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Clinically relevant genetic biomarkers from the brain in alcoholism with representation on high resolution chromosome ideograms

Ann M. Manzardo^{a,*}, Austen McGuire^a, Merlin G. Butler^{a,b}

^aDepartment of Psychiatry & Behavioral Sciences, University of Kansas Medical Center, Kansas City, KS 66160, USA

^bDepartment of Pediatrics, University of Kansas Medical Center, Kansas City, KS 66160, USA

Abstract

Objective: Alcoholism arises from combined effects of multiple biological factors including genetic and non-genetic causes with gene/environmental interaction. Intensive research and advanced genetic technology has generated a long list of genes and biomarkers involved in alcoholism neuropathology. These markers reflect complex overlapping and competing effects of possibly hundreds of genes which impact brain structure, function, biochemical alcohol processing, sensitivity and risk for dependence.

Method: We compiled a tabular list of clinically relevant genetic biomarkers for alcoholism targeting expression disturbances in the human brain through an extensive search of keywords related to alcoholism, alcohol abuse, and genetics from peer reviewed medical research articles and related nationally sponsored websites. Gene symbols were then placed on high resolution human chromosome ideograms with gene descriptions in tabular form.

Results: We identified 337 clinically relevant genetic biomarkers and candidate genes for alcoholism and alcohol-responsiveness from human brain research. Genetic biomarkers included neurotransmitter pathways associated with brain reward processes for dopaminergic (e.g., *DRD2*, *MAOA*, and *COMT*), serotonergic (e.g., *HTR3A*, *HTR1B*, *HTR3B*, and *SLC6A4*), GABAergic (e.g., *GABRA1*, *GABRA2*, and *GABRG1*), glutaminergic (*GADI*, *GRIK3*, and *GRIN2C*) and opioid (e.g., *OPRM1*, *OPRD1*, and *OPRK1*) pathways which presumably impact reinforcing properties of alcohol. Gene level disturbances in cellular and molecular networks impacted by alcohol and alcoholism pathology include transketolase (TKT), transferrin (TF), and myelin (e.g., MBP, MOBP, and MOG).

Conclusions: High resolution chromosome ideograms provide investigators, physicians, geneticists and counselors a convenient visual image of the distribution of alcoholism genetic biomarkers from brain research with alphabetical listing of genes in tabular form allowing comparison between alcoholism-related phenotypes, and clinically-relevant alcoholism gene(s) at the chromosome band level to guide research, diagnosis, and treatment. Chromosome ideograms

*Corresponding author at: University of Kansas Medical Center, Department of Psychiatry & Behavioral Sciences, 3901 Rainbow Boulevard, MS 4015, Kansas City, Kansas 66160, USA. amanzardo@kumc.edu (A.M. Manzardo).

may facilitate gene-based personalized counseling of alcohol dependent individuals and their families.

Keywords

High resolution chromosome ideograms; Alcoholism; Genetic biomarkers; Brain; Chromosome band location; Gene

1. Introduction

Alcoholism arises from the combined effects of multiple biological factors including a wide range of possible genetic variations and/or abnormalities, as well as non-genetic causes including interpersonal and psychosocial relationships, neuroadaptive responses, and gene/environmental interaction (epigenetics) (Enoch, 2013; Koob, 2013; Mayfield et al., 2008; Morozova et al., 2014; Rietschel and Treutlein, 2013). The risk to develop alcoholism is strongly related to the family history, childhood environment particularly the number of life stressors and presence or absence of co-occurring mental disorders (Bierut et al., 1998; Brady and Back, 2012; Brady and Sinha, 2005; Enoch, 2013; Keyes et al., 2012; Schepis et al., 2011). The interface of these relationships are complex and involve overlapping and competing effects of many genes impacting brain development, structure, and function, as well as, alcohol processing and sensitivity (Enoch, 2013; Koob, 2013).

