,593 33,505,593 33,530,374 33,646,891 33,662,211	584 460 376 916 474 467 633 567 474 377 331 753	9 9 9 12 9 16 10 11 11 13 9 13 10 9	KPS18, B3GALT4, ZBTB22, ZBTB22, DAXX, KIFC1, KIFC1, CUTA, SYNGAP1, ZBTB9, GGNBP1, Z02017 6 2	VPS52 TAPBP TAPBP ZBTB22 DAXX KIFC1 RPL35AP4 PHF1 SYNGAP1 CUTA CUTA CUTA BAK1	4,522 481 3,297 5,132 317 235 2,326 572 1,693 11,076 35,954 5,410	WDR46 DAXX DAXX AL662799.16-2 AL662799.16-2 CUTA PHF1 PHF1 PHF1 PHF1 BAK1	1,208 3,134 442 8,451 7,791 6,097 1,465 12,925 37,803 1,411
6 6 6 6 6 6 6 6 6	33,393,411 33,398,620 33,399,082 33,466,889 33,467,556 33,485,567 33,493,659 33,505,119 33,529,997 33,646,560 33,646,560	33,391,179 33,393,871 33,398,996 33,399,998 33,467,363 33,468,023 33,468,023 33,446,200 33,494,226 33,505,593 33,505,593 33,505,593 33,646,891 33,664,891	584 460 376 916 474 467 633 567 474 377 331 753	9 9 9 12 9 16 10 11 13 9 13 10 9	KPS18, B3GALT4, ZBTB22, ZBTB22, DAXX, KIFC1, KIFC1, CUTA, SYNGAP1, ZSYNGAP1, ZBTB9, GGNBP1, Z93017.6-2, ITDP2	VPS52 TAPBP TAPBP ZBTB22 DAXX KIFC1 RPL35AP4 PHF1 SYNGAP1 CUTA CUTA CUTA BAK1	4,522 481 3,297 5,132 317 235 2,326 572 1,693 11,076 35,954 5,410	WDR46 DAXX DAXX AL662799.16-2 AL662799.16-2 CUTA PHF1 PHF1 PHF1 PHF1 BAK1	1,208 3,134 442 8,451 7,791 6,097 1,465 12,925 37,803 1,411
6 6 6 6 6 6 6 6 6 6 6	33,393,411 33,398,620 33,399,082 33,466,889 33,467,556 33,485,567 33,493,659 33,505,119 33,529,997 33,646,560 33,646,560 33,661,458 33,697,637	33,391,179 33,393,871 33,398,996 33,399,998 33,467,363 33,468,023 33,468,023 33,446,200 33,494,226 33,505,593 33,505,593 33,505,593 33,646,891 33,646,891 33,662,211	584 460 376 916 474 467 633 567 474 377 331 753 493	9 9 9 12 9 16 10 10 11 13 9 13 10 9 9	KPS18, B3GALT4, ZBTB22, ZBTB22, DAXX, KIFC1, KIFC1, CUTA, SYNGAP1, ZSYNGAP1, ZBTB9, GGNBP1, Z93017.6-2, ITPR3,	VPS52 TAPBP TAPBP ZBTB22 DAXX KIFC1 RPL35AP4 PHF1 SYNGAP1 CUTA CUTA CUTA BAK1 Z93017.6-2	4,522 481 3,297 5,132 317 235 2,326 572 1,693 11,076 35,954 5,410 28,544	WDR46 DAXX DAXX AL662799.16-2 AL662799.16-2 CUTA PHF1 PHF1 PHF1 PHF1 BAK1 BAK1	1,208 3,134 442 8,451 7,791 6,097 1,465 12,925 37,803 1,411 32,856 5,555
6 6 6 6 6 6 6 6 6 6 6	33,393,411 33,398,620 33,399,082 33,466,889 33,467,556 33,485,567 33,493,659 33,505,119 33,529,997 33,646,560 33,646,560 33,661,458 33,697,637 33,767,483	33,391,179 33,393,871 33,398,996 33,399,998 33,467,363 33,468,023 33,468,023 33,446,200 33,494,226 33,505,593 33,505,593 33,505,593 33,646,891 33,646,891 33,662,211 33,698,130 33,767,900	584 460 376 916 474 467 633 567 474 377 331 753 493 493	9 9 9 12 9 16 10 10 11 13 9 13 10 9 9 11	RPS18, B3GALT4, ZBTB22, ZBTB22, DAXX, KIFC1, KIFC1, CUTA, SYNGAP1, ZSYNGAP1, ZBTB9, GGNBP1, Z93017.6-2, ITPR3, ITPR3,	VPS52 TAPBP TAPBP ZBTB22 DAXX KIFC1 RPL35AP4 PHF1 SYNGAP1 CUTA CUTA CUTA BAK1 Z93017.6-2	4,522 481 3,297 5,132 317 235 2,326 572 1,693 11,076 35,954 5,410 28,544	WDR46 DAXX DAXX AL662799.16-2 AL662799.16-2 CUTA PHF1 PHF1 PHF1 PHF1 BAK1 GGNBP1 C60rf125	1,208 3,134 442 8,451 7,791 6,097 1,465 12,925 37,803 1,411 32,856 5,422
6 6 6 6 6 6 6 6 6 6 6 6 6	33,393,411 33,398,620 33,399,082 33,466,889 33,467,556 33,485,567 33,493,659 33,505,119 33,529,997 33,646,560 33,646,560 33,661,458 33,697,637 33,767,483 33,819,786	33,391,179 33,393,871 33,399,996 33,399,998 33,467,363 33,468,023 33,468,023 33,446,200 33,494,226 33,505,593 33,505,593 33,505,593 33,646,891 33,646,891 33,662,211 33,698,130 33,767,902 33,820,542	584 460 376 916 474 467 633 567 474 377 331 753 493 419 756	9 9 9 12 9 16 10 11 11 13 9 13 10 9 13 9 9 11 11 9	RPS18, B3GALT4, ZBTB22, ZBTB22, DAXX, KIFC1, KIFC1, CUTA, SYNGAP1, ZSYNGAP1, ZBTB9, GGNBP1, Z93017.6-2, ITPR3, ITPR3, IP6K3,	VPS52 TAPBP TAPBP ZBTB22 DAXX KIFC1 RPL35AP4 PHF1 SYNGAP1 CUTA CUTA CUTA BAK1 Z93017.6-2 C6orf125	4,522 481 3,297 5,132 317 235 2,326 572 1,693 11,076 35,954 5,410 28,544 32,304	WDR46 DAXX DAXX AL662799.16-2 AL662799.16-2 CUTA PHF1 PHF1 PHF1 PHF1 BAK1 GGNBP1 C6orf125 LEMD2	1,208 3,134 442 8,451 7,791 6,097 1,465 12,925 37,803 1,411 32,856 5,422 26,435
6 6 6 6 6 6 6 6 6 6 6 6 6	33,393,411 33,398,620 33,399,082 33,466,889 33,467,556 33,485,567 33,493,659 33,505,119 33,529,997 33,646,560 33,646,560 33,661,458 33,697,637 33,767,483 33,819,786 33,837,118	33,391,179 33,393,871 33,399,996 33,399,998 33,467,363 33,468,023 33,468,023 33,448,200 33,494,226 33,505,593 33,505,593 33,505,593 33,646,891 33,662,211 33,698,130 33,767,902 33,820,542 33,837,744	584 460 376 916 474 467 633 567 474 377 331 753 493 419 756 626	9 9 9 12 9 16 10 11 11 13 9 13 10 9 9 11 11 9 9	RPS18, B3GALT4, ZBTB22, ZBTB22, DAXX, KIFC1, KIFC1, CUTA, SYNGAP1, ZSYNGAP1, ZBTB9, GGNBP1, Z93017.6-2, ITPR3, ITPR3, IP6K3,	VPS52 TAPBP TAPBP ZBTB22 DAXX KIFC1 RPL35AP4 PHF1 SYNGAP1 CUTA CUTA CUTA BAK1 Z93017.6-2 C6orf125	4,522 481 3,297 5,132 317 235 2,326 572 1,693 11,076 35,954 5,410 28,544 32,304	WDR46 DAXX DAXX AL662799.16-2 AL662799.16-2 CUTA PHF1 PHF1 PHF1 PHF1 BAK1 GGNBP1 C6orf125 LEMD2 LEMD2	1,208 3,134 442 8,451 7,791 6,097 1,465 12,925 37,803 1,411 32,856 5,422 26,435 9,233
6 6	33,393,411 33,398,620 33,399,082 33,466,889 33,467,556 33,485,567 33,493,659 33,505,119 33,529,997 33,646,560 33,661,458 33,697,637 33,767,483 33,819,786 33,837,118 33,844,208	33,391,179 33,393,871 33,398,996 33,399,998 33,467,363 33,468,023 33,468,023 33,448,200 33,494,226 33,505,593 33,505,593 33,505,593 33,646,891 33,662,211 33,698,130 33,767,902 33,820,542 33,837,744 33,844,626	584 460 376 916 474 467 633 567 474 377 331 753 493 493 419 756 626 418	9 9 9 12 9 16 10 11 11 13 9 13 10 9 9 11 9 9 11	RPS18, B3GALT4, ZBTB22, ZBTB22, DAXX, KIFC1, KIFC1, CUTA, SYNGAP1, ZSYNGAP1, ZBTB9, GGNBP1, Z93017.6-2, ITPR3, ITPR3, IP6K3,	VPS52 TAPBP TAPBP ZBTB22 DAXX KIFC1 RPL35AP4 PHF1 SYNGAP1 CUTA CUTA CUTA BAK1 Z93017.6-2 C6orf125	4,522 481 3,297 5,132 317 235 2,326 572 1,693 11,076 35,954 5,410 28,544 32,304	WDR46 DAXX DAXX AL662799.16-2 AL662799.16-2 CUTA PHF1 PHF1 PHF1 PHF1 BAK1 GGNBP1 C6orf125 LEMD2 LEMD2 LEMD2 LEMD2	1,208 3,134 442 8,451 7,791 6,097 1,465 12,925 37,803 1,411 32,856 5,422 26,435 9,233 2,351
6 6	33,393,411 33,398,620 33,399,082 33,466,889 33,467,556 33,485,567 33,493,659 33,505,119 33,529,997 33,646,560 33,661,458 33,697,637 33,767,483 33,819,786 33,837,118 33,844,208 34,271,884	33,391,179 33,393,871 33,398,996 33,399,998 33,467,363 33,468,023 33,468,023 33,468,023 33,448,200 33,494,226 33,505,593 33,505,593 33,505,593 33,505,593 33,646,891 33,662,211 33,698,130 33,767,902 33,820,542 33,837,744 33,844,626 34,272,411	584 460 376 916 474 467 633 567 474 377 331 753 493 419 756 626 418 527	9 9 9 12 9 16 10 11 11 13 9 13 10 9 9 11 11 9 9 11 10	RPS18, B3GALT4, ZBTB22, ZBTB22, DAXX, KIFC1, KIFC1, CUTA, SYNGAP1, ZSYNGAP1, ZBTB9, GGNBP1, Z93017.6-2, ITPR3, ITPR3, IP6K3,	VPS52 TAPBP TAPBP ZBTB22 DAXX KIFC1 RPL35AP4 PHF1 SYNGAP1 CUTA CUTA CUTA BAK1 Z93017.6-2 C6orf125 AL354740.29	4,522 481 3,297 5,132 317 235 2,326 572 1,693 11,076 35,954 5,410 28,544 32,304 22,716	WDR46 DAXX DAXX AL662799.16-2 AL662799.16-2 CUTA PHF1 PHF1 PHF1 PHF1 BAK1 GGNBP1 C6orf125 LEMD2 LEMD2 LEMD2 LEMD2 C6orf1	1,208 3,134 442 8,451 7,791 6,097 1,465 12,925 37,803 1,411 32,856 5,422 26,435 9,233 2,351 49,725
6 6	33,393,411 33,398,620 33,399,082 33,466,889 33,467,556 33,485,567 33,493,659 33,505,119 33,505,119 33,529,997 33,646,560 33,661,458 33,697,637 33,767,483 33,819,786 33,837,118 33,844,208 34,271,884 34,468,029	33,391,179 33,393,871 33,398,996 33,399,998 33,467,363 33,468,023 33,468,023 33,448,200 33,494,226 33,505,593 33,505,593 33,505,593 33,505,593 33,646,891 33,662,211 33,698,130 33,767,902 33,820,542 33,837,744 33,844,626 34,272,411 34,468,975	584 460 376 916 474 467 633 567 474 377 331 753 493 419 756 626 418 527 946	9 9 9 12 9 16 10 11 11 13 9 13 10 9 9 11 9 9 11 10 9 9 9 11 10 9 9	RPS18, B3GALT4, ZBTB22, ZBTB22, DAXX, KIFC1, CUTA, SYNGAP1, ZSYNGAP1, ZBTB9, GGNBP1, Z93017.6-2, ITPR3, ITPR3, ITPR3, IP6K3, NUDT3,	VPS52 TAPBP TAPBP ZBTB22 DAXX KIFC1 RPL35AP4 PHF1 SYNGAP1 CUTA CUTA CUTA BAK1 Z93017.6-2 C6orf125 AL354740.29	4,522 481 3,297 5,132 317 235 2,326 572 1,693 11,076 35,954 5,410 28,544 32,304 22,716	WDR46 DAXX DAXX AL662799.16-2 AL662799.16-2 CUTA PHF1 PHF1 PHF1 PHF1 BAK1 GGNBP1 C6orf125 LEMD2 LEMD2 LEMD2 LEMD2 C6orf1 RPS10	1,208 3,134 442 8,451 7,791 6,097 1,465 12,925 37,803 1,411 32,856 5,422 26,435 9,233 2,351 49,725 24,234

6	34,538,138	34,538,750	612	9		PACSIN1	3,133	BX255972.1	7,795
6	34,867,060	34.867.849	789	9	UHRF1BP1.	Y RNA	29.351	SNRPC	17.515
6	34 867 880	34 869 000	1 120	9	UHRF1BP1	Y RNA	28 200	SNRPC	18 335
6	34 963 583	34 964 310	727	12	TAF11	ANKS1A	706		
6	35 257 420	35 258 385	965	.2	.,,	SCUBE3	31 783		
6	35 335 039	35 335 779	740	12	ZNE76	COODEO	01,100	SCUBE3	8 4 5 2
6	35 417 830	35 418 378	548	11				DEF6	20,306
6	35 400 743	35 /01 321	578	10			27 478	DEIO	20,000
6	35 543 223	35 543 593	350	10	TTAND,		27,470	EANCE	374
0	35,545,235	35,545,565	350	9		RFLIUA	575		374
0	35,543,721	35,544,405	004	14	RPLIUA,				002
6	35,544,648	35,545,829	1,181	11	RPL10A,	00.001	40 744		1,789
6	35,763,334	35,764,119	785	12	FKBP5,	C60rf81	48,714	AL157823.9	12,635
6	35,802,852	35,803,447	595	10	FKBP5,	C6orf81	9,386		
6	35,803,756	35,804,428	672	9	FKBP5,	C6orf81	8,405		
6	35,811,986	35,812,390	404	11		C6orf81	443		
6	35,995,544	35,995,959	415	10	SRPK1,			SLC26A8	23,314
6	36,001,634	36,002,024	390	9		SRPK1	4,692		
6	36,103,157	36,103,730	573	18	MAPK14,	SLC26A8	2,802		
6	36,170,880	36,171,428	548	12	MAPK14,	Z95152.1-1	2,810		
6	36,378,112	36,378,730	618	11	PNPLA1,			C6orf222	12,787
6	36,459,570	36,460,222	652	9	ETV7,			PXT1	6,084
6	36,498,666	36,499,567	901	12		KCTD20	18,955	SRP_euk_arch	27,103
6	36,517,084	36,517,462	378	9		KCTD20	1,060	SRP_euk_arch	9,208
6	36,518,401	36,519,582	1,181	9	KCTD20,			SRP euk arch	7,088
6	36,669,367	36,670,342	975	16	SFRS3,	STK38	46,133		
6	36.698.927	36,699,334	407	13	,			SFRS3	19,740
6	36 742 633	36 743 465	832	12		AI 121715 15	6 059		,
6	36 753 524	36 754 697	1 173	9	CDKN1A		0,000	AI 121715 15	2 498
6	36 852 614	36 852 966	352	10	CPNE5	785996 1-2	19 459	RP3-431A14.4	38 873
6	36 949 524	36 951 060	1 536	q	PPII 1 Coorf89	CPNE5	33 768		00,070
6	36 961 335	36 962 174	1,000	10	C6orf80		10 588		
6	37 003 818	37 004 616	709	10	DDI 12D2		31 901		
0	57,035,010	57,054,010	730	10	FGD2	WITCHT	51,051		
6	37 135 283	37 135 744	461	10	RPI 12P2			FGD2	30 897
6	37 178 429	37 178 810	381	11	TT E1212,			RPI 12P2	10 834
6	37 180 038	37 181 184	246	10				RDI 12D2	13 3/3
6	37,100,000	37 211 013	270	10		DIM1	34 051		10,040
6	37,210,101	37 224 300	401	9		DIM1	21 574		42,500
6	37 247 828	37 24,390	491 550	9			21,374		30 547
6	37,247,020	27 296 521	209	10	FINIT,				39,347
6	37,203,013	27 200,521	612	10			24.040		1,413
6	37,297,900	27 224 255	1 4 2 4	10			54,940	AL353579.17	20,379
0	37,332,021	37,334,255	1,434	9		AL353579.17	5,762		
6	27 420 545	27 420 022	100	10	DNEO	SPD out oroh	6 006		
0	37,429,545	37,430,033	400	10		SRP_euk_arch	6,906		20.070
o c	37,508,570	37,509,442	8/2	11		AL 252507 00	40.004		38,079
o c	31,535,535	37,530,1/1	030	9		AL303097.20	40,931		22,506
o c	37,560,007	37,560,717	/10	9	Conf129,				1,/25
6	37,565,406	37,565,884	4/8	10	Сюопті29,		- ^^^	FISJD2	7,124
6	37,781,577	37,782,079	502	9		MDGA1	7,833		
6	37,783,561	37,783,855	294	10		MDGA1	9,817		
6	37,867,077	37,867,836	759	9		ZFAND3	27,449	SRP_euk_arch	40,833
6	38,715,317	38,715,922	605	15		BTBD9	41,469	GLO1	35,760
6	38,986,870	38,987,321	451	9	DNAH8,	RP1-207H1.2	16,464		
6	39,136,796	39,137,795	999	9	GLP1R,	RP1-202I21.3	21,057	DNAH8	30,251
6	39,190,286	39,191,442	1,156	9	C6orf64,			RP1-202l21.5	1,580
6	39,396,881	39,397,160	279	10	KCNK16,	KCNK17	6,667		
6	39,423,578	39,423,999	421	13	KIF6,	RP1-137F1.3	5,502		
6	39,437,468	39,438,143	675	10	KIF6,			RP1-137F1.3	7,542
6	39,447,455	39,447,807	352	9	KIF6,	KCNK16	49,161	RP1-137F1.3	17,529
6	39,527,600	39,527,930	330	9	KIF6,	No non-overlappi	ng genes wit	hin 50,000bp	
6	40.010.147	40,010.513	366	11	MOCS1.			RP1-278E11.3	23.618
6	40.384.184	40.384.828	644	9				AL139275.30	35.234
6	40.425.675	40.426.165	490	.9	AL139275.30.	AL591063.6-2	27.889	LRFN2	41.142
6	40,553,002	40.553.927	925	9	LRFN2.	No non-overlappi	na aenes wit	hin 50.000bp	.,
6	40 880 590	40 880 886	296	a	····,	No non-overlappi	na aenes wit	hin 50 000bp	
v	-0,000,000	-0,000,000	200	9		non-ovenappi	ng genes wit		

6	41,347,838	41,348,060	222	11		RP1-229K20.5	1,883	TREM1	3,415
6	41.354.655	41.355.137	482	10	TREM1.	RP1-229K20.5	8.700		
6	41,394,106	41,394,919	813	9	,	AL672212.2-1	9.822		
6	41 443 415	41 443 847	432	9			0,011	NCR2	16 835
6	41 444 622	41 445 244	622	g				NCR2	18 042
6	41 460 540	41 460 855	315	a				NCR2	33,960
6	41 478 318	41 478 830	512	a		No non-overlanni	na aenes wit	hin 50 000hn	00,000
6	41,525,603	41 527 275	1 672	9		No non-overlappi	ng genes wit	hin 50,000bp	
6	41,525,005	41,527,275	662	14		No non overlappi	ng genes wit	hin 50,000bp	
6	41,551,092	41,552,554	2002	14				nin 50,000p	
6	41,021,003	41,021,991	300	10		FUAF4	101	AL 120221 10	20.759
0	41,053,390	41,054,065	009		FUXP4,			AL 139331.19	29,750
6	41,654,476	41,655,064	588	9	FOXP4,			AL139331.19	28,779
6	41,678,643	41,679,075	432	9				FOXP4	544
6	41,757,671	41,758,374	703	11				TFEB	1,320
6	41,811,175	41,811,752	577	13	TFEB, PGC,	C6orf49	44,726	FRS3	34,140
6	41,842,565	41,843,216	651	9				FRS3	2,676
6	41,879,939	41,880,262	323	9	USP49,	FRS3	24,331	TOMM6	14,325
6	41,996,522	41,997,443	921	10	TRFP, BYSL,	Y_RNA	3,280		
6	42,121,172	42,121,894	722	9	CCND3,	TAF8	4,335		
6	42,126,131	42,126,940	809	9	TAF8,	CCND3	1,729		
6	42,293,343	42,294,156	813	10	MRPS10,			TRERF1	6,491
6	42,586,465	42,586,781	316	9		AL591473.3	5,143		
6	42,639,194	42,640,210	1,016	13	UBR2,	No non-overlappi	ng genes wit	hin 50,000bp	
6	42,706,478	42.707.016	538	9	UBR2.	U6	32.862	, ,	
6	42,820,896	42.821.772	876	9	TBCC.	KIAA0240	902		
6	42 822 727	42 823 099	372	13	KIAA0240	TBCC	191		
6	42 859 119	42 859 459	340	10	KIAA0240	TBCC	36 583		
Ŭ	42,000,110	42,000,400	040	10	AI 353716 18	1000	00,000		
6	42 966 052	42 966 917	865	11	AL 353716 18			RPI 7I 1	440
Ŭ	12,000,002	12,000,011	000		C6orf226				
6	43 004 792	43 005 785	993	11	AL 353716 18			PTCRA	3 241
Ŭ	10,001,102	10,000,100	000		CNPY3.				0,211
6	43 084 823	43 085 385	562	9	PPP2R5D	KI HDC3	4 570	MFA1	2 558
6	43 089 670	43 090 043	373	g	KLHDC3	MFA1	74	PPP2R5D	1 616
6	43 134 987	43 135 570	583	12	MRPL2 KLC4		5 355		1,010
6	43 152 089	43 153 446	1 357	9	PTK7	002/	0,000	KI C4	1 274
6	43,132,009	43 247 305	1,007	9	SDF				8 644
6	43,240,079	43,247,303	1,220	9			9.014		0,044
6	43,240,307	43,240,900	242	9		CUL9	7.057		
0	43,250,330	43,250,643	313	10	SRF,	COL9	1,257	DTKZ	40.200
0	43,250,833	43,258,552	1,719	10	SRF, CUL9,	00	04.400		19,398
6	43,326,369	43,327,204	835	9	TTBK1,	C60ff108	21,180	CUL9	26,066
6	43,327,586	43,327,954	368	9	TTBK1,	C6orf108	22,397	CUL9	27,283
6	43,339,285	43,339,606	321	9	TTBK1,	C6orf108	34,096	CUL9	38,982
6	43,345,822	43,346,319	497	11	TTBK1,	SLC22A7	27,657	CRIP3	34,870
6	43,465,827	43,466,183	356	9		ZNF318	20,668	RPS2P28	25,841
6	43,467,260	43,467,542	282	9		ZNF318	22,101	RPS2P28	27,274
6	43,480,940	43,481,548	608	9		5S_rRNA	12,262	RPS2P28	40,954
6	43,502,875	43,503,938	1,063	9	ABCC10,			5S_rRNA	8,970
6	43,582,202	43,582,819	617	9	RP3-337H4.1,	POLR1C	9,950	YIPF3	4,725
					C6orf154,				
6	43,683,936	43,684,549	613	9	POLH,	MAD2L1BP	24,118	GTPBP2	11,416
6	43,689,788	43,690,219	431	9	POLH,			GTPBP2	5,746
6	43,704,309	43,704,834	525	11	GTPBP2,	MAD2L1BP	3,833		
6	43,704,990	43,706,151	1,161	9		GTPBP2	29		
6	43,711.104	43,711.802	698	10	MAD2L1BP.	GTPBP2	6.143		
6	43.777.721	43.779.008	1.287	.9	- ,	1	.,	RP1-261G23.4	2.656
6	43,785,266	43,785,603	,_0.	11		RP1-261G23 4	2 800		_,
6	43 799 386	43 800 536	1 150	. I Q		RP1-261G23 4	16,920		
6	43 834 100	43,000,000	372	0		1.4 1 201020.4	10,020	AL 136131 15 2	5 520
6	43,034,190	40,004,071	313	9	VECE			AL 136121 4E 2	10 044
6	43,040,977	43,047,437	400	11	VEGE			AL 136121 4E 2	20,000
0 C	43,848,674	43,849,002	328	9	VEGF,	Cearfood	00 474	AL130131.15-2	20,008
0 C	44,047,379	44,047,843	464	9		00011223	28,474	00 - #000	20.044
6	44,116,908	44,117,616	708	10					36,044
6	44,134,004	44,134,750	/46	9				AL109615.42-1	30,213
6	44,148,480	44,149,291	811	9				AL109615.42-1	15,672

6	44,149,834	44,150,220	386	12				AL109615.42-1	14,743
6	44,248,340	44,248,831	491	9	CAPN11,	MRPL14	45,171	TMEM63B	17,106
6	44,312,906	44,313,491	585	9		HSP90AB1	9,311	SLC29A1	3,040
6	44,322,055	44,323,160	1,105	13	HSP90AB1,			SLC35B2	6,651
6	44,345,258	44,345,651	393	9		TMEM151B	807		
6	44,388,919	44,389,376	457	20	TMEM151B, AARS2,	TCTE1	15,514	AL353588.25	34,968
6	44,463,060	44,463,581	521	10	CDC5L,			TMEM151B	8,388
6	44,491,935	44,492,519	584	9	CDC5L,			TMEM151B	37,263
6	44,706,051	44,706,479	428	11		No non-overlappi	ng genes wit	hin 50,000bp	
6	44,806,190	44,807,246	1,056	9		No non-overlappi	ng genes wit	hin 50,000bp	
6	44,876,821	44,877,489	668	9				SUPT3H	26,958
6	45,453,426	45,454,078	652	15	SUPT3H, RUNX2,	No non-overlappi	ng genes wit	hin 50,000bp	
6	45,741,156	45,741,424	268	10				AL161907.17	19,258
6	45,761,731	45,762,051	320	9				AL161907.17	39,833
6	45,790,442	45,790,793	351	10		No non-overlappi	ng genes wit	hin 50,000bp	
6	45,912,215	45,912,705	490	9		No non-overlappi	ng genes wit	hin 50,000bp	
6	46,205,010	46,205,970	960	10	ENPP4,	CLIC5	49,072	ENPP5	28,915
6	46,266,640	46,267,244	604	9		AL035701.13	13,677	RCAN2	29,184
6	46,296,618	46,297,307	689	9	RCAN2,	ENPP5	49,942	AL035701.13	15,389
6	46,727,919	46,728,381	462	10	CYP39A1,	SLC25A27	257		
6	46,731,477	46,731,843	366	9	SLC25A27,	CYP39A1	2,995	000111	
6	47,061,147	47,061,460	313	9		GPR116	30,508	GPR110	13,616
6	47,159,289	47,159,612	323	10		GPR110	41,248		
6	47,175,862	47,176,687	825	9		No non-overlappi	ng genes wit	hin 50,000bp	
6	47,384,300	47,384,643	343	9	INFRSF21,	No non-overlappi	ng genes wit	hin 50,000bp	
6	47,490,253	47,490,534	281	10	000444	No non-overlappi	ng genes wit	nin 50,000bp	00.075
6	47,732,017	47,732,466	449	12	GPR111,	GPR115	29,093	CD2AP	29,073
6	47,856,282	47,856,732	450	9	00 auf 1 1 1	UPN5	1,025		44 070
6	49,626,056	49,626,617	561	10	С60П141,	No non survis		KP11-28H17.4	14,979
b C	51,183,262	52 100 101	390	10		No non-overlappi	ng genes wit		0.045
0 C	52,128,/13	52,129,181	468	9				nsa-mir-1330	6,915
6	52,200,915	52,207,524	609	10		No per overlage			1,914
6	52 202 400	52 302 00F	3/0	11		No non-overlappi	ng genes wit		11 054
6	52 476 740	52 477 102	1,419	10	TRAM2				11,954 0 170
6	52 5/8 756	52 5/0 221	575	10	TRAM2	No non-overlappi	na aenes wit	hin 50 000hn	0,170
6	52 540 412	52 540 754	341	9	TRAM2	No non-overlappi	ng genes wit	hin 50,000bp	
6	52 567 805	52 568 164	350	9 10	· · · · · · · · · · · · · · · · · · ·	TRAM2	17 984	iiii 30,000bp	
6	52 966 746	52 967 104	363	10 Q	GSTA4	7SK	1 268	ICK	6 959
6	52 967 674	52 968 676	1 002	12	GSTA4 7SK		1,200	ICK	5 302
6	52,968,766	52 969 117	351	10		GSTA4	667	7SK	50,002
6	53 034 386	53 034 863	477	13	ICK	FBXO9	2 802		
6	53 144 448	53 144 991	543	15 Q	ivit,	GCM1	2,032	RP11-506F9 1	24 486
6	53 434 491	53 434 900	409	9 Q			22,002	AI 591034 5-2	5 202
6	53.517 309	53.517 667	358	11	GCLC.	No non-overlappi	na aenes wit	hin 50.000bp	0,202
6	53.623 947	53.624 558	611	10	KLHL31.	AL157773 13	12 369		
6	53.767.003	53.767.845	842	10	LRRC1.	No non-overlappi	ng genes wit	hin 50,000bp	
6	53,767,862	53,768,271	409	10	LRRC1.	No non-overlappi	na genes wit	hin 50.000bp	
6	54.819.075	54,820.077	1.002	10	FAM83B	No non-overlappi	na aenes wit	hin 50.000bp	
6	54.852.062	54.852.626	564	.0	FAM83B.	No non-overlappi	ng genes wit	hin 50,000bp	
6	55,019,465	55,019.938	473	10	,	No non-overlappi	ng genes wit	hin 50,000bp	
6	55,551,357	55,552.096	739	9	HMGCLL1.	No non-overlappi	ng genes wit	hin 50,000bp	
6	55,750,679	55,751,213	534	9	BMP5,	No non-overlappi	ng genes wit	hin 50,000bp	
6	55,958,353	55,958,660	307	9		AL589796.7	44,972		
6	56,220,112	56,220,521	409	10	COL21A1,			RP11- 323I14 A.1	28,765
6	56,354.296	56,354.746	450	9	COL21A1.			RP3-361I14.1	49.969
6	56,515,234	56,515.894	660	10	, DST,	No non-overlappi	ng genes wit	hin 50,000bp	.,
6	56,783,778	56,784,213	435	9	DST,	No non-overlappi	ng genes wit	hin 50,000bp	
6	56,815,631	56,816,044	413	10	DST,	RP11-472M19.3	27,904		
6	56,816,617	56,817,233	616	11	DST,	RP11-472M19.3	26,715		
6	56,824,564	56,824,957	393	11	DST,	RP11-472M19.3	18,991		
6	56,927,862	56,928,925	1,063	11	BEND6,	DST	499	U6	9,268

6	57,019,156	57,019,483	327	10	KIAA1586,	ZNF451	43,304	BEND6	19,059
6	57,249,645	57,250,019	374	11		PRIM2	37,543		
6	57,290,037	57,290,657	620	10	PRIM2,	No non-overlappi	ng genes wit	hin 50,000bp	
6	57,322,800	57,323,457	657	9	PRIM2,	No non-overlappi	ng genes wit	hin 50,000bp	
6	57,352,612	57,353,220	608	11	PRIM2,	No non-overlappi	ng genes wit	hin 50,000bp	
6	57,401,918	57,402,312	394	9	PRIM2,	No non-overlappi	ng genes wit	hin 50,000bp	
6	57,419,504	57,419,893	389	9	PRIM2,	No non-overlappi	ng genes wit	hin 50,000bp	
6	57,433,868	57,434,289	421	9	PRIM2,	No non-overlappi	ng genes wit	hin 50,000bp	
6	57,436,434	57,436,969	535	11	PRIM2,	No non-overlappi	ng genes wit	hin 50,000bp	
6	57,503,727	57,504,106	379	11	PRIM2,	No non-overlappi	ng genes wit	hin 50,000bp	
6	57,520,134	57,520,599	465	12	PRIM2,	No non-overlappi	ng genes wit	hin 50,000bp	
6	57,539,624	57,540,127	503	9	PRIM2,	No non-overlappi	ng genes wit	hin 50,000bp	
6	57.548.434	57.548.779	345	10	PRIM2.	No non-overlappi	na aenes wit	hin 50.000bp	
6	57.600.161	57.601.107	946	9	PRIM2.	No non-overlappi	na aenes wit	hin 50.000bp	
6	57,633,008	57,633,526	518	9				PRIM2	11,674
6	57.648.370	57.648.772	402	9				PRIM2	27.036
6	62 823 552	62 823 960	408	9	KHDRBS2	No non-overlappi	na aenes wit	hin 50 000bp	
6	64 019 653	64 020 006	353	9		RP11-184C23 4	21 453	RP11-184C23 3	24 057
6	64 039 258	64 039 617	359	9			21,100	LGSN	7 904
6	64 295 535	64 295 888	353	10		PTP4A1	43 991	RPI 7AP34	20 684
6	64 339 506	64 340 257	751	9	ΡΤΡ4Δ1	RPI 7AP34	22 128	RPI 9P18	43 434
6	64 341 410	64 341 783	373	11	PTP4Δ1	RPI 74P34	24,120	RPI 9P18	41 908
6	64 366 328	64 366 716	388	15	1 11 1 71,	PHE3	36 984		14 881
6	64 308 234	64 308 637	403	10		DHE3	5 063		14,001
6	64 716 126	64 716 482	356	9		No non-overlanni	na aenes wit	hin 50 000hn	
6	64 780 018	64 780 300	391			No non-overlappi	ng genes wit	hin 50,000bp	
6	64,760,016	64,005,120	400	9		No non-overlappi	ng genes wit	hin 50,000bp	
6	67 024 420	67 024 912	423	9		No non-overiappi	ng genes wit		10 226
6	60 401 546	60 402 059	513	9	DA12	DD11 261E10 1	26 540	AL390074.0	10,220
6	60 702 092	60 704 252	260	0	DAIS,	No non overlanni	30,340	03 hin 50 000hn	29,013
0	60,903,300	60,002,704	309	9	DAIS,	No non-overlappi	ng genes wit	hin 50,000bp	
0	70 624 022	70 624 279	395	9		No non-overlappi	ng genes wit	hin 50,000bp	
0	70,034,033	70,034,376	345	11	COLIGAI,	No non-overlappi	ng genes wit	hin 50,000bp	
6	70,001,177	70,062,295	1,118	9	COLIBAI,		ng genes wit	nin 50,000p	
6	71,135,745	71,130,075	330	10		FAMI 135A	43,753	hia 50 000ha	
0	71,179,302	71,100,300	970	12	FAIVITSDA,	No non-ovenappi	ng genes wit		20.045
6	71,050,780	71,051,280	000	9	B3GAT2,			SMAP1	22,345
0	71,721,906	71,723,102	1,194		DIMO1	No non-overlappi	ng genes wit	hin 50,000bp	
0	72,940,004	72,949,040	1,112	9	KINIST,	No non-ovenappi	ng genes wit	quuu,uuup	
0	73,300,220	73,300,701	232	9		AL 132073.17	22,143		
6	73,388,764	73,389,147	383	15	KCNQ5,	AL132073.17	22,081		
0	73,389,434	73,389,874	440	10		AL132073.17	23,351		45.040
σ	74,075,534	74,077,134	1,600	9	KHUCI,	308K22 10	12,147	KP11-398K22.9	15,813
6	74 140 614	74 140 060	346	0	OOEP	RP11_308K22.3	007	C6orf221	0 000
6	74,140,014	74,140,300	904	10			5 262	DD11 209K22 5	1,555
6	74 229 004	74 220 272	960	12	MTO1		1 640	NETT-390NZZ.3	1,032
6	74 287 020	74 297 721	711	10	FEF1A1	00	1,040	RP11-505D4 5	5 157
6	74 280 056	74 200 222	277	10			1 610	DD11_505D4.5	0,407 2 QEE
6	74 420 646	71 101 100	577	12			1,012	NETT-505F4.5	2,000
6	74 111 700	74 11 251	562	9			10 994		
6	71 167 155	74 462 020	200	9		SI C1745	19,004		
6	75 041 404	75 011 654	250	9	COI 1241	No non overlanni	+1,737	hin 50 000hn	
6	75 074 445	75 070 044	200	9	COL 12A 1	No non-ovenappi	ng genes wit		24 070
0	75,971,415	75,972,641	1,420	11	COLIZAI,				31,270
0	76,010,142	76,010,560	410	15	COX7A2,				0,009
0	10,023,113	10,023,543	370	9	TMEM30A				JO,8UJ
6	76 050 756	76 051 700	1 043	10		COX742	27 544		10 547
6	76 260 061	76 260 355	2043	01		RP11_47/1 11 2	5 726		10,047
6	76 376 040	76 277 220	294	9		INF -4/4 L .Z	5,700	DD11_4741 44 E	260
0	78 220 745	70,011,009	390	9		DD11 551 440 4	22 220	NF 11-4/4L11.5	208
0	10,220,115	10,229,119	404	- 11	111R1D,	No pop overland	33,376	hin EO OOOhn	
0 E	70,470,190	70 942 750	300	9			ng genes wit	nin 50,000bp	
0	70 040,000	70 045 100	450	20	гин г , рцір	DD11 47752 0	0,720		
0	19,044,227	19,040,400	1,1/3	13		DD11 46011 0	9,003		
O	00,000,046	00,001,346	100	9	Ceart E2	NF 11-40D11.2	43,195	hin EQ QQ0hr	
~		811 411 867	4/2	14	0.0011152	uno non-overianni	na aenes wit		

6	80,397,249	80,398,166	917	12	C6orf152,	No non-overlappi	ng genes wit	hin 50,000bp	
					SH3BGRL2,			1	
6	80,477,992	80,478,368	376	9	C6orf152,			SH3BGRL2	7,904
6	80,636,001	80,636,309	308	11		AL132875.22	42,680	RP1-92C4.1	13,933
6	80,747,866	80,748,145	279	9		ттк	22,931	RP3-357D13.3	16,911
6	80,770,440	80,770,764	324	9		ттк	312		
6	81,104,648	81,105,111	463	9	BCKDHB,			RPL17P25	35,340
6	82,356,817	82,357,172	355	9		5S_rRNA	31,464		
6	82,512,980	82,513,280	300	9	FAM46A,	SNORA70	17,180		
6	82,517,993	82,518,244	251	9	FAM46A,	SNORA70	12,216		
6	82,518,649	82,519,099	450	12	FAM46A,	SNORA70	11,361		
6	82,519,580	82,520,101	521	10		FAM46A	370		
6	82,520,213	82,520,530	317	10		FAM46A	1,003		
6	83,013,200	83,013,858	658	11	IBTK,	AL050333.18-1	36,324	RP3-492P14.2	16,574
6	83,013,915	83,015,133	1,218	9	IBTK,	AL050333.18-1	37,039	RP3-492P14.2	15,299
6	83,981,598	83,981,959	361	9	ME1,	PGM3	21,908	RWDD2A	18,623
6	84,278,148	84,278,798	650	9		PRSS35	192		
6	84,475,400	84,475,898	498	11	SNAP91,	No non-overlappi	ng genes wit	hin 50,000bp	
6	84,983,703	84,984,158	455	9	KIAA1009,	No non-overlappi	ng genes wit	hin 50,000bp	
6	84,993,659	84,993,991	332	11	KIAA1009,	No non-overlappi	ng genes wit	hin 50,000bp	
6	85,346,368	85,347,030	662	9		No non-overlappi	ng genes wit	hin 50,000bp	
6	85,529,672	85,530,022	350	10	TBX18,			AL035694.8	16,461
6	85,531,133	85,531,647	514	12		TBX18	460		
6	85,534,910	85,535,475	565	14		TBX18	4,237		
6	85,540,705	85,541,647	942	9		TBX18	10,032	AL035694.8	27,494
6	85,782,462	85,782,901	439	9		RP3-435K13.1	49,400		
6	86,043,557	86,044,092	535	9		RP11-30P6.1	8,421		
6	86,249,154	86,249,788	634	11	NT5E,			SNX14	22,145
6	86,359,664	86,360,860	1,196	11	SNX14,			SYNCRIP	18,459
6	86,409,242	86,409,930	688	11	SYNCRIP,	SNX14	48,894	RP11-33E24.1	16,399
6	86,410,171	86,410,730	559	11		SYNCRIP	425		
6	86,444,893	86,446,006	1,113	14	AL355615.12-1,	SNORD50	798		
6	87,702,503	87,702,785	282	9		HTR1E	1,190		
6	87,845,444	87,845,791	347	10		AL138827.16	3,885	CGA	6,144
6	87,921,451	87,922,445	994	9	ZNF292,	AL139274.17	32,421	RP11-393I2.2	17,360
6	88,174,549	88,175,278	729	12	C6orf165,			C6orf164	4,278
6	88,356,088	88,356,787	699	9	RARS2, ORC3L,	No non-overlappi	ng genes wit	hin 50,000bp	
6	88,468,207	88,469,007	800	14	AKIRIN2,	AL133211.9	18,345	ORC3L	34,319
6	89,547,167	89,547,580	413	10	RNGTT,	No non-overlappi	ng genes wit	hin 50,000bp	
6	89,729,642	89,730,551	909	9	RNGTT,	AL079342.17-1	414		
6	89,814,481	89,814,921	440	9		RP1-72A23.1	11,145	U2	15,017
6	89,885,277	89,885,968	691	10		RP11-63L7.3	758		
6	89,905,557	89,906,061	504	9		PM20D2	6,427		
6	89,912,445	89,913,017	572	9	PM20D2,	RP11-63L7.3	27,926	GABRR1	31,674
6	90,138,358	90,138,717	359	9	RRAGD,	AL138717.6	8,821		
6	90,152,15 <mark>2</mark>	90,152,721	569	9	RRAGD,	AL138717.6	22,615	RP11-11D8.3	35,816
6	90,175,865	90,176,548	683	9	RRAGD,	ANKRD6	23,068	RP11-11D8.3	11,989
6	90,179,015	90,179,921	906	9		RRAGD	301	RP11-11D8.3	8,616
6	90,265,252	90,265,555	303	10	ANKRD6,			AL136971.7-1	20,381
6	90,327,177	90,327,561	384	9	ANKRD6,	No non-overlappi	ng genes wit	hin 50,000bp	
6	90,585,383	90,585,769	386	12	MDN1,	AL353692.14-1	3,966	RP11-63K6.1	3,480
6	90,595,765	90,596,769	1,004	9	CASP8AP2,	MDN1	9,602	AL353692.14-1	5,930
6	90,982,375	90,982,815	440	11	BACH2,	No non-overlappi	ng genes wit	hin 50,000bp	
6	90,984,461	90,985,503	1,042	9	BACH2,	No non-overlappi	ng genes wit	hin 50,000bp	
6	90,985,542	90,986,552	1,010	9	BACH2,	No non-overlappi	ng genes wit	hin 50,000bp	
6	91,131,999	91,132,545	546	9		No non-overlappi	ng genes wit	hin 50,000bp	
6	91,135,303	91,135,874	571	9		No non-overlappi	ng genes wit	hin 50,000bp	
6	91,245,763	91,246,699	936	9				MAP3K7	35,375
6	91,353,470	91,353,933	463	10	MAP3K7,	No non-overlappi	ng genes wit	hin 50,000bp	
6	91,442,813	91,443,452	639	9		No non-overlappi	ng genes wit	hin 50,000bp	
6	92,143,141	92,143,476	335	10		No non-overlappi	ng genes wit	hin 50,000bp	
6	93,603,838	93,604,119	281	10				U3	46,735
6	93,803,304	93,804,265	961	9		No non-overlappi	ng genes wit	hin 50,000bp	
6	96,132,151	96,132,616	465	10	MANEA,	No non-overlappi	ng genes wit	hin 50,000bp	

6	97,076,128	97,076,709	581	9	KIAA0776,	FHL5	40,447		
6	97,248,561	97,249,322	761	9		RP11-304C16.3	20,995	RP11-304C16.2	39,822
6	97,479,226	97,479,699	473	14	KLHL32,	SRP euk arch	9,634		
6	97,769,740	97.770.413	673	10	C6orf167.	No non-overlappi	na aenes wit	hin 50.000bp	
6	97,837,214	97,838,020	806	11	C6orf167,	No non-overlappi	ng genes wit	hin 50,000bp	
6	99,323,846	99,324,140	294	10				RP11-67P15.1	10,719
6	99,328,682	99,329,205	523	9				RP11-67P15.1	5,654
6	99,388,660	99,389,001	341	9		POU3F2	300		
6	99,400,263	99,400,807	544	10				POU3F2	6,882
6	99.580.743	99.581.108	365	11		No non-overlappi	na aenes wit	hin 50.000bp	,
6	99.889.239	99.889.667	428	9	C6orf168.			COQ3	34.330
6	99,979,689	99,980,716	1,027	12	SFRS18,			USP45	6,195
6	100,069,249	100,069,581	332	10	USP45,	Y RNA	11,113	CCNC	27,404
6	100,070,668	100,071,048	380	9		USP45	639		
6	100,122,946	100,123,594	648	16	CCNC,	RP1-199J3.5	6,715		
6	100,167,881	100,169,586	1,705	9	PRDM13,	CCNC	44,470	Y RNA	27,248
6	100,556,445	100,556,798	353	10		MCHR2	7,625	_	
6	100,662,097	100,662,416	319	10		AL080285.6	28,342		
6	100,821,191	100,821,873	682	9		No non-overlappi	ng genes wit	hin 50,000bp	
6	101.015.164	101.015.523	359	10	SIM1.		00	ASCC3	47.268
6	101.018.855	101.019.512	657	10	SIM1.			ASCC3	43.279
6	103,355,717	103,356.073	356	9		No non-overlappi	ng genes wit	hin 50,000bp	, -
6	105,495,433	105,495,978	545	10		AL135911.16-1	338		
6	105,511,578	105,512,376	798	11	LIN28B,	AL135911.16-1	16,483		
6	105,734,053	105,734,462	409	9	POPDC3,			AL359709.15	1,255
6	105,957,220	105,957,650	430	10	PREP,	No non-overlappi	ng genes wit	hin 50,000bp	,
6	106.162.623	106.163.149	526	9	,	No non-overlappi	na aenes wit	hin 50.000bp	
6	106.549.195	106.549.822	627	11		No non-overlappi	na aenes wit	hin 50.000bp	
6	106,640,053	106,640,553	500	9		PRDM1	335	· · ·	
6	106,762,255	106,762,631	376	9	ATG5,	No non-overlappi	ng genes wit	hin 50,000bp	
6	106,879,756	106,880,563	807	9	ATG5,	AL133509.8	41,477	· · ·	
6	106,914,791	106,915,527	736	9	,	ATG5	34,403		
6	107.032.124	107.032.667	543	9		AIM1	33.756	Y RNA	22.627
6	107,194,263	107,194,765	502	9	QRSL1,	RP11-294H11.4	2,266	-	
6	107,541,918	107,542,462	544	10	BEND3,	AL355586.27-2	18,507	PDSS2	37,994
6	107,543,735	107,544,625	890	10		BEND3	569		
6	107,886,753	107,888,236	1,483	12	PDSS2,	SOBP	29,774		
6	108,083,205	108,083,522	317	9	SOBP,			SCML4	46,538
6	108,094,226	108,094,592	366	10	-			SOBP	5,031
6	108,275,978	108,276,527	549	12		SCML4	23,764	SEC63	21,688
6	108,345,498	108,345,864	366	10	SEC63,	RP1-191J18.2	13,833		
6	108,499,510	108,500,129	619	9	OSTM1,	No non-overlappi	ng genes wit	hin 50,000bp	
6	108,688,731	108,689,678	947	10	SNX3,			5S_rRNA	8,327
6	108,953,815	108,954,402	587	9				LACE1	2,873
6	108,986,367	108,987,486	1,119	11		FOXO3	233		
6	108,987,495	108,987,750	255	9	FOXO3,			LACE1	36,553
6	108,989,826	108,990,907	1,081	12	FOXO3,			LACE1	38,884
6	109,105,366	109,105,725	359	10	FOXO3,	No non-overlappi	ng genes wit	hin 50,000bp	
6	109,136,469	109,136,814	345	9		Z95118.1	42,738	FOXO3	23,805
6	109,149,382	109,149,753	371	10		Z95118.1	29,799	FOXO3	36,718
6	109,165,672	109,166,360	688	9		Z95118.1	13,192	ZNF259P	47,225
6	109,202,314	109,202,766	452	9				Z95118.1	5,300
6	109,210,096	109,211,017	921	9				ZNF259P	2,568
6	109,263,083	109,263,531	448	9		ARMC2	12,781	RP11-249L21.2	20,765
6	109,375,174	109,375,710	536	11	ARMC2,	RP11-249L21.4	39,405	SESN1	38,630
6	109,809,939	109,810,457	518	14	CD164,			PPIL6	10,170
6	109,810,787	109,811,370	583	9		CD164	447	PPIL6	9,257
6	109,869,003	109,869,644	641	9	PPIL6, SMPD2,			MICAL1	2,317
6	109,883,775	109,884,136	361	9	MICAL1,			ZBTB24	6,276
6	110,114,417	110,114,726	309	9	AKD2,	FIG4	4,435		
6	110,118,707	110,119,717	1,010	11	AKD2, FIG4,	No non-overlappi	ng genes wit	hin 50,000bp	
6	110,265,579	110,265,964	385	9				FIG4	12,252
6	110,791,724	110,792,338	614	9		C6orf186	5,556		
6	111,241,987	111,242,552	565	10	CDC2L6,	SNORA40	33,890		

6	111,242,634	111,243,269	635	10	CDC2L6,	SNORA40	33,173		
6	111,243,357	111,244,384	1,027	13	CDC2L6,	SNORA40	32,058		
6	111,303,275	111,304,580	1,305	12	AMD1,	RP11-397G5.2	46,882	Z84480.1-1	16,232
6	111,307,018	111,307,401	383	10	AMD1,	RP11-397G5.2	44,061	Z84480.1-1	19,975
6	111.909.976	111.910.321	345	9	REV3L.			RP3-415N12.1	12,566
6	111,911,118	111,911,646	528	10	REV3L,			RP3-415N12.1	11,241
6	111,911,810	111,912,303	493	12		REV3L	685		
6	111,980,137	111,980,642	505	13				TRAF3IP2	6,194
6	112,004,379	112,004,628	249	10	TRAF3IP2,	No non-overlappi	ng genes wit	hin 50,000bp	
6	112,018,878	112,019,787	909	11	TRAF3IP2,	No non-overlappi	ng genes wit	hin 50,000bp	
6	112,033,251	112,034,134	883	10	TRAF3IP2,			Z97989.1	40,091
6	112,153,803	112,154,132	329	10	FYN,	No non-overlappi	ng genes wit	hin 50,000bp	
6	112,210,375	112,210,762	387	9	FYN,	No non-overlappi	ng genes wit	hin 50,000bp	
6	112,269,894	112,270,291	397	9	FYN,	No non-overlappi	ng genes wit	hin 50,000bp	
6	112,299,624	112,300,630	1,006	9	FYN,	No non-overlappi	ng genes wit	hin 50,000bp	
6	112,301,074	112,301,915	841	9	FYN,	No non-overlappi	ng genes wit	hin 50,000bp	
6	112,342,313	112,342,693	380	9		FYN	40,993		
6	112,385,621	112,386,089	468	12		No non-overlappi	ng genes wit	hin 50,000bp	
6	112,407,976	112,408,361	385	9		No non-overlappi	ng genes wit	hin 50,000bp	
6	112,424,865	112,425,282	417	10		No non-overlappi	ng genes wit	hin 50,000bp	
6	112,471,430	112,471,963	533	13		WISP3	10,008	TUBE1	26,712
6	112,494,691	112,495,092	401	9	WISP3,			TUBE1	3,583
6	112,515,072	112,515,713	641	9	TUBE1,			WISP3	16,208
					C6orf225,				
6	112,681,730	112,682,395	665	14	LAMA4,	No non-overlappi	ng genes wit	hin 50,000bp	
6	112,899,035	112,899,362	327	9		AL357514.19	5,259		
6	114,284,598	114,285,282	684	10	MARCKS,	AL671966.1-2	46,124	RPL30P8	17,097
6	114,286,201	114,287,355	1,154	13	MARCKS,	AL671967.1	44,640	RPL30P8	18,700
6	114,397,596	114,398,351	755	11	HDAC2,			AL671967.1	48,097
6	114,398,939	114,399,723	784	9	HDAC2,	No non availanti		RP11-446G24.4	47,755
6	115,083,500	115,083,770	210	10			ng genes wit		22 519
6	116,707,003	116,700,111	1,040	10	ISPILI,	AL050551.11-1	20,092		55,510
6	116 959 880	116,075,200	426	3 Q	BET3I		38 970	FAM26E	13 479
U	110,000,000	110,000,000	420	Ŭ	FAM26D.		00,070	1711202	10,470
6	116,998,579	116,999,539	960	12	RWDD1,	BET3L	25,209	FAM26D	11,855
6	117,043,600	117,044,574	974	9	RSPH4A,	AL132795.12	9,326		
6	117,122,685	117,123,039	354	9	KPNA5,	ZUFSP	26,035		
6	117,910,250	117,910,723	473	10	DCBLD1,	U6	24,556	RP1-92C8.2	49,952
6	117,910,797	117,911,647	850	9	DCBLD1,	U6	25,103		
6	118,029,729	118,030,794	1,065	11	GOPC,	RP11-117013.2	30,768	DCBLD1	32,020
6	118,347,594	118,347,919	325	10	SLC35F1,	No non-overlappi	ng genes wit	hin 50,000bp	
6	118,791,951	118,792,232	281	10				SLC35F1	46,430
6	119,045,316	119,046,081	765	9	C6orf204,			RP3-509L4.1	27,826
6	119,078,878	119,079,920	1,042	9	C6orf204,	No non-overlappi	ng genes wit	hin 50,000bp	
6	119,204,465	119,204,771	306	10		RP11-	5,909		
6	110 000 007	110 220 500	050	10		A.1	00 044	MCMO	10 704
6	110 110 570	110 440 000	1 651	10	E0M194A	hea_mir 510h	20,311		12,731
6	110 505 120	110 505 159	1,001	9	FAM184A	RP3-354NI10 1	16 702	ΜΑΝΊΔΊ	35 510
6	119,505,120	119,505,450	451	Q1	ΜΔΝ1Δ1	N 5-554N 19.1	10,703	RP3-354N10 3	31 451
6	119 644 282	119 644 559	277	9	MAN1A1	RP3-354N19.3	11 704	141 0 0041410.0	01,401
6	121 049 336	121 049 721	385	12	5S rRNA	No non-overlappi	na aenes wit	hin 50 000hn	
6	121,697 049	121,697 927	878	12	C6orf170	U6	19 272	Y RNA	43 715
6	121,763,370	121,764,004	634	11		AL139098.15-1	7,383		
6	122,212,203	122,212,719	516	9			.,	RP3-438G17.1	8,377
6	122,744,427	122,744,703	276	9		HSF2	17,791		.,
6	122,761,965	122,762,787	822	10	HSF2,			SERINC1	43,408
6	123,151,993	123,152,917	924	10	SMPDL3A,			FABP7	5,078
6	123,193,839	123,194,193	354	9				SMPDL3A	21,278
6	124,166,755	124,167,349	594	9	TCBA1,	No non-overlappi	ng genes wit	hin 50,000bp	
6	124,609,737	124,610,193	456	9	TCBA1,	No non-overlappi	ng genes wit	hin 50,000bp	
6	124,913,190	124,913,500	310	9	TCBA1,	No non-overlappi	ng genes wit	hin 50,000bp	
6	125,153,956	125,154,294	338	9	TCBA1,	No non-overlappi	ng genes wit	hin 50,000bp	
6	125,244,979	125,245,441	462	9		No non-overlappi	ng genes wit	hin 50,000bp	

6	125,408,767	125,409,422	655	9	RNF217,	No non-overlappi	ng genes wit	hin 50,000bp	
6	125,462,146	125,462,945	799	9				RNF217	15,583
6	125,516,350	125,517,161	811	11	TPD52L1,	No non-overlappi	ng genes wit	hin 50,000bp	
6	125,664,449	125,665,356	907	9	HDDC2.	F F	55	TPD52L1	37,197
6	125 725 593	125 727 062	1 469	9	,	No non-overlappi	na aenes wit	hin 50 000bp	
6	125 874 604	125 874 933	329	12		No non-overlappi	ng genes wit	hin 50 000bp	
6	125,014,004	125,014,000	480	9		No non-overlappi	ng genes wit	hin 50,000bp	
6	125,044,303	125,047,002	470	12		No non overlappi	ng gonos wit	hin 50,000bp	
6	125,947,352	125,947,022	4/0	12				1111 30,000bp	
0	120,072,729	120,073,035	1,100	9			30,000		
6	126,111,747	126,112,366	619	y	HEY2,	ESNA1	31,634		
6	126,112,419	126,113,484	1,065	9	HEY2,	ESNA1	30,516		
6	126,143,028	126,144,223	1,195	10	ESNA1,			HEY2	18,920
6	126,151,995	126,153,756	1,761	9	ESNA1,			HEY2	27,887
6	126,154,336	126,154,713	377	9	ESNA1,			HEY2	30,228
6	126,258,331	126,258,764	433	11	ESNA1,			7SK	20,010
6	126,272,046	126,272,359	313	10	ESNA1,	HINT3	47,205	7SK	33,725
6	126 276 613	126 277 079	466	9	ESNA1	HINT3	42 485	7SK	38 292
6	126 319 260	126 320 639	1 379	g	HINT3	TRMT11	28,630	AL 035689 26	22 080
6	126,349,053	126,349,685	632	11	TPMT11	AL 035680 26	6 280	HINT3	5 997
6	126,349,033	126,349,003	220	12		AL035009.20	7 019		6 725
0	120,349,791	120,350,150	339	13		AL03009.20	7,010		0,735
0	126,426,411	126,427,295	884	11					24,296
6	127,066,003	127,066,402	399	9				RP1-179E13.1	19,324
6	127,705,723	127,706,595	872	9	ECHDC1,	AL109939.13-2	12,044		
6	127,879,180	127,879,941	761	9	AL096711.9,	C6orf174	40,628		
6	128,335,722	128,336,184	462	9	PTPRK,	No non-overlappi	ng genes wit	hin 50,000bp	
6	128,853,178	128,853,560	382	9	PTPRK,	No non-overlappi	ng genes wit	hin 50,000bp	
6	128,882,487	128,883,105	618	10	PTPRK,	No non-overlappi	ng genes wit	hin 50,000bp	
6	129.007.841	129.008.132	291	9	,	RP1-6P5.2	5.350		
6	129 231 745	129 232 152	407	9		LAMA2	13 827		
6	120,037,765	120,038,515	750	9		2,	10,021		455
6	120,007,700	120,000,010	297	0	C6orf101	DD11 17407 3	20.240	DD11 17407 2	400
0	130,212,249	130,212,030	307	9		RFTI-17407.3	29,240	KF11-17407.2	47,740
6	130,728,039	130,728,776	131	14	SAMD3,	No non-overlappi	ng genes wit	nin 50,000p	
•	404 000 057	404 000 000	700	0	KIAA 1913,	N		him 50 000hm	
6	131,296,257	131,296,966	709	9	EPB41L2,	No non-overlappi	ng genes wit		
6	131,331,303	131,331,572	269	y	EPB41L2,	No non-overlappi	ng genes wit	nin 50,000bp	
6	131,562,331	131,562,797	466	9	AKAP7,	RP1-209B5.2	14,012		
6	131,656,061	131,656,695	634	9				AKAP7	9,695
6	131,990,783	131,991,352	569	19	CRSP3,	ENPP3	8,783		
6	132,300,754	132,301,260	506	10				CTGF	9,754
6	132,312,938	132,313,908	970	11	CTGF,	No non-overlappi	ng genes wit	hin 50,000bp	
6	132,313,930	132,314,322	392	10	CTGF,	No non-overlappi	ng genes wit	hin 50,000bp	
6	132,698,289	132,698,626	337	11	MOXD1.	No non-overlappi	na aenes wit	hin 50.000bp	
6	132 764 122	132 765 130	1 008	9	MOXD1	No non-overlappi	na aenes wit	hin 50 000bp	
6	132 873 821	132 874 368	547	۵ ۵	STX7			RP11-205F4 4	7 204
6	102,070,021	102,074,000	470	9	0177,	00012	050	111-23014.4	1,294
0	100,170,039	100,170,518	4/9	10	DDC40	RP312	000		
Ø	133,176,853	133,177,779	926	12	RP312,	SNUKU101	360		0.0
6	133,523,521	133,523,843	322	11				кР11-203B4.1	9,872
6	133,603,891	133,604,593	702	11	EYA4,	AL121959.15	31,043		
6	133,635,489	133,635,973	484	18	EYA4,	No non-overlappi	ng genes wit	hin 50,000bp	
					AL121959.15,				
6	134,104,365	134,104,728	363	11		No non-overlappi	ng genes wit	hin 50,000bp	
6	134,200,464	134,200,956	492	12		No non-overlappi	ng genes wit	hin 50,000bp	
6	134,315,148	134,316,691	1,543	9	TBPL1,			SLC2A12	33,273
6	134,474,012	134,474,362	350	12				HMGA1L7	3,064
6	134,799.377	134,799.677	300	11		AL096815.18	42.646		
6	135,416,876	135 418 300	1.424	9	HBS1L.	No non-overlappi	ng genes wit	hin 50.000bp	
6	135 545 640	135 545 947	307	10	MYB	No non-overlappi	ng genes wit	hin 50 000bp	
6	135 5/6 555	135 5/6 076	121	12	MYB	No non-overlappi	ng genes wit	hin 50,000bp	
0 e	105,040,000	125 000 754	421	10				nin 30,000bp	
0	130,000,115	100,000,701	0.00	10			22,075	hin EO OOOka	
Ø	130,214,300	130,214,620	320	12		No non-overlappi	ng genes wit		
6	130,4/0,639	130,477,021	382	15	PDE/B,	No non-overlappi	ng genes wit		
6	136,612,794	136,613,786	992	13	FAM54A,			BCLAF1	7,633
6	136,652,230	136,653,108	878	14	BCLAF1,	RP3-406A7.1	27,718		
6	136,768,435	136,768,683	248	10	MAP7,	RP3-406A7.5	14,002	RP3-406A7.3	41,142
6	136.971.002	136.971.452	450	10	MAP3K5,	5S rRNA	21,619		

6	137,153,953	137,154,637	684	14	MAP3K5,	PEX7	30,779		
6	137,185,163	137,185,605	442	10	PEX7,	MAP3K5	29,814	SNORA27	32,924
6	137,520,845	137,521,157	312	9	IL22RA2,			IFNGR1	39,165
6	137,666,941	137,667,264	323	10		No non-overlappi	ng genes wit	hin 50,000bp	
6	137,671,973	137,672,408	435	10		No non-overlappi	ng genes wit	hin 50,000bp	
6	138,060,259	138,060,757	498	9				RP11-95M15.2	7,496
6	138,229,832	138,230,319	487	9	TNFAIP3,	No non-overlappi	ng genes wit	hin 50,000bp	
6	138,240,336	138,240,679	343	10	TNFAIP3,	No non-overlappi	ng genes wit	hin 50,000bp	
6	138,345,157	138,345,724	567	9		RP11-240M16.2	12,376		
6	138,387,708	138,388,085	377	11				RP11-240M16.2	28,731
6	138,460,996	138,461,528	532	9	PERP,	No non-overlappi	ng genes wit	hin 50,000bp	
6	138,472,677	138,473,031	354	13		PERP	2,397		
6	138,782,064	138,782,848	784	9				NHSL1	2,028
6	138,934,899	138,935,644	745	11		NHSL1	158		
6	139,054,335	139,055,836	1,501	11		RP11-390P2.2	40,532		
6	139,333,908	139,334,398	490	9	REPS1,	No non-overlappi	ng genes wit	hin 50,000bp	
6	139,391,296	139,391,814	518	10	C6orf115,	REPS1	40,200		
6	139,498,570	139,499,389	819	9	HECA,	No non-overlappi	ng genes wit	hin 50,000bp	
6	139,737,181	139,737,656	475	16	CITED2,			RP11-12A2.1	34,771
6	139,737,836	139,739,130	1,294	14		CITED2	358		
6	139,859,351	139,859,916	565	9		No non-overlappi	ng genes wit	hin 50,000bp	
6	140,244,514	140,245,104	590	9		No non-overlappi	ng genes wit	hin 50,000bp	
6	140,412,924	140,413,502	578	9		No non-overlappi	ng genes wit	hin 50,000bp	
6	141,084,835	141,085,303	468	9		RP11-65C6.1	39,056		
6	142,509,720	142,510,085	365	1/		VIA1	2		
6	143,055,517	143,056,339	822	9		No non-overlappi	ng genes wit	hin 50,000bp	
6	143,303,176	143,303,769	593	y Q	HIVEP2,	No non-overlappi	ng genes wit	nin 50,000bp	
6	143,308,986	143,309,641	655	9		HIVEP2	955		
6	143,309,767	143,310,174	407	10		HIVEP2	1,736		
6	143,310,310	143,310,708	398	9	4104	HIVEP2	2,279		10.007
6	143,642,390	143,642,693	303	10	AIG1,	RP1-95L4.3	47,412	RP1-95L4.2	18,907
6	143,686,526	143,687,114	588	9	AIG1,	RP1-95L4.3	2,991		
6	143,813,377	143,814,119	742	13	ADATZ, PEX3,			55_IRNA	636
6	143,873,731	143,874,501	830	12	FUCAZ,	FUCA2	1.665	RP1-20N2.4	19,534
0	143,070,221	143,070,313	292	9		FUCA2	1,000		45.072
6	143,900,170	143,900,441	599	10		No pop ovorlappi	25,014	hin 50 000hn	45,975
6	144,100,310	144,100,090	314	10		No non-overlappi	ng genes wit	hin 50,000bp	
6	144 128 044	144 128 465	421	10	PHACTR2	No non-overlappi	ng genes wit	hin 50,000bp	
6	144 205 404	144 206 756	1 352	11	I TV/1	FAM164B	20 561		11 390
6	144 212 428	144 212 955	527	9	LTV1,	FAM164B	14 362		18 414
6	144 376 189	144 376 671	482	11	LIVI,		4 955		10,414
6	144 457 907	144 458 595	688	10	SE3B5	RP1-197I 1 1	40.685		
6	144 579 105	144 579 668	563	26		RP1-83M4 2	15 310	STX11	27 911
6	144.628.898	144.629 271	373	10		RP1-91J24 1	8 445		
6	145,260,159	145,260.632	473	.0				UTRN	44.300
6	145,776,759	145,777,285	526	9				U1	48,782
6	146,176,753	146,177.260	507	10	FBXO30.	AL023806.1	22.241	SHPRH	49.892
6	146,177.397	146,178,096	699	9	FBXO30,	AL023806.1	22.885	SHPRH	49.056
6	146,718,457	146,718,742	285	9	GRM1,			RP1-69B13.2	9,009
6	147,220,249	147,220,997	748	14				C6orf103	41,958
6	147,276,647	147,277,170	523	9		AL138916.14-2	14,349		
6	147,871,274	147,871,946	672	9	SAMD5,	No non-overlappi	ng genes wit	hin 50,000bp	
6	147,924,513	147,924,939	426	9	SAMD5,	No non-overlappi	ng genes wit	hin 50,000bp	
6	148,540,382	148,540,809	427	9		No non-overlappi	ng genes wit	hin 50,000bp	
6	148,705,082	148,705,667	585	9	SASH1,	No non-overlappi	ng genes wit	hin 50,000bp	
6	148,784,877	148,785,184	307	12	SASH1,	No non-overlappi	ng genes wit	hin 50,000bp	
6	148,922,651	148,923,466	815	10				RP3-323M4.3	6,741
6			340	11		RP3-323M4.3	10,588	SASH1	26,194
	148,941,071	148,941,420	549	11					
6	148,941,071 149,153,593	148,941,420 149,153,947	354	10	UST,	No non-overlappi	ng genes wit	hin 50,000bp	
6 6	148,941,071 149,153,593 149,335,293	148,941,420 149,153,947 149,335,647	354 354 354	10 9	UST, UST,	No non-overlappi	ng genes wit	hin 50,000bp AL590485.7	23,323
6 6 6	148,941,071 149,153,593 149,335,293 149,374,791	148,941,420 149,153,947 149,335,647 149,375,132	354 354 354 341	10 9 9	UST, UST, UST,	No non-overlappi No non-overlappi	ng genes wit ng genes wit	hin 50,000bp AL590485.7 hin 50,000bp	23,323
6 6 6	148,941,071 149,153,593 149,335,293 149,374,791 149,489,207	148,941,420 149,153,947 149,335,647 149,375,132 149,489,524	354 354 354 341 317	10 10 9 9 9	UST, UST, UST,	No non-overlappi No non-overlappi RP11-365H23.1	ng genes wit ng genes wit 13,706	hin 50,000bp AL590485.7 hin 50,000bp UST	23,323 49,389

6	149,855,913	149,856,465	552	9		RP1-281H8.3	795		
6	149,928,208	149,928,759	551	10		C6orf72	475		
6	150,011,155	150,011,851	696	9	KATNA1,			LATS1	11,893
6	150,109,018	150,109,634	616	10	NUP43,	PCMT1	2,639		i
6	150,112,292	150,113,306	1.014	9	PCMT1.	NUP43	2.785		
6	150,326,364	150,327,291	927	13	ULBP1,	RP11-472G23.3	13,009	RP11-244K5.7	10,832
6	150,511,853	150,512,259	406	9	PPP1R14C,	AL355497.14-3	15,154		
6	150,558,540	150.558.914	374	9	PPP1R14C.			AL355497.14-3	31.025
6	150.615.778	150.616.156	378	9	,			PPP1R14C	2.596
6	150 766 200	150 766 673	473	11	IYD	RP3-422F24 2	18 251		
6	150 963 192	150 964 087	895	10	PI FKHG1	No non-overlappi	na aenes wit	hin 50 000hn	
6	151 572 274	151 572 605	331	11	,		ing gonee int	AI 451072 14	8 001
6	151 603 829	151 604 696	867	10	ΔΚΔΡ12	AL 356535 19	15 054	AL 451072 14	39 556
6	151 752 325	151 753 140	815	10	78TB2	Y RNA	11 308		14 542
6	151,752,020	151,753,140	276	10	ZBTB2, ZBTB2	Y RNA	12 332	RMND1	14,342
6	151 814 667	151 815 587	020	10	PMND1	PP11_351K16 /	37 786		14,147
0	131,014,007	131,013,307	320		C6orf211	NI 11-551N10.4	57,700		
6	151 857 206	151 857 563	357	10	C6orf97	RMND1	42 107	C6orf211	24 281
6	152 743 687	152 744 172	485	10	SYNE1	5S rRNA	28 931	00011211	24,201
6	152,740,007	152,744,172	346	10	SVNE1		20,001	59 rDNA	17 600
6	152,730,312	152,791,230	444	9	STNLT,	No non overlanni	na aonos wit	bin 50 000hn	17,030
6	152,915,395	152,915,059	220	9			ng genes wit		4 120
6	153,345,722	153,340,031	1 026	12	FBXO5				4,139
0	153,346,069	153,347,095	1,020	10	FBAUS,				3,095
0	153,365,485	153,305,787	302	9	MIRFIL,	DD11 400M0 0	47.004	RSGI7	7,763
6	154,863,632	154,864,439	807	9	MAGI1,	RP11-486M3.2	47,904	DD11 400M0 0	4 000
6	154,917,728	154,918,125	397	9				RP11-486M3.2	4,660
6	154,978,398	154,978,836	438	10				RPS4P8	38,493
6	155,336,744	155,337,655	911	9	T 1 4 4 40	No non-overlappi	ng genes wit	nin 50,000bp	
6	155,564,361	155,564,758	397	9	TIAM2,	No non-overlappi	ng genes wit	nin 50,000bp	
6	155,586,909	155,587,295	386	9	TIAM2,	CLDN20	39,544	IFB1M	33,193
6	155,677,642	155,677,928	286	10		TFB1M	331		
6	156,980,185	156,980,566	381	14		RP11-230C9.1	44,310		
6	157,083,076	157,083,416	340	9		No non-overlappi	ng genes wit	nin 50,000bp	
6	157,094,301	157,094,673	372	11		ARID1B	46,083		
6	157,232,804	157,233,421	617	9	ARID1B,	No non-overlappi	ng genes wit	nin 50,000bp	
6	157,340,601	157,341,124	523	9	ARID1B,			RP11-2J18.1	706
6	157,384,019	157,384,920	901	14	ARID1B,			RP11-2J18.1	44,124
6	157,473,978	157,474,520	542	10	ARID1B,	No non-overlappi	ng genes wit	nin 50,000bp	
6	157,521,709	157,522,061	352	10	ARID1B,	No non-overlappi	ng genes wit	nin 50,000bp	
6	157,655,522	157,656,103	581	9	C6orf35,	RP11-96F3.2	14,491		
6	157,663,863	157,664,832	969	11	C6orf35,	RP11-96F3.2	22,832	AL390955.20	42,173
6	157,664,938	157,665,544	606	9		C6orf35	157		
6	157,720,613	157,721,220	607	9		ZDHHC14	1,325		
6	158,097,688	158,098,502	814	9		AL133510.13	44,578		
6	158,098,623	158,099,010	387	9		AL133510.13	45,513		
6	158,249,684	158,249,970	286	9	SNX9,	RP3-403L10.2	15,452		
6	158,323,032	158,324,242	1,210	9	SYNJ2,			SNX9	36,935
6	158,349,825	158,350,203	378	9	SYNJ2,	No non-overlappi	ng genes wit	hin 50,000bp	
6	158,367,148	158,367,716	568	13	SYNJ2,	No non-overlappi	ng genes wit	hin 50,000bp	
6	158,381,073	158,381,458	385	10	SYNJ2,	No non-overlappi	ng genes wit	hin 50,000bp	
6	158,413,085	158,413,566	481	11	SYNJ2,			SERAC1	36,971
6	158,508,695	158,510,022	1,327	9	SERAC1,	AL590703.15	5,982		
					GTF2H5,				
6	158,583,534	158,583,896	362	9	RP1-274L14.2,	No non-overlappi	ng genes wit	hin 50,000bp	
6	158,876,992	158,877,997	1,005	10	TMEM181,	RP11-107N4.1	19,743	TULP4	24,150
6	158,979,899	158,980,245	346	10	DYNLT1,			TMEM181	3,451
6	159,158,949	159,159,308	359	11	VIL2,			OSTCL	22,840
6	159,194,301	159,194,974	673	11	OSTCL,	C6orf99	15,985		
6	159,210.940	159,211,292	352	10	C6orf99,	OSTCL	12,286		
6	159,340.342	159,341.453	1,111	13	RSPH3,		, , , , ,	TAGAP	34.564
6	159,421.229	159,421.888	659	9	- ,	TAGAP	35.057		. ,
6	159.498.988	159,499,405	417	9		FNDC1	11.012		
6	159,511.207	159,511.696	489	10	FNDC1,	No non-overlappi	ng genes wit	hin 50,000bp	
0	, ,=	,,				Nie nen eurodenni	3.0		
6	159,593,956	159,594,606	650	9	FNDC1,	No non-overlappi	ng genes wit	nin 50,000bp	
6 6	159,593,956 160,099,317	159,594,606 160,100,091	650 774	9	FNDC1,	ACAT2	ng genes wit 2,952	NIN 50,000bp WTAP	1,978

6	160,103,886	160,104,307	421	10	ACAT2,			WTAP	6,547
6	160,130,366	160,130,885	519	10	TCP1,	MRPL18	603		
6	160,131,152	160,131,917	765	9	MRPL18,	TCP1	427		
6	160,479,332	160,479,673	341	9	SLC22A1,			RP11-317M22.1	24,888
6	160,876,234	160,876,740	506	9	LPA,	LPAL2	24,088		
6	161,271,282	161,272,268	986	9				RP11-235G24.2	16,622
6	161,333,241	161,333,899	658	9	MAP3K4,	No non-overlappi	ng genes wit	hin 50,000bp	
6	161,585,779	161,586,063	284	9	AGPAT4,	No non-overlappi	ng genes wit	hin 50,000bp	
6	161,614,876	161,615,573	697	11	AGPAT4,	No non-overlappi	ng genes wit	hin 50,000bp	
6	161,780,109	161.780.446	337	12	PARK2.	No non-overlappi	na aenes wit	hin 50.000bp	
6	161.839.315	161.839.649	334	9	PARK2.	No non-overlappi	na aenes wit	hin 50.000bp	
6	161.869.243	161.869.592	349	9	PARK2.	No non-overlappi	na aenes wit	hin 50.000bp	
6	162 902 322	162 902 748	426	9	PARK2	AP000888.3	7 218		
6	162 943 154	162 943 537	383	9	PARK2		.,	AP000888 3	32 404
6	163 854 750	163 855 244	494	9	QKI	No non-overlappi	na aenes wit	hin 50 000bp	,
6	164 000 069	164 000 346	277	9	x ,	No non-overlappi	na aenes wit	hin 50 000bp	
6	165 780 456	165 780 911	455	9			ng gonoo mi	5S rRNA	37 301
6	165 997 021	165 998 501	1 480	9	T DE TOA,	AI 121789 38	080		57,501
6	166 007 558	166 008 405	8/7	9		AL 121780 38	11 526	116	43 308
6	166 207 373	166 207 806	/122	0		No non overlanni	na aonos wit	bin 50 000hn	43,300
6	166 715 205	166 715 800		10			30 277	DDS6KA2	27.044
6	166 924 477	166 925 001	500	10	DREAKAD	311201	39,211	haa mir 1012	17 021
6	100,024,477	100,023,001	620	10	RESURAZ,		26.640	115a-1111-1913	17,031
0	167,694,720	100,957,215	020	9	RPSONAZ,	RP3-421A4.2	30,040	DD2 266N22 4	2 1 9 0
0	107,004,720	107,000,420	705	10				RP3-300IN23.4	3,109
0	168,391,216	168,391,769	553	10	0140.00			AL606970.12	38,007
6	168,662,051	168,663,001	950	9	SMOC2,	No non-overlappi	ng genes wit		
6	169,037,057	169,037,424	367	10		No non-overlappi	ng genes wit	hin 50,000bp	
6	169,212,449	169,212,969	520	9		No non-overlappi	ng genes wit	hin 50,000bp	10.071
6	169,796,511	169,796,955	444	9	WDR27,	C6orf120	47,227	PHF10	48,974
6	169,843,798	169,844,184	386	15	WDR27,			PHF10	1,745
-					C60ff120,	511576		<u></u>	
6	169,893,126	169,894,292	1,166	9		PHF10	27,100	C60ff120	44,800
6	160 072 619	160.074.004	476	10	10123,	No non overlenni	na aonoo wit	hin EQ QQQhn	
0	109,973,010	109,974,094	4/0	10		No non-ovenappi	ng genes wit		
0	170,404,770	170,405,105	307	10	FAIVI I ZUB,	DLLI	23,154	DOMD1	4 996
0	170,000,001	170,001,240	307	10		тор	1 104	POIVIDI	4,000
0	170,703,766	170,704,260	492	10			1,104		44.054
0	170,735,520	170,730,153	033	9		PSIVIB I	31,206	IBP	11,001
7	2,103,795	2,104,107	312	10		NUDT4	ng genes wit		1.000
7	2,239,023	2,239,448	425	9		NUDIT	8,935	FISJZ	1,006
/	3,922,252	3,922,085	433	9	SDK1,	No non-ovenappi	ng genes wit	nin 50,000p	
/	4,647,697	4,648,258	561	9	50)////	FUXK1	40,198	1007005440	00.040
/	4,728,588	4,728,948	360	9	FUXK1,			AC072054.10	32,848
7	5,425,202	5,425,444	242	11	INRC18B,			AC093620.3	1,045
7	6,277,168	6,277,596	428	10	CYTH3,	No non-overlappi	ng genes wit	nin 50,000bp	
7	6,277,878	6,278,258	380	9	CYTH3,	No non-overlappi	ng genes wit	hin 50,000bp	
7	6,354,976	6,355,425	449	9	AC009412.5,	RAC1	25,226		
7	6,712,894	6,713,569	675	9	ZNF12,	PMS2CL	2,711	1000-	
7	20,790,978	20,791,399	421	9	SP8,	AC005251.1-4	42,045	ABCB5	27,821
7	22,565,891	22,566,361	470	9	AC002480.1-1,	AC002480.1-2	47,809		
7	23,187,859	23,188,400	541	10	AC005082.3,			KLHL7	6,298
_					NUPL2,				
7	23,279,340	23,279,862	522	11	GPNMB,	C7orf30	25,603	IGF2BP3	36,492
7	23,283,192	23,283,829	637	9				GPNMB	1,944
7	23,476,396	23,476,980	584	12	IGF2BP3,			Y_RNA	20,956
7	23,537,707	23,538,321	614	10	TRA2A,	AC023105.7-1	467		
7	24,290,366	24,290,745	379	9	NPY,	AC004485.2-2	22,508		
7	26,206,636	26,207,356	720	11	HNRPA2B1,	CBX3	268		
7	26,485,819	26,486,202	383	9	AC004540.1,	No non-overlappi	ng genes wit	hin 50,000bp	
7	27,668,477	27,669,359	882	10	HIBADH,	No non-overlappi	ng genes wit	hin 50,000bp	
7	28,416,752	28,417,579	827	9	CREB5,	No non-overlappi	ng genes wit	hin 50,000bp	
7	28,962,488	28,963,064	576	10	AC005013.3,			CPVL	38,708
7	29,041,455	29,041,867	412	9	CPVL,	No non-overlappi	ng genes wit	hin 50,000bp	
7	30,032,434	30,033,265	831	9	FKBP14,	PLEKHA8	1,301		
7	30,511,016	30,511,612	596	9		GGCT	39		

7	32,947,778	32,948,041	263	9	AVL9, RP9P,	FKBP9	15,536		
					AC018648.5,				
7	32,963,601	32,964,018	417	12	AVL9, FKBP9,	RP9P	14,294	AC083863.2	44,079
7	39,572,073	39,573,176	1,103	9	C7orf36,	No non-overlappi	ng genes wit	hin 50,000bp	
7	39,739,963	39,740,322	359	10		AC004987.2-1	34,144	RALA	25,723
7	39,955,049	39,955,896	847	9		CDC2L5	588		
7	40,140,593	40,141,038	445	11	C7orf11,	C7orf10	62		
7	42,894,078	42,894,715	637	14		MRPL32	43,749	C7orf25	20,684
7	44,129,861	44,130,236	375	9		POLD2	206	AEBP1	9,178
7	44,496,300	44,497,227	927	9	NUDCD3,			U6	12,670
7	44,587,709	44,588,782	1,073	9	TMED4,	DDX56	7,047		
7	44,621,444	44,622,104	660	9	OGDH,	TMED4	33,092		
7	44,802,061	44,802,420	359	9		PPIA	385		
7	45,098,326	45,098,788	462	9		NACAD	6,141	TBRG4	7,437
7	45,117,364	45,118,232	868	9	TBRG4,	SNORA5	5,141		
7	45,926,951	45,927,265	314	11	IGFBP3,			IGFBP1	27,160
7	46,359,416	46,359,680	264	9		No non-overlappi	ng genes wit	hin 50,000bp	
7	46,474,923	46,475,295	372	10		No non-overlappi	ng genes wit	hin 50,000bp	
7	48,642,710	48,643,111	401	17	ABCA13,	No non-overlappi	ng genes wit	hin 50,000bp	
7	50,197,924	50,198,200	276	9				AC020743.7	28,242
7	51,325,341	51,325,623	282	9	COBL,	No non-overlappi	ng genes wit	hin 50,000bp	
7	51,641,886	51,642,393	507	9		No non-overlappi	ng genes wit	hin 50,000bp	
7	55,302,933	55,303,417	484	9		No non-overlappi	ng genes wit	hin 50,000bp	
7	56,141,711	56,142,034	323	10		CHCHD2	26	AC006970.6	7,835
7	63,295,693	63,295,898	205	9				AC091685.4	14,987
7	63,748,711	63,749,111	400	9		ZNF588	14,835		
7	65,217,131	65,217,578	447	9	CRCP,	AC068533.7-1	43,207	ASL	21,375
					AC068533.7-2,				
7	65,595,852	65,596,365	513	11				AC008267.6-3	11,235
7	65,783,663	65,784,009	346	9				AC027644.9	29,994
7	69,037,211	69,037,825	614	9	AUTS2,	No non-overlappi	ng genes wit	hin 50,000bp	
7	72,786,843	72,787,402	559	11		AC073846.6	1,719	ABHD11	961
7	72,791,100	72,791,734	634	9	ABHD11,	AC073846.6	5,976		
7	73,322,170	73,322,521	351	10		RFC2	15,496	LAT2	40,071
7	75,515,044	75,515,423	379	10	STYXL1, MDH2,	AC005077.5-1	39,276		
7	75,781,496	75,781,840	344	13			,	HSPB1	9.948
7	75.825.967	75.826.332	365	10	YWHAG.	AC005522.2-1	2.051		
7	77,265,084	77,266,348	1,264	9	TMEM60,		,	RSBN1L	18,028
					PHTF2,				
7	78,919,851	78,921,140	1,289	9	MAGI2,	No non-overlappi	ng genes wit	hin 50,000bp	
7	80,800,662	80,801,215	553	17	SSU_rRNA_5,	AC004541.1	20,476		
					AC004866.1-1,				
7	84,653,180	84,654,437	1,257	9		No non-overlappi	ng genes wit	hin 50,000bp	
7	86,812,527	86,812,972	445	9	TP53TG1,	No non-overlappi	ng genes wit	hin 50,000bp	
					CROT,				
7	87,401,222	87,401,730	508	13	AC005075.2, AD	AM22, ADAM22,		DBF4	24,430
7	90,096,619	90,097,007	388	9	PFTK1,	AC000059.1	2,149		
7	90,731,460	90,731,859	399	11	FZD1,	No non-overlappi	ng genes wit	hin 50,000bp	
7	90,732,416	90,732,904	488	10	FZD1,	No non-overlappi	ng genes wit	hin 50,000bp	
7	91,347,583	91,348,175	592	10	MTERF,	No non-overlappi	ng genes wit	hin 50,000bp	
7	91,600,908	91,602,039	1,131	10	CYP51A1,			AC000120.1-1	15,118
7	91,712,365	91,712,805	440	9	KRIT1,	ANKIB1	679		
7	91,891,584	91,892,136	552	11		GATAD1	22,565	ANKIB1	22,950
7	94,124,049	94,124,840	791	11	PEG10,	SGCE	592		
7	95,864,230	95,864,601	371	9		No non-overlappi	ng genes wit	hin 50,000bp	
7	98,358,515	98,358,770	255	10	TRRAP,	AC004991.1	37,866		
7	98,966,828	98,967,318	490	9	ZKSCAN5,	ZNF655	26,663	C7orf38	14,549
7	99,863,701	99,864,019	318	10	ZCWPW1,	MEPCE	1,171	C7orf47	6,829
7	99,995,291	99,995,693	402	10	AGFG2,	AC069281.6-2	6,964		
7	100,141,420	100,141,896	476	9	POP7,	EPO	14,463	GNB2	26,687
7	100,263,135	100,263,490	355	9		EPHB4	56		
7	100,272,737	100,273,358	621	9		EPHB4	9,658		
7	100,310,156	100,310,743	587	10	SRRT,			TRIP6	1,152
7	100,402,932	100,403,233	301	10				MUC3B	4,600
7	100,489,353	100,489,715	362	12				MUC17	493

7	100,507,580	100,507,864	284	10		TRIM56	7,576		
7	100,573,817	100,574,508	691	9		AP1S1	9,898	SERPINE1	4,791
7	100,712,775	100,713,277	502	9				AZGP1P2	4,060
7	101,818,085	101,818,409	324	10	AC073517.6,	PRKRIP1	5,455		
7	102,772,245	102,772,684	439	11	DNAJC2,	PSMC2	2,641	SLC26A5	7,729
7	102,874,765	102,875,072	307	10		SLC26A5	931		
7	103,658,993	103,659,588	595	9		ORC5L	23,294		
7	104,311,194	104,312,174	980	9		AC007384.3-1	11,831		
7	104,371,266	104,371,600	334	11		AC007384.3-3	46,181	SRP_euk_arch	31,390
7	104,372,673	104,373,032	359	11		AC007384.3-3	44,749	SRP_euk_arch	32,797
7	104,440,076	104,440,834	758	10		MLL5	1,039		
7	105,712,841	105,713,448	607	9	PBEF1,	No non-overlappi	ng genes wit	hin 50,000bp	
7	107,170,632	107,171,961	1,329	9	CBLL1,			SLC26A3	21,195
7	111,589,369	111,589,740	371	12		ZNF277	44,139		
7	111,877,468	111,878,707	1,239	9	IFRD1,	C7orf53	29,575		
7	113,512,669	113,513,111	442	11		No non-overlappi	ng genes wit	hin 50,000bp	
7	114,080,481	114,080,978	497	9	FOXP2,	5S_rRNA	39,284		
7	114,944,091	114,944,444	353	9		No non-overlappi	ng genes wit	hin 50,000bp	
7	115,926,423	115,926,790	367	10	CAV2,	CAV1	25,285		
7	115,927,426	115,927,812	386	10	CAV2,	CAV1	24,263		
7	116,381,167	116,381,805	638	11	ST7, ST7OT4,	AC106873.3-1	9,463		
7	116,447,268	116,447,763	495	10	ST7,	AC106873.2	47,067		
7	117,641,593	117,642,333	740	9		ANKRD7	9,620		
7	120,283,878	120,284,199	321	9	TSPAN12,	No non-overlappi	ng genes wit	hin 50,000bp	
7	122,314,560	122,315,033	473	10		CADPS2	770		
7	127,271,510	127,271,813	303	11	SND1,	No non-overlappi	ng genes wit	hin 50,000bp	
7	127,770,795	127,771,392	597	9	RBM28,			IMPDH1	48,176
7	127,903,636	127,904,187	551	9	METTL2B,			AC010655.7-2	7,147
7	128,210,564	128,210,983	419	15		OPN1SW	7,477		
7	128,257,930	128,258,230	300	11	FLNC,			CCDC136	8,511
7	128,481,569	128,482,556	987	13	TNPO3,	AC018639.8	6,265		
7	129,632,351	129,632,725	374	10	TMEM209,	C7orf45	2,229		
7	130,375,776	130,376,236	460	9				U6	13,949
7	131,194,421	131,194,750	329	11		No non-overlappi	ng genes wit	hin 50,000bp	
7	133,462,305	133,462,932	627	11	LRGUK,	No non-overlappi	ng genes wit	hin 50,000bp	
7	134,114,453	134,115,015	562	9	CALD1,	No non-overlappi	ng genes wit	hin 50,000bp	
			455	11	NUP205,	CNOT4	47,612		
7	134,893,003	134,893,458	400	11					
7 7	134,893,003 134,893,508	134,893,458 134,893,833	325	9	NUP205,	CNOT4	48,117		
7 7 7	134,893,003 134,893,508 136,678,563	134,893,458 134,893,833 136,679,228	325 665	9	NUP205, PTN,	CNOT4	48,117	DGKI	45,697
7 7 7 7	134,893,003 134,893,508 136,678,563 138,468,805	134,893,458 134,893,833 136,679,228 138,469,296	325 665 491	9	NUP205, PTN, TTC26,	CNOT4 ZC3HAV1	48,117 23,800	DGKI	45,697
7 7 7 7 7	134,893,003 134,893,508 136,678,563 138,468,805 138,675,359	134,893,458 134,893,833 136,679,228 138,469,296 138,676,218	325 665 491 859	9 9 9 9 19	NUP205, PTN, TTC26,	CNOT4 ZC3HAV1 C7orf55	48,117 23,800 396	DGKI	45,697
7 7 7 7 7 7 7	134,893,003 134,893,508 136,678,563 138,468,805 138,675,359 138,694,833	134,893,458 134,893,833 136,679,228 138,469,296 138,676,218 138,695,436	325 665 491 859 603	9 9 9 9 19 14	NUP205, PTN, TTC26, LUC7L2,	CNOT4 ZC3HAV1 C7orf55 AC083883.6	48,117 23,800 396 29,030	DGKI C7orf55	45,697
7 7 7 7 7 7 7 7 7	134,893,003 134,893,508 136,678,563 138,468,805 138,675,359 138,694,833 139,853,061	134,893,458 134,893,833 136,679,228 138,469,296 138,676,218 138,695,436 139,853,472	325 665 491 859 603 411	9 9 9 19 14 10	NUP205, PTN, TTC26, LUC7L2,	CNOT4 ZC3HAV1 C7orf55 AC083883.6 MKRNP6	48,117 23,800 396 29,030 27,290	DGKI C7orf55 DENND2A	45,697 13,228 11,227
7 7 7 7 7 7 7 7 7 7 7	134,893,003 134,893,508 136,678,563 138,468,805 138,675,359 138,694,833 139,853,061 140,417,628	134,893,458 134,893,833 136,679,228 138,469,296 138,676,218 138,695,436 139,853,472 140,418,026	325 665 491 859 603 411 398	9 9 9 19 14 10 11	NUP205, PTN, TTC26, LUC7L2,	CNOT4 ZC3HAV1 C7orf55 AC083883.6 MKRNP6	48,117 23,800 396 29,030 27,290	DGKI C7orf55 DENND2A U4	45,697 13,228 11,227 18,949
7 7 7 7 7 7 7 7 7 7 7 7	134,893,003 134,893,508 136,678,563 138,468,805 138,675,359 138,694,833 139,853,061 140,417,628 141,084,202	134,893,458 134,893,833 136,679,228 138,469,296 138,676,218 138,695,436 139,853,472 140,418,026 141,084,844	325 665 491 859 603 411 398 642	9 9 9 19 14 10 11 10	NUP205, PTN, TTC26, LUC7L2, SSBP1,	CNOT4 ZC3HAV1 C7orf55 AC083883.6 MKRNP6	48,117 23,800 396 29,030 27,290	DGKI C7orf55 DENND2A U4 WEE2	45,697 13,228 11,227 18,949 6,662
7 7 7 7 7 7 7 7 7 7 7 7 7	134,893,003 134,893,508 136,678,563 138,468,805 138,675,359 138,694,833 139,853,061 140,417,628 141,084,202 141,759,652	134,893,458 134,893,833 136,679,228 138,469,296 138,676,218 138,695,436 139,853,472 140,418,026 141,084,844 141,759,991	325 665 491 859 603 411 398 642 339	9 9 9 19 14 10 11 10 10	NUP205, PTN, TTC26, LUC7L2, SSBP1,	CNOT4 ZC3HAV1 C7orf55 AC083883.6 MKRNP6 U66059.1-16	48,117 23,800 396 29,030 27,290 413	DGKI C7orf55 DENND2A U4 WEE2 U66059.1-15	45,697 13,228 11,227 18,949 6,662 1,518
7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	134,893,003 134,893,508 136,678,563 138,468,805 138,675,359 138,694,833 139,853,061 140,417,628 141,084,202 141,759,652 142,655,928	134,893,458 134,893,833 136,679,228 138,469,296 138,676,218 138,695,436 139,853,472 140,418,026 141,084,844 141,759,991 142,656,281	430 325 665 491 859 603 411 398 642 339 353	9 9 9 19 14 10 11 10 10 9	NUP205, PTN, TTC26, LUC7L2, SSBP1,	CNOT4 ZC3HAV1 C7orf55 AC083883.6 MKRNP6 U66059.1-16 GSTK1	48,117 23,800 396 29,030 27,290 413 14,363	DGKI C7orf55 DENND2A U4 WEE2 U66059.1-15 TAS2R40	45,697 13,228 11,227 18,949 6,662 1,518 25,634
7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	134,893,003 134,893,508 136,678,563 138,468,805 138,675,359 138,694,833 139,853,061 140,417,628 141,084,202 141,759,652 142,655,928 144,163,081	134,893,458 134,893,833 136,679,228 138,469,296 138,676,218 138,695,436 139,853,472 140,418,026 141,084,844 141,759,991 142,656,281 144,163,540	1325 665 491 859 603 411 398 642 339 353 459	9 9 9 19 14 10 11 10 10 9 14	NUP205, PTN, TTC26, LUC7L2, SSBP1, TPK1,	CNOT4 ZC3HAV1 C7orf55 AC083883.6 MKRNP6 U66059.1-16 GSTK1	48,117 23,800 396 29,030 27,290 413 14,363	DGKI C7orf55 DENND2A U4 WEE2 U66059.1-15 TAS2R40 7SK	45,697 13,228 11,227 18,949 6,662 1,518 25,634 14,241
7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	134,893,003 134,893,508 136,678,563 138,468,805 138,675,359 138,694,833 139,853,061 140,417,628 141,084,202 141,759,652 142,655,928 144,163,081 145,624,170	134,893,458 134,893,833 136,679,228 138,469,296 138,676,218 138,695,436 139,853,472 140,418,026 141,084,844 141,759,991 142,656,281 144,163,540 145,624,543	1325 665 491 859 603 411 398 642 339 353 459 373	9 9 9 19 14 10 11 10 10 9 14 9	NUP205, PTN, TTC26, LUC7L2, SSBP1, TPK1, CNTNAP2,	CNOT4 ZC3HAV1 C7orf55 AC083883.6 MKRNP6 U66059.1-16 GSTK1 No non-overlappi	48,117 23,800 396 29,030 27,290 413 14,363 ng genes wit	DGKI C7orf55 DENND2A U4 WEE2 U66059.1-15 TAS2R40 7SK hin 50,000bp	45,697 13,228 11,227 18,949 6,662 1,518 25,634 14,241
7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	134,893,003 134,893,508 136,678,563 138,468,805 138,675,359 138,694,833 139,853,061 140,417,628 141,084,202 141,759,652 142,655,928 144,163,081 145,624,170 146,036,397	134,893,458 134,893,833 136,679,228 138,469,296 138,676,218 138,695,436 139,853,472 140,418,026 141,084,844 141,759,991 142,656,281 144,163,540 145,624,543 146,036,802	325 325 665 491 859 603 411 398 642 339 353 459 373	9 9 9 19 14 10 11 10 10 9 14 9 12	NUP205, PTN, TTC26, LUC7L2, SSBP1, TPK1, CNTNAP2, CNTNAP2,	CNOT4 ZC3HAV1 C7orf55 AC083883.6 MKRNP6 U66059.1-16 GSTK1 No non-overlappi No non-overlappi	48,117 23,800 396 29,030 27,290 413 14,363 ng genes wit ng genes wit	DGKI C7orf55 DENND2A U4 WEE2 U66059.1-15 TAS2R40 7SK hin 50,000bp hin 50,000bp	45,697 13,228 11,227 18,949 6,662 1,518 25,634 14,241
7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	134,893,003 134,893,508 136,678,563 138,468,805 138,675,359 138,694,833 139,853,061 140,417,628 141,084,202 141,759,652 142,655,928 144,163,081 145,624,170 146,036,397 148,233,063	134,893,458 134,893,833 136,679,228 138,469,296 138,676,218 138,695,436 139,853,472 140,418,026 141,084,844 141,759,991 142,656,281 144,163,540 145,624,543 146,036,802 148,233,565	133 325 665 491 859 603 411 398 642 339 353 459 373 405 502	9 9 9 19 14 10 11 10 10 9 14 9 12 10	NUP205, PTN, TTC26, LUC7L2, SSBP1, TPK1, CNTNAP2, CNTNAP2,	CNOT4 ZC3HAV1 C7orf55 AC083883.6 MKRNP6 U66059.1-16 GSTK1 No non-overlappi No non-overlappi EZH2	48,117 23,800 396 29,030 27,290 413 14,363 ng genes wit ng genes wit 20,716	DGKI C7orf55 DENND2A U4 WEE2 U66059.1-15 TAS2R40 7SK hin 50,000bp hin 50,000bp SRP_euk_arch	45,697 13,228 11,227 18,949 6,662 1,518 25,634 14,241 14,523
7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	134,893,003 134,893,508 136,678,563 138,468,805 138,675,359 138,694,833 139,853,061 140,417,628 141,084,202 141,759,652 142,655,928 144,163,081 145,624,170 146,036,397 148,233,063 148,270,355	134,893,458 134,893,833 136,679,228 138,469,296 138,676,218 138,695,436 139,853,472 140,418,026 141,084,844 141,759,991 142,656,281 144,163,540 145,624,543 146,036,802 148,233,565 148,270,862	133 325 665 491 859 603 411 398 642 339 353 459 373 405 502 507	9 9 9 19 14 10 11 10 10 9 14 9 12 10 9	NUP205, PTN, TTC26, LUC7L2, SSBP1, TPK1, CNTNAP2, CNTNAP2,	CNOT4 ZC3HAV1 C7orf55 AC083883.6 MKRNP6 U66059.1-16 GSTK1 No non-overlappi No non-overlappi EZH2	48,117 23,800 396 29,030 27,290 413 14,363 ng genes wit 20,716	DGKI C7orf55 DENND2A U4 WEE2 U66059.1-15 TAS2R40 7SK hin 50,000bp hin 50,000bp SRP_euk_arch RNY5	45,697 13,228 11,227 18,949 6,662 1,518 25,634 14,241 14,523 759
7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	134,893,003 134,893,508 136,678,563 138,468,805 138,675,359 138,694,833 139,853,061 140,417,628 141,084,202 141,759,652 142,655,928 144,163,081 145,624,170 146,036,397 148,233,063 148,270,355 148,311,620	134,893,458 134,893,833 136,679,228 138,469,296 138,676,218 138,695,436 139,853,472 140,418,026 141,084,844 141,759,991 142,656,281 144,163,540 145,624,543 146,036,802 148,233,565 148,270,862 148,311,968	133 325 665 491 859 603 411 398 642 339 353 459 373 405 502 507 348	9 9 9 19 14 10 11 10 10 9 14 9 12 10 9 9 9 9	NUP205, PTN, TTC26, LUC7L2, SSBP1, TPK1, CNTNAP2, CNTNAP2, Y_RNA,	CNOT4 ZC3HAV1 C7orf55 AC083883.6 MKRNP6 U66059.1-16 GSTK1 No non-overlappi No non-overlappi EZH2	48,117 23,800 396 29,030 27,290 413 14,363 ng genes wit 20,716	DGKI C7orf55 DENND2A U4 WEE2 U66059.1-15 TAS2R40 7SK hin 50,000bp hin 50,000bp SRP_euk_arch RNY5 Y_RNA	45,697 13,228 11,227 18,949 6,662 1,518 25,634 14,241 14,523 759 3,193
7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	134,893,003 134,893,508 136,678,563 138,468,805 138,675,359 138,694,833 139,853,061 140,417,628 141,084,202 141,759,652 142,655,928 144,163,081 145,624,170 146,036,397 148,233,063 148,270,355 148,311,620 148,315,048	134,893,458 134,893,833 136,679,228 138,469,296 138,676,218 138,695,436 139,853,472 140,418,026 141,084,844 141,759,991 142,656,281 144,163,540 145,624,543 146,036,802 148,233,565 148,270,862 148,311,968 148,316,353	133 325 665 491 859 603 411 398 642 339 353 459 373 405 502 507 348 1,305	9 9 9 19 14 10 11 10 10 9 14 9 12 10 9 9 11	NUP205, PTN, TTC26, LUC7L2, SSBP1, TPK1, CNTNAP2, CNTNAP2, Y_RNA, Y_RNA,	CNOT4 ZC3HAV1 C7orf55 AC083883.6 MKRNP6 U66059.1-16 GSTK1 No non-overlappi No non-overlappi EZH2	48,117 23,800 396 29,030 27,290 413 14,363 ng genes wit ng genes wit 20,716	DGKI C7orf55 DENND2A U4 WEE2 U66059.1-15 TAS2R40 7SK hin 50,000bp hin 50,000bp SRP_euk_arch RNY5 Y_RNA Y_RNA	45,697 13,228 11,227 18,949 6,662 1,518 25,634 14,241 14,523 759 3,193 3,167
7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	134,893,003 134,893,508 136,678,563 138,468,805 138,675,359 138,694,833 139,853,061 140,417,628 141,084,202 141,759,652 142,655,928 144,163,081 145,624,170 146,036,397 148,233,063 148,270,355 148,311,620 148,315,048 148,638,114	134,893,458 134,893,833 136,679,228 138,469,296 138,676,218 138,695,436 139,853,472 140,418,026 141,084,844 141,759,991 142,656,281 144,163,540 145,624,543 146,036,802 148,233,565 148,270,862 148,311,968 148,316,353 148,638,419	133 325 325 665 491 859 603 411 398 642 339 353 459 373 405 502 507 348 1,305 305	9 9 9 19 14 10 11 10 10 10 9 14 9 12 10 9 9 9 11	NUP205, PTN, TTC26, LUC7L2, SSBP1, TPK1, CNTNAP2, CNTNAP2, Y_RNA, Y_RNA, Y_RNA,	CNOT4 ZC3HAV1 C7orf55 AC083883.6 MKRNP6 U66059.1-16 GSTK1 No non-overlappi No non-overlappi EZH2 AC004941.4	48,117 23,800 396 29,030 27,290 413 14,363 ng genes wit 20,716 23,629	DGKI C7orf55 DENND2A U4 WEE2 U66059.1-15 TAS2R40 7SK hin 50,000bp hin 50,000bp SRP_euk_arch RNY5 Y_RNA Y_RNA AC004941.5	45,697 13,228 11,227 18,949 6,662 1,518 25,634 14,241 14,523 759 3,193 3,167 11,470
7 7	134,893,003 134,893,508 136,678,563 138,468,805 138,675,359 138,694,833 139,853,061 140,417,628 141,084,202 141,759,652 142,655,928 144,163,081 145,624,170 146,036,397 148,233,063 148,270,355 148,311,620 148,315,048 148,638,114 148,895,406	134,893,458 134,893,833 136,679,228 138,469,296 138,676,218 138,695,436 139,853,472 140,418,026 141,084,844 141,759,991 142,656,281 144,163,540 145,624,543 146,036,802 148,233,565 148,270,862 148,311,968 148,311,968 148,316,353 148,638,419 148,895,731	133 325 325 665 491 859 603 411 398 642 339 353 459 373 405 502 507 348 1,305 305 325	9 9 9 19 14 10 11 10 10 10 9 14 9 12 10 9 9 9 11 10 9 9 11	NUP205, PTN, TTC26, LUC7L2, SSBP1, TPK1, CNTNAP2, CNTNAP2, Y_RNA, Y_RNA, Y_RNA, ZNF767,	CNOT4 ZC3HAV1 C7orf55 AC083883.6 MKRNP6 U66059.1-16 GSTK1 No non-overlappi EZH2 AC004941.4 AC004932.4-1	48,117 23,800 396 29,030 27,290 413 14,363 ng genes wit 20,716 23,629 31,565	DGKI C7orf55 DENND2A U4 WEE2 U66059.1-15 TAS2R40 7SK hin 50,000bp hin 50,000bp SRP_euk_arch RNY5 Y_RNA Y_RNA AC004941.5	45,697 13,228 11,227 18,949 6,662 1,518 25,634 14,241 14,523 759 3,193 3,167 11,470
7 7	134,893,003 134,893,508 136,678,563 138,468,805 138,675,359 138,694,833 139,853,061 140,417,628 141,084,202 141,759,652 142,655,928 144,163,081 145,624,170 146,036,397 148,233,063 148,270,355 148,311,620 148,315,048 148,638,114 148,895,406 149,018,919	134,893,458 134,893,833 136,679,228 138,469,296 138,676,218 138,695,436 139,853,472 140,418,026 141,084,844 141,759,991 142,656,281 144,163,540 145,624,543 146,036,802 148,233,565 148,270,862 148,311,968 148,311,968 148,316,353 148,638,419 148,895,731 149,019,379	133 325 325 665 491 859 603 411 398 642 339 353 459 373 405 502 507 348 1,305 305 325 460	9 9 9 19 14 10 11 10 10 9 14 9 12 10 9 9 9 11 10 9 9 11 10 0 20	NUP205, PTN, TTC26, LUC7L2, SSBP1, SSBP1, CNTNAP2, CNTNAP2, CNTNAP2, Y_RNA, Y_RNA, Y_RNA, ZNF767,	CNOT4 ZC3HAV1 C7orf55 AC083883.6 MKRNP6 U66059.1-16 GSTK1 No non-overlappi EZH2 AC004941.4 AC004932.4-1 KRBA1	48,117 23,800 396 29,030 27,290 413 14,363 ng genes wit 20,716 23,629 31,565 23,702	DGKI C7orf55 DENND2A U4 WEE2 U66059.1-15 TAS2R40 7SK hin 50,000bp hin 50,000bp SRP_euk_arch RNY5 Y_RNA Y_RNA AC004941.5	45,697 13,228 11,227 18,949 6,662 1,518 25,634 14,241 14,523 759 3,193 3,167 11,470
7 7	134,893,003 134,893,508 136,678,563 138,468,805 138,675,359 138,694,833 139,853,061 140,417,628 141,084,202 141,759,652 142,655,928 144,163,081 145,624,170 146,036,397 148,233,063 148,270,355 148,311,620 148,315,048 148,638,114 148,895,406 149,018,919 149,115,263	134,893,458 134,893,833 136,679,228 138,469,296 138,676,218 138,695,436 139,853,472 140,418,026 141,084,844 141,759,991 142,656,281 144,163,540 145,624,543 146,036,802 148,233,565 148,270,862 148,311,968 148,316,353 148,638,419 148,895,731 149,019,379 149,116,250	133 325 325 665 491 859 603 411 398 642 339 353 459 373 405 502 507 3488 1,305 305 325 460 987	9 9 9 19 14 10 11 10 10 9 14 9 12 10 9 9 11 11 10 0 9 9 9 9 9	NUP205, PTN, TTC26, LUC7L2, SSBP1, SSBP1, TPK1, CNTNAP2, CNTNAP2, CNTNAP2, Y_RNA, Y_RNA, Y_RNA, ZNF767, AC004877.1-2,	CNOT4 ZC3HAV1 C7orf55 AC083883.6 MKRNP6 U66059.1-16 GSTK1 No non-overlappi No non-overlappi EZH2 AC004941.4 AC004932.4-1 KRBA1	48,117 23,800 396 29,030 27,290 413 14,363 ng genes wit 20,716 23,629 31,565 23,702	DGKI C7orf55 DENND2A U4 WEE2 U66059.1-15 TAS2R40 7SK hin 50,000bp hin 50,000bp SRP_euk_arch RNY5 Y_RNA Y_RNA AC004941.5 AC004877.1-1	45,697 13,228 11,227 18,949 6,662 1,518 25,634 14,241 14,523 759 3,193 3,167 11,470 297
7 7	134,893,003 134,893,508 136,678,563 138,468,805 138,675,359 138,694,833 139,853,061 140,417,628 141,084,202 141,759,652 142,655,928 144,163,081 145,624,170 146,036,397 148,233,063 148,270,355 148,311,620 148,315,048 148,638,114 148,895,406 149,018,919 149,115,263 149,182,671	134,893,458 134,893,833 136,679,228 138,469,296 138,676,218 138,695,436 139,853,472 140,418,026 141,084,844 141,759,991 142,656,281 144,163,540 145,624,543 146,036,802 148,233,565 148,270,862 148,311,968 148,316,353 148,638,419 148,895,731 149,019,379 149,116,250 149,183,071	133 325 325 665 491 859 603 411 398 642 339 353 459 373 405 502 507 3488 1,305 305 325 460 987 400	9 9 9 19 14 10 11 10 10 10 9 14 9 12 10 9 9 11 11 10 0 0 9 9 11	NUP205, PTN, TTC26, LUC7L2, SSBP1, SSBP1, TPK1, CNTNAP2, CNTNAP2, CNTNAP2, Y_RNA, Y_RNA, Y_RNA, ZNF767, AC004877.1-2, ZNF862,	CNOT4 ZC3HAV1 C7orf55 AC083883.6 MKRNP6 U66059.1-16 GSTK1 No non-overlappi EZH2 AC004941.4 AC004932.4-1 KRBA1 ATP6V0E2	48,117 23,800 396 29,030 27,290 413 14,363 ng genes wit 20,716 23,629 31,565 23,702 17,919	DGKI C7orf55 DENND2A U4 WEE2 U66059.1-15 TAS2R40 7SK hin 50,000bp hin 50,000bp SRP_euk_arch RNY5 Y_RNA Y_RNA AC004941.5 AC004877.1-1 AC004877.1-3	45,697 13,228 11,227 18,949 6,662 1,518 25,634 14,241 14,523 759 3,193 3,167 11,470 297 12,648
7 7	134,893,003 134,893,508 136,678,563 138,468,805 138,675,359 138,694,833 139,853,061 140,417,628 141,084,202 141,759,652 142,655,928 144,163,081 145,624,170 146,036,397 148,233,063 148,270,355 148,311,620 148,315,048 148,638,114 148,895,406 149,018,919 149,115,263 149,182,671 149,201,548	134,893,458 134,893,833 136,679,228 138,469,296 138,676,218 138,695,436 139,853,472 140,418,026 141,084,844 141,759,991 142,656,281 144,163,540 145,624,543 146,036,802 148,233,565 148,270,862 148,311,968 148,316,353 148,638,419 148,895,731 149,019,379 149,116,250 149,183,071 149,202,239	133 325 325 665 491 859 603 411 398 642 339 353 459 373 405 502 507 3488 1,305 325 460 987 400 691	9 9 9 19 14 10 11 10 10 9 14 9 12 10 9 9 11 10 0 0 9 9 11 10 10	NUP205, PTN, TTC26, LUC7L2, SSBP1, SSBP1, TPK1, CNTNAP2, CNTNAP2, CNTNAP2, Y_RNA, Y_RNA, Y_RNA, ZNF767, AC004877.1-2, ZNF862, AC004877.1-3,	CNOT4 ZC3HAV1 C7orf55 AC083883.6 MKRNP6 U66059.1-16 GSTK1 No non-overlappi EZH2 AC004941.4 AC004932.4-1 KRBA1 ATP6V0E2	48,117 23,800 396 29,030 27,290 413 14,363 ng genes wit 20,716 23,629 31,565 23,702 17,919	DGKI C7orf55 DENND2A U4 WEE2 U66059.1-15 TAS2R40 7SK hin 50,000bp hin 50,000bp SRP_euk_arch RNY5 Y_RNA Y_RNA AC004941.5 AC004877.1-1 AC004877.1-3 ZNF862	45,697 13,228 11,227 18,949 6,662 1,518 25,634 14,241 14,523 759 3,193 3,167 11,470 297 12,648 6,050
7 7	134,893,003 134,893,508 136,678,563 138,468,805 138,675,359 138,694,833 139,853,061 140,417,628 141,084,202 141,759,652 144,163,081 145,624,170 146,036,397 148,233,063 148,270,355 148,311,620 148,315,048 148,638,114 148,895,406 149,018,919 149,115,263 149,182,671 149,201,548	134,893,458 134,893,833 136,679,228 138,469,296 138,676,218 138,695,436 139,853,472 140,418,026 141,084,844 141,759,991 142,656,281 144,163,540 145,624,543 146,036,802 148,233,565 148,270,862 148,311,968 148,316,353 148,638,419 148,895,731 149,019,379 149,116,250 149,183,071 149,202,239	133 325 325 665 491 859 603 411 398 642 339 353 459 373 405 502 507 348 1,305 325 460 987 400 691	9 9 9 19 14 10 11 10 10 10 9 14 9 12 10 10 9 9 9 11 11 10 20 9 9 11 11	NUP205, PTN, TTC26, LUC7L2, SSBP1, SSBP1, TPK1, CNTNAP2, CNTNAP2, CNTNAP2, Y_RNA, Y_RNA, Y_RNA, ZNF767, AC004877.1-2, ZNF862, AC004877.1-3, ATP6V0E2,	CNOT4 ZC3HAV1 C7orf55 AC083883.6 MKRNP6 U66059.1-16 GSTK1 No non-overlappi No non-overlappi EZH2 AC004941.4 AC004932.4-1 KRBA1 ATP6V0E2	48,117 23,800 396 29,030 27,290 413 14,363 ng genes wit 20,716 23,629 31,565 23,702 17,919	DGKI C7orf55 DENND2A U4 WEE2 U66059.1-15 TAS2R40 7SK hin 50,000bp hin 50,000bp SRP_euk_arch RNY5 Y_RNA Y_RNA AC004941.5 AC004877.1-1 AC004877.1-3 ZNF862	45,697 13,228 11,227 18,949 6,662 1,518 25,634 14,241 14,523 759 3,193 3,167 11,470 297 12,648 6,050
7 7	134,893,003 134,893,508 136,678,563 138,468,805 138,675,359 138,694,833 139,853,061 140,417,628 141,084,202 141,759,652 142,655,928 144,163,081 145,624,170 146,036,397 148,233,063 148,270,355 148,311,620 148,315,048 148,638,114 148,895,406 149,018,919 149,115,263 149,182,671 149,201,548	134,893,458 134,893,833 136,679,228 138,469,296 138,676,218 138,695,436 139,853,472 140,418,026 141,084,844 141,759,991 142,656,281 144,163,540 145,624,543 146,036,802 148,233,565 148,270,862 148,311,968 148,316,353 148,638,419 148,895,731 149,019,379 149,116,250 149,183,071 149,202,239	133 325 665 491 859 603 411 398 642 339 353 459 373 405 502 507 348 1,305 325 460 987 400 691 420	9 9 9 19 14 10 11 10 10 9 14 12 10 10 9 9 9 11 11 10 20 9 9 111 10	NUP205, PTN, TTC26, LUC7L2, SSBP1, SSBP1, TPK1, CNTNAP2, CNTNAP2, Y_RNA, Y_RNA, Y_RNA, ZNF767, AC004877.1-2, ZNF862, AC004877.1-3, ATP6V0E2, 	CNOT4 ZC3HAV1 C7orf55 AC083883.6 MKRNP6 U66059.1-16 GSTK1 No non-overlappi No non-overlappi EZH2 AC004941.4 AC004932.4-1 KRBA1 ATP6V0E2 REPIN1 THUE	48,117 23,800 396 29,030 27,290 413 14,363 ng genes wit 20,716 23,629 31,565 23,702 17,919 510	DGKI C7orf55 DENND2A U4 WEE2 U66059.1-15 TAS2R40 7SK hin 50,000bp hin 50,000bp SRP_euk_arch RNY5 Y_RNA Y_RNA AC004941.5 AC004877.1-1 AC004877.1-3 ZNF862	45,697 13,228 11,227 18,949 6,662 1,518 25,634 14,241 14,523 759 3,193 3,167 11,470 297 12,648 6,050
7 7	134,893,003 134,893,508 136,678,563 138,468,805 138,675,359 138,694,833 139,853,061 140,417,628 141,084,202 141,759,652 142,655,928 144,163,081 145,624,170 146,036,397 148,233,063 148,270,355 148,311,620 148,315,048 148,638,114 148,895,406 149,018,919 149,115,263 149,182,671 149,201,548 149,695,882 150,415,894	134,893,458 134,893,833 136,679,228 138,469,296 138,676,218 138,695,436 139,853,472 140,418,026 141,084,844 141,759,991 142,656,281 144,163,540 145,624,543 146,036,802 148,233,565 148,270,862 148,311,968 148,316,353 148,638,419 148,895,731 149,019,379 149,116,250 149,183,071 149,202,239	133 325 665 491 859 603 411 398 642 339 353 459 373 405 502 507 348 1,305 325 460 987 400 691 420 427	9 9 9 19 14 10 11 10 10 9 14 9 12 10 10 9 9 11 11 10 20 9 9 111 10 20 9 9 111	NUP205, PTN, TTC26, LUC7L2, SSBP1, SSBP1, TPK1, CNTNAP2, CNTNAP2, Y_RNA, Y_RNA, Y_RNA, ZNF767, AC004877.1-2, ZNF862, AC004877.1-3, ATP6V0E2, AGAP3, DMA5252	CNOT4 ZC3HAV1 C7orf55 AC083883.6 MKRNP6 U66059.1-16 GSTK1 No non-overlappi No non-overlappi EZH2 AC004941.4 AC004932.4-1 KRBA1 ATP6V0E2 REPIN1 TMUB1	48,117 23,800 396 29,030 27,290 413 14,363 ng genes wit 20,716 23,629 31,565 23,702 17,919 510 4,391	DGKI C7orf55 DENND2A U4 WEE2 U66059.1-15 TAS2R40 7SK hin 50,000bp hin 50,000bp SRP_euk_arch RNY5 Y_RNA Y_RNA AC004941.5 AC004877.1-1 AC004877.1-3 ZNF862	45,697 13,228 11,227 18,949 6,662 1,518 25,634 14,241 14,523 759 3,193 3,167 11,470 297 12,648 6,050

7	150,605,079	150,605,595	516	10	SMARCD3,	ABCF2	49,829	AC021097.5	38,241
7	151,739,512	151,739,779	267	10	MLL3,	FABP5L3	25,134	AC104692.1	44,234
7	151,739,959	151,740,920	961	9	MLL3,	FABP5L3	23,993	AC104692.1	44,681
7	151,791,357	151,791,644	287	10		MLL3	27,334	CCT8L1	16,070
7	154,375,707	154,376,309	602	9	PAXIP1,			AC093726.6	7,666
7	154,930,361	154,930,958	597	9		EN2	12,627	CNPY1	28,704
7	155,129,392	155,129,876	484	10	AC009403.2,	RBM33	30		
7	155,282,316	155,282,721	405	9				SHH	5,598
7	156,623,970	156,624,421	451	17		UBE3C	4		
7	156,872,547	156,872,885	338	9	DNAJB6,	No non-overlappi	ng genes wit	hin 50,000bp	
7	158,189,814	158,190,729	915	9	NCAPG2,	AC019084.7	14,453	FAM62B	25,721
8	1.947.525	1.947.973	448	9			,	KBTBD11	5.016
8	10.823.377	10.823.748	371	10	XKR6.	No non-overlappi	na aenes wit	hin 50.000bp	·
8	11,796,790	11,797,393	603	10	-)	AC107918.5-2	10.817	AC107918.5-1	26.117
8	13.976.087	13.976.291	204	10				SGCZ	15.453
8	17 992 552	17 992 863	311	9		ASAH1	5 765		,
8	22 050 744	22 051 139	395	9		HR	5 4 1 8	RFFP4	339
8	29 189 465	29 189 841	376	9		AC084262.6	5 968		000
8	33 449 927	33 450 340	413	10	FUT10	MAK16	11 919	C8orf41	25 440
8	37 575 054	37 575 425	371	10	10110,	No non-overlanni	na aenes wit	bin 50 000bn	23,440
0	37,976,493	37 926 753	270	12	PDE2		ng genes wit	CPP124	5 835
0 0	39 073 107	39 073 019	721	12	TM2D2				9 3 20
0	30,973,197	30,973,910	121	12	ΔΠΔΜ9				0,329
8	30 000 414	30 000 701	377	14			10.840		
8	42 816 895	42 817 234	330	10		1002	10,040	DNE170	7 857
0 0	42,010,095	56 018 030	405	10	AC018607 12 1		36,000	TGS1	16.097
0 0	59 290 716	50,910,039	490	12	AC010007.12-1,		30,909	AC025674 10 2	21 002
0	59 294 705	50,201,300	764	13				AC025074.10-2	21,003
0	56,204,795	56,265,559	104	11			10.074	AC025074.10-2	25,902
0	00,700,700	00,709,234	490	11	ARING I,		10,274	T_RNA	41,149
8	67,187,993	67,188,474	481	13		AC084082.5	192		
8	67,188,687	67,189,125	438	9	0.00544	AC084082.5	886		
8	70,764,728	70,765,317	589	68	SLCO5A1,	AC091047.10-2	9,696		
Q	72 436 576	72 436 880	304	0	EVA1	No non ovorlanni	na aonos wit	hin 50 000hn	
0 0	72,430,370	72,430,000	277	12	LIAI,	No non-overlappi	ng genes wit	hin 50,000bp	
0	80 830 050	80 840 350	301	12		No non overlappi	ng genes wit	hin 50,000bp	
0	80,839,959	80,840,350	391	10		No non-overlappi	ng genes wit	hin 50,000bp	
0	00,042,275	00,042,007	332	10	neti,	NO HOH-OVEHapph	ng genes wit	quoo,ocop	
0	02,917,033	02,917,011	4/0 502	0		SINATO	40		8 000
0	92,000,107	92,000,090	563	9		No non overlenni	na aonoo wit	hin EQ 000hn	0,990
0	96,214,966	90,215,530	072	11	PLENIFZ,	No non-ovenappi	ng genes wit	qauuu,ue niin	
0	90,300,704	90,351,027	013	y Aller		COorf27	140		
8	100,577,085	100 577 500	404	14		C8orf37	149	haa min 500	40 504
8	400 007 400	100,577,506	421	14	VPS13B,	C8orf37 Y_RNA	149 31,724	hsa-mir-599	40,534
8	102,287,160	100,577,506 102,287,536	421	14 13	VPS13B,	C8orf37 Y_RNA ZNF706	149 31,724 24	hsa-mir-599	40,534
•	102,287,160 119,550,247	100,577,506 102,287,536 119,550,640	421 376 393	14 13 9	VPS13B, SAMD12,	C8orf37 Y_RNA ZNF706 No non-overlappi	149 31,724 24 ng genes wit	hsa-mir-599 hin 50,000bp	40,534
8	102,287,160 119,550,247 124,238,456	100,577,506 102,287,536 119,550,640 124,238,962	421 376 393 506	14 13 9 20	VPS13B, SAMD12,	C8orf37 Y_RNA ZNF706 No non-overlappi	149 31,724 24 ng genes wit	hsa-mir-599 hin 50,000bp WDR67	40,534
8 9	102,287,160 119,550,247 124,238,456 5,822,810	100,577,506 102,287,536 119,550,640 124,238,962 5,823,059	421 376 393 506 249	14 13 9 20 11	VPS13B, SAMD12, ERMP1,	C8orf37 Y_RNA ZNF706 No non-overlappi	149 31,724 24 ng genes wit	hsa-mir-599 hin 50,000bp WDR67 RP11-546N22.2	40,534
8 9 9	102,287,160 119,550,247 124,238,456 5,822,810 5,876,165	100,577,506 102,287,536 119,550,640 124,238,962 5,823,059 5,876,514	421 376 393 506 249 349	14 13 9 20 11 9	VPS13B, SAMD12, ERMP1,	C8orf37 Y_RNA ZNF706 No non-overlappi AL365360.9	149 31,724 24 ng genes wit	hsa-mir-599 hin 50,000bp WDR67 RP11-546N22.2	40,534
8 9 9 9	102,287,160 119,550,247 124,238,456 5,822,810 5,876,165 6,584,548 6,747,727	100,577,506 102,287,536 119,550,640 124,238,962 5,823,059 5,876,514 6,584,924	421 376 393 506 249 349 376	14 13 9 20 11 9 9	VPS13B, SAMD12, ERMP1, GLDC,	C8orf37 Y_RNA ZNF706 No non-overlappi AL365360.9 RPL23AP57	149 31,724 24 ng genes wit 3,636 44,202	hsa-mir-599 hin 50,000bp WDR67 RP11-546N22.2 RP11-472F14.4	40,534 4,885 22,722 25,188
8 9 9 9 9	102,287,160 119,550,247 124,238,456 5,822,810 5,876,165 6,584,548 6,747,737	100,577,506 102,287,536 119,550,640 124,238,962 5,823,059 5,876,514 6,584,924 6,748,145	421 376 393 506 249 349 376 408	14 13 9 20 11 9 9 9 9 12	VPS13B, SAMD12, ERMP1, GLDC, JMJD2C,	C8orf37 Y_RNA ZNF706 No non-overlappi AL365360.9 RPL23AP57 AL354707.17	149 31,724 24 ng genes wit 3,636 44,202 8,756	hsa-mir-599 hin 50,000bp WDR67 RP11-546N22.2 RP11-472F14.4	40,534 4,885 22,722 25,188
8 9 9 9 9 9 9	102,287,160 119,550,247 124,238,456 5,822,810 5,876,165 6,584,548 6,747,737 12,766,121	100,577,506 102,287,536 119,550,640 124,238,962 5,823,059 5,876,514 6,584,924 6,748,145 12,766,778	421 376 393 506 249 349 376 408 657	14 13 9 20 11 9 9 9 12 12 10	VPS13B, SAMD12, ERMP1, GLDC, JMJD2C, C9orf150,	C8orf37 Y_RNA ZNF706 No non-overlappi AL365360.9 RPL23AP57 AL354707.17 AL38753.8-2	149 31,724 24 ng genes wit 3,636 44,202 8,756 11,076	hsa-mir-599 hin 50,000bp WDR67 RP11-546N22.2 RP11-472F14.4 AL138753.8-1	40,534 4,885 22,722 25,188 43,951
8 9 9 9 9 9 9 9 9	102,287,160 119,550,247 124,238,456 5,822,810 5,876,165 6,584,548 6,747,737 12,766,121 14,312,176	100,577,506 102,287,536 119,550,640 124,238,962 5,823,059 5,876,514 6,584,924 6,748,145 12,766,778 14,312,637	421 376 393 506 249 349 376 408 657 461	14 14 13 9 20 11 9 9 9 12 12 10 10	VPS13B, SAMD12, ERMP1, GLDC, JMJD2C, C9orf150, NFIB,	C8orf37 Y_RNA ZNF706 No non-overlappi AL365360.9 RPL23AP57 AL354707.17 AL138753.8-2 No non-overlappi	149 31,724 24 ng genes wit 3,636 44,202 8,756 11,076 ng genes wit	hsa-mir-599 hin 50,000bp WDR67 RP11-546N22.2 RP11-472F14.4 AL138753.8-1 hin 50,000bp	40,534 4,885 22,722 25,188 43,951
8 9 9 9 9 9 9 9 9 9	102,287,160 119,550,247 124,238,456 5,822,810 5,876,165 6,584,548 6,747,737 12,766,121 14,312,176 16,695,214	100,577,506 102,287,536 119,550,640 124,238,962 5,823,059 5,876,514 6,584,924 6,748,145 12,766,778 14,312,637 16,695,583	421 376 393 506 249 349 376 408 657 461 369	14 14 13 9 20 11 9 9 9 12 12 10 10 10	VPS13B, SAMD12, ERMP1, GLDC, JMJD2C, C9orf150, NFIB, BNC2,	C8orf37 Y_RNA ZNF706 No non-overlappi AL365360.9 RPL23AP57 AL354707.17 AL138753.8-2 No non-overlappi No non-overlappi	149 31,724 24 ng genes wit 3,636 44,202 8,756 11,076 ng genes wit ng genes wit	hsa-mir-599 hin 50,000bp WDR67 RP11-546N22.2 RP11-472F14.4 AL138753.8-1 hin 50,000bp hin 50,000bp	40,534 4,885 22,722 25,188 43,951
8 9 9 9 9 9 9 9 9 9 9 9	102,287,160 119,550,247 124,238,456 5,822,810 5,876,165 6,584,548 6,747,737 12,766,121 14,312,176 16,695,214 19,369,916	100,577,506 102,287,536 119,550,640 124,238,962 5,823,059 5,876,514 6,584,924 6,748,145 12,766,778 14,312,637 16,695,583 19,370,679	421 376 393 506 249 349 376 408 657 461 369 763	14 13 9 20 11 9 9 12 10 10 10 10 11 11	VPS13B, SAMD12, ERMP1, GLDC, JMJD2C, C9orf150, NFIB, BNC2, RPS6,	C8orf37 Y_RNA ZNF706 No non-overlappi AL365360.9 RPL23AP57 AL354707.17 AL138753.8-2 No non-overlappi No non-overlappi	149 31,724 24 ng genes wit 3,636 44,202 8,756 11,076 ng genes wit ng genes wit	hsa-mir-599 hin 50,000bp WDR67 RP11-546N22.2 RP11-472F14.4 AL138753.8-1 hin 50,000bp hin 50,000bp RP11-513M16.5	40,534 4,885 22,722 25,188 43,951 2,541
8 9 9 9 9 9 9 9 9 9 9 9	102,287,160 119,550,247 124,238,456 5,822,810 5,876,165 6,584,548 6,747,737 12,766,121 14,312,176 16,695,214 19,369,916 21,324,971	100,577,506 102,287,536 119,550,640 124,238,962 5,823,059 5,876,514 6,584,924 6,748,145 12,766,778 14,312,637 16,695,583 19,370,679 21,325,401	421 376 393 506 249 349 376 408 657 461 369 763 430	14 13 9 20 11 9 9 12 10 10 10 10 11 11 9 9	VPS13B, SAMD12, ERMP1, GLDC, JMJD2C, C9orf150, NFIB, BNC2, RPS6, KLHL9,	C8orf37 Y_RNA ZNF706 No non-overlappin AL365360.9 RPL23AP57 AL354707.17 AL138753.8-2 No non-overlappin No non-overlappin IFNA5	149 31,724 24 ng genes wit 3,636 44,202 8,756 11,076 ng genes wit ng genes wit 29,660	hsa-mir-599 hin 50,000bp WDR67 RP11-546N22.2 RP11-472F14.4 AL138753.8-1 hin 50,000bp hin 50,000bp RP11-513M16.5 RP11-380P16.7	40,534 4,885 22,722 25,188 43,951 2,541 13,145
8 9 9 9 9 9 9 9 9 9 9 9 9 9 9	102,287,160 119,550,247 124,238,456 5,822,810 5,876,165 6,584,548 6,747,737 12,766,121 14,312,176 16,695,214 19,369,916 21,324,971 21,979,269	100,577,506 102,287,536 119,550,640 124,238,962 5,823,059 5,876,514 6,584,924 6,748,145 12,766,778 14,312,637 16,695,583 19,370,679 21,325,401 21,979,924	421 376 393 506 249 349 376 408 657 461 369 763 430 655	14 13 9 20 11 9 9 12 10 10 10 10 11 11 9 9 9	VPS13B, SAMD12, ERMP1, GLDC, JMJD2C, C9orf150, NFIB, BNC2, RPS6, KLHL9, MTAP, SOUVER	C8orf37 Y_RNA ZNF706 No non-overlappin AL365360.9 RPL23AP57 AL354707.17 AL138753.8-2 No non-overlappin No non-overlappin IFNA5 AL354709.15	149 31,724 24 ng genes wit 3,636 44,202 8,756 11,076 ng genes wit ng genes wit 29,660 22,230	hsa-mir-599 hin 50,000bp WDR67 RP11-546N22.2 RP11-472F14.4 AL138753.8-1 hin 50,000bp hin 50,000bp RP11-513M16.5 RP11-380P16.7 CDKN2B	40,534 4,885 22,722 25,188 43,951 2,541 13,145 12,985
8 9 9 9 9 9 9 9 9 9 9 9 9 9	102,287,160 119,550,247 124,238,456 5,822,810 5,876,165 6,584,548 6,747,737 12,766,121 14,312,176 16,695,214 19,369,916 21,324,971 21,979,269 21,999,034	100,577,506 102,287,536 119,550,640 124,238,962 5,823,059 5,876,514 6,584,924 6,748,145 12,766,778 14,312,637 16,695,583 19,370,679 21,325,401 21,979,924 21,999,743	421 376 393 506 249 349 376 408 657 461 369 763 430 655 709	14 13 9 20 111 9 9 9 12 10 10 10 10 11 11 9 9 9 13	VPS13B, SAMD12, ERMP1, GLDC, JMJD2C, C9orf150, NFIB, BNC2, RPS6, KLHL9, MTAP, CDKN2A, MTAP,	C8orf37 Y_RNA ZNF706 No non-overlappin AL365360.9 RPL23AP57 AL354707.17 AL138753.8-2 No non-overlappin No non-overlappin IFNA5 AL354709.15 AL354709.15	149 31,724 24 ng genes wit 3,636 44,202 8,756 11,076 ng genes wit ng genes wit 29,660 22,230 2,411	hsa-mir-599 hin 50,000bp WDR67 RP11-546N22.2 RP11-472F14.4 AL138753.8-1 hin 50,000bp hin 50,000bp RP11-513M16.5 RP11-380P16.7 CDKN2B	40,534 4,885 22,722 25,188 43,951 2,541 13,145 12,985
8 9 9 9 9 9 9 9 9 9 9 9 9	102,287,160 119,550,247 124,238,456 5,822,810 5,876,165 6,584,548 6,747,737 12,766,121 14,312,176 16,695,214 19,369,916 21,324,971 21,979,269 21,999,034	100,577,506 102,287,536 119,550,640 124,238,962 5,823,059 5,876,514 6,584,924 6,748,145 12,766,778 14,312,637 16,695,583 19,370,679 21,325,401 21,979,924 21,999,743	421 376 393 506 249 349 376 408 657 461 369 763 430 655 709	14 13 9 20 11 9 9 9 12 10 10 10 10 11 11 9 9 9 13	VPS13B, SAMD12, ERMP1, GLDC, JMJD2C, C9orf150, NFIB, BNC2, RPS6, KLHL9, MTAP, CDKN2A, MTAP, CDKN2B,	C8orf37 Y_RNA ZNF706 No non-overlappin AL365360.9 RPL23AP57 AL354707.17 AL138753.8-2 No non-overlappin No non-overlappin IFNA5 AL354709.15 AL354709.15	149 31,724 24 ng genes wit 3,636 44,202 8,756 11,076 ng genes wit 29,660 22,230 2,411	hsa-mir-599 hin 50,000bp WDR67 RP11-546N22.2 RP11-472F14.4 AL138753.8-1 hin 50,000bp hin 50,000bp RP11-513M16.5 RP11-380P16.7 CDKN2B	40,534 4,885 22,722 25,188 43,951 2,541 13,145 12,985
8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	102,287,160 119,550,247 124,238,456 5,822,810 5,876,165 6,584,548 6,747,737 12,766,121 14,312,176 16,695,214 19,369,916 21,324,971 21,979,269 21,999,034 23,810,808	100,577,506 102,287,536 119,550,640 124,238,962 5,823,059 5,876,514 6,584,924 6,748,145 12,766,778 14,312,637 16,695,583 19,370,679 21,325,401 21,979,924 21,999,743 23,811,310	421 376 393 506 249 349 376 408 657 461 369 763 430 655 709 502	14 13 9 20 11 9 9 9 12 10 10 10 10 11 11 11 9 9 9 13 10	VPS13B, SAMD12, ERMP1, GLDC, JMJD2C, C9orf150, NFIB, BNC2, RPS6, KLHL9, MTAP, CDKN2A, MTAP, CDKN2B, ELAVL2,	C8orf37 Y_RNA ZNF706 No non-overlappin AL365360.9 RPL23AP57 AL354707.17 AL138753.8-2 No non-overlappin IFNA5 AL354709.15 No non-overlappin No non-overlappin	149 31,724 24 ng genes wit 3,636 44,202 8,756 11,076 ng genes wit 29,660 22,230 2,411 ng genes wit	hsa-mir-599 hin 50,000bp WDR67 RP11-546N22.2 RP11-472F14.4 AL138753.8-1 hin 50,000bp RP11-513M16.5 RP11-380P16.7 CDKN2B	40,534 4,885 22,722 25,188 43,951 2,541 13,145 12,985
8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	102,287,160 119,550,247 124,238,456 5,822,810 5,876,165 6,584,548 6,747,737 12,766,121 14,312,176 16,695,214 19,369,916 21,324,971 21,979,269 21,999,034 23,810,808 23,810,137	100,577,506 102,287,536 119,550,640 124,238,962 5,823,059 5,876,514 6,584,924 6,748,145 12,766,778 14,312,637 16,695,583 19,370,679 21,325,401 21,979,924 21,999,743 23,811,310 23,816,698	421 376 393 506 249 349 376 408 657 461 369 763 430 655 709 502 561	14 13 9 20 11 9 9 9 12 10 10 10 10 11 11 9 9 9 13 9 9 9 9 9 9 9	VPS13B, SAMD12, ERMP1, GLDC, JMJD2C, C9orf150, NFIB, BNC2, RPS6, KLHL9, MTAP, CDKN2A, MTAP, CDKN2B, ELAVL2, ELAVL2, ELAVL2,	C8orf37 Y_RNA ZNF706 No non-overlappin AL365360.9 RPL23AP57 AL354707.17 AL354707.17 AL138753.8-2 No non-overlappin No	149 31,724 24 ng genes wit 3,636 44,202 8,756 11,076 ng genes wit 29,660 22,230 2,411 ng genes wit ng genes wit	hsa-mir-599 hin 50,000bp WDR67 RP11-546N22.2 RP11-472F14.4 AL138753.8-1 hin 50,000bp RP11-513M16.5 RP11-380P16.7 CDKN2B hin 50,000bp hin 50,000bp	40,534 4,885 22,722 25,188 43,951 2,541 13,145 12,985
8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	102,287,160 119,550,247 124,238,456 5,822,810 5,876,165 6,584,548 6,747,737 12,766,121 14,312,176 16,695,214 19,369,916 21,324,971 21,979,269 21,999,034 23,810,808 23,810,808	100,577,506 102,287,536 119,550,640 124,238,962 5,823,059 5,876,514 6,584,924 6,748,145 12,766,778 14,312,637 16,695,583 19,370,679 21,325,401 21,979,924 21,999,743 23,811,310 23,816,698 23,820,400	421 376 393 506 249 349 376 408 657 461 369 763 430 655 709 502 561 779	14 14 13 9 20 11 11 9 9 12 10 10 10 10 11 11 11 9 9 9 13 0 9 9 9 9 9 9	VPS13B, SAMD12, ERMP1, GLDC, JMJD2C, C9orf150, NFIB, BNC2, RPS6, KLHL9, MTAP, CDKN2A, MTAP, CDKN2B, ELAVL2, ELAVL2,	C8orf37 Y_RNA ZNF706 No non-overlappin AL365360.9 RPL23AP57 AL354707.17 AL354707.17 AL138753.8-2 No non-overlappin No	149 31,724 24 ng genes wit 3,636 44,202 8,756 11,076 ng genes wit 29,660 22,230 2,411 ng genes wit ng genes wit 3,286	hsa-mir-599 hin 50,000bp WDR67 RP11-546N22.2 RP11-472F14.4 AL138753.8-1 hin 50,000bp RP11-513M16.5 RP11-380P16.7 CDKN2B hin 50,000bp hin 50,000bp	40,534 4,885 22,722 25,188 43,951 2,541 13,145 12,985
8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	102,287,160 119,550,247 124,238,456 5,822,810 5,876,165 6,584,548 6,747,737 12,766,121 14,312,176 16,695,214 19,369,916 21,324,971 21,979,269 21,999,034 23,810,808 23,810,808 23,816,137 23,819,621 27,237,732	100,577,506 102,287,536 119,550,640 124,238,962 5,823,059 5,876,514 6,584,924 6,748,145 12,766,778 14,312,637 16,695,583 19,370,679 21,325,401 21,979,924 21,999,743 23,811,310 23,816,698 23,820,400 27,238,086	421 376 393 506 249 349 376 408 657 461 369 763 430 655 709 502 561 779 354	14 14 13 9 20 11 11 9 9 9 12 10 10 10 10 11 11 9 9 9 13 0 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	VPS13B, SAMD12, ERMP1, GLDC, JMJD2C, C9orf150, NFIB, BNC2, RPS6, KLHL9, MTAP, CDKN2A, MTAP, CDKN2B, ELAVL2, ELAVL2,	C8orf37 Y_RNA ZNF706 No non-overlappin AL365360.9 RPL23AP57 AL354707.17 AL354707.17 AL138753.8-2 No non-overlappin No	149 31,724 24 ng genes wit 3,636 44,202 8,756 11,076 ng genes wit 29,660 22,230 2,411 ng genes wit ng genes wit 3,286	hsa-mir-599 hin 50,000bp WDR67 RP11-546N22.2 RP11-472F14.4 AL138753.8-1 hin 50,000bp RP11-513M16.5 RP11-380P16.7 CDKN2B hin 50,000bp hin 50,000bp hin 50,000bp TEK	40,534 4,885 22,722 25,188 43,951 2,541 13,145 12,985
8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	102,287,160 119,550,247 124,238,456 5,822,810 5,876,165 6,584,548 6,747,737 12,766,121 14,312,176 16,695,214 19,369,916 21,324,971 21,979,269 21,999,034 23,810,808 23,810,808 23,816,137 23,819,621 27,237,732 30,845,263	100,577,506 102,287,536 119,550,640 124,238,962 5,823,059 5,876,514 6,584,924 6,748,145 12,766,778 14,312,637 16,695,583 19,370,679 21,325,401 21,979,924 21,999,743 23,811,310 23,816,698 23,820,400 27,238,086 30,845,649	421 376 393 506 249 349 376 408 657 461 369 763 430 655 709 502 561 779 354 386	14 14 13 9 20 11 11 9 9 12 10 10 10 10 11 11 9 9 9 13 13 9 9 9 9 9 9 9 9 9 9 9	VPS13B, SAMD12, ERMP1, GLDC, JMJD2C, C9orf150, NFIB, BNC2, RPS6, KLHL9, MTAP, CDKN2A, MTAP, CDKN2B, ELAVL2, ELAVL2, ELAVL2,	C8orf37 Y_RNA ZNF706 No non-overlappin AL365360.9 RPL23AP57 AL354707.17 AL354707.17 AL138753.8-2 No non-overlappin No non-overlappin No non-overlappin No non-overlappin No non-overlappin No non-overlappin ELAVL2 RPS26P2	149 31,724 24 ng genes wit 3,636 44,202 8,756 11,076 ng genes wit 29,660 22,230 2,411 ng genes wit 3,286 23,016	hsa-mir-599 hin 50,000bp WDR67 RP11-546N22.2 RP11-472F14.4 AL138753.8-1 hin 50,000bp RP11-513M16.5 RP11-380P16.7 CDKN2B hin 50,000bp hin 50,000bp hin 50,000bp	40,534 4,885 22,722 25,188 43,951 2,541 13,145 12,985 12,985
8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	102,287,160 119,550,247 124,238,456 5,822,810 5,876,165 6,584,548 6,747,737 12,766,121 14,312,176 16,695,214 19,369,916 21,324,971 21,979,269 21,999,034 23,810,808 23,810,808 23,816,137 23,819,621 27,237,732 30,845,263 32,540,093	100,577,506 102,287,536 119,550,640 124,238,962 5,823,059 5,876,514 6,584,924 6,748,145 12,766,778 14,312,637 16,695,583 19,370,679 21,325,401 21,979,924 21,999,743 23,811,310 23,816,698 23,820,400 27,238,086 30,845,649 32,541,154	421 376 393 506 249 349 376 408 657 461 369 763 430 655 709 502 561 779 354 386 1,061	14 14 13 9 20 11 1 9 9 9 12 10 10 10 10 10 11 11 11 9 9 9 9 13 13 10 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	VPS13B, SAMD12, ERMP1, GLDC, JMJD2C, C9orf150, NFIB, BNC2, RPS6, KLHL9, MTAP, CDKN2A, MTAP, CDKN2B, ELAVL2, ELAVL2, ELAVL2,	C8orf37 Y_RNA ZNF706 No non-overlappin AL365360.9 RPL23AP57 AL354707.17 AL354707.17 AL138753.8-2 No non-overlappin No non-overlappin No non-overlappin No non-overlappin No non-overlappin No non-overlappin ELAVL2 RPS26P2 AL353671.6-3	149 31,724 24 ng genes wit 3,636 44,202 8,756 11,076 ng genes wit ng genes wit 29,660 22,230 2,411 ng genes wit 3,286 23,016 1,606	hsa-mir-599 hin 50,000bp WDR67 RP11-546N22.2 RP11-472F14.4 AL138753.8-1 hin 50,000bp RP11-513M16.5 RP11-380P16.7 CDKN2B hin 50,000bp hin 50,000bp TEK AL353671.6-2	40,534 4,885 22,722 25,188 43,951 2,541 13,145 12,985 12,985 17,561 1,945