1.1. Candidate gene strategies

Alcohol-responsive brain networks have been reported and identified by case-control, population and family-based studies incorporating candidate gene approach with whole-genome methodology in individuals with and without alcoholism (Edenberg, 2012; Edenberg and Foroud, 2006, 2013; Enoch, 2013; Morozova et al., 2014; Yan et al., 2014). Candidate gene strategies have considered neurobiological and neurodevelopmental pathways which are key to brain function by emphasizing emotion and reward pathways as well as biochemical processes associated with the physiologic effects and molecular targets of alcohol itself particularly those impacting alcohol metabolism (Blum et al., 1990; Bolos et al., 1990; Chai et al., 2005; Edenberg et al., 2006, 2008; Enoch, 2013; Feinn et al., 2005; Kapoor et al., 2014; Luo et al., 2005; Macgregor et al., 2009; Radel et al., 2005; Tolstrup et al., 2008; Wetherill et al., 2014; Zhang et al., 2008). Further, genetic biomarkers including chromosome regions have been identified by overlapping genetic linkage and functional data with alcoholism-related phenotypes of interest and refined to develop a molecular signature of alcoholism phenotype (Ehlers et al., 2004; Enoch, 2013; Kapoor et al., 2014; Wetherill et al., 2014). A representative example of a candidate gene/biomarker analysis is the alcohol dehydrogenase enzyme (ADH) which is responsible for alcohol metabolism and linked to the ADH gene family located in the 4q23 chromosome band (Chai et al., 2005; Edenberg et al., 2006; Macgregor et al., 2009; Tolstrup et al., 2008). The 4q23 chromosome band has been strongly associated with alcoholism vulnerability in several genome-wide linkage studies (Long et al., 1998; Reich et al., 1998). The activity of alcohol metabolizing enzymes (e.g., ADH) influences sensitivity to alcohol, its effects on the body and the accumulation of metabolites (e.g., acetaldehyde) which may be toxic. Genetic variants that increase production or slow the processing of alcohol intermediates (e.g., ADH1B, ADH1C,

ALDH2) influence the likelihood of developing a drinking problem (Chai et al., 2005; Edenberg et al., 2006; Macgregor et al., 2009; Tolstrup et al., 2008). Human genetic studies have similarly identified alcoholism candidate genes involving neurotransmitter pathways associated with brain reward processes including the dopaminergic (e.g., *DRD2*, *MAOA*, *COMT*), serotonergic (e.g., *HTR3A*, *HTR1B*, *HTR3B*), GABAergic (e.g., *GABRA1*, *GABRA2*), glutaminergic (*GAD1*, *GRIK3*, *GRIN2C*) and opioid (e.g., *OPRM1*, *OPRD1*; Blum et al., 1990; Bolos et al., 1990; Edenberg, 2012; Edenberg and Foroud, 2013; Edenberg et al., 2008; Feinn et al., 2005; Luo et al., 2005; Radcl et al., 2005; Zhang et al., 2008). These genes presumably directly impact the reinforcing properties of alcohol driving the motivation to seek and use alcohol to excess. Whole-genome studies have shown abnormalities of chromosomes and identified specific regions (e.g., 4p12, 7q31.32, 13q14.2) where known or candidate genes for alcoholism are located and for alcoholism-related phenotypes such as age of drinking onset (3q26.1, 5q11.2, and 12q32.2; Edenberg, 2012; Edenberg and Foroud, 2013; Enoch, 2013; Kapoor et al., 2014; Morozova et al., 2014; Radcl et al., 2005; Yan et al., 2014).

1.2. Whole genome investigation

Advances in genetic technology beyond linkage or cytogenetic analysis of affected families with alcoholism or other complex disorders using COGA, SAGE, and other resources have led to genome-wide association studies (GWAS) involving hundreds of affected and control individuals analyzing the distribution and clustering of hundreds and thousands of SNPs to search for candidate genes (Edenberg, 2012; Edenberg and Foroud, 2013; Enoch, 2013; Morozova et al., 2014; Rietschel and Treutlein, 2013; Yan et al., 2014). GWAS studies have identified genetic linkage to primary disease risk, alcoholism-related phenotypes and responsiveness such as consumption, level of response to alcohol's effects and event-related potential. Examples of candidate genes identified by GWAS studies include functional roles in cell adhesion important for brain development and implicated in Autism Spectrum Disorder (e.g., *AUTS2*, *CDH13*, *EFNA5*), molecular transporters (e.g., *SLC1A3*, *SLC5A11*, *SLC6A4*), and growth factors (e.g., *BDNF*) (Edenberg, 2012; Edenberg and Foroud, 2006, 2013; Enoch, 2013; Morozova et al., 2014; Rietschel and Treutlein, 2013; Yan et al., 2014).