9	33,500,849	33,501,211	362	9		SUGT1P	140		
9	34,038,298	34,039,010	712	9	UBAP2,	AL354989.13-1	954		
9	34,319,327	34,319,852	525	10	NUDT2,	KIF24	129	RP11-571F15.6	9,674
9	34,602,263	34,603,029	766	9		C9orf23	162	DCTN3	520
9	34,636,605	34,636,906	301	10	GALT,	IL11RA	7,026		
9	35,062,158	35,062,952	794	9	VCP,			FANCG	885
9	35,093,001	35,093,357	356	10	STOML2,	PIGO	6,422	KIAA1539	752
9	35,647,400	35,648,252	852	10	RNase_MRP,	CCDC107	49	C9orf100	1,089
9	35,657,887	35,658,258	371	9	C9orf100,	SRP_euk_arch	3,515	CCDC107	6,487
9	35,895,961	35,896,253	292	10	HRCT1,	RP11-112J3.13	30,770	RP11-327L3.4	36,954
9	36,180,498	36,181,316	818	9	CLTA,			CCIN	19,178
9	36,248,364	36,248,772	408	10	GNE,	U4	9,008		
9	36,562,463	36,562,967	504	12	MELK,	No non-overlappi	ng genes wit	hin 50,000bp	
9	36,738,695	36,738,980	285	9		No non-overlappi	ng genes wit	hin 50,000bp	
9	36,893,862	36,894,391	529	9	PAX5,	No non-overlappi	ng genes wit	hin 50,000bp	
9	44,010,547	44,010,954	407	9		CR848007.2	670	CR848007.1	5,410
9	44,819,048	44,819,880	832	9		RP11-160N1.7	1,178	RP11-160N1.6	1,017
9	44,933,001	44,933,401	400	10		RP11-374M1.6	884	RP11-374M1.8	1,114
9	66,223,495	66,224,001	506	9				RP11-262H14.6	5,113
9	66,233,799	66,234,264	465	14	RP11-262H14.5,	RP11-262H14.6	4,061		
					AL512625.10-1,				
9	67,902,402	67,903,186	784	14		RP11-764K9.3	347	RP11-764K9.2	116
9	67,904,136	67,904,339	203	9		RP11-764K9.2	120	5S_rRNA	5,274
9	67,905,107	67,905,348	241	10		RP11-764K9.2	1,091	5S_rRNA	6,245
9	67,906,543	67,907,355	812	10		RP11-764K9.2	2,527	5S_rRNA	7,681
9	67,908,116	67,909,544	1,428	24		RP11-764K9.2	4,100	RP11-764K9.4	8,137
9	67,910,132	67,911,300	1,168	15		RP11-764K9.2	6,116	RP11-764K9.4	6,381
9	67,911,762	67,912,220	458	14		RP11-764K9.2	7,746	RP11-764K9.4	5,461
9	67,913,642	67,914,925	1,283	15		RP11-764K9.2	9,626	RP11-764K9.4	2,756
9	67,915,326	67,915,699	373	15				RP11-764K9.4	1,982
9	67,915,862	67,917,128	1,266	12				RP11-764K9.4	553
9	72,223,087	72,223,861	774	14		KLF9	3,694		
9	72,371,503	72,371,823	320	9	TRPM3,			AL358786.21-1	12,076
9	72,566,079	72,566,428	349	10	TRPM3,			hsa-mir-204	48,283
9	/3,/15,/22	73,716,651	929	9	FAM108B1,	Y_RNA	8,436		
0	76 802 010	76 803 510	600	10	C901165,	No non overlanni	na aonos wit	hin 50 000hn	
9	70,092,910	70,093,510	000	10	OSTE1	No non-ovenappi	ng genes wit	nin 50,000bp	
9	77 042 636	77 043 606	970	9				116	39 723
9	77 697 063	77 697 403	340	11	PCSK5	No non-overlanni	na aenes wit	hin 50 000hn	00,120
9	78 376 280	78,376,862	582	54	AI 161626 20-2	AI 161626 20-1	21 776	PRUNE2	39 250
9	78 710 791	78 711 549	758	12	PRUNE2	712101020.201	21,110	RP11-159H20 1	24 448
9	79 835 432	79 835 768	336	9	GNAQ	No non-overlappi	na aenes wit	hin 50 000hp	21,110
9	80 044 224	80 044 559	335	9	CEP78		ng gonoo mi	RP11-336N8 4	20 131
9	80 101 137	80 101 658	521	10	02.10,	PSAT1	221		
9	81,472,771	81.473.319	548	.0	TLE4.	No non-overlappi	na aenes wit	hin 50.000bp	
9	84.766.261	84.766.598	337	9	,		0.01.100.11	RASEF	20.546
9	85,783.850	85,784.304	454	10	HNRNPK.	RMI1	1.213		,0.0
9	85,785.218	85,785.553	335	10	HNRNPK, RMI1	hsa-mir-7-1	10.626		
9	87,546,640	87,547,510	870	10	AGTPBP1,	RP11-213G2.1	10,531		
9	88,158.775	88,159.271	496	11	ZCCHC6.		-,	AL353678.11	19.907
9	91,407,690	91,408,297	607	9		GADD45G	1,451		,
9	94,095,438	94,096,063	625	12	IARS,		,	NOL8	3,398
9	95,252,814	95,253,254	440	9	FAM120AOS,	FAM120A	740		
9	97,119,540	97,119,899	359	9	FANCC,			AL157384.8	22,435
9	97,264,550	97,265,004	454	9	PTCH1,	MT1P1	48,930		
9	97,401,397	97,401,772	375	9		No non-overlappi	ng genes wit	hin 50,000bp	
9	97,677,518	97,677,898	380	15	AL354861.11,	5S_rRNA	29,210		
					C9orf130,				
_					C9orf102,	00.000			
9	97,678,093	97,678,515	422	10	C9ort102,	C9ort130	14		
9	98,019,859	98,020,775	916	9				HSD17B3	16,635
9	98,656,538	98,656,875	337	10	<u> </u>	∠NF782	1,363		
9	99,724,058	99,724,400	342	13	C9ort156,			HEMGN	4,494
9	99,724,424	99,724,886	462	9	C9orf156,			HEMGN	4,008

9	100,598,583	100,599,047	464	10	ANKS6,	GALNT12	10,755		
9	100,717,157	100,717,490	333	9		COL15A1	28,469	RP11-92C4.4	23,117
9	100,776,932	100,777,404	472	9	COL15A1,	No non-overlappi	ng genes wit	hin 50,000bp	
9	101,023,643	101,024,462	819	11	ALG2, SEC61B,	AL162427.24	35,674	· · ·	
9	103,251,221	103,251,834	613	9		ALDOB	13,295	C9orf125	23,440
9	103,289,068	103,289,446	378	9	C9orf125,	RNF20	46,508	RP11-490D19.8	14,300
9	106,765,177	106,765,505	328	9		ABCA1	34,920		
9	108,499,920	108,500,562	642	9		RP11-308N19.5	23,890	7SK	17,527
9	110,353,289	110,354,011	722	9		No non-overlappi	ng genes wit	hin 50,000bp	
9	110,735,832	110,736,254	422	11	IKBKAP,	C9orf6	28	CTNNAL1	8,425
9	112,838,596	112,838,866	270	9	LPAR1,	No non-overlappi	ng genes wit	hin 50,000bp	
9	113,286,324	113,286,705	381	10	KIAA0368,	ZNF483	40,555		
9	113,432,723	113,433,535	812	12	C9orf29,	PTGR1	30,767		
					DNAJC25-				
					GNG10,				
9	114,646,780	114,647,301	521	9	SNX30,			SLC46A2	33,721
9	114,705,276	114,705,642	366	11		SLC46A2	12,365	SNX30	28,189
9	115,151,818	115,152,163	345	9	BSPRY,	WDR31	9,430		
9	115,423,359	115,424,021	662	9				RGS3	23,520
9	116,200,247	116,200,554	307	9		AKNA	3,741	DFNB31	3,627
9	116,389,352	116,390,085	733	9	ATP6V1G1,	AL160275.14-1	21,899	RP11-402G3.6	13,885
9	121,358,164	121,358,510	346	10		No non-overlappi	ng genes wit	hin 50,000bp	
9	122,876,759	122,877,092	333	12	CEP110,	RP11-525G7.2	1,459		
9	122,877,579	122,877,899	320	9	CEP110,	RP11-525G7.2	652		
9	125,071,308	125,071,603	295	10		STRBP	590	C9orf56	2,233
9	126,217,439	126,217,835	396	11	PSMB7,	GPR144	35,409		
9	126,539,443	126,539,798	355	9	NR6A1,	OLFML2A	39,460	hsa-mir-181b-2	43,545
9	128,345,694	128,345,988	294	9		AL356309.23	12,603	AL161908.13	32,642
9	129,252,995	129,253,959	964	9	RPL12,	SNORA65	2,265	ZNF79	5,524
0	400 070 404	400.070.400	201		LRSAIVIT,		44.004		
9	129,372,124	129,372,488	304	9	FAIVI129B,	SIXBPI	41,901	TTC16	227
9	129,536,509	129,530,613	304	9	TURZA,		E 765		231
9	129,743,721	129,740,112	256	12	FAIVITUZA,	DFINZ	5,705	DTCES2	2 624
9	129,919,004	129,920,100	1 003	12	DTGES2		20 527	FIGE32 SLC25A25	18 206
9	129,929,041	129,930,044	1,003	9	F 10L32,		20,327	SL025A25	5 732
a	130,141,304	130,142,303	503	اب ۵	SET	PKN3	17 680	RP11-216B9 4	32 103
a	130,400,300	130 620 888	565	10			17,000	C9orf114	3 279
a	130 941 859	130 942 379	520	10	PPP2R4	CRAT	28 955	IER5I	35 273
9	130 979 899	130 980 503	604	9	IFR5I		20,000	PPP2R4	28 853
Ŭ	100,010,000	100,000,000	001	Ũ	AL158151.16-1,				20,000
9	131,241,357	131,241,943	586	9		AL391056.25-1	49,798		
9	131,553,843	131,554,343	500	9	PTGES,	RP11-5J2.2	38,953	PRRX2	29,073
9	131,939,674	131,940,451	777	9	GPR107,			AL360004.22	2,259
9	132,316,611	132,317,237	626	9	ASS1,			AL354898.10-1	1,449
9	132,547,579	132,548,017	438	9	PRDM12,	EXOSC2	10,971	RP11-57C19.2	29,988
9	132,558,726	132,559,763	1,037	9	EXOSC2,	ABL1	19,224	PRDM12	10,521
9	132,711,706	132,712,100	394	11	ABL1,			QRFP	46,536
9	132,731,278	132,732,196	918	9	ABL1,			QRFP	26,440
9	132,879,254	132,879,629	375	9	LAMC3,	No non-overlappi	ng genes wit	hin 50,000bp	
9	132,911,858	132,912,248	390	10	LAMC3,	AIF1L	49,485		
9	133,067,052	133,067,439	387	9	NUP214,	RP11-544A12.5	38,456		
9	133,282,215	133,282,624	409	10	BAT2L,	No non-overlappi	ng genes wit	hin 50,000bp	
9	133,283,704	133,284,013	309	10	BAT2L,	No non-overlappi	ng genes wit	hin 50,000bp	
9	133,620,746	133,621,211	465	9		RAPGEF1	15,464	RP11-323H21.2	26,567
9	134,809,555	134,810,057	502	10	TSC1,	GFI1B	696		
9	134,896,688	134,897,067	379	9	GTF3C5,	CEL	30,134	AL593851.6-1	10,606
9	135,012,405	135,013,201	796	9	RALGDS,			GBGT1	4,960
9	135,014,494	135,014,832	338	20	RALGDS,			GBGT1	3,329
9	135,045,077	135,045,557	480	10		GBGT1	15,950	OBP2B	24,931
9	135,205,836	135,206,389	553	9	RPL7A,	SNORD36	382	SURF4	277
	105 050 51	405 050 550			SNORD24,				
9	135,272,515	135,273,653	1,138	9	REXO4,	ADAMTS13	3,288		
9	135,953,948	135,954,402	454	11		BKD3	30,470		
9	135,990,200	135,990,856	656	13		WDR5	175		

9	136,019,285	136,019,782	497	9	U6atac,			WDR5	4,371
9	136,025,675	136,026,093	418	11		U6atac	6,168		
9	136,359,586	136,359,924	338	9	RXRA,	No non-overlappi	ng genes wit	hin 50,000bp	
9	136,701,910	136,702,464	554	9	COL5A1,	C9orf104	17,400		
9	137,375,429	137,375,919	490	10	C9orf62,	No non-overlappi	ng genes wit	hin 50,000bp	
9	137,860,015	137,860,360	345	11	CAMSAP1,			KCNT1	33,629
9	138,276,488	138,277,156	668	9	QSOX2,	LHX3	39,712		
9	138,423,803	138,424,160	357	9	SDCCAG3,	PMPCA	771		
9	138,742,262	138,742,823	561	9		SNORA17	1,110	FAM69B	3,939
9	138,880,367	138,880,745	378	9	EDF1,			MAMDC4	5,297
9	139,043,588	139,043,933	345	9	C9orf139,	ABCA2	393	FUT7	514
9	139,183,665	139,184,026	361	10	LRRC26,	AL929554.20-2	6,673	GRIN1	637
9	139,250,544	139,251,105	561	9	SLC34A3,	TUBB2C	4,427	BX255925.17-3	5,839
9	139,308,628	139,308,985	357	12				NRARP	6,872
9	139,436,994	139,437,915	921	9	EXD3, BX322799	9.22, NOXA1,		ENTPD8	10,722
9	139,592,789	139,593,306	517	9	WDR85,			ZMYND19	3,046
10	1,024,591	1,024,861	270	9	GTPBP4,	AL359878.13-2	310		
10	2,246,467	2,246,875	408	9				U6	14,785
10	5,895,106	5,896,164	1,058	9	GDI2,			ANKRD16	47,533
10	5,935,468	5,935,932	464	9				ANKRD16	7,765
10	7,493,088	7,493,440	352	9	SFMBT2,	No non-overlappi	ng genes wit	hin 50,000bp	
10	7,869,690	7,870,154	464	11	KIN, ATP5C1,	TAF3	30,353	ITIH2	38,202
10	8,922,334	8,922,618	284	10		No non-overlappi	ng genes wit	hin 50,000bp	
10	11,904,913	11,905,577	664	9	C10orf47,	No non-overlappi	ng genes wit	hin 50,000bp	
10	12,276,995	12,277,976	981	9	NUDT5,			SEC61A2	25,033
					CDC123,				
10	12,278,067	12,278,671	604	9	NUDT5,			SEC61A2	26,105
10	40.050.040	40.050.400	000	0	CDC123,	NI		bia 50.000ba	
10	13,058,019	13,058,402	383	9		No non-overlappi	ng genes wit	nin 50,000p	
10	14,919,814	14,920,516	702	10	ARMETLT,	50V39H2	40,352		
10	16 518 816	16 510 180	373	٩		AL 360230 20-1	38.052		
10	17 310 231	17 310 841	610	11	T T ∟ IX,	VIM	409		
10	18 833 037	18 833 362	325	9	CACNB2		400	NSUN6	41 135
10	21 824 517	21 825 083	566	10	C10orf114			hsa-mir-1915	414
10	22 557 882	22 558 546	664	14	0.000,			RP11-108B14 4	2 923
10	22.645.235	22.645.662	427	11	COMMD3.	BMI1	4,484		_,0_0
10	22.881.856	22.882.276	420	9	PIP5K2A.	No non-overlappi	na aenes wit	hin 50.000bp	
10	22.893.671	22.894.027	356	9	PIP5K2A.	No non-overlappi	na aenes wit	hin 50.000bp	
10	22,902,855	22,903,200	345	9	PIP5K2A,	No non-overlappi	ng genes wit	hin 50,000bp	
10	25,503,423	25,503,811	388	10	,	GPR158	485		
10	27,027,293	27,027,627	334	10	PDSS1,	RP13-16H11.6	15,930	SSH3BP	47,901
10	27,484,522	27,485,151	629	9	MASTL,	YME1L1	1,195		-
10	27,518,009	27,518,354	345	9	-			MASTL	2,155
10	27,569,066	27,569,735	669	9	ACBD5,			RP11-85G18.4	5,550
10	27,570,480	27,571,483	1,003	9	ACBD5,			RP11-85G18.4	3,802
10	28,722,869	28,723,243	374	11		RP11-351M16.1	41,893	AC022021.10-1	13,731
10	29,173,946	29,174,284	338	9		C10orf126	1,059		
10	29,268,255	29,268,674	419	13		RP11-492M23.2	39,836		
10	29,583,535	29,584,111	576	12		LYZL1	33,885		
10	30,677,429	30,678,353	924	9	MTPAP,	DNM1P17	4,288		
10	31,571,688	31,572,023	335	12		AL117340.3-1	16,511		
10	32,674,998	32,675,806	808	9	EPC1,			U6	47,686
					AL391839.9-2,				
10	32,774,820	32,775,454	634	10	CCDC7,	AL391839.9-1	35,188		
10	34,077,553	34,077,826	273	9		No non-overlappi	ng genes wit	hin 50,000bp	
10	35,011,385	35,011,889	504	9	PARD3,	AL138768.23	6,410		
10	35,141,633	35,141,906	273	10	PARD3,	No non-overlappi	ng genes wit	hin 50,000bp	
10	38,037,316	38,037,764	448	10		No non-overlappi	ng genes wit	hin 50,000bp	
10	38,423,111	38,423,425	314	9	ZNF37A,	RP11-508N22.5	2,126		
10	42,568,554	42,568,883	329	12		BMS1	29,382		
10	42,597,914	42,598,351	437	12	BMS1,			AL022344.3-1	27,332
10	42,953,564	42,953,967	403	9	CSGALNACT2,				7,759
10	43,222,984	43,223,833	849	9			07 740	AL450326.30-1	8,870
10	43,459,415	43,459,852	437	9	ZNF32,	KP11-402L1.1	37,710	KP11-402L1.12	12,579

10	44,672,944	44,673,641	697	9				RP11-18M11.1	49,267
10	46,387,722	46,388,485	763	9	SYT15,	GPRIN2	25,067	FAM35B	28,568
10	46,403,532	46,404,465	933	11		GPRIN2	9,087		
10	46,413,108	46,413,527	419	10		GPRIN2	25		
10	46,413,549	46,414,035	486	13	GPRIN2,	SYT15	22,731		
10	46,416,900	46,417,746	846	9	GPRIN2,	SYT15	26,082		
10	46,474,245	46,475,305	1,060	9		PPYR1	28,235		
10	46.480.274	46.480.587	313	9		PPYR1	22,953		
10	46,496,084	46,496,590	506	9		PPYR1	6,950		
10	46 500 268	46 501 000	732	9		PPYR1	2 540		
10	46 501 088	46 501 590	502	10		PPYR1	1,950		
10	46 501 981	46 502 592	611	13		PPYR1	948		
10	46 510 177	46,502,002	443	11		AI 391137 11-1	925	PPYR1	1 851
10	46 523 199	46,524,284	1 085	9	ΔI 301137 11-1		020	PPVR1	14 873
10	46 527 488	46 528 086	598	10	ΔI 301137 11-1			PPVR1	19 162
10	46 530 932	46 531 201	350	11	AL301137.11-1,			PD11_31/P12 3	22 053
10	46,530,932	46,531,231	559	0	AL391137.11-1,			DD11 214D12 2	6 202
10	40,540,403	40,540,901	1 021	9	AL391137.11-1,			RF11-314F12.3	0,303
10	40,550,747	40,001,770	1,031	9	AL391137.11-1,		4 500	RP11-314P12.3	1,000
10	40,000,402	40,000,910	403	10	AL391137.11-1,	RP11-314P12.3	4,526	MOMP	0.455
10	51,234,751	51,235,416	665	13	NCOA4,	NI			2,155
10	51,847,363	51,847,762	399	9	SGMS1,	No non-overlappi	ng genes wit		
10	52,570,632	52,571,022	390	10	PRKG1,	No non-overlappi	ng genes wit	hin 50,000bp	
10	53,128,983	53,129,673	690	9	PRKG1,	No non-overlappi	ng genes wit	hin 50,000bp	
10	57.000.405	57 000 000	404		CSTF21,		0.005		
10	57,800,405	57,800,869	464	11	TEANA	ZVVINI	9,365		40.000
10	59,814,405	59,815,944	1,539	9	TFAM,	100000777	04.070	UBE2D1	13,890
10	61,140,013	61,140,337	324	9	SLC16A9,	AC022027.7	21,879		
10	62,430,592	62,430,943	351	11	RHOBTB1,	No non-overlappi	ng genes wit	hin 50,000bp	
10	63,022,272	63,022,623	351	9		No non-overlappi	ng genes wit	hin 50,000bp	
10	63,333,291	63,333,625	334	9	ARID5B,	AC067742.7	23,076		
10	64,562,641	64,563,324	683	9	NRBF2,			U6	22,629
10	64,698,494	64,699,265	771	9	JMJD1C,			RP11-444I9.2	45,683
10	65,059,089	65,059,559	470	10				REEP3	4,202
10	65,060,461	65,060,738	277	10				RP11-111N20.3	3,345
10	65,470,941	65,471,415	474	9		No non-overlappi	ng genes wit	hin 50,000bp	
10	69,193,986	69,194,534	548	11		RP11-57G10.1	29,000	AL607022.11	12,990
10	69,761,461	69,761,977	516	10	PBLD,			RUFY2	11,295
					HNRNPH3,				
10	69,762,565	69,762,890	325	11	PBLD,			RUFY2	10,382
					HNRNPH3,				
10	69,991,086	69,991,515	429	10	TET1,	TMEM14D	16,404		
10	70,331,293	70,331,665	372	9	DDX50,			STOX1	6,099
10	71,483,398	71,484,173	775	9	H2AFY2,			AIFM2	43,812
10	71,833,534	71,834,024	490	9	EIF4EBP2,	AC022532.13-2	391		
10	71,891,154	71,891,457	303	11		KIAA1274	17,113	RP11-104F15.7	23,641
10	72,591,386	72,591,759	373	9		No non-overlappi	ng genes wit	hin 50,000bp	
10	73,702,426	73,703,151	725	9		DDIT4	532		
10	73,704,605	73,704,960	355	9	DDIT4,			C10orf104	38,983
10	73,783,750	73,785,166	1,416	9	DNAJB12,	U6	36,562	CBARA1	11,938
10	74,526,294	74,526,954	660	10	P4HA1,			AL731563.9-2	854
10	74,597,531	74,597,929	398	10	ECD,	FAM149B1	1		
10	74,676,588	74,677,223	635	9	DNAJC9,			MRPS16	1,386
10	74,925,119	74,925,533	414	10	PPP3CB,			USP54	1,769
10	75,160,064	75,160,436	372	10		GLUDP3	504		
10	75,229,554	75,230,036	482	9	KIAA0913,			NDST2	1,639
10	75,605,991	75,606,377	386	9	ADK,	AP3M1	25,159		
10	76,665.610	76,666.139	529	9	COMTD1,			VDAC2	4,402
10	76,838,787	76,839,768	981	9		ZNF503	7.268		,
10	78,835.577	78,835.858	281	10	KCNMA1.		,	RP11-417C21.2	27.478
10	79,459.003	79,460.037	1.034	11	POLR3A.	RPS24	3.543		,
10	79.476 899	79.477 589	690	12			5,510	RPS24	6.422
10	80 404 373	80 404 826	453	<u>، ۲</u>		No non-overlappi	na aenes wit	hin 50.000bp	5,122
10	81 654 198	81 654 707	509	9	AI 512662 8-2	AI 512662 8-1	11 424	SETPD	32 771
10	81 828 107	81 828 646	530	10	RP11-369.121.6	RP11-369.121 4	37 328		<i>52,11</i>
10	82 194 470	82 194 823	353	11		TSPAN14	9 178		
.0	5_,107,770	52,104,020	000		l		5,170	I	

10	83,900,001	83,900,647	646	9	NRG3,	No non-overlappi	ng genes wit	hin 50,000bp	
10	85,888,935	85,889,493	558	9	GHITM,	C10orf99	34,041		
10	86,017,087	86,017,481	394	9				RGR	7,392
10	87,667,689	87,668,131	442	9	GRID1,	No non-overlappi	ng genes wit	hin 50,000bp	
10	88,149,523	88,149,993	470	11	-	GRID1	33,394	WAPAL	35,000
10	88,460,899	88,461,262	363	10	LDB3,	BMPR1A	45,114	AC067750.5	34,348
10	88,710,192	88,710,786	594	9	SNCG,	MMRN2	2,840		
10	89,612,497	89,613,376	879	12	PTEN,	AC022016.7-1	29,670	AC022016.7-2	18,517
10	89,864,076	89,864,737	661	12		No non-overlappi	ng genes wit	hin 50,000bp	,
10	91.009.965	91.010.444	479	9	LIPA.	IFIT2	41.248	, ,	
10	92,606,915	92.607.720	805	9	HTR7.	RPP30	13,969	Y RNA	22.057
10	94.039.856	94.041.507	1.651	9	CPEB3. 5-Mar.	Y RNA	17.868		,
10	94,342,501	94,343,284	783	10	KIF11.		,	RP11-366I13.3	3.305
10	95,245,354	95,245,784	430	9	,	CEP55	595		- ,
10	95,452,246	95,452,584	338	11	C10orf4.			PDE6C	36.829
10	97,309,881	97.310.397	516	9	SORBS1.	AL356632.12	23.326	ALDH18A1	45,280
10	97 337 589	97 337 952	363	9		RPS3AP36	6 393	AI 356632 12	3 792
10	97 443 733	97 444 177	444	10	TCTN3	ENTPD1	17 349		0,102
10	97 879 304	97 880 536	1 232	9	ZNE518	Litti Di	11,010	U6	16 706
10	98 262 275	98 262 727	452	11	TI I 2			TM9SE3	7 697
10	98 551 142	98 551 685	543	33	1222,	LCOR	30 344	hsa-mir-607	26 731
10	99 157 148	99 157 543	305	10		RRP12	6 061	1130-1111-007	20,701
10	00 433 640	00 131 000	360	11			0,001	ΡΙΛΚ2Δ	7 463
10	00 618 006	00 610 733	827	0					1,405
10	99,010,900	99,019,755	221	9	CRTACI,			GOLGA7B	21 547
10	101 079 719	101 070 220	601	10	CNINIM1	No non overlenni	na aonoo wit	GOLGATB	21,347
10	101,076,716	101,079,339	021	9	CININIVI I,	No non-ovenappi	12 FO2		
10	101,209,741	101,270,197	400	10		INRAZ-3	12,503		1 200
10	102,035,931	102,036,594	003	11	BLUC 152,	Ne nen evenlenni		PKDZLI	1,299
10	102,420,573	102,421,508	935	9			ng genes wit		07.000
10	102,628,102	102,629,059	957	9	1 77.00	FAMI178A	33,257		27,862
10	102,748,115	102,749,128	1,013	10	LZ I 52,			PEUT	3,967
10	102,764,130	102,764,522	392	10	PDZD7,			LZTSZ	6,547
10	103,103,404	103,104,573	1,169	10	BIRC,			U2	10,019
10	103,114,384	103,114,802	418	18	BTRC, U2,			AL133387.8-2	6,800
10	103,589,256	103,589,791	535	9	KCNIP2,			C100ff/6	5,555
10	103,736,342	103,736,755	413	9	C10orf76,	Y_RNA	33,891		10.1
10	103,817,944	103,818,235	291	11				HPS6	164
10	103,869,268	103,869,656	388	9		LDB1	4,576		
10	103,901,966	103,902,522	556	9	NOLC1,			PPRC1	1,888
10	103,995,038	103,995,716	678	11	GBF1,	PITX3	3,817		
10	104,181,409	104,182,720	1,311	14	CUEDC2,	hsa-mir-146b	3,539	FBXL15	8,526
10	104,668,222	104,668,708	486	10	CNNM2,	RP11-753C18.8	30,287	AS3MT	16,576
10	105,117,523	105,117,920	397	10	TAF5,	PCGF6	16,642	USMG5	20,868
10	105,482,855	105,483,414	559	9	SH3PXD2A,	No non-overlappi	ng genes wit	hin 50,000bp	
10	105,522,074	105,522,410	336	9	SH3PXD2A,	No non-overlappi	ng genes wit	hin 50,000bp	
10	105,821,272	105,821,635	363	9	COL17A1,			AL138761.12	7,781
10	105,871,258	105,871,763	505	14		C10orf78	43	C10orf79	7,873
10	109,802,345	109,802,667	322	9		No non-overlappi	ng genes wit	hin 50,000bp	
10	111,958,892	111,959,486	594	9	MXI1,	RP11-549L6.2	47,326		
10	111,960,911	111,961,402	491	9	MXI1,	RP11-549L6.2	45,410		
10	111,971,386	111,971,950	564	9	MXI1,	RP11-549L6.2	34,862		
10	111,975,798	111,976,353	555	13	MXI1,	RP11-549L6.2	30,459		
10	112,607,205	112,607,700	495	9		PDCD4	13,886	RBM20	17,989
10	114,505,437	114,506,029	592	9	VTI1A,	No non-overlappi	ng genes wit	hin 50,000bp	
10	115,428,547	115,429,018	471	9	CASP7,	NRAP	14,671	AL592546.7-1	24,387
10	115,429,461	115,430,026	565	10	CASP7,	NRAP	15,585	AL592546.7-1	23,379
10	116,571,035	116,572,003	968	9	FAM160B1,			RP11-106M7.2	10,116
10	118,546,581	118,546,879	298	10				AC016825.12	46,653
10	118,750,209	118,750,597	388	9	KIAA1598,			RP11-5G18.2	22,578
10	118,753,898	118,754,297	399	9	KIAA1598,			RP11-5G18.2	18,878
10	118,917,567	118,918,116	549	9		AL731557.7	6,483		
10	119,291,979	119,292,263	284	9	EMX2,	No non-overlappi	ng genes wit	hin 50,000bp	
10	119,795,956	119,796,444	488	9	RAB11FIP2,	CASC2	62		
10	120,650,794	120,651,147	353	9		RP11-215A21.2	28,690	RP11-498J9.1	31,029

10	120,948,858	120,949,222	364	10		GRK5	7,869		
10	121,346,186	121,347,076	890	9	TIAL1,	RP11-179H18.4	23,494		
10	122,600,593	122,600,976	383	10	WDR11,	No non-overlappi	ng genes wit	hin 50,000bp	
10	123,793,734	123,794,079	345	9	TACC2,	No non-overlappi	ng genes wit	hin 50,000bp	
10	124,628,549	124,629,632	1,083	13	FAM24B,	AC073585.8-1	3,653		
10	124,703,490	124,704,331	841	11	C10orf88,	PSTK	25,215	IKZF5	38,858
10	125,843,686	125,844,032	346	9		RP11-47G11.1	1,788		
10	126,407,534	126,407,891	357	10	FAM53B,	Y_RNA	36,864	METTL10	29,505
10	126,470,241	126,470,866	625	11	METTL10,	FAM175B	9,478		
10	127,168,279	127,168,717	438	10		RP11-359B3.1	15,788		
10	127,200,378	127,201,016	638	9		RP11-359B3.1	47,887		
10	127,564,460	127,564,950	490	15		DHX32	4,586	U2	4,085
10	127,565,234	127,565,643	409	14		DHX32	5,360	U2	3,392
10	127,565,704	127,566,027	323	11		DHX32	5,830	U2	3,008
10	127,567,939	127,568,378	439	9		FANK1	6,720	U2	657
10	127,568,805	127,570,166	1,361	12	U2,	FANK1	4,932		
10	127.570.568	127.571.276	708	12		U2	1.331		
10	127.573.914	127,574,706	792	12		FANK1	392		
10	127.574.824	127,575,656	832	13	FANK1.	U2	5.587		
10	127 926 254	127 926 778	524	10	ADAM12	AC026226.9	24 599		
10	130 215 054	130 215 596	542		, <u> </u>	No non-overlappi	na aenes wit	hin 50 000bp	
10	131 650 218	131 650 832	614	Q Q	EBF3.	No non-overlappi	na genes wit	hin 50,000bp	
10	132 263 509	132 263 861	352	9 Q	2010,	No non-overlappi	ng genee wit	hin 50,000bp	
10	133 886 564	133 887 133	569	9	STK32C		ng gonoo mi	DPYSL4	17 308
10	134 196 158	134 196 665	507	g	011020,		4 678		17,000
10	135 002 338	135 002 747	409	g			1 909	RP11-122K13.8	5 390
11	1 617 807	1 618 312	505	g		DIAD III	1,505	KRTAP5-5	9 294
11	1,017,007	1,010,012	468	10				PPM1	28 803
11	8 660 667	8 660 005	328	10		SNODA3	1 355		20,000
11	0,000,007	0,000,995	365	12	NFL27A,	SNORAJ	1,555	7NE1/3	684
11	9,507,551	9,307,090	300	9				ZNI 143	4 977
11	9,735,901	9,730,203	505	10				AC020250.10	20.446
11	10,504,049	10,505,154	277	10				AC100805.5-2	29,440
11	17 260 662	10,000,020	400	9		KON 111	2 4 4 0	AC 100605.5-2	30,740
11	17,309,003	17.370.003	400	9		KUNJII	3,449	ADUUO	940
11	20 026 271	20,026,740	379	10		No non ovorlanni	na aonos wit	hin 50 000hn	
11	29,926,371	29,926,749	378	10		No non-overlappi	ng genes wit	hin 50,000bp	
11 11 11	29,926,371 34,336,503 35,504,301	29,926,749 34,337,263	378 760	10 9		No non-overlappi ABTB2	ng genes wit 1,125	hin 50,000bp	
11 11 11	29,926,371 34,336,503 35,504,301 36,488,267	29,926,749 34,337,263 35,504,896	378 760 595	10 9 9	TDAE6	No non-overlappi ABTB2 AC090625.5-2	ng genes wit 1,125 146	hin 50,000bp	44.038
11 11 11 11	29,926,371 34,336,503 35,504,301 36,488,267	29,926,749 34,337,263 35,504,896 36,488,829	378 760 595 562	10 9 9 9	TRAF6,	No non-overlappi ABTB2 AC090625.5-2	ng genes wit 1,125 146	hin 50,000bp AC009656.11	44,938
11 11 11 11 11	29,926,371 34,336,503 35,504,301 36,488,267 45,804,638	29,926,749 34,337,263 35,504,896 36,488,829 45,804,874	378 760 595 562 236	10 9 9 9 10	TRAF6, AC044839.16-1,	No non-overlappi ABTB2 AC090625.5-2 CRY2	ng genes wit 1,125 146 20,731	hin 50,000bp AC009656.11 SLC35C1	44,938 13,496
11 11 11 11 11 11	29,926,371 34,336,503 35,504,301 36,488,267 45,804,638 46,217,345	29,926,749 34,337,263 35,504,896 36,488,829 45,804,874 46,217,737	378 760 595 562 236 392	10 9 9 9 10 9	TRAF6, AC044839.16-1,	No non-overlappi ABTB2 AC090625.5-2 CRY2 Y_RNA	ng genes wit 1,125 146 20,731 4,549	hin 50,000bp AC009656.11 SLC35C1	44,938 13,496
11 11 11 11 11 11 11	29,926,371 34,336,503 35,504,301 36,488,267 45,804,638 46,217,345 46,678,881 47,226,700	29,926,749 34,337,263 35,504,896 36,488,829 45,804,874 46,217,737 46,679,184	378 760 595 562 236 392 303	10 9 9 9 10 9 10	TRAF6, AC044839.16-1, ZNF408,	No non-overlappi ABTB2 AC090625.5-2 CRY2 Y_RNA ARHGAP1	ng genes wit 1,125 146 20,731 4,549 185	hin 50,000bp AC009656.11 SLC35C1	44,938 13,496
11 11 11 11 11 11 11 11	29,926,371 34,336,503 35,504,301 36,488,267 45,804,638 46,217,345 46,678,881 47,226,799	29,926,749 34,337,263 35,504,896 36,488,829 45,804,874 46,217,737 46,679,184 47,227,335	378 760 595 562 236 392 303 536	10 9 9 9 10 9 10 9 10	TRAF6, AC044839.16-1, ZNF408, ACP2, NR1H3, C11of21	No non-overlappi ABTB2 AC090625.5-2 CRY2 Y_RNA ARHGAP1	ng genes wit 1,125 146 20,731 4,549 185	hin 50,000bp AC009656.11 SLC35C1 DDB2 TMX2	44,938 13,496 9,460
11 11 11 11 11 11 11 11 11	29,926,371 34,336,503 35,504,301 36,488,267 45,804,638 46,217,345 46,678,881 47,226,799 57,265,107	29,926,749 34,337,263 35,504,896 36,488,829 45,804,874 46,217,737 46,679,184 47,227,335 57,265,865	378 760 595 562 236 392 303 536 758	10 9 9 9 10 9 10 9 9 9	TRAF6, AC044839.16-1, ZNF408, ACP2, NR1H3, C110rf31,	No non-overlappi ABTB2 AC090625.5-2 CRY2 Y_RNA ARHGAP1	ng genes wit 1,125 146 20,731 4,549 185	hin 50,000bp AC009656.11 SLC35C1 DDB2 TMX2	44,938 13,496 9,460 87
11 11 11 11 11 11 11 11 11 11 11 11 11 11	29,926,371 34,336,503 35,504,301 36,488,267 45,804,638 46,217,345 46,678,881 47,226,799 57,265,107 58,808,550	29,926,749 34,337,263 35,504,896 36,488,829 45,804,874 46,217,737 46,679,184 47,227,335 57,265,865 58,808,899 50,075,204	378 760 595 562 236 392 303 536 758 349	10 9 9 9 10 9 10 9 9 9 9	TRAF6, AC044839.16-1, ZNF408, ACP2, NR1H3, C11orf31,	No non-overlappi ABTB2 AC090625.5-2 CRY2 Y_RNA ARHGAP1 AP002358.3-3	ng genes wit 1,125 146 20,731 4,549 185 468	hin 50,000bp AC009656.11 SLC35C1 DDB2 TMX2 SRP_euk_arch	44,938 13,496 9,460 87 6,203
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11	29,926,371 34,336,503 35,504,301 36,488,267 45,804,638 46,217,345 46,678,881 47,226,799 57,265,107 58,808,550 59,074,523 59,000,112	29,926,749 34,337,263 35,504,896 36,488,829 45,804,874 46,217,737 46,679,184 47,227,335 57,265,865 58,808,899 59,075,304 59,000,460	378 760 595 562 236 392 303 536 758 349 781	10 9 9 10 9 10 9 9 10 12	TRAF6, AC044839.16-1, ZNF408, ACP2, NR1H3, C11orf31,	No non-overlappi ABTB2 AC090625.5-2 CRY2 Y_RNA ARHGAP1 AP002358.3-3	ng genes wit 1,125 146 20,731 4,549 185 468	hin 50,000bp AC009656.11 SLC35C1 DDB2 TMX2 SRP_euk_arch OSBP	44,938 13,496 9,460 87 6,203 23,143 7,097
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11	29,926,371 34,336,503 35,504,301 36,488,267 45,804,638 46,217,345 46,678,881 47,226,799 57,265,107 58,808,550 59,074,523 59,090,112	29,926,749 34,337,263 35,504,896 36,488,829 45,804,874 46,217,737 46,679,184 47,227,335 57,265,865 58,808,899 59,075,304 59,090,460	378 760 595 562 236 392 303 536 758 349 781 348	10 9 9 10 9 10 9 9 10 12 11	TRAF6, AC044839.16-1, ZNF408, ACP2, NR1H3, C11orf31,	No non-overlappi ABTB2 AC090625.5-2 CRY2 Y_RNA ARHGAP1 AP002358.3-3	ng genes wit 1,125 146 20,731 4,549 185 468	hin 50,000bp AC009656.11 SLC35C1 DDB2 TMX2 SRP_euk_arch OSBP OSBP	44,938 13,496 9,460 87 6,203 23,143 7,987
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11	29,926,371 34,336,503 35,504,301 36,488,267 45,804,638 46,217,345 46,678,881 47,226,799 57,265,107 58,808,550 59,074,523 59,090,112 62,115,540	29,926,749 34,337,263 35,504,896 36,488,829 45,804,874 46,217,737 46,679,184 47,227,335 57,265,865 58,808,899 59,075,304 59,090,460 62,115,844	378 760 595 562 236 392 303 536 758 349 781 348 304	10 9 9 10 9 10 9 9 10 12 11 11	TRAF6, AC044839.16-1, ZNF408, ACP2, NR1H3, C11orf31, TUT1,	No non-overlappi ABTB2 AC090625.5-2 CRY2 Y_RNA ARHGAP1 AP002358.3-3 EEF1G	ng genes wit 1,125 146 20,731 4,549 185 468 8,918	hin 50,000bp AC009656.11 SLC35C1 DDB2 TMX2 SRP_euk_arch OSBP OSBP MTA2	44,938 13,496 9,460 87 6,203 23,143 7,987 1,407
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11	29,926,371 34,336,503 35,504,301 36,488,267 45,804,638 46,217,345 46,678,881 47,226,799 57,265,107 58,808,550 59,074,523 59,090,112 62,115,540 62,365,5498	29,926,749 34,337,263 35,504,896 36,488,829 45,804,874 46,217,737 46,679,184 47,227,335 57,265,865 58,808,899 59,075,304 59,090,460 62,115,844 62,365,9424	378 760 595 562 236 392 303 536 758 349 781 348 304 524	10 9 9 10 9 10 9 9 10 12 11 11 10	TRAF6, AC044839.16-1, ZNF408, ACP2, NR1H3, C11orf31, TUT1, U2, C11orf2	No non-overlappi ABTB2 AC090625.5-2 CRY2 Y_RNA ARHGAP1 AP002358.3-3 EEF1G WDR74	ng genes wit 1,125 146 20,731 4,549 185 468 8,918 1,789 7,000	hin 50,000bp AC009656.11 SLC35C1 DDB2 TMX2 SRP_euk_arch OSBP OSBP MTA2	44,938 13,496 9,460 87 6,203 23,143 7,987 1,407
$ \begin{array}{c} 11\\ 11\\ 11\\ 11\\ 11\\ 11\\ 11\\ 11\\ 11\\ 11$	29,926,371 34,336,503 35,504,301 36,488,267 45,804,638 46,217,345 46,678,881 47,226,799 57,265,107 58,808,550 59,074,523 59,090,112 62,115,540 62,365,498 64,619,890	29,926,749 34,337,263 35,504,896 36,488,829 45,804,874 46,217,737 46,679,184 47,227,335 57,265,865 58,808,899 59,075,304 59,090,460 62,115,844 62,365,903 64,620,421	378 760 595 562 236 392 303 536 758 349 781 348 304 405 531	10 9 9 10 9 10 9 9 10 12 11 11 10 49	TRAF6, AC044839.16-1, ZNF408, ACP2, NR1H3, C11orf31, TUT1, U2, C11orf2, KATE	No non-overlappi ABTB2 AC090625.5-2 CRY2 Y_RNA ARHGAP1 AP002358.3-3 EEF1G WDR74 AP003068.3-1	ng genes wit 1,125 146 20,731 4,549 185 468 8,918 1,789 7,080	hin 50,000bp AC009656.11 SLC35C1 DDB2 TMX2 SRP_euk_arch OSBP OSBP MTA2 ZFPL1 DNA5EU20	44,938 13,496 9,460 87 6,203 23,143 7,987 1,407 7,440
11 11	29,926,371 34,336,503 35,504,301 36,488,267 45,804,638 46,217,345 46,678,881 47,226,799 57,265,107 58,808,550 59,074,523 59,090,112 62,115,540 62,365,498 64,619,890 65,235,897	29,926,749 34,337,263 35,504,896 36,488,829 45,804,874 46,679,184 47,227,335 57,265,865 58,808,899 59,075,304 59,090,460 62,115,844 62,365,903 64,620,421 65,236,288	378 760 595 562 236 392 303 536 758 349 781 348 304 405 531 445	10 9 9 10 9 10 9 9 10 12 11 11 10 49 11 9	TRAF6, AC044839.16-1, ZNF408, ACP2, NR1H3, C11orf31, TUT1, U2, C11orf2, KAT5, CEL 1	No non-overlappi ABTB2 AC090625.5-2 CRY2 Y_RNA ARHGAP1 AP002358.3-3 EEF1G WDR74 AP003068.3-1	ng genes wit 1,125 146 20,731 4,549 185 468 8,918 1,789 7,080 2,224	hin 50,000bp AC009656.11 SLC35C1 DDB2 TMX2 SRP_euk_arch OSBP OSBP MTA2 ZFPL1 RNASEH2C SNIX22	44,938 13,496 9,460 87 6,203 23,143 7,987 1,407 7,440 5,432 2,254
11 11	29,926,371 34,336,503 35,504,301 36,488,267 45,804,638 46,217,345 46,678,881 47,226,799 57,265,107 58,808,550 59,074,523 59,090,112 62,115,540 62,365,498 64,619,890 65,235,847 65,381,000	29,926,749 34,337,263 35,504,896 36,488,829 45,804,874 46,679,184 47,227,335 57,265,865 58,808,899 59,075,304 59,090,460 62,115,844 62,365,903 64,620,421 65,236,288 65,381,577	378 760 595 562 236 392 303 536 758 349 781 348 304 405 531 441	10 9 9 10 9 10 9 9 10 12 11 11 10 49 11 9 9	TRAF6, AC044839.16-1, ZNF408, ACP2, NR1H3, C11orf31, TUT1, U2, C11orf2, KAT5, CFL1,	No non-overlappi ABTB2 AC090625.5-2 CRY2 Y_RNA ARHGAP1 AP002358.3-3 EEF1G WDR74 AP003068.3-1 MUS81 AD004403.5.4	ng genes wit 1,125 146 20,731 4,549 185 468 8,918 1,789 7,080 3,224 200	hin 50,000bp AC009656.11 SLC35C1 DDB2 TMX2 SRP_euk_arch OSBP OSBP MTA2 ZFPL1 RNASEH2C SNX32	44,938 13,496 9,460 87 6,203 23,143 7,987 1,407 7,440 5,432 3,254
11 11	29,926,371 34,336,503 35,504,301 36,488,267 45,804,638 46,217,345 46,678,881 47,226,799 57,265,107 58,808,550 59,074,523 59,090,112 62,115,540 62,365,498 64,619,890 65,235,847 65,381,000 65,871,946	29,926,749 34,337,263 35,504,896 36,488,829 45,804,874 46,679,184 47,227,335 57,265,865 58,808,899 59,075,304 59,090,460 62,115,844 62,365,903 64,620,421 65,236,288 65,381,577 65,872,357	378 760 595 562 236 392 303 536 758 349 781 348 304 405 531 441 577	10 9 9 10 9 10 9 9 10 12 11 11 10 49 11 9 9 9	TRAF6, AC044839.16-1, ZNF408, ACP2, NR1H3, C11orf31, TUT1, U2, C11orf2, KAT5, CFL1, NDAS4	No non-overlappi ABTB2 AC090625.5-2 CRY2 Y_RNA ARHGAP1 AP002358.3-3 EEF1G WDR74 AP003068.3-1 MUS81 AP001107.5-1 SNOE 4.12	ng genes wit 1,125 146 20,731 4,549 185 468 8,918 1,789 7,080 3,224 209 10,707	hin 50,000bp AC009656.11 SLC35C1 DDB2 TMX2 SRP_euk_arch OSBP OSBP MTA2 ZFPL1 RNASEH2C SNX32 MRDL11	44,938 13,496 9,460 87 6,203 23,143 7,987 1,407 7,440 5,432 3,254
11 11	29,926,371 34,336,503 35,504,301 36,488,267 45,804,638 46,217,345 46,678,881 47,226,799 57,265,107 58,808,550 59,074,523 59,090,112 62,115,540 62,365,498 64,619,890 65,235,847 65,381,000 65,871,946 65,945,392 66,440,700	29,926,749 34,337,263 35,504,896 36,488,829 45,804,874 46,679,184 47,227,335 57,265,865 58,808,899 59,075,304 59,090,460 62,115,844 62,365,903 64,620,421 65,236,288 65,381,577 65,872,357 65,946,076	378 760 595 562 236 392 303 536 758 349 781 348 304 405 531 441 577 411 684	10 9 9 10 9 10 9 9 10 12 11 11 10 9 9 11 9 9 18 9	TRAF6, AC044839.16-1, ZNF408, ACP2, NR1H3, C11orf31, TUT1, U2, C11orf2, KAT5, CFL1, NPAS4, DEM4	No non-overlappi ABTB2 AC090625.5-2 CRY2 Y_RNA ARHGAP1 AP002358.3-3 EEF1G WDR74 AP003068.3-1 MUS81 AP001107.5-1 SNORA43	ng genes wit 1,125 146 20,731 4,549 185 468 8,918 1,789 7,080 3,224 209 10,737 4,572	hin 50,000bp AC009656.11 SLC35C1 DDB2 TMX2 SRP_euk_arch OSBP OSBP MTA2 ZFPL1 RNASEH2C SNX32 MRPL11	44,938 13,496 9,460 87 6,203 23,143 7,987 1,407 7,440 5,432 3,254 13,806
11 11	29,926,371 34,336,503 35,504,301 36,488,267 45,804,638 46,217,345 46,678,881 47,226,799 57,265,107 58,808,550 59,074,523 59,090,112 62,115,540 62,365,498 64,619,890 65,235,847 65,381,000 65,871,946 65,945,392 66,140,709 60,700,500	29,926,749 34,337,263 35,504,896 36,488,829 45,804,874 46,679,184 47,227,335 57,265,865 58,808,899 59,075,304 59,090,460 62,115,844 62,365,903 64,620,421 65,236,288 65,381,577 65,872,357 65,946,076 66,141,134	378 760 595 562 236 392 303 536 758 349 781 348 304 405 531 441 577 411 684 425	10 9 9 10 9 10 9 9 10 12 11 11 10 49 9 111 9 9 18 9 9	TRAF6, AC044839.16-1, ZNF408, ACP2, NR1H3, C11orf31, TUT1, U2, C11orf2, KAT5, CFL1, NPAS4, RBM4, FADD	No non-overlappi ABTB2 AC090625.5-2 CRY2 Y_RNA ARHGAP1 AP002358.3-3 EEF1G WDR74 AP003068.3-1 MUS81 AP001107.5-1 SNORA43 U4	ng genes wit 1,125 146 20,731 4,549 185 468 468 8,918 1,789 7,080 3,224 209 10,737 1,572	hin 50,000bp AC009656.11 SLC35C1 DDB2 TMX2 SRP_euk_arch OSBP OSBP MTA2 ZFPL1 RNASEH2C SNX32 MRPL11	44,938 13,496 9,460 87 6,203 23,143 7,987 1,407 7,440 5,432 3,254 13,806
$\begin{array}{c} 11 \\ 11 \\ 11 \\ 11 \\ 11 \\ 11 \\ 11 \\ 11$	29,926,371 34,336,503 35,504,301 36,488,267 45,804,638 46,217,345 46,678,881 47,226,799 57,265,107 58,808,550 59,074,523 59,090,112 62,115,540 62,365,498 64,619,890 65,235,847 65,381,000 65,871,946 65,945,392 66,140,709 69,726,593	29,926,749 34,337,263 35,504,896 36,488,829 45,804,874 46,679,184 47,227,335 57,265,865 58,808,899 59,075,304 59,090,460 62,115,844 62,365,903 64,620,421 65,236,288 65,381,577 65,872,357 65,946,076 66,141,134 69,727,341	378 760 595 562 236 392 303 536 758 349 781 348 304 405 531 441 577 411 684 425 778	10 9 9 10 9 9 10 9 9 10 12 11 11 10 49 9 111 9 9 9 18 9 9	TRAF6, AC044839.16-1, ZNF408, ACP2, NR1H3, C11orf31, TUT1, U2, C11orf2, KAT5, CFL1, NPAS4, RBM4, FADD, CLPD	No non-overlappi ABTB2 AC090625.5-2 CRY2 Y_RNA ARHGAP1 AP002358.3-3 EEF1G WDR74 AP003068.3-1 MUS81 AP001107.5-1 SNORA43 U4	ng genes wit 1,125 146 20,731 4,549 185 468 468 1,789 7,080 3,224 209 10,737 1,572	hin 50,000bp AC009656.11 SLC35C1 DDB2 TMX2 SRP_euk_arch OSBP OSBP MTA2 ZFPL1 RNASEH2C SNX32 MRPL11 ANO1 his 50,0001	44,938 13,496 9,460 87 6,203 23,143 7,987 1,407 7,440 5,432 3,254 13,806 13,312
11 11	29,926,371 34,336,503 35,504,301 36,488,267 45,804,638 46,217,345 46,678,881 47,226,799 57,265,107 58,808,550 59,074,523 59,090,112 62,115,540 62,365,498 64,619,890 65,235,847 65,381,000 65,871,946 65,945,392 66,140,709 69,726,593 71,822,797	29,926,749 34,337,263 35,504,896 36,488,829 45,804,874 46,679,184 47,227,335 57,265,865 58,808,899 59,075,304 59,090,460 62,115,844 62,365,903 64,620,421 65,236,288 65,381,577 65,872,357 65,946,076 66,141,134 69,727,341 71,823,387	378 760 595 562 236 392 303 536 758 349 781 348 304 405 531 441 577 411 684 425 748 590	10 9 9 10 9 9 10 9 9 10 12 11 10 49 11 9 9 11 9 9 15 9 12	TRAF6, AC044839.16-1, ZNF408, ACP2, NR1H3, C11orf31, TUT1, U2, C11orf2, KAT5, CFL1, NPAS4, RBM4, FADD, CLPB,	No non-overlappi ABTB2 AC090625.5-2 CRY2 Y_RNA ARHGAP1 AP002358.3-3 EEF1G WDR74 AP003068.3-1 MUS81 AP001107.5-1 SNORA43 U4 No non-overlappi	ng genes wit 1,125 146 20,731 4,549 185 468 468 8,918 1,789 7,080 3,224 209 10,737 1,572 ng genes wit	hin 50,000bp AC009656.11 SLC35C1 DDB2 TMX2 SRP_euk_arch OSBP OSBP MTA2 ZFPL1 RNASEH2C SNX32 MRPL11 ANO1 hin 50,000bp	44,938 13,496 9,460 87 6,203 23,143 7,987 1,407 7,440 5,432 3,254 13,806 13,312
11 11	29,926,371 34,336,503 35,504,301 36,488,267 45,804,638 46,217,345 46,678,881 47,226,799 57,265,107 58,808,550 59,074,523 59,090,112 62,115,540 62,365,498 64,619,890 65,235,847 65,381,000 65,871,946 65,945,392 66,140,709 69,726,593 71,822,797 72,531,193	29,926,749 34,337,263 35,504,896 36,488,829 45,804,874 46,217,737 46,679,184 47,227,335 57,265,865 58,808,899 59,075,304 59,090,460 62,115,844 62,365,903 64,620,421 65,236,288 65,381,577 65,872,357 65,946,076 66,141,134 69,727,341 71,823,387 72,531,492	378 760 595 562 236 392 303 536 758 349 781 348 304 405 531 441 577 411 684 425 748 590 299	10 9 9 10 9 9 10 9 9 10 12 11 10 49 11 9 9 18 9 9 15 9 12	TRAF6, AC044839.16-1, ZNF408, ACP2, NR1H3, C11orf31, TUT1, U2, C11orf2, KAT5, CFL1, NPAS4, RBM4, FADD, CLPB, MDEL 46	No non-overlappi ABTB2 AC090625.5-2 CRY2 Y_RNA ARHGAP1 AP002358.3-3 EEF1G WDR74 AP003068.3-1 MUS81 AP001107.5-1 SNORA43 U4 No non-overlappi FCHSD2	ng genes wit 1,125 146 20,731 4,549 185 468 468 8,918 1,789 7,080 3,224 209 10,737 1,572 ng genes wit 239 202	hin 50,000bp AC009656.11 SLC35C1 DDB2 TMX2 SRP_euk_arch OSBP OSBP MTA2 ZFPL1 RNASEH2C SNX32 MRPL11 ANO1 hin 50,000bp	44,938 13,496 9,460 87 6,203 23,143 7,987 1,407 7,440 5,432 3,254 13,806 13,312
$\begin{array}{c} 11\\ 11\\ 11\\ 11\\ 11\\ 11\\ 11\\ 11\\ 11\\ 11$	29,926,371 34,336,503 35,504,301 36,488,267 45,804,638 46,217,345 46,678,881 47,226,799 57,265,107 58,808,550 59,074,523 59,090,112 62,115,540 62,365,498 64,619,890 65,235,847 65,381,000 65,871,946 65,945,392 66,140,709 69,726,593 71,822,797 72,531,193 73,176,760	29,926,749 34,337,263 35,504,896 36,488,829 45,804,874 46,679,184 47,227,335 57,265,865 58,808,899 59,075,304 59,090,460 62,115,844 62,365,903 64,620,421 65,236,288 65,381,577 65,872,357 65,946,076 66,141,134 69,727,341 71,823,387 72,531,492 73,177,028	378 760 595 562 236 392 303 536 758 349 781 348 304 405 531 441 577 411 684 425 748 590 299 209	10 9 9 10 9 9 10 9 9 10 12 11 10 49 9 11 9 9 15 9 12 11 10	TRAF6, AC044839.16-1, ZNF408, ACP2, NR1H3, C11orf31, TUT1, U2, C11orf2, KAT5, CFL1, NPAS4, RBM4, FADD, CLPB, MRPL48,	No non-overlappi ABTB2 AC090625.5-2 CRY2 Y_RNA ARHGAP1 AP002358.3-3 EEF1G WDR74 AP003068.3-1 MUS81 AP001107.5-1 SNORA43 U4 No non-overlappi FCHSD2 RAB6A OD000	ng genes wit 1,125 146 20,731 4,549 185 468 8,918 1,789 7,080 3,224 209 10,737 1,572 ng genes wit 239 26,911	hin 50,000bp AC009656.11 SLC35C1 DDB2 TMX2 SRP_euk_arch OSBP OSBP MTA2 ZFPL1 RNASEH2C SNX32 MRPL11 ANO1 hin 50,000bp 7SK	44,938 13,496 9,460 87 6,203 23,143 7,987 1,407 7,440 5,432 3,254 13,806 13,312 44,042
11 11	29,926,371 34,336,503 35,504,301 36,488,267 45,804,638 46,217,345 46,678,881 47,226,799 57,265,107 58,808,550 59,074,523 59,090,112 62,115,540 62,365,498 64,619,890 65,235,847 65,381,000 65,871,946 65,945,392 66,140,709 69,726,593 71,822,797 72,531,193 73,176,760 74,337,410	29,926,749 34,337,263 35,504,896 36,488,829 45,804,874 46,679,184 47,227,335 57,265,865 58,808,899 59,075,304 59,090,460 62,115,844 62,365,903 64,620,421 65,236,288 65,381,577 65,872,357 65,946,076 66,141,134 69,727,341 71,823,387 72,531,492 73,177,028 74,337,950	378 760 595 562 236 392 303 536 758 349 781 348 304 405 531 441 577 411 684 425 748 590 299 268 590	10 9 9 10 9 9 10 9 9 10 12 11 10 49 9 11 9 9 15 9 12 11 11 10 0	TRAF6, AC044839.16-1, ZNF408, ACP2, NR1H3, C11orf31, TUT1, U2, C11orf2, KAT5, CFL1, NPAS4, RBM4, FADD, CLPB, MRPL48, XRRA1,	No non-overlappi ABTB2 AC090625.5-2 CRY2 Y_RNA ARHGAP1 AP002358.3-3 EEF1G WDR74 AP003068.3-1 MUS81 AP001107.5-1 SNORA43 U4 No non-overlappi FCHSD2 RAB6A SPCS2 WAUT44	ng genes wit 1,125 146 20,731 4,549 185 468 8,918 1,789 7,080 3,224 209 10,737 1,572 ng genes wit 239 26,911 25 02,545	hin 50,000bp AC009656.11 SLC35C1 DDB2 TMX2 SRP_euk_arch OSBP OSBP MTA2 ZFPL1 RNASEH2C SNX32 MRPL11 ANO1 hin 50,000bp 7SK	44,938 13,496 9,460 87 6,203 23,143 7,987 1,407 7,440 5,432 3,254 13,806 13,312 44,042
$\begin{array}{c} 11\\ 11\\ 11\\ 11\\ 11\\ 11\\ 11\\ 11\\ 11\\ 11$	29,926,371 34,336,503 35,504,301 36,488,267 45,804,638 46,217,345 46,678,881 47,226,799 57,265,107 58,808,550 59,074,523 59,090,112 62,115,540 62,365,498 64,619,890 65,235,847 65,381,000 65,871,946 65,945,392 66,140,709 69,726,593 71,822,797 72,531,193 73,176,760 74,337,410 75,623,935	29,926,749 34,337,263 35,504,896 36,488,829 45,804,874 46,217,737 46,679,184 47,227,335 57,265,865 58,808,899 59,075,304 59,090,460 62,115,844 62,365,903 64,620,421 65,236,288 65,381,577 65,872,357 65,946,076 66,141,134 69,727,341 71,823,387 72,531,492 73,177,028 74,337,950 75,624,740	378 760 595 562 236 392 303 536 758 349 781 348 304 405 531 441 577 411 684 425 748 590 299 268 540 805	10 9 9 10 9 9 10 9 9 10 12 11 10 49 9 11 9 9 15 9 12 11 11 10 10	TRAF6, AC044839.16-1, ZNF408, ACP2, NR1H3, C11orf31, TUT1, U2, C11orf2, KAT5, CFL1, NPAS4, RBM4, FADD, CLPB, MRPL48, XRRA1,	No non-overlappi ABTB2 AC090625.5-2 CRY2 Y_RNA ARHGAP1 AP002358.3-3 EEF1G WDR74 AP003068.3-1 MUS81 AP001107.5-1 SNORA43 U4 No non-overlappi FCHSD2 RAB6A SPCS2 WNT11	ng genes wit 1,125 146 20,731 4,549 185 468 8,918 1,789 7,080 3,224 209 10,737 1,572 ng genes wit 239 26,911 25 28,713	hin 50,000bp AC009656.11 SLC35C1 DDB2 TMX2 SRP_euk_arch OSBP OSBP MTA2 ZFPL1 RNASEH2C SNX32 MRPL11 ANO1 hin 50,000bp 7SK	44,938 13,496 9,460 87 6,203 23,143 7,987 1,407 7,440 5,432 3,254 13,806 13,312 44,042
$\begin{array}{c} 11\\ 11\\ 11\\ 11\\ 11\\ 11\\ 11\\ 11\\ 11\\ 11$	29,926,371 34,336,503 35,504,301 36,488,267 45,804,638 46,217,345 46,678,881 47,226,799 57,265,107 58,808,550 59,074,523 59,090,112 62,115,540 62,365,498 64,619,890 65,235,847 65,381,000 65,871,946 65,945,392 66,140,709 69,726,593 71,822,797 72,531,193 73,176,760 74,337,410 75,623,935 77,274,993	29,926,749 34,337,263 35,504,896 36,488,829 45,804,874 46,679,184 47,227,335 57,265,865 58,808,899 59,075,304 59,090,460 62,115,844 62,365,903 64,620,421 65,236,288 65,381,577 65,872,357 65,946,076 66,141,134 69,727,341 71,823,387 72,531,492 73,177,028 74,337,950 75,624,740 77,275,392	378 760 595 562 236 392 303 536 758 349 781 348 304 405 531 441 577 411 684 425 748 590 299 268 540 805 399	10 9 9 10 9 9 10 9 9 10 12 11 10 49 11 10 9 9 15 9 12 11 10 10 10 11	TRAF6, AC044839.16-1, ZNF408, ACP2, NR1H3, C11orf31, TUT1, U2, C11orf2, KAT5, CFL1, NPAS4, RBM4, FADD, CLPB, MRPL48, XRRA1, INTS4, AD002812.2	No non-overlappi ABTB2 AC090625.5-2 CRY2 Y_RNA ARHGAP1 AP002358.3-3 EEF1G WDR74 AP003068.3-1 MUS81 AP001107.5-1 SNORA43 U4 No non-overlappi FCHSD2 RAB6A SPCS2 WNT11	ng genes wit 1,125 146 20,731 4,549 185 468 8,918 1,789 7,080 3,224 209 10,737 1,572 ng genes wit 239 26,911 25 28,713	hin 50,000bp AC009656.11 SLC35C1 DDB2 TMX2 SRP_euk_arch OSBP MTA2 ZFPL1 RNASEH2C SNX32 MRPL11 ANO1 hin 50,000bp 7SK C11orf67	44,938 13,496 9,460 87 6,203 23,143 7,987 1,407 7,440 5,432 3,254 13,806 13,312 44,042 9,248
11 11	29,926,371 34,336,503 35,504,301 36,488,267 45,804,638 46,217,345 46,678,881 47,226,799 57,265,107 58,808,550 59,074,523 59,090,112 62,115,540 62,365,498 64,619,890 65,235,847 65,381,000 65,871,946 65,945,392 66,140,709 69,726,593 71,822,797 72,531,193 73,176,760 74,337,410 75,623,935 77,274,993	29,926,749 34,337,263 35,504,896 36,488,829 45,804,874 46,679,184 47,227,335 57,265,865 58,808,899 59,075,304 59,090,460 62,115,844 62,365,903 64,620,421 65,236,288 65,381,577 65,872,357 65,946,076 66,141,134 69,727,341 71,823,387 72,531,492 73,177,028 74,337,950 75,624,740 77,275,392	378 760 595 562 236 392 303 536 758 349 781 348 304 405 531 441 577 411 684 425 748 590 299 268 540 805 399	10 9 9 10 9 9 10 9 9 10 12 11 10 49 11 10 9 9 15 9 12 11 10 10 10 10	TRAF6, AC044839.16-1, ZNF408, ACP2, NR1H3, C11orf31, TUT1, U2, C11orf2, KAT5, CFL1, NPAS4, RBM4, FADD, CLPB, MRPL48, XRRA1, INTS4, AP002812.3, CCCDC002	No non-overlappi ABTB2 AC090625.5-2 CRY2 Y_RNA ARHGAP1 AP002358.3-3 EEF1G WDR74 AP003068.3-1 MUS81 AP001107.5-1 SNORA43 U4 No non-overlappi FCHSD2 RAB6A SPCS2 WNT11	ng genes wit 1,125 146 20,731 4,549 185 468 8,918 1,789 7,080 3,224 209 10,737 1,572 ng genes wit 239 26,911 25 28,713	hin 50,000bp AC009656.11 SLC35C1 DDB2 TMX2 SRP_euk_arch OSBP MTA2 ZFPL1 RNASEH2C SNX32 MRPL11 ANO1 hin 50,000bp 7SK C11orf67	44,938 13,496 9,460 87 6,203 23,143 7,987 1,407 7,440 5,432 3,254 13,806 13,312 44,042 9,248
11 11	29,926,371 34,336,503 35,504,301 36,488,267 45,804,638 46,217,345 46,678,881 47,226,799 57,265,107 58,808,550 59,074,523 59,090,112 62,115,540 62,365,498 64,619,890 65,235,847 65,381,000 65,871,946 65,945,392 66,140,709 69,726,593 71,822,797 72,531,193 73,176,760 74,337,410 75,623,935 77,274,993 82,674,975	29,926,749 34,337,263 35,504,896 36,488,829 45,804,874 46,679,184 47,227,335 57,265,865 58,808,899 59,075,304 59,090,460 62,115,844 62,365,903 64,620,421 65,236,288 65,381,577 65,872,357 65,946,076 66,141,134 69,727,341 71,823,387 72,531,492 73,177,028 74,337,950 75,624,740 77,275,392 82,675,350	378 760 595 562 236 392 303 536 758 349 781 348 304 405 531 441 577 411 684 425 748 590 299 268 540 805 399	10 9 9 9 10 9 9 10 10 12 11 10 49 11 10 9 9 12 11 10 10 10 11 11	TRAF6, AC044839.16-1, ZNF408, ACP2, NR1H3, C11orf31, TUT1, U2, C11orf2, KAT5, CFL1, NPAS4, RBM4, FADD, CLPB, MRPL48, XRRA1, INTS4, AP002812.3, CCDC90B, DLC2	No non-overlappi ABTB2 AC090625.5-2 CRY2 Y_RNA ARHGAP1 AP002358.3-3 EEF1G WDR74 AP003068.3-1 MUS81 AP001107.5-1 SNORA43 U4 No non-overlappi FCHSD2 RAB6A SPCS2 WNT11	ng genes wit 1,125 146 20,731 4,549 185 468 8,918 1,789 7,080 3,224 209 10,737 1,572 ng genes wit 239 26,911 25 28,713	hin 50,000bp AC009656.11 SLC35C1 DDB2 TMX2 SRP_euk_arch OSBP OSBP MTA2 ZFPL1 RNASEH2C SNX32 MRPL11 ANO1 hin 50,000bp 7SK C11orf67 ANKRD42	44,938 13,496 9,460 87 6,203 23,143 7,987 1,407 7,440 5,432 3,254 13,806 13,312 44,042 9,248 30,285
11 11	29,926,371 34,336,503 35,504,301 36,488,267 45,804,638 46,217,345 46,678,881 47,226,799 57,265,107 58,808,550 59,074,523 59,090,112 62,115,540 62,365,498 64,619,890 65,235,847 65,381,000 65,871,946 65,945,392 66,140,709 69,726,593 71,822,797 72,531,193 73,176,760 74,337,410 75,623,935 77,274,993 82,674,975 84,872,506	29,926,749 34,337,263 35,504,896 36,488,829 45,804,874 46,217,737 46,679,184 47,227,335 57,265,865 58,808,899 59,075,304 59,090,460 62,115,844 62,365,903 64,620,421 65,236,288 65,381,577 65,872,357 65,946,076 66,141,134 69,727,341 71,823,387 72,531,492 73,177,028 74,337,950 75,624,740 77,275,392 82,675,350 84,872,951	378 760 595 562 236 392 303 536 758 349 781 348 304 405 531 441 577 411 684 405 531 411 684 425 748 590 299 268 540 805 399 375 445	10 9 9 9 10 9 9 10 10 12 11 10 49 9 11 10 9 9 12 11 10 10 10 11 11 11 10	TRAF6, AC044839.16-1, ZNF408, ACP2, NR1H3, C11orf31, TUT1, U2, C11orf2, KAT5, CFL1, NPAS4, RBM4, FADD, CLPB, MRPL48, XRRA1, INTS4, AP002812.3, CCDC90B, DLG2, AP003035 2-1	No non-overlappi ABTB2 AC090625.5-2 CRY2 Y_RNA ARHGAP1 AP002358.3-3 EEF1G WDR74 AP003068.3-1 MUS81 AP001107.5-1 SNORA43 U4 No non-overlappi FCHSD2 RAB6A SPCS2 WNT11	ng genes wit 1,125 146 20,731 4,549 185 468 8,918 1,789 7,080 3,224 209 10,737 1,572 ng genes wit 239 26,911 25 28,713	hin 50,000bp AC009656.11 SLC35C1 DDB2 TMX2 SRP_euk_arch OSBP MTA2 ZFPL1 RNASEH2C SNX32 MRPL11 ANO1 hin 50,000bp 7SK C11orf67 ANKRD42	44,938 13,496 9,460 87 6,203 23,143 7,987 1,407 7,440 5,432 3,254 13,806 13,312 44,042 9,248 30,285

11	85,633,554	85,633,981	427	11	EED,	No non-overlappi	ng genes wit	hin 50,000bp	
11	86,426,318	86,426,863	545	9	TMEM135,	No non-overlappi	ng genes wit	hin 50,000bp	
11	87,917,125	87,917,469	344	9	GRM5,	No non-overlappi	ng genes wit	hin 50,000bp	
11	91,772,494	91,772,884	390	9	FAT3,	No non-overlappi	ng genes wit	hin 50,000bp	
11	95,716,058	95,716,343	285	10				CCDC82	9,246
11	103,539,819	103,540,345	526	9	PDGFD,	No non-overlappi	ng genes wit	hin 50,000bp	
11	109,672,264	109,672,588	324	9	RDX,	No non-overlappi	ng genes wit	hin 50,000bp	
11	111,312,894	111,313,286	392	9	DIXDC1,	CRYAB	25,190	C11orf52	10,090
11	111,449,865	111,450,328	463	12	PIH1D2,			DLAT	9,541
					C11orf57,				
11	112,337,009	112,337,406	397	9	NCAM1,	No non-overlappi	ng genes wit	hin 50,000bp	
11	114,957,922	114,958,268	346	10				AP000997.1	44,744
11	116,211,647	116,212,219	572	9	APOA1,			APOC3	2,649
11	116,244,069	116,244,377	308	10	AP006216.9,	APOA1	30,498	APOC3	35,071
11	118,303,874	118,304,280	406	9		SRP_euk_arch	2,850		
11	119,728,572	119,728,941	369	9	ARHGEF12,			TMEM136	22,016
11	119,886,756	119,887,318	562	9		AP002348.3	403		
11	122,437,768	122,438,503	735	9	HSPA8.	SNORD14	2.428	AP000926.6-1	9.742
11	122,806,797	122.807.074	277	10	,	No non-overlappi	na aenes wit	hin 50.000bp	- 1
11	125.000.816	125,001,168	352	17		CHEK1	379	STT3A	4.654
12	928.618	929.667	1.049	9	RAD52.	ERC1	40,998	WNK1	37,739
12	1 570 129	1 570 414	285	10	FBXI 14	WNT5B	26,069		01,100
12	1 571 841	1,572,613	772	10	FBXL14	WNT5B	23,870		
12	1,371,041	1,372,013	307	10		WINISE	20,070		7 507
12	1,775,012	1,775,919	046	10			18 123		7,507
12	2 014 297	2 014 796	400	9	DCF ID,		40,423		
12	2,014,207	2,014,700	499	10		CACINA IC	17,939	AC006122.24	2 204
12	4,300,049	4,300,303	400	0			113	AC000122.24	3,294
12	4,516,075	4,316,703	571	9	RADSTAPT,	ACUUOU12.0	140 na aonao wit	hin EQ QQQhn	
12	5,407,913	0,400,404	000	9			ng genes wit		
12	0,174,889	0,175,518	629	9		CD9	3,624		0.000
12	6,314,870	0,315,453	583	11	INFROFIA,			PLEKHGO	6,960
12	6,472,429	6,472,903	4/4	9	MRPL51,	NCAPD2	626		0.070
12	0,514,353	6,514,869	010	9	GAPDH,		000	NCAPDZ	2,972
12	0,587,735	0,588,034	299	10		CHD4	923		774
12	6,596,998	6,597,491	493	9	1104	4.0405404.0.0	0.004		771
12	6,642,241	6,643,058	817	10	ING4,	AC125494.2-2	3,631	ZNF384	2,846
12	6,671,830	6,672,362	532	10		ZNF384	2,900	C120ff53	859
12	6,732,826	6,733,398	572	9		MLF2	296		
12	6,743,619	6,744,093	4/4	11	000400	PIMS	1,709	0.5.4	0 700
12	6,803,999	6,805,310	1,311	9	GPR162,	LEPREL2	2,523	CD4	3,762
12	6,903,664	6,904,160	496	11	AIN1,	0.10.777		ENO2	544
12	6,917,263	6,917,675	412	18	AIN1,	C120ff57	5,789		10.001
12	8,270,233	8,270,562	329	9	FAM90A1,			ZNF705A	46,324
12	8,993,204	8,993,721	517	10	M6PR,			PHC1	7,879
12	10,197,184	10,197,496	312	16				ULR1	4,675
12	10,407,964	10,409,039	1,075	9	KLRK1,			KLRC4	42,211
12	10,657,285	10,657,586	301	11	MAGOHB,	077/1/1		STYK1	5,463
12	10,765,833	10,766,403	570	9	CSDA,	STYK1	47,675		
12	10,793,954	10,794,424	470	9	T100	CSDA	26,776		
12	11,214,823	11,215,596	773	9	TAS2R14,			AC134349.2	7,791
12	11,530,745	11,531,143	398	10		No non-overlappi	ng genes wit	hin 50,000bp	
12	11,692,653	11,693,531	878	9		ETV6	524		
12	13,299,929	13,300,349	420	9				EMP1	38,955
12	14,301,713	14,302,411	698	10		AC092112.17	7,172		
12	14,342,304	14,342,591	287	9		AC092112.17	47,763		
12	15,926,261	15,926,650	389	11	STRAP,	No non-overlappi	ng genes wit	hin 50,000bp	
12	20,595,454	20,595,915	461	91	PDE3A,	No non-overlappi	ng genes wit	hin 50,000bp	
					AC112777.7,				
12	21,481,626	21,482,102	476	10	PYROXD1,	AC006559.6-1	20,710	AC006559.6-2	28,654
12	22,026,055	22,026,371	316	9		ABCC9	40,452		
12	22,379,343	22,379,888	545	9		ST8SIA1	428		
12	22,588,673	22,589,099	426	10	KIAA0528,	No non-overlappi	ng genes wit	hin 50,000bp	
12	22,669,719	22,670,430	711	9	ETNK1,	No non-overlappi	ng genes wit	hin 50,000bp	
12	24,605,177	24,605,476	299	9				C12orf67	5,689
12	26,158,035	26,158,629	594	9				BHLHE41	5,599