1.3. Functional genomic biomarkers from brain

Additional functional genomic biomarker studies using high resolution microarrays have identified regionally distinct gene and exon level expression disturbances in post-mortem brain impacting neuronal growth and function which may influence alcoholism onset and progression (Flatscher-Bader et al., 2005, 2006, 2010; Lewohl et al., 2000; Liu et al., 2004, 2006; Manzardo et al., 2014; Mayfield et al., 2002; Sokolov et al., 2003). Functional gene expression profiling has identified disturbances in selected brain regions associated with reward processing and prefrontal inhibitory control mechanisms relevant to the development and propagation of abuse behaviors (Flatscher-Bader et al., 2005, 2006, 2010; Lewohl et al., 2000; Liu et al., 2004, 2006; Manzardo et al., 2014; Mayfield et al., 2002; Sokolov et al., 2003). An overrepresentation of down-regulated vs up-regulated genes at the mRNA level have been reported in addiction-related brain regions and functional disturbances impacting myelination, cellular signaling and energy production influencing brain structure, function, growth and development (Lewohl et al., 2000; Liu et al., 2004, 2006; Manzardo et al., 2014;

Mayfield et al., 2002; Sokolov et al., 2003). These effects have been correlated with medical and psychiatric co-morbidities such as cirrhotic liver disease, smoking status and/or nutritional deficiency (Liu et al., 2007) and become potential genetic biomarkers for considerations in assessment and treatment development.

Advanced genetic platforms incorporating sophisticated bioinformatics techniques have enhanced our ability to identify SNPs and bio-markers involved in the genetics of alcoholism including risk factors for the development and progression of illness and have provided invaluable insight into the molecular and cellular mechanisms underlying the pathophysiology of alcoholism and the addictions. This insight has contributed to the development of the first targeted, clinically-validated and FDA approved drug treatments for alcoholism. The field will continue to advance through the use of next generation sequencing (whole genome or exome) which will yield additional valuable information on the location and description of genes contributing to alcoholism, enabling the identification of specific and recurring mutations of single genes impacting upon alcoholism-related phenotypes such as tolerance, withdrawal sensitivity, and craving which may provide novel therapeutic targets for future interventions. A current list of clinically relevant genetic biomarkers from brain in alcoholism are summarized and incorporated into high resolution chromosome ideograms (850 band level) to facilitate research, diagnostic testing and genetic counseling options for families in the clinical setting. The location of the 337 genes now recognized by searching literature and website information as playing a role in alcoholism are also presented in tabular form listing the individual gene symbol, name and chromosome location.

2. Materials and methods

We searched key words such as genetics, genes, alcoholism, alcohol abuse and alcohol dependence, mutations or gene variants and gene expression related to molecular disturbances in humans and alcoholism using computer-based internet sources including peer-reviewed medical literature (e.g., PubMed), federally sponsored (e.g., National Center for Biotechnology Information) and other informative websites (e.g., Online Mendelian Inheritance in Man; Ethanol-Related Gene Resource) (Guo et al., 2009) to compile a list of genetic biomarkers. The research articles ascertained were examined for evidence of gene or genetic biomarker involvement in alcoholism causation or pathology. These searches included whole-genome microarray and sequencing data and results from genome-wide association studies (GWAS) of alcoholism and families with and without a history of alcoholism as well as functional gene expression profiles using human brain. This list included a total of 337 genes identified with at least one mechanism related to alcoholism, or that could contribute to behavioral or neurological disturbances seen in alcoholism although not necessarily implicated in disease risk or causality (Table 1). The genetic biomarkers recognized, to date, as playing a role in alcoholism susceptibility or causation generally appear to impact alcohol metabolism and major neuro-transmitter pathways related to brain reward such as dopamine, serotonin, GABA, glutamate and opiate receptors and their metabolic pathways. Additional influences are noted for neurodevelopmental, molecular transport and cellular signaling pathways associated with alcohol exposure and pathophysiology and functionally disturbed in brain expression studies with possible impact

on disease course. We include gene symbols representing each biomarker, their expanded name and chromosome band location in Table 1 for the 337 separate genes with a possible role in alcoholism. The position for each gene is plotted on high resolution chromosome ideograms (850 band level) as shown in Figure 1.

3. Discussions and conclusion

Decades of intensive research involving international collaborative networks utilizing large databases and tissue banks and advanced genetic technology and bioinformatics have led to significant discoveries in recognition of genetic variants and biomarkers implicated in the causation and course of alcoholism. Improved commercial platforms available for alcoholism research with potential application in the clinical setting have permitted the identification and characterization of the molecular signatures for novel or disturbed gene or exon expression and disease-specific profiles and patterns of interconnected disturbed gene pathways for alcoholism and other psychiatric or aberrant behavioral disorders in a growing body of genetic data and evidence. Significant discoveries have been made using microarray technology and now next generation sequencing with readily available tissue such as peripheral blood, autopsy specimens, established lymphoblastoid cell lines and/or saliva hold promise for more advances in alcoholism biomarker research by enabling the identification of new, clinically relevant genes impacting causation and disease mechanisms stimulating discovery of treatment modalities.