12	26,169,582	26,170,026	444	10		BHLHE41	469		
12	26 318 856	26 319 306	450	11				SSPN	41 722
12	27 047 837	27 048 201	100	0	TM7SE3	MED21	18 / 50	EGER1OP2	27 566
12	27,047,007	27,040,231	202	9	11017-01-0,		10, 4 09	hin 50 000hn	27,500
12	27,223,903	27,224,303	744	9	CTI/201	No non-overlappi	ng genes wit	hin 50,000bp	
12	27,200,011	27,200,700	744	10	STRJOL,	No non-ovenappi	ng genes wit		7.054
12	27,377,506	27,378,080	5/4	9	ARNTLZ,	10000500 7 4		SIKJOL	7,351
12	27,711,734	27,712,167	433	9	PPFIBP1,	AC009509.7-1	28,528		
12	30,799,238	30,799,810	572	9		CAPRIN2	523		
12	30,841,042	30,841,374	332	9		AC010198.8	23,438		
12	30,994,693	30,994,978	285	9	TSPAN11,	AC008013.8-1	44,996		
12	34,263,685	34,264,101	416	35	AC140847.4-2,			5S_rRNA	13,666
12	36,730,861	36,731,160	299	10		No non-overlappi	ng genes wit	hin 50,000bp	
12	36,735,840	36,736,476	636	9		No non-overlappi	ng genes wit	hin 50,000bp	
12	36,829,860	36,830,269	409	9				5S_rRNA	11,266
12	37,585,223	37,586,416	1,193	9	CPNE8,	No non-overlappi	ng genes wit	hin 50,000bp	
12	37,586,787	37,587,067	280	12	CPNE8,	No non-overlappi	ng genes wit	hin 50,000bp	
12	40.774.231	40.774.713	482	9	GLT8D3.		00	AC023513.21	14,280
12	41 005 731	41 006 411	680	9	ZCRB1			AC020629 6-3	37 102
	11,000,701	11,000,111	000	0	PPHLN1.			/10020020.0 0	01,102
12	44,407,591	44,408,052	461	10	,	ARID2	1.835		
12	44 408 742	44 409 223	481	9		ARID2	664		
12	44 670 570	44 670 923	353	10	SERS2IP	No non-overlanni	na aenes wit	hin 50 000hn	
12	45.062.099	45,070,520	500	10	011(0211,		2 411	1111 30,000bp	
12	45,005,000	45,005,052	373	10	CL C 20 A 4	SLCJOAZ	2,411	hin EO 000hn	
12	45,477,195	45,477,507	312	9	SLUJOA4,	No non-ovenappi	ng genes wit		22.000
12	40,438,031	46,439,496	605	9	RAPGEF3,	SLC48A1	13,762		23,280
12	46,701,507	46,702,388	881	9		COL2A1	16,955	SENP1	20,560
12	46,786,169	46,786,574	405	10		SENP1	283		
12	47,396,542	47,397,008	466	10	CCNT1,	C12orf41	34,272	ADCY6	49,240
12	47,475,817	47,476,312	495	9		ADCY6	6,730		
12	47,570,596	47,571,080	484	9				U6	1,100
12	47,583,982	47,584,808	826	9	CCDC65,	U6	11,704	FKBP11	17,211
12	47,790,489	47,791,326	837	9	LMBR1L,	DHH	15,620	TUBA1B	16,510
12	47,807,259	47,807,601	342	9				TUBA1B	235
12	47,868,838	47,869,538	700	9	TUBA1A,	AC010173.27	21,633		
12	47,968,390	47,969,162	772	10		PRPH	4,590		
12	47,972,982	47,973,915	933	9	PRPH,	TROAP	29,323	TUBA1C	19,599
12	48,421,536	48,421,825	289	10	TMBIM6,	FMNL3	34,072	KIAA1602	49,377
12	48,548,844	48,549,436	592	9	AC131157.4-3,			AC131157.4-4	8,310
					FAIM2,				
12	48,963,495	48,964,111	616	9	LIMA1,	AC140061.14-1	6,900	AC008147.31-1	605
12	49,706,153	49,706,427	274	9	SLC11A2,	U6	11,122	CSRNP2	34,830
12	49.727.919	49.728.911	992	9	LETMD1.	SLC11A2	19.644	U6	10.267
12	50 051 453	50 051 956	503	10	GALNT6	SI C4A8	19 443		-, -
12	50 705 309	50 706 348	1 039	. 0 Q			,	GRASP	9 394
12	50 749 416	50 749 808	392	12		C12orf44	217	NR4A1	9 858
12	51 660 732	51 661 253	521	12		FIF4R	25 076	KRT18P10	27 781
12	51 830 477	51 830 810	333	10	CSAD		20,070	AC.073573 27-2	4 936
10	51 950 016	51 960 704	202 205	9	CSAD		2 010	AUU13313.21-2	4,900
12	52 356 016	52 256 272	257	9	ATP502	AC072504 24	10 01		21 707
12	52,350,010	52,300,373	35/	15	AIFOGZ,	70013394.31	42,814		54,/9/
12	52,098,543	52,699,049	anc	10					5,729
12	52 712 269	52 712 004	526	0	HOXC4	hsa_mir_615	07	HOXCE	2 /0/
12	52,715,500	52,715,904	550	9		115a-1111-015	57	TIOACO	2,494
12	52 732 662	52 733 300	638	٥	HOXC4			HOXC5	17 250
12	52 877 083	52 877 840	766	۵ ۵		SMUG1	8 050		11,200
12	53 072 775	53 073 104	/10	9		ZNE3854	1 //2		2 122
10	53 112 050	53 112 052	704	9			10 7/4	GTSF1	2,122
12	53 229 677	53 220 100	194	11			10 100		23,100
12	52,530,077	52 627 044	431	9		No pop overlar	10,133	hin EO OOOka	
12	53,030,538	53,037,214	0/0	9	riaau148,	No non-overlappi	ng genes wit		04 500
12	53,731,591	53,731,914	323	9			E 00 /		21,526
12	54,417,185	54,417,500	315	9		GUETT	5,831	ACUU9//9.18	5,208
12	54,654,381	54,054,763	382	10	KAB5B,	SILV	7,616		1,549
12	54,796,259	54,796,976	/17	9	7001110	2C3H10	1,321	PA2G4P4	3,060
12	54,797,714	54,798,849	1,135	9	ZC3H10,	FAM62A	9,469	PA2G4P4	4,515
12	54,808,043	54,808,540	497	10	FAM62A,			ZC3H10	5,498

12	54,868,634	54,869,153	519	12	SMARCC2,	OBFC2B	35,257	RNF41	15,402
12	54,870,079	54,870,610	531	13		SMARCC2	461		
12	54,903,909	54,904,445	536	10	OBFC2B,	RNF41	1,938		
12	55,274,017	55,274,382	365	12				BAZ2A	1,265
12	55,316,790	55,317,444	654	10		BAZ2A	360	ATP5B	786
12	55,893,376	55,893,738	362	10	LRP1,	NXPH4	3,107		
12	56,585,365	56,585,802	437	9		XRCC6BP1	35,825		
12	59,476,761	59,477,135	374	10		No non-overlappi	ng genes wit	hin 50,000bp	
12	62,459,934	62,460,327	393	9	TMEM5,	No non-overlappi	ng genes wit	hin 50,000bp	
12	62,523,761	62,524,281	520	11		SRGAP1	527		
12	62,902,223	62,902,791	568	10	C12orf66,			U6	17,277
12	63,460,965	63,461,520	555	11		TBC1D30	4,538		
12	64,408,887	64,409,891	1,004	9				RPSAP52	28,179
12	64,810,344	64,811,236	892	10	LLPH,			TMBIM4	5,749
12	65,949,058	65,949,661	603	10	CAND1,	No non-overlappi	ng genes wit	hin 50,000bp	
12	67,119,921	67,120,388	467	9		No non-overlappi	ng genes wit	hin 50,000bp	
12	67,366,751	67,367,323	572	10	NUP107,	AC015550.19-2	43,750	RAP1B	26,197
12	67,487,966	67,488,468	502	9	MDM2,			SLC35E3	41,846
12	67,488,656	67,489,193	537	9	MDM2,			CPM	42,034
12	68,922,554	68,923,666	1,112	9	CNOT2,	No non-overlappi	ng genes wit	hin 50,000bp	
12	69,045,122	69,045,641	519	9		KCNMB4	688		
12	69,046,800	69,047,288	488	9	KCNMB4,			CNOT2	11,760
12	74,070,852	74,071,578	726	11	CAPS2,			GLIPR1L1	20,420
10	74 404 047	74 404 070	050	0	GLIPR1L2,				0.005
12	74,191,317	74,191,976	659	9	KRR1,			GLIPR1	9,335
12	75,265,890	75,266,782	892	9	BBS10,	NI		USBPL8	2,938
12	75,681,617	75,682,391	//4	9	ZDHHC17,	No non-overlappi	ng genes wit	nin 50,000bp	
12	78,608,737	78,609,561	824	9	PAWR,	No non-overlappi	ng genes wit	nin 50,000p	
12	78,631,082	78,031,318	230	9		PAWR	22,101		
12	78,858,253	78,858,537	284	10		PPP1R12A	5,411		
12	79,105,588	79,105,888	300	10	040	C120ff64	20,226		
12	79,134,852	79,135,269	417	9	C120ff64,	No non-overlappi	ng genes wit	nin 50,000p	
12	81,276,036	81,276,702	000	17	CCDC59, C12orf26	AC083811.22	15,416		
12	02 360 020	02 360 303	364	10	LIBE2N		25.008		18 230
12	92,300,029	92,300,393	792	10 Q	MRPL 42	Y RNA	<u> </u>		10,233
12	02 003 1/2	92,000,101	528	3 0		No non-overlanni	0,000 na aenes wit	hin 50 000hn	
12	94 035 259	94 035 549	290	9	FGD6	NR2C1	43 760	AC126615 7	16 336
12	94 135 503	94 136 260	757	11	VEZT	FGD6	132	A0120010.1	10,000
12	94 953 630	94 954 075	445	14	VL21,	ТА4Н	134		
12	97 421 237	97 421 689	452	21		TMPO	11 847		
12	97 421 946	97 422 315	369	12		TMPO	11 221		
12	97 562 804	97 563 344	540	10	AC013283 23-2	APAF1	,	AC013283 23-3	38 935
12	100 325 790	100 326 314	524	11	710010200.20 2,	ARI 1	87	710010200.20 0	00,000
12	102 874 776	102 875 570	794	12	C12orf73	TDG	8 171	HSP90B1	8 967
12	102 883 388	102 884 269	881	10	TDG.	C12orf73	8 337		0,007
12	103,204 837	103.205 373	536	.0	TXNRD1		0,007	RPL18AP3	21 018
12	103.876 415	103.876 772	357	<u>9</u>		C12orf45	27 456	AC090051.8	17,885
12	104.025.069	104.026.079	1.010		KIAA1033.	AC016257.22	21.716		,000
12	105.275.532	105.276.592	1.060	.9	POLR3B.		,0	TCP11L2	10.612
12	107.046.787	107.047.256	469	9		WSCD2	385		
12	107,434,254	107,434,857	603	9	FICD.			SART3	5.265
12	108.399.552	108.399.883	331	10	UBE3B.	KCTD10	14		-,
12	108.575.135	108.575.754	619	9	/			7SK	9.297
12	108.970.557	108.971.057	500	10	AC007546.6-1.			AC007546.6-2	2,113
12	109,390,489	109.391.076	587	10	C12orf24,	GPN3	42		_,•
12	109.391.196	109.391.663	467	11	C12orf24	GPN3	749		
12	110,103.264	110,103.576	312	10	CUX2.	No non-overlappi	ng genes wit	hin 50,000bp	
12	110,318.971	110,319.509	538	9	. ,	SH2B3	8.626		
12	110.500.791	110.501 142	351		ATXN2.	No non-overlappi	ng genes wit	hin 50,000bp	
12	110,936,166	110,936.578	412	12	ERP29.	TMEM116	840		
12	111,038,735	111,039,217	482	9	- ,	C12orf30	7,755		
12	111,331.202	111,332,115	913	13	RPL6P27,	PTPN11	8,804		
12	112,361,670	112,362,030	360	9	,			SDSL	1,207
12	113,604,635	113,604,994	359	10	TBX3,	Y_RNA	24,385		

12	113,606,136	113,606,835	699	9	TBX3,	Y_RNA	25,886		
12	115,464,835	115,465,390	555	9				NCRNA00173	7,126
12	117.024.277	117.024.710	433	9	AC131238.3.	PEBP1	33,543	TAOK3	47.282
12	119 214 187	119 214 628	441	10		U4	98	U4	655
12	119 247 670	119 248 007	337	10	PLA2G1B	114	32 247	SIRT4	12 240
12	119 352 673	119 353 031	358	15	,	COX6A1	7 256		,
12	119 359 940	119 360 503	563	10	COX6A1	GATC	8 150	TRIAP1	5 645
12	110,000,040	110,000,000	708	a	TRIAP1 GATC	0,110	0,100	AL 021546 3	3 850
12	110 / 17 0/2	110,000,772	518	10				COO5	7,006
12	119,417,942	119,410,400	310	10	CARD1		20.022	0000	7,000
12	119,306,934	119,509,399	440	9			39,933		
12	119,571,297	119,571,869	5/2	10	CABP1,	MLEC	37,463		0.040
12	119,927,513	119,927,955	442	9	C12orf43,			HNF1A	2,818
12	120,274,335	120,274,902	567	10	ANAPC5,	RNF34	47,402		
12	120,365,403	120,365,768	365	9	FBXL10,			RNF34	18,865
12	120,547,060	120,547,432	372	10		ORAI1	1,426		
12	120,810,356	120,811,274	918	14	PSMD9,	HPD	29,204		
12	121,450,425	121,450,761	336	9	CLIP1,	No non-overlappi	ng genes wit	hin 50,000bp	
12	121,551,237	121,551,986	749	10	ZCCHC8,			RSRC2	3,240
12	121,802,823	121,803,442	619	10		DENR	760		
12	121,945,876	121,946,142	266	10	VPS37B,			HIP1R	32,416
12	122,508,442	122,508,999	557	9	AC145423.8,	RILPL2	21,225	RILPL1	13,317
12	122,582,661	122,583,035	374	9	RILPL1.	No non-overlappi	na aenes wit	hin 50.000bp	,
12	122 632 625	122 633 032	407	11		TMED2	1 997		
12	123 795 360	123 795 732	372	12			1,001	SCARB1	32 407
12	123,822,453	123,822,821	368	12				SCARB1	5 318
12	123,022,455	123,022,021	500	10				AC126300.8	12 080
12	123,903,033	123,903,002	207	10	060,		6 602	AC120309.0	12,900
12	123,972,133	123,972,420	207	11			0,003		40 700
12	123,978,195	123,978,533	338	15		OBC	12,665	DHX37	18,793
12	123,989,998	123,990,728	730	19				DHX37	6,598
12	123,990,828	123,991,490	662	14				DHX37	5,836
12	124,043,199	124,043,708	509	9		BRI3BP	439		
12	124,046,055	124,046,392	337	9	BRI3BP,	DHX37	6,435		
40	126 216 249	126 217 091	033	57	AC070040 45	No non ovorlanni	na aonoo wit	hin EO OOOhn	
12	120,210,240	120,217,001	000	51	A0073343.43,	No non-ovenappi	ng genes wit	1111 30,000bp	
12 12	130,031,893	130,032,262	369	9	GPR133,	No non-ovenappi	ng genes wit	AC078925.18	47,912
12 12 12	130,031,893 130,761,260	130,032,262 130,761,925	369 665	9	GPR133, SFRS8,		ng genes wit	AC078925.18 5S_rRNA	47,912 49,588
12 12 12 12 12	130,031,893 130,761,260 131,853,864	130,032,262 130,761,925 131,854,268	369 665 404	9 9 11	GPR133, SFRS8,	ANKLE2	5,340	AC078925.18 5S_rRNA GOLGA3	47,912 49,588 1,300
12 12 12 12 12 12	120,210,248 130,031,893 130,761,260 131,853,864 131,915,470	120,217,081 130,032,262 130,761,925 131,854,268 131,915,802	369 665 404 332	9 9 11 11	GPR133, SFRS8,	ANKLE2 GOLGA3	5,340 109	AC078925.18 5S_rRNA GOLGA3	47,912 49,588 1,300
12 12 12 12 12 12 12 12	130,031,893 130,761,260 131,853,864 131,915,470 132,166,614	130,032,262 130,761,925 131,854,268 131,915,802 132,166,962	369 665 404 332 348	9 9 11 11 10	GPR133, SFRS8,	ANKLE2 GOLGA3 ZNF140	5,340 109 148	AC078925.18 5S_rRNA GOLGA3 Y_RNA	47,912 49,588 1,300 7,210
12 12 12 12 12 12 12 12 13	130,031,893 130,761,260 131,853,864 131,915,470 132,166,614 26,931,536	130,032,262 130,761,925 131,854,268 131,915,802 132,166,962 26,932,147	369 665 404 332 348 611	9 9 11 11 10 39	GPR133, SFRS8,	ANKLE2 GOLGA3 ZNF140 MTIF3	5,340 5,340 109 148 8,825	AC078925.18 5S_rRNA GOLGA3 Y_RNA	47,912 49,588 1,300 7,210
12 12 12 12 12 12 12 13 13	$\begin{array}{r} 120,210,248\\ 130,031,893\\ 130,761,260\\ 131,853,864\\ 131,915,470\\ 132,166,614\\ 26,931,536\\ 30,089,915 \end{array}$	130,032,262 130,761,925 131,854,268 131,915,802 132,166,962 26,932,147 30,090,269	369 665 404 332 348 611 354	9 9 11 11 10 39 9	GPR133, SFRS8, USPL1,	ANKLE2 GOLGA3 ZNF140 MTIF3 HMGB1	5,340 5,340 109 148 8,825 181	AC078925.18 5S_rRNA GOLGA3 Y_RNA	47,912 49,588 1,300 7,210
12 12 12 12 12 12 12 13 13 13	130,031,893 130,761,260 131,853,864 131,915,470 132,166,614 26,931,536 30,089,915 30,681,361	130,032,262 130,761,925 131,854,268 131,915,802 132,166,962 26,932,147 30,090,269 30,681,939	369 665 404 332 348 611 354 578	9 9 11 11 10 39 9 9	USPL1, B3GALTL.	ANKLE2 GOLGA3 ZNF140 MTIF3 HMGB1 HSPH1	5,340 5,340 109 148 8,825 181 47,244	AC078925.18 5S_rRNA GOLGA3 Y_RNA	47,912 49,588 1,300 7,210
12 12 12 12 12 12 13 13 13 13 13	$\begin{array}{r} 120,210,248\\ 130,031,893\\ 130,761,260\\ 131,853,864\\ 131,915,470\\ 132,166,614\\ 26,931,536\\ 30,089,915\\ 30,681,361\\ 47,510,005 \end{array}$	130,032,262 130,761,925 131,854,268 131,915,802 132,166,962 26,932,147 30,090,269 30,681,939 47,510,363	369 665 404 332 348 611 354 578 358	9 9 111 11 10 39 9 9 9 9	USPL1, B3GALTL, NUDT15.	ANKLE2 GOLGA3 ZNF140 MTIF3 HMGB1 HSPH1 SUCLA2	5,340 109 148 8,825 181 47,244 36,542	AC078925.18 5S_rRNA GOLGA3 Y_RNA MED4	47,912 49,588 1,300 7,210 37,730
12 12 12 12 12 12 13 13 13 13 13	$\begin{array}{r} 120,210,243\\ 130,031,893\\ 130,761,260\\ 131,853,864\\ 131,915,470\\ 132,166,614\\ 26,931,536\\ 30,089,915\\ 30,681,361\\ 47,510,005\\ 47,566,697\\ \end{array}$	130,032,262 130,761,925 131,854,268 131,915,802 132,166,962 26,932,147 30,090,269 30,681,939 47,510,363 47,567,395	369 665 404 332 348 611 354 578 358 698	9 9 111 11 10 39 9 9 9 9 9 9	USPL1, B3GALTL, NUDT15, MED4	ANKLE2 GOLGA3 ZNF140 MTIF3 HMGB1 HSPH1 SUCLA2	5,340 109 148 8,825 181 47,244 36,542	AC078925.18 5S_rRNA GOLGA3 Y_RNA MED4 AI 158196.24	47,912 49,588 1,300 7,210 37,730 39,100
12 12 12 12 12 12 13 13 13 13 13 13 13	120,210,243 130,031,893 130,761,260 131,853,864 131,915,470 132,166,614 26,931,536 30,089,915 30,681,361 47,510,005 47,566,697 50,384,088	$\begin{array}{r} 120,217,03\\ 130,032,262\\ 130,761,925\\ 131,854,268\\ 131,915,802\\ 132,166,962\\ 26,932,147\\ 30,090,269\\ 30,681,939\\ 47,510,363\\ 47,567,395\\ 50,384,551\\ \end{array}$	369 665 404 332 348 611 354 578 358 698 463	9 9 111 11 10 39 9 9 9 9 9 9	USPL1, B3GALTL, NUDT15, MED4, RNASEH2B	ANKLE2 GOLGA3 ZNF140 MTIF3 HMGB1 HSPH1 SUCLA2	5,340 109 148 8,825 181 47,244 36,542	AC078925.18 5S_rRNA GOLGA3 Y_RNA MED4 AL158196.24 bin 50 000bp	47,912 49,588 1,300 7,210 37,730 39,100
12 12 12 12 12 12 13 13 13 13 13 13 13 13	120,210,248 130,031,893 130,761,260 131,853,864 131,915,470 132,166,614 26,931,536 30,089,915 30,681,361 47,510,005 47,566,697 50,384,088 51,922,465	$\begin{array}{r} 120,217,03\\ 130,032,262\\ 130,761,925\\ 131,854,268\\ 131,915,802\\ 132,166,962\\ 26,932,147\\ 30,090,269\\ 30,681,939\\ 47,510,363\\ 47,567,395\\ 50,384,551\\ 51,923,047\\ \end{array}$	369 665 404 332 348 611 354 578 358 698 463 582	9 9 111 11 10 39 9 9 9 9 9 9 11	USPL1, B3GALTL, NUDT15, MED4, RNASEH2B, VPS36	ANKLE2 GOLGA3 ZNF140 MTIF3 HMGB1 HSPH1 SUCLA2 No non-overlappi CKAP2	5,340 109 148 8,825 181 47,244 36,542 ng genes wit	AC078925.18 5S_rRNA GOLGA3 Y_RNA MED4 AL158196.24 hin 50,000bp	47,912 49,588 1,300 7,210 37,730 39,100
12 12 12 12 12 12 13 13 13 13 13 13 13 13 13 13	$\begin{array}{r} 120,210,248\\ 130,031,893\\ 130,761,260\\ 131,853,864\\ 131,915,470\\ 132,166,614\\ 26,931,536\\ 30,089,915\\ 30,681,361\\ 47,510,005\\ 47,566,697\\ 50,384,088\\ 51,922,465\\ 59,868,122\end{array}$	$\begin{array}{r} 120,217,063\\ 130,032,262\\ 130,761,925\\ 131,854,268\\ 131,915,802\\ 132,166,962\\ 26,932,147\\ 30,090,269\\ 30,681,939\\ 47,510,363\\ 47,567,395\\ 50,384,551\\ 51,923,047\\ 59,868,454\end{array}$	369 665 404 332 348 611 354 578 358 698 463 582 332	9 9 111 11 10 39 9 9 9 9 9 9 11 11 14	USPL1, B3GALTL, NUDT15, MED4, RNASEH2B, VPS36,	ANKLE2 GOLGA3 ZNF140 MTIF3 HMGB1 HSPH1 SUCLA2 No non-overlappi CKAP2 TDRD3	5,340 109 148 8,825 181 47,244 36,542 ng genes wit 4,449 138	AC078925.18 5S_rRNA GOLGA3 Y_RNA MED4 AL158196.24 hin 50,000bp	47,912 49,588 1,300 7,210 37,730 39,100
12 12 12 12 12 13 13 13 13 13 13 13 13 13 13 13 13	$\begin{array}{r} 120,210,248\\ 130,031,893\\ 130,761,260\\ 131,853,864\\ 131,915,470\\ 132,166,614\\ 26,931,536\\ 30,089,915\\ 30,681,361\\ 47,510,005\\ 47,566,697\\ 50,384,088\\ 51,922,465\\ 59,868,122\\ 72,199,774\end{array}$	$\begin{array}{r} 120,217,063\\ 130,032,262\\ 130,761,925\\ 131,854,268\\ 131,915,802\\ 132,166,962\\ 26,932,147\\ 30,090,269\\ 30,681,939\\ 47,510,363\\ 47,567,395\\ 50,384,551\\ 51,923,047\\ 59,868,454\\ 72,200,230\\ \end{array}$	369 665 404 332 348 611 354 578 358 698 463 582 332 455	9 9 111 11 10 39 9 9 9 9 9 9 111 14 14	USPL1, B3GALTL, NUDT15, MED4, RNASEH2B, VPS36, C13orf37	ANKLE2 GOLGA3 ZNF140 MTIF3 HMGB1 HSPH1 SUCLA2 No non-overlappi CKAP2 TDRD3 LI6	5,340 109 148 8,825 181 47,244 36,542 ng genes wit 4,449 138 21 512	AC078925.18 5S_rRNA GOLGA3 Y_RNA MED4 AL158196.24 hin 50,000bp	47,912 49,588 1,300 7,210 37,730 39,100
12 12 12 12 12 13 13 13 13 13 13 13 13 13 13 13 13 13 13 13 13	$\begin{array}{r} 120,210,248\\ 130,031,893\\ 130,761,260\\ 131,853,864\\ 131,915,470\\ 132,166,614\\ 26,931,536\\ 30,089,915\\ 30,681,361\\ 47,510,005\\ 47,566,697\\ 50,384,088\\ 51,922,465\\ 59,868,122\\ 72,199,774 \end{array}$	$\begin{array}{r} 120,217,03\\ 130,032,262\\ 130,761,925\\ 131,854,268\\ 131,915,802\\ 132,166,962\\ 26,932,147\\ 30,090,269\\ 30,681,939\\ 47,510,363\\ 47,567,395\\ 50,384,551\\ 51,923,047\\ 59,868,454\\ 72,200,229\\ \end{array}$	363 369 665 404 332 348 611 354 578 358 698 463 582 332 455	9 9 111 11 10 39 9 9 9 9 9 9 111 14 14 10 9	USPL1, B3GALTL, NUDT15, MED4, RNASEH2B, VPS36, C13orf37, C13orf34	ANKLE2 GOLGA3 ZNF140 MTIF3 HMGB1 HSPH1 SUCLA2 No non-overlappi CKAP2 TDRD3 U6	109 genes wit 5,340 109 148 8,825 181 47,244 36,542 ng genes wit 4,449 138 21,512	AC078925.18 5S_rRNA GOLGA3 Y_RNA MED4 AL158196.24 hin 50,000bp RP11-11C5.1	47,912 49,588 1,300 7,210 37,730 39,100 23,497
12 12 12 12 12 13 13 13 13 13 13 13 13 13 13 13 13 13	120,210,248 130,031,893 130,761,260 131,853,864 131,915,470 132,166,614 26,931,536 30,089,915 30,681,361 47,510,005 47,566,697 50,384,088 51,922,465 59,868,122 72,199,774	120,217,081 130,032,262 130,761,925 131,854,268 131,915,802 132,166,962 26,932,147 30,090,269 30,681,939 47,510,363 47,567,395 50,384,551 51,923,047 59,868,454 72,200,229	363 369 665 404 332 348 611 354 578 358 698 463 582 332 455	9 9 11 11 10 39 9 9 9 9 9 9 9 11 14 10 9	USPL1, B3GALTL, NUDT15, MED4, RNASEH2B, VPS36, C13orf37, C13orf34,	ANKLE2 GOLGA3 ZNF140 MTIF3 HMGB1 HSPH1 SUCLA2 No non-overlappi CKAP2 TDRD3 U6	5,340 109 148 8,825 181 47,244 36,542 ng genes wit 4,449 138 21,512	AC078925.18 5S_rRNA GOLGA3 Y_RNA MED4 AL158196.24 hin 50,000bp RP11-11C5.1 DCT	47,912 49,588 1,300 7,210 37,730 39,100 23,497
12 12 12 12 12 12 12 12 13 13 13 13 13 13 13 13 13 13 13 13 13	120,210,248 130,031,893 130,761,260 131,853,864 131,915,470 132,166,614 26,931,536 30,089,915 30,681,361 47,510,005 47,566,697 50,384,088 51,922,465 59,868,122 72,199,774 93,877,640	120,217,08 130,032,262 130,761,925 131,854,268 131,915,802 132,166,962 26,932,147 30,090,269 30,681,939 47,510,363 47,567,395 50,384,551 51,923,047 59,868,454 72,200,229 93,877,951	363 369 665 404 332 348 611 354 578 358 698 463 582 332 455 311	9 9 9 11 11 10 39 9 9 9 9 9 9 9 9 9 9 11 11 14 10 9 9 9 9	USPL1, B3GALTL, NUDT15, MED4, RNASEH2B, VPS36, C13orf37, C13orf34,	ANKLE2 GOLGA3 ZNF140 MTIF3 HMGB1 HSPH1 SUCLA2 No non-overlappi CKAP2 TDRD3 U6	5,340 109 148 8,825 181 47,244 36,542 ng genes wit 4,449 138 21,512	AC078925.18 5S_rRNA GOLGA3 Y_RNA MED4 AL158196.24 hin 50,000bp RP11-11C5.1 DCT	47,912 49,588 1,300 7,210 37,730 39,100 23,497 11,893
12 12 12 12 12 12 12 12 13	120,210,248 130,031,893 130,761,260 131,853,864 131,915,470 132,166,614 26,931,536 30,089,915 30,681,361 47,510,005 47,566,697 50,384,088 51,922,465 59,868,122 72,199,774 93,877,640 99,538,950	120,217,08 130,032,262 130,761,925 131,854,268 131,915,802 132,166,962 26,932,147 30,090,269 30,681,939 47,510,363 47,567,395 50,384,551 51,923,047 59,868,454 72,200,229 93,877,951 99,539,293 440,044,550	363 369 665 404 332 348 611 354 578 358 698 463 582 332 455 3111 364	9 9 9 11 11 10 39 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	GPR133, GPR133, SFRS8, USPL1, B3GALTL, NUDT15, MED4, RNASEH2B, VPS36, C13orf37, C13orf37, C13orf34,	ANKLE2 GOLGA3 ZNF140 MTIF3 HMGB1 HSPH1 SUCLA2 No non-overlappi CKAP2 TDRD3 U6 PCCA	5,340 109 148 8,825 181 47,244 36,542 ng genes wit 4,449 138 21,512 45	AC078925.18 5S_rRNA GOLGA3 Y_RNA MED4 AL158196.24 hin 50,000bp RP11-11C5.1 DCT	47,912 49,588 1,300 7,210 37,730 39,100 23,497 11,893
12 12 12 12 12 12 12 13	120,210,248 130,031,893 130,761,260 131,853,864 131,915,470 132,166,614 26,931,536 30,089,915 30,681,361 47,510,005 47,566,697 50,384,088 51,922,465 59,868,122 72,199,774 93,877,640 99,538,950 112,910,908	120,217,08 130,032,262 130,761,925 131,854,268 131,915,802 132,166,962 26,932,147 30,090,269 30,681,939 47,510,363 47,567,395 50,384,551 51,923,047 59,868,454 72,200,229 93,877,951 99,539,293 112,911,569 440,202,868	363 369 665 404 332 348 611 354 578 358 698 463 582 332 455 311 343 661	9 9 9 11 11 10 39 9 9 9 9 9 9 9 11 11 14 14 10 9 9 9 9 9 9 9 16	GPR133, GPR133, SFRS8, USPL1, B3GALTL, NUDT15, MED4, RNASEH2B, VPS36, C13orf37, C13orf37, C13orf34, PCID2, CUL4A,	ANKLE2 GOLGA3 ZNF140 MTIF3 HMGB1 HSPH1 SUCLA2 No non-overlappi CKAP2 TDRD3 U6 PCCA	5,340 109 148 8,825 181 47,244 36,542 ng genes wit 4,449 138 21,512 45	AC078925.18 5S_rRNA GOLGA3 Y_RNA MED4 AL158196.24 hin 50,000bp RP11-11C5.1 DCT PROZ	47,912 49,588 1,300 7,210 37,730 39,100 23,497 11,893 36,213
12 12 12 12 12 12 12 13 14	120,210,248 130,031,893 130,761,260 131,853,864 131,915,470 132,166,614 26,931,536 30,089,915 30,681,361 47,510,005 47,566,697 50,384,088 51,922,465 59,868,122 72,199,774 93,877,640 99,538,950 112,910,908 113,286,611	120,217,08 130,032,262 130,761,925 131,854,268 131,915,802 132,166,962 26,932,147 30,090,269 30,681,939 47,510,363 47,567,395 50,384,551 51,923,047 59,868,454 72,200,229 93,877,951 99,539,293 112,911,569 113,286,998	363 369 665 404 332 348 611 354 578 358 698 463 582 332 455 311 343 661 387	9 9 9 11 11 10 39 9 9 9 9 9 9 9 11 11 14 14 10 9 9 9 9 9 16 12	GPR133, GPR133, SFRS8, USPL1, B3GALTL, NUDT15, MED4, RNASEH2B, VPS36, C13orf37, C13orf37, C13orf34, PCID2, CUL4A,	ANKLE2 GOLGA3 ZNF140 MTIF3 HMGB1 HSPH1 SUCLA2 No non-overlappi CKAP2 TDRD3 U6 PCCA TFDP1	19 genes wit 5,340 109 148 8,825 181 47,244 36,542 ng genes wit 4,449 138 21,512 45 59	AC078925.18 SS_rRNA GOLGA3 Y_RNA MED4 AL158196.24 hin 50,000bp RP11-11C5.1 DCT PROZ	47,912 49,588 1,300 7,210 37,730 39,100 23,497 11,893 36,213
12 12 12 12 12 12 12 12 13	120,210,248 130,031,893 130,761,260 131,853,864 131,915,470 132,166,614 26,931,536 30,089,915 30,681,361 47,510,005 47,566,697 50,384,088 51,922,465 59,868,122 72,199,774 93,877,640 99,538,950 112,910,908 113,286,611 113,848,630	120,217,08 130,032,262 130,761,925 131,854,268 131,915,802 132,166,962 26,932,147 30,090,269 30,681,939 47,510,363 47,567,395 50,384,551 51,923,047 59,868,454 72,200,229 93,877,951 99,539,293 112,911,569 113,286,998 113,848,980	363 369 665 404 332 348 611 354 578 358 698 463 582 332 455 311 343 661 387 350	9 9 9 11 11 10 39 9 9 9 9 9 9 11 11 14 14 10 9 9 9 9 9 9 16 12 12	GPR133, GPR133, SFRS8, USPL1, B3GALTL, NUDT15, MED4, RNASEH2B, VPS36, C13orf37, C13orf37, C13orf34, PCID2, CUL4A, RASA3,	ANKLE2 GOLGA3 ZNF140 MTIF3 HMGB1 HSPH1 SUCLA2 No non-overlappi CKAP2 TDRD3 U6 PCCA TFDP1 No non-overlappi	5,340 109 148 8,825 181 47,244 36,542 ng genes wit 4,449 138 21,512 45 59 ng genes wit	AC078925.18 5S_rRNA GOLGA3 Y_RNA MED4 AL158196.24 hin 50,000bp RP11-11C5.1 DCT PROZ hin 50,000bp	47,912 49,588 1,300 7,210 37,730 39,100 23,497 11,893 36,213
12 12 12 12 12 12 12 12 13 13 13 13 13 13 13 13 13 13 13 13 13 13 13 13 13 13 14	120,210,248 130,031,893 130,761,260 131,853,864 131,915,470 132,166,614 26,931,536 30,089,915 30,681,361 47,510,005 47,566,697 50,384,088 51,922,465 59,868,122 72,199,774 93,877,640 99,538,950 112,910,908 113,286,611 113,848,630 20,147,135	120,217,03 130,032,262 130,761,925 131,854,268 131,915,802 132,166,962 26,932,147 30,090,269 30,681,939 47,510,363 47,567,395 50,384,551 51,923,047 59,868,454 72,200,229 93,877,951 99,539,293 112,911,569 113,286,998 113,848,980 20,147,640	333 369 665 404 332 348 611 354 578 358 698 463 582 332 455 311 343 661 387 350 505	9 9 9 11 11 10 39 9 9 9 9 9 9 11 11 14 14 10 9 9 9 9 9 16 12 10 9 9	GPR133, GPR133, SFRS8, USPL1, B3GALTL, NUDT15, MED4, RNASEH2B, VPS36, C13orf37, C13orf37, C13orf34, PCID2, CUL4A, RASA3,	ANKLE2 GOLGA3 ZNF140 MTIF3 HMGB1 HSPH1 SUCLA2 No non-overlappi CKAP2 TDRD3 U6 PCCA TFDP1 No non-overlappi	5,340 109 148 8,825 181 47,244 36,542 ng genes wit 4,449 138 21,512 45 59 ng genes wit	AC078925.18 SS_rRNA GOLGA3 Y_RNA MED4 AL158196.24 hin 50,000bp RP11-11C5.1 DCT PROZ hin 50,000bp AL163195.5	47,912 49,588 1,300 7,210 37,730 39,100 23,497 11,893 36,213 1,999
12 12 12 12 12 12 12 13 13 13 13 13 13 13 13 13 13 13 13 13 13 13 13 13 14	120,210,248 130,031,893 130,761,260 131,853,864 131,915,470 132,166,614 26,931,536 30,089,915 30,681,361 47,510,005 47,566,697 50,384,088 51,922,465 59,868,122 72,199,774 93,877,640 99,538,950 112,910,908 113,286,611 113,848,630 20,147,135 20,148,087	120,217,03 130,032,262 130,761,925 131,854,268 131,915,802 132,166,962 26,932,147 30,090,269 30,681,939 47,510,363 47,567,395 50,384,551 51,923,047 59,868,454 72,200,229 93,877,951 99,539,293 112,911,569 113,286,998 113,848,980 20,147,640 20,148,482	333 369 665 404 332 348 611 354 578 358 698 463 582 332 455 311 343 661 387 350 505 395	9 9 9 11 11 10 39 9 9 9 9 9 9 9 11 11 14 14 10 9 9 9 9 16 12 10 9 9 9	GPR133, GPR133, SFRS8, USPL1, B3GALTL, NUDT15, MED4, RNASEH2B, VPS36, C13orf37, C13orf37, C13orf34, PCID2, CUL4A, RASA3,	ANKLE2 GOLGA3 ZNF140 MTIF3 HMGB1 HSPH1 SUCLA2 No non-overlappi CKAP2 TDRD3 U6 PCCA TFDP1 No non-overlappi	5,340 109 148 8,825 181 47,244 36,542 ng genes wit 4,449 138 21,512 45 59 ng genes wit	AC078925.18 SS_rRNA GOLGA3 Y_RNA MED4 AL158196.24 hin 50,000bp RP11-11C5.1 DCT PROZ hin 50,000bp AL163195.5 AL163195.5	47,912 49,588 1,300 7,210 37,730 39,100 23,497 11,893 36,213 1,999 2,951
12 12 12 12 12 12 12 13 13 13 13 13 13 13 13 13 13 13 13 13 13 13 13 13 14 14	120,210,248 130,031,893 130,761,260 131,853,864 131,915,470 132,166,614 26,931,536 30,089,915 30,681,361 47,510,005 47,566,697 50,384,088 51,922,465 59,868,122 72,199,774 93,877,640 99,538,950 112,910,908 113,286,611 113,848,630 20,147,135 20,148,087 20,151,248	120,217,03 130,032,262 130,761,925 131,854,268 131,915,802 132,166,962 26,932,147 30,090,269 30,681,939 47,510,363 47,567,395 50,384,551 51,923,047 59,868,454 72,200,229 93,877,951 99,539,293 112,911,569 113,286,998 113,848,980 20,147,640 20,148,482 20,152,101	363 369 665 404 332 348 611 354 578 358 698 463 582 332 455 311 343 661 387 350 505 395 853	9 9 9 11 11 10 39 9 9 9 9 9 9 9 11 11 14 14 10 9 9 9 9 9 16 12 10 9 9	GPR133, GPR133, SFRS8, USPL1, B3GALTL, NUDT15, MED4, RNASEH2B, VPS36, C13orf37, C13orf37, C13orf34, PCID2, CUL4A, RASA3,	ANKLE2 GOLGA3 ZNF140 MTIF3 HMGB1 HSPH1 SUCLA2 No non-overlappi CKAP2 TDRD3 U6 PCCA TFDP1 No non-overlappi	5,340 109 148 8,825 181 47,244 36,542 ng genes wit 4,449 138 21,512 45 59 ng genes wit	AC078925.18 SS_rRNA GOLGA3 Y_RNA MED4 AL158196.24 hin 50,000bp RP11-11C5.1 DCT PROZ hin 50,000bp AL163195.5 AL163195.5 AL163195.5	47,912 49,588 1,300 7,210 37,730 39,100 23,497 11,893 36,213 36,213 1,999 2,951 6,112
12 12 12 12 12 12 12 13 13 13 13 13 13 13 13 13 13 13 13 13 13 14 14 14	120,210,248 130,031,893 130,761,260 131,853,864 131,915,470 132,166,614 26,931,536 30,089,915 30,681,361 47,510,005 47,566,697 50,384,088 51,922,465 59,868,122 72,199,774 93,877,640 99,538,950 112,910,908 113,286,611 113,848,630 20,147,135 20,148,087 20,151,248 20,170,610	120,217,03 130,032,262 130,761,925 131,854,268 131,915,802 132,166,962 26,932,147 30,090,269 30,681,939 47,510,363 47,567,395 50,384,551 51,923,047 59,868,454 72,200,229 93,877,951 99,539,293 112,911,569 113,286,998 113,848,980 20,147,640 20,148,482 20,152,101 20,171,597	363 369 665 404 332 348 611 354 578 358 698 463 582 332 455 311 343 661 387 350 505 395 853 987	9 9 9 11 11 10 39 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	GPR133, GPR133, SFRS8, USPL1, B3GALTL, NUDT15, MED4, RNASEH2B, VPS36, C13orf37, C13orf37, C13orf34, PCID2, CUL4A, RASA3,	ANKLE2 GOLGA3 ZNF140 MTIF3 HMGB1 HSPH1 SUCLA2 No non-overlappi CKAP2 TDRD3 U6 PCCA TFDP1 No non-overlappi	5,340 109 148 8,825 181 47,244 36,542 ng genes wit 4,449 138 21,512 45 59 ng genes wit	AC078925.18 SS_rRNA GOLGA3 Y_RNA MED4 AL158196.24 hin 50,000bp RP11-11C5.1 DCT PROZ hin 50,000bp AL163195.5 AL163195.5 AL163195.5 OR6S1	47,912 49,588 1,300 7,210 37,730 39,100 23,497 11,893 36,213 36,213 1,999 2,951 6,112 7,098
12 12 12 12 12 12 12 13 13 13 13 13 13 13 13 13 13 13 13 13 13 14 14 14 14	120,210,248 130,031,893 130,761,260 131,853,864 131,915,470 132,166,614 26,931,536 30,089,915 30,681,361 47,510,005 47,566,697 50,384,088 51,922,465 59,868,122 72,199,774 93,877,640 99,538,950 112,910,908 113,286,611 113,848,630 20,147,135 20,148,087 20,151,248 20,170,610 20,195,083	120,217,03 130,032,262 130,761,925 131,854,268 131,915,802 132,166,962 26,932,147 30,090,269 30,681,939 47,510,363 47,567,395 50,384,551 51,923,047 59,868,454 72,200,229 93,877,951 99,539,293 112,911,569 113,286,998 113,848,980 20,147,640 20,148,482 20,152,101 20,171,597 20,195,894	363 369 665 404 332 348 611 354 578 358 698 463 582 332 455 311 343 661 387 350 505 395 853 987 811	9 9 9 111 110 399 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	GPR133, GPR133, SFRS8, USPL1, B3GALTL, NUDT15, MED4, RNASEH2B, VPS36, C13orf37, C13orf37, C13orf34, PCID2, CUL4A, RASA3,	ANKLE2 GOLGA3 ZNF140 MTIF3 HMGB1 HSPH1 SUCLA2 No non-overlappi CKAP2 TDRD3 U6 PCCA TFDP1 No non-overlappi	5,340 109 148 8,825 181 47,244 36,542 ng genes wit 4,449 138 21,512 45 59 ng genes wit	AC078925.18 SS_rRNA GOLGA3 Y_RNA MED4 AL158196.24 hin 50,000bp RP11-11C5.1 DCT PROZ hin 50,000bp AL163195.5 AL163195.5 AL163195.5 OR6S1 AL163636.7-1	47,912 49,588 1,300 7,210 37,730 39,100 23,497 11,893 36,213 36,213 1,999 2,951 6,112 7,098 11,280
12 12 12 12 12 12 12 13 13 13 13 13 13 13 13 13 13 13 13 13 14 14 14 14 14	120,210,248 130,031,893 130,761,260 131,853,864 131,915,470 132,166,614 26,931,536 30,089,915 30,681,361 47,510,005 47,566,697 50,384,088 51,922,465 59,868,122 72,199,774 93,877,640 99,538,950 112,910,908 113,286,611 113,848,630 20,147,135 20,148,087 20,151,248 20,170,610 20,195,083 20,200,829	120,217,08 130,032,262 130,761,925 131,854,268 131,915,802 132,166,962 26,932,147 30,090,269 30,681,939 47,510,363 47,567,395 50,384,551 51,923,047 59,868,454 72,200,229 93,877,951 99,539,293 112,911,569 113,286,998 113,848,980 20,147,640 20,148,482 20,152,101 20,171,597 20,195,894 20,201,409	363 369 665 404 332 348 611 354 578 358 698 463 582 332 455 311 343 661 387 350 505 395 853 987 811 580	9 9 9 111 110 399 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	GPR133, GPR133, SFRS8, USPL1, B3GALTL, NUDT15, MED4, RNASEH2B, VPS36, C13orf37, C13orf37, C13orf34, PCID2, CUL4A, RASA3,	ANKLE2 GOLGA3 ZNF140 MTIF3 HMGB1 HSPH1 SUCLA2 No non-overlappi CKAP2 TDRD3 U6 PCCA TFDP1 No non-overlappi OR6S1	15,340 109 148 8,825 181 47,244 36,542 ng genes wit 4,449 138 21,512 45 59 ng genes wit 59 ng genes wit	AC078925.18 SS_rRNA GOLGA3 Y_RNA MED4 AL158196.24 hin 50,000bp RP11-11C5.1 DCT PROZ hin 50,000bp AL163195.5 AL163195.5 AL163195.5 OR6S1 AL163636.7-1 AL163636.7-1	47,912 49,588 1,300 7,210 37,730 39,100 23,497 11,893 36,213 36,213 1,999 2,951 6,112 7,098 11,280 5,765
12 12 12 12 12 12 12 13 13 13 13 13 13 13 13 13 13 13 13 13 13 14 14 14 14 14 14 14	120,210,248 130,031,893 130,761,260 131,853,864 131,915,470 132,166,614 26,931,536 30,089,915 30,681,361 47,510,005 47,566,697 50,384,088 51,922,465 59,868,122 72,199,774 93,877,640 99,538,950 112,910,908 113,286,611 113,848,630 20,147,135 20,148,087 20,151,248 20,170,610 20,195,083 20,200,829 20,220,931	120,217,03 130,032,262 130,761,925 131,854,268 131,915,802 132,166,962 26,932,147 30,090,269 30,681,939 47,510,363 47,567,395 50,384,551 51,923,047 59,868,454 72,200,229 93,877,951 99,539,293 112,911,569 113,286,998 113,848,980 20,147,640 20,148,482 20,152,101 20,171,597 20,195,894 20,221,587	363 369 665 404 332 348 611 354 578 358 698 463 582 332 455 311 343 661 387 350 505 395 853 987 811 580 656	9 9 9 111 110 399 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	GPR133, GPR133, SFRS8, USPL1, B3GALTL, NUDT15, MED4, RNASEH2B, VPS36, C13orf37, C13orf37, C13orf34, PCID2, CUL4A, RASA3,	ANKLE2 GOLGA3 ZNF140 MTIF3 HMGB1 HSPH1 SUCLA2 No non-overlappi CKAP2 TDRD3 U6 PCCA TFDP1 No non-overlappi OR6S1 OR6S1	15,340 109 148 8,825 181 47,244 36,542 ng genes wit 4,449 138 21,512 45 59 ng genes wit 59 ng genes wit	AC078925.18 SS_rRNA GOLGA3 Y_RNA MED4 AL158196.24 hin 50,000bp RP11-11C5.1 DCT PROZ hin 50,000bp AL163195.5 AL163195.5 AL163195.5 OR6S1 AL163636.7-1 Y_RNA	47,912 49,588 1,300 7,210 37,730 39,100 23,497 11,893 36,213 36,213 1,999 2,951 6,112 7,098 11,280 5,765 3,420
12 12 12 12 12 12 12 13 13 13 13 13 13 13 13 13 13 13 13 13 14 14 14 14 14 14 14 14 14 14 14 14 14 14	120,210,248 130,031,893 130,761,260 131,853,864 131,915,470 132,166,614 26,931,536 30,089,915 30,681,361 47,510,005 47,566,697 50,384,088 51,922,465 59,868,122 72,199,774 93,877,640 99,538,950 112,910,908 113,286,611 113,848,630 20,147,135 20,148,087 20,151,248 20,170,610 20,195,083 20,220,931 20,221,905	120,217,03 130,032,262 130,761,925 131,854,268 131,915,802 132,166,962 26,932,147 30,090,269 30,681,939 47,510,363 47,567,395 50,384,551 51,923,047 59,868,454 72,200,229 93,877,951 99,539,293 112,911,569 113,286,998 113,848,980 20,147,640 20,148,482 20,152,101 20,171,597 20,195,894 20,221,587 20,222,529	363 369 665 404 332 348 611 354 578 358 698 463 582 332 455 311 343 661 387 350 505 395 853 987 811 580 656 624	9 9 9 111 110 39 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	GPR133, GPR133, SFRS8, USPL1, B3GALTL, NUDT15, MED4, RNASEH2B, VPS36, C13orf37, C13orf37, C13orf34, PCID2, CUL4A, RASA3, RASA3,	ANKLE2 GOLGA3 ZNF140 MTIF3 HMGB1 HSPH1 SUCLA2 No non-overlappi CKAP2 TDRD3 U6 PCCA TFDP1 No non-overlappi OR6S1 OR6S1 RNASE4 ANG	15,340 109 148 8,825 181 47,244 36,542 ng genes wit 4,449 138 21,512 45 59 ng genes wit 59 ng genes wit 15,393 625 84	AC078925.18 SS_rRNA GOLGA3 Y_RNA MED4 AL158196.24 hin 50,000bp RP11-11C5.1 DCT PROZ PROZ hin 50,000bp AL163195.5 AL163195.5 AL163195.5 OR6S1 AL163636.7-1 Y_RNA Y RNA	47,912 49,588 1,300 7,210 37,730 39,100 23,497 11,893 36,213 36,213 36,213 1,999 2,951 6,112 7,098 11,280 5,765 3,420 4,394
12 12 12 12 12 12 12 13 13 13 13 13 13 13 13 13 13 13 13 13 13 14 14 14 14 14 14 14	120,210,248 130,031,893 130,761,260 131,853,864 131,915,470 132,166,614 26,931,536 30,089,915 30,681,361 47,510,005 47,566,697 50,384,088 51,922,465 59,868,122 72,199,774 93,877,640 99,538,950 112,910,908 113,286,611 113,848,630 20,147,135 20,148,087 20,151,248 20,170,610 20,195,083 20,220,931 20,221,905 22,468,408	120,217,03 130,032,262 130,761,925 131,854,268 131,915,802 132,166,962 26,932,147 30,090,269 30,681,939 47,510,363 47,567,395 50,384,551 51,923,047 59,868,454 72,200,229 93,877,951 99,539,293 112,911,569 113,286,998 113,848,980 20,147,640 20,148,482 20,152,101 20,171,597 20,195,894 20,221,587 20,222,529 22,469,018	363 369 665 404 332 348 611 354 578 358 698 463 582 332 455 311 343 661 387 350 505 395 853 987 811 580 656 624 610	9 9 9 111 110 399 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	GPR133, GPR133, SFRS8, USPL1, B3GALTL, NUDT15, MED4, RNASEH2B, VPS36, C13orf37, C13orf37, C13orf34, PCID2, CUL4A, RASA3, RASA3, RNASE4, PRMT5,	ANKLE2 GOLGA3 ZNF140 MTIF3 HMGB1 HSPH1 SUCLA2 No non-overlappi CKAP2 TDRD3 U6 PCCA TFDP1 No non-overlappi OR6S1 OR6S1 RNASE4 ANG RBM23	15,340 109 148 8,825 181 47,244 36,542 18 47,244 36,542 138 21,512 45 59 ng genes wit 59 ng genes wit 15,393 625 84 10,172	AC078925.18 SS_rRNA GOLGA3 Y_RNA MED4 AL158196.24 hin 50,000bp RP11-11C5.1 DCT PROZ PROZ hin 50,000bp AL163195.5 AL163195.5 AL163195.5 OR6S1 AL163636.7-1 Y_RNA Y_RNA Y_RNA C14orf94	47,912 49,588 1,300 7,210 37,730 39,100 23,497 11,893 36,213 36,213 36,213 1,999 2,951 6,112 7,098 11,280 5,765 3,420 4,394 16,260
12 12 12 12 12 12 12 13 13 13 13 13 13 13 13 13 13 13 13 13 13 14 14 14 14 14 14	120,210,248 130,031,893 130,761,260 131,853,864 131,915,470 132,166,614 26,931,536 30,089,915 30,681,361 47,510,005 47,566,697 50,384,088 51,922,465 59,868,122 72,199,774 93,877,640 99,538,950 112,910,908 113,286,611 113,848,630 20,147,135 20,148,087 20,151,248 20,170,610 20,195,083 20,200,829 20,220,931 20,221,905 22,468,408 23,700 031	120,217,03 130,032,262 130,761,925 131,854,268 131,915,802 132,166,962 26,932,147 30,090,269 30,681,939 47,510,363 47,567,395 50,384,551 51,923,047 59,868,454 72,200,229 93,877,951 99,539,293 112,911,569 113,286,998 113,848,980 20,147,640 20,148,482 20,152,101 20,171,597 20,195,894 20,221,587 20,222,529 22,469,018 23,700,396	363 369 665 404 332 348 611 354 578 358 698 463 582 332 455 311 343 661 387 350 505 395 853 987 811 580 656 624 610 365	9 9 9 111 110 399 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	GPR133, GPR133, SFRS8, USPL1, B3GALTL, NUDT15, MED4, RNASEH2B, VPS36, C13orf37, C13orf37, C13orf34, PCID2, CUL4A, RASA3, RASA3, RASA3, C130F3G, C130F	ANKLE2 GOLGA3 ZNF140 MTIF3 HMGB1 HSPH1 SUCLA2 No non-overlappi CKAP2 TDRD3 U6 PCCA TFDP1 No non-overlappi OR6S1 OR6S1 RNASE4 ANG RBM23	15,340 109 148 8,825 181 47,244 36,542 ng genes wit 4,449 138 21,512 45 59 ng genes wit 15,393 625 84 10,172	AC078925.18 SS_rRNA GOLGA3 Y_RNA MED4 AL158196.24 hin 50,000bp RP11-11C5.1 DCT PROZ hin 50,000bp AL163195.5 AL163195.5 AL163195.5 AL163636.7-1 AL163636.7-1 Y_RNA Y_RNA Y_RNA C14orf94 RNF31	47,912 49,588 1,300 7,210 37,730 39,100 23,497 11,893 36,213 36,213 36,213 1,999 2,951 6,112 7,098 11,280 5,765 3,420 4,394 16,260 3,21
12 12 12 12 12 12 12 13 13 13 13 13 13 13 13 13 13 13 13 13 13 14 14 14 14 14 14 14	120,210,248 130,031,893 130,761,260 131,853,864 131,915,470 132,166,614 26,931,536 30,089,915 30,681,361 47,510,005 47,566,697 50,384,088 51,922,465 59,868,122 72,199,774 93,877,640 99,538,950 112,910,908 113,286,611 113,848,630 20,147,135 20,148,087 20,151,248 20,170,610 20,195,083 20,200,829 20,220,931 20,221,905 22,468,408 23,700,031 23,905,627	120,217,03 130,032,262 130,761,925 131,854,268 131,915,802 132,166,962 26,932,147 30,090,269 30,681,939 47,510,363 47,567,395 50,384,551 51,923,047 59,868,454 72,200,229 93,877,951 99,539,293 112,911,569 113,286,998 113,848,980 20,147,640 20,148,482 20,152,101 20,171,597 20,195,894 20,221,587 20,222,529 22,469,018 23,700,396 23,906,791	363 369 665 404 332 348 611 354 578 358 698 463 582 332 455 311 343 661 387 350 505 395 853 987 811 580 624 610 365 164	9 9 9 111 110 399 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	GPR133, GPR133, SFRS8, USPL1, B3GALTL, NUDT15, MED4, RNASEH2B, VPS36, C13orf37, C13orf37, C13orf34, PCID2, CUL4A, RASA3, RASA3, RASA3, C130F35, ISGF3G,	ANKLE2 GOLGA3 ZNF140 MTIF3 HMGB1 HSPH1 SUCLA2 No non-overlappi CKAP2 TDRD3 U6 PCCA TFDP1 No non-overlappi OR6S1 OR6S1 RNASE4 ANG RBM23 NFATC4	19 genes wit 5,340 109 148 8,825 181 47,244 36,542 ng genes wit 4,449 138 21,512 45 59 ng genes wit 15,393 625 84 10,172 303	AC078925.18 SS_rRNA GOLGA3 Y_RNA MED4 AL158196.24 hin 50,000bp RP11-11C5.1 DCT PROZ hin 50,000bp AL163195.5 AL163195.5 AL163195.5 OR6S1 AL163636.7-1 Y_RNA Y_RNA Y_RNA Y_RNA C14orf94 RNF31	47,912 49,588 1,300 7,210 37,730 39,100 23,497 11,893 36,213 36,213 36,213 1,999 2,951 6,112 7,098 11,280 5,765 3,420 4,394 16,260 321

14	28,048,113	28,048,322	209	9		No non-overlappi	ng genes wit	hin 50,000bp	
14	28,290,482	28,290,756	274	10		FOXG1B	14,045		
14	30,745,965	30,746,714	749	9	HECTD1,	Y_RNA	37,004		
14	33,489,607	33,490,083	476	10	EGLN3,	No non-overlappi	ng genes wit	hin 50,000bp	
14	34,584,858	34,585,125	267	10	C14orf24,			SRP54	16,336
14	44,791,995	44,792,500	505	9	C14orf106,			U6	20,812
14	49,388,756	49,389,338	582	9	SDCCAG1,	AL627171.1-1	7,454	SRP_euk_arch	748
14	49,390,180	49,390,571	391	9	SRP_euk_arch,	SDCCAG1	891	SRP_euk_arch	8,450
14	50,097,345	50,097,773	428	11	SPG3A,	MAP4K5	28,219		
14	57,776,174	57,776,503	329	9		PSMA3	4,843	ACTR10	4,070
14	61,126,923	61,127,288	365	10				PRKCH	39,480
14	64,076,607	64,077,222	615	10	HSPA2,	C14orf50	9,151	ZBTB1	6,446
14	66,043,909	66,044,715	806	9	GPHN,			C14orf53	8,886
14	66,580,956	66,581,366	410	11	GPHN,	No non-overlappi	ng genes wit	hin 50,000bp	
14	67,063,068	67,063,415	347	10		PLEKHH1	6,346		
14	69,121,458	69,121,904	446	9		AL133445.4-1	23,518		
14	69,355,156	69,355,509	353	9		SNORA11	14,355	SFRS5	46,681
14	74,300,503	74,300,802	299	9	YLPM1,			FCF1	27,367
14	76,594,384	76,594,852	468	10		C14orf4	30,496		
14	78,470,543	78,470,750	207	12	NRXN3,	No non-overlappi	ng genes wit	hin 50,000bp	
14	87,307,192	87,307,715	523	60		No non-overlappi	ng genes wit	hin 50,000bp	
14	87,529,316	87,529,675	359	9	GALC,			AL157955.5	2,770
14	88,360,737	88,361,126	389	10	TTC8,			U4	4,208
14	88,515,056	88,515,429	373	10		No non-overlappi	ng genes wit	hin 50,000bp	
14	89,410,946	89,411,349	403	10	C14orf143,	No non-overlappi	ng genes wit	hin 50,000bp	
					AL163011.3,				
14	92,649,261	92,649,652	391	10	ITPK1,	No non-overlappi	ng genes wit	hin 50,000bp	
14	93,649,837	93,650,371	534	11	IFI27,	DDX24	32,526	IFI27L1	11,029
14	101,484,079	101,484,945	866	16		DYNC1H1	15,789	PPP2R5C	20,251
14	103,036,317	103,036,716	399	9	MARK3,	TRMT61A	28,585	CKB	19,033
14	104,558,329	104,558,688	359	9	CDCA4,	AHNAK2	42,590	C14orf79	25,429
14	104,624,079	104,624,444	365	9		GPR132	21,280		
14	105,019,183	105,019,535	352	10		AL928654.1	4,164	CRIP2	1,640
14	105,856,620	105,857,033	413	9	IGHVII-28-1,	AB019439.1-5	4,630	IGHV3-29	1,380
14	105,873,196	105,873,668	472	11		IGHV3-30-2	1,394	AB019439.1-7	2,584
14	105,875,428	105,875,772	344	17		IGHV3-30-2	3,626	AB019439.1-7	480
14	105,875,935	105,876,150	215	9		IGHV3-30-2	4,133	AB019439.1-7	102
15	29,471,679	29,471,941	262	9				KLF13	14,286
15	35,180,582	35,180,963	381	12	MEIS2,	No non-overlappi	ng genes wit	hin 50,000bp	
15	38,586,469	38,586,879	410	9		U6	22,182	D4ST1	33,826
15	39,122,036	39,122,248	212	9	INO80,	No non-overlappi	ng genes wit	hin 50,000bp	
15	40,136,366	40,136,730	364	9		PLA2G4E	5,686		
15	41,854,899	41,855,494	595	9	ELL3,	SERF2	1,096	PDIA3	2,806
15	42,273,783	42,274,192	409	10	FRMD5,	No non-overlappi	ng genes wit	hin 50,000bp	
15	42,506,401	42,507,691	1,290	9	CTDSPL2,			CASC4	11,154
15	43,277,943	43,278,381	438	10	SHF,	0.471 <i>(</i>		SNORA11	16,015
15	43,481,183	43,482,089	906	9	SPATA5L1,	GATM	22,911	AC025580.8-1	43,865
15	53,398,431	53,398,762	331	10	PIGB,	RAB27A	29,138	5S_rRNA	32,734
15	54,325,477	54,325,812	335	11		RFX7	2,702		
15	56,555,329	56,555,658	329	9	LIPC,	No non-overlappi	ng genes wit	hin 50,000bp	
15	62,466,713	62,467,319	606	10	TRIP4,	KIAA0101	5,958		
15	63,384,051	63,384,708	657	15	U5,			U5	8,494
15	63,596,325	63,597,309	984	11	DPP8,	PTPLAD1	12,569	AC011846.16-1	14,101
15	63,613,794	63,614,045	251	10	PTPLAD1,	DPP8	16,706	U6	18,427
15	63,690,189	63,690,873	684 	11	C15ort44,	SLC24A1	12,599	PTPLAD1	32,443
15	63,948,656	63,949,230	574	12	RAB11A,			MEGF11	25,458
15	64,373,353	64,374,140	787	11	DIS3L,	MEGF11	40,214		42,090
15	64,435,100	64,436,259	1,159	9	TIPIN,	SCARNA14	8,366	Y_RNA	7,333
15	64,465,498	64,466,339	841	9	014005	MAP2K1	335		1
15	64,577,011	64,577,638	627	13	SNAPC5,	ZWILCH	6,847	KPL4	1,070
15	64,777,478	64,778,086	608	13	0140.50	SMAD6	3,602		
15	64,781,151	64,782,585	1,434	9	SMAD6,	No non-overlappi	ng genes wit	nin 50,000bp	
15	64,983,019	64,983,393	374	9		No non-overlappi	ng genes wit	nin 50,000bp	
15	65,143,371	65,143,660	289	12		SMAD3	1,589		
15	65,536,171	65,536,570	399	10	IQCH,	No non-overlappi	ng genes wit	hin 50,000bp	
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15	65,600,846	65,601,292	446	10	C15orf61,	MAP2K5	20,783	IQCH	19,653
15	65,621,732	65,622,176	444	9	MAP2K5,			C15orf61	15,786
15	65,796,799	65,797,248	449	12	MAP2K5,	No non-overlappi	ng genes wit	hin 50,000bp	
15	65,919,072	65,919,516	444	14	U6,			LBXCOR1	5,844
15	65,919,605	65,919,907	302	10		U6	168	LBXCOR1	6,377
15	65,933,863	65,934,201	338	9		U6	14,426	LBXCOR1	20,635
15	65,962,833	65,963,321	488	9		U6	43,396	LBXCOR1	49,605
15	66,003,857	66,004,336	479	9		No non-overlappi	ng genes wit	hin 50,000bp	
15	66,299,234	66,299,693	459	13	CLN6,	CALML4	13,732	PIAS1	31,778
15	66,356,890	66,358,718	1,828	9	FEM1B,	CLN6	47,811	ITGA11	22,386
15	66,385,711	66,386,262	551	10	ITGA11,			FEM1B	15,020
15	66,638,826	66,639,655	829	10		CORO2B	18,707		
15	66,657,504	66,658,174	670	11		CORO2B	188		
15	67,153,778	67,154,248	470	13		TMEM84	5,945		
15	67,160,168	67,160,609	441	10	TMEM84,			NOX5	24,041
15	67.161.465	67.161.739	274	10	,			TMEM84	789
15	67.205.076	67,205,441	365	9		GLCE	34,586	TMEM84	44,400
15	67.225.292	67.225.909	617	10		GLCE	14.118		,
15	67.239.414	67.240.126	712	10	GLCE.	No non-overlappi	na aenes wit	hin 50.000bp	
15	67,493,937	67.494.440	503	10	KIF23.			PAQR5	6.897
15	67 532 445	67 533 053	608	12	RPI P1			KIF23	231
15	67.588.569	67.588.914	345	10	-,	No non-overlappi	na aenes wit	hin 50.000bp	1
15	67.615.436	67.615.751	315	11		No non-overlappi	na aenes wit	hin 50.000bp	
15	67.673.203	67.673.902	699	9		No non-overlappi	na aenes wit	hin 50.000bp	
15	67 973 255	67 973 734	479	9		No non-overlappi	na aenes wit	hin 50 000bp	
15	68 055 720	68 056 108	388	10		No non-overlappi	ng genes wit	hin 50 000bp	
15	68 102 670	68 103 479	809	9			ng gonoo mi	TI E3	24 118
15	68 171 406	68 172 235	829	9	TI E3	hsa-mir-629	12 545	1220	21,110
15	68 275 643	68 277 001	1 358	9	1220,		12,010	116	2 906
15	68 283 885	68 284 261	376	9				16	11 148
15	68 310 887	68 311 236	349	9				16	38 150
15	68 562 747	68 563 453	706	9		No non-overlanni	na aenes wit	bin 50 000bn	00,100
15	68 564 384	68 564 777	303	a a		No non-overlappi	ng genes wit	hin 50,000bp	
15	68 605 488	68 606 300	812	9		No non-overlappi	ng genes wit	hin 50 000bp	
15	68 795 576	68 795 904	328	10	LIACA	No non-overlappi	ng genes wit	hin 50,000bp	
15	68 842 687	68 843 125	438	10			ng genes wit	AC009269 6	32 903
15	69 358 415	69 358 979	564	13	THSD4			RPI 17P33	49 406
15	69 863 931	69 864 521	590	10	11100 1,			THSD4	1 155
15	70 197 183	70 198 489	1 306	9				GRAMD2	40 713
10	70,107,100	70,100,400	1,000	Ū	SENP8.				40,710
15	70.278.966	70.279.585	619	9	PKM2.	GRAMD2	1.786		
15	70.309.950	70,311.074	1,124	9	PKM2,		, , , , , , , , , , , , , , , , , , , ,	PARP6	9.503
15	70,315,875	70,316.679	804	9		PKM2	5,137	PARP6	3,898
15	70.351.986	70.352.392	406	10		PARP6	1.304	-	.,
15	70.455.120	70.456.059	939	11	HEXA.	TMEM202	21.645		
15	70.553.492	70.553.817	325	11	ARIH1.		,	AC079322.5	24.134
15	70.554.543	70.555.017	474	11	ARIH1.			AC079322.5	22.934
15	70.765.210	70,766,296	1.086		HIGD2B BBS4			GOLGA6B	18.419
15	70.862.313	70.863.782	1.469	9	ADPGK.			BBS4	44.444
15	71.047.262	71.047.902	640	12	,	No non-overlappi	ng genes wit	hin 50,000bp	,
15	71.127.916	71.128.449	533			NEO1	3.479		
15	71 556 761	71 557 061	300	9	C15orf60	No non-overlappi	na aenes wit	hin 50 000bp	
15	71.711.203	71.712.114	911	.9	NPTN.	No non-overlappi	ng genes wit	hin 50,000bp	
15	71.712.688	71.713 170	482	11	NPTN.	No non-overlappi	ng genes wit	hin 50.000bp	
15	71.715 833	71.716.363	530	11	,	NPTN	3 027	,	
15	71,756,555	71,757 050	495	11		CD276	6 625		
15	71 764 414	71 764 707	293	11	CD276	No non-overlappi	na aenes wit	hin 50.000bp	
15	72 044 137	72 044 830	702	۰. ۵		PMI	29 228	I OXI 1	12 606
15	72 215 503	72 215 786	283	10	ISI R2	AC010931 17	35 864	STRA6	43 077
15	72 278 003	72 278 362	350	۰. ۵	STRA6	AC023300 19	18 304	ISIR	21 737
15	72 302 524	72 302 938	414	10			10,004	AC023300 19	1 802
15	72 302 946	72 303 339	303	13				AC023300 19	2 224
15	72 394 907	72 395 331	424	۰. ۵	CCDC33			CYP11A1	21 822
.0	12,004,001	12,000,001	747	5		1		• · · · · · · ·	- 1,022

15	72,401,160	72,401,533	373	9	CCDC33,			CYP11A1	15,620
15	72,452,867	72,454,154	1,287	9		CYP11A1	5,733		
15	72,454,282	72,454,910	628	9		CYP11A1	7,148		
15	72,621,209	72,621,584	375	9	ARID3B,	No non-overlappi	ng genes wit	hin 50,000bp	
15	72,866,798	72,867,642	844	10	CSK,	LMAN1L	24,595	CYP1A2	30,804
15	72,921,908	72,922,602	694	10	ULK3,			SCAMP2	1,648
15	72,950,054	72,950,583	529	10	SCAMP2,	MPI	18,867	C15orf17	28,799
15	72,977,327	72,977,606	279	10	MPI,			C15orf17	1,776
15	72,985,319	72,986,123	804	9	C15orf17,			MPI	7,697
15	73,029,733	73,030,379	646	10				RPP25	3,431
15	73,074,305	73,075,040	735	13	SCAMP5,	Y_RNA	11,535		
15	73,102,634	73,103,096	462	14	PPCDC,			SCAMP5	1,745
15	73,389,066	73,389,466	400	9		DNM1P34	6,726		
15	73,415,102	73,415,504	402	9	COMMD4,	NEIL1	10,959	hsa-mir-631	17,501
15	73,446,879	73,447,341	462	9	MAN2C1,			SIN3A	1,432
15	73,447,346	73,447,596	250	10	MAN2C1,			SIN3A	1,177
15	73,447,795	73,448,238	443	10	MAN2C1,			SIN3A	535
15	73,535,385	73,535,815	430	10		SIN3A	208		
15	73,704,896	73,705,505	609	9	SNUPN,	AC105020.18-1	3,470		
15	73,718,672	73,720,019	1,347	9	IMP3,	SH3PX3	8,384	AC105020.18-1	9,445
15	73,726,672	73,727,262	590	10	IMP3,	SH3PX3	1,141		
15	73,775,118	73,775,463	345	9	CSPG4,	ODF3L1	27,911	AC105020.18-2	14,970
15	73,983,007	73,983,393	386	13	FBXO22,			UBE2Q2	2,572
15	73,983,546	73,984,010	464	10	FBXO22,			UBE2Q2	3,111
15	74,138,455	74,138,974	519	9		C15orf27	380		
15	74,139,523	74,139,787	264	9	C15orf27,	NRG4	47,681		
15	74,266,517	74,266,861	344	9	C15orf27,			ETFA	28,785
15	74,282,497	74,282,945	448	9	C15orf27,			ETFA	12,701
15	74,400,699	74,401,077	378	9		ETFA	9,834		
15	74,406,368	74,406,814	446	9		ISL2	9,388		
15	74,406,961	74,407,614	653	10		ISL2	8,588		
15	74,416,577	74,416,880	303	11	ISL2,	ETFA	25,712	SCAPER	10,713
15	74,984,513	74,985,163	650	15	SCAPER,	RCN2	25,971		
15	75,080,738	75,081,019	281	9	PSTPIP1,	AC090181.9-1	24,132	TSPAN3	44,368
15	75,488,285	75,488,587	302	9		HMG20A	11,698		
15	75,499,197	75,500,565	1,368	10	HMG20A,	No non-overlappi	ng genes wit	hin 50,000bp	
15	75,622,488	75,623,064	576	10		No non-overlappi	ng genes wit	hin 50,000bp	
15	75,696,438	75,697,429	991	9	LINGO1,	No non-overlappi	ng genes wit	hin 50,000bp	
15	75,712,637	75,713,213	576	11		LINGO1	750		
15	75,886,659	75,887,137	478	9		No non-overlappi	ng genes wit	hin 50,000bp	
15	76,038,756	76,039,244	488	10		AC104758.12-1	14,760	TBC1D2B	35,139
15	76,117,966	76,118,444	478	9	TBC1D2B, hsa- mir-1827,	SH2D7	38,761		
15	76,141,270	76,141,558	288	9	TBC1D2B,	SH2D7	15,647	hsa-mir-1827	23,278
15	76,147,723	76,148,117	394	11	TBC1D2B,	SH2D7	9,088		
15	76,155,308	76,155,649	341	9	TBC1D2B,	SH2D7	1,556		
15	76,216,041	76,216,462	421	9		CIB2	5,108		
15	76,256,859	76,257,194	335	9	ACSBG1,			IDH3A	6,921
15	76,291,652	76,292,448	796	10	ACSBG1,			IDH3A	41,714
15	76,502,035	76,502,598	563	10		IREB2	14,975		
15	76,517,383	76,517,678	295	10	IREB2,	No non-overlappi	ng genes wit	hin 50,000bp	
15	76,586,679	76,587,189	510	12	AC027228.16,			IREB2	5,826
15	76,830,416	76,830,770	354	9				ADAMTS7	7,831
15	76,939,817	76,940,237	420	14		MORF4L1	11,990	AC103975.9	28,393
15	76,951,592	76,952,345	753	9	MORF4L1,			AC011944.12-2	25,893
15	76,952,846	76,953,336	490	11	MORF4L1,			AC011944.12-2	24,902
15	77,391,142	77,391,714	572	9	TMED3,	No non-overlappi	ng genes wit	hin 50,000bp	
15	77,675,350	77,675,677	327	12		No non-overlappi	ng genes wit	hin 50,000bp	
15	77,957,517	77,957,917	400	10	MTHFS,			ST20	20,323
15	77,975,751	77,976,500	749	10	MTHFS,			ST20	1,740
15	78,430,398	78,430,894	496	9		No non-overlappi	ng genes wit	hin 50,000bp	
15	78,561,940	78,562,198	258	10	ARNT2,	No non-overlappi	ng genes wit	hin 50,000bp	
15	78,694,693	78,695,174	481	9		U6	47,994	ARNT2	17,369
15	79,069,381	79,069,948	567	9		MESDC2	121		

15	79,103,445	79,103,826	381	9		MESDC2	34,185	MESDC1	20,045
15	79,403,635	79,404,440	805	9		STARD5	56	TMC3	7,306
15	79,417,897	79,418,338	441	9	TMC3,	STARD5	14,318	IL16	24,443
15	79,654,941	79,655,388	447	10		No non-overlappi	ng genes wit	hin 50,000bp	
15	80,101,022	80,102,005	983	9		AC026956.20	21,686	RKHD3	19,178
15	80,125,755	80,126,480	725	9		RKHD3	339	AC026956.20	1,983
15	80,341,225	80,342,293	1,068	9	EFTUD1, FAM154B,	No non-overlappi	ng genes wit	hin 50,000bp	
15	81,445,391	81,445,942	551	10		FAM103A1	33		
15	81,667,726	81,668,299	573	10	AC024270.6,			BNC1	47,360
15	81,707,777	81,708,496	719	9				BNC1	7,163
15	81,907,855	81,908,397	542	9	SH3GL3,	No non-overlappi	ng genes wit	hin 50,000bp	
15	82,233,499	82,233,805	306	10	ADAMTSL3,	No non-overlappi	ng genes wit	hin 50,000bp	
15	82,290,282	82,290,569	287	9	ADAMTSL3,	U6	5,558		
15	82,997,701	82,998,849	1,148	13	WDR73,			NMB	515
15	82,998,943	82,999,366	423	10	NMB,	WDR73	418		
15	83,079,337	83,079,673	336	10		SEC11A	18,659		
15	83,324,593	83,325,005	412	11	PDE8A,	U6	40,635	SLC28A1	34,560
15	83,325,174	83,325,901	727	21	PDE8A,	U6	41,216	SLC28A1	35,141
15	83,336,778	83,337,105	327	11	PDE8A,			SLC28A1	46,745
15	84,198,580	84,198,955	375	11		No non-overlappi	ng genes wit	hin 50,000bp	
15	84,900,268	84,900,884	616	9	AGBL1,	No non-overlappi	ng genes wit	hin 50,000bp	
15	86,600,647	86,601,049	402	9	NTRK3,	No non-overlappi	ng genes wit	hin 50,000bp	
15	87,148,450	87,149,040	590	9	ACAN,	No non-overlappi	ng genes wit	hin 50,000bp	
15	87,255,948	87,256,657	709	9	MFGE8,	HAPLN3	16,174	ACAN	37,232
15	87.385.654	87.386.674	1.020	9	/	ABHD2	45.755		
15	87.401.443	87.402.066	623	11		ABHD2	30.363		
15	87.521.883	87.522.254	371	11	ABHD2.			AC124068.6	22.746
15	87.678.914	87.679.531	617	20	POLG.	hsa-mir-9-3	32.721	FANCI	17.548
15	87.844.667	87.845.354	687	13	,	RHCG	3.848	_	
15	88 238 071	88 238 935	864	13	AP3S2	U6	7 244	C15orf38	5 901
15	88 509 917	88 510 435	518	.0	,	AC091167 19-2	37		0,001
15	88.558.891	88,559,240	349	11	SEMA4B.	C15orf58	23.486	CIB1	15.247
15	88 732 445	88 733 217	772		IQGAP1	AC018946 12	39 012	ZNF774	25.612
15	89,298,894	89.299.827	933	9	RCCD1.		00,012	UNC45A	568
15	89.335.842	89,336,466	624	9	PRC1.			VPS33B	6.312
15	89 338 430	89 339 478	1 048	9	PRC1			VPS33B	3 300
15	90.441.505	90,442,848	1.343	9	SLCO3A1.	No non-overlappi	na aenes wit	hin 50.000bp	-,
15	90.542.107	90.542.497	390	9	,			SLCO3A1	34.324
15	90.625.536	90.625.844	308	9		AC116903.3	4.218		
15	91,153,024	91,154,234	1.210	10		No non-overlappi	na aenes wit	hin 50.000bp	
15	91.164.490	91,165,013	523	13		No non-overlappi	na aenes wit	hin 50.000bp	
15	91.175.719	91,176,529	810	10		No non-overlappi	na aenes wit	hin 50.000bp	
15	91.248.273	91.248.974	701	9	CHD2.	No non-overlappi	na aenes wit	hin 50.000bp	
15	91.264.950	91.265.684	734	.9	CHD2.	No non-overlappi	ng genes wit	hin 50,000bp	
15	91.379.975	91.380.493	518	.9	,		0.01.100.111	RGMA	7.148
15	91,408.354	91,408.932	578	9	RGMA,			AC087641.5	956
15	91,432,387	91,433.057	670	9	RGMA,	AC087641.5	21,790	-	
15	92,414.534	92,415.154	620	10	,		,	AC080032.12	10.177
15	93,775.384	93,775.815	431	10		No non-overlappi	ng genes wit	hin 50,000bp	- ,
15	93,901,228	93,902.030	802	11		No non-overlappi	ng genes wit	hin 50,000bp	
15	94,391,376	94,392,201	825	9		No non-overlappi	ng genes wit	hin 50,000bp	
15	94,595.276	94.595.521	245	10				AC016251.9	36.763
15	94,668.092	94,668.524	432	11		NR2F2	2.019		.,
15	94,680,498	94,680,822	324	9	NR2F2,		,	hsa-mir-1469	2.958
15	94,700,752	94,701.655	903	12	*			NR2F2	16.256
15	94,704.084	94,704,763	679	9				NR2F2	19,588
15	96,092,723	96,093.053	330	9		No non-overlappi	ng genes wit	hin 50,000bp	.,
15	96,443,681	96,444,351	670	9		U6	8,166		
15	96,672,363	96,672,952	589	9		No non-overlappi	ng genes wit	hin 50,000bp	
15	96,789.852	96,790.465	613	9				FAM169B	7.449
15	96,803,178	96,803,575	397	11	FAM169B.	No non-overlappi	ng genes wit	hin 50,000bp	,
15	96,914,940	96,915,443	503	10	,	No non-overlappi	ng genes wit	hin 50,000bp	
15	97,007.875	97,008.655	780	14		IGF1R	1,647		
· · · · ·	, ,	, ., -				1	,		

15	97,011,249	97,011,719	470	9	IGF1R,	No non-overlappi	ng genes wit	hin 50,000bp	
15	97,140,297	97,140,715	418	13	IGF1R,	No non-overlappi	ng genes wit	hin 50,000bp	
15	97,265,194	97,265,570	376	10	IGF1R,	No non-overlappi	ng genes wit	hin 50,000bp	
15	97,390,281	97,390,572	291	10		AC069029.9	23,967		
15	97,403,676	97,404,063	387	9		AC069029.9	37,362		
15	97,417,357	97,418,084	727	9		SYNM	44,845		
15	97,462,439	97,462,954	515	14	SYNM,			TTC23	31,097
15	97.923.378	97.923.923	545	14	MEF2A.	No non-overlappi	na aenes wit	hin 50.000bp	,
15	97.924.277	97.924.719	442	9	MEF2A.	No non-overlappi	na aenes wit	hin 50.000bp	
15	98.091.332	98.091.668	336	10	,	AC022692.11-1	160	,	
15	98 699 403	98 700 515	1 1 1 2	9	ADAMTS17			AC015723 8	1 671
15	98 707 747	98 708 273	526	10	AC015723 8	ADAMTS17	8 041		.,
15	98 959 400	98 959 928	528	13	LINS1	ASB7	409		
15	98 959 995	98 960 446	451	17	ASB7	LINS1	68		
15	99 230 552	99 231 129	577	9	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	ALDH1A3	6 451		
15	99 235 090	99 235 527	437	10		ALDH1A3	2 053		
15	00, <u>2</u> 00,000	99 366 683	544	C		No non-overlanni	na aenes wit	hin 50 000hn	
15	99 615 762	99 616 852	1 000	9			6 102	IIII 30,0000p	
15	00 652 447	00 653 450	1,000	12			0,102	PCSK6	8 207
15	99,052,447	00 854 373	1,000	11		PCSK6	6.643	1 0010	0,207
15	99,054,059	99,054,575	792	0		PCSK6	10 139		
15	99,007,004	99,050,510	242	9		PCSK6	15,150		
15	99,003,302	99,003,004	242	9		PCSKO	10,900		
15	99,000,703	99,007,105	322	10		PCSKO	39,307		
15	99,894,685	99,895,215	530	10		PUSKO	47,289	hin 50 000hn	
15	99,901,865	99,902,156	291	11		No non-overlappi	ng genes wit		07.050
15	99,970,961	99,971,627	666	13				TM2D3	27,953
15	99,973,422	99,974,174	752	11	T1 (0D0	4 0 0 0 0 4 0 4 0 0		TM2D3	25,406
15	100,009,795	100,010,842	1,047	13	TM2D3,	AC090164.22	3,757	TARSL2	637
15	100,045,308	100,045,664	356	9	TARSL2,	4.0.407077.40.0	00.045	AC027559.17	3,977
15	100,067,049	100,067,400	351	9	TARSL2,	AC107977.13-2	36,245	AC027559.17	25,718
15	100,070,800	100,071,148	348	9	TARSL2,	AC10/9/7.13-2	32,497	AC027559.17	29,469
15	100,077,416	100,077,937	521	10	TARSL2,	AC10/9/7.13-2	25,708	AC027559.17	36,085
15	100,081,593	100,082,184	591	16	TARSL2,	AC10/9/7.13-2	21,461	AC027559.17	40,262
15	100,082,411	100,082,919	508	9		TARSL2	243		a
16	171,126	171,793	667	12	HBQ1,			Y_RNA	2,471
16	381,831	382,225	394	12		NME4	4,501	Z97634.3	4,597
16	391,919	392,181	262	10	DECR2,			NME4	1,165
16	626,146	626,858	712	12	C16orf13,	C16orf14	4,992	WFIKKN1	2,029
16	680,059	680,591	532	9	WDR24,	JMJD8	5,529	FBXL16	1,910
16	1,403,692	1,404,064	372	13	C16orf28,			C16orf91	5,881
16	1,954,627	1,955,094	467	11	RPS2,	SNORA64	1,519	NDUFB10	2,650
16	2,330,798	2,331,329	531	11		ABCA3	50		
16	2,672,336	2,672,840	504	9	KCTD5,	AC092117.4-1	1,463		
16	2,901,518	2,902,338	820	9	FLYWCH1,	AC004034.2	15,326	FLYWCH2	12,159
16	3,013,830	3,014,545	715	10	HCFC1R1,	CLDN6	3,757	TNFRSF12A	1,448
40	0.000.0	0.000 -0-	001	-	THOC6,	715005			
16	3,096,256	3,096,587	331	9		ZNF205	5,977	101001010101	<u> </u>
16	3,140,402	3,141,166	764	9	101001010101			AC108134.3-1	1,444
16	3,142,290	3,143,182	892	11	AC108134.3-1,	A 1000 (17 ()	0.04	ZNF213	9,485
16	3,164,046	3,164,416	370	9		AJ003147.1-1	3,014	71/5000	0-04-
16	3,173,989	3,174,407	418	10		AJ003147.1-2	11,747	ZNF200	37,919
16	3,179,502	3,179,948	446	10		AJ003147.1-2	6,206		
16	3,181,490	3,182,138	648	10		AJ003147.1-2	4,016	1.00055555	
16	3,390,935	3,391,748	813	9	ZNF434,	AC025283.6-6	29,953	AC025283.6-7	17,236
10	0 400 700	0 404 000	500		$\angle NF1/4$,	010-100	E 0/0		
16	3,490,709	3,491,269	560	11	GLUAP'I,	C100H90	5,248		0.0
16	4,243,522	4,244,319	797	10					2,870
16	4,496,121	4,496,898	777	9	HMUX2,	4.0000000000	1- 00-	C160ff5	3,779
16	4,528,662	4,529,123	461	10	C160ff5,	AC023830.9-2	17,369	HMOX2	28,313
16	4,614,157	4,614,991	834	10	MGRN1,	FAM100A	9,229		a
16	4,758,097	4,758,916	819	9		∠NF500	930	12-Sep	8,700
16	4,932,977	4,933,427	450	10		PPL .	5,840	Y_RNA	8,348
16	6,746,724	6,747,012	288	9		No non-overlappi	ng genes wit	nin 50,000bp	
16	8,557,728	8,558,106	378	9		No non-overlappi	ng genes wit	hin 50,000bp	
16	8,798,818	8,799,179	361	9	C16orf51,	PMM2	14		

16	9,182,573	9,182,781	208	11		AC087190.5-2	24,334		
16	10,943,817	10,944,170	353	10	DEXI,	CLEC16A	1,676		
16	11,917,191	11,917,578	387	9	GSPT1,	TNFRSF17	48,887		
16	12,804,559	12,805,070	511	13	CPPED1,			SNORA27	38,775
16	14,286,421	14,286,879	458	9				Y_RNA	9,463
16	14,287,110	14,287,691	581	15		hsa-mir-193b	17,634	Y_RNA	10,152
16	14,290,971	14,291,409	438	10		hsa-mir-193b	13,916	Y_RNA	14,013
16	14,488,184	14,488,605	421	28	PARN,	AC092291.3-1	32,528	AC092291.3-2	15,629
16	15,592,176	15,592,664	488	10				C16orf45	2,758
16	19,804,993	19,805,489	496	9		GPRC5B	1,341		
16	19,826,136	19,826,501	365	9		GPRC5B	22,484	IQCK	49,778
16	21,518,074	21,518,413	339	11	METTL9,	U6	42,467	AC005632.2-1	11,387
16	22,107,354	22,108,089	735	9	SDR42E2,	EEF2K	17,004	VWA3A	31,579
16	22,110,995	22,111,320	325	9				SDR42E2	1,828
16	22,114,373	22,114,743	370	18				SDR42E2	5,206
16	22,215,792	22,216,287	495	13	POLR3E,			EEF2K	8,225
16	22,216,400	22,216,606	206	9	POLR3E,			EEF2K	8,833
16	22,216,848	22,217,106	258	11	POLR3E,			EEF2K	9,281
16	22,217,162	22,217,494	332	20	POLR3E,			EEF2K	9,595
16	22,599,580	22,599,911	331	10		No non-overlappi	ng genes wit	hin 50,000bp	
16	23,475,695	23,476,023	328	10	EARS2, UBFD1,	GGA2	46,386	NDUFAB1	23,815
16	23.514.923	23.515.307	384	10	NDUFAB1.		,	PALB2	6.677
16	23.515.685	23.516.211	526	9	,	NDUFAB1	545	PALB2	5.773
16	24.925.235	24.925.761	526	9	ARHGAP17.	No non-overlappi	na aenes wit	hin 50.000bp	-, -
16	25,176,771	25.177.414	643	11	- ,	ZKSCAN2	428	,	
16	27 880 970	27 881 258	288	10	GSG1I			U6	35 859
16	28 100 298	28 100 657	359	.0	XPO6	Y RNA	1 483	SNORA25	2 253
16	28 761 669	28 762 155	486	9	TUFM		.,	ATXN2I	5 612
16	28 764 310	28 765 465	1 155	9	TUFM			ATXN2I	8 253
16	28 781 834	28 782 701	867	9	i or m,	SH2B1	24	, (I) (ILE	0,200
16	29 723 428	29 724 033	605	9	KIF22	MAZ	1 323		
16	29 724 216	29 724 765	549	15		MAZ	591	KIF22	9
16	29 726 277	29 727 077	800	10	MA7	PRRT2	3 833	KIF22	2 070
16	20,720,277	29,727,077	700	11	ΜΔΖ,	PRRT2	254	KIE22	5 749
16	29,725,340	29,736,194	854	a	C16orf53	MVP	3 095	PRRT2	638
16	20,782,082	20,700,104	736	11	AC120114 2-2		3,000	SE76L2	7 514
16	20,702,002	29,863,374	1 215	a	A0120114.2-2,	AC120114 2-1	13 107		37 283
16	20,880,451	29,880,758	307	11		TMEM219	94	AOLIDI	57,205
16	29,000,401	29,972,856	524	9		PPP4C	21 983	AC093512.2	28 808
16	20,072,002	29,983,470	871	11		PPP4C	11 369	TBX6	20,000
16	30 015 359	30 016 090	731	9	ZNE688	VPEL3	321	GDPD3	7 542
16	30,013,339	30,010,030	631	9	ZNF688		521		1,542
10	50,274,110	30,274,743	001	5	CD2BP2.				1,175
16	30 289 727	30 290 100	373	10	ZNF688	TBC1D10B	641	1-Sep	6 858
16	30 318 180	30,319,811	1 631		ZNE688 ZNE48	ZNF771	6 626		0,000
16	30 336 636	30 337 450	814	14	ZNF688		0,020	SNORA42	997
	22,200,000	22,207,100	514		ZNF771,				001
16	30,348,788	30,349,349	561	13	ZNF688,	SNORA42	10,207	ZNF771	10,559
					DCTPP1,				
16	30,364,046	30,365,057	1,011	9	ZNF688,			Y_RNA	7,762
					SEPHS2,				
16	30,476,896	30,477,478	582	12	ZNF688,	ZNF747	23,156	ITGAL	34,890
					ZNF764,				
16	30,528,882	30,529,551	669	11	ZNF689,	ZNF688	24,371		
16	30,553,262	30,553,822	560	9		PRR14	15,902	AC093249.4-1	40,300
16	30,576,047	30,576,985	938	11		FBRS	805	PRR14	813
16	30,617,339	30,617,900	561	12		SRCAP	63	U6	2,251
16	30,680,418	30,681,506	1,088	10	AC106886.3-1,			PHKG2	4,235
					RNF40,				
16	30,693,917	30,694,994	1,077	10	RNF40,			ZNF629	2,277
16	30,732,943	30,733,406	463	11				AC106886.3-2	6,565
16	30,793,648	30,794,649	1,001	14	BCL7C,	CTF1	17,226	AC135048.2-1	46,769
16	30,813,008	30,813,422	414	11	CTF1,	BCL7C	108	AC135048.2-2	207
16	30,840,676	30,842,218	1,542	11	AC135048.2-1,	FBXL19	701		
16	30,868,817	30,869,139	322	10	ORAI3,	SETD1A	6,977	FBXL19	1,212

16	30,875,560	30,876,174	614	10	SETD1A,			ORAI3	1,803
16	30,876,232	30,876,805	573	12	SETD1A,			ORAI3	2,475
16	30,951,496	30,952,502	1,006	9	STX4,	STX1B2	22,220	ZNF668	27,170
16	30.991.572	30,992,193	621	12	ZNF668.	ZNF646	1.070		
16	31,098,328	31,099,787	1,459	9	TRIM72, FUS,	PRSS36	29,412	PYCARD	20,523
16	33,829,407	33,830,720	1,313	13		AC136932.4-2	38,433		
16	33.841.600	33.843.362	1.762	9		AC136932.4-2	25.791		
16	33.844.006	33.844.837	831	9		AC136932.4-2	24,316		
16	33.857.623	33,858,160	537	40		AC136932.4-2	10,993		
16	33 858 362	33 858 737	375	18		AC136932 4-2	10,416		
16	33 858 779	33 858 982	203	15		AC136932 4-2	10,171		
16	33 860 372	33 861 073	701	53		AC136932 4-2	8 080		
16	33,863,040	33 863 518	/01	20		AC136032.4-2	5,635		
16	33,863,860	33 864 180	320	20		AC136032.4-2	1 964		
16	33,864,453	33,865,427	074	47		AC136032.4-2	3 726		
16	22 966 091	22 967 211	1 1 2 0	47		AC130932.4-2	3,720		
10	33,000,001	33,007,211	1,130	30		AC130932.4-2	1,942		
10	33,868,413	33,868,975	200	25		AC136932.4-2	1/8	10100000 1.0	00.4
16	33,869,901	33,871,700	1,799	133	SSU_IRNA_5,	5_85_IRNA	1,227	AC136932.4-2	634
16	33,872,761	33,873,545	/84	28	5_8S_rRNA,			SSU_rRNA_5	2,109
16	45,475,115	45,475,977	862	9	GPT2,	AC007225.2	39,117		
16	46,096,026	46,096,875	849	12	PHKB,	ITFG1	43,507		
					AC007599.6-1,				
					AC007599.6-2,				
16	49 440 112	49 440 491	260	11	55_IRNA,	7115400	20,602		
10	40,449,112	40,449,401	309	11	01100	ZINF423	30,093	hin 50 000hn	
10	51,040,099	51,040,527	420	12	СПD9,		ng genes wit		40.000
16	52,141,310	52,141,657	347	9		FIS	46,639	RPGRIP1L	49,668
16	52,328,194	52,328,524	330	9	F10,	RPGRIP1L	32,922		
16	53,520,492	53,521,426	934	9		IRX5	1,186	202214	
16	55,836,182	55,836,581	399	9	ARL2BP,			RSPRY1	5,741
16	55,891,267	55,892,239	972	16		PLLP	15,195	ARL2BP	46,221
16	56,013,698	56,014,209	511	9				CIAPIN1	5,378
16	56,111,024	56,111,408	384	9	CCDC102A,	GPR114	22,694	POLR2C	47,602
16	56,182,842	56,183,131	289	10	GPR114,	AC018552.6	11,420		
16	56,713,306	56,713,691	385	10	C16orf80,	Y_RNA	38,733	CSNK2A2	35,629
16	56,720,420	56,721,356	936	9	C16orf80,	Y_RNA	45,847	CSNK2A2	27,964
16	57,103,382	57,103,681	299	13	NDRG4,	SETD6	3,206	CNOT1	7,678
16	63,484,905	63,485,246	341	10				CDH11	49,911
16	64,005,715	64,006,076	361	9		No non-overlappi	ng genes wit	hin 50,000bp	
16	65,765,141	65,765,770	629	10	NOL3,			EXOC3L	1,238
16	65,839,261	65,839,542	281	9		FHOD1	335		
16	65,870,757	65,871,174	417	9	PLEKHG4,			SLC9A5	7,163
16	66,153,188	66,153,784	596	9	,	CTCF	27		
16	66 397 909	66 398 434	525	9	RANBP10	TSNAXIP1	77		
16	66 407 805	66 408 455	650	9	TSNAXIP1	RANBP10	9 749		
16	67 434 828	67 435 873	1 045	a	TMCO7		0,170	CDH1	7 885
16	67 808 016	67 808 360	353	0	SNTB2	116	<u>40 835</u>	Y RNA	25 380
16	67 021 260	67 922 500	621	11	COG8 COG8	NIP7	9,000 8 5/17	VPS44	5 102
16	68 122 025	68 122 /5/	<u>410</u>	0		NFAT5	34 044	hsa-mir-1538	34 759
16	68 038 131	68 938 850	710	9			34,044		12 001
10	60 245 226	60 245 670	119	9	11 3/			MTSS1	12,901 6 020
10	60 566 074	60 566 570	400	9		No non overlanni		hin 50 000hn	0,929
16	60,579,700	60 570 217	510	9		No non-overlappi	ng genes wit	hin 50,000bp	
10	09,070,799	09,579,317	010	9		No non-overlappi	ng genes wit	hin 50,000bp	
16	69,610,374	69,611,064	690	10	HYDIN,	No non-overlappi	ng genes wit		
16	69,613,273	69,613,793	520	9	HYDIN,	No non-overlappi	ng genes wit		
16	70,017,704	70,018,580	876	10				ZNF23	20,421
16	70,052,974	70,053,328	354	9	∠NF23,			ZNF19	12,149
16	70,400,074	70,400,558	484	12	AP1G1,	No non-overlappi	ng genes wit	hin 50,000bp	
16	71,628,735	71,629,205	470	9	ATBF1,	No non-overlappi	ng genes wit	hin 50,000bp	
16	71,956,531	71,957,244	713	9		No non-overlappi	ng genes wit	hin 50,000bp	
16	73,739,652	73,740,708	1,056	9	ZFP1,	LDHD	31,486	ZNRF1	37,259
16	73,896,541	73,897,208	667	9	CFDP1,	BCAR1	37,089		
16	74,024,396	74,025,021	625	19	CFDP1,			TMEM170A	13,405
16	75,781,695	75,782,728	1,033	10	MON1B,	AC009139.8	15,044		
16	76,594,441	76,594,848	407	9		CLEC3A	19,096	VAT1L	22,937

16	81,736,169	81,736,535	366	9	CDH13,	No non-overlappi	ng genes wit	hin 50,000bp	
16	82,707,769	82,708,255	486	10	MBTPS1,			HSDL1	5,134
16	83,397,546	83,398,270	724	9		CRISPLD2	12,843	USP10	26,520
16	84,011,800	84,012,246	446	11		No non-overlappi	ng genes wit	hin 50,000bp	
16	84,144,970	84,145,711	741	9		No non-overlappi	ng genes wit	hin 50,000bp	
16	85,974,823	85,975,491	668	10	FBXO31,	MAP1LC3B	7,829		
16	85,979,223	85,979,573	350	10		MAP1LC3B	3,747		
16	86,194,026	86,194,391	365	11	JPH3,	No non-overlappi	ng genes wit	hin 50,000bp	
16	87,403,553	87,404,032	479	9	APRT,			CDT1	387
16	87,451,346	87,451,841	495	9	TRAPPC2L,	GALNS	461	AC092384.5-1	5,754
16	88,196,802	88,197,118	316	9				CPNE7	5,647
16	88,468,715	88,469,130	415	10	TCF25,			SPIRE2	3,487
16	88,607,101	88,607,709	608	9	DBNDD1,	GAS8	8,800		
17	288,645	289,249	604	9				FAM101B	759
17	290,401	290,790	389	9	FAM101B,			C17orf97	16,639
17	602,499	602,905	406	9	AC087392.10-2,	GEMIN4	248	GLOD4	6,537
17	783.003	783,744	741	10	NXN.	No non-overlappi	na aenes wit	hin 50.000bp	,
17	814,792	815.295	503	9	NXN.	TIMM22	31.812	ABR	38.215
17	906,028	906,535	507	9	ABR,	No non-overlappi	ng genes wit	hin 50,000bp	,
17	920,063	920,707	644	9	ABR,	No non-overlappi	ng genes wit	hin 50,000bp	
17	923.330	923.671	341	11	ABR,	No non-overlappi	ng genes wit	hin 50,000bp	
17	1,212.236	1,212.899	663	10	YWHAE,	No non-overlappi	ng genes wit	hin 50,000bp	
17	1,249,524	1,250,501	977	9	YWHAE,	· · · · · · · · · · · · · · · · ·		CRK	21,689
17	1,366.349	1.366.931	582	10	SKIP,			PITPNA	1.106
17	1.479.982	1,480,358	376	10	,	SLC43A2	1.102	SCARF1	3.545
17	1 679 110	1 679 923	813	9	SMYD4	RPA1	172		-,
17	1 846 879	1 847 763	884	9		DPH1	32 418		
17	1 880 022	1 880 809	787	11	DPH1	OVCA2	11 218	hsa-mir-132	19 143
17	1 891 496	1 893 109	1 613		DPH1_OVCA2	0.0.12	,=	hsa-mir-132	6 843
17	2 185 836	2 186 278	442	9	TSR1	SGSM2	1 278		0,010
17	2 209 285	2 209 950	665	10	SGSM2	TSR1	21 857	MNT	24 155
17	2.361.363	2.362.274	911	9	METT10D.			AC015799.23-1	45.244
17	2 444 569	2 444 980	411	10	PAFAH1B1	SRP euk arch	36 431		,
17	2 561 789	2 562 137	348	10		KIAA0664	7 195		
17	2 825 502	2 825 968	466	12	GARNI 4	No non-overlappi	na aenes wit	hin 50 000bp	
17	3 519 083	3 519 505	422	9	TMFM93	TAX1BP3	361	P2RX5	2 992
17	3 763 908	3 764 242	334	10	P2RX1			ATP2A3	5 376
17	3 993 674	3 994 403	729	.0	CYB5D2	77FF1	672		0,010
17	4,113,709	4,114,375	666	13	ANKFY1.			UBE2G1	4,886
17	4 114 379	4 114 743	364	9	,	ANKFY1	356	UBE2G1	4 518
17	4.215.089	4.215.902	813	9	UBE2G1.	No non-overlappi	na aenes wit	hin 50.000bp	.,
17	4 216 648	4 217 091	443	9	UBF2G1	No non-overlappi	na aenes wit	hin 50 000bp	
17	4.263.008	4,263,546	538	10		SPNS3	20.422		
17	4 298 419	4 299 019	600	.0	SPNS3	SPNS2	49 863		
17	4.559.844	4.560.316	472	15	,	ARRB2	217		
17	4,569.622	4,570.476	854	9	ARRB2,	MED11	10.981	CXCL16	13.101
17	4,581.279	4,581.825	546	14	MED11,	ZMYND15	8.732	CXCL16	1.752
17	4.783.709	4.784.489	780	18	SLC25A11	-	-, -	GP1BA	5.110
	, , 0	, ,			RNF167,				.,
17	4,790,405	4,790,700	295	10	PFN1,	ENO3	4,431	RNF167	1,145
17	4,831,180	4,831,890	710	10	CAMTA2,			AC004771.1-2	259
					AC004771.1-1,				
17	4,841,351	4,841,874	523	11	AC004771.1-2,	KIF1C	97	AC004771.1-1	9,655
17	4,955,713	4,956,078	365	10	ZNF232,	USP6	4,379		
17	5,035,423	5,036,508	1,085	9	ZNF594,			USP6	16,370
17	5,127,627	5,128,298	671	9	RABEP1,	C17orf87	48,766		
17	5,262,802	5,263,600	798	9	NUP88,	RPAIN	85		
17	5,264,294	5,264,948	654	9	RPAIN,	NUP88	574		
17	5,277,579	5,277,884	305	10	C1QBP,			RPAIN	659
17	5,312,800	5,313,262	462	9	DHX33,			DERL2	5,075
17	5,330,577	5,331,247	670	9	MIS12,	DERL2	356		
17	6,484,760	6,485,664	904	13	KIAA0753,			MED31	1,693
					TXNL5,				
17	6,831,421	6,831,831	410	9	AC027763.2,	ALOX12	8,277		
					ວວ_rkna,				

17	6,857,017	6,857,788	771	9	RNASEK,	AC027763.2	640	ALOX12	2,238
47	0.000.005	0 000 770			AC040977.10-1,	01.040444	0.000	01.040440	0.040
17	6,890,205	6,890,770	565	11		SLC16A11	2,239	SLC16A13	6,042
17	6,896,147	6,896,575	428	9		SLC16A11	8,181		
17	7,063,475	7,064,168	693	9	DLG4, ACADVL,			hsa-mir-324	3,172
17	7,064,611	7,065,314	703	10	ACADVL,	DLG4	830	hsa-mir-324	2,026
17	7,065,504	7,066,362	858	9	ACADVL,	DLG4	1,723	hsa-mir-324	978
17	7,085,884	7,086,490	606	9	GABARAP,	PHF23	2,335	DULLARD	1,165
17	7,096,829	7,097,408	579	10	C17orf81,	DULLARD	846	CLDN7	6,545
17	7,124,639	7,125,522	883	9		SLC2A4	256	YBX2	6,773
17	7,152,577	7,154,025	1,448	9	EIF5A,			GPS2	2,677
17	7,173,347	7,173,916	569	13	NEURL4,	AC026954.6	579		
17	7,328,173	7,328,703	530	11	ZBTB4,			CHRNB1	26,517
17	7 346 210	7 346 688	478	Q	POLR2A, POLR2A	7BTB4	17 969		34 449
17	7,040,210	7,340,000	700	11		SNOR448	1 / 35		611
17	7,410,020	7,417,320	700	11			1,433	SEINES	692
17	7,422,010	7,423,730	920	11	EIF4AT, CD00,		4,110	SNURA07	003
17	7,501,157	7,501,476	319	10	ATP1B2,	SA12	29,245	TP53	10,969
17	7,529,838	7,530,624	786	9	TP53,	WRAP53	1,740		
17	7,531,408	7,531,801	393	13	TP53,	WRAP53	563		
17	7,560,745	7,561,206	461	11		DNAH2	1,540	EFNB3	5,331
17	7,561,210	7,561,622	412	11		DNAH2	1,124	EFNB3	5,796
17	7,589,884	7,590,161	277	10	DNAH2,	AC087388.9	8,269		
17	7.678.737	7.679.185	448	11		JMJD3	4.762	DNAH2	954
17	7,679,824	7,680,123	299	,q		JMJD3	3 824	DNAH2	2 041
17	7 680 788	7 681 566	778	g		JMJD3	2 381	DNAH2	3,005
17	7,000,700	7,001,000	507	10			10 105		10,616
17	7,000,399	7,000,900	760	10			10,195		10,010
17	7,700,971	7,701,733	/62	10	LSMDT,		305		829
17	7,775,991	7,776,437	446	9	CNTROB,	TRAPPCT	3		
17	7,834,037	7,834,538	501	11		GUCY2D	12,175	CNTROB	40,417
17	7,860,676	7,861,021	345	9	GUCY2D,	ALOX15B	22,062		
17	7,923,212	7,923,857	645	10	ALOX12B, AC12	9492.6,		ALOXE3	16,086
17	7,962,629	7,963,388	759	16		ALOXE3	97	HES7	1,636
17	7,963,661	7,963,883	222	10		ALOXE3	1,129	HES7	1,141
17	7,964,121	7,964,548	427	18		ALOXE3	1,589	HES7	476
17	7.964.659	7.965.136	477	15	HES7.	ALOXE3	2.127		
17	7 982 529	7 983 739	1 2 1 0	20	- ,			PFR1	795
17	7 998 037	7 998 369	332	10		PFR1	1 610	VAMP2	4 777
17	8 002 628	8 003 131	503	14		PER1	6 201		15
17	8 016 631	8 018 354	1 723	14		AC120402.6.1	0,201		15
17	0,010,031	0,010,354	1,723	9	$TIVIEIVITU_{7}, U0,$	AC129492.0-1	9,014	017-50	4 707
17	8,030,158	8,030,589	431	15		TIVIEIVITU7	9,719		1,787
17	8,030,768	8,032,252	1,484	22				C17orf59	124
17	8,054,339	8,054,670	331	10	AURKB,	C17orf59	19,389	C17orf44	10,040
17	8,064,722	8,065,091	369	14	C17orf44,			C17orf68	5,827
17	8,065,234	8,067,746	2,512	19	C17orf44,			C17orf68	3,172
17	8,069,868	8,071,394	1,526	11	C17orf68,	C17orf44	1,782		
17	8,091,426	8,092,047	621	9	C17orf68,	PFAS	1,315		
17	8,132,434	8,133,032	598	9	SLC25A35,	ARHGEF15	21,283	PFAS	17,906
17	8 120 009	8 120 956	750	0	RANGRF,			PANCEE	4 070
11	0,139,090	0,139,000	001	9	VDDA0				4,970
17	ö,220,471	ö,221,315	844	12	KKBAZ,		A AA-	KPLZ0	244
17	8,226,981	8,227,709	728	13	RPL26,	KRBA2	6,227	RNF222	7,043
17	8,280,165	8,280,861	696	9	NDEL1,	RNF222	38,296	MYH10	37,387
17	8,475,125	8,475,730	605	9		MYH10	321		
17	8,928,207	8,928,708	501	9	NTN1,	No non-overlappi	ng genes wit	hin 50,000bp	
17	9,488,972	9,489,544	572	11		USP43	131	WDR16	1,475
17	9,680,233	9,680,504	271	9	GLP2R,	AC027045.21	14,105		
17	10,171.640	10,171,906	266	10	MYH13,	No non-overlappi	ng genes wit	hin 50.000bp	
17	10 462 088	10,462,566	478	. 0 . Q	-,		5 5 5	MYH3	10 002
17	11 641 427	11 642 112	685	12	DNAH9	No non-overlappi	na aenes wit	hin 50 000hn	. 5,002
17	11 831 707	11 832 601	000	12	ZNE18		32 175		17 851
17	11 040 000	11 040 070	1 070	9	ZNI 10,		32,173		17,001
1/	11,040,998	11,042,276	1,2/8	9	ZINF 10,	IVIAPZR4	22,590		27,142
17	12,045,002	12,045,783	/81	9		No non-overlappi	ng genes wit	nin 50,000bp	
17	12,389,697	12,390,344	647	9		AC005358.1	3,667		
17	12,509,169	12,509,489	320	9		MYOCD	450		

17	12,632,865	12,633,656	791	9	AC005277.1,			MYOCD	25,141
17	12,958,547	12.958.899	352	10		No non-overlappi	na aenes wit	hin 50.000bp	,
17	13 414 511	13 414 852	341	9	HS3ST3A1	hsa-mir-548h-3	26 823		
17	13 445 305	13 445 695	390	9	HS3ST3A1	No non-overlanni	na aenes wit	hin 50 000hn	
17	13 446 260	13 446 689	429	13	100010/11,	HS3ST3A1	201		
17	13 913 212	13 913 907	695	10	COX10	No non-overlanni	na aenes wit	hin 50 000hn	
17	14 144 524	14 145 137	613	11	00/(10,	HS3ST3B1	38		
17	14 153 057	14 153 777	720	0	HS3ST3B1	No non-overlanni	na aenes wit	hin 50 000hn	
17	14,105,007	14,135,777	120	10	110001001,	No non overlappi	ng genes wit	hin 50,000bp	
17	14,295,000	14,290,113	400	10		No non-overlappi	ng genes wit	hin 50,000bp	
17	14,315,123	14,315,442	319	10		No non-overlappi	ng genes wit	hin 50,000bp	
17	14,975,538	14,976,154	616	9		No non-overlappi	ng genes wit		15 7 10
17	15,101,095	15,102,104	1,009	9	PMP22,	AC005703.2-1	19,180	TEK13	45,749
17	15,106,466	15,107,663	1,197	9	PMP22,	AC005703.2-1	24,551	TEKT3	40,190
17	16,061,008	16,061,622	614	12	PIGL,	NCOR1	1,438		
17	16,224,520	16,225,929	1,409	9	UBB,	CENPV	26,983		
17	16,379,604	16,380,182	578	10		C17orf76	43,412	ZNF287	15,244
17	16,886,853	16,887,475	622	11	MPRIP,	No non-overlappi	ng genes wit	hin 50,000bp	
17	16,888,778	16,889,815	1,037	9	MPRIP,	No non-overlappi	ng genes wit	hin 50,000bp	
17	17,049,814	17,050,754	940	9	PLD6,			FLCN	5,500
17	17,125,033	17,125,742	709	9	COPS3,	NT5M	21,632	AC055811.5	38,108
17	17,146,994	17,147,511	517	9	NT5M,	COPS3	21,678		
17	17,198,977	17,199,283	306	10				NT5M	7,275
17	17,200,064	17,200,523	459	14				NT5M	8,362
17	17,507,371	17,508,063	692	12		RAI1	17,449		- ,
17	17 527 170	17 527 796	626	10	RAI1	No non-overlappi	na aenes wit	hin 50 000bp	
17	17 537 437	17 537 872	435	9	RΔI1	No non-overlappi	ng genee wit	hin 50,000bp	
17	17 583 181	17 583 716	535	9		No non-overlappi	ng genes wit	hin 50,000bp	
17	17,505,101	17,505,710	413	10			ng genes wit		238
17	17,000,700	17,000,140	413	10					230
17	17,000,220	17,000,019	299	10	SREDFI,		0.700		120
17	17,083,840	17,084,304	458	9	TONALO	SREBF1	2,796	TOMILZ	3,244
17	17,689,064	17,689,761	697	9	TOM1L2,	SREBFI	8,014	0.17 (00	0.045
17	17,915,088	17,915,442	354	10				C17off39	2,645
17	17,931,509	17,932,411	902	11	DRG2,	MYO15A	20,334	C17orf39	19,066
17	17,938,004	17,938,376	372	9	DRG2,	MYO15A	14,369	C17orf39	25,561
17	18,026,064	18,027,865	1,801	10	ALKBH5,			MYO15A	2,223
17	18,092,198	18,093,071	873	9	FLII,			LLGL1	3,284
17	18,158,690	18,159,913	1,223	9	TOP3A,			AC127537.7	1,124
					SMCR8,				
17	18,413,502	18,414,046	544	9	CCDC144B,	RPS28	2,745		
17	18,699,871	18,700,441	570	12	PRPSAP2,			AC107982.4	13,469
17	18,804,708	18,805,172	464	10	SLC5A10,	AC090286.16-1	6,521	FAM83G	7,655
17	19,206,630	19,207,176	546	14	B9D1,	MAPK7	14,483	MFAP4	20,172
17	19,351,830	19,352,549	719	24		SLC47A1	25,210	RPL17P43	10,396
17	19,492,587	19,493,036	449	10	ALDH3A2,			AC115989.6	367
17	19,836,706	19,837,222	516	9		5S rRNA	4,371		
17	20,458,807	20,459.597	790	9		AC087499.9	5,292	AC087499.5	894
17	20.550.814	20,551,137	323	9		AC126365.1	9.251	AC087499.8	3.195
17	20,752,106	20,753,113	1.007	9		CCDC144NL	12.061		.,
17	20.837 014	20.837 359	345	10			_,	USP22	6 139
17	20.887 278	20,888 240	962	.0		USP22	334		-,
17	21,057,986	21 058 420	434	10	TMEM11	001 22		SRP euk arch	14 821
17	21,007,000	21,000,420	818	9		SRP euk arch	2 341	C17orf103	6 088
17	21,073,074	21,070,092	596	11			4 222	01701105	0,000
17	21,123,742	21,124,328	1 4 4 0		MADOKO	No non overlare	4,233	hin EO OOgha	
17	21,149,001	21,150,419	1,418	9	MADOKO	No non-overlappi	ng genes wit	hin 50,000bp	
17	21,152,485	21,153,309	684	12	IVIAMZKJ,	No non-overiappi	ng genes wit		4.004
17	21,160,319	21,160,887	568	12					1,201
17	21,164,985	21,165,999	1,014	11				MAP2K3	5,867
17	21,168,648	21,169,046	398	9				MAP2K3	9,530
17	21,169,217	21,169,957	740	9				MAP2K3	10,099
17	21,170,790	21,171,136	346	10		KCNJ12	49,156	MAP2K3	11,672
17	21,177,387	21,179,022	1,635	9		KCNJ12	41,270	MAP2K3	18,269
17	21,180,003	21,181,154	1,151	9		KCNJ12	39,138	MAP2K3	20,885
17	21,181,240	21,181,515	275	9		KCNJ12	38,777	MAP2K3	22,122
17	21,181,847	21,183,193	1,346	9		KCNJ12	37,099	MAP2K3	22,729

17	21 192 027	21 192 855	828	11		KCNJ12	27 437	MAP2K3	32 909
17	21 193 291	21 193 686	395	9		KCN.I12	26 606	MAP2K3	34 173
17	21,100,201	21,100,000	709	12	KCN112	No non ovorlanni		hin 50 000hn	04,170
17	21,245,209	21,240,007	190	12	KCNU12	No non-overlappi	ng genes wit	hin 50,000bp	
17	21,240,372	21,247,354	902	10	KCINJ IZ,	No non-overlappi	ng genes wit	hin 50,000bp	
17	21,247,990	21,248,031	641	9	KGNJ12,	No non-overlappi	ng genes wit		
17	21,254,369	21,255,230	861	9	KCNJ12,	No non-overlappi	ng genes wit	hin 50,000bp	
17	21,828,558	21,829,025	467	10		No non-overlappi	ng genes wit	hin 50,000bp	
17	21,944,629	21,945,042	413	35		AC131055.10-3	324	AC131055.10-2	394
17	22,627,822	22,628,161	339	10		RPS16P8	3,429		
17	22,644,528	22,644,891	363	9		WSB1	342		
17	22,666,496	22,666,883	387	9				WSB1	1,724
17	22,683,604	22,684,692	1,088	10				WSB1	18,832
17	22,707,196	22,707,914	718	9				WSB1	42,424
17	22 789 976	22 790 312	336	9		KSR1	17 485		,
17	22 928 214	22 930 073	1 850	a a	KSR1	AC069366.8	40 838		
17	22,020,214	22,000,070	1,000	11	AC015699 11	A0000000.0	40,000		4 080
47	23,003,095	23,000,140	440	11	AC015000.11,			LGAL39	4,909
17	23,129,677	23,130,004	327	10	NU52,	No non-overlappi	ng genes wit	nin 50,000p	
17	23,259,213	23,259,604	391	9		AC005697.1	14,677	0110 D 1 D 0	
17	23,335,766	23,336,219	453	9		SCARNA20	33,704	SNORA70	37,264
17	23,578,465	23,579,273	808	9	PYY2,			AC061975.6-1	7,123
17	23,602,401	23,603,110	709	10				AC061975.6-3	2,528
17	23,686,252	23,686,928	676	10	IFT20,			TMEM97	6,415
					TNFAIP1,				
17	23,756,835	23,757,344	509	10	SLC46A1,			SARM1	4,662
17	23,845,763	23,846,573	810	9	SLC13A2,	AC005726.1-1	26,968	AC015917.30-3	16,661
17	23,927,963	23,928,399	436	9	ALDOC,	PIGS	5,299	SPAG5	336
17	23,949,572	23,951,214	1.642	9	SPAG5.	AC005726.1-6	2,195	AC005726.6	7.895
17	24 070 443	24 071 270	827	11	RPI 23A	RAB34	1 115	TI CD1	4 234
17	24 075 635	24 076 429	794	14		NEK8	3 530	RPI 23A	557
17	24,075,000	24,070,420	625	10			2,001		1 255
17	24,070,433	24,077,056	020	10	TLCD1,		2,901		1,300
17	24,077,842	24,078,336	494	14	TLCD1,	NEK8	1,623	RPL23A	2,764
17	24,094,110	24,094,797	687	9		TRAF4	353	NEK8	199
17	24,101,235	24,101,524	289	12	TRAF4,			NEK8	7,324
17	24,107,510	24,107,887	377	9				C17orf63	1,528
17	24,205,320	24,205,756	436	9		ERAL1	404	hsa-mir-451	6,757
17	24,248,050	24,248,724	674	11	FLOT2,			DHRS13	204
17	24,253,337	24,253,639	302	10	DHRS13,	FLOT2	4,496	PHF12	2,778
17	24,254,114	24,254,661	547	10		DHRS13	25	PHF12	1,756
17	24,302,573	24,303,956	1,383	12	PHF12,			SEZ6	2,119
17	24,462,897	24,463,370	473	11	MYO18A,	TIAF1	37,554		
17	24,499,895	24,500,709	814	9	MYO18A,	No non-overlappi	ng genes wit	hin 50,000bp	
17	24,645,032	24,645,697	665	10	NUFIP2.		<u> </u>	CRYBA1	39,406
17	24 741 074	24 741 532	458	19		TAOK1	537	114	1 247
17	24,820,802	24,830,326	400	0			33 348	0-	1,2-17
17	24,020,002	24,000,020	425	10	TD52112	AC104564 11 1	1 757		4 262
11	24,919,925	24,920,000	420	10	CIT1	AUKPD120	1,/0/		4,203
17	24,935,095	24,935,432	337	9	GITT,	ANKRUIJB	9,160		
17	24,942,611	24,943,761	1,150	12	FFOADE		851		
17	25,455,614	25,456,467	853	9	EFCAB5,	nsa-mir-423	11,756		
	05 004 005	05 000 05-	4=4	-	UUU005,				
17	25,661,628	25,662,078	450	9				TMIGD1	5,414
17	25,950,988	25,951,540	552	9	LRRC37B2,	AC006050.3	28,299	5S_rRNA	17,503
17	26,059,733	26,060,196	463	10		AC005562.1	5,814		
17	26,175,121	26,175,457	336	10	CRLF3,	ATAD5	7,689		
17	26,176,820	26,177,359	539	11		CRLF3	916		
17	26,446,596	26,447,753	1,157	9	NF1,	No non-overlappi	ng genes wit	hin 50,000bp	
17	26,901,175	26,901,725	550	18		hsa-mir-193a	9,403		
17	26,936,156	26,936.859	703	9				hsa-mir-365-2	9.503
17	27 478 642	27.478.999	357	9		RHOT1	14 587	AC090616 2	13 359
17	27 670 561	27 671 032	<u>4</u> 71	a	RHBDL3	hsa-mir-632	30 200	C17orf75	11 473
17	27 603 170	27 603 680	510	11	C17orf75	hsa_mir_632	7 550		11,773
17	27,080,179	27 702 405	1 102	10	bea mir 622	C17orf75	7,002		
17	21,100,992	21,102,105	1,193	12	7NF207	0170175	1,090		
17	27 705 270	27 705 700	510	11			10 100		10 710
17	21,130,219	21,190,192	513	11			42,422		7 004
1/	20,1/3,502	20,174,140	384	60	ACCNI	No non overland	ng generativ''		7,204
17	28,871,295	28,872,047	/52	9	ACCN1,	No non-overlappi	ng genes wit	nin 50,000bp	

17	29,551,033	29,551,488	455	9		ACCN1	43,369		
17	29,975,434	29,975,901	467	9	TMEM132E,	C17orf102	44,933		
17	30,331,359	30,331,725	366	9	LIG3,	CCT6B	18,740	ZNF830	17,182
17	30,414,683	30,415,167	484	10	RFFL,	AC004223.1-1	9,057		
17	30,470,884	30,471,353	469	10	RAD51L3,	FNDC8	1,391	NLE1	1,553
17	30,502,061	30,502,609	548	96	UNC45B,	NLE1	8,626		
17	30,593,438	30,593,882	444	11		SLFN5	317		
17	30,594,081	30,594,824	743	9	SLFN5,	AMAC1	48,521		
17	30,595,807	30,596,227	420	9	SLFN5,	No non-overlappi	ng genes wit	hin 50,000bp	
17	30,918,786	30,919,132	346	10		snoZ30	5,657	PEX12	6,796
17	30,929,068	30,930,223	1,155	13	PEX12,	AP2B1	8,172	snoZ30	4,183
17	30,938,332	30,939,165	833	12	AP2B1,	PEX12	8,637		
17	30,940,661	30,940,944	283	12	AP2B1,	PEX12	10,966	snoZ30	15,776
17	31,078,018	31,078,642	624	9		RASL10B	4,150	AP2B1	471
17	31,146,291	31,146,758	467	10	MMP28,	TAF15	13,838	C17orf50	30,080
17	31,160,267	31,161,308	1,041	9	TAF15,	MMP28	13,514	C17orf50	44,056
17	31.320.514	31.320.971	457	9	,			CCL16	6.680
17	31.470.035	31.470.682	647	13		CCL3	28.416	CCL4	12.257
17	31,500,342	31,501,463	1.121	13				TBC1D3F	15,782
17	31,916,287	31,916,741	454	11	ZNHIT3.			AC126327.6-1	4,430
17	31 964 316	31 965 361	1 045	11	MYO19	PIGW	155		.,
17	31 965 445	31 965 945	500	12	PIGW	MYO19	69		
17	31 975 385	31 975 991	606	10	ZNF403			PIGW	6 122
17	32 033 459	32 033 809	350	10	MRM1			DHRS11	2 135
17	32 332 819	32 333 108	370	11		LHX1	35 4 1 4	DIIKOTT	2,100
17	32,380,150	32,380,883	724	0	ΔΔΤΕ		33,414	L HX1	5 563
17	22,300,139	32,300,003	201	9	ААП,				9.061
17	22,490,344	32,490,045	414	10			1 / 20	AATT	0,001
17	32,922,212	32,922,020	4 14	10			1,430		
17	32,922,769	32,923,902	1,113	9		DUSP 14	10 201		10.070
17	33,750,699	33,751,140	441	10	GPR179,	50057	10,391		18,072
17	33,825,168	33,825,909	741	9			40.000	50057	15,627
17	33,833,442	33,833,758	316	9		ARHGAP23	42,920	50057	23,901
1/	33 864 677	33 865 050	373	11		ARHGAP23	11 628		
17	00,001,017	00,000,000	477		10115000 0		11,020		
17	34,008,267	34,008,744	477	14	AC115090.8,	No non-overlappi	ng genes wit	hin 50,000bp	
17 17 17	34,008,267 34,009,259	34,008,744 34,009,612	477	14	AC115090.8, AC115090.8,	No non-overlappi No non-overlappi	ng genes wit	hin 50,000bp hin 50,000bp	
17 17 17 17 17	34,008,267 34,009,259 34,016,112	34,009,612 34,016,595	477 353 483	14 9 15	AC115090.8, AC115090.8,	No non-overlappi No non-overlappi AC115090.8	ng genes wit ng genes wit 403	hin 50,000bp hin 50,000bp	0.000
17 17 17 17 17 17	34,008,267 34,009,259 34,016,112 34,077,150	34,008,744 34,009,612 34,016,595 34,077,484	477 353 483 334	14 9 15 10	AC115090.8, AC115090.8,	No non-overlappi No non-overlappi AC115090.8	ng genes wit ng genes wit 403	hin 50,000bp hin 50,000bp C17orf96	3,998
17 17 17 17 17 17 17	34,008,267 34,009,259 34,016,112 34,077,150 34,114,640	34,008,744 34,009,612 34,016,595 34,077,484 34,115,041	477 353 483 334 401	14 9 15 10 9	AC115090.8, AC115090.8,	No non-overlappi No non-overlappi AC115090.8 MLLT6	ng genes wit ng genes wit 403 358	hin 50,000bp hin 50,000bp C17orf96	3,998
17 17 17 17 17 17 17 17	34,008,267 34,009,259 34,016,112 34,077,150 34,114,640 34,161,197	34,008,744 34,009,612 34,016,595 34,077,484 34,115,041 34,161,871	477 353 483 334 401 674	14 9 15 10 9 10	AC115090.8, AC115090.8,	No non-overlappi No non-overlappi AC115090.8 MLLT6 PSMB3	ng genes wit ng genes wit 403 358 657	hin 50,000bp hin 50,000bp C17orf96	3,998
17 17 17 17 17 17 17 17 17	34,008,267 34,009,259 34,016,112 34,077,150 34,114,640 34,161,197 34,162,032	34,008,744 34,009,612 34,016,595 34,077,484 34,115,041 34,161,871 34,162,674	477 353 483 334 401 674 642	14 9 15 10 9 10 9	AC115090.8, AC115090.8, PSMB3,	No non-overlappi No non-overlappi AC115090.8 MLLT6 PSMB3 PCGF2	ng genes wit ng genes wit 403 358 657 3,948	hin 50,000bp hin 50,000bp C17orf96	3,998
17 17 17 17 17 17 17 17 17 17	34,008,267 34,009,259 34,016,112 34,077,150 34,114,640 34,161,197 34,162,032 34,234,682	34,008,744 34,009,612 34,016,595 34,077,484 34,115,041 34,161,871 34,162,674 34,235,423	477 353 483 334 401 674 642 741	14 9 15 10 9 10 9 10 9 10	AC115090.8, AC115090.8, PSMB3, CCDC49,	No non-overlappi No non-overlappi AC115090.8 MLLT6 PSMB3 PCGF2	ng genes wit ng genes wit 403 358 657 3,948	hin 50,000bp hin 50,000bp C17orf96 C17orf98	3,998
17 17	34,008,267 34,009,259 34,016,112 34,077,150 34,114,640 34,161,197 34,162,032 34,234,682 34,262,574	34,008,744 34,009,612 34,016,595 34,077,484 34,115,041 34,161,871 34,162,674 34,235,423 34,263,820	477 353 483 334 401 674 642 741 1,246	14 9 15 10 9 10 9 10 9 13 11	AC115090.8, AC115090.8, PSMB3, CCDC49, RPL23, SNORA21,	No non-overlappi No non-overlappi AC115090.8 MLLT6 PSMB3 PCGF2 C17orf98	ng genes wit ng genes wit 403 358 657 3,948 11,406	hin 50,000bp hin 50,000bp C17orf96 C17orf98	3,998 9,444
17 17	34,008,267 34,009,259 34,016,112 34,077,150 34,114,640 34,161,197 34,162,032 34,234,682 34,262,574 34,271,060	34,008,744 34,009,612 34,016,595 34,077,484 34,115,041 34,161,871 34,162,674 34,235,423 34,263,820 34,271,744	477 353 483 334 401 674 642 741 1,246 684	114 9 155 100 9 100 9 130 111 114	AC115090.8, AC115090.8, PSMB3, CCDC49, RPL23, SNORA21,	No non-overlappi No non-overlappi AC115090.8 MLLT6 PSMB3 PCGF2 C17orf98 RPL23	ng genes wit ng genes wit 403 358 657 3,948 11,406 7,481	hin 50,000bp hin 50,000bp C17orf96 C17orf98	3,998 9,444
17 17	34,008,267 34,009,259 34,016,112 34,077,150 34,114,640 34,161,197 34,162,032 34,234,682 34,262,574 34,262,574 34,271,060 34,277,150	34,008,744 34,009,612 34,016,595 34,077,484 34,115,041 34,161,871 34,162,674 34,235,423 34,263,820 34,271,744 34,277,560	477 353 483 334 401 674 642 741 1,246 684 410	114 9 15 100 9 100 9 100 9 13 113 111 14 14	AC115090.8, AC115090.8, PSMB3, CCDC49, RPL23, SNORA21,	No non-overlappi No non-overlappi AC115090.8 MLLT6 PSMB3 PCGF2 C17orf98 RPL23 LASP1	11,020 ng genes wit 403 358 657 3,948 11,406 7,481 2,334	hin 50,000bp hin 50,000bp C17orf96 C17orf98	3,998 9,444
17 17	34,008,267 34,009,259 34,016,112 34,077,150 34,114,640 34,161,197 34,162,032 34,234,682 34,262,574 34,271,060 34,277,150 34,278,958	34,008,744 34,009,612 34,016,595 34,077,484 34,115,041 34,161,871 34,162,674 34,235,423 34,263,820 34,271,744 34,277,560 34,279,615	477 353 483 334 401 674 642 741 1,246 684 410 657	114 9 15 100 9 100 9 100 9 103 113 111 14 14	AC115090.8, AC115090.8, PSMB3, CCDC49, RPL23, SNORA21,	No non-overlappi No non-overlappi AC115090.8 MLLT6 PSMB3 PCGF2 C17orf98 RPL23 LASP1 LASP1	11,020 ng genes wit 403 358 657 3,948 11,406 7,481 2,334 279	hin 50,000bp hin 50,000bp C17orf96 C17orf98	3,998 9,444
17 17	34,008,267 34,009,259 34,016,112 34,077,150 34,114,640 34,161,197 34,162,032 34,234,682 34,262,574 34,271,060 34,277,150 34,278,958 34,279,618	34,008,744 34,009,612 34,016,595 34,077,484 34,115,041 34,161,871 34,162,674 34,235,423 34,263,820 34,271,744 34,277,560 34,279,615 34,280,084	477 353 483 334 401 674 642 741 1,246 684 410 657 466	114 9 15 100 9 100 9 100 9 103 113 111 14 14 114 111	AC115090.8, AC115090.8, PSMB3, CCDC49, RPL23, SNORA21, LASP1,	No non-overlappi No non-overlappi AC115090.8 MLLT6 PSMB3 PCGF2 C17orf98 RPL23 LASP1 LASP1 RPL23	11,020 ng genes wit 403 358 657 3,948 11,406 7,481 2,334 279 16,039	hin 50,000bp hin 50,000bp C17orf96 C17orf98	3,998 9,444
17 17	34,008,267 34,009,259 34,016,112 34,077,150 34,114,640 34,161,197 34,162,032 34,234,682 34,262,574 34,271,060 34,277,150 34,278,958 34,279,618 34,290,100	34,008,744 34,009,612 34,016,595 34,077,484 34,115,041 34,161,871 34,162,674 34,235,423 34,263,820 34,271,744 34,277,560 34,279,615 34,280,084 34,290,440	477 353 483 334 401 674 642 741 1,246 684 410 657 466 340	114 99 155 100 99 100 99 103 113 111 14 144 114 111 111	AC115090.8, AC115090.8, PSMB3, CCDC49, RPL23, SNORA21, LASP1, LASP1,	No non-overlappi No non-overlappi AC115090.8 MLLT6 PSMB3 PCGF2 C17orf98 RPL23 LASP1 LASP1 RPL23 RPL23 RPL23 RPL23	ng genes wit ng genes wit 403 358 657 3,948 11,406 7,481 2,334 279 16,039 26,521	hin 50,000bp hin 50,000bp C17orf96 C17orf98	3,998 9,444
17 17	34,008,267 34,009,259 34,016,112 34,077,150 34,114,640 34,161,197 34,162,032 34,234,682 34,262,574 34,271,060 34,277,150 34,278,958 34,279,618 34,290,100 34,295,491	34,008,744 34,009,612 34,016,595 34,077,484 34,115,041 34,161,871 34,162,674 34,235,423 34,263,820 34,271,744 34,277,560 34,279,615 34,280,084 34,290,440 34,295,870	477 353 483 334 401 674 642 741 1,246 684 410 657 466 340 379	114 99 155 100 99 100 99 103 10 99 133 111 14 14 14 111 111 99	AC115090.8, AC115090.8, PSMB3, CCDC49, RPL23, SNORA21, LASP1, LASP1, LASP1, LASP1,	No non-overlappi No non-overlappi AC115090.8 MLLT6 PSMB3 PCGF2 C17orf98 RPL23 LASP1 LASP1 RPL23 RPL23 RPL23 RPL23 RPL23	n, 620 ng genes wit 403 358 657 3,948 11,406 7,481 2,334 279 16,039 26,521 31,912	hin 50,000bp hin 50,000bp C17orf96 C17orf98	3,998 9,444
17 17	34,008,267 34,009,259 34,016,112 34,077,150 34,114,640 34,161,197 34,162,032 34,234,682 34,262,574 34,271,060 34,277,150 34,278,958 34,279,618 34,290,100 34,295,491 34,315,856	34,008,744 34,009,612 34,016,595 34,077,484 34,115,041 34,161,871 34,162,674 34,235,423 34,263,820 34,271,744 34,277,560 34,279,615 34,280,084 34,290,440 34,295,870 34,316,206	477 353 483 334 401 674 642 741 1,246 684 410 657 466 340 379 350	114 99 155 100 99 100 99 133 111 144 144 114 111 110 99 99	AC115090.8, AC115090.8, PSMB3, CCDC49, RPL23, SNORA21, LASP1, LASP1, LASP1, LASP1, LASP1,	No non-overlappi No non-overlappi AC115090.8 MLLT6 PSMB3 PCGF2 C17orf98 RPL23 LASP1 LASP1 RPL23 RPL23 RPL23 RPL23	ng genes wit ng genes wit 403 358 657 3,948 11,406 7,481 2,334 279 16,039 26,521 31,912	hin 50,000bp hin 50,000bp C17orf96 C17orf98 C17orf98 FBXO47	3,998 9,444 30,038
17 17	34,008,267 34,009,259 34,016,112 34,077,150 34,114,640 34,161,197 34,162,032 34,234,682 34,262,574 34,271,060 34,277,150 34,278,958 34,279,618 34,290,100 34,295,491 34,315,856 34,563,285	34,008,744 34,009,612 34,016,595 34,077,484 34,115,041 34,161,871 34,162,674 34,235,423 34,263,820 34,271,744 34,277,560 34,279,615 34,280,084 34,290,440 34,295,870 34,316,206 34,564,450	477 353 483 334 401 674 642 741 1,246 684 410 657 466 340 379 350 1,165	114 99 155 100 99 100 99 133 111 144 144 114 111 110 99 99 188	AC115090.8, AC115090.8, PSMB3, CCDC49, RPL23, SNORA21, LASP1, LASP1, LASP1, LASP1, LASP1,	No non-overlappi No non-overlappi AC115090.8 MLLT6 PSMB3 PCGF2 C17orf98 RPL23 LASP1 LASP1 RPL23 RPL23 RPL23 RPL23 RPL23 PLXDC1	11,625 ng genes wit 403 358 657 3,948 11,406 7,481 2,334 279 16,039 26,521 31,912 1,987	hin 50,000bp hin 50,000bp C17orf96 C17orf98 C17orf98 FBXO47 ARL5C	3,998 9,444 30,038 5.904
17 17	34,008,267 34,009,259 34,016,112 34,077,150 34,114,640 34,161,197 34,162,032 34,234,682 34,262,574 34,271,060 34,277,150 34,278,958 34,279,618 34,290,100 34,295,491 34,315,856 34,563,285 34,641,663	34,008,744 34,009,612 34,016,595 34,077,484 34,115,041 34,161,871 34,162,674 34,235,423 34,263,820 34,271,744 34,277,560 34,279,615 34,280,084 34,290,440 34,295,870 34,316,206 34,564,450 34,642,214	477 353 483 334 401 674 642 741 1,246 684 410 657 466 340 379 350 1,165 551	114 99 155 100 99 100 99 103 100 99 113 111 114 114 111 110 99 99 118 99	AC115090.8, AC115090.8, PSMB3, CCDC49, RPL23, SNORA21, LASP1, LASP1, LASP1, LASP1, LASP1,	No non-overlappi No non-overlappi AC115090.8 MLLT6 PSMB3 PCGF2 C17orf98 RPL23 LASP1 LASP1 RPL23 RPL23 RPL23 RPL23 RPL23 PLXDC1 STAC2	11,625 ng genes wit 403 358 657 3,948 11,406 7,481 2,334 279 16,039 26,521 31,912 1,987 6,163	hin 50,000bp hin 50,000bp C17orf96 C17orf98 C17orf98 FBXO47 ARL5C	3,998 9,444 30,038 5,904
17 17	34,008,267 34,009,259 34,016,112 34,077,150 34,114,640 34,161,197 34,162,032 34,234,682 34,262,574 34,277,150 34,277,150 34,277,150 34,278,958 34,279,618 34,290,100 34,295,491 34,315,856 34,563,285 34,641,663 34,653,904	34,008,744 34,009,612 34,016,595 34,077,484 34,115,041 34,161,871 34,162,674 34,235,423 34,263,820 34,271,744 34,277,560 34,279,615 34,280,084 34,290,440 34,295,870 34,316,206 34,564,450 34,642,214 34,654,935	477 353 483 334 401 674 642 741 1,246 684 410 657 466 340 379 350 1,165 551 1,031	114 99 115 100 99 100 99 103 100 99 113 111 114 114 111 110 99 99 118 99 99	AC115090.8, AC115090.8, PSMB3, CCDC49, RPL23, SNORA21, LASP1, LASP1, LASP1, LASP1, LASP1,	No non-overlappi No non-overlappi AC115090.8 MLLT6 PSMB3 PCGF2 C17orf98 RPL23 LASP1 LASP1 LASP1 RPL23 RPL23 RPL23 RPL23 RPL23 RPL23 STAC2 STAC2	n, 620 ng genes wit 403 358 657 3,948 11,406 7,481 2,334 279 16,039 26,521 31,912 1,987 6,163 18,404	hin 50,000bp hin 50,000bp C17orf96 C17orf98 C17orf98 FBXO47 ARL5C FBXL20	3,998 9,444 30,038 5,904 15,439
17 17	34,008,267 34,008,267 34,009,259 34,016,112 34,077,150 34,114,640 34,161,197 34,162,032 34,234,682 34,262,574 34,271,060 34,277,150 34,278,958 34,279,618 34,290,100 34,295,491 34,315,856 34,563,285 34,641,663 34,653,904 34,870,960	34,008,744 34,009,612 34,016,595 34,077,484 34,115,041 34,161,871 34,162,674 34,235,423 34,263,820 34,271,744 34,277,560 34,279,615 34,280,084 34,290,440 34,295,870 34,316,206 34,564,450 34,642,214 34,654,935 34,871,463	477 353 483 334 401 674 642 741 1,246 684 410 657 466 340 379 350 1,165 551 1,031 503	114 99 115 100 99 100 99 103 100 99 113 111 114 114 111 110 99 99 118 99 99 26	AC115090.8, AC115090.8, PSMB3, CCDC49, RPL23, SNORA21, LASP1, LASP1, LASP1, LASP1, LASP1, LASP1, CRKRS.	No non-overlappi No non-overlappi AC115090.8 MLLT6 PSMB3 PCGF2 C17orf98 RPL23 LASP1 LASP1 LASP1 RPL23 RPL23 RPL23 RPL23 RPL23 RPL23 RPL23 PLXDC1 STAC2 STAC2 PPARBP	11,620 ng genes wit 403 358 657 3,948 11,406 7,481 2,334 279 16,039 26,521 31,912 1,987 6,163 18,404 9 907	hin 50,000bp hin 50,000bp C17orf96 C17orf98 C17orf98 FBXO47 ARL5C FBXL20	3,998 9,444 30,038 5,904 15,439
17 17	34,008,267 34,008,267 34,009,259 34,016,112 34,077,150 34,114,640 34,161,197 34,162,032 34,234,682 34,262,574 34,271,060 34,277,150 34,278,958 34,279,618 34,290,100 34,295,491 34,315,856 34,563,285 34,641,663 34,653,904 34,870,960 35,073,443	34,008,744 34,009,612 34,016,595 34,077,484 34,115,041 34,161,871 34,162,674 34,235,423 34,263,820 34,271,744 34,277,560 34,279,615 34,280,084 34,290,440 34,295,870 34,316,206 34,564,450 34,642,214 34,654,935 34,871,463 35,073,769	477 353 483 334 401 674 642 741 1,246 684 410 657 466 340 379 350 1,165 551 1,031 503 326	114 99 115 100 99 100 99 103 100 99 113 111 114 114 114 111 110 99 99 188 99 99 266 11	AC115090.8, AC115090.8, CCDC49, RPL23, SNORA21, LASP1, LASP1, LASP1, LASP1, CRKRS,	No non-overlappi No non-overlappi AC115090.8 MLLT6 PSMB3 PCGF2 C17orf98 RPL23 LASP1 LASP1 LASP1 RPL23 RPL23 RPL23 RPL23 RPL23 RPL23 PLXDC1 STAC2 STAC2 PPARBP TCAP	n, 620 ng genes wit 403 358 657 3,948 11,406 7,481 2,334 279 16,039 26,521 31,912 1,987 6,163 18,404 9,907 197	hin 50,000bp hin 50,000bp C17orf96 C17orf98 C17orf98 FBXO47 ARL5C FBXL20 STARD3	3,998 9,444 30,038 5,904 15,439
17 17	34,008,267 34,009,259 34,016,112 34,077,150 34,114,640 34,161,197 34,162,032 34,234,682 34,262,574 34,271,060 34,277,150 34,278,958 34,279,618 34,290,100 34,295,491 34,315,856 34,563,285 34,641,663 34,653,904 34,870,960 35,073,443 35,146,319	34,008,744 34,009,612 34,016,595 34,077,484 34,115,041 34,161,871 34,162,674 34,235,423 34,263,820 34,271,744 34,277,560 34,279,615 34,280,084 34,290,440 34,295,870 34,316,206 34,564,450 34,654,935 34,871,463 35,073,769 35 146 666	477 353 483 334 401 674 642 741 1,246 684 410 657 466 340 379 350 1,165 551 1,031 503 326 347	114 99 115 100 99 100 99 103 103 111 114 114 114 114 111 110 99 99 118 99 266 111	AC115090.8, AC115090.8, CCDC49, RPL23, SNORA21, LASP1, LASP1, LASP1, LASP1, CRKRS,	No non-overlappi No non-overlappi AC115090.8 MLLT6 PSMB3 PCGF2 C17orf98 RPL23 LASP1 LASP1 LASP1 RPL23 RPL23 RPL23 RPL23 RPL23 RPL23 PLXDC1 STAC2 STAC2 PPARBP TCAP GRB7	11,620 ng genes wit 403 358 657 3,948 11,406 7,481 2,334 279 16,039 26,521 31,912 1,987 6,163 18,404 9,907 197	hin 50,000bp hin 50,000bp C17orf96 C17orf98 C17orf98 FBXO47 ARL5C FBXL20 STARD3 ERBB2	3,998 9,444 30,038 5,904 15,439 195 7 878
17 17	34,008,267 34,009,259 34,016,112 34,077,150 34,114,640 34,161,197 34,162,032 34,234,682 34,262,574 34,277,150 34,277,150 34,277,150 34,279,618 34,279,618 34,290,100 34,295,491 34,315,856 34,653,285 34,641,663 34,653,904 34,870,960 35,073,443 35,146,319 35,163,602	34,008,744 34,009,612 34,016,595 34,077,484 34,115,041 34,161,871 34,162,674 34,235,423 34,263,820 34,271,744 34,277,560 34,279,615 34,280,084 34,290,440 34,295,870 34,316,206 34,564,450 34,642,214 34,654,935 34,871,463 35,073,769 35,146,666 35,164,414	477 353 483 334 401 674 642 741 1,246 684 410 657 466 340 350 1,165 551 1,031 503 326 342	114 9 15 100 9 100 9 100 9 100 9 100 9 111 111 1	AC115090.8, AC115090.8, CCDC49, RPL23, SNORA21, LASP1, LASP1, LASP1, LASP1, CRKRS,	No non-overlappi No non-overlappi AC115090.8 MLLT6 PSMB3 PCGF2 C17orf98 RPL23 LASP1 LASP1 LASP1 RPL23 RPL3 RPL23 RPL23 RPL23 RPL23 RPL23 RPL23 RPL3 RPL3 RPL3 RPL3 RPL3 RPL3 RPL3 RPL	n, 9 genes wit ng genes wit 403 358 657 3,948 11,406 7,481 2,334 279 16,039 26,521 31,912 1,987 6,163 18,404 9,907 197 1,047	hin 50,000bp hin 50,000bp C17orf96 C17orf98 C17orf98 FBXO47 ARL5C FBXL20 FBXL20 STARD3 ERBB2 GRB7	3,998 9,444 30,038 5,904 15,439 195 7,878 6 532
17 17	34,008,267 34,008,267 34,009,259 34,016,112 34,077,150 34,114,640 34,161,197 34,162,032 34,234,682 34,262,574 34,277,150 34,277,150 34,277,150 34,277,150 34,279,618 34,279,618 34,290,100 34,295,491 34,315,856 34,563,285 34,641,663 34,653,904 34,870,960 35,073,443 35,146,319 35,163,602 35,210,365	34,008,744 34,009,612 34,016,595 34,017,484 34,115,041 34,161,871 34,162,674 34,235,423 34,263,820 34,271,744 34,277,560 34,279,615 34,280,084 34,290,440 34,295,870 34,316,206 34,564,450 34,642,214 34,654,935 34,871,463 35,073,769 35,146,666 35,164,414 35,210,751	477 353 483 334 401 674 642 741 1,246 684 410 657 466 340 359 1,165 551 1,031 503 326 347 386	114 9 15 100 9 100 9 100 9 100 9 100 9 111 111 1	AC115090.8, AC115090.8, AC115090.8, PSMB3, CCDC49, RPL23, SNORA21, LASP1, LASP1, LASP1, LASP1, CRKRS,	No non-overlappi No non-overlappi AC115090.8 MLLT6 PSMB3 PCGF2 C17orf98 RPL23 LASP1 LASP1 LASP1 RPL23 RPL3 RPL23 RPL3 RPL3 RPL23 RPL3 RPL3 RPL3 RPL3 RPL3 RPL3 RPL3 RPL	n, genes wit ng genes wit 403 358 657 3,948 11,406 7,481 2,334 279 16,039 26,521 31,912 1,987 6,163 18,404 9,907 197 1,047	hin 50,000bp hin 50,000bp C17orf96 C17orf98 C17orf98 FBXO47 ARL5C FBXL20 FBXL20 STARD3 ERBB2 GRB7 AC079199 2	3,998 9,444 30,038 5,904 15,439 195 7,878 6,532 38 397
17 17	34,008,267 34,009,259 34,016,112 34,077,150 34,114,640 34,161,197 34,162,032 34,234,682 34,224,682 34,262,574 34,277,150 34,277,150 34,279,618 34,279,618 34,290,100 34,295,491 34,315,856 34,653,904 34,653,904 34,653,904 34,653,904 35,073,443 35,163,602 35,210,365 35,20,325	34,008,744 34,009,612 34,016,595 34,077,484 34,115,041 34,161,871 34,162,674 34,235,423 34,263,820 34,271,744 34,277,560 34,279,615 34,280,084 34,290,440 34,295,870 34,316,206 34,564,450 34,642,214 34,654,935 34,871,463 35,073,769 35,146,666 35,164,414 35,210,751 35,349,728	4.77 353 483 334 401 674 642 741 1,246 684 410 657 466 340 350 1,165 551 1,031 503 326 347 812 386 403	114 9 15 100 9 100 9 100 9 100 9 100 9 111 111 1	AC115090.8, AC115090.8, AC115090.8, PSMB3, CCDC49, RPL23, SNORA21, LASP1	No non-overlappi No non-overlappi AC115090.8 MLLT6 PSMB3 PCGF2 C17orf98 RPL23 LASP1 LASP1 LASP1 LASP1 RPL23	n, genes wit ng genes wit 403 358 657 3,948 11,406 7,481 2,334 279 16,039 26,521 31,912 1,987 6,163 18,404 9,907 197 1,047	hin 50,000bp hin 50,000bp C17orf96 C17orf98 C17orf98 FBXO47 ARL5C FBXL20 STARD3 ERBB2 GRB7 AC079199.2	3,998 9,444 30,038 5,904 15,439 195 7,878 6,532 38,397
17 17	34,008,267 34,009,259 34,016,112 34,016,112 34,077,150 34,114,640 34,161,197 34,162,032 34,234,682 34,234,682 34,262,574 34,277,150 34,277,150 34,277,150 34,279,618 34,279,618 34,290,100 34,295,491 34,315,856 34,653,904 34,653,904 34,653,904 34,653,904 34,653,904 35,073,443 35,163,602 35,210,365 35,349,325 35,368,746	34,008,744 34,009,612 34,016,595 34,077,484 34,115,041 34,161,871 34,162,674 34,235,423 34,263,820 34,271,744 34,277,560 34,279,615 34,280,084 34,290,440 34,295,870 34,316,206 34,564,450 34,642,214 34,654,935 34,871,463 35,146,666 35,164,414 35,210,751 35,349,728 35,369,390	3.70 477 353 483 334 401 674 642 741 1,246 684 410 657 466 340 350 1,165 551 1,031 503 326 347 812 386 403 644	11 14 9 15 10 9 10 9 10 10 9 13 11 14 14 14 14 14 14 14 14 14	AC115090.8, AC115090.8, CCDC49, RPL23, SNORA21, LASP1, LAS	No non-overlappi No non-overlappi AC115090.8 MLLT6 PSMB3 PCGF2 C17orf98 RPL23 LASP1 LASP1 LASP1 LASP1 RPL23 RPL3 RPL23 RPL3 RPL23 RPL3 RPL3 RPL3 RPL3 RPL3 RPL3 RPL3 RPL	n, genes wit ng genes wit 403 358 657 3,948 11,406 7,481 2,334 279 16,039 26,521 31,912 1,987 6,163 18,404 9,907 197 1,047	hin 50,000bp hin 50,000bp C17orf96 C17orf98 C17orf98 FBXO47 ARL5C FBXL20 STARD3 ERBB2 GRB7 AC079199.2	3,998 9,444 9,444 30,038 5,904 15,439 195 7,878 6,532 38,397
17 17	$\begin{array}{r} 34,008,267\\ 34,009,259\\ 34,016,112\\ 34,077,150\\ 34,114,640\\ 34,161,197\\ 34,162,032\\ 34,234,682\\ 34,262,574\\ 34,277,150\\ 34,277,150\\ 34,277,150\\ 34,277,150\\ 34,277,150\\ 34,277,150\\ 34,279,618\\ 34,290,100\\ 34,295,491\\ 34,315,856\\ 34,563,285\\ 34,641,663\\ 34,653,904\\ 34,870,960\\ 35,073,443\\ 35,146,319\\ 35,163,602\\ 35,210,365\\ 35,349,325\\ 35,368,746\\ 35,900,275\\ \end{array}$	34,008,744 34,009,612 34,016,595 34,077,484 34,115,041 34,161,871 34,162,674 34,235,423 34,263,820 34,271,744 34,277,560 34,279,615 34,280,084 34,290,440 34,295,870 34,316,206 34,564,450 34,564,450 34,642,214 34,654,935 34,871,463 35,164,414 35,210,751 35,349,728 35,369,390 35,391,360	477 353 483 334 401 674 642 741 1,246 684 410 657 466 340 350 1,165 551 1,031 503 326 347 812 386 403 644	114 9 15 10 9 10 9 10 9 10 9 10 9 11 11 11 11 11 11 11 11 10 9 9 9 9	AC115090.8, AC115090.8, AC115090.8, PSMB3, CCDC49, RPL23, SNORA21, LASP1	No non-overlappiNo non-overlappiAC115090.8MLLT6PSMB3PCGF2C17orf98RPL23LASP1LASP1LASP1STAC2PPARBPTCAPGRB7AC090844.7GSDMA	n, genes wit ng genes wit 403 358 657 3,948 11,406 7,481 2,334 279 16,039 26,521 31,912 1,987 6,163 18,404 9,907 197 1,047 3,531 3,362	hin 50,000bp hin 50,000bp C17orf96 C17orf98 C17orf98 FBXO47 ARL5C FBXL20 STARD3 ERBB2 GRB7 AC079199.2 GSDMA	3,998 9,444 9,444 30,038 5,904 15,439 195 7,878 6,532 38,397 2,730
17 17	$\begin{array}{r} 34,008,267\\ 34,009,259\\ 34,016,112\\ 34,077,150\\ 34,114,640\\ 34,161,197\\ 34,162,032\\ 34,234,682\\ 34,262,574\\ 34,277,150\\ 34,277,150\\ 34,277,150\\ 34,277,150\\ 34,277,150\\ 34,277,150\\ 34,279,618\\ 34,279,618\\ 34,290,100\\ 34,295,491\\ 34,315,856\\ 34,563,285\\ 34,641,663\\ 34,653,904\\ 34,870,960\\ 35,073,443\\ 35,146,319\\ 35,163,602\\ 35,514,6319\\ 35,349,325\\ 35,349,345\\ 35,349,345\\ 35,349,345\\ 35,349,345\\ 35,349,345\\ 35,349,345\\ 35,349,345\\ 35,349,345$	34,008,744 34,009,612 34,016,595 34,077,484 34,115,041 34,161,871 34,162,674 34,235,423 34,263,820 34,271,744 34,277,560 34,279,615 34,280,084 34,290,440 34,295,870 34,316,206 34,564,450 34,564,450 34,642,214 34,654,935 34,871,463 35,073,769 35,146,666 35,164,414 35,210,751 35,349,728 35,369,390 35,391,360 35,521,831	477 353 483 334 401 674 642 741 1,246 684 410 657 466 340 379 350 1,165 551 1,031 555 1,031 555 1,031 326 347 812 386 403 644 1,085 404	114 9 15 10 9 10 9 10 9 10 9 10 9 11 11 11 11 11 11 11 11 11 10 9 9 9 9	AC115090.8, AC115090.8, AC115090.8, PSMB3, CCDC49, RPL23, SNORA21, LASP1, LASP1, LASP1, LASP1, LASP1, LASP1, LASP1, LASP1, LASP1, LASP1, LASP1, SNORA21, CRKRS,	No non-overlappi No non-overlappi AC115090.8 MLLT6 PSMB3 PCGF2 C17orf98 RPL23 LASP1 LASP1 LASP1 LASP1 LASP1 RPL23 RPL23 RPL23 RPL23 RPL23 RPL23 RPL23 RPL23 RPL23 RPL23 RPL23 RPL23 RPL23 C17orf98 RPL23 RPL3 RPL23 RPL23 RPL3 RPL3 RPL3 RPL3 RPL3 RPL3 RPL3 RPL	n, genes wit ng genes wit 403 358 657 3,948 11,406 7,481 2,334 279 16,039 26,521 31,912 1,987 6,163 18,404 9,907 197 1,047 3,531 3,362	hin 50,000bp hin 50,000bp C17orf96 C17orf98 C17orf98 FBXO47 ARL5C FBXL20 STARD3 ERBB2 GRB7 AC079199.2 GSDMA AC068669 21-2	3,998 9,444 9,444 30,038 5,904 15,439 195 7,878 6,532 38,397 2,730 5,248
17 17	$\begin{array}{r} 34,008,267\\ 34,009,259\\ 34,016,112\\ 34,077,150\\ 34,114,640\\ 34,161,197\\ 34,162,032\\ 34,234,682\\ 34,262,574\\ 34,277,150\\ 34,277,150\\ 34,277,150\\ 34,277,150\\ 34,277,150\\ 34,277,150\\ 34,279,618\\ 34,279,618\\ 34,290,100\\ 34,295,491\\ 34,315,856\\ 34,563,285\\ 34,641,663\\ 34,653,904\\ 34,870,960\\ 35,073,443\\ 35,146,319\\ 35,163,602\\ 35,514,6319\\ 35,349,325\\ 35,349,325\\ 35,521,427\\ 35,522,640\\ \end{array}$	34,008,744 34,009,612 34,016,595 34,077,484 34,115,041 34,161,871 34,162,674 34,235,423 34,263,820 34,271,744 34,277,560 34,279,615 34,280,084 34,290,440 34,295,870 34,316,206 34,564,450 34,644,50 34,644,50 34,644,50 34,644,50 34,644,50 34,644,50 34,644,50 35,164,414 35,210,751 35,349,728 35,369,390 35,391,360 35,521,831 35,523,310	477 353 483 334 401 674 642 741 1,246 684 410 657 466 340 350 1,165 551 1,031 503 326 347 812 386 403 644 1,085 404	114 9 15 100 9 10 9 10 9 10 9 10 11 11 11 11 11 11 11 11 11 10 9 9 9 9	AC115090.8, AC115090.8, AC115090.8, PSMB3, CCDC49, RPL23, SNORA21, LASP1, LASP1, LASP1, LASP1, LASP1, LASP1, LASP1, LASP1, LASP1, LASP1, LASP1, LASP1, SNORA21, CRKRS,	No non-overlappi No non-overlappi AC115090.8 MLLT6 PSMB3 PCGF2 C17orf98 RPL23 LASP1 LASP1 LASP1 LASP1 RPL23 RPL23 RPL23 RPL23 RPL23 RPL23 RPL23 RPL23 RPL23 RPL23 RPL23 RPL23 RPL23 C17orf98 RPL23 RPL3 RPL23 RPL3 RPL23 RPL3 RPL23 RPL3 RPL3 RPL3 RPL3 RPL3 RPL3 RPL3 RPL	n, genes wit ng genes wit 403 358 657 3,948 11,406 7,481 2,334 279 16,039 26,521 31,912 1,987 6,163 18,404 9,907 197 1,047 3,531 3,362	hin 50,000bp hin 50,000bp C17orf96 C17orf98 C17orf98 FBXO47 ARL5C FBXL20 STARD3 ERBB2 GRB7 AC079199.2 GSDMA AC068669.21-2 AC068669.21-2	3,998 9,444 9,444 30,038 5,904 15,439 195 7,878 6,532 38,397 2,730 5,248 3,760
17 17	34,008,267 34,009,259 34,016,112 34,077,150 34,114,640 34,161,197 34,162,032 34,234,682 34,224,682 34,262,574 34,277,150 34,277,150 34,277,150 34,277,150 34,277,150 34,279,618 34,279,618 34,290,100 34,295,491 34,315,856 34,563,285 34,641,663 34,653,904 34,870,960 35,073,443 35,146,319 35,163,602 35,210,365 35,390,275 35,521,427 35,522,427	34,008,744 34,009,612 34,016,595 34,017,484 34,115,041 34,161,871 34,162,674 34,235,423 34,263,820 34,271,744 34,277,560 34,279,615 34,280,084 34,290,440 34,295,870 34,316,206 34,564,450 34,642,214 34,654,935 34,871,463 35,073,769 35,146,666 35,164,414 35,210,751 35,349,728 35,369,390 35,391,360 35,521,831 35,523,310 35,523,310	477 353 483 334 401 674 674 674 684 410 684 410 657 466 340 350 1,165 551 1,031 503 326 347 386 403 644 1,085 404 670	114 9 15 100 9 100 9 103 10 9 10 10 9 9 10 10 9 9 10 10 9 9 10 10 9 9 9 9 9 9 9 9 9 9 9 9 9	AC115090.8, AC115090.8, AC115090.8, PSMB3, CCDC49, RPL23, SNORA21, LASP1, LASP1, LASP1, LASP1, LASP1, LASP1, LASP1, LASP1, BSP1, LASP1, LASP1, LASP1, ASP1,	No non-overlappi No non-overlappi AC115090.8 MLLT6 PSMB3 PCGF2 C17orf98 RPL23 LASP1 LASP1 LASP1 LASP1 RPL23	n, genes wit ng genes wit 403 358 657 3,948 11,406 7,481 2,334 279 16,039 26,521 31,912 1,987 6,163 18,404 9,907 197 1,047 3,531 3,362 9,083	hin 50,000bp hin 50,000bp C17orf96 C17orf98 C17orf98 FBXO47 ARL5C FBXL20 STARD3 ERBB2 GRB7 AC079199.2 GSDMA AC068669.21-2 AC068669.21-2	3,998 9,444 9,444 30,038 5,904 15,439 195 7,878 6,532 38,397 2,730 5,248 3,769