We identified 337 clinically relevant or known gene biomarkers for alcoholism based on computer searches of key words from peer reviewed medical literature reports or nationally sponsored web sites. These genetic biomarkers may be causative in nature or transient reflecting physiological responses to alcohol use or environmental influences such as poor nutrition, sanitation, and exposure to other drugs, illnesses, and viruses, common in chronic alcoholism. Transient, potentially modifiable genomic imbalances are important considerations in discovery, treatment and assessment of phenotypic outcomes in alcoholism. Future studies should also consider the impact of copy number variation, segmental deletions and duplications and regions of homozygosity in the genome for determination of identical by descent for calculation of inbreeding coefficients or consanguinity status along with uniparental disomy of individual chromosomes and areas of genomic imprinting on alcoholism risk and course of illness.

Our summary of the current status and number of clinically relevant human genetic biomarkers associated with alcoholism — targeting disturbed brain networks along with their position on high resolution chromosome ideograms will enhance the development of genetic testing options including DNA or gene testing panels for alcoholism and encourage genetic counseling of family members with a high density of alcoholism in biological relatives. The number of genes identified may vary in future studies based upon size and selected subject characteristics, tissue type and genetic technique used. The authors encourage the use of this current collection of genetic biomarkers from brain in alcoholism in their evaluation of patients and families to improve diagnosis and genetic counseling of selected patients, at-risk individuals and their families.

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Abbreviations:

COGA	collaborative study on the genetics of alcoholism
DNA	deoxyribonucleic acid
FDA	Food and Drug Administration
GWAS	genome-wide association studies
mRNA	messenger ribonucleic acid
SAGE	study of addiction: genetics and environment
SNPs	single nucleotide polymorphisms

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A

B

Fig. 1. High resolution human chromosome ideograms (850 band level) with alcoholism gene symbols positioned at the chromosome band location. The upper 'p' and lower 'q' arms for each chromosome are separated by the centromere area highlighted in black. The gene symbol in alphabetical order, expanded name of the gene and precise chromosome band position are found in Table 1.

Table 1

Genetic biomarkers for alcoholism and alcohol-responsiveness in human brain.

Gene symbol	Gene name	Location	References
<i>AADAC</i>	Arylacetamide deacetylase	3q25.1	Flatscher-Bader et al. (2005)
<i>ABCA1</i>	ATP-binding cassette, subfamily A, member 1	9q31.1	Liu et al. (2007)
<i>ABCA8</i>	ATP-binding cassette, subfamily A, member 8	17q24.2	Manzardo et al. (2014)
<i>ACACB</i>	Acetyl-CoA carboxylase-beta	12q24.11	Manzardo et al. (2014)
<i>ACN9</i>	ACN9, S. cerevisiae, homolog of	7q21.3	Dick et al. (2008)
<i>ACO1</i>	Aconitase 1, soluble	9p21.1	Flatscher-Bader et al. (2005)
<i>ACOT12</i>	Acyl-CoA thioesterase 12	5q14.1	Flatscher-Bader et al. (2005)
<i>ACTG1</i>	Actin, gamma-1	17q25.3	Hill et al. (2004)
<i>ACTN4</i>	Actinin, alpha-4	19q13.2	Joslyn et al. (2010); Yu et al. (2008)
<i>ADH1A</i>	Alcohol dehydrogenase 1A, class I, alpha polypeptide	4q23	Morozova et al. (2014)
<i>ADH1B</i>	Alcohol dehydrogenase 1B, class I, beta polypeptide	4q23	Edenberg (2007)
<i>ADH1C</i>	Alcohol dehydrogenase 1C, class I, gamma polypeptide	4q23	Rietschel and Treutlein (2013)
<i>ADH4</i>	Alcohol dehydrogenase 4	4q23	Zuo et al. (2011)
<i>ADH5</i>	Alcohol dehydrogenase 5, chi polypeptide	4q23	Zuo et al. (2011)
<i>ADH6</i>	Alcohol dehydrogenase 6	4q23	Flatscher-Bader et al. (2005)
<i>ADO</i>	2-aminoethanethiol dioxxygenase	10q21.3	Guo et al. (2009)
<i>AGT</i>	Angiotensinogen	1q42.2	Liu et al. (2006)
<i>ALDH1A1</i>	Aldehyde dehydrogenase 1 family, member A1	9q21.13	Morozova et al. (2014)
<i>ALDH1B1</i>	Aldehyde dehydrogenase 1 family, member B1	9p13.2	Linneberg et al. (2010)
<i>ALDH2</i>	Aldehyde dehydrogenase 2 family	12q24.12	Cui et al. (2009)
<i>ALDOC</i>	Aldolase C, fructose-bisphosphate	17q11.2	Guo et al. (2009)
<i>ALK</i>	Anaplastic lymphoma kinase	2p23.2-p23.1	Wang et al. (2011b)
<i>AMPH</i>	Amphipysin	7p14.1	Flatscher-Bader et al. (2005)
<i>ANKK1</i>	Ankyrin repeat and kinase domain containing 1	11q23.2	Yang et al. (2008)
<i>ANKRD7</i>	Ankyrin repeat domain 7	7q31.31	Chen et al. (2012)
<i>ANKS1A</i>	Ankyrin repeat and sterile alpha motif domain containing 1A	6p21.31	Heath et al. (2011)
<i>ANLN</i>	Anillin, actin binding protein	7p14.2	Manzardo et al. (2014)
<i>ANP32E</i>	Acidic leucine-rich nuclear phosphoprotein 32 family, member E	1q21.2	Liu et al. (2006)