17	35,697,327	35,698,146	819	10	CDC6,			WIPF2	5,362
17	35,735,083	35,735,834	751	9	RARA,	AC080112.15-1	41,895	CDC6	22,144
17	35,764,339	35,765,183	844	9	RARA.			GJD3	5.578
17	35.827.013	35.827.575	562	10	TOP2A.	IGFBP4	25.627	AC080112.15-1	48,794
17	35,828,180	35,828,630	450	9	- /	TOP2A	246		-, -
17	36.029.825	36.030.171	346	9		-		AC004585.1-2	6.290
17	36.057.267	36.057.870	603	9	SMARCE1.	AC004585.1-2	20.439	AC004585.1-1	38,170
	,,	,,			KRT222P,		,		,
17	37,072,215	37,072,969	754	9		KRT42P	22,238		
17	37.075.491	37.076.089	598	10		EIF1	22.564		
17	37.101.929	37.102.684	755	9				EIF1	505
17	37,147,462	37,148,842	1.380	9		HAP1	3.040		
17	37 195 918	37 196 479	561	14	JUP	FKBP10	26 248	AC130686 6	15 246
17	37 211 292	37 211 671	379	11				AC130686.6	54
17	37 274 978	37 275 466	488	11	KI HI 11			ACLY	1 230
17	37 327 748	37 328 223	475	10	ACLY	TTC25	12 201	1021	1,200
17	37 329 039	37 329 464	425	13	//OE1,		241		
17	37 338 050	37 330 285	326	13		TTC25	1 130		
17	37,330,939	37,339,203	520 608	9	TTC25	ACLV	1,139		11 555
17	27 244 562	27 245 251	690	14	TTC25,		16,951		41,555
17	37,344,303	37,343,231	210	9	CND	ACLI	15,705		50,731
17	37,301,124	37,301,434	310	11	CNP,				240
17	31,422,169	31,423,252	483	10	DINAJUT,			LINESOSC	7,808
17	27 550 272	27 550 627	264	0	DADEC				2 002
17	37,559,273	37,559,037	304	9	RADOC,	OTATED	00		2,002
17	37,002,040	37,002,000	400	9		STATED	90		
17	37,082,043	37,683,024	381	9	07470	STATSB	693	074754	40 704
17	37,728,275	37,728,919	644	17	STAT3,	STAT5B	46,325	STAT5A	10,791
17	37,793,935	37,794,679	/44	15	STAT3,	AC107993.9	9,874		
17	37,812,842	37,813,510	668	9	PIRF,	D705		AC107993.9	8,207
17	37,833,901	37,834,290	389	10		PIRF	5,101		
17	37,923,096	37,923,415	319	11	ATP6V0A1,	NAGLU	18,062		
17	37,967,123	37,967,783	660	10	COASY,	MLX	4,821	HSD17B1	6,373
17	37,972,125	37,972,844	719	9	MLX,			COASY	304
17	38,066,087	38,066,493	406	9	TUBG2,			PLEKHH3	6,970
17	38,083,289	38,083,836	547	9		PLEKHH3	794	CCR10	1,110
17	38,084,004	38,084,371	367	10		PLEKHH3	1,509	CCR10	575
17	38,149,473	38,149,728	255	10	EZH1,			AC100793.8	9,749
17	38,178,715	38,179,155	440	10	VPS25,	WNK4	7,067		
17	38,369,707	38,370,248	541	13	AARSD1,	RUNDC1	15,860	Y_RNA	33,211
17	38,386,590	38,387,070	480	10	RUNDC1,	AARSD1	557		
17	38,403,501	38,404,319	818	15	Y_RNA, RPL27,	IF135	8,032	RUNDC1	4,268
17	38,427,204	38,427,597	393	9	VAT1,	RND2	3,187	IFI35	7,206
17	38,576,397	38,577,919	1,522	9	AC109326.11,	BRCA1	45,403	NBR2	26,637
17	38,737,099	38,737,991	892	38				TMEM106A	9,984
17	38,755,454	38,756,805	1,351	46				TMEM106A	28,339
17	38,818,974	38,819,562	588	15	AC087650.12-3,			U2	558
17	38,819,983	38,820,554	571	14	AC087650.12-4,		<u> </u>	AC087650.12-2	8,333
					AC087650.12-4,				
17	38 821 383	38 822 092	709	45	02, AC087650 12-3	112	1 072	AC087650 12-2	6 795
.,	00,021,000	00,022,002	100	-10	AC087650.12-4,	02	1,072	10001000.12 2	0,700
17	38,831,217	38,831,561	344	10		ARL4D	318		
17	38,916,434	38,916.869	435	17	DHX8,			RPL29P31	6,875
17	38,916,998	38,917,747	749	9	DHX8,			RPL29P31	7,439
17	39,102.901	39,103,477	576	10		MEOX1	8.113		,
17	39,325.469	39,325,934	465	12	MPP2,		-,	CD300LG	28.949
17	39,340.235	39,341.367	1,132	9	MPP2,			PPY	32.331
17	39,439.724	39,440.610	886	9	NAGS,	PYY	2.361	TMEM101	3.475
17	39,447 520	39,448,060	540	15	TMEM101		,	NAGS	5.561
17	39.543 553	39.544 531	978	9	HDAC5	C17orf53	30 321	U6	24,246
17	39,556 628	39,556,952	324	10	,	HDAC5	88		,0
17	39,574 537	39,575,011	474	13	C17orf53	U6	5 654		
17	39.654 086	39.655 478	1 392	9	,	UBTF	310		
17	39,966 366	39,966,918	552	13		FZD2	23 533		
	,,,,	, ,	202	.0	1		_0,000	1	

17	39,989,989	39,990,390	401	10		FZD2	61		
17	40,088,764	40,089,608	844	9	AC091152.1,			CCDC43	20,726
17	40.122.217	40.123.392	1.175	12	CCDC43.	DBF4B	18.110	AC091152.1	13.800
17	40,141,318	40,142,089	771	10	DBF4B, AC005180.3	CCDC43	18,645	AC091152.1	32,901
17	40,172,159	40,172,480	321	9	DBF4B,	ADAM11	19,614		
17	40 207 420	40 209 615	1 1 9 6	0	AC005160.3,				22 272
17	40,207,429	40,206,615	1,100	9	ADAMIT,				22,272
17	40,211,654	40,212,502	848	9	ADAMITI,	10015000 11	44.004	GJUT	18,840
17	40,298,024	40,298,392	368	10	EFTUDZ,	AC015936.14	14,284	HIGDIB	14,058
17	40,334,268	40,334,602	334	9	FAM187A,	EFTUDZ	1,979	GFAP	3,917
17	40,494,023	40,494,447	424	10	NMT1,	DCAKD	111		
17	40,565,771	40,566,363	592	10		PLCD3	354		
17	40,568,149	40,568,787	638	10	ACBD4,	PLCD3	2,732		
17	40,580,802	40,581,149	347	10	HEXIM1,			ACBD4	3,478
17	40,581,381	40,581,949	568	13	HEXIM1,			ACBD4	4,057
17	40,593,666	40,594,125	459	10	HEXIM2,			HEXIM1	8,415
17	40,594,447	40,595,012	565	10	HEXIM2,			HEXIM1	9,196
17	40,668,806	40,669,224	418	13	FMNL1,			C17orf46	18,319
17	40.710.374	40.710.835	461	9	MAP3K14.	C17orf46	15.112	FMNL1	29.910
17	40.804.173	40,804,526	353	13		5S rRNA	43.527	ARHGAP27	22,532
17	40 818 605	40 818 985	380	15			,	ARHGAP27	8 073
17	41 015 101	10,010,000	452	10		AC126544 5-1	3 467	/	0,010
17	41,013,101	41,019,000	563	10		AC120544.5-1	013		
17	41,017,044	41,010,107	303	12		AC120344.5-1	913	A C 0000000 0	40.000
17	41,327,204	41,327,962	/ 58	14		NI		AC003662.3	46,992
17	41,534,321	41,534,782	461	10	KIAA1267,	No non-overlapp	ing genes wit	nin 50,000bp	
17	41,570,785	41,571,307	522	9	KIAA1267,	No non-overlapp	ing genes wit	hin 50,000bp	
17	41,625,685	41,626,116	431	12	KIAA1267,	AC005829.1-3	600		
17	41,626,844	41,627,604	760	9	AC005829.1-3,	KIAA1267	901		
17	41,700,157	41,700,785	628	12		AC005829.1-2	6,408		
17	42,214,808	42,215,055	247	10	WNT3,			NSF	24,808
17	42,355,074	42,355,812	738	11	GOSR2,			U6atac	1,460
17	42,372,872	42,373,506	634	10	GOSR2,			U6atac	19,258
17	42,499,469	42,500,068	599	9	,			AC068152.11-2	16,108
17	42 567 926	42 568 324	398	21	CDC27			AC002558 1	16 970
17	42 568 466	42 568 985	519	36	CDC27			AC002558 1	17 510
17	42,000,400	42,000,000	512	11				AC002558 1	18 405
17	42,500,001	42,505,075	441	10				AC002550.1	10,403
17	42,570,955	42,371,374	441	10				AC002558.1	19,977
17	42,574,044	42,574,454	410	13	CDC27,			AC002558.1	23,088
17	42,576,060	42,576,459	399	12	CDC27,			AC002558.1	25,104
17	42,589,099	42,589,562	463	30	CDC27,			AC002558.1	38,143
17	42,590,380	42,590,825	445	18	CDC27,			AC002558.1	39,424
17	42,604,112	42,604,526	414	10	CDC27,	MYL4	36,901		
17	42,613,731	42,614,166	435	17	CDC27,	MYL4	27,261		
17	42,621,136	42,621,804	668	22	CDC27,	MYL4	19,623		
17	42,651,108	42,651,409	301	9	MYL4,	CDC27	29,444		
17	42,662,198	42,662,721	523	9				MYL4	6,154
17	43,081,032	43,081,913	881	9		KPNB1	361		
17	43,081,936	43,082,452	516	9	KPNB1,	TBKBP1	45.177	NPEPPS	26.296
17	43,373 063	43,374 527	1.464	9	PNPO.			ATAD4	9 808
17	43 402 746	43 403 273	527	12		CDK5RAP3	155		0,000
17	43 403 352	43 403 880	522	10			13 2/2	PNPO	21 670
17	43,469,750	43,400,000	520	10			13,243	haa mir 150	10,000
17	40,400,709	40,409,020	1 000	12			Z 1,394	113a-1111-113Z	10,200
11	43,533,091	43,534,129	1,038	11	UDAI,		5,790		
17	43,539,518	43,540,321	803	12	SNX11,	CBX1	5,712		
17	43,595,271	43,596,149	878	9	SKAP1,	nsa-mir-1203	6,399		
17	43,613,998	43,614,433	435	9	SKAP1,	hsa-mir-1203	25,126	U6	14,608
17	43,715,734	43,716,484	750	9	SKAP1,	No non-overlappi	ing genes wit	hin 50,000bp	
17	43,730,253	43,730,680	427	9	SKAP1,	No non-overlapp	ing genes wit	hin 50,000bp	
17	43,916,030	43,917,072	1,042	9				Y_RNA	4,471
17	43,938,311	43,938,750	439	9				HOXB1	23,056
17	43,987,373	43,987,991	618	9	HOXB3,	HOXB2	9,981		
17	44,009,500	44,010.218	718	9	HOXB4.	HOXB3	2.691	hsa-mir-10a	1.981
17	44,022,261	44,022,666	405	10		hsa-mir-10a	9.953	HOXB5	953

17	44,026,215	44,026,726	511	11		HOXB5	88	HOXB6	1,372
17	44,078,418	44,080,099	1,681	9		hsa-mir-196a-1	13,498	AC103702.3	39,647
17	44,110,807	44,111,125	318	11		hsa-mir-196a-1	45,887	PRAC	42,966
17	44,340,445	44,341,196	751	9	UBE2Z,	AC068531.9-2	40,965	ATP5G1	12,216
17	44,427,728	44,428,495	767	11	,	IGF2BP1	1,278	AC091133.11-2	6,774
17	44,428,561	44,429,104	543	10		IGF2BP1	669	AC091133.11-2	7,607
17	44,429,566	44,430,265	699	9	IGF2BP1,			AC091133.11-2	8,612
17	44.448.502	44,448,807	305	9	IGF2BP1.	U6	19.906	AC091133.11-2	27.548
17	44.464.535	44,465,332	797	9	IGF2BP1.	U6	3.381		,
17	44,624,270	44.624.528	258	11	- ,	ABI3	18.060	GNGT2	14.068
17	44 624 734	44 625 184	450	20		ABI3	17 404	GNGT2	13 412
17	44 625 205	44 625 598	393	10		ABI3	16,990	GNGT2	12 998
17	44 846 722	44 847 468	746	10	PHR	7.010	10,000	Y RNA	1 637
17	45 002 217	45 002 792	575	11	т н в ,		5 4 2 7		1,007
17	45 110 494	45,002,732	345	16	SPOP		5,427	SI C35B1	22 850
17	45 136 086	45,110,000	605	0	SI C35B1			EAM117A	5 997
17	45,130,000	45,130,031	1 220	0					1 766
17	45,139,702	45,140,922	1,220	9	SLUSSBI,		04.004		1,700
17	45,220,719	45,222,262	1,543	9	IVIYSIZ,	FAMITI/A	24,201	TAC4	48,408
17	45,277,294	45,277,635	341	9	TAC4,	AC027801.10	636	1000700110	04.000
17	45,313,066	45,313,656	590	9		TAC4	32,688	AC027801.10	31,868
17	45,400,640	45,401,019	379	11		ULX4	542		
17	45,483,303	45,483,681	378	10		IIGA3	4,807		
17	45,526,676	45,527,074	398	10		PDK2	621	ITGA3	3,834
17	45,547,197	45,547,645	448	9	SAMD14,			PDK2	3,778
17	45,571,920	45,572,803	883	12	PPP1R9B,	SAMD14	9,744		
17	45,584,334	45,584,715	381	10		PPP1R9B	1,461		
17	45,593,294	45,594,043	749	11		SGCA	4,322	HILS1	9,830
17	45,632,778	45,633,563	785	9	COL1A1,	HILS1	27,942	SGCA	24,487
17	45,702,254	45,702,918	664	12		TMEM92	3,914		
17	45,794,844	45,795,179	335	9				XYLT2	1,333
17	45,805,232	45,806,004	772	9	MRPL27, EME1,			LRRC59	7,595
17	45,829,776	45,830,137	361	17	LRRC59,	Y_RNA	11,170	EME1	15,959
17	46,140,198	46,140,636	438	12		ANKRD40	158		
17	46,152,142	46,152,500	358	10	AC005921.3-1,	ANKRD40	12,102	Y_RNA	23,022
17	46,243,792	46,244,263	471	9		WFIKKN2	23,341		
17	46,389,728	46,389,974	246	9				SPAG9	7,109
17	46,478,828	46,479,356	528	10	SPAG9,	No non-overlappi	ng genes wit	hin 50,000bp	
17	46,551,678	46,552,005	327	9	SPAG9,	AC005839.1	21,045		
17	46,552,171	46,552,490	319	11	SPAG9,	AC005839.1	21,538		
17	46.553.335	46.553.791	456	11		SPAG9	131		
17	46,554,085	46,554,557	472	11		SPAG9	881		
17	46,585,659	46,586,157	498	29	NME1-NME2.	SPAG9	32,455	MBTD1	23.628
17	46 599 254	46 599 873	619	9	NMF1-NMF2		,	MBTD1	9,912
17	46 691 918	46 693 575	1 657	9	MBTD1 UTP18	No non-overlappi	na aenes wit	hin 50 000bp	0,012
17	46 734 586	46,734,796	210	10				UTP18	4 297
17	46 803 903	46,804 400	497	11		No non-overlappi	na aenes wit	hin 50.000bp	1,201
17	46 867 947	46 868 378	431	11		No non-overlappi	na aenes wit	hin 50 000bp	
17	46 803 062	46 894 231	260	0				RPI 7P48	40 617
17	47 072 201	47 072 227	016	9	CA10	No non-overlanni	na aenes wit	hin 50 000bp	-0,017
17	47 154 072	47 155 654	683	9	CA10,	No non-overlappi	ng genes wit	hin 50,000bp	
17	47,104,972	47,103,034	277	9	CA10,	No non-overlappi	ng genes wit	hin 50,000bp	
17	47,190,730	47,197,015	211	10	CATU,	No non-overlappi	ng genes wit	hin 50,000bp	
17	40,000,200	40,000,020	300	9	TOM11 1	No non-overlappi	ng genes wit	hin 50,000bp	
17	50,333,016	50,334,005	909	14		No non-ovenappi	ng genes wit		0.544
17	50,400,850	50,401,403	553	13				TOWITET	6,541
17	50 660 400	50 660 720	200	~	51ADF4,		07 500		
17	50,009,409	50,009,732	323	9			27,508		
17	50,740,940	50,741,613	6/3	9	nlf,		17,222		
17	50,806,227	50,866,766	539	9			11,887	hin EO OOOka	
1/	51,872,894	51,873,286	392	9	ANKEN1,	No non-overlappi	ng genes wit	qq000,0c min	
17	52,024,735	52,025,761	1,026	12	NOO	NUG	513		
17	52,026,341	52,027,299	958	11	NUG,	No non-overlappi	ng genes wit	nin 50,000bp	
17	52,265,270	52,265,756	486	9	C17ort67,	DGKE	796		
17	52,393,063	52,393,625	562	9	COIL,	SCPEP1	16,842		
17	52,675,455	52,675,807	352	11		MSI2	13,123	AC003950.1	23,899

17	53,097,071	53,097,434	363	9	MSI2,			SRP_euk_arch	46,313
17	53,265,113	53,265,649	536	11				MRPS23	6,198
17	53,296,835	53,297,172	337	9	CUEDC1,	MRPS23	14,428		
17	53,357,563	53,357,907	344	11	CUEDC1,			VEZF1	46,002
17	53,381,471	53,381,835	364	10	CUEDC1,			VEZF1	22,074
17	53,388,785	53,389,315	530	9		CUEDC1	1,102		
17	53,427,627	53,428,375	748	10		VEZF1	7,013	SFRS1	4,908
17	53,439,468	53,440,107	639	13	SFRS1,	VEZF1	18,854		
17	53,526,158	53,526,482	324	10				DYNLL2	4,348
17	53,715,871	53,716,153	282	10		MPO	2,576		
17	53,732,750	53,733,065	315	11				BZRAP1	532
17	53,749,747	53,750,483	736	9	BZRAP1,	MPO	36,452	hsa-mir-142	13,109
17	53,772,385	53,772,812	427	9		hsa-mir-142	8,707	SUPT4H1	4,726
17	53,823,659	53,824,418	759	9	RNF43,	SUPT4H1	39,097	HSF5	28,110
17	53,849,751	53,850,147	396	17	RNF43,			HSF5	2,381
17	54,063,330	54,064,540	1,210	9	TEX14, U3,			U1	26,969
17	54,091,209	54,091,813	604	20	TEX14, U1,			U1	7,084
17	54,187,896	54,188,999	1,103	14	PPM1E,			RAD51C	21,207
17	54,538,791	54,539,179	388	11	TRIM37,			FAM33A	2,911
17	54,539,324	54,539,635	311	10		TRIM37	313	FAM33A	2,455
17	54,641,956	54,642,217	261	12	C17orf71,			PRR11	7,250
17	54,652,283	54,653,140	857	9	GDPD1,			C17orf71	4,893
17	54,872,907	54,873,295	388	9				YPEL2	39,030
17	54,997,121	54,998,170	1,049	11	DHX40,	U4	27,479		
17	55,396,173	55,397,415	1,242	9	RNFT1,			RPS6KB1	13,609
17	55,469,023	55,469,604	581	9				HEATR6	5,740
17	55,957,644	55,958,073	429	9	APPBP2,	No non-overlappi	ng genes wit	hin 50,000bp	
17	55,958,087	55,958,665	578	12	APPBP2,	No non-overlappi	ng genes wit	hin 50,000bp	
17	56,031,317	56,032,843	1,526	9	PPM1D,	No non-overlappi	ng genes wit	hin 50,000bp	
17	56,073,855	56,074,246	391	12	PPM1D,	BCAS3	35,752	U6	20,230
17	56,843,984	56,844,918	934	10	C17orf82,			TBX2	2,377
17	56,899,773	56,900,160	387	11	TBX4,	No non-overlappi	ng genes wit	hin 50,000bp	
17	57,177,485	57,177,793	308	9	BRIP1,	No non-overlappi	ng genes wit	hin 50,000bp	
17	57,196,166	57,196,636	470	10	BRIP1,	No non-overlappi	ng genes wit	hin 50,000bp	
17	57,295,307	57,295,893	586	10	BRIP1,			INTS2	1,624
1/	57,359,651	57,360,421	//0	17		INTS2	807		
17	57,541,533	57,542,011	478	10	MDCO	Y_RNA	12,452	TL 1/2	40 770
17	50,050,520	50,059,033	205	9	MRC2,			TLK2	13,773
17	50,003,004	50,004,101	357	9	MRC2,	116	25.942		19,049
17	59 102 277	59,079,150	299	10	MRC2,		10 450	1_KINA 20002	13,000
17	58 210 121	58 210 414	202	10	IVIRCZ, 10 Mar	I_RNA No non ovorlanni	10,459	59002 hin 50 000hn	20,039
17	58 082 120	58 082 725	293	10	KCNH6		10 220 40 220		21 600
17	50,502,450	50,502,755	505	5	WDR68	000044	49,230	00	21,000
17	59.031 665	59.032 159	494	13	KCNH6.			WDR68	6.294
	,001,000	,,		.0	CCDC44,				0,201
17	59,106,494	59,107,441	947	9	KCNH6,			LIMD2	19,541
					MAP3K3,				
17	59,204,634	59,205,353	719	13	CCDC47,	STRADA	31,687	KCNH6	43,737
<u> </u>					UDX42,				
17	59,251,028	59,251,345	317	10	FTSJ3,	PSMC5	7,197	DDX42	620
17	59,265,950	59,266,237	287	10	SMARCD2,	FISJ3	7,762	PSMC5	2,832
17	59,272,517	59,272,966	449	11	SMARCD2,		45 400	PSIVIUS	9,399
17	59,273,624	59,274,100	4/6	19	SMARCD2,	FISJ3	15,436	P51VIC5	10,506
17	59,280,051	59,280,490	439	10			0,390		
17	50 576 622	50 577 700	1 157	17			5,086	TEX2	700
17	59,570,032	59,577,769	1,157	9	SNORA76				139
17	59 645 851	59 646 665	814	Q	TFX2	No non-overlappi	na aenes wit	hin 50 000hn	
17	59.671 874	59.672 546	672	9	TEX2.	No non-overlappi	ng genes wit	hin 50.000bp	
17	59.692.807	59.693.854	1.047	9	TEX2,			AC016489.1	45.554
17	59,932,829	59,933,621	792	12	DDX5, CCDC45.	POLG2	9,198		.,
17	60,482,116	60,482,620	504	10	GNA13,	AC015821.9	20,105		
17	60,549,793	60,550,197	404	9	-	RGS9	13,814	AC015821.9	46,903
· ·		60 701 000	780	0		No non-overlanni	na aenes wit	hin 50 000hn	

17	60,921,831	60,922,383	552	10				AXIN2	32,760
17	61,627,293	61,627,613	320	10		CCDC46	8,858		-
17	61,731,397	61,731,746	349	11	PRKCA,			AC006120.1	36,986
17	61,836,365	61,836,750	385	9	PRKCA.			AC009452.21-1	45,466
17	62.054.443	62.054.859	416	9	PRKCA.	AC006947.2	9.992		-,
17	62,333,058	62,333,739	681	9			,	CACNG5	21,201
17	62.672.051	62.672.449	398	11		HELZ	270		, -
17	62,792,811	62,793,332	521	10	PSMD12.	PITPNC1	11.054	AC110921.9-1	41.090
17	62.801.123	62.801.602	479	12		PITPNC1	2.784		,
17	62 803 298	62 803 939	641	12		PITPNC1	447		
17	63,144,034	63,144,679	645	15	NOL11.	SNORA38	22.568	PITPNC1	23.927
17	63,144,720	63.144.979	259	10	NOL11.	SNORA38	22.268	PITPNC1	24.613
17	63.226.759	63.227.334	575	9	- ,	FALZ	24.908	AC006534.10	14,891
17	63.419.611	63.419.962	351	10	C17orf58.		,	FALZ	8.655
17	63,446,269	63.446.710	441	27	,	KPNA2	15.600	FALZ	35.313
17	63.446.887	63.447.173	286	9		KPNA2	15.137	FALZ	35.931
17	63,712,958	63,713,426	468	10			-, -	AC005332.1-3	4,927
17	63 755 394	63 756 299	905	11	AMZ2			SI C16A6	19 634
17	63 798 808	63 799 459	651		SI C16A6	ARSG	15 313	AM72	22 174
17	63,964,091	63,964,662	571	10	WIPI1.	hsa-mir-635	31.807	ARSG	33.624
17	64,267,575	64,268,431	856	9	,	No non-overlappi	na aenes wit	hin 50.000bp	,
17	64,834,456	64.835.257	801	13	ABCA5.			AC115085.4	27.611
17	65,727,862	65,728,405	543	9	/			KCNJ2	40,107
17	66.185.945	66.186.515	570	9		No non-overlappi	na aenes wit	hin 50.000bp	-, -
17	66.345.631	66.345.964	333	9		No non-overlappi	na aenes wit	hin 50.000bp	
17	66,467,658	66,468,004	346	9			33	AC005181.1	46,746
17	67.019.181	67.019.818	637	9		No non-overlappi	na aenes wit	hin 50.000bp	
17	67,914,427	67.915.911	1.484	9		No non-overlappi	na aenes wit	hin 50.000bp	
17	67,945,260	67,945,749	489	9		No non-overlappi	na aenes wit	hin 50.000bp	
17	68.065.422	68.066.114	692	9		No non-overlappi	na aenes wit	hin 50.000bp	
17	68,493,907	68,494,221	314	10	SLC39A11.	No non-overlappi	na aenes wit	hin 50.000bp	
17	68,600,207	68.600.693	486	9	SLC39A11.	No non-overlappi	na aenes wit	hin 50.000bp	
17	68,663,586	68.664.416	830	9	,	SSTR2	8.339		
17	68,739,093	68,739,705	612	10	FAM104A.	C17orf80	666		
17	68,763,356	68,763,764	408	9	CPSF4L.			C17orf80	6.670
17	68.812.548	68.813.142	594	11	CDC42EP4.	CPSF4L	42.462	SDK2	28,976
17	68.816.034	68.816.336	302	10	CDC42EP4.	CPSF4L	45.948	SDK2	25.782
17	68,818,350	68,818,719	369	10	CDC42EP4,	CPSF4L	48,264	SDK2	23,399
17	68,937,077	68,937,590	513	9	SDK2,	No non-overlappi	ng genes wit	hin 50,000bp	,
17	69.550.536	69.550.883	347	10		No non-overlappi	na aenes wit	hin 50.000bp	
17	69.592.985	69.593.367	382	9		No non-overlappi	na aenes wit	hin 50.000bp	
17	69.597.665	69.598.046	381	11		No non-overlappi	na aenes wit	hin 50.000bp	
17	69.707.117	69.707.628	511	10		RPL38	3.762		
17	69,711,138	69,711,828	690	18	RPL38,	TTYH2	9,463		
17	69,720.964	69,721,347	383	12	TTYH2,		,	RPL38	3,361
17	69,834,478	69,834.971	493	9	KIF19,	GPR142	40,269	DNAI2	11,861
17	69,843,506	69,843,863	357	9	KIF19,	GPR142	31,377	BTBD17	20,287
17	69,875,729	69,876,317	588	9	GPR142,	BTBD17	6,176		
17	69,939,379	69,940,101	722	11	GPRC5C,	5S_rRNA	13,941		
17	70,252,400	70,252,883	483	10	RAB37,	SLC9A3R1	3,480		
17	70,349,634	70,351,041	1,407	9	GRIN2C,			TMEM104	3,421
17	70,489,694	70,490,086	392	10		CDR2L	5,236		-
17	70,519,380	70,521,205	1,825	9	ICT1,			CDR2L	5,890
17	70,539,736	70,540,336	600	10		SRP_euk_arch	9,089	ATP5H	6,214
17	70,541,439	70,541,672	233	11		SRP_euk_arch	7,753	ATP5H	4,878
17	70,541,736	70,542,262	526	20		SRP_euk_arch	7,163	ATP5H	4,288
17	70,542,584	70,543,432	848	22		SRP_euk_arch	5,993	ATP5H	3,118
17	70,554,101	70,554,928	827	10	ATP5H, KCTD2,		· · ·	SRP_euk_arch	4,404
17	70,617,375	70,617,888	513	9	ARMC7,			SLC16A5	3,534
17	70,621,411	70,622,263	852	9	ARMC7,			SLC16A5	7,570
17	70,639,035	70,639,416	381	10	NT5C,			ARMC7	1,080
17	70,662,364	70,662,757	393	11	HN1,	AC022211.5-2	157	AC022211.5-1	8,913
17	70,690,489	70,691,062	573	26		NUP85	22,130	AC022211.5-1	37,038
17	70,746,145	70,746,656	511	13	GGA3,			NUP85	2,696

17	70,769,111	70,770,141	1,030	9	GGA3, MRPS7,			MIF4GD	3,767
17	70,775,287	70,775,782	495	11	MIF4GD,	GGA3	6,015	MRPS7	1,238
17	70,777,903	70,778,771	868	9	MIF4GD,	GGA3	8,631	SLC25A19	1,898
17	70,778,880	70,779,620	740	10	MIF4GD,	GGA3	9,608	SLC25A19	1,049
17	70,901,196	70,901,987	791	12	GRB2,	Y_RNA	37,679	U6	14,775
17	71,023,031	71,023,786	755	10	CASKIN2,	TSEN54	418		
17	71,057,235	71,057,856	621	9	LLGL2,	CASKIN2	34,013	TSEN54	24,820
17	71,140,336	71,141,812	1,476	9	RECQL5,	AC087749.12-2	4,297	MYO15B	5,818
17	71,271,701	71,272,874	1,173	9	GALK1,			ITGB4	6,208
17	71,291,706	71,293,488	1,782	9	UNK,	H3F3B	4,251		
17	71,362,953	71,363,483	530	11	WBP2,	UNC13D	10,560	TRIM47	18,359
17	71,380,148	71,381,076	928	9				TRIM47	766
17	71,385,949	71,386,263	314	11	TRIM47,	WBP2	22,853	TRIM65	10,377
17	71,448,516	71,449,490	974	10	FBF1, ACOX1,	MRPL38	35,427		
17	71,486,617	71,487,487	870	9	ACOX1, AC040980.1, CDK3,	FBF1	37,903	EVPL	27,035
17	71,537,045	71,537,623	578	9		EVPL	1,943	SRP68	9,163
17	71,589,343	71,589,640	297	9	ZACN, EXOC7,	SRP68	9,141	GALR2	4,175
17	71,611,371	71,611,919	548	10	EXOC7,	SRP68	31,169	ZACN	21,029
17	71,649,123	71,649,542	419	12		FOXJ1	157	RNF157	1,909
17	71,861,351	71,861,911	560	9	PRPSAP1,	SPHK1	30,415	U6	16,253
17	71,891,552	71,893,842	2,290	9	SPHK1,			UBE2O	3,649
17	71,905,362	71,906,326	964	9	UBE2O,			SPHK1	9,826
17	72,048,239	72,048,764	525	11	PRCD,	CYGB	2,678		
17	72,065,082	72,065,773	691	14	SNORD1C,	snoR38	695	ST6GALNAC2	7,283
17	72,065,912	72,066,498	586	11	SNORD1C, snoR38,	snoR38	2,288	ST6GALNAC2	6,558
17	72,105,764	72,106,253	489	9		ST6GALNAC2	12,240	ST6GALNAC1	26,189
17	72,210,574	72,211,214	640	9	MXRA7,			Y_RNA	95
17	72,215,432	72,217,741	2,309	9	MXRA7,	Y_RNA	4,028	JMJD6	6,622
17	72,234,717	72,235,634	917	9	C17orf95, SFRS2,	JMJD6	464	hsa-mir-636	8,493
17	72,243,911	72,244,247	336	10	SFRS2, hsa-mir- 636,	MFSD11	1,131	C17orf95	2,355
17	72,244,736	72,245,507	771	9	SFRS2, MFSD11,	hsa-mir-636	511	C17orf95	3,180
17	72,341,682	72,342,088	406	9		MGAT5B	34,045		
17	72,375,696	72,376,245	549	9	MGAT5B,	No non-overlappi	ng genes wit	hin 50,000bp	
17	72,563,999	72,564,307	308	9		AC015815.14-2	24,917	AC015815.14-1	24,006
17	72,595,994	72,596,595	601	12		SCARNA16	389	AC015815.14-4	986
17	72,630,251	72,630,527	276	9		SEC14L1	18,120	AC015815.14-6	19,002
17	72,648,024	72,648,370	346	10		SEC14L1	277		
17	73,002,449	73,002,991	542	10	9-Sep,	AC111170.11-1	46,301	AC111170.11-2	45,773
17	73,341,946	73,342,353	407	10				AC015804.14	44,351
17	73,467,877	73,468,468	591	10		No non-overlappi	ng genes wit	hin 50,000bp	
17	73,684,203	73,684,602	399	9	тК1,			SYNGR2	3,599
17	73,821,808	73,822,477	669	9		AC087645.19-2	35,640	SOCS3	41,982
17	73,822,595	73,823,348	753	11	2001	AC087645.19-2	36,427	SOCS3	41,111
17	73,885,754	73,886,554	800	9	PGS1,	SRP_euk_arch	6,943		
17	74,216,141	74,216,534	393	10	CYTH1,	AC099804.3	11,667		
17	74,348,171	74,349,635	1,464	9	USP36,			TIMP2	11,023
17	74,440,979	74,441,293	314	9		TIMP2	7,912		
17	74,442,018	74,442,815	797	9		TIMP2	8,951		
17	74,531,644	74,532,060	416	9	AC073624.1, C1QTNF1,	CAN11	14,189		
17	74,649,848	74,650,679	831	9	AC021534.1,	No non-overlappi	ng genes wit	hin 50,000bp	
17	74,899,491	74,900,023	532	9	AC021534.1,	No non-overlappi	ng genes wit	hin 50,000bp	
17	75,247,299	75,247,610	311	9		AC105337.7	48,060		
17	75,328,558	75,329,420	862	9	ENPP7,	CBX2	37,168	AC105337.7	31,179
17	75,365,241	75,366,219	978	9	0.5%	CBX2	369	0.5.1/2	4- 0
17	/5,366,543	/5,366,915	372	10	CBX2,			CBX8	15,858
17	75,428,083	75,428,420	337	16		UBX4	275	AC100704 45	44.005
1/	10,009,885	10,010,151	200	9		000040	07 000	AC100791.15	14,995
17	10,090,001	10,591,100	433	10	סועוססו,	UUUU40	27,930		

17	75,620,431	75,620,832	401	9	TBC1D16,	CCDC40	4,198		
17	75,705,535	75,705,927	392	9	GAA,			CCDC40	16,528
17	75,735,320	75,736,042	722	11	EIF4A3,	CARD14	30,827	GAA	27,047
17	75,784,445	75,784,813	368	16	CARD14,	SLC26A11	24,011	SGSH	12,872
17	75,812,339	75,812,781	442	10	SLC26A11,	SGSH	3,620		
17	76,042,638	76,043,386	748	11				NPTX1	11,842
17	76,133,099	76,133,500	401	12	AC127496.5-2,			AC109327.10	2,099
17	76,163,759	76,164,183	424	9	AC127496.5-2,			AC109327.1	26,761
17	76,421,431	76,422,085	654	11	AC127496.5-2,	No non-overlappi	ng genes wit	hin 50,000bp	
17	76,623,535	76,623,791	256	9	BAIAP2,	AC127496.5-3	567		
17	76,683,194	76,683,797	603	10	BAIAP2,			AATK	21,906
17	76,689,851	76,690,557	706	10	BAIAP2,			AATK	15,146
17	76,731,070	76,731,829	759	9	AATK,	hsa-mir-1250	9,367		
17	76,757,933	76,759,009	1,076	9		AATK	3,466		
17	76,827,335	76,827,776	441	10	C17orf56,			SLC38A10	5,620
17	76,832,827	76,833,385	558	10		C17orf56	5,377	SLC38A10	11
17	76,841,398	76,842,638	1,240	9	SLC38A10,	C17orf56	13,948	C17orf55	48,581
17	76,883,212	76,883,534	322	10	SLC38A10,			C17orf55	7,685
17	76,979,604	76,980,254	650	9		AC139149.5-1	7,307		
17	76,982,013	76,983,012	999	9		AC139149.5-1	4,549		
17	76,983,288	76,983,819	531	11		AC139149.5-1	3,742		
17	76,987,132	76,987,769	637	9	AC139149.5-1,	50.0110		AC110285.14	16,621
17	77,065,875	77,066,510	635	9	10TO /	FSCN2	43,643	AC139149.5-1	17,922
17	77,092,810	77,093,475	665	9	ACTG1,	FSCN2	16,678	C17orf70	23,913
17	77,130,875	77,131,507	632	15		C17orf70	1,027	NPLOC4	2,852
17	77,178,931	77,179,651	720	9	NPLOC4,	TSPAN10	40,103	Y_RNA	27,866
17	77,213,416	77,214,381	965	9	NPLOC4,	TSPAN10	5,373		
17	77,214,482	77,214,843	361	10	NPLOC4,	TSPAN10	4,911		
17	77,248,601	77,249,108	507	9	CCDC137,	C17orf90	4,578	ARL16	9,502
17	77,295,180	77,295,586	406	9	SLC25A10,	ARL16	33,920	MRPL12	10,229
17	77,410,424	77,411,203	779	9	P4HB,			ARHGDIA	7,684
17	77,411,559	77,412,233	674	10	P4HB,			ARHGDIA	6,654
17	77,417,967	77,419,825	1,858	10	ARHGDIA,	P4HB	6,134		
17	77,422,521	77,423,598	1,077	9	ARHGDIA,	P4HB	10,688	THOC4	15,419
17	77,461,183	77,461,864	681	10	PCY12,	0.075		SIR17	1,243
17	77,477,322	77,477,708	386	10	MAFG,	SIRT7	7,990	PYCR1	5,852
17	77,478,925	77,479,442	517	10	DUCA	MAFG	46	PYCR1	4,118
17	77,010,909	77,017,189	280	12	DUSTL,		14 150	GPS1	8,274
17	77,039,020	77,039,400	400	9			14,156	CD7	20,347
17	77,903,386	77,904,005	019	9		AC132938.1	6,406		
17	77,909,558	77,909,899	341	9		AC132938.1	512		5 000
17	78,045,358	78,046,247	889	10					5,928
17	78,302,954	70,303,309	415	11	TBCD,			FINON	292
1/	10,323,922	10,320,501	5/9	12		No pop overlaggi		hin 50.000km	23,500
10	201,315	200,238	003	14		No non-overlappi	ng genes wit	hin 50,000bp	
10	439,532	439,820	294	11		No non-overlappi	ng genes wit	hin 50,000bp	
10	440,027	440,700	203	10		No non-overlappi	ng genes wit	hin 50,000bp	
10	400,903	487,294	311	10	CULEUIZ,	No non-overiappi	ng genes wit		7 700
IQ	048,017	048,882	805	13	TYMS			GLULT	1,126
18	802 435	803 300	87/	12	1 1 10,	YES1	10.9		
18	3 052 982	3 053 481	499	10		1201	100	MYOM1	3 324
18	3 236 135	3 236 416	281	12		MYI 12Δ	1 1 1 2		0,024
18	3 237 300	3 237 718	201	11	MYI 124	MYI 12R	14 417		
18	3 761 161	3 761 650	409	۱۱ ۵	DI GAP1	AP002478 3-1	39 658		
18	3 974 127	3 974 498	371	a 3	520/11,	No non-overlappi	na aenes wit	hin 50 000hn	
18	5 284 536	5 285 102	566	10	ZFP161	No non-overlappi	ng genes wit	hin 50,000bp	
18	5 285 960	5 287 037	1 077	10	ZFP161	No non-overlappi	ng genes wit	hin 50,000bp	
18	5 821 764	5 822 167	403	19	,	No non-overlappi	ng genes wit	hin 50 000bp	
18	6 209 037	6 209 389	352	9	I 3MBTI 4	No non-overlappi	na aenes wit	hin 50 000bp	
18	6 391 644	6 392 038	394	10	L 3MBTI 4	No non-overlappi	na aenes wit	hin 50 000bp	
18	6 719 062	6 719 698	636	16	,	No non-overlappi	na aenes wit	hin 50 000bp	
18	6 719 706	6 720 083	377	10		No non-overlappi	ng genes wit	hin 50 000bp	
18	6 909 963	6 910 527	564	a		no non ovenappi	ing genes wit	ARHGAP28	4 264
.0	0,000,000	0,010,021	004	5	1	1			7,207

18	7,106,028	7,106,690	662	9	LAMA1,	No non-overlappi	ng genes wit	hin 50,000bp	
18	8,697,107	8,697,464	357	10	KIAA0802,			AP000864.4	12,571
18	8.833.184	8.833.528	344	12				KIAA0802	10.408
18	8,973,952	8,974,435	483	9		No non-overlappi	na aenes wit	hin 50.000bp	-,
18	12 692 501	12 692 916	415	10	CEP76	SPIRE1	44 368	AP005482 1	43 789
	12,002,001	12,002,010	110	10	TNFSF5IP1,		11,000	/	10,100
18	12.787.706	12.788.060	354	10	PTPN2.			Y RNA	36.889
18	12 938 297	12 938 697	400	10	SFH1I	No non-overlappi	na aenes wit	hin 50 000bp	,
18	13 206 150	13 206 567	417	9	,	C18orf1	2 228		
18	13 212 416	13 212 946	530	9	C18orf1	No non-overlappi	na aenes wit	hin 50 000hp	
18	13 601 645	13 602 149	504	9	C18orf1	No non-overlappi	ng genes wit	hin 50 000bp	
18	13 790 687	13 791 260	573	10		MC5R	24 283	AP001525.6-2	22 654
18	14 969 017	14 969 400	383	10		No non-overlanni	na aenes wit	hin 50 000hn	22,004
10	17,076,725	17,077,224	600	0	KIA A 1770	No non-overlappi	ng genes wit	hin 50,000bp	
10	17,070,725	17,077,334	4 077	9	RIAA 1772,		ing genes wit		40.524
18	17,433,645	17,435,322	1,677	9	ESCO1,	SNRPDI	10,936	АВНОЗ	49,534
18	17,574,473	17,574,909	436	11		MIB1	634		
18	17,825,062	17,825,478	416	9		No non-overlappi	ng genes wit	hin 50,000bp	
18	18,002,359	18,002,815	456	9		GATA6	599		
18	18,003,730	18,004,508	778	9	GATA6,			U6	9,563
18	18,176,570	18,176,868	298	9		No non-overlappi	ng genes wit	hin 50,000bp	
18	18,180,326	18,180,846	520	11		No non-overlappi	ng genes wit	hin 50,000bp	
18	18,397,071	18,397,709	638	9		No non-overlappi	ng genes wit	hin 50,000bp	
18	18,969,217	18,969,495	278	12		CABLES1	230	AC105247.16	902
18	18.975.205	18.975.997	792	9	CABLES1.	AC105247.16	4.731	-	
18	19 276 363	19 276 711	348	11	,	C18orf45	4 440		
18	19 420 194	19 420 539	345	12	NPC1	Y RNA	4 111		
10	20 004 271	20,004,672	402	12		1_111/4	4,111	AC000772.0.1	0 220
10	20,004,271	20,004,073	402	12	55 rDNA			AC090772.9-1	0,330
10	21 022 074	21 024 257	263	10	SC_1111A,	DSMA8	13 557		
10	21,923,974	21,924,237	200	10		F SIVIAO	43,337	hin EQ QQQhn	
10	22,350,924	22,351,254	330	9		No non-overlappi	ng genes wit	hin 50,000bp	
18	23,921,027	23,921,530	503	9	CDH2,	No non-overlappi	ng genes wit	nin 50,000bp	
18	24,011,272	24,011,781	509	10		CDH2	83		
18	24,502,408	24,502,710	302	11				AC090365.7	2,561
18	26,875,235	26,875,844	609	10	DSC3,			DSC2	24,161
18	27,040,771	27,041,272	501	11		DSC1	43,954		
18	27,258,282	27,258,613	331	9		DSG3	23,117	DSG4	10,405
18	27,556,299	27,556,692	393	9				7SK	3,126
18	27,808,021	27,808,397	376	9		KIAA1012	30,932	AC009831.21-1	10,439
18	28.011.528	28.012.080	552	9		5S rRNA	1.399		,
18	28 095 546	28 095 830	284	10			.,	Y RNA	1 266
18	28 207 825	28 208 540	715	9	ΕΔΜ59Δ			AC021224 7	36,929
10	20,207,020	20,200,040	509	12	ASYL 3	No non ovorlanni	na aonos wit	hin 50 000hn	00,020
10	29,412,903	29,413,411	762	12	NOL4	No non-overlappi	ng genes wit	hin 50,000bp	
10	30,050,570	30,057,333	/03	10	NUL4,	No non-overlappi	ng genes wit		
18	31,439,970	31,440,235	265	11	GALNII,	No non-overlappi	ng genes wit		
18	31,806,303	31,806,675	372	9	C18ort21,			KPRD1A	17,110
18	31,963,024	31,963,772	748	11	SLC39A6,	STATIP1	109		
18	32,624,171	32,624,660	489	9				C18orf10	5,373
18	32,662,065	32,662,913	848	9	C18orf10,	KIAA1328	165		
18	37,939,575	37,940,094	519	9				PIK3C3	24,133
18	40,512,902	40,513,202	300	10		SETBP1	1,659		
18	41.046.687	41.047.215	528	11		No non-overlappi	ng genes wit	hin 50,000bp	
18	41.911.735	41.912.055	320	9		PSTPIP2	5.511	ATP5A1	6.053
18	42 007 254	42 007 603	349	12		C18orf25	383		0,000
18	42 007 630	42 008 258	610	15	C18orf25		000	CCDC5	45 343
19	42 154 541	42 15/ 060	107	10	51001120,	RNE165	12 017		-5,5-5
10	12,104,041	12 167 174	721	10		DNE165	714		
10	42,107,107	42,107,471	204	12	DIAGO	No por survive '	/ 14	hin EO OOOka	
18	42,702,473	42,702,965	492	9	PIASZ,	No non-overlappi	ng genes wit	nin 50,000p	
18	42,751,238	42,751,495	257	10	PIAS2,	KAINAL2	29,290		
18	43,554,137	43,554,869	732	9		AC026898.8	6,976		
18	43,711,581	43,711,970	389	9		SMAD2	71		
18	43,814,226	43,814,640	414	9	ZBTB7C,	No non-overlappi	ng genes wit	hin 50,000bp	
18	44,192,708	44,193,089	381	9		No non-overlappi	ng genes wit	hin 50,000bp	
18	44,753,812	44,755,047	1,235	9		SMAD7	22,733		
18	45,266,929	45,268,174	1,245	9	C18orf32, hsa-			SNORD58	1,439
l I					mir-1539,				

18	45,272,085	45,273,053	968	9	SNORD58,	AC100778.5	273	hsa-mir-1539	4,295
18	45,341,658	45,342,561	903	9	LIPG,	No non-overlappi	ng genes wit	hin 50,000bp	
18	45,593,583	45,594,338	755	9	ACAA2,	SCARNA17	163	MYO5B	8,761
18	45,656,795	45,657,106	311	10	MYO5B,	Y RNA	4,761		
18	45,940,666	45,941,415	749	9	MYO5B,			AC105224.8	45,951
18	46,067,679	46,068,633	954	9	CXXC1,	MBD1	5,537		
18	46,299,570	46,299,988	418	9		MAPK4	40,494		
18	46,975,891	46,976,209	318	11	MEX3C,	No non-overlappi	ng genes wit	hin 50,000bp	
18	48,572,953	48,573,408	455	18	DCC,	No non-overlappi	ng genes wit	hin 50,000bp	
18	49,590,324	49,590,662	338	9		No non-overlappi	ng genes wit	hin 50,000bp	
18	50,003,925	50,004,236	311	11	MBD2,	SNORA30	1,145		
18	50,005,003	50,005,533	530	10	MBD2,	SNORA30	2,223		
18	50,138,594	50,139,193	599	9	C18orf54,	STARD6	3,653		
18	50,646,694	50,647,124	430	10	RAB27B,	No non-overlappi	ng genes wit	hin 50,000bp	
18	50,912,969	50,913,469	500	9		No non-overlappi	ng genes wit	hin 50,000bp	
18	51,052,936	51,053,166	230	10	TCF4,	No non-overlappi	ng genes wit	hin 50,000bp	
18	51,118,936	51,119,282	346	10	TCF4,	No non-overlappi	ng genes wit	hin 50,000bp	
18	51,421,908	51,422,264	356	9	TCF4,	No non-overlappi	ng genes wit	hin 50,000bp	
18	51,515,923	51,516,399	476	10		No non-overlappi	ng genes wit	hin 50,000bp	
18	53,255,994	53,256,623	629	9	ONECUT2,	AC090340.6	18,437		
18	53,316,243	53,316,769	526	9				ONECUT2	6,716
18	53,439,871	53,440,438	567	10	NARS,	FECH	34,883	ATP8B1	24,218
18	53,607,341	53,608,218	877	9		AC022724.8-1	48,488	U6	33,611
18	53,863,039	53,863,621	582	9	NEDD4L,	AC090324.7	25,748		
18	54,586,597	54,587,242	645	12		SRP_euk_arch	33,991	MALT1	18,247
18	54,957,928	54,958,278	350	10	SEC11L3,	No non-overlappi	ng genes wit	hin 50,000bp	
18	54,958,383	54,958,750	367	9	SEC11L3,	No non-overlappi	ng genes wit	hin 50,000bp	
18	55,220,579	55,221,105	526	9		LMAN1	43,116	CCBE1	31,024
18	55,272,812	55,274,382	1,570	9	CCBE1,	No non-overlappi	ng genes wit	hin 50,000bp	
18	55,606,154	55,606,789	635	9				AC098847.4	38,185
18	55,655,696	55,656,032	336	9		No non-overlappi	ng genes wit	hin 50,000bp	
18	55,731,117	55,731,504	387	9				PMAIP1	8,599
18	55,776,100	55,776,596	496	10		AC090377.15-1	11,821		
18	57,711,117	57,712,142	1,025	9	RNF152,	No non-overlappi	ng genes wit	hin 50,000bp	
18	58,176,410	58,176,695	285	10	TNFRSF11A,			Y_RNA	27,283
18	58,342,822	58,343,279	457	9	ZCCHC2,	No non-overlappi	ng genes wit	hin 50,000bp	
18	58,403,929	58,404,190	261	11				ZCCHC2	7,156
18	58,406,348	58,406,705	357	10				ZCCHC2	9,575
18	58,414,681	58,415,408	727	9				ZCCHC2	17,908
18	58,973,479	58,974,042	563	9	BCL2,	No non-overlappi	ng genes wit	hin 50,000bp	
18	61,569,299	61,569,786	487	12	CDH7,	No non-overlappi	ng genes wit	hin 50,000bp	
18	66,023,715	66,024,293	578	12	RTTN,	No non-overlappi	ng genes wit	hin 50,000bp	
18	70,207,110	70,207,472	362	9				AC008021.10	29,712
18	70,330,613	70,330,910	297	10	CNDP2,	CNDP1	21,762		
18	71,049,044	71,049,522	478	9	ZADH2,	TSHZ1	2,197		
18	71,051,571	71,052,013	442	10	TSHZ1,	ZADH2	1,466		
18	72,278,676	72,279,221	545	9	ZNF516,	No non-overlappi	ng genes wit	hin 50,000bp	
18	72,333,392	72,334,203	811	9	ZNF516,	AC018413.10	2,262		
18	72,336,339	72,336,755	416	11	AC018413.10,	ZNF516	205		
18	72,366,243	72,366,619	376	11		ZNF516	30,109	AC018413.10	27,210
18	72,644,652	72,645,099	447	10		ZNF236	20,005		
18	72,664,006	72,665,006	1,000	9		ZNF236	98		
18	72,717,685	72,717,971	286	9	ZNF236,	No non-overlappi	ng genes wit	hin 50,000bp	
18	72,929,829	72,930,181	352	10	MBP,	No non-overlappi	ng genes wit	hin 50,000bp	
18	73,951,672	73,952,008	336	9		No non-overlappi	ng genes wit	hin 50,000bp	
18	74,499,850	74,500,457	607	9		No non-overlappi	ng genes wit	hin 50,000bp	
18	75,539,949	75,540,459	510	10	AC068473.19,	CTDP1	330	0705	
18	75,652,765	75,653,099	334	10				CTDP1	37,270
18	75,883,530	75,884,048	518	12				AC090360.9	9,477
18	76,105,583	/6,106,152	569	9	PARD6G,	No non-overlappi	ng genes wit		7 000
19	542,431	542,789	358	9	HCN2,		0 477	BSG	7,939
19	947,277	947,960	683	9		GKIN3B	3,4/7		1,708
19	1,217,119	1,217,557	438	10		CIKBP	2,779		6,980
19	1,334,314	1,335,004	690	20	NDUES7,			MUM1	4,887

19	1,358,010	1,358,563	553	16		DAZAP1	21		
19	1,389,009	1,389,587	578	11	RPS15P5,			DAZAP1	2,326
19	1,442,153	1,442,625	472	9	REEP6.	PCSK4	746		
19	1,703,008	1,703,333	325	9		ONECUT3	1,329		
19	1,856,623	1,856,905	282	10	AC012615.4,	FAM108A4	20,129	C19orf34	46,621
					SCAMP4,				,
					ADAT3,				
19	2,220,093	2,220,433	340	16		OAZ1	87	C19orf35	5,198
19	2,458,128	2,458,483	355	10		AC005512.1-1	3,990	AC005512.1-2	3,735
19	2,969,014	2,969,310	296	9	TLE2,			TLE6	22,838
19	3,055,113	3,055,543	430	9	GNA11,	GNA15	31,648		
19	3,201,651	3,202,040	389	18	BRUNOL5,			NCLN	41,079
19	3,275,416	3,275,796	380	14		NFIC	34,820	BRUNOL5	27,345
19	3,277,963	3,278,364	401	9		NFIC	32,252	BRUNOL5	29,892
19	3,316,497	3,316,885	388	9	NFIC,	No non-overlappi	ng genes wit	hin 50,000bp	
19	3,451,642	3,452,196	554	10	RAX2,	DOHH	21		
19	3,577,235	3,578,627	1,392	9	RAX2,			PIP5K1C	2,555
10	0.000.400	0.000 545	040	10	C190ff29,	DADKO	4 070		4 5 4 0
19	3,922,196	3,922,515	319	10		DAPK3	1,370	EEF2	4,540
19	3,936,213	3,936,734	521	10	EEF2,	SNORD37	2,643		0.007
19	4,184,438	4,184,739	301	10	EBI3,			ANKRD24	8,627
19	4,197,515	4,198,259	/44	11	CCDC94,		-	EBI3	9,000
19	4,351,498	4,351,854	356	13		SH3GL1	2		
19	4,518,393	4,519,101	708	9		SEMA6B	8,886		
19	4,584,123	4,584,568	445	12		TNFAIP8L1	5,962		
19	4,674,799	4,675,273	474	15	DPP9,	C19orf30	44,879	AC005594.1	37,839
19	4,675,503	4,675,807	304	20		DPP9	628		
19	4,741,815	4,742,638	823	9		FEM1A	90		
19	5,259,833	5,260,521	688	9	PTPRS,	No non-overlappi	ng genes wit	hin 50,000bp	
19	5,474,139	5,474,478	339	9		No non-overlappi	ng genes wit	hin 50,000bp	
19	5,640,848	5,641,768	920	12	RPL36,	C19orf70	8,937	LONP1	1,077
19	5,778,940	5,779,531	591	9	NRTN,			FUT6	2,106
19	5,854,450	5,855,032	582	13	FUT5, AC024592.5,	AC104532.2	853		
10	E 072 425	5 072 022	200	0	NDULATI,		44 274		
19	5,975,425	5,975,025	590	9	KFAZ,	RAINDES	44,274		42.090
19	0,110,700	0,117,413	252	9	ACSBGZ,		2 0 4 2		43,900
10	7 506 545	7 507 024	470	0	DNDLA6		2,943		1 691
19	7,300,345	7,307,024	4/9 510	9	FINELAO,	MADOKZ			1,001
19	7,074,245	7,074,703	240	9			2		1,339
19	0,415,509	0,415,910	549	10	ELAVLI, HNRNPM			Z-IVIAI	5,074
19	8 484 516	8 485 000	484	9	7NF414			MYO1F	6 689
19	8 783 163	8 783 554	391	9	ZNE558	MBD3I 1	30 778	AC008734 7	36,967
19	9 281 446	9 281 803	357	11		ZNF699	4 651		00,007
19	9 757 482	9 758 147	665	Q Q		ZNF846	17 072	FBXI 12	23 800
19	9 818 681	9 819 016	335	<u>0</u>	PIN1.		,072	OLFM2	6 422
19	9 999 205	9 999 642	437	10	,			RDH8	5 251
19	10 090 653	10 092 073	1 420	.0 Q	EIF3G			P2RY11	3 588
19	10 304 475	10 305 084	609	10	RAVER1			ICAM3	371
19	10 305 795	10 306 443	648	10	ICAM3	RAVER1	481		071
19	10.388 305	10.388 771	466	33	PDE4A.	CDC37	13 034		
19	10 552 729	10 553 020	291	10	AP1M2	CDKN2D	12 074	ATG4D	27 636
19	10,616,182	10 616 718	536	۰۵ ۵	SI C44A2	II F3	9 270	AC011475.6	7 111
10	10,688,898	10,610,710	668	q		hsa-mir-638	514		3 858
10	10 807 404	10 808 751	1 347	9	TMED1		514	DNM2	3 825
10	10,007,404	10,000,731	407	9	VIPE2			CARM1	5 758
13	10,000,200	10,000,010	-07	9	C19orf52				5,750
19	10.933 773	10.934 283	510	9	SMARCA4	YIPF2	33 416	C19orf52	31,859
19	11.066 560	11.067.024	464	9	LDLR.			SMARCA4	32.607
19	11.316.086	11.316.492	406	12	TMEM205.	RAB3D	4,765		
	,,,				AC024575.6-1.		.,. 50		
19	11,318,086	11,318,463	377	11	AC024575.6-1.	TMEM205	126		
19	11,354,352	11,354,809	457	11	EPOR,			RGL3	1,379
19	11,500,395	11,500,719	324	9	ECSIT,	CNN1	9,860	AC008481.9-3	4,749

19	11,738,360	11,738,979	619	9	ZNF441,	ZNF823	27,600		
19	11,852,754	11,853,466	712	9		ZNF69	6,204		
19	12,134,724	12,135,344	620	9	ZNF136,	ZNF625	6,195		
19	12,522,988	12.523.818	830	9	ZNF564.	AC010422.7-1	7.555		
19	12.549.875	12.550.264	389	9	ZNF490.	ZNF564	26.548	AC010422.7-1	16.956
19	12.643.821	12.644.275	454	11	AC010422.7-3.	C19orf56	2.372	DHPS	3.262
19	12.648.056	12.648.656	600	9	DHPS.	C19orf56	6,607	AC010422.7-3	411
19	12 667 250	12 667 660	410	11	FBXW9	AC018761 6-1	8 849	TNPO2	3 357
19	12 749 438	12 749 848	410	9	. 27(110)	HOOK2	2 004		0,001
10	12,740,400	12,740,040	2/1	10		ILINB	820		6 153
10	12,702,240	12,702,401	733	10	גאטמט		0.457		3 114
10	12,700,250	12,700,971	133	11			4,637		9 225
19	12,775,559	12,773,791	1 2 2 2	0	EADSA		4,037	JOND	0,235
19	12,905,129	12,900,402	1,333	9	FARSA,	CALK	3,901		2.005
19	12,949,052	12,950,155	503	14					3,005
19	12,955,312	12,956,037	725	16	TOMT	14004	4 4 9 9	DAND5	8,745
19	13,088,417	13,088,920	503	13	IRMI1,	NACC1	1,189		
19	13,124,684	13,126,139	1,455	9	IER2,	STX10	2,632	AC011446.6	3,582
19	13,289,965	13,290,366	401	9	CACNA1A,	No non-overlappi	ng genes wit	hin 50,000bp	
19	13,746,002	13,746,580	578	9	MRI1, C19orf53,			AC008686.8	5,304
19	14,467,877	14,468,555	678	9	GIPC1,	PTGER1	20,703	DNAJB1	18,027
19	14,477,392	14,477,726	334	9		GIPC1	9,448	DNAJB1	8,856
19	15,527,544	15,528,097	553	14				CYP4F22	3,417
19	16,808,494	16,809,069	575	9	SIN3B,			NWD1	18,738
19	17,274,932	17,275,427	495	9	ABHD8,	MRPL34	2,050		
19	17,277,142	17,277,519	377	11	MRPL34,	ABHD8	1,860		
19	17,308,405	17.309.542	1.137	13	GTPBP3.	ANO8	1,767		
19	17 425 073	17 425 455	382	12		AC010319 10	3 604	NXNI 1	1 781
19	17 441 231	17 441 605	374			SI C27A1	695		.,
19	17 978 743	17 979 185	442	10	ARRDC2	0202//11	000	KCNN1	7 813
10	18 157 005	18 157 625	530	10	AITIDOZ,	AC068400 1	7 / 15	IEI30	7,010
10	18 311 680	19 312 669	088	10		AC000433.1	7,413	AC008307 7 1	6 207
19	10,311,000	10,312,000	900	10			20.972	AC006397.7-1	0,297
19	10,330,000	10,337,096	290	9	PGPEP1,	GDF 15	20,072		25,659
19	18,529,200	18,529,635	435	9	С190п50,	DEVANUE	5 054	PGPEP1	2,339
19	19,157,834	19,158,157	323	10	MEF2B,	REXANK	5,851		
19	19,163,860	19,164,233	373	15	MEF2B, AC002126.1, REXANK			NR2C2AP	8,993
19	19,173,583	19,173,940	357	9	RFXANK, NR2C2AP,	AC002126.1	9,645		
19	19,590,519	19,590,997	478	9	PBX4,			LPAR2	4,480
19	20,024,213	20,024,678	465	9		ZNF682	12,936	AC006539.1	27,330
19	21,882,195	21,882,734	539	9		No non-overlappi	ng genes wit	hin 50,000bp	
19	23,224,953	23,225,271	318	10				AC092329.3-1	9,332
19	23,975,315	23,975,699	384	24				AC092279.2-2	216
19	23,975,734	23,976,147	413	30	AC092279.2-2,			5 8S rRNA	2,853
19	23,976,332	23,976,996	664	29	,	AC092279.2-2	327	5 8S rRNA	2,004
19	32,976.113	32,977.575	1,462	11		No non-overlappi	ng genes wit	hin 50,000bp	,
19	33,138,178	33,138,463	285	10		No non-overlappi	na aenes wit	hin 50.000bp	
19	33 351 190	33 351 876	686	9		No non-overlappi	na aenes wit	hin 50 000hp	
10	33 648 981	33 649 553	572	a a		No non-overlappi	ng genee wit	hin 50 000bp	
10	33 651 450	33 651 754	304	0		No non-overlappi	ng genes wit	hin 50,000bp	
10	22 767 070	22 767 427	267	3		No non-overlappi	ng genes wit	hin 50,000bp	
19	33,707,070	24 241 020	307	9		No non-overlappi	ng genes wit	hin 50,000bp	
19	34,241,530	34,241,920	390	9		No non-overlappi	ng genes wit	hin 50,000bp	
19	34,468,689	34,469,084	395	9		No non-overlappi	ng genes wit		
19	34,650,610	34,650,917	307	10	DOD 4	No non-overlappi	ng genes wit		11.00
19	34,788,429	34,789,443	1,014	9				VSTM2B	41,384
19	34,854,272	34,854,738	466	10	PLEKHF1,			C19orf12	26,896
19	34,877,359	34,877,772	413	13				C19orf12	3,862
19	34,954,565	34,954,890	325	12		CCNE1	39,851		
19	35,145,596	35,145,893	297	10	C19orf2,	AC008507.11-1	5,861		
19	35,353,516	35,353,763	247	10		No non-overlappi	ng genes wit	hin 50,000bp	
19	35,642,683	35,643,206	523	10	ZNF536,	No non-overlappi	ng genes wit	hin 50,000bp	
19	36,221,494	36,222,144	650	9		No non-overlappi	ng genes wit	hin 50,000bp	
19	36,237,208	36,237,888	680	10		No non-overlappi	ng genes wit	hin 50,000bp	

19	36,361,414	36,361,976	562	9		No non-overlappi	ng genes wit	hin 50,000bp	
19	36,934,773	36,935,350	577	10				U6	34,544
19	37.049.900	37.050.261	361	10		No non-overlappi	na aenes wit	hin 50.000bp	- /-
19	37 093 022	37 093 352	330			AC011456 2	15 967		
19	37 287 208	37 287 849	641	10		No non-overlanni	na aenes wit	hin 50 000hn	
10	37 523 110	37 523 587	477	9		ZNE507	4 806	1111 30,00000	
10	37 528 000	37 528 540	5/0	9	ZNE507	No non-overlanni	ng genes wit	hin 50 000hn	
10	37,520,000	37,520,540	654	9			F21	nin 50,000bp	
10	27 974 257	27 975 111	0.04	9	AINKKD27,		16 215	DCCOPD	12 211
19	37,874,237	37,675,111	004	9	NUDT 19,	ANKRUZI	10,315	RGS9DF	13,211
19	38,234,929	38,235,239	310	10	RHPNZ,	DUDNO	40.000	AC008521.5	/11
19	38,263,700	38,264,516	816	10	GPATCH1,	RHPN2	16,066	AC008521.5	29,482
19	38,359,365	38,360,319	954	16		01.074.00		WDR88	820
19	38,415,790	38,416,135	345	10		SLC/A10	7,194		
19	38,476,449	38,477,250	801	9		AC008738.7	8,652	CEBPA	5,293
19	38,548,611	38,548,953	342	10		CEBPG	7,496		
19	38,555,762	38,556,716	954	12	CEBPG,			PEPD	12,989
19	38,613,385	38,613,862	477	9	PEPD,			CEBPG	47,954
19	38,805,617	38,805,865	248	9		No non-overlappi	ng genes wit	hin 50,000bp	
19	38,977,989	38,978,926	937	9		KCTD15	681		
19	39,316,910	39,317,741	831	10		LSM14A	37,542		
19	39,354,778	39,355,120	342	12		LSM14A	163		
19	39,500,751	39,501,272	521	9	KIAA0355,	AC010614.8	21,269		
19	39,540,162	39,540,489	327	9	,	GPI	7,420	KIAA0355	1.851
19	39 541 428	39 541 852	424	11		GPI	6 057	KIAA0355	3 117
19	39 547 923	39 548 973	1 050	9	GPI	0	0,001	KIAA0355	9.612
10	39 586 707	30 587 485	778	0				GPI	3 631
10	20 502 009	20 502 265	267	9					0,001
19	39,392,098	39,392,303	207	9	FDCD2L,				9,022
19	39,013,530	39,013,030	320	9	UBAZ,				4,020
19	39,684,191	39,684,559	368	12		71/5000	4 000	WTP	266
19	39,859,555	39,860,893	1,338	12		ZNF302	4,620		
19	39,872,608	39,873,301	693	9				ZNF302	4,626
19	39,916,265	39,916,829	564	9		ZNF181	104		
19	39,916,868	39,917,398	530	11	ZNF181,	AC020910.7	11,599	ZNF599	23,421
19	39,942,698	39,943,079	381	9	ZNF599,	AC020910.7	37,429	ZNF181	17,086
19	39,954,200	39,954,552	352	9	ZNF599,	AC020910.7	48,931	ZNF181	28,588
19	39,973,862	39,974,519	657	9		ZNF599	11,637	ZNF181	48,250
19	40,109,408	40,110,081	673	14		ZNF30	15,324	ZNF792	29,017
19	40,155,437	40,156,586	1,149	9		ZNF792	8,644		
19	40,162,798	40,163,246	448	9		ZNF792	16,005	ZNF30	34,884
19	40,181,870	40,182,477	607	12		GRAMD1A	609		,
19	40 297 230	40 297 772	542	11		EXYD3	867	AC020907 6-3	2 360
19	40 306 848	40 308 127	1 279	9	EXYD3 I GI4	FXYD1	13 441	AC020907 6-3	11 978
10	40 318 125	40 318 561	436	10		I GI4	181	AC020907 6-1	3 01/
10	40,306,400	40,010,001	00	0			34 300	FAM187B	10 447
10	40,000,400	40 420 002	765	10		ISP	407		10,447
10	40,430,227	40,430,992	700 E00	12			407		
19	40,431,434	40,432,024	090	10	LON,		19,/12		004
19	40,400,920	40,401,242	310	10			494	LUR	221
19	40,719,526	40,719,854	328	10	GAPUHS,	SRON	8,433		1 500
19	40,727,852	40,728,416	564	10	GAPDHS,			ATP4A	4,520
10	10 750 500	40.750.000	<u> </u>	-	TNEN1147,				
19	40,750,598	40,750,989	391	9		ATP4A	4,198		0- • •
19	40,758,162	40,758,746	584	58	AD000090.1,	ATP4A	11,762	IMEM147	27,894
19	40,811,150	40,812,139	989	11	RBM42,			KIAA0841	4,799
19	40,825,988	40,827,088	1,100	9	ETV2,	COX6B1	3,907	RBM42	5,562
19	40,827,355	40,827,788	433	10	ETV2,	COX6B1	3,207	RBM42	6,929
19	40,830,807	40,831,335	528	15	COX6B1,			ETV2	3,194
19	40,876,559	40,876,935	376	10		ZBTB32	18,735	UPK1A	15,352
19	40,899,223	40,900,605	1,382	9	ZBTB32,	AD000671.3	156		
19	40,922,932	40,923,775	843	10	TMEM149,	PSENEN	4,559	AD000671.3	1,313
19	40,927,540	40,927,980	440	14	U2AF1L4,	PSENEN	354	AD000671.3	5,921
19	40,930.861	40,931,319	458	11		LIN37	20	PSENEN	1.118
19	40.940.580	40.941.061	481	10	C19orf55.	HSPB6	781	LIN37	3.323
19	41.002 722	41.003.053	331	15	C19orf55	PRODH2	6 699	NPHS1	5 653
19	41.028 148	41.028 690	542	.0 .0	NPHS1		2,000	C19orf55	8 466
	,0_0,110	,020,000		0		1	1		5,100

19	41,082,924	41,083,295	371	11	NFKBID,	HCST	1,927	TYROBP	3,857
19	41,114,211	41,115,057	846	12		LRFN3	4,533		
19	41,118,820	41,119,261	441	9		LRFN3	329		
19	41,156,144	41,156,642	498	9		AF038458.1	21,299	LRFN3	28,220
19	41,177,503	41,178,897	1,394	13	AF038458.1,			C19orf46	6,945
19	41,196,808	41,197,521	713	9	ALKBH6, CLIP3,	C19orf46	5,296		
19	41,201,306	41,201,997	691	9	CLIP3,	ALKBH6	4,325		
19	41,233,829	41,234,686	857	9	THAP8,	WDR62	2,937	Y_RNA	1,863
19	41,236,382	41,236,680	298	10	THAP8,	WDR62	943	Y_RNA	4,416
19	41,241,201	41,241,751	550	9	WDR62,	THAP8	3,697	Y_RNA	9,235
19	41,276,472	41,276,959	487	10	WDR62,	AD001527.1	16,890	POLR2I	19,493
19	41,296,792	41,298,284	1,492	9	POLR2I, TBCB,			AD001527.1	339
19	41,310,425	41,311,156	731	17				TBCB	1,736
19	41,376,988	41,377,756	768	9	ZNF565,			Y_RNA	8,333
19	41,397,135	41,398,380	1,245	9	ZNF565,	Y_RNA	10,934		
					ZNF146,				
19	41,399,539	41,399,846	307	10	ZNF146,	ZNF565	1,713		
19	41,561,278	41,562,166	888	13	ZFP14,	AC092296.2-1	42,113	ZFP82	12,535
19	41,600,613	41,601,707	1,094	9	ZFP82,	AC092296.2-1	2,572		
19	41,671,466	41,672,538	1,072	16	ZNF566,			ZNF260	23,796
19	41,755,650	41,756,162	512	11	ZNF529,	ZNF382	31,899	AC092295.2	10,643
19	41,787,050	41,787,622	572	9		ZNF382	439		
19	41,787,644	41,788,810	1,166	9	ZNF382,	ZNF529	31,614	ZNF461	31,313
19	41,849,339	41,849,912	573	11	ZNF461,	ZNF567	22,230	ZNF382	37,755
19	41,869,749	41,871,040	1,291	12		ZNF567	1,102		
19	41,980,045	41,980,628	583	11		AC020928.7	24,489	ZNF790	19,548
19	42,020,556	42,021,719	1,163	10	ZNF790,	ZNF345	11,384	Y_RNA	19,250
19	42,098,601	42,099,463	862	16	ZNF829,			ZNF345	36,295
10	10.000.005	40.004.047	400	40	ZNF568,	10010000 0 1	10.057	7155054	00.400
19	42,260,885	42,261,347	462	12	ZNF420,	AC012309.8-1	46,257	ZNF585A	28,132
19	42,400,648	42,401,817	1,169	11	ZNF383,	ZNF585B	7,355		0.077
19	42,553,272	42,554,145	8/3	9	ZNF527,	711570	4 0 4 0	HKRI	6,077
19	42,049,912	42,650,509	397	12	ZNE570		1,313		
19	42,001,004	42,002,443	759	14	ZINF570,		1,505		21 217
19	42,009,399	42,009,919	1 532	12	7NE571	ZNF793	24,207	ZNF370	17 420
15	42,110,492	42,770,024	1,552	15	ZNF540.	AC022140.0-2	21,000	AC022140.0-0	17,425
19	42.838.369	42.839.142	773	12		ZFP30	216		
19	42.902.212	42.902.656	444	10	ZNF607.	AC093227.3	25.907	ZNF573	18.387
19	42,961,249	42,961,690	441	11	ZNF573,	AC016582.9	23,796		-,
19	42,961,765	42,962,525	760	12	ZNF573,	AC016582.9	22,961		
19	43,088,683	43,089,321	638	12	WDR87,	SIPA1L3	387		
19	43,089,331	43,089,773	442	10	SIPA1L3,	WDR87	174		
19	43,114,684	43,115,209	525	9	SIPA1L3,	WDR87	25,527		
19	43,407,118	43,407,393	275	10		DPF1	490		
19	43,518,010	43,518,448	438	10	C19orf15,			KCNK6	6,530
19	43,556,793	43,558,890	2,097	9	PSMD8,			C19orf15	3,370
19	43,584,196	43,584,545	349	9		FAM98C	1,070	SPRED3	5,485
19	43,661,048	43,661,439	391	10	RYR1,	No non-overlappi	ng genes wit	hin 50,000bp	
19	43,726,690	43,727,483	793	10	RYR1,			MAP4K1	42,638
19	43,800,526	43,800,901	375	9		MAP4K1	43		
19	43,801,097	43,801,856	759	12	EIF3K,	MAP4K1	614		
19	43,829,744	43,830,358	614	17	ACTN4,	MAP4K1	29,261	EIF3K	10,309
19	43,844,548	43,844,919	371	10	ACTN4,	MAP4K1	44,065	EIF3K	25,113
19	43,866,485	43,867,216	731	9	ACTN4,			CAPN12	45,456
19	43,912,101	43,912,473	372	10	ACTN4,			CAPN12	199
19	44,013,678	44,014,615	937	10	ECH1,			HNRNPL	4,254
19	44,030,827	44,031,668	841	9	HNRNPL,	ECH1	16,490	RINL	18,642
19	44,082,035	44,082,837	802	9	SIRT2, NFKBIB,	RINL	21,301	SARS2	14,914
19	44,112,525	44,113,107	582	12	SARS2,	MRPS12	81		
19	44,113,305	44,113,708	403	10	SARS2,	SIRT2	30,963	FBXO17	10,174
					MRPS12,				
19	44,144,654	44,144,913	259	10	FBXO17,	AC011455.6	16,107	MRPS12	29,157
19	44,157,567	44,157,960	393	13	FBXU17,	AC011455.6	29,020	MRPS12	42,070
19	44,158,364	44,158,756	392	11		FBXO17	144		

19	44,304,440	44,305,017	577	10		PAK4	3,243		
19	44,307,730	44,308,552	822	9	PAK4,			AC011443.6	14,412
19	44,308,881	44,309,537	656	9	PAK4,			AC011443.6	15,563
19	44,502,478	44,503,042	564	9		LRFN1	4,662	GMFG	7,808
19	44,523,606	44,524,655	1,049	11		SAMD4B	293		
19	44,573,109	44,574,296	1,187	14	PAF1, MED29,			SAMD4B	5,734
19	44,579,903	44,580,400	497	9	MED29,	PAF1	6,317		
19	44,584,808	44,585,294	486	10		ZFP36	3,999	MED29	1,767
19	44,594,267	44,595,488	1,221	14	PLEKHG2,			ZFP36	2,414
19	44,627,858	44,628,413	555	15	SUPT5H,	RPS16P10	9,400	AC011500.7-1	3,936
19	44,662,874	44,663,342	468	9	TIMM50,			SUPT5H	3,724
19	44,680,748	44,681,173	425	9		DLL3	254	TIMM50	7,380
19	44,689,210	44,689,645	435	10	DLL3,	AC011500.7-2	7,948		
19	44,689,673	44,690,376	703	9	DLL3,	AC011500.7-2	7,217		
19	44,714,417	44,715,867	1,450	12	EID2B,			EID2	4,863
19	44,813,240	44,813,912	672	9				LGALS13	23,287
19	44,975,455	44,975,936	481	12				LEUTX	7,029
19	45,005,927	45,006,414	487	9				DYRK1B	1,419
19	45,006,787	45,007,298	511	12				DYRK1B	535
19	45,016,139	45,016,588	449	12	DYRK1B,			FBL	350
19	45,025,127	45,025,466	339	9	FBL,	DYRK1B	8,446		
19	45,168,264	45,168,924	660	11	PSMC4,	ZNF546	25,945		
19	45,194,067	45,194,667	600	9		ZNF546	202	501101	
19	45,194,676	45,195,515	839	11	ZNF546,	71157000		PSMC4	15,485
19	45,288,346	45,289,054	708	10	ZNF780A,	ZNF780B	34,394	AC011496.7	23,327
19	45,419,475	45,420,126	651	10	CNTD2,	TTC9B	3,329	MAP3K10	6,161
19	45,423,434	45,423,818	384	9	CNTD2,	I I C9B	7,288	AKIZ	4,246
19	45,483,137	45,484,614	1,477	9			32		5 200
19	45,545,497	45,546,534	1,037	10	C 1901147, PLD3,		0,000		5,309
19	45,010,939	45,019,340	407	10			12 220	SERTADI SEDTAD2	905
19	45,025,342	45,024,330	1,014	9	SERTADI,	FRA	12,229		14,230
19	45,040,450	45,041,078	1,220	9	SERTADS,	No non ovorlanni	na aonos wit		3,003
10	45,721,004	45,721,549	1 070	13	SPTBN4,	SHKBD1	19 genes wit	nin 50,000bp	
10	40,720,001	TU.I CI.UIU	1,075	10			+0,000		
19	45 796 203	45 796 664	461	12	I TRP4			SHKBP1	7 062
19 19	45,796,203 45 801 479	45,796,664 45,801,838	461 359	12 12	LTBP4, I TBP4			SHKBP1 SHKBP1	7,062
19 19 19	45,796,203 45,801,479 45,801,925	45,796,664 45,801,838 45,802,695	461 359 770	12 12 9	LTBP4, LTBP4, LTBP4.			SHKBP1 SHKBP1 SHKBP1	7,062 12,338 12,784
19 19 19 19	45,796,203 45,801,479 45,801,925 45,803,110	45,796,664 45,801,838 45,802,695 45,803,798	461 359 770 688	12 12 9 10	LTBP4, LTBP4, LTBP4, LTBP4.			SHKBP1 SHKBP1 SHKBP1 SHKBP1	7,062 12,338 12,784 13,969
19 19 19 19 19	45,796,203 45,801,479 45,801,925 45,803,110 45,832,263	45,796,664 45,801,838 45,802,695 45,803,798 45,832,564	461 359 770 688 301	12 12 9 10 13	LTBP4, LTBP4, LTBP4, LTBP4,			SHKBP1 SHKBP1 SHKBP1 SHKBP1 LTBP4	7,062 12,338 12,784 13,969 4,698
19 19 19 19 19 19	45,796,203 45,801,479 45,801,925 45,803,110 45,832,263 45,913,218	45,796,664 45,801,838 45,802,695 45,803,798 45,832,564 45,913,615	461 359 770 688 301 397	12 12 9 10 13 12	LTBP4, LTBP4, LTBP4, LTBP4, ADCK4,	ІТРКС	1,233	SHKBP1 SHKBP1 SHKBP1 SHKBP1 LTBP4	7,062 12,338 12,784 13,969 4,698
19 19 19 19 19 19 19	45,796,203 45,801,479 45,801,925 45,803,110 45,832,263 45,913,218 45,915,370	45,796,664 45,801,838 45,802,695 45,803,798 45,832,564 45,913,615 45,916,245	461 359 770 688 301 397 875	12 12 9 10 13 12 12	LTBP4, LTBP4, LTBP4, LTBP4, ADCK4, ITPKC,	ITPKC ADCK4	1,233 930	SHKBP1 SHKBP1 SHKBP1 SHKBP1 LTBP4	7,062 12,338 12,784 13,969 4,698
191919191919191919	45,796,203 45,801,479 45,801,925 45,803,110 45,832,263 45,913,218 45,915,370 45,948,522	45,796,664 45,801,838 45,802,695 45,803,798 45,832,564 45,913,615 45,916,245 45,949,598	461 359 770 688 301 397 875 1,076	12 12 9 10 13 12 12 12 11	LTBP4, LTBP4, LTBP4, LTBP4, ADCK4, ITPKC, SNRPA,	ITPKC ADCK4 C19orf54	1,233 930 274	SHKBP1 SHKBP1 SHKBP1 SHKBP1 LTBP4 ITPKC	7,062 12,338 12,784 13,969 4,698 9,919
1919191919191919191919	45,796,203 45,801,479 45,801,925 45,803,110 45,832,263 45,913,218 45,915,370 45,948,522 45,975,102	45,796,664 45,801,838 45,802,695 45,803,798 45,832,564 45,913,615 45,916,245 45,949,598 45,976,854	461 359 770 688 301 397 875 1,076 1,752	12 12 9 10 13 12 12 12 11 10	LTBP4, LTBP4, LTBP4, LTBP4, ADCK4, ITPKC, SNRPA, MIA, RAB4B,	ITPKC ADCK4 C19orf54 EGLN2	1,233 930 274 20,105	SHKBP1 SHKBP1 SHKBP1 SHKBP1 LTBP4 ITPKC SNRPA	7,062 12,338 12,784 13,969 4,698 9,919 11,972
19 19 19 19 19 19 19 19 19 19	45,796,203 45,801,479 45,803,110 45,832,263 45,913,218 45,915,370 45,948,522 45,975,102 45,997,823	45,796,664 45,801,838 45,802,695 45,803,798 45,832,564 45,913,615 45,916,245 45,949,598 45,976,854 45,998,175	461 359 770 688 301 397 875 1,076 1,752 352	12 12 9 10 13 12 12 12 11 11 9	LTBP4, LTBP4, LTBP4, LTBP4, ADCK4, ITPKC, SNRPA, MIA, RAB4B, EGLN2,	ITPKC ADCK4 C19orf54 EGLN2	1,233 930 274 20,105	SHKBP1 SHKBP1 SHKBP1 LTBP4 ITPKC SNRPA RAB4B	7,062 12,338 12,784 13,969 4,698 9,919 11,972 3,136
19191919191919191919191919	45,796,203 45,801,479 45,801,925 45,803,110 45,832,263 45,913,218 45,915,370 45,948,522 45,975,102 45,997,823 46,004,210	45,796,664 45,801,838 45,802,695 45,803,798 45,832,564 45,913,615 45,916,245 45,949,598 45,976,854 45,998,175 46,005,093	461 359 770 688 301 397 875 1,076 1,752 352 883	12 12 9 10 13 12 12 12 11 10 9 11	LTBP4, LTBP4, LTBP4, ADCK4, ITPKC, SNRPA, MIA, RAB4B, EGLN2, EGLN2,	ITPKC ADCK4 C19orf54 EGLN2	1,233 930 274 20,105	SHKBP1 SHKBP1 SHKBP1 LTBP4 ITPKC SNRPA RAB4B RAB4B	7,062 12,338 12,784 13,969 4,698 9,919 11,972 3,136 9,523
19191919191919191919191919	45,796,203 45,801,479 45,801,925 45,803,110 45,832,263 45,913,218 45,915,370 45,948,522 45,975,102 45,997,823 46,004,210 46,172,293	45,796,664 45,801,838 45,802,695 45,803,798 45,832,564 45,913,615 45,916,245 45,949,598 45,976,854 45,998,175 46,005,093 46,172,679	461 359 770 688 301 397 875 1,076 1,752 352 883 386	12 12 9 10 13 12 12 12 11 10 9 11 11	LTBP4, LTBP4, LTBP4, ADCK4, ITPKC, SNRPA, MIA, RAB4B, EGLN2, EGLN2,	ITPKC ADCK4 C19orf54 EGLN2 CYP2B6	1,233 930 274 20,105 16,365	SHKBP1 SHKBP1 SHKBP1 LTBP4 ITPKC SNRPA RAB4B RAB4B CYP2B7P1	7,062 12,338 12,784 13,969 4,698 9,919 11,972 3,136 9,523 23,890
19191919191919191919191919191919	45,796,203 45,801,479 45,801,925 45,803,110 45,832,263 45,913,218 45,915,370 45,948,522 45,975,102 45,997,823 46,004,210 46,172,293 46,459,480	45,796,664 45,801,838 45,802,695 45,803,798 45,832,564 45,913,615 45,916,245 45,949,598 45,976,854 45,998,175 46,005,093 46,172,679 46,460,627	461 359 770 688 301 397 875 1,076 1,752 352 883 386 1,147	12 12 9 10 13 12 12 11 10 9 111 10 9 9	LTBP4, LTBP4, LTBP4, ADCK4, ITPKC, SNRPA, MIA, RAB4B, EGLN2, EGLN2, AXL, NUEDUT	ITPKC ADCK4 C19orf54 EGLN2 CYP2B6 AC011510.7-1	1,233 930 274 20,105 16,365 19,426	SHKBP1 SHKBP1 SHKBP1 LTBP4 ITPKC SNRPA RAB4B RAB4B CYP2B7P1 SRP_euk_arch	7,062 12,338 12,784 13,969 4,698 9,919 11,972 3,136 9,523 23,890 23,542
19 19	45,796,203 45,801,479 45,801,925 45,803,110 45,832,263 45,913,218 45,915,370 45,948,522 45,975,102 45,997,823 46,004,210 46,172,293 46,459,480	45,796,664 45,801,838 45,802,695 45,803,798 45,832,564 45,913,615 45,916,245 45,949,598 45,976,854 45,998,175 46,005,093 46,172,679 46,460,627	461 359 770 688 301 397 875 1,076 1,752 352 883 386 1,147	12 12 9 10 13 12 12 12 11 10 9 111 10 9	LTBP4, LTBP4, LTBP4, ADCK4, ITPKC, SNRPA, MIA, RAB4B, EGLN2, EGLN2, AXL, HNRNPUL1,	ITPKC ADCK4 C19orf54 EGLN2 CYP2B6 AC011510.7-1	1,233 930 274 20,105 16,365 19,426	SHKBP1 SHKBP1 SHKBP1 LTBP4 ITPKC SNRPA RAB4B CYP2B7P1 SRP_euk_arch	7,062 12,338 12,784 13,969 4,698 9,919 11,972 3,136 9,523 23,890 23,542
19 19 19 19 19 110	45,796,203 45,801,479 45,801,925 45,803,110 45,832,263 45,913,218 45,915,370 45,948,522 45,975,102 45,997,823 46,004,210 46,172,293 46,459,480 46,506,189	45,796,664 45,801,838 45,802,695 45,803,798 45,832,564 45,913,615 45,916,245 45,949,598 45,976,854 45,998,175 46,005,093 46,172,679 46,460,627 46,506,732	461 359 770 688 301 397 875 1,076 1,752 352 883 386 1,147 543	12 12 9 10 13 12 12 12 11 10 9 111 10 9 10	LTBP4, LTBP4, LTBP4, ADCK4, ITPKC, SNRPA, MIA, RAB4B, EGLN2, EGLN2, AXL, HNRNPUL1, CORDOCT	ITPKC ADCK4 C19orf54 EGLN2 CYP2B6 AC011510.7-1 CCDC97	1,233 930 274 20,105 16,365 19,426 1,202	SHKBP1 SHKBP1 SHKBP1 LTBP4 ITPKC SNRPA RAB4B CYP2B7P1 SRP_euk_arch HNRNPUL1	7,062 12,338 12,784 13,969 4,698 9,919 11,972 3,136 9,523 23,890 23,542 751
19 19	45,796,203 45,801,479 45,801,925 45,803,110 45,832,263 45,913,218 45,915,370 45,948,522 45,975,102 45,997,823 46,004,210 46,172,293 46,459,480 46,506,189 46,507,539	45,796,664 45,801,838 45,802,695 45,803,798 45,832,564 45,913,615 45,916,245 45,949,598 45,976,854 45,998,175 46,005,093 46,172,679 46,460,627 46,506,732 46,508,393	461 359 770 688 301 397 875 1,076 1,752 352 883 386 1,147 543	12 12 9 10 13 12 12 12 11 10 9 11 10 9 10 10 2	LTBP4, LTBP4, LTBP4, ADCK4, ITPKC, SNRPA, MIA, RAB4B, EGLN2, EGLN2, EGLN2, AXL, HNRNPUL1, CCDC97, DO(C97,	ITPKC ADCK4 C19orf54 EGLN2 CYP2B6 AC011510.7-1 CCDC97	1,233 930 274 20,105 16,365 19,426 1,202	SHKBP1 SHKBP1 SHKBP1 LTBP4 ITPKC SNRPA RAB4B RAB4B CYP2B7P1 SRP_euk_arch HNRNPUL1 HNRNPUL1	7,062 12,338 12,784 13,969 4,698 9,919 11,972 3,136 9,523 23,890 23,542 751 2,101
19 19	45,796,203 45,801,479 45,801,925 45,803,110 45,832,263 45,913,218 45,915,370 45,948,522 45,975,102 45,997,823 46,004,210 46,172,293 46,459,480 46,506,189 46,507,539 46,595,224	45,796,664 45,801,838 45,802,695 45,803,798 45,832,564 45,913,615 45,916,245 45,949,598 45,976,854 45,998,175 46,005,093 46,172,679 46,460,627 46,506,732 46,506,732 46,508,393 46,595,612	461 359 770 688 301 397 875 1,076 1,752 352 883 386 1,147 543 854 388	12 12 9 10 13 12 12 12 11 10 9 11 10 9 10 10 12	LTBP4, LTBP4, LTBP4, LTBP4, ADCK4, ITPKC, SNRPA, MIA, RAB4B, EGLN2, EGLN2, EGLN2, AXL, HNRNPUL1, CCDC97, BCKDHA, ITPEC	ITPKC ADCK4 C19orf54 EGLN2 CYP2B6 AC011510.7-1 CCDC97 EXOSC5	1,233 930 274 20,105 16,365 19,426 1,202 128 0 277	SHKBP1 SHKBP1 SHKBP1 LTBP4 ITPKC SNRPA RAB4B RAB4B CYP2B7P1 SRP_euk_arch HNRNPUL1 HNRNPUL1	7,062 12,338 12,784 13,969 4,698 9,919 11,972 3,136 9,523 23,890 23,542 751 2,101
19 19	45,796,203 45,801,479 45,801,925 45,803,110 45,832,263 45,913,218 45,915,370 45,948,522 45,975,102 45,997,823 46,004,210 46,172,293 46,459,480 46,506,189 46,507,539 46,595,224 46,637,602	45,796,664 45,801,838 45,802,695 45,803,798 45,832,564 45,913,615 45,916,245 45,949,598 45,976,854 45,998,175 46,005,093 46,172,679 46,460,627 46,506,732 46,506,732 46,508,393 46,595,612 46,638,025	461 359 770 688 301 397 875 1,076 1,752 352 883 386 1,147 543 854 388 424	12 12 9 10 13 12 12 12 11 10 9 11 10 9 10 10 9 9	LTBP4, LTBP4, LTBP4, ADCK4, ITPKC, SNRPA, MIA, RAB4B, EGLN2, EGLN2, EGLN2, AXL, HNRNPUL1, CCDC97, BCKDHA, ATP5SL, BCADC	ITPKC ADCK4 C19orf54 EGLN2 CYP2B6 AC011510.7-1 CCDC97 EXOSC5 C19orf69	1,233 930 274 20,105 16,365 19,426 1,202 128 2,877	SHKBP1 SHKBP1 SHKBP1 LTBP4 ITPKC SNRPA RAB4B RAB4B CYP2B7P1 SRP_euk_arch HNRNPUL1 HNRNPUL1 BCKDHA	7,062 12,338 12,784 13,969 4,698 9,919 11,972 3,136 9,523 23,890 23,542 751 2,101 8,512
19 19	45,796,203 45,801,479 45,801,925 45,803,110 45,832,263 45,913,218 45,915,370 45,948,522 45,975,102 45,997,823 46,004,210 46,172,293 46,459,480 46,506,189 46,507,539 46,595,224 46,637,602 47,055,632	45,796,664 45,801,838 45,802,695 45,803,798 45,832,564 45,913,615 45,916,245 45,949,598 45,976,854 45,998,175 46,005,093 46,172,679 46,460,627 46,506,732 46,508,393 46,595,612 46,638,026 47,056,274	461 359 770 688 301 397 875 1,076 1,752 352 883 386 1,147 543 854 388 424 639	12 12 9 10 13 12 12 12 11 10 9 11 10 9 10 10 9 12 10 9	LTBP4, LTBP4, LTBP4, LTBP4, ADCK4, ITPKC, SNRPA, MIA, RAB4B, EGLN2, EGLN2, EGLN2, AXL, HNRNPUL1, CCDC97, BCKDHA, ATP5SL, RPS19P3, ADU6554	ITPKC ADCK4 C19orf54 EGLN2 CYP2B6 AC011510.7-1 CCDC97 EXOSC5 C19orf69	1,233 930 274 20,105 16,365 19,426 1,202 128 2,877	SHKBP1 SHKBP1 SHKBP1 LTBP4 ITPKC SNRPA RAB4B CYP2B7P1 SRP_euk_arch HNRNPUL1 HNRNPUL1 BCKDHA DMRTC2	7,062 12,338 12,784 13,969 4,698 9,919 11,972 3,136 9,523 23,890 23,542 751 2,101 8,512 7,394
19 19	45,796,203 45,801,479 45,801,925 45,803,110 45,832,263 45,913,218 45,915,370 45,948,522 45,975,102 45,997,823 46,004,210 46,172,293 46,459,480 46,506,189 46,507,539 46,595,224 46,637,602 47,055,632 47,055,632	45,796,664 45,801,838 45,802,695 45,803,798 45,832,564 45,913,615 45,913,615 45,949,598 45,976,854 45,998,175 46,005,093 46,172,679 46,460,627 46,506,732 46,508,393 46,595,612 46,638,026 47,056,271 47,080,744	461 359 770 688 301 397 875 1,076 1,752 352 883 386 1,147 543 854 388 424 639 1,122	12 12 9 10 13 12 12 12 11 10 9 11 10 9 10 12 10 9 12 12 13	LTBP4, LTBP4, LTBP4, LTBP4, ADCK4, ITPKC, SNRPA, MIA, RAB4B, EGLN2, EGLN2, EGLN2, AXL, HNRNPUL1, CCDC97, BCKDHA, ATP5SL, RPS19P3, ARHGEF1,	ITPKC ADCK4 C19orf54 EGLN2 CYP2B6 AC011510.7-1 CCDC97 EXOSC5 C19orf69	1,233 930 274 20,105 16,365 19,426 1,202 128 2,877	SHKBP1 SHKBP1 SHKBP1 LTBP4 ITPKC SNRPA RAB4B RAB4B CYP2B7P1 SRP_euk_arch HNRNPUL1 HNRNPUL1 BCKDHA DMRTC2 CD79A	7,062 12,338 12,784 13,969 4,698 9,919 11,972 3,136 9,523 23,890 23,542 751 2,101 8,512 7,394 2,343 22,270
19 19	45,796,203 45,801,479 45,801,925 45,803,110 45,832,263 45,913,218 45,915,370 45,948,522 45,975,102 45,997,823 46,004,210 46,172,293 46,459,480 46,506,189 46,507,539 46,595,224 46,637,602 47,055,632 47,079,622 47,079,622 47,125,816	45,796,664 45,801,838 45,802,695 45,803,798 45,832,564 45,913,615 45,916,245 45,949,598 45,976,854 45,998,175 46,005,093 46,172,679 46,460,627 46,506,732 46,508,393 46,595,612 46,638,026 47,056,271 47,080,744 47,126,113	461 359 770 688 301 397 875 1,076 1,752 352 883 386 1,147 543 854 388 424 639 1,122 297	12 12 9 10 13 12 12 12 11 10 9 9 11 10 9 10 12 10 9 9 12 13 9 9	LTBP4, LTBP4, LTBP4, LTBP4, ADCK4, ITPKC, SNRPA, MIA, RAB4B, EGLN2, EGLN2, EGLN2, AXL, HNRNPUL1, CCDC97, BCKDHA, ATP5SL, RPS19P3, ARHGEF1, ZNE574	ITPKC ADCK4 C19orf54 EGLN2 CYP2B6 AC011510.7-1 CCDC97 EXOSC5 C19orf69	1,233 930 274 20,105 16,365 19,426 1,202 128 2,877	SHKBP1 SHKBP1 SHKBP1 LTBP4 ITPKC SNRPA RAB4B RAB4B CYP2B7P1 SRP_euk_arch HNRNPUL1 HNRNPUL1 BCKDHA DMRTC2 CD79A ARHGEF1	7,062 12,338 12,784 13,969 4,698 9,919 11,972 3,136 9,523 23,890 23,542 7,51 2,101 8,512 7,394 2,343 22,379
19 19	45,796,203 45,801,479 45,801,925 45,803,110 45,832,263 45,913,218 45,915,370 45,948,522 45,975,102 45,997,823 46,004,210 46,172,293 46,459,480 46,506,189 46,507,539 46,595,224 46,637,602 47,055,632 47,079,622 47,125,816 47,266,894	45,796,664 45,801,838 45,802,695 45,803,798 45,832,564 45,913,615 45,916,245 45,949,598 45,976,854 45,998,175 46,005,093 46,172,679 46,460,627 46,506,732 46,508,393 46,595,612 46,638,026 47,056,271 47,080,744 47,126,113 47,267,156	461 359 770 688 301 397 875 1,076 1,752 352 883 386 1,147 543 854 386 1,147 543 854 388 424 639 1,122 297 675	12 12 9 10 13 12 12 12 12 11 10 9 9 11 10 9 10 12 10 9 9 12 13 9 9 9	LTBP4, LTBP4, LTBP4, LTBP4, ADCK4, ITPKC, SNRPA, MIA, RAB4B, EGLN2, EGLN2, EGLN2, CCDC97, BCKDHA, ATP5SL, RPS19P3, ARHGEF1, ZNF574, POU/2E2	ITPKC ADCK4 C19orf54 EGLN2 CYP2B6 AC011510.7-1 CCDC97 EXOSC5 C19orf69 GRIK5 CPIK5	1,233 930 274 20,105 16,365 19,426 1,202 128 2,877 5,097	SHKBP1 SHKBP1 SHKBP1 LTBP4 ITPKC SNRPA RAB4B RAB4B CYP2B7P1 SRP_euk_arch HNRNPUL1 HNRNPUL1 BCKDHA DMRTC2 CD79A ARHGEF1	7,062 12,338 12,784 13,969 4,698 9,919 11,972 3,136 9,523 23,890 23,542 7,51 2,101 8,512 7,394 2,343 22,379
19 19	45,796,203 45,801,479 45,801,925 45,803,110 45,832,263 45,913,218 45,915,370 45,948,522 45,975,102 45,997,823 46,004,210 46,172,293 46,459,480 46,506,189 46,507,539 46,595,224 46,637,602 47,055,632 47,079,622 47,125,816 47,266,894 47,304,453	45,796,664 45,801,838 45,802,695 45,803,798 45,832,564 45,913,615 45,916,245 45,949,598 45,976,854 45,998,175 46,005,093 46,172,679 46,506,732 46,506,732 46,508,393 46,595,612 46,638,026 47,056,271 47,080,744 47,126,113 47,267,569	461 359 770 688 301 397 875 1,076 1,752 352 883 386 1,147 543 854 388 424 639 1,122 297 675 374	12 12 9 10 13 12 12 12 12 11 10 9 11 10 9 10 10 12 10 9 9 12 13 3 9 9 9 10	LTBP4, LTBP4, LTBP4, ADCK4, ITPKC, SNRPA, MIA, RAB4B, EGLN2, EGLN2, EGLN2, CCDC97, BCKDHA, ATP5SL, RPS19P3, ARHGEF1, ZNF574, POU2F2, AC006486 1	ITPKC ADCK4 C19orf54 EGLN2 CYP2B6 AC011510.7-1 CCDC97 EXOSC5 C19orf69 GRIK5 GRIK5 GRIK5 GRIK5	1,233 930 274 20,105 16,365 19,426 1,202 128 2,877 5,097 42,656 1 9,42	SHKBP1 SHKBP1 SHKBP1 LTBP4 ITPKC SNRPA RAB4B RAB4B CYP2B7P1 SRP_euk_arch HNRNPUL1 HNRNPUL1 BCKDHA DMRTC2 CD79A ARHGEF1 ZNF574 ERE	7,062 12,338 12,784 13,969 4,698 9,919 11,972 3,136 9,523 23,890 23,542 7,51 2,101 8,512 7,394 2,343 22,379 26,896 2,554
19 19	45,796,203 45,801,479 45,801,925 45,803,110 45,832,263 45,913,218 45,915,370 45,948,522 45,975,102 45,997,823 46,004,210 46,172,293 46,459,480 46,506,189 46,507,539 46,595,224 46,637,602 47,055,632 47,079,622 47,125,816 47,266,894 47,304,453 47,440,539 47,440,539	45,796,664 45,801,838 45,802,695 45,803,798 45,832,564 45,913,615 45,916,245 45,949,598 45,976,854 45,998,175 46,005,093 46,172,679 46,506,732 46,508,393 46,508,393 46,595,612 46,638,026 47,056,271 47,080,744 47,126,113 47,267,569 47,304,827 47,441,010 47,442,610	461 359 770 688 301 397 875 1,076 1,752 352 883 386 1,147 543 854 388 424 639 1,122 297 675 374 471 437	12 12 9 10 13 12 12 12 11 10 9 11 10 9 10 12 10 9 9 12 13 9 9 9 9 10 14	LTBP4, LTBP4, LTBP4, ADCK4, ITPKC, SNRPA, MIA, RAB4B, EGLN2, EGLN2, EGLN2, CCDC97, BCKDHA, ATP5SL, RPS19P3, ARHGEF1, ZNF574, POU2F2, AC006486.1,	ITPKC ADCK4 C19orf54 EGLN2 CYP2B6 AC011510.7-1 CCDC97 EXOSC5 C19orf69 GRIK5 GRIK5 GRIK5 GSK3A GSK3A	1,233 930 274 20,105 16,365 19,426 1,202 128 2,877 5,097 42,656 1,948 3 582	SHKBP1 SHKBP1 SHKBP1 LTBP4 ITPKC SNRPA RAB4B RAB4B CYP2B7P1 SRP_euk_arch HNRNPUL1 HNRNPUL1 BCKDHA DMRTC2 CD79A ARHGEF1 ZNF574 ERF ERF	7,062 12,338 12,784 13,969 4,698 9,919 11,972 3,136 9,523 23,890 23,542 751 2,101 8,512 7,394 2,343 22,379 26,896 2,554 954
19 19	45,796,203 45,801,479 45,801,925 45,803,110 45,832,263 45,913,218 45,915,370 45,948,522 45,975,102 45,997,823 46,004,210 46,172,293 46,459,480 46,506,189 46,507,539 46,595,224 46,637,602 47,055,632 47,079,622 47,125,816 47,266,894 47,304,453 47,440,539 47,442,173 47,442,173	45,796,664 45,801,838 45,802,695 45,803,798 45,832,564 45,913,615 45,916,245 45,949,598 45,976,854 45,998,175 46,005,093 46,172,679 46,506,732 46,508,393 46,595,612 46,638,026 47,056,271 47,080,744 47,126,113 47,267,569 47,304,827 47,441,010 47,442,610 47,464,426	461 359 770 688 301 397 875 1,076 1,752 352 883 386 1,147 543 854 388 424 639 1,122 297 675 374 471 437 912	12 12 9 10 13 12 12 12 11 10 9 11 10 9 10 12 10 10 12 10 9 9 10 12 13 9 9 9 10 10 12 13 3 9 9 9 10	LTBP4, LTBP4, LTBP4, ADCK4, ITPKC, SNRPA, MIA, RAB4B, EGLN2, EGLN2, EGLN2, CCDC97, BCKDHA, ATP5SL, RPS19P3, ARHGEF1, ZNF574, POU2F2, AC006486.1,	ITPKC ADCK4 C19orf54 EGLN2 CYP2B6 AC011510.7-1 CCDC97 EXOSC5 C19orf69 GRIK5 GRIK5 GRIK5 GSK3A GSK3A FRF	1,233 930 274 20,105 16,365 19,426 1,202 128 2,877 42,656 1,948 3,582 12,421	SHKBP1 SHKBP1 SHKBP1 LTBP4 ITPKC SNRPA RAB4B RAB4B CYP2B7P1 SRP_euk_arch HNRNPUL1 HNRNPUL1 BCKDHA DMRTC2 CD79A ARHGEF1 ZNF574 ERF ERF AC006486 1	7,062 12,338 12,784 13,969 4,698 9,919 11,972 3,136 9,523 23,890 23,542 751 2,101 8,512 7,394 2,343 22,379 26,896 2,554 954
19 19	45,796,203 45,801,479 45,801,925 45,803,110 45,832,263 45,913,218 45,915,370 45,948,522 45,975,102 45,997,823 46,004,210 46,172,293 46,459,480 46,506,189 46,507,539 46,595,224 46,637,602 47,055,632 47,079,622 47,125,816 47,266,894 47,304,453 47,440,539 47,442,173 47,463,514 47,464,439	45,796,664 45,801,838 45,802,695 45,803,798 45,832,564 45,913,615 45,916,245 45,949,598 45,976,854 45,998,175 46,005,093 46,172,679 46,400,627 46,506,732 46,508,393 46,595,612 46,638,026 47,056,271 47,080,744 47,126,113 47,267,569 47,304,827 47,441,010 47,442,610 47,464,426 47,465,176	461 359 770 688 301 397 875 1,076 1,752 352 883 386 1,147 543 854 388 424 639 1,122 297 675 374 471 437 912 737	12 12 9 10 13 12 12 12 12 11 10 9 11 10 9 10 12 10 10 12 10 9 9 10 112 13 9 9 9 10 14 14 2 9 9 9	LTBP4, LTBP4, LTBP4, LTBP4, ADCK4, ITPKC, SNRPA, MIA, RAB4B, EGLN2, EGLN2, EGLN2, EGLN2, CCDC97, BCKDHA, ATP5SL, RPS19P3, ARHGEF1, ZNF574, POU2F2, AC006486.1,	ITPKC ADCK4 C19orf54 EGLN2 CYP2B6 AC011510.7-1 CCDC97 EXOSC5 C19orf69 GRIK5 GRIK5 GRIK5 GSK3A ERF ERF	1,233 930 274 20,105 16,365 19,426 1,202 128 2,877 5,097 42,656 1,948 3,582 12,421 13 346	SHKBP1 SHKBP1 SHKBP1 LTBP4 ITPKC SNRPA RAB4B RAB4B CYP2B7P1 SRP_euk_arch HNRNPUL1 HNRNPUL1 BCKDHA DMRTC2 CD79A ARHGEF1 ZNF574 ERF ERF AC006486.1 AC006486.1	7,062 12,338 12,784 13,969 4,698 9,919 11,972 3,136 9,523 23,542 751 2,101 8,512 7,394 2,343 22,379 26,896 2,554 954 22,549 23,474
19 19	45,796,203 45,801,479 45,801,925 45,803,110 45,832,263 45,913,218 45,915,370 45,948,522 45,975,102 45,997,823 46,004,210 46,172,293 46,459,480 46,506,189 46,507,539 46,595,224 46,637,602 47,055,632 47,079,622 47,125,816 47,266,894 47,304,453 47,440,539 47,442,173 47,463,514 47,464,439 47,497,913	45,796,664 45,801,838 45,802,695 45,803,798 45,832,564 45,913,615 45,916,245 45,949,598 45,976,854 45,998,175 46,005,093 46,172,679 46,460,627 46,506,732 46,508,393 46,595,612 46,638,026 47,056,271 47,080,744 47,126,113 47,267,569 47,304,827 47,441,010 47,442,610 47,465,176 47,498,817	461 359 770 688 301 397 875 1,076 1,752 352 883 386 1,147 543 854 388 424 639 1,122 297 675 374 471 437 912 737 904	12 12 9 10 13 12 12 12 12 12 11 10 9 11 10 9 10 12 10 10 12 10 9 9 10 12 13 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	LTBP4, LTBP4, LTBP4, LTBP4, ADCK4, ITPKC, SNRPA, MIA, RAB4B, EGLN2, EGLN2, EGLN2, EGLN2, CCDC97, BCKDHA, ATP5SL, RPS19P3, ARHGEF1, ZNF574, POU2F2, AC006486.1, PAFAH1B3.	ITPKC ADCK4 C19orf54 EGLN2 CYP2B6 AC011510.7-1 CCDC97 EXOSC5 C19orf69 GRIK5 GRIK5 GRIK5 GSK3A ERF ERF	1,233 930 274 20,105 16,365 19,426 1,202 128 2,877 42,656 1,948 3,582 12,421 13,346	SHKBP1 SHKBP1 SHKBP1 LTBP4 ITPKC SNRPA RAB4B RAB4B CYP2B7P1 SRP_euk_arch HNRNPUL1 HNRNPUL1 BCKDHA DMRTC2 CD79A ARHGEF1 ZNF574 ERF ERF AC006486.1 AC006486.1 CIC	7,062 12,338 12,784 13,969 4,698 9,919 11,972 3,136 9,523 23,890 23,542 751 2,101 8,512 7,394 2,343 22,379 26,896 2,554 954 22,549 23,474 6,124
19 19 19 <	45,796,203 45,801,479 45,801,925 45,803,110 45,832,263 45,913,218 45,913,218 45,915,370 45,948,522 45,975,102 45,997,823 46,004,210 46,172,293 46,459,480 46,506,189 46,507,539 46,595,224 46,637,602 47,055,632 47,079,622 47,125,816 47,266,894 47,304,453 47,440,539 47,442,173 47,463,514 47,464,439 47,497,913	45,796,664 45,801,838 45,802,695 45,803,798 45,832,564 45,913,615 45,916,245 45,949,598 45,976,854 45,998,175 46,005,093 46,172,679 46,460,627 46,506,732 46,508,393 46,595,612 46,638,026 47,056,271 47,080,744 47,126,113 47,267,569 47,304,827 47,441,010 47,442,610 47,465,176 47,498,817	461 359 770 688 301 397 875 1,076 1,752 383 386 1,147 543 854 388 424 639 1,122 297 675 374 471 437 912 737 904	12 12 9 10 13 12 12 12 11 10 9 11 10 9 11 10 9 10 12 10 9 9 10 10 12 13 9 9 9 10 10 12 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	LTBP4, LTBP4, LTBP4, LTBP4, ADCK4, ITPKC, SNRPA, MIA, RAB4B, EGLN2, EGLN2, EGLN2, AXL, HNRNPUL1, CCDC97, BCKDHA, ATP5SL, RPS19P3, ARHGEF1, ZNF574, POU2F2, AC006486.1, PAFAH1B3, PRR19, PRR19,	ITPKC ADCK4 C19orf54 EGLN2 CYP2B6 AC011510.7-1 CCDC97 EXOSC5 C19orf69 GRIK5 GRIK5 GSK3A GSK3A ERF ERF	1,233 930 274 20,105 16,365 19,426 1,202 128 2,877 5,097 42,656 1,948 3,582 12,421 13,346	SHKBP1 SHKBP1 SHKBP1 SHKBP1 LTBP4 ITPKC SNRPA RAB4B RAB4B CYP2B7P1 SRP_euk_arch HNRNPUL1 HNRNPUL1 BCKDHA DMRTC2 CD79A ARHGEF1 ZNF574 ERF ERF AC006486.1 AC006486.1 CIC	7,062 12,338 12,784 13,969 4,698 9,919 11,972 3,136 9,523 23,890 23,542 751 2,101 8,512 7,394 2,343 22,379 26,896 2,554 954 22,549 23,474 6,124
19 19 19 <	45,796,203 45,801,479 45,801,925 45,803,110 45,832,263 45,913,218 45,913,218 45,915,370 45,948,522 45,975,102 45,997,823 46,004,210 46,172,293 46,459,480 46,506,189 46,507,539 46,507,539 46,595,224 46,637,602 47,055,632 47,079,622 47,125,816 47,266,894 47,304,453 47,440,539 47,442,173 47,463,514 47,464,439 47,497,913	45,796,664 45,801,838 45,802,695 45,803,798 45,832,564 45,913,615 45,916,245 45,949,598 45,976,854 45,998,175 46,005,093 46,172,679 46,460,627 46,506,732 46,508,393 46,595,612 46,638,026 47,056,271 47,080,744 47,126,113 47,267,569 47,304,827 47,441,010 47,442,610 47,465,176 47,498,817 47,583,486	461 359 770 688 301 397 875 1,076 1,752 383 386 1,175 543 883 386 1,147 543 854 388 424 639 1,122 297 675 374 471 437 912 737 904 681	12 12 9 10 13 12 12 12 11 10 9 11 10 9 11 10 10 12 10 10 12 10 10 12 10 10 12 10 10 9 9 10 12 13 9 9 9 9 9 9 9 10 10 13 13 12 12 12 12 12 12 12 12 12 12 12 12 12	LTBP4, LTBP4, LTBP4, LTBP4, ADCK4, ITPKC, SNRPA, MIA, RAB4B, EGLN2, EGLN2, EGLN2, CCDC97, BCKDHA, ATP5SL, RPS19P3, ARHGEF1, ZNF574, POU2F2, AC006486.1, PAFAH1B3, PRR19, CNFN,	ITPKC ADCK4 C19orf54 EGLN2 CYP2B6 AC011510.7-1 CCDC97 EXOSC5 C19orf69 GRIK5 GRIK5 GSK3A GSK3A ERF ERF	1,233 930 274 20,105 16,365 19,426 1,202 128 2,877 5,097 42,656 1,948 3,582 12,421 13,346	SHKBP1 SHKBP1 SHKBP1 SHKBP1 LTBP4 ITPKC SNRPA RAB4B RAB4B CYP2B7P1 SRP_euk_arch HNRNPUL1 HNRNPUL1 BCKDHA DMRTC2 CD79A ARHGEF1 ZNF574 ERF ERF AC006486.1 AC006486.1 AC006486.1	7,062 12,338 12,784 13,969 4,698 9,919 11,972 3,136 9,523 23,890 23,542 7,51 2,101 8,512 7,394 2,343 22,379 26,896 2,554 954 22,549 23,474 6,124 8,044

19	48,387,619	48,387,985	366	11		PSG5	5,091	PSG4	709
19	48,486,554	48,487,009	455	9		CEACAMP11	6,244		
19	48,512,567	48,513,427	860	11		CEACAMP4	12,052	AC005392.8	13,909
19	48.670.781	48.671.655	874	9	PHLDB3.	LYPD3	9,110		,
19	48,699,344	48,700,149	805	9	PHLDB3,			ETHE1	2,563
19	48,728,392	48,729,401	1,009	9	ZNF575,	ETHE1	5,156	XRCC1	9,903
19	48,751,177	48,751,644	467	10	XRCC1,	AC006276.1	24,950	ZNF575	19,055
19	48.791.884	48.792.848	964	10	ZNF576.	IRGQ	368		-,
19	48.815.104	48.815.614	510	10	ZNF428.			CADM4	2.748
19	48 944 148	48 944 778	630	9	C19orf61			KCNN4	17 747
19	48 950 568	48 951 374	806	9	C19orf61			KCNN4	11 151
19	49 023 027	49 023 463	436	15	ZNE283	LYPD5	24 588	7NF404	44 896
19	49 097 567	49 098 083	516	12	2111 200,	ZNF404	21,000	ZNF45	10 540
10	40,007,007	40,000,000	493	14	7NF221	ZNF45	15 693	2111 40	10,040
10	40,170,771	49 181 069	1 208	9	ZNF155	ZNE230	14 167	7NF221	16 070
10	40,108,722	40,101,000	710	10	ZNF230	ZNF222	8 072	ZNF155	4 405
10	40,100,122	49,100,441	725	18	2111 200,	ZNF223	2 963	2111100	4,405
10	49,247,402	49,240,207	1 25	10		2111 223	2,903	7115000	4 150
10	49,207,422	49,200,077	1,200	1 0	ZINI 204, ZNE294	SPD out oroh	14.057	ZINI 223 ZNE222	4,152
19	49,273,097	49,274,040	043	9	ZNF204,		14,057	SPD out arch	10,427
19	49,269,941	49,290,765	044	10	ZNFZZ4,				1,344
19	49,309,118	49,309,574	400	12	ZINFZZƏ,	7115024	0.000		4,601
19	49,330,800	49,338,398	1,538	11	7115006	LINF 234	o,290		1,105
19	49,360,771	49,361,486	/15	13	ZNF226,	715007	4 400	ZNF234	6,442
19	49,403,197	49,404,088	891	14	715007	ZNF227	4,436	71/5000	04 504
19	49,408,207	49,409,339	1,132	11	ZNF227,	ZNF233	36,819	ZNF226	34,531
19	49,455,789	49,456,107	318	11	ZNF233,			ZNF227	22,529
19	49,500,720	49,501,195	475	11	ZNF235,			ZFP112	21,351
19	49,644,327	49,644,763	436	10	ZNF229,	AC069278.1	23,440	ZNF180	26,938
19	49,695,117	49,695,585	468	9	ZNF180,			CEACAM20	6,466
19	49,918,891	49,919,511	620	9				CEACAM16	3,550
19	49,979,508	49,979,792	284	10	CBLC,	BCAM	24,386	AC092066.6	18,947
19	49,995,202	49,995,855	653	9	CBLC,	BCAM	8,323		
19	50,039,849	50,040,258	409	10		PVRL2	975		
19	50,040,365	50,040,922	557	9		PVRL2	311		
19	50,085,332	50,086,047	715	12		TOMM40	287	PVRL2	1,007
19	50,196,074	50,196,473	399	10		RELB	66	CLPTM1	7,636
19	50,230,885	50,231,181	296	10	RELB,	SFRS16	2,957		
19	50,274,067	50,274,603	536	9	GEMIN7,	ZNF296	2,539	SFRS16	8,013
19	50,286,671	50,287,020	349	11		LRRC68	1,038	GEMIN7	49
19	50,287,620	50,288,251	631	11	LRRC68,			GEMIN7	998
19	50,600,146	50,600,821	675	11		PPP1R13L	10	ERCC1	3,891
19	50,637,468	50,637,769	301	10		ERCC1	18,451	CD3EAP	31,604
19	50,641,466	50,641,718	252	11		FOSB	21,375	CD3EAP	35,602
19	50,673,386	50,674,088	702	14		AC138534.3	9,787	FOSB	3,132
19	50,680,332	50,680,635	303	10	RTN2,	AC138534.3	3,240		
19	50,779,636	50,780,310	674	11	OPA3,			GPR4	4,565
19	50,886,759	50,888,162	1,403	9	SNRPD2,	-		GIPR	9,215
					QPCTL,				
19	50,964,396	50,965,440	1,044	10	DMPK,	SIX5	244		
19	50,965,609	50,965,934	325	9	DMPK,	SIX5	1,457		
19	51,078,359	51,078,676	317	11				IRF2BP1	442
19	51,081,528	51,082,686	1,158	9		IRF2BP1	656	MYPOP	2,439
19	51,097,790	51,098,377	587	10		MYPOP	88		
19	51,235,895	51,236,685	790	9	IGFL4,	PGLYRP1	17,751	hsa-mir-769	21,748
19	51,272,560	51,272,941	381	10		AC007785.1-2	74		
19	51,494,235	51,494,597	362	9	HIF3A,			U6	6,970
19	51,769,262	51,769,723	461	9		CALM3	26,629	PTGIR	45,843
19	51,795,749	51,796,308	559	24		CALM3	44		· · · ·
19	51,961,600	51,962,147	547	9				SLC1A5	7,835
19	51,983,449	51,983,842	393	10	SLC1A5,	STRN4	41,889	FKRP	29,868
19	52,035,516	52,035,905	389	10	AP2S1,	No non-overlappi	ng genes wit	hin 50,000bp	
19	52,045,816	52,046.309	493	11	AP2S1,	No non-overlappi	ng genes wit	hin 50,000bp	
19	52,054,988	52,055,373	385	12		AP2S1	8,945		
19	52,058,737	52,059,217	480	10		AP2S1	12,694		
	-								

19	52,221,977	52,222,272	295	9	NPAS1,			TMEM160	18,736
19	52,243,052	52,243,399	347	10	TMEM160,			NPAS1	2,179
19	52,308,112	52,309,303	1,191	10	ZC3H4,	SAE1	16,725		
19	52,326,025	52,326,800	775	9	SAE1,	ZC3H4	17,176		
19	52,427,515	52,428,101	586	9	BBC3,	CCDC9	23,531	SAE1	22,228
19	52,439,139	52,439,646	507	14		BBC3	11,440	SAE1	33,852
19	52,500,321	52,500,766	445	10		C5AR1	4,178		
19	52,678,762	52,679,140	378	15	KPTN,			NAPA	3,563
19	52,893,069	52,893,599	530	15	GLTSCR1,	EHD2	14,903		
19	52,902,290	52,902,683	393	9		EHD2	5,819	GLTSCR1	3,999
19	52,938,450	52,939,075	625	9		GLTSCR2	1,545	EHD2	248
19	53,058,533	53,059,121	588	10				SULT2A1	6,561
19	53,398,805	53,399,118	313	10	AC011466.6,			CARD8	4,207
19	53,516,743	53,517,338	595	10	CCDC114,	EMP3	3,116		
19	53,586,147	53,587,010	863	9	KDELR1,	GRIN2D	2,934		
19	53,640,702	53,641,528	826	9	GRWD1,	KCNJ14	9,050	GRIN2D	703
19	53,769,630	53,770,143	513	10	SULT2B1,	hsa-mir-220c	14,207	FAM83E	25,526
19	53,779,197	53,779,755	558	9	SULT2B1.	SPACA4	22.057	FAM83E	15.914
19	53,783,686	53,784,254	568	9	SULT2B1.	SPACA4	17.558	FAM83E	11.415
19	53.813.331	53,814,626	1.295	10	RPL18, SPHK2,	FAM83E	4,825		, -
19	53,990,304	53,990,737	433	9	BCAT2.	U6	1,977		
19	54 030 674	54 031 121	447	9	HSD17B14		.,	PI FKHA4	1 046
19	54 067 343	54 067 959	616	9	PPP1R15A	PI FKHA4	3 673	TUI P2	8 082
19	54 067 964	54 069 011	1 047	9	PPP1R15A	PI FKHA4	4 294	TUI P2	7 030
19	54 301 576	54 302 071	495	9	SNRNP70	LIN7B	7 322	10212	1,000
10	54 646 694	54 647 116	400	11			1 209		
10	54 691 022	54 691 454	432	14	RPS11P5	SNORD35	1,200		3 652
10	54 871 198	54 871 876	678	14		PRMT1	474	BCI 2I 12	2 214
10	54 875 518	54 876 093	575	9	PRMT1			BCI 2I 12	6 534
10	54 061 183	54 061 662	470	9		AD2A1	330	DOLLETZ	0,004
10	55 064 541	55 064 973	432	10	AKT191		1 011		8 730
10	55 071 802	55,004,975	1 1 1 2	10	AKT101,		0.262	11001	0,755
19	55,071,092	55,075,010	1,110	10	TBC1D17		9,202		
19	55 220 946	55 221 242	296	10	ZNF473	VRK3	329		
19	55 331 010	55 331 396	386	9	2111 470,	VICO	020	C19orf41	16 221
19	55 528 479	55 529 342	863	9	NAPSB	KCNC3	4 033		10,221
10	55 571 151	55 571 541	390	12	NR1H2		7 879		
10	56 031 337	56 031 819	482	9	NIX1112,		4 746		
10	56 211 693	56 212 216	523	10	KI K10	KIKQ	7 044	KI K11	5 085
10	56 899 084	56 899 700	616	11	AC018755 3-4		7,044	HAS1	8 477
10	57 082 844	57 083 224	380	11	ZNE577			7NE649	1 077
10	57 223 025	57 223 537	512	10	ZNF614			ZNF432	4 636
10	57 333 011	57 335 164	1 253	9	ZNF616	AC011468 8-2	4 506	2111 402	4,000
10	57 765 306	57 765 710	412	9	ZNF701		-,500	ZNE808	5 777
10	58 626 520	58 627 150	630	0	AC022137.6.1	AC022127.6.2	17 200	ZNE765	10 455
10	58 715 151	58 716 249	704	9	7NF331	AUUZZ 137.0-Z	11,290	ZNE813	16 602
10	59 102 250	59 103 114	7 34 585	9		CACNG7	057	PRKCG	1/6
10	50 310 521	59 311 102	500	10	TEPT PPDE31		901		041
10	50 651 760	59 652 120	202	14	TTTT, INFEST,		70	AC0087/6 5	1 722
10	60 363 7/1	60 364 016	275	9	C19orf51		2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	A0000740.0	1,132
10	60 / 82 071	60 /83 /04	213 213	10	HSPRD1	BRSK1	2,029		
10	60 509 922	60 500 512	400	10	RDSK1	BIXOICI	5,735		6 526
10	60 621 102	60 601 674	404	10			10.046	AC135502.2	14 664
19	60,621,163	60,621,674	491	12	AC125502.2		10,046	AC 135592.2	14,001
19	60 707 404	60 707 570	35/	9	AC009725 0	00020	29,392	13002 NAT14	10,202
19	60,707,104	60,707,576	472	9	AC008735.9,	15062	42,200		10,357
19	60.846.400	60.846.000	200	9			5,411	2INF024	1,800
19	00,040,423	00,040,900	400	13	ZINF 300, ZNE 591	CCDC 106	3,000		
10	61 344 124	61 344 720	500	11	ZNE444			AC024580 6 1	0 507
19	61 455 629	61 /56 707	1 1 1 10		ZINI 444, 790 ANEA			AC011506 2	0,00/
10	61 506 247	61 506 692	1,149	9	ZUCANUA,	7NE583	10 0/0	ZNE542	+,912 11 700
10	61 506 700	61 507 179	430	40	ZINI JOZ,	ZNE582	10,040	ZINI JHZ	14,132
10	62 275 407	62 375 005	407	10			4 750		
10	62 302 010	62 304 065	1 0/6	11	ZNE264		72 751		
10	62 522 705	62 524 224	520	9	ZNE542		20,201		06 E 47
19	02,323,795	02,024,331	230	9	ZINF043,	LINE JU4	30,156		∠0,547