Gene symbol	Gene name	Location	References
<i>APOA1</i>	Apolipoprotein A-I	11q23.3	Mayfield et al. (2002)
<i>APOD</i>	Apolipoprotein D	3q29	Mayfield et al. (2002)
<i>APP</i>	Amyloid beta A4 precursor protein	21q21.3	Flatscher-Bader et al. (2005)
<i>AQP4</i>	Aquaporin 4	18q11.2	Liu et al. (2007)
<i>ARF1</i>	ADP-ribosylation factor 1	1q42.13	Liu et al. (2004)
<i>ARF4</i>	ADP-ribosylation factor 4	3p14.3	Liu et al. (2004)
<i>ARID5A</i>	AT rich interaction domain-containing protein 5A (MRFI-like)	2q11.2	Zlojutro et al. (2010)
<i>ARH1</i>	Ariadne, Drosophila, homolog of, 1	15q24.1	Morozova et al. (2014)
<i>ARHGAP11A</i>	RHO (rhodopsin) GTPase-activating protein 11A	15q13.3	Morozova et al. (2012)
<i>ARHGAP28</i>	RHO (rhodopsin) GTPase-activating protein 28	18p11.31	Morozova et al. (2012)
<i>ARL2</i>	ADP-ribosylation factor-like 2	11q13.1	Liu et al. (2004)
<i>ARL4D</i>	ADP-ribosylation factor-like 4D	17q21.31	Liu et al. (2004)
<i>ARL15</i>	ADP-ribosylation factor-like 15	5q11.2	Kapoor et al. (2014)
<i>ART3</i>	ADP-ribosyltransferase 3	4q21.1	Mayfield et al. (2002)
<i>ASPA</i>	Aspartoacylase	17p13.2	Manzardo et al. (2014)
<i>ATP5A1</i>	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit 1	18q21.1	Guo et al. (2009)
<i>ATP6V1B2</i>	ATPase, H+ transporting, lysosomal 56/58 kDa, V1 subunit B2	8p21.3	Guo et al. (2009)
<i>ATXN1</i>	Ataxin 1	6p22.3	Mayfield et al. (2002)
<i>AUTS2</i>	Autism susceptibility 2	7q11.22	Schumann et al. (2011)
<i>BBX</i>	Bobby sox homolog (Drosophila)	3q13.12	Edenberg et al. (2010)
<i>BDNF</i>	Brain-derived neurotrophic factor	11p14.1	Zhao et al. (2012)
<i>BNIP3</i>	BCL2/adenovirus E1B 19 kDa interacting protein 3	10q26.3	Flatscher-Bader et al. (2005)
<i>C15ORF32</i>	Chromosome 15 open reading frame 32	15q26.1	Heath et al. (2011)
<i>C4BPB</i>	Complement component 4-binding protein, beta chain	1q32.2	Liu et al. (2006)
<i>CA2</i>	Carbonic Anhydrase II	8q21.2	Flatscher-Bader et al. (2005)
<i>CACNG1</i>	Calcium channel, voltage-dependent, gamma-1 subunit	17q24.2	Mayfield et al. (2002)
<i>CALM2</i>	Calmodulin 2	2p21	Mayfield et al. (2002)
<i>CANX</i>	Calnexin	5q35.3	Liu et al. (2006)
<i>CAPN3</i>	Calpain 3	15q15.1	Liu et al. (2006)
<i>CAST</i>	Calpastatin	5q15	Morozova et al. (2014)
<i>CAT</i>	Catalase	11p13	Lind et al. (2012)