10 2,2,92,005 62,2,92,005 62,2,92,005 70,2,702,297 70,375 70,777	19	62,554,268	62,554,688	420	13	ZNF304,	ZNF547	12,015	ZNF543	20,312
19 02.14.224 62.14.579 355 10 DWF73. DWF74 DWF73. DWF74 DWF756 DWF76 DWF76 DWF76 DWF76 DWF77 DWF76 DWF77 DWF76 DWF77 DWF77 <thdwf77< th=""> DWF77 DWF77 <</thdwf77<>	19	62,592,605	62,593,469	864	9	ZNF548,		,	ZNF547	9,870
16 52,702,851 62,702,951 72,702,951 72,702,951 72,702,951 72,702,973 72,702,973 72,702,973 72,702,973 72,702,973 72,702,973 72,702,973 72,702,973 72,702,973 72,702,973 72,702,973 72,702,973 72,702,973 72,702,973 72,702,973 72,702,973 72,702,973 72,702,973 72,703,973 72,703,973 72,703,973 72,703,973 72,703,973 72,703,973 72,703,973 73,703,973 73,703,973 73,703,973 73,703,973 73,703,973 74,974 74,703,973,774 74,974<	19	62 614 224	62 614 579	355	10	ZNF17			ZNE548	9 627
Image: 10 EXTRACT	19	62 702 851	62 703 209	358		ZNE773			ZNF419	4 991
10 62 943 300 62 944 586 656 0 2NPT6 2SPAP11 2SE0N4 27 550 NPT6 13.37 10 62 972 584 62 972 586 210 2NPT6 2NPF76 41.869 NPT76 11.357 10 63 367 214 63 433 278 317 11 2NP546 22051 63 387 214 13.222 10 63 432 201 63 433 278 317 11 2NP544 2NP54 44 5852 AC020915.6 13.222 10 63 508 172 63 508 507 731 9 AC010842.5-1 6,358 ANP54 9 10 63 565 077 500 9 2NF544 AC012313.7-2 880 2NP534 55 10 63 65 070 91 9 2NF344 8.032 PNF344 55 55 11 63 702 455 63 702 457 112 11 2NF344 8.032 2NF544 55 10 52 56 63 570 75 90 10 5C2745 71	19	62 781 647	62 782 467	820	9	ZNF416	7IK1	4 855		1,001
10 62 949 745 62 949 745 62 949 745 62 950 555 910 2 NPT76 2 NPF71 14 889 NPT76 11.357 19 63 342 054 63 387 319 557 11 2 NP574 AC020915.6 32.036 11.357 19 63 420 051 63 430 207 311 11 2 NP574 AC020915.6 32.038 13.222 19 63 430 1741 63 440 207 314 11 2 NP574 AC01042.5-1 6,358 2NP5 5.08 19 63 361.016 63 650.075 91 2 NP564 AC012313.7.1 1.138 5.08 10 63 650.075 91 01 2 NP594 AC012313.7.1 1.138 5.08 10 63 650.075 91 01 2 NP594 S.127A5 7.111 11 NP524 8.332 VP584 5.312 10 63 200.0757 1.12 11 2 NP324 Z.NP486 8.332 VP524 5.183 4.4791 221420 13.854 10 2 Z55.65 5.23.366 1.051 11 2 NP324 Z.NP324 Z.NP324 Z.NP324 Z.NP324 <t< td=""><td>19</td><td>62 843 920</td><td>62 844 556</td><td>636</td><td>9</td><td>ZNF211</td><td>ZSCAN4</td><td>27 559</td><td>7NF134</td><td>19 337</td></t<>	19	62 843 920	62 844 556	636	9	ZNF211	ZSCAN4	27 559	7NF134	19 337
10 62:072.094 62:072.096 29:07.096 29:07.096 29:07.096 29:07.096 29:07.096 20:07.096 11:07 10 63:36.07.67 63:37.01 55:7 11 2NF54 2NF85 44.852 AC020915.6 13.222 10 63:36.07.47 63:36.088 71 9 AC010642.5-1 6:368 2NF8 73 - 10 63:36.07.67 50:08 2/NF497 AC012313.7-2 880 2NF837 5:080 10 63:36.089 63:07.075 111 2/NF584 AC012313.7-1 1:135 - 10 63:36:0.89 63:07.075 1:11 12/NF584 AC012313.7-1 1:35 - 10 63:36:0.89 63:07.075 1:12 11 2/NF324 2/NF324 8:52 2/NF324 8:52 10 63:72:356 63:72:346 1:05 1:2274.5 7:111 - 2 2:56:56 2:33:83.04 1:05 1:05 2:05:05 0:05 0:05:05 0:05 0:05	19	62 949 745	62 950 555	810	9	ZNF776	ZNE671	18 950		10,007
Image: 1 Control (1) Control (1) <thcontrol (1)<="" th=""> <thcontrol (1)<="" th=""> <t< td=""><td>10</td><td>62 972 694</td><td>62,000,000</td><td>202</td><td>10</td><td>ZNF586</td><td>ZNE671</td><td>41 800</td><td>7NE776</td><td>11 357</td></t<></thcontrol></thcontrol>	10	62 972 694	62,000,000	202	10	ZNF586	ZNE671	41 800	7NE776	11 357
1 25.05.0 25.05.0 25.05.0 25.05.0 12.222 10 63.481,743 63.482,087 314 9 2NF8 73 73 10 63.508,098 63.303,848 755 9 ZSCAN22, AC010642.5-1 6,358.0P8 9,306 10 63.508,098 63.303,848 755 9 ZSCAN22, AC01021317.2 806 QMF837 5,008 10 63.811,610 63.612,224 614 11 ZMF544, AC012313.7.1 1,135 5,008 10 63.666,653 63.70.675 1,112 11 ZMF544, AC012313.7.1 1,135 5,308 10 82.722.556 235.306 10 SLC27A5, 7,111 1 13.864 10 255.069 255.365 386 9 SOX12, NRSN2 20.213 ZCCHC3 26.104 20 255.069 255.456 386 9 SOX12, NRSN2 20.213 ZCCHC3 26.104 20 256.06 00 10 SCR27, SRN14 14.010 20 2	10	63 386 762	63 387 310	557	11	ZNF274	AC020015.6	32 036	2111770	11,007
10 0.142.50 0.132.20 0.11 12.14.04.7. 2.NF8 7.10 4.00.2 [PC203] 13.21.00 13.	10	63 432 061	63 433 278	317	11	ZINI 274, ZNE544	7NE9	48 852	AC020015.6	13 222
In In< In In In In In In< In In In In In In< In In In	19	62 491 742	62 492 057	214	0	ZINI 344,		40,052	AC020915.0	13,222
10 0.300 11 9 2XXV000-23-1 0.300 2XV000-23-1 0.300 2XV00-23-1 2XV00-2	19	62 509 172	62 508 080	017	9		ZINFO	6 259		0.106
Instructure	19	03,506,172	03,500,969	017	9	7004100	AC010042.5-1	0,300		9,100
19 63,365,297 63,365,797 300 9 2(M+97, 200 AC012313,7-2 880 2(M+337, 200 5008 19 65,661,008 63,665,079 981 9 ZNF324B ZNF324B 5,416 19 65,665,038 33,702,857 399 10 SLC27A5, 11 ZNF324, 225,2956 ZNF324B 8,552 19 63,702,458 63,702,457 399 10 SLC27A5, 11 ZBF1845, SLC27A5, 255,537 THIN28 44,791 ZBF1845 13,854 20 255,900 256,646 816 9 SOX12, 9 SOX12, 255,800 SOX12, 256,800 266,646 9 SOX12, 9 SOX12, 258,900 NRSN2 20,213 ZCCHC3 268,866 20 535,500 566,660 660 10 SCRT2, 335,817 SXX11 14,010 200 20 535,900 566,660 660 SOX12, 32,893,866 73 10 SCRT2, 32,894,804 SXX11 14,010 200 2,399,863 2,399,963 328 10 SNRP8, 9,042 YRAA 17,6851 10,767 1,706,303 10,767 1,706,303 10,767 1,706,303 10,767 1,7	19	63,530,093	63,530,848	755	9	ZSCANZZ,	10010010 7 0		AC010642.5-2	7,330
19 66,56,008 63,867,224 614 11 2/M*954, 9 2/M*924B, 2/M*942B 2/M*934, 2/M*942B 2/M*934, 2/M*942B 2/M*934, 2/M*942B 5/M*944 5/M*944 19 65,702,468 63,702,457 3/M 10 SLC27A5, 112 M*934B TMF446 8,932 2/M*934B 8,552 19 63,702,468 63,702,468 63,702,468 3/M 11 ZBT845, 112 M*172 SLC27A5, 2/2D 7/M*172 8/M 1 2/M*172 8/M 1 2/2D 2/2D<	19	03,505,297	63,565,797	500	9	ZNF497,	AC012313.7-2	880	ZNF837	5,008
19 65,854,038 63,035,078 381 9 2012 2012 2013 2014	19	63,611,610	03,012,224	614	11	ZNF584,	AC012313.7-1	1,135	7115504	5 440
19 63,669,663 63,670,676 1,12 11 2/H*324 2/H*324 8,552 19 63,702,368 63,702,368 63,723,369 10 SLC27A5, TRIM28 44,791 ZBTB45 13,864 19 63,702,368 412 9 SOX12 871 20 20 255,969 253,368 412 9 SOX12 NRSN2 20,213 ZOCHC3 28,646 20 255,800 266,484 816 9 SOX12 NRSN2 20,202 ZOCHC3 28,686 20 335,817 336,495 678 10 RBCK1 202 TRB3 9,620 20 744,561 745,031 450 9 SOX12 NRSN2 20,217 ZOB 740 2,308 2,309,366 23 9 TGM3, No non-overtapping genes with 30,000bp 2,343,932 40 77 10 77 10 10,775 17,661 ZNF343 10,767 11,821 10 2,740,807 2,441,41	19	63,654,098	63,655,079	981	9	ZNF324B,			ZNF584	5,416
19 63,702,458 64,714 74,111 11 25,878 96,800 660 10 SCR12 SKN11 14,010 23,002 74,4581 74,5031 460,724 24,804 12,014 73,000 73,00 73,000 10,014,014 11 No non-overlapping genes within 50,000p 23,093,68 23,909,666 328 10,0767 No non-overlapping genes within 50,000p 24,43,012 24,43,012 11,0767 110,0148 5,687 0 2,2,641,653 2,2,642,643 33	19	63,669,563	63,670,675	1,112	11	ZNF324,	ZNF446	8,932	ZNF324B	8,552
19 63,722,355 63,723,406 10,051 11,28TB45, 120 SLC27A5 7,11 20 255,069 255,455 386 9 SOX12, NRSN2 871 20,110 20 255,069 255,455 386 9 SOX12, NRSN2 19,000 20,010 26,865 20 335,817 336,495 678 10 RBCK1 202 71,000 20,868 20 745,81 745,011 450 9 CC00765 17,035 RPF310 23,012 20 1,395,169 1,395,936 767 11 NSF.1C, 2,399,368 2,249,060 2,246,046 2,463,392 40 No non-overlapping genes with 50,000bp 2,465,012 2,463,432 420 10 ZNF34,3 10,707 2 2,560,526 2,581,356 830 9 NDF56, NDF54,3 ThC2 11,821 467 7,553 20 2,646,879 2,769,400 521 14 FAM113A, PFFA, 2,474 7,553 20 2,7	19	63,702,458	63,702,857	399	10	SLC27A5,	TRIM28	44,791	ZBTB45	13,854
20 252,956 253,368 412 9 SOX12 871 20 255,680 256,648 818 9 SOX12, NRSN2 20,213 ZCCHC3 26,614 20 255,830 256,648 818 9 SOX12, NRSN2 10,020 CCHC3 26,865 20 335,817 336,495 678 10 RECK1 202 TRUB3 9,620 20 744,581 745,031 450 9 C20off55 17,325 RFs10L 23,012 2,399,366 767 11 NSF1C, SIRPB2 7,300 20 1,705,756 1,705,360 604 9 RP4-673020.1 7,605 Z,649,342 420 10 ZNF343, TMC2 11,821 10,760 23,912 2,453,452 420 10 ZNF343, TMC2 11,821 10,760 24,643,615-2 7,176 20 2,646,637 2,741,176 309 9 C20orf141 2,481 C20orf141 2,481 </td <td>19</td> <td>63,722,355</td> <td>63,723,406</td> <td>1,051</td> <td>11</td> <td>ZBTB45,</td> <td>SLC27A5</td> <td>7,111</td> <td></td> <td></td>	19	63,722,355	63,723,406	1,051	11	ZBTB45,	SLC27A5	7,111		
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20 16,658,275 16,658,965 690 9 SNRPB2, OTOR 18,038 Image: Signal State St	20	16,508,988	16,509,340	352	9		C20orf23	6,910	RPLP0P1	5,638
20 19,590,965 19,591,340 375 9 SLC24A3, No non-overlapping genes within 50,000bp 20 21,696,315 21,696,722 407 9 SLC25A6P1 24,600 RPL41P1 12,327 20 26,136,662 26,137,515 853 89 hsa-mir-663, No non-overlapping genes within 50,000bp 12,327 20 26,137,695 26,138,424 729 136 hsa-mir-663 781 1 20 28,214,262 28,214,647 385 9 FRG1B 10,871 MLLT10L 36,813 20 28,251,290 28,251,719 429 13 FRG1B, MLLT10L, AL441988.11-2 329 20 28,259,819 28,260,259 440 20 FRG1B, MLLT10L 8,098 AL441988.11-2 8,858 20 28,262,129 28,262,551 422 9 FRG1B, MLLT10L 10,408 AL441988.11-2 11,168 20 28,265,219 28,265,982 763 11 FRG1B, <	20	16,658,275	16,658,965	690	9	SNRPB2,	OTOR	18,038		
20 21,696,315 21,696,722 407 9 SLC25A6P1 24,600 RPL41P1 12,327 20 26,136,662 26,137,515 853 89 hsa-mir-663, No non-overlapping genes within 50,000bp 20 26,137,695 26,138,424 729 136 hsa-mir-663 781 20 28,214,262 28,214,647 385 9 FRG1B 10,871 MLLT10L 36,813 20 28,251,290 28,251,719 429 13 FRG1B, MLLT10L, MLLT10L 8,098 AL441988.11-2 329 20 28,259,819 28,260,259 440 20 FRG1B, MLLT10L 8,098 AL441988.11-2 8,858 20 28,262,129 28,265,982 763 11 FRG1B, MLLT10L 10,408 AL441988.11-2 11,168 20 28,265,219 28,265,982 763 11 FRG1B, MLLT10L 13,498 AL441988.11-2 14,258 20 28,266,622 28,267,489 867 10 FRG1B 807 20 29,565,700 29,565,969 269 28 HM13, RP3	20	19,590,965	19,591,340	375	9	SLC24A3,	No non-overlappi	ng genes wit	hin 50,000bp	
20 26,136,662 26,137,515 853 89 hsa-mir-663, No non-overlapping genes within 50,000bp 20 26,137,695 26,138,424 729 136 hsa-mir-663 781 20 28,214,262 28,214,647 385 9 FRG1B 10,871 MLLT10L 36,813 20 28,251,290 28,251,719 429 13 FRG1B, MLLT10L, AL441988.11-2 329 20 28,259,819 28,260,259 440 20 FRG1B, MLLT10L, 8,098 AL441988.11-2 8,858 20 28,262,129 28,260,259 440 20 FRG1B, MLLT10L 10,408 AL441988.11-2 11,168 20 28,265,219 28,265,982 763 11 FRG1B, MLLT10L 13,498 AL441988.11-2 14,258 20 28,266,622 28,267,489 867 10 FRG1B, MLLT10L 13,498 AL441988.11-2 14,258 20 29,565,700 29,565,969 269 28	20	21,696,315	21,696,722	407	9		SLC25A6P1	24,600	RPL41P1	12,327
20 26,137,695 26,138,424 729 136 hsa-mir-663 781 20 28,214,262 28,214,647 385 9 FRG1B 10,871 MLLT10L 36,813 20 28,251,290 28,251,719 429 13 FRG1B, MLLT10L, AL441988.11-2 329 20 28,259,819 28,260,259 440 20 FRG1B, MLLT10L 8,098 AL441988.11-2 8,858 20 28,262,129 28,265,551 422 9 FRG1B, MLLT10L 10,408 AL441988.11-2 11,168 20 28,265,219 28,265,982 763 11 FRG1B, MLLT10L 13,498 AL441988.11-2 14,258 20 28,266,622 28,267,489 867 10 FRG1B, MLLT10L 13,498 AL441988.11-2 14,258 20 29,565,700 29,565,969 269 28 HM13, RP3-324017.4 32,999 REM1 29,332 20 30,409,222 30,409,716 494 12 ASXL1 98 441983C 823 20 <td>20</td> <td>26,136,662</td> <td>26,137,515</td> <td>853</td> <td>89</td> <td>hsa-mir-663,</td> <td>No non-overlappi</td> <td>ng genes wit</td> <td>hin 50,000bp</td> <td></td>	20	26,136,662	26,137,515	853	89	hsa-mir-663,	No non-overlappi	ng genes wit	hin 50,000bp	
20 28,214,262 28,214,647 385 9 FRG1B 10,871 MLLT10L 36,813 20 28,251,290 28,251,719 429 13 FRG1B, MLLT10L, AL441988.11-2 329 20 28,259,819 28,260,259 440 20 FRG1B, MLLT10L 8,098 AL441988.11-2 8,858 20 28,262,129 28,262,551 422 9 FRG1B, MLLT10L 10,408 AL441988.11-2 11,168 20 28,265,219 28,265,982 763 11 FRG1B, MLLT10L 13,498 AL441988.11-2 14,258 20 28,266,622 28,267,489 867 10 FRG1B, MLLT10L 13,498 AL441988.11-2 14,258 20 29,565,700 29,565,969 269 28 HM13, RP3-324017.4 32,999 REM1 29,332 20 30,409,222 30,409,716 494 12 ASXL1 98 F 450 450 450 453 20 33,335,285 33,336,127 842 9 EIF6,	20	26,137,695	26,138,424	729	136		hsa-mir-663	781		
20 28,251,290 28,251,719 429 13 FRG1B, MLLT10L, AL441988.11-2 329 20 28,259,819 28,260,259 440 20 FRG1B, MLLT10L 8,098 AL441988.11-2 8,858 20 28,262,129 28,262,551 422 9 FRG1B, MLLT10L 10,408 AL441988.11-2 11,168 20 28,265,219 28,265,982 763 11 FRG1B, MLLT10L 13,498 AL441988.11-2 14,258 20 28,266,622 28,267,489 867 10 FRG1B 807 20 29,565,700 29,565,969 269 28 HM13, RP3-324017.4 32,999 REM1 29,332 20 30,409,222 30,409,716 494 12 ASXL1 98 441983.12 423 20 33,335,285 33,336,127 842 9 EIF6, FAM83C 823	20	28,214,262	28,214,647	385	9		FRG1B	10,871	MLLT10L	36,813
Image: Marcol	20	28,251,290	28,251,719	429	13	FRG1B,			AL441988.11-2	329
20 28,259,819 28,260,259 440 20 FRG1B, MLLT10L 8,098 AL441988.11-2 8,858 20 28,262,129 28,262,551 422 9 FRG1B, MLLT10L 10,408 AL441988.11-2 11,168 20 28,265,219 28,265,982 763 11 FRG1B, MLLT10L 13,498 AL441988.11-2 14,258 20 28,266,622 28,267,489 867 10 FRG1B 807 20 29,565,700 29,565,969 269 28 HM13, RP3-324O17.4 32,999 REM1 29,332 20 30,409,222 30,409,716 494 12 ASXL1 98 44832 20 33,335,285 33,336,127 842 9 EIF6, FAM83C 823						MLLT10L,				
20 28,262,129 28,262,551 422 9 FRG1B, MLLT10L 10,408 AL441988.11-2 11,168 20 28,265,219 28,265,982 763 11 FRG1B, MLLT10L 13,498 AL441988.11-2 14,258 20 28,266,622 28,267,489 867 10 FRG1B 807 20 29,565,700 29,565,969 269 28 HM13, RP3-324O17.4 32,999 REM1 29,332 20 30,409,222 30,409,716 494 12 ASXL1 98	20	28,259,819	28,260,259	440	20	FRG1B,	MLLT10L	8,098	AL441988.11-2	8,858
20 28,265,219 28,265,982 763 11 FRG1B, MLLT10L 13,498 AL441988.11-2 14,258 20 28,266,622 28,267,489 867 10 FRG1B 807 20 29,565,700 29,565,969 269 28 HM13, RP3-324O17.4 32,999 REM1 29,332 20 30,409,222 30,409,716 494 12 ASXL1 98 9 20 33,335,285 33,336,127 842 9 EIF6, FAM83C 823	20	28,262,129	28,262,551	422	9	FRG1B,	MLLT10L	10,408	AL441988.11-2	11,168
20 28,266,622 28,267,489 867 10 FRG1B 807 20 29,565,700 29,565,969 269 28 HM13, RP3-324O17.4 32,999 REM1 29,332 20 30,409,222 30,409,716 494 12 ASXL1 98 9 EIF6, FAM83C 823	20	28,265,219	28,265,982	763	11	FRG1B,	MLLT10L	13,498	AL441988.11-2	14,258
20 29,565,700 29,565,969 269 28 HM13, RP3-324O17.4 32,999 REM1 29,332 20 30,409,222 30,409,716 494 12 ASXL1 98	20	28,266,622	28,267,489	867	10				FRG1B	807
20 30,409,222 30,409,716 494 12 ASXL1 98 20 33,335,285 33,336,127 842 9 EIF6, FAM83C 823	20	29,565,700	29,565,969	269	28	HM13,	RP3-324017.4	32,999	REM1	29,332
20 33,335,285 33,336,127 842 9 EIF6, FAM83C 823	20	30.409.222	30,409,716	494	12		ASXL1	98		

20	33,793,439	33,793,861	422	16	RBM39,	AL357374.11-1	10,388	AL357374.11-2	27,260
20	34,287,629	34,287,933	304	13	C20orf4,			EPB41L1	3,494
20	34,667,083	34,667,525	442	9	SLA2.	C20orf24	56		
20	34 925 849	34 926 116	267	9		C20orf117	346		
20	36 497 288	36 497 766	478	9		AL 080249 26-1	117		
20	36 508 695	36 509 065	370	9	SNHG11	SNORA71	1 076	SNORA71	4 469
20	36 988 036	36 988 401	365	10			1,070		2 955
20	44 022 202	44 022 771	270	10	TANIOSD,				2,900
20	44,033,393	44,033,771	5/0	9	ZINF 333,				3,524
20	44,033,957	44,034,497	540	10	ZNF335,			FILP	2,798
20	44,075,906	44,076,367	461	10	MMP9,	AL162458.10-1	1,151		
20	40 022 142	49 022 460	226	10	AL102430.10-3,	SNA11	165	116	0.097
20	40,032,143	40,032,409	320	10		COOorf175	400	00	9,907
20	48,781,168	48,781,534	300	15	PARD6B,	C2000175	39,696		00 700
20	49,612,101	49,612,662	561	9		NFATC2	19,436	ATP9A	33,798
20	55,591,417	55,592,064	647	14				PCK1	16,495
20	56,659,475	56,659,925	450	10	STX16,	NPEPL1	41,438	AL050327.6	45,786
20	57,191,371	57,191,710	339	9		C20orf174	7,760		
20	62,050,439	62,050,799	360	9	UCKL1,	UCKL10S	4,652	ZNF512B	7,700
20	62,081,905	62,082,147	242	10	ZNF512B,	SAMD10	466		
20	62,082,457	62,082,958	501	9	ZNF512B,	SAMD10	1,018		
					PRPF6,				
21	10,077,649	10,078,220	571	9	BAGE2,	No non-overlappi	ng genes wit	hin 50,000bp	
21	10,082,420	10,083,154	734	9	BAGE2,	No non-overlappi	ng genes wit	hin 50,000bp	
21	10.086.778	10.087.750	972	9	BAGE2.	No non-overlappi	ng genes wit	hin 50,000bp	
21	10 093 102	10 093 575	473	10	BAGE2	No non-overlappi	na aenes wit	hin 50 000hp	
21	10 116 384	10,000,010	258	12	BAGE2	No non-overlappi	ng genee wit	hin 50,000bp	
21	10,120,900	10,110,042	504	12	DAGEZ,		10 102		44 214
21	10,130,600	10,131,394	1594	13			10,192		44,314
21	10,133,144	10,133,597	453	9		BAGE2	12,536		42,111
21	10,134,518	10,135,638	1,120	11		BAGE2	13,910	VN1R7P	40,070
21	10,139,956	10,140,267	311	10		BAGE2	19,348	VN1R/P	35,441
21	10,140,999	10,141,456	457	9		BAGE2	20,391	VN1R7P	34,252
21	10,141,535	10,142,281	746	10		BAGE2	20,927	VN1R7P	33,427
21	10,142,953	10,143,310	357	10		BAGE2	22,345	VN1R7P	32,398
21	10,150,025	10,150,675	650	10		BAGE2	29,417	VN1R7P	25,033
21	10,151,897	10,152,898	1,001	9		BAGE2	31,289	VN1R7P	22,810
21	10,155,690	10,156,084	394	13		BAGE2	35,082	VN1R7P	19,624
21	10.157.148	10.157.586	438	11		BAGE2	36.540	VN1R7P	18,122
21	10 165 366	10 166 107	741	9				VN1R7P	9 601
21	10 166 346	10 168 621	2 275	12				VN1R7P	7 087
21	10 195 453	10,106,021	662					EIE3S5P	6 676
21	10,100,400	10,100,110	3/8	0		EIE395D	662		0,070
21	10,204,540	10,204,030	505	11			2 050		
21	10,207,045	10,200,240	1 000	11	OTOU	EIF330F	3,959	400040	44 500
21	14,676,805	14,678,068	1,203	9	SICH,			ABCC13	44,599
21	15,498,972	15,499,797	825	9		No non-overlappi	ng genes wit		
21	15,777,221	15,777,708	487	9	004 55			CYCSP42	7,012
21	16,829,223	16,829,567	344	9	C21orf34,	nsa-mir-99a	3,713		
24	17 740 700	17 740 000	E A A	10	02101134,				22.000
21	17,748,736	17,749,280	544	18	CYADD			AP000952.2	22,900
21	17,807,865	17,808,475	610	10	UXADK,			APUUU963.2	4,237
21	17,905,562	17,906,069	507	11	BIG3,			CXADR	17,794
21	17,906,849	17,907,449	600	9	BTG3,			CXADR	19,081
21	24,246,292	24,246,670	378	9		No non-overlappi	ng genes wit	hin 50,000bp	
21	25,901,530	25,901,850	320	24	MRPL39,	JAM2	31,605	hsa-mir-155	33,303
21	26,029,005	26,029,776	771	11	ATP5J, GABPA,			JAM2	17,260
21	26,149,780	26,150,179	399	15	· ·			APP	24,554
21	26,465,251	26,465.822	571	9		APP	248		
21	27.010.095	27.010.480	385	10		No non-overlappi	ng genes wit	hin 50,000bp	
21	27.026.219	27.026.666	447	9		No non-overlappi	ng genes wit	hin 50.000bp	
21	27 129 266	27 129 547	281	10				ADAMTS1	932
21	27 137 771	27 138 184	412	10	ΔΠΔΜΤς1	No non-overlanni	na aenes wit	hin 50 000bp	552
21	27 130 222	27,130,104	710	10	ΔΠΔΜΤς1	No non-overlappi	ng genes wit	hin 50,000bp	
21	27 140 204	27 144 450	050	10			The genes will	iiii 30,000p	
21	27,140,301	27,141,159	000	12		ADAIVITST	/02	hin EQ QQQha	
21	21,259,885	21,260,324	439	14	ADAMI155,	No non-overlappi	ng genes wit		
21	28,811,219	28,811,648	429	10		No non-overlappi	ng genes wit		. == .
21	29,179,061	29,179,901	840	12	HEMK2,			HSPDP7	1,572

21	29,285,912	29,287,479	1,567	9	RNF160,			AF129075.3-1	4,326
21	29,367,674	29,368,246	572	16	CCT8,	C21orf7	3,579		
21	29,593,483	29,594,177	694	9	BACH1,			AF124731.2	11,086
21	29,666,648	29,666,981	333	9				BACH1	10,560
21	30.143.593	30,144,298	705	9	GRIK1.	No non-overlappi	na aenes wit	hin 50.000bp	- ,
21	30,642,582	30,643,012	430	9	KRTAP23-1,			KRTAP13P2	7,692
21	31.392.729	31,393,118	389	10	- ,	UBE3AP2	35.371	TIAM1	19,489
21	31.572.484	31,572,763	279	9	TIAM1.	No non-overlappi	na genes wit	hin 50.000bp	,
21	31.645.654	31,645,993	339	11	TIAM1.	No non-overlappi	na aenes wit	hin 50.000bp	
21	31 837 303	31 837 662	359	9	TIAM1	No non-overlappi	ng genes wit	hin 50 000bp	
21	31 852 817	31 853 448	631	11	TIAM1	No non-overlappi	ng genes wit	hin 50 000bp	
21	31 853 581	31 854 543	962	9		TIAM1	420	iiii 00,0000p	
21	31 882 899	31 883 235	336	9		TIAM1	29 738	FRXW11P1	38 076
21	31 977 187	31 977 592	405	9	SFRS15	HMGN1L2	23 147	SOD1	14 072
21	32 026 406	32 027 692	1 286	9	011(010,	SFRS15	147	0001	14,072
21	32,020,400	32,027,032	/1200	0		011010	147	TDT1D	30.016
21	22,174,007	22,174,473	416	9	C21orf45	MDAD	10 705		21,000
21	32,372,794	32,373,210	251	9	62101145,		12,703	UKDI	31,990
21	32,573,901	32,374,232	351	10	Colorfeo		10 765		
21	32,706,971	32,707,521	550	9	62101163,	URBI	19,765	004 - 1577	0.004
21	32,863,343	32,864,326	983	10	004 (50	0.0.75000		C210ff77	2,094
21	32,906,561	32,907,323	762	12	C210rf59,	OR/E23P	7,907		
21	33,066,032	33,066,440	408	15	C21orf66,	SYNJ1	43,849	C21orf62	21,306
04	00.045.044	00.045.770	10.1	•	C210ff49,	01100	1.004		
21	33,315,314	33,315,778	464	9		OLIG2	4,331	01100	
21	33,349,404	33,349,745	341	9		OLIG1	14,575	OLIG2	26,030
21	33,521,562	33,522,284	722	9		IFNAR2	1,817		
21	33,619,182	33,619,677	495	11	IFNAR1,	AP000297.1	9,070		
21	33,641,997	33,642,275	278	10	IFNAR1,			AP000297.1	12,725
21	33,836,471	33,837,461	990	13	GART, SON,	AP000303.1	23,186	DONSON	32,192
21	33,935,246	33,935,739	493	10	CRYZL1,	ITSN1	837		
21	33,936,155	33,936,544	389	9		ITSN1	32		
21	34,095,794	34,096,074	280	10	ITSN1,	No non-overlappi	ng genes wit	hin 50,000bp	
21	34,112,089	34,112,582	493	10	ITSN1,	No non-overlappi	ng genes wit	hin 50,000bp	
21	34,188,875	34,189,559	684	10				ITSN1	4,427
21	34,209,557	34,210,449	892	9	ATP5O,			AP000313.1-1	2,436
21	34,669,154	34,670,073	919	10	C21orf51,			KCNE2	3,847
21	34,737,557	34,738,043	486	9				KCNE1	2,815
21	34,800,224	34,800,539	315	9	KCNE1,	SNORA11	49,819	DSCR1	10,113
21	34,804,767	34,805,096	329	10	KCNE1,			DSCR1	5,556
21	34,820,777	34,821,392	615	11	DSCR1,	KCNE1	14,334		
21	35,128,826	35,129,207	381	9	RUNX1,	No non-overlappi	ng genes wit	hin 50,000bp	
21	35,169,041	35,169,539	498	9	RUNX1,	No non-overlappi	ng genes wit	hin 50,000bp	
21	35,181,951	35,183,050	1,099	9	RUNX1,	No non-overlappi	ng genes wit	hin 50,000bp	
21	35,318,240	35,318,579	339	11	RUNX1,	AF015262.2	14,183		
21	36,066,843	36,067,205	362	9		RPS20P1	47,575		
21	36,419,628	36,420.059	431	10		AP000689.1-1	4,480		
21	36,429,281	36,430,234	953	11	CBR3,		,	AP000689.1-2	2.081
21	36.449.688	36.450.075	387	10	,	DOPEY2	8.628	CBR3	8.960
21	36,716,234	36,716,589	355	12			2,020	CHAF1B	5.240
21	36 724 218	36 724 658	440	10		ATP5J2LP	40 938	CHAF1B	13 224
21	36 866 119	36 866 518	399	11	CLDN14	No non-overlappi	na aenes wit	hin 50 000hp	
21	36 925 767	36 926 093	326	9	olbhin,	No non-overlappi	ng genes wit	hin 50 000bp	
21	36 997 476	36 997 763	287	a a	SIM2			HICS	47 303
21	37 284 233	37 284 945	712	11			3 212	TILOO	+7,505
21	37 303 077	37 304 372	306	10	DSCR6	HLCS	10 604		14 722
∠ I 21	37 266 020	37 366 101	286	14	PIGP	TTC3	1 017		17,132
∠ I 21	37 366 504	37 369 112	1 840	10		1103	1,017	116	26 700
∠ I 01	37 515 472	37 515 705	1,049	10	1101, 1103,			DSCR3	20,700
21	51,010,473	37,513,795	322	10				SDD out arch	1,003
∠	37 553 000		010	10	030K3,				42,017
04	37,552,889	37,553,205	600	40	08002	No non overland	na aonao wit	hin 50 000hn	
21	37,552,889 37,561,370	37,553,205	622	13	DSCR3,	No non-overlappi	ng genes wit	hin 50,000bp	
21 21	37,552,889 37,561,370 37,633,304	37,553,205 37,561,992 37,633,689	622 385	13	DSCR3,	No non-overlappi DYRK1A	ng genes wit 28,060	hin 50,000bp	40.000
21 21 21	37,552,889 37,561,370 37,633,304 37,857,933	37,553,205 37,561,992 37,633,689 37,858,515	622 385 582	13 9 11	DSCR3,	No non-overlappi DYRK1A	ng genes wit 28,060	hin 50,000bp	48,383
21 21 21 21 21	37,552,889 37,561,370 37,633,304 37,857,933 37,982,671	37,553,205 37,561,992 37,633,689 37,858,515 37,983,050	622 385 582 379	13 9 11 9	DSCR3, KCNJ6,	No non-overlappi DYRK1A No non-overlappi	ng genes wit 28,060 ng genes wit	hin 50,000bp DYRK1A hin 50,000bp	48,383

21	38,768,586	38,769,129	543	9	ERG,	AP001037.1	27,110		
21	39,416,502	39,416,899	397	9		RPL23AP12	4,465		
21	39.475.728	39,476,550	822	9	PSMG1.	AF129408.11	9,826	BRWD1	2.724
21	39.476.863	39.477.927	1.064	9	PSMG1.		-,	BRWD1	1.347
21	39.607.266	39,608,269	1.003	12	BRWD1.			HMGN1	27.848
21	39.644.058	39.644.837	779	9	AF064861.5.	HMGN1	615		
21	39.673.942	39,674,419	477	11	WRB.	AF064861.93	3.080		
21	39 893 047	39 893 470	423		B3GALT5	No non-overlappi	na aenes wit	hin 50 000bp	
	00,000,011	00,000,110	120	0	C21orf88.		ng gonoo mi	inii 00,0000p	-
21	39.947.107	39.947.476	369	10	B3GALT5.	C21orf88	40.489		
21	40.082.100	40.082.639	539	12	IGSF5.	No non-overlappi	na aenes wit	hin 50.000bp	
21	40,137,109	40,137,838	729	9		PCP4	23.379	IGSF5	41.216
21	40 581 725	40 582 070	345	10	DSCAM	No non-overlappi	na aenes wit	hin 50 000bp	,
21	40 670 944	40 671 246	302	9	DSCAM	No non-overlappi	na aenes wit	hin 50 000hp	
21	41 362 725	41 363 238	513	10	200, 111,	No non-overlappi	ng genes wit	hin 50 000bp	
21	41 501 290	41 502 013	723	9	BACE2	AI 773572 1	21 151	iiii 00,0000p	
21	41 971 608	41 972 596	988	g	Di (OLZ,	No non-overlanni	na aenes wit	hin 50 000hn	
21	42 053 033	42 053 550	517	10	RIPK4		ing genes wit	PRDM15	37 904
21	42,053,000	42,053,000	502	11	RIPK4			PRDM15	36 530
21	42,004,422	42,004,024	202	10	PPDM15	AP001610 1-1	12 127		15 048
21	42,102,342	42,103,240	230	10	T INDIMITS,	C2CD2	42,427	02002	15,040
21	42,247,200	42,247,575	512	16	ZNE205	No non ovorlanni	na aonos wit	hin 50 000hn	
21	42,303,079	42,303,391	512	10	ZINI 295,		17 096	1111 30,000bp	
21	42,320,051	42,321,225	5/4	10	40004	ZNF295	17,086	A D004000 4 4	27.005
21	42,551,671	42,552,168	497	10	ABCG1,			AP001622.1-1	37,205
21	42,760,600	42,761,002	402	11				TSGA2	4,666
21	43,014,188	43,014,710	522	9	PDE9A,	No non-overlappi	ng genes wit	nin 50,000bp	00.040
21	43,102,781	43,103,357	5/6	11				WDR4	32,918
21	43,172,453	43,173,010	557	10	WDR4,	NDUEV3	13,437	AP001629.1	36,985
21	43,185,737	43,186,569	832	9	NDUEV3,	WDR4	12,990	AP001629.1	23,426
21	43,186,582	43,187,371	789	9	NDUFV3,	WDR4	13,835	AP001629.1	22,624
21	43,268,429	43,268,951	522	10	PKNOX1,	AP001629.1	49,604		
21	43,670,070	43,670,492	422	9	SIK1,	C21orf125	23,840	C21orf84	35,910
21	43,853,801	43,854,636	835	9	HSF2BP,	KIAA0179	49,224	H2BFS	43,873
21	43,903,678	43,904,345	667	10	HSF2BP,	No non-overlappi	ng genes wit	hin 50,000bp	
				-	KIAA0179,				
21	43,970,144	43,970,442	298	9	PDXK,	C21orf124	7,929		
21	43,972,456	43,973,305	849	9	PDXK,	C21orf124	5,066		
21	44,015,253	44,015,877	624	9				CSTB	2,383
21	44,019,822	44,020,657	835	10	CSTB,	RRP1	13,165	PDXK	13,206
21	44,055,010	44,055,571	561	11	AP001053.1,			RRP1	5,408
21	44,183,316	44,183,666	350	11	AGPAT3,	U6	19,106		
21	44,269,056	44,269,608	552	9	TRAPPC10,	AB001523.1	28,343	H2AFZP	21,048
21	44,583,443	44,584,003	560	9	C21orf2,			AP001062.1	7,385
21	45,062,161	45,062,631	470	10	SUMO3,	UBE2G2	15,995	PTTG1IP	31,297
21	45,116,004	45,116,526	522	10	PTTG1IP,			ITGB2	13,770
21	45,319,399	45,320,105	706	9	ADARB1,	No non-overlappi	ng genes wit	hin 50,000bp	
21	45,381,288	45,381,889	601	9	ADARB1,	No non-overlappi	ng genes wit	hin 50,000bp	
21	45,436,642	45,437,062	420	10	ADARB1,	C21orf89	41,633		
21	45,683,268	45,684,042	774	10	COL18A1,	C21orf123	13,855		
21	45,722,434	45,722,680	246	10	COL18A1,			SLC19A1	17,997
21	45,800,078	45,800,746	668	9		SLC19A1	13,265	COL18A1	42,016
21	46,024,798	46,025,144	346	9	PCBP3,			AL592528.1	47,159
21	46,167,472	46,168,093	621	9	PCBP3,			PCBP3OT	4,193
21	46,217,844	46,218,647	803	9		COL6A1	7,444		
21	46,387,921	46,388,245	324	11	FTCD,			COL6A2	10,732
21	46,529,961	46,531,004	1,043	12	MCM3AP,	PCNT	37,479	C21orf58	10,012
					C21orf57,				
21	46,879,632	46,880,400	768	9	PRMT2,	S100B	30,083	AP000339.4	17,498
21	46,894,372	46,894,750	378	9	PRMT2,			AP000339.4	3,148
22	16,260,595	16,260,889	294	10		AC004019.10	16,855		
22				-	A CO16026 15			MICAL3	4 035
22	16,692,645	16,693,069	424	9	AC016026.15,			NIIO/ LO	.,
22	16,692,645 17,012,459	16,693,069 17,013,133	424 674	9	USP18,			TUBA8	17,961
22 22 22	16,692,645 17,012,459 17,258,302	16,693,069 17,013,133 17,258,709	424 674 407	9 9 20	USP18,	DGCR6	15,070	TUBA8 PRODH	17,961
22 22 22 22	16,692,645 17,012,459 17,258,302 17,260,459	16,693,069 17,013,133 17,258,709 17,260,703	424 674 407 244	9 9 20 12	USP18,	DGCR6 DGCR6	15,070 13,076	TUBA8 PRODH PRODH	17,961 21,586 19,592

22	17,798,159	17,798.485	326	12	HIRA,	MRPL40	1,551	C22orf39	9,924
22	17,799,618	17,800,153	535	12	MRPL40,	HIRA	399	C22orf39	8,256
22	18,478,504	18,479,156	652	10	DGCR8,	RANBP1	5,791	HTF9C	242
22	19,077,857	19,078,562	705	9	USP41, ZNF74,			U6	22,525
22	19,569,773	19,570,548	775	11	SNAP29,	PI4KA	26,703		
22	19,601,179	19,602,148	969	11	CRKL,	AC002470.17-1	28,785	SNAP29	27,070
22	19,666,174	19,667,935	1,761	9	LZTR1,			AIFM3	525
22	19,686,166	19,686,605	439	10	THAP7,			LZTR1	2,841
22	19,786,985	19,787,483	498	10	AP000550.1-2,			AP000550.1-1	12,628
22	20.251.596	20.252.132	536	10	UBE2L3.	RIMBP3C	16.476	AP000557.2-1	11,968
22	20.256.963	20.257.640	677	10	UBE2L3.	RIMBP3C	21.843	AP000557.2-1	17.335
22	20.313.418	20.313.934	516	10	YDJC.	CCDC116	3.152	UBE2L3	6.843
22	20.325.705	20.326.175	470	9	,	SDF2L1	367	CCDC116	4.090
22	20 552 271	20 552 671	400	9		MAPK1	301	0020110	.,
22	20,667,008	20 667 394	386	10	ТОРЗВ			PRAMEI	8 103
22	21 115 773	21 116 245	472			IGI V1-36	91	IGI V5-37	3 402
22	21 192 496	21 193 401	905	11	7NF280B			ZNF280A	4 662
22	22 211 716	22 212 056	340	10	2111 2000,				33 256
22	22,211,710	22,212,000	1 066	13	SMARCB1			MMD11	2 3/1
22	22,430,043	22,439,909	1,000	10		A D000350 10	6 870	CSTT2P	2,541
22	22,020,007	22,023,000	410	20		AD000351 13	2,666	031120	517
22	22,737,370	22,737,709	419	20	CABINI,	AF000331.13	2,000		
22	22,072,040	22,073,090	450	12	CADINT,	503D2	34,340		29.016
22	23,201,400	23,202,127	009	13	SNPPD3	6611	27,591	UFDI	20,910
22	23 677 030	23 678 500	561	10	SINITI DS,		5 277		
22	23,077,939	23,070,500	353	10			7.640		
22	23,000,311	23,000,004	094	0	CTA 221C0 5		7,049	hin 50 000hn	
22	23,030,304	23,037,340	352	9	CTA-22109.5,		ng genes wit		3 050
22	23,901,700	23,902,130	410	9		No non overlanni	na aonoo wit	bin 50 000hn	3,950
22	24,744,120	24,744,009	419	10		No non-overlappi	ng genes wit	hin 50,000bp	
22	24,943,492	24,943,796	500	10	SEZOL,	No non-ovenappi	ng genes wit		20.005
22	25,086,215	25,086,716	501	10	SEZOL,			ALU/8460.6	29,905
22	25,384,744	25,385,288	544	12				299774.1	8,308
22	20,107,000	20,100,243	200	9	0000117		ng genes wit		14.961
22	27,490,304	27,490,702	390	11		UTERZ	30,342		14,001
22	27,000,301	27,000,020	440	11	KREIVIEN I,		205	06	20,273
22	27,931,175	27,931,506	331	10			395		0.400
22	28,028,647	28,029,007	360	11		GAS2L1	3,990	EWSRI	2,132
22	28,196,017	28,196,399	382	10	10000		9,820		
22	28,563,717	28,564,045	328	9	ASCC2,	ZMA15	19,627	10000011	10.000
22	28,718,948	28,719,352	404	9	MTMR3,			AC003681.1	48,663
22	29,013,265	29,013,995	730	12	RP1-130H16.13,			TBC1D10A	3,987
22	29,014,035	29,014,655	620	9	RP1-130H16.13,			TBC1D10A	3,327
22	29,149,667	29,150,532	865	11	SEC14L2,	MTP18	1,188	06	2,530
22	20.200.400	00 004 074	570	10	AC004832.3-4,		710	TONO	7 454
22	29,300,498	29,301,074	5/6	10	CMTN	SLUSSE4	/19		7,451
22	29,815,168	29,815,602	434	9	SIVEEN,	RP3-412A9.12	23,401	SELIVI	15,156
22	29,833,636	29,834,154	518	9	SELIVI,	RP3-412A9.12	4,849	SIVI I IN	3,027
22	30,073,131	30,073,714	583	9		PAIZI	882		
22	30,215,722	30,216,356	634	10	EIF4ENIF1,	SFIL	5,905		05.007
22	31,059,824	31,060,206	382	9	000	KFPL3	20,666	KFPL3S	25,687
22	31,137,978	31,138,467	489	9	02201128,	770070 4	00 -	BPIL2	1,367
22	31,573,113	31,573,584	4/1	9	SYN3, HMP3,	Z73979.1	32,741	298256.1	12,422
22	32,647,198	32,647,656	458	11		LARGE	788		
22	33,983,226	33,983,826	600	10	HMGXB4,	TOM1	42,035		
22	34,025,145	34,025,690	545	9		IOM1	171	HMGXB4	3,346
22	34,247,526	34,247,903	377	10		RP4-569D19.5	17,947		
22	34,561,986	34,562,323	337	10	RBM9, RPL41,	No non-overlappi	ng genes wit	hin 50,000bp	
22	34,849,820	34,850,215	395	10		Z95114.19-1	3,895		
22	34,947,775	34,948,121	346	9	APOL3,			APOL2	4,080
22	35,057,320	35,057,757	437	11	MYH9,	No non-overlappi	ng genes wit	hin 50,000bp	
22	35,180,876	35,181,209	333	10		WI2-80423F1.1	33,241	TXN2	11,830
22	35,277,966	35,278,318	352	9		AL022313.1	14,369	CACNG2	11,732
22	35,507,978	35,508,599	621	9		RABL4	5,863		
22	35,582,161	35,582,857	696	12		NCF4	4,119		
						i da se		i da se	

22	35 924 938	35 926 136	1 198	11				SSTR3	5 962
22	36,002,782	36,003,166	394	0					780
22	30,092,782	30,093,100	074	9			1 0 0 0	LNNC02	700
22	36,158,314	36,158,985	671	9		LRRC62	4,863		
22	36,407,525	36,407,917	392	10		NOL12	4,373	LGALS1	1,772
22	36,411,991	36,412,402	411	13	NOL12,			LGALS1	6,238
22	36,570,263	36,570,805	542	11	ANKRD54, hsa- mir-658,	EIF3EIP	4,469	hsa-mir-659	2,826
22	36,725,469	36,726,252	783	9	POLR2F, AI 031587 3	SOX10	12,094	RP5-1039K5.16	31,866
22	37 015 320	37 015 850	530	Q				CSNK1E	794
22	27 197 202	27 107 771	270	0		KONIA	6 242	CONTRACT	704
22	37,107,392	37,107,771	379	9	TON 41 400	KCNJ4	0,243	10004	0.400
22	37,407,516	37,408,150	634	12	TOIVIIVIZZ,	1000		JO2D1	3,480
22	37,426,441	37,427,616	1,175	9		JOSD1	36		
22	37,430,811	37,431,210	399	11		GTPBP1	543		
22	37,431,307	37,432,015	708	13	GTPBP1,	JOSD1	4,902		
22	37,570,110	37,570,798	688	9		NPTXR	147		
22	37,649,717	37,650,150	433	10		APOBEC3A	28,552		
22	37,650,439	37.650.755	316	9		APOBEC3A	27.947		
22	37 659 830	37 660 378	548	9		APOBEC3A	18 324		
22	29 042 121	29 042 629	517	0			10,024		2 262
22	30,042,121	30,042,030	317	9	RFLJ,	51100030	003	SNURD43	2,303
22	38,125,319	38,126,033	/14	10	MAP3K/IP1,			SYNGR1	13,782
22	38,246,080	38,246,687	607	10	ATF4,			SMCR7L	2,001
22	38,248,973	38,249,666	693	9				ATF4	336
22	38,254,622	38,255,545	923	9	RPS19BP1,			ATF4	5,985
22	38,258,503	38,259,102	599	13	RPS19BP1.			ATF4	9,866
22	38 348 763	38 349 462	699	12	CACNA1I	AL 022319 2	3 090		-,
22	20 522 542	20 522 212	760	0		No non overlenni		hin 50 000hn	
22	30,332,343	30,333,312	709	9					
22	38,656,334	38,656,943	609	9	GRAP2,	ENTHD1	36,594		
22	38,902,949	38,903,300	351	9	INRC6B,	No non-overlappi	ng genes wit	hin 50,000bp	
22	39,362,246	39,363,436	1,190	9	MKL1,	Z86090.10-1	37,126	Z86090.10-2	17,997
22	39,377,499	39,378,321	822	10		MKL1	14,848	CTA-229A8.6	21,118
22	40,170,129	40,171,050	921	11	TOB2,	ACO2	24,025	PHF5A	14,618
22	40,172,669	40.173.137	468	13	TOB2.	ACO2	21,938	PHF5A	12,531
22	40 174 204	40 174 739	535	15	- ,	TOB2	1 231		,
22	40,250,330	40,250,714	375	11		TOBE	1,201	ACO2	4 400
22	40,259,559	40,259,714	575	11			4 555	ACOZ	4,400
22	40,414,432	40,414,938	506	11	NHP2L1,	CTA-216E10.9	1,555	06	8,665
22	40,816,257	40,817,110	853	9	NDUFA6,			C22orf32	6,024
22	41,341,259	41,341,732	473	15	U12,	POLDIP3	353	CYB5R3	3,033
22	41,690,495	41,691,688	1,193	9	PACSIN2,	No non-overlappi	ng genes wit	hin 50,000bp	
22	41,741,891	41,742,271	380	9		PACSIN2	796		
22	41.876.792	41.877.414	622	9		TSPO	65		
22	41 989 810	41 990 754	944	Q	SCUBE1	No non-overlanni	na aenes wit	hin 50 000hn	
22	43 400 015	43 401 202	377	15	COODE I,		25 087		
22	43,400,913	43,401,292	511	10		RF 1-10109.2	25,007		
22	43,823,231	43,823,812	581	9		FUF21R	38,758		0 1 0 0 -
22	44,092,278	44,092,664	386	9	FAM118A,			UPK3A	21,860
22	44,555,926	44,556,342	416	10	A I ⁻ XN10,		<u> </u>	RP1-37M3.8	10,620
22	44,750,816	44,751,189	373	9	WNT7B,	No non-overlappi	ng genes wit	hin 50,000bp	
22	44,846,624	44,847,439	815	9	RP4- 695O20B.10,	C22orf26	17,936		
22	45,024.900	45,025,188	288	10		C22orf40	43	PKDREJ	5.036
22	45,577 874	45,578 199	325	10	TBC1D22A	Z97351.1	44 268		- ,
22	48 281 710	48 282 046	327	 Q	· - · - · -· · ·,	No non-overlappi	na aenes wit	hin 50 000hn	
22	18 710 6/4	18 710 042	2021	10			ing genes wit		3 452
22	40,710,044	40,710,942	290	10					3,452
22	49,203,951	49,204,332	381	9	5AP52,			SBF1	27,718
22	49,405,688	49,406,402	714	9				ARSA	3,914
22	49,515,264	49,515,660	396	9	SHANK3,	ACR	7,858		
Х	139,778	140,071	293	10	PLCXD1,	BX000483.7	18,409	GTPBP6	19,954
Х	204,409	205,156	747	9				PPP2R3B	9.814
X	267 552	268 351	799	20	PPP2R3B	No non-overlappi	na aenes wit	hin 50 000hn	-,
X	275 506	275 885	370	20		PPP2R3R	7 870		
	210,000	210,000	260	9		No non overlage:	1,079	hin 50 000hn	
X	004,407	004,769	362	9		No non-overlappi	ng genes wit	qa000,00 min	
Х	1,325,662	1,326,277	615	9		CSF2RA	21,416		
Х	1,465,161	1,465,496	335	9	SLC25A6,			IL3RA	3,580
Х	1,497,063	1,497,593	530	10	ASMTL,	SLC25A6	26,070	IL3RA	35,482
Х	1,630,040	1,630,376	336	11		P2RY8	14,040		

Х	1,634,237	1,634,621	384	9		P2RY8	18,237		
Х	1,878,721	1,879,081	360	10		No non-overlappi	ng genes wit	hin 50,000bp	
Х	2,605,564	2,606,191	627	9		CD99	13,037		
Х	2,747,621	2,748,442	821	9		AC138085.2	8,285	XG	3,666
Х	4,833,837	4,834,159	322	9		No non-overlappi	ng genes wit	hin 50,000bp	
Х	12,099,641	12,100,304	663	9	FRMPD4,			Y_RNA	22,363
Х	12,699,325	12,699,835	510	10		PRPS2	19,579	FRMPD4	46,762
Х	12,874,790	12,875,346	556	12		TMSB4X	27,804	TLR8	23,581
Х	12,878,703	12,879,323	620	9		TMSB4X	23,827	TLR8	27,494
Х	13,289,397	13,290,202	805	9		ATXN3L	41,405	RP11-142G7.1	16,573
Х	13,390,953	13,391,303	350	9		No non-overlappi	ng genes wit	hin 50,000bp	
Х	13,581,240	13,581,723	483	9	TCEANC,	RAB9A	35,539	EGFL6	19,626
Х	13,618,818	13,619,194	376	10	RAB9A,	OFD1	43,591	TRAPPC2	21,088
Х	13,621,391	13,621,877	486	9	RAB9A,	OFD1	40,908	TRAPPC2	18,405
х	13,662,223	13,663,196	973	11	TRAPPC2, OFD1,			RAB9A	24,542
Х	13,862,119	13,863,038	919	9	GPM6B,	No non-overlappi	ng genes wit	hin 50,000bp	
Х	13,950,134	13,950,796	662	9	GEMIN8,	No non-overlappi	ng genes wit	hin 50,000bp	
Х	14,527,051	14,527,445	394	11	GLRA2,	No non-overlappi	ng genes wit	hin 50,000bp	
Х	16,647,140	16,647,955	815	9	SYAP1,	CTPS2	6,160		
Х	17,693,251	17,693,701	450	9				RP3-389A20.2	3,345
Х	18,464,077	18,464,436	359	10	CDKL5, RP1-	No non-overlappi	ng genes wit	hin 50,000bp	
					245G19.2,				
Х	18,602,822	18,603,166	344	14		RS1	2,672		
Х	21,666,574	21,666,939	365	10	SMPX,	No non-overlappi	ng genes wit	hin 50,000bp	
Х	21,767,382	21,768,032	650	13	MBTPS2,	YY2	15,994		
Х	21,900,900	21,901,231	331	10	SMS,	No non-overlappi	ng genes wit	hin 50,000bp	
Х	23,322,296	23,322,686	390	9	PTCHD1,			RP11-654E17.2	42,808
Х	23,426,524	23,426,828	304	10				AC096507.7	8,421
Х	23,836,790	23,837,129	339	10	CXorf58,	APOO	832		
Х	23,982,119	23,983,111	992	11	EIF2S3,	KLHL15	26,895		
Х	24,009,583	24,010,401	818	9				EIF2S3	2,737
Х	24,052,615	24,053,142	527	11		SNORA68	8,082		
Х	24,079,385	24,079,771	386	9	ZFX,			SNORA68	18,030
Х	24,117,178	24,117,487	309	9	ZFX,	No non-overlappi	ng genes wit	hin 50,000bp	
Х	25,037,286	25,037,663	377	9		AC002504.1-2	48,309		
Х	31,054,342	31,054,725	383	9	DMD,	No non-overlappi	ng genes wit	hin 50,000bp	
X	31,259,747	31,260,414	667	9	DMD,	No non-overlappi	ng genes wit	hin 50,000bp	
X	32,188,982	32,189,500	518	9	DMD,	No non-overlappi	ng genes wit	hin 50,000bp	
X	34,238,390	34,238,703	313	10		No non-overlappi	ng genes wit	hin 50,000bp	
х	37,062,951	37,063,288	337	9		PRRG1	30,179		26,551
v	27 571 000	27 572 444	500	10					0 5 1 2
×	37,371,909	37,372,441	202	10	SDDV				0,010
^ V	20 201 442	20 201 001	400	9	SRFA,	No non overlanni	na aonoo wit	bin E0 000hn	22,019
^ Y	40 500 920	40 600 155	208	10			19 genes Wil	ΔC002474 3 2	10 600
~	40,000,029	40,000,100	501	10			23,070	RD11_460E10 4	6 465
^ V	40,020,412	40,020,913	100	11			919	DD11_/60E10.1	0,400 6 000
^ Y	40,020,930	40,023,301	401 201	9			4/1	RP11_/60E10.1	15 002
X	40 851 052	40 852 252	1 305	9	USP9X			RP11_460F10 1	30.002
X	40,001,900	40,000,200	3/0	9		No non-overlanni	na aenes wit	hin 50 000hn	30,000
X	41 077 153	41 077 436	283	3 0	001 97,		159	IIII 30,0000p	
X	41 077 559	41 079 108	1 549	11		RP13-13A3 1	10 251	SRP euk arch	10 671
X	41 001 454	41 001 820	366	Q		SRP euk arch	1 381		10,071
X	41 124 793	41 125 126	333	9	DDAJA,	SRP euk arch	34 720	22200	30 327
X	41 365 346	41 365 932	586	9	CASK	No non-overlanni	na aenes wit	bin 50 000bn	50,521
X	44 419 416	44 419 919	503	10				AI 136137 15	25 507
X	44.659.681	44.659.980	299	10	UTX.	No non-overlappi	na genes wit	hin 50.000bp	_0,001
X	45 568 960	45 569 257	297	<u>.0</u>	,	No non-overlappi	ng genes wit	hin 50,000bp	
X	46.471.795	46.472.215	420		SLC9A7.	AL512633.6	1.598	,p	
Х	46,937.616	46,938.406	790	13	UBA1,		.,	RBM10	6.460
X	46.976.921	46.977.276	355	12	USP11.			PCTK1	2.585
Х	47,105.926	47,106.438	512	9	,	ZNF157	8.505		_,000
X	47.402.716	47.403.836	1.120	11	UXT.	ELK1	7.752		
Х	48,920,816	48,921,361	545	9	PRICKLE3,		,	PLP2	2,437

Х	48,929,378	48,929,908	530	9	PRICKLE3,			SYP	1,293
Х	49,050,837	49,051,230	393	10	GAGE13,	GAGE2E	33,297	PPP1R3F	19,336
					GAGE10,				
					GAGE12J,				
Х	49,629,252	49,629,686	434	9	CLCN5,	hsa-mir-532	24,808		
Х	52,980,270	52,980,662	392	11				FAM156A	12,525
Х	53,271,004	53,271,606	602	10	JARID1C,			IQSEC2	7,178
Х	53,300,416	53,300,774	358	11	IQSEC2,	JARID1C	29,087		
Х	53,333,313	53,334,082	769	9	IQSEC2,	RP6-29D12.4	34,830	RP6-29D12.3	49,632
Х	53,363,206	53,363,582	376	9	IQSEC2,	RP6-29D12.4	5,330		
Х	53,437,727	53,438,201	474	9	SMC1A,	RIBC1	28,374	HSD17B10	36,730
Х	53,465,515	53,467,162	1,647	14	SMC1A, RIBC1,			HSD17B10	7,769
Х	53,727,699	53,728,256	557	12	HUWE1,	No non-overlappi	ng genes wit	hin 50,000bp	
Х	54,483,551	54,484,132	581	9	TSR2,			FGD1	4,482
Х	54,487,838	54,488,184	346	9	TSR2,			FGD1	430
Х	54,850,501	54,851,519	1,018	9	MAGED2,	SNORA11	6,009		
Х	55,189,096	55,189,501	405	10	FAM104B,	AL590240.5-1	26,374	RP11-266l3.5	31,864
Х	55,765,339	55,765,793	454	9	RRAGB,	No non-overlappi	ng genes wit	hin 50,000bp	
Х	61,980,308	61,981,158	850	9	RP1-267M5.2,	BX119964.4-1	5,659	BX119964.4-5	388
Х	62,046,306	62,046,725	419	9		RP1-267M5.3	25,269		
Х	62.219.263	62.219.631	368	9		No non-overlappi	na aenes wit	hin 50.000bp	
Х	63.398.251	63.398.703	452	9			00	MTMR8	5.984
Х	63,910,650	63.910.856	206	10		RP13-100A9.2	46.997		- ,
Х	64,498,452	64,498,813	361	11		RP11-151G12.2	4,300		
X	64 706 437	64 706 897	460	9		RP3-475B7 3	17 411		
X	64,731,897	64.732.622	725	9		RP3-475B7.3	42.871		
X	65 489 998	65 490 572	574	9			,	RP13-238N7 2	6 761
X	65 775 770	65 776 149	379	12		FDA2R	162		0,101
X	65 865 350	65 865 930	580	9		No non-overlanni	na aenes wit	hin 50 000hn	
X	66 414 635	66 415 102	467	9		No non-overlappi	ng genes wit	hin 50,000bp	
X	67 276 107	67 276 534	337	0			ng genes wit	RP11_516A11 3	6 104
X	67 378 056	67 378 307	3/1	0		No non-overlanni	na aenes wit	hin 50 000hn	0,104
X	67 553 112	67 553 879	767	0		AL 672138 10-1	36 967	IIII 30,0000p	
×	67 508 830	67 500 280	450	0	OF TINT,	AL072130.10-1	30,307	AL 672138 10 1	7 001
×	67 627 123	67 627 300	267	10			9 221	AL072130.10-1	7,301
X	67 849 244	67 849 848	604	10	STAPD8	No non-overlanni	0,221 na aenes wit	hin 50 000hn	
X	67 890 592	67 890 888	206	10	STANDO,	RP13-178D16 1	17 002		28 100
X	67 940 107	67 940 722	615	10		FENR1	24 834	AL 353587 11	18 470
X	67 965 0/3	67 965 772	720	10	EENB1		24,004	AL353587.11	10,470
×	67 068 142	67 068 620	123	10				AL353507.11	46,505
X	68 243 834	68 244 839	1 005	10		No non-overlanni	na aenes wit	hin 50 000hn	+0,505
×	68 300 775	68 301 215	1,005	0			0 477	nin 30,000bp	
~	69 224 201	69 224 655	254	9	CVorfe2	RF 13-331122.2	3,477	DD12 55U22 2	12 016
~	69 247 909	69 249 242	304	9	CA01102,	FJAI	22,212	CVorfe2	1 406
~	69 250 570	69 251 162	440 502	10				CX01102	1,400
	68 366 005	68 267 400	593	9				CXorf62	4,078
	68 461 270	68 461 004	504	9		No non ovorlanni		6701102 hip 50.000hp	20,493
^ V	60.067.540	60.067.000	220	40	EDA	No non-overlappi	ng genes wit		E 004
^	09,007,540	09,007,920	380	12	LDA,			237E13 P 2	5,ŏ21
Y	60 166 000	60 167 420	101	0	EDA			ΔI 1581/1 1/ F	7 401
~ ~	60 260 507	60 270 044	421	9		ICBP1	n	AL 100141.14-0	1,491
	60 356 000	60 357 335	220	10			2	AL 357752 10 1	1 950
	09,300,000	09,337,223	339	13	0000			AL337732.19-1	1,300
	09,000,023	60,500,927	404	9					3,002
X	09,501,840	69,562,536	690	9	GDPDZ,		00.040		4,385
X	70,204,855	70,205,249	394	31	SNATZ,	KP5-1091N2.2	22,810		35,313
X	70,265,290	70,266,689	1,399	9	IVIED 12,	INLGIN3	14,747		25,180
X	70,288,339	70,288,829	490	9	NLGN3,	7.4.1/1.40	10	MED12	9,311
X	70,391,734	70,392,551	817	9	41 500700 0 0	ZMYM3	13	TAF 4	4
X	70,612,290	70,612,641	351	10	AL590763.2-2,	AL590763.2-1	16,246		11,265
X	70,651,235	70,651,915	680	9	AL590763.2-2,	UGI	17,743	AL590763.5	12,474
V	70.000 700	70.000.000	4 050	4.0	AL590763.2-1,	41 500700 5	4 000	AL 500700 0 1	4 000
X	10,668,708	70,669,960	1,252	13	AL590763.2-2,	AL590763.5	1,908	AL590763.2-1	1,608
×	70 006 119	70 006 645	FUZ	0	001,			DD11 402D6 6	10 520
	71 127 205	71 107 700	307	9			24 700	NF 11-40200	10,539
X I	11,131,385	11,131,182	397	10	1	00	34,730		

Х	71,158,286	71,159,314	1,028	10		RPS26P11	21,670		
Х	71,160,004	71,160,369	365	9		RPS26P11	20,615		
Х	71,166,569	71,166,919	350	12		RPS26P11	14,065		
Х	71.250.867	71.251.432	565	9		NHSL2	18,792	BX119917.9-2	37.479
Х	71,279,022	71,279,790	768	9				NHSL2	1,085
Х	71,412,892	71,414,021	1,129	14	RPS4X,	ERCC6L	37,290	CITED1	24,201
Х	71,443,383	71,444,026	643	12	CITED1.	RPS4X	29.517	HDAC8	22.065
Х	71,496,014	71,496,445	431	9	HDAC8.	_	- , -	U2	17.109
Х	71,505,444	71,505,858	414	9	HDAC8.			U2	7.696
х	71 682 066	71 682 471	405	10	HDAC8			PHKA1	32 918
X	72 536 340	72 536 758	418			U6	2 142		0_,010
X	72 955 707	72 956 216	509	11			_,	RP11-108A15.2	48 724
X	72 958 455	72 959 027	572	11		No non-overlappi	na aenes wit	hin 50 000bp	
X	72 965 371	72 965 857	486			EXYD8	45 741		
X	72 987 424	72 988 599	1 175	16		EXYD8	22 999		
X	72 989 016	72 989 450	434	10		EXYD8	22,000		
X	72 001 085	72 992 903	918	10		EXYD8	18 695		
X	73,006,513	73,007,008	495	9		FXYD8	4 590		
X	73,000,010	73,007,000	417	31		No non-overlanni	na aenes wit	hin 50 000hn	
X	73,000,000	73,001,000	417	0		RD13_36C14 2	15 750	IIII 30,0000p	
X	73,131,001	73 105 620	550	9		AI 130/00 0	7 023		
×	73,195,070	73,195,020	561	0		DD13 204A15 4	2 797	DD13 204A15 2	0.706
Ŷ	73 375 200	73 375 601	262	10		11 10-204A10.4	2,101	AC00/386 1 1	3,100
^ V	73,373,320	73,373,091	503	10	SI C1642	AL 120001 15 2	22 040	AC004360.1-1	3,470
^ V	73,337,721	73,000,000	242	0	SLCTOAZ,	AL 130091.15-2	23,640	AC004073.1-1	19,001
	73,370,000	73,371,220	342	9	SLCTOAZ,	AL130091.13-2	37,005	AC004073.1-2	10,923
X	73,601,378	73,601,712	334	12	SLC16AZ,		00 770	AC004073.4	7,803
X	73,750,882	73,751,513	031	10	RLINI,	CTD-2530H13.2	30,776	AL513007.5	27,172
X	73,794,793	73,795,082	289	9		06	21,531		00 700
X	74,439,279	74,439,596	317	10	UPRI,		0.440	RP11-311P8.2	23,736
X	75,560,762	75,561,103	341	9		MAGEE1	3,418		
X	75,691,692	75,692,201	509	9		No non-overlappi	ng genes wit	nin 50,000bp	
X	76,440,156	76,440,487	331	11	4701	No non-overlappi	ng genes wit		11001
X	76,884,876	76,885,573	697	9	ATRX,	75.400		RP3-34606.2	14,664
X	79,125,162	79,125,673	511	9		TBX22	31,238		
X	79,326,088	79,326,436	348	9		No non-overlappi	ng genes wit	hin 50,000bp	10.000
X	80,519,258	80,519,990	732	9		RP13-52K8.1	31,103	RP11-346E8.1	12,933
х	80,699,226	80,699,759	533	9		XXyac-	42,468		
V	00 707 004	00 700 404	500	0		TRIZUBD.I		hin 50 000hm	
	00,797,001	00,790,101	320	9		No non-overlappi	ng genes wit	hin 50,000bp	
	01,423,231	01,425,501	330	10		No non-overlappi	ng genes wit	hin 50,000bp	
	02,197,711	02,197,990	2/9	11			ng genes wit	nin 50,000p	
	02,735,947	02,730,310	303	9		RP 1-223D 17.1	33,97 I	hin EQ QQQhn	
	02,000,300	02,000,000	440	10		No non-ovenappi	ng genes wit		20.020
^ V	03,030,221	00,000,000	385	9			05 000	GILGI	∠9,939
X	83,8/1,425	04,700,540	313	10		KP1-30P20.1	25,062	hin EQ QQQka	
X	84,762,164	84,762,540	3/6	9	DACUS	No non-overlappi	ng genes wit	hin 50,000bp	
X	85,964,489	85,964,860	3/1	9	DACHZ,	No non-overlappi	ng genes wit	hin 50,000bp	
×		00,008,541	524	9		No non-overlappi	ng genes wit	hin 50,000bp	
×	00,725,259	00,120,039	380	10	rl⊓l4,	No non-overlappi	ng genes wit		2 000
×	00,040,529	00,041,000	4//	10		No pop overlage:		203010.1	3,993
X	80,970,083	80,977,548	208	9		No non-overlappi	ng genes wit	nin 50,000bp	
×	00,313,809	00,314,245	3/0	11		no non-overiappi	ng genes wit		14.055
×	92,588,209	92,500,044	435	9			10.070	ALU23280.1	14,255
× ×	95,126,941	95,127,342	401	9		RPD-901K14.1	10,972	hin 50 000km	
× ×	90,738,992	90,739,345	353	9	DIAPTIZ,	No non-overlappi	ng genes wit	hin 50,000bp	
×	91,049,908	91,000,007	039	9		No non-overlappi	ng genes wit	hin 50,000bp	
×	99,543,552	99,543,960	408	9		TO HOM-overlappi	ng genes wit		22.000
× ×	99,791,849	99,792,181	1 070	9	SKPAZ,	ISPANO	13,399		23,963
× ×	100,239,439	100,240,809	1,3/0	9		סדע	4 400		1,430
X	100,532,274	100,532,972	098	12	RPL30A,	DIK	4,436		6,463
X	100,549,149	100,550,360	1,211	9	RPL30A, GLA,		21,311	ALU35422.12-2	18,677
X	102,005,362	102,005,638	2/6	10		No non-overlappi	ng genes wit		40.054
X	102,092,835	102,093,311	4/6	10				KAB4UAL	12,951
Х	102,356,501	102,356,996	495	9	вех4,	KP4-635G19.1	8,018		
Х	102,512,142	102,512,527	385	9		NGFRAP1	5,383		
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Х	102,770,086	102,770,710	624	9	TCEAL1,			TCEAL3	18,575
Х	103,267,687	103,268,022	335	9	MCART6,	CXorf39	29,935	ZCCHC18	21,017
Х	103,320,907	103,321,189	282	10	CXorf39,	MCART6	32,543		
Х	103,850,841	103,851,233	392	9	IL1RAPL2,	No non-overlappi	ng genes wit	hin 50,000bp	
Х	105,395,440	105,395,794	354	11		No non-overlappi	ng genes wit	hin 50,000bp	
Х	105,667,830	105,668,325	495	9				RP13-483F6.1	24,335
Х	106,487,183	106,487,551	368	9		AC004081.1	4,455		
Х	106,807,111	106,807,623	512	9				PRPS1	26,202
Х	106,859,993	106,860,291	298	12	DIP,	No non-overlappi	ng genes wit	hin 50,000bp	
Х	108,184,068	108,184,624	556	66	AL928646.3,	No non-overlappi	ng genes wit	hin 50,000bp	
					CTD-2328D6.1,				
Х	108,519,833	108,520,250	417	10	GUCY2F,			AL034403.19	47,323
Х	108,604,970	108,605,292	322	9	GUCY2F,	No non-overlappi	ng genes wit	hin 50,000bp	
Х	108,970,135	108,970,746	611	9		AC003013.1	12,453		
Х	109,101,791	109,102,216	425	9		TMEM164	30,763		
Х	109,153,750	109,154,427	677	9	TMEM164,	hsa-mir-652	30,786		
Х	111,443,170	111,443,710	540	10		No non-overlappi	ng genes wit	hin 50,000bp	
Х	111,809,834	111,810,126	292	10	LHFPL1,	AL034450.1	9,679		
Х	114,425,155	114,425,464	309	9		LUZP4	5,084		
Х	114,650,240	114,650,628	388	9		No non-overlappi	ng genes wit	hin 50,000bp	
Х	114,955,154	114,955,503	349	9		No non-overlappi	ng genes wit	hin 50,000bp	
Х	115,814,014	115,814,434	420	9		RP11-232D9.1	47,141		
Х	116,824,146	116,824,490	344	9		No non-overlappi	ng genes wit	hin 50,000bp	
Х	116,963,208	116,963,749	541	9	KLHL13,	Y_RNA	30,872		
Х	117,514,482	117,514,875	393	10	DOCK11,			WDR44	39,505
Х	118,439,029	118,439,797	768	9	SLC25A43,	U1	1,936		
Х	118,606,432	118,606,746	314	10	NKRF,			UBE2A	4,023
Х	118,695,609	118,696,095	486	9	6-Sep,	hsa-mir-766	30,770		
Х	118,870,610	118,871,059	449	9	UPF3B.	NDUFA1	18,703	RNF113A	17,407
Х	119,503,752	119,504,117	365	10	,	LAMP2	16.563	CUL4B	38.359
Х	119,568,283	119.568.587	304	9	CUL4B.			AC002476.1	5.983
Х	121,055,371	121,056,101	730	9		No non-overlappi	ng genes wit	hin 50,000bp	
Х	121,411,061	121,411,355	294	9			3.3	AL513487.3	21.904
Х	122,136,919	122,137,239	320	9		GRIA3	8.448		
Х	122,465,286	122,465,638	352	9		AL590139.11	10.367	GRIA3	12,839
Х	126,205,083	126.205.665	582	9		No non-overlappi	na aenes wit	hin 50.000bp	,
X	126,402,657	126,403,047	390	9				RP3-428A13.1	48,468
X	126.610.995	126.611.372	377	11		No non-overlappi	na aenes wit	hin 50.000bp	,
X	127,933,346	127.933.804	458	11		No non-overlapping genes within 50.000bp			
Х	128.097.451	128.097.986	535	9		No non-overlapping genes within 50.000bp			
X	128,568,580	128,569,134	554	10				AL022162.1	14.371
X	128 666 565	128 667 103	538	.0		XPNPEP2	33 524		,0
X	128 668 919	128 669 258	339	9		XPNPFP2	31 369		
X	128 892 936	128 893 255	319	q			0.,000	UTP14A	1 528
X	128 943 838	128 944 161	323	<u>0</u>		BCORI 1	189		1,020
X	129 012 882	129 013 447	565	9	BCORI 1			ELF4	13 092
X	129 592 698	129 593 296	598	9	ENOX2	RP5-875H3 2	14 082		10,002
X	129 878 259	129 878 839	580	q	,	FNOX2	13 370		
x	130 505 861	130 506 225	364	a 3	OR13H1	RP11-324A3 1	18 168		
X	130 689 944	130 691 493	1 549	9		No non-overlappi	na aenes wit	hin 50 000hn	
X	130 745 116	130 745 561	445	14			ng genes wit	AI 121572 14	11 799
X	130 754 692	130 755 232	540	11				ΔI 121572 14	2 128
X	130 774 889	130 776 119	1 230	9		RP1-197017 2	9 4 3 9	AL121012.14	2,120
X	130 783 865	130 784 640	78/	9		RP1-197017.2	18 415		
X	130 702 373	130 702 807	524	12		RP1-197017.2	26 022		
x	130 085 670	130 086 089	<u>المح</u> 12	13	RP6-213H10 1	No non-overlappi	na aenes wit	hin 50 000hn	
× ×	131 0/6 225	131 0/6 600	365	9	FRMD7		ng genes wit	RP6-213H10 1	8 5 9 2
Ŷ	131 500 260	131 500 606	200	9	HSAST2	116	10 100	110-2131119.1	0,000
^ Y	131 502 /22	131 50/ 000	520	9	HS6ST2,	No non-ovorlanni	40,430	hin 50 000hn	
\sim	131 709 670	131 700 250	670	9	H96972,	No non-overlapping genes within 50,000bp			
~	131,700,079	131,708,308	019	9	1130312, LICECTO	No non-overlapping genes within 50,000bp			
^ V	122 072 040	122 074 420	344	9	CDC2	No non-overlappi	ng genes wit	hin 50,000bp	
^ V	132,073,010	132,074,130	312	9			14 470		20.007
^	133,000,208	133,001,048	040	9	FLAUI,	NF 11-300B3.4	11,478	NF 11-30089.3	JU,88/

Х	133,647,283	133,647,739	456	10				AL672032.6-1	8,316
Х	133,652,881	133,653,241	360	9		PLAC1	32,702	AL672032.6-1	13,914
Х	134,446,060	134.446.564	504	9		DDX26B	35.686	RP11-265D19.5	45.835
X	134 954 760	134 955 136	376	9	SI C9A6	AI 732579 5	32 532		,
X	134 974 677	134 974 990	313	10	0200.10,	AL 732579.5	12 678	SI C9A6	17 585
X	135 390 975	135 391 344	369	9		BRS3	6 4 4 7	0200/10	11,000
X	135 425 869	135 426 383	514	9		BIXOU	0,111	ΗΤΔΤΩΕ1	3 734
X	135 932 560	135 033 368	808	9				PP11_308D16.2	1 256
×	136 104 003	136 104 208	205	10		No non ovorlanni	na aonos wit	hin 50 000hn	1,230
×	130,104,003	130,104,290	290	10			ng genes wit		2.050
	130,347,090	130,340,223	329	44				ALU22370.2	2,000
X	138,112,304	138,112,870	506	9	470440	No non-overlappi	ng genes wit	nin 50,000bp	
X	138,736,405	138,736,943	538	9	ATP11C,	No non-overlappi	ng genes wit		
X	138,966,654	138,967,186	532	9		SRP_euk_arch	28,494	RP11-364B14.2	23,349
Х	139,036,279	139,036,643	364	9				RP11-364B14.3	33,893
Х	139,390,632	139,390,984	352	10		RP11-51C14.2	9,527		
Х	139,675,763	139,676,103	340	10		AL078639.5	9,956		
Х	142,530,423	142,530,713	290	9				SLITRK4	12,897
Х	142,716,088	142,716,376	288	9		RP11-2906.2	776		
Х	142,969,707	142,970,036	329	9		No non-overlappi	ng genes wit	hin 50,000bp	
Х	144,155,145	144,155,493	348	9				SPANXN1	9,723
Х	147,465,091	147,465,467	376	9	AFF2,	No non-overlappi	ng genes wit	hin 50,000bp	
Х	147,477,371	147,477,661	290	11	AFF2,	No non-overlappi	ng genes wit	hin 50,000bp	
Х	147 885 169	147 885 529	360	9	AFF2	No non-overlappi	na aenes wit	hin 50 000bp	
X	148 221 812	148 222 217	405	9	· · · · _,	AF011889 1-2	20 243		
X	148 525 434	148 525 722	288	10	HSEX1		4 059		
X	148 014 723	148,020,722	558	0		No non-overlanni	na aenes wit	hin 50 000hn	
×	140,314,723	140,313,201	313				12 674	nin 30,000bp	
×	149,239,222	149,239,333	405	9			42,074	hin EQ QQQhn	
~	149,294,042	149,294,407	420	9	IVIAIVILDI,	No non-ovenappi	ng genes wit		0.002
X	149,415,543	149,415,880	337	10	IVIAIVILDT,	N 477 N 4 4	04 504	AC109994.2	6,963
X	149,455,771	149,456,133	362	12		MTM1	31,594	MAMLD1	22,665
Х	149,497,115	149,497,615	500	9	MTM1,	No non-overlappi	ng genes wit	hin 50,000bp	
Х	149,615,480	149,615,808	328	11	MTMR1,			MTM1	23,027
Х	149,684,265	149,684,846	581	9				MTMR1	32
Х	150,515,290	150,515,702	412	9	PASD1,	No non-overlappi	ng genes wit	hin 50,000bp	
Х	151,740,061	151,740,554	493	10		NSDHL	9,613	CETN2	5,975
Х	151,877,996	151,878,556	560	9	ZNF185,			PNMA5	29,469
Х	151,982,702	151,982,985	283	11		PNMA6A	8,536	PNMA3	3,227
Х	152,426,100	152,426,682	582	9	BGN,	ATP2B3	9,646		
Х	152,452,720	152,453,477	757	10	ATP2B3,	UCHL5IP	38,552	BGN	24,522
Х	152,515,608	152,516,230	622	9	FAM58A,	AF274858.3-2	8,936	AF274858.3-1	6,963
Х	152.845.706	152.846.094	388	10		ARHGAP4	798	ARD1A	2.467
X	152 846 858	152 847 325	467	11		ARHGAP4	1 950	ARD1A	1 236
X	152 889 985	152 890 811	826	<u>,</u> 0	HCFC1	TMEM187	.,230		.,200
X	152 891 872	152 892 394	522	a 0	TMFM187	HCEC1	1 850		
X	153 180 610	153 100 /09	780			TEX28	12 861	OPN1M\//2	37 666
^ Y	153 270 604	153 220 202	510	9		SNORA70	1 612		2 57,000
N V	153 210 005	153 210 414	400	10		BY036247 2	1,013		2,370
^ V	153,310,005	153,310,414	409	10	AIFUAFI,	07900347.3	10		0,740
X V	153,300,395	153,300,773	3/8	9	LAGEJ,				4,481
X	153,360,811	153,361,193	382	9			21	UBL4A	4,061
X	153,374,385	153,374,933	548	12		SLC10A3	2,189	SRP_euk_arch	2,428
Х	153,408,456	153,409,161	705	9				G6PD	3,639
Х	153,416,187	153,416,562	375	12	G6PD,	IKBKG	7,110		
Х	153,427,442	153,427,893	451	11	G6PD, IKBKG,	CXorf52	24,780		
Х	153,596,428	153,596,711	283	10	GAB3,	DKC1	40,629		
Х	153,599,126	153,599,653	527	11	GAB3,	DKC1	37,687		
Х	153,643,093	153,643,460	367	9	DKC1,	SNORA36	6,537		
Х	154,128,210	154,128,923	713	9				VBP1	6,919
Y	10,629.058	10,629,579	521	23		AC006987.7	8,724	AC006987.8	7,242
Y	10.629.697	10,630,130	433	15		AC006987.7	9.363	AC010970.1	7.856
Y	10.631.750	10.632.162	412	18			-,- 30	AC010970.1	5.824
Ŷ	10 632 248	10 632 661	413	33				AC010970 1	5 325
Ŷ	10 632 741	10 634 111	1 370	16		AC010970 3-2	2AR 0	AC010970 1	3 875
Y	10 634 084	10 635 433	440	33		AC010970 3-2	8 546	AC010970 1	2 552
I.	10 626 540	10,000,400	449	33		AC010070.3-2	7 000	AC010070.1	4 005
· · ·	10 n sh 510	10 030 951	441	11	1	ACU109/0.3-2	/.028	ACU10970.1	1.035

Y	10,639,340	10,639,843	503	29	AC010970.1,	AC010970.3-2	4,136	AC010970.2	6,270
Y	10,641,203	10,642,165	962	26		AC010970.1	1,296	AC010970.2	3,948
Y	10,643,313	10,643,728	415	14		AC010970.3-2	251	AC010970.2	2,385
Y	10,644,835	10,645,652	817	23	SSU_rRNA_5,	AC010970.3-1	2,194	AC010970.2	461
Y	10,645,694	10,646,317	623	34	AC010970.2,	AC010970.3-1	1,529	SSU_rRNA_5	177
Y	10,646,348	10,646,755	407	18	AC010970.2,	AC010970.3-1	1,091	SSU_rRNA_5	831
Y	10,647,613	10,648,040	427	36	AC010970.3-1,	AC010970.2	902	SSU_rRNA_5	2,096
Y	11,922,939	11,923,667	728	9		AC134882.2-3	3,591	AC134882.2-2	106
Y	11,929,602	11,930,200	598	24				AC134882.2-2	6,769
Y	11,931,430	11,932,146	716	9				AC134882.2-2	8,597
Y	11,932,306	11,932,704	398	16				AC134882.2-2	9,473
Y	11,936,877	11,937,280	403	10		AC134882.2-1	10,727	AC134882.2-2	14,044
Y	11,938,206	11,938,491	285	9		AC134882.2-1	9,516		
Y	11,947,089	11,947,496	407	12		AC134882.2-1	511	AC134882.2-4	8,820
Y	11,947,675	11,947,996	321	10		AC134882.2-1	11	AC134882.2-4	8,320
Y	11,948,649	11,949,094	445	13	AC134882.2-1,			AC134882.2-4	7,222
Y	11,949,105	11,950,229	1,124	19	AC134882.2-1,			AC134882.2-4	6,087
Y	57,392,433	57,392,645	212	11		AC025226.2	18,134		