Gene symbol	Gene name	Location	References
<i>CCR1</i>	Chemokine (C–C motif) receptor 1	<i>3p21.31</i>	Mayfield et al. (2002)
<i>CCT3</i>	Chaperonin containing TCP1 (T-complex 1), subunit 3	<i>1q22</i>	Guo et al. (2009)
<i>CD33</i>	CD33 Antigen	<i>19q13.41</i>	Flatscher-Bader et al. (2005)
<i>CDC14A</i>	Cell division cycle 14, S. Cerevisiae, homolog A	<i>1p21.2</i>	Flatscher-Bader et al. (2005)
<i>CDKL5</i>	Cyclin-dependent kinase-like 5	<i>Xp22.13</i>	Liu et al. (2006)()
<i>CDH13</i>	Cadherin 13	<i>16q23.3</i>	Rietschel and Treutlein (2013)
<i>CDHR2</i>	Cadherin-related family member 2	<i>5q35.2</i>	Wetherill et al. (2014)
<i>CEBPG</i>	CCAAT/enhancer binding protein (C/EBP), gamma	<i>19q13.11</i>	Flatscher-Bader et al. (2005)
<i>CHRM2</i>	Cholinergic receptor, muscarinic, 2	<i>7q33</i>	Luo et al. (2005)
<i>CHRNA3</i>	Cholinergic receptor, neuronal nicotinic, alpha polypeptide 3	<i>15q25.1</i>	Zuo et al. (2011)
<i>CHRNA5</i>	Cholinergic receptor, neuronal nicotinic, alpha polypeptide 5	<i>15q25.1</i>	Wang et al. (2009)
<i>CHRNA2</i>	Cholinergic receptor, neuronal nicotinic, beta polypeptide 2	<i>1q21.3</i>	Ehringer et al. (2007)
<i>CKB</i>	Creatine kinase, brain type	<i>14q32.32</i>	Hill et al. (2004)
<i>CLCN4</i>	Chloride channel 4	<i>Xp22.2</i>	Flatscher-Bader et al. (2005)
<i>CLDN11</i>	Claudin 11	<i>3q26.2</i>	Liu et al. (2004); Manzardo et al. (2014)
<i>CNP</i>	Cyclic nucleotide phosphodiesterase	<i>17q21.2</i>	Liu et al. (2006)
<i>COMT</i>	Catechol-O-methyltransferase	<i>22q11.21</i>	Yang et al. (2008)
<i>COPB2</i>	Coatomer protein complex, subunit beta-2	<i>3q23</i>	Morozova et al. (2014)
<i>CPE</i>	Carboxypeptidase E	<i>4q32.3</i>	Mayfield et al. (2002)
<i>CREM</i>	cAMP responsive element modulator	<i>10p11.21</i>	Mayfield et al. (2002)
<i>CRMP1</i>	Collapsin response mediator protein 1	<i>4p16.2</i>	Guo et al. (2009)
<i>CRYAA</i>	Crystallin, alpha-A	<i>21q22.3</i>	Mayfield et al. (2002)
<i>CRYAB</i>	Crystallin, alpha-B	<i>11q23.1</i>	Mayfield et al. (2002)
<i>CSMD1</i>	CUB (complement C1r/C1s, Uegf, Bmp1) and sushi multiple domains 1	<i>8p23.2</i>	Morozova et al. (2012)
<i>CSMD2</i>	CUB and sushi multiple domains 2	<i>1p34.3</i>	Morozova et al. (2012)
<i>CTNNA3</i>	Catenin, alpha-3	<i>10q21.3</i>	Manzardo et al. (2014)
<i>CTNND2</i>	Catenin, delta-2	<i>5p15.2</i>	Morozova et al. (2012)
<i>CXCL12</i>	Chemokine (C-X-C motif) ligand 12	<i>10q11.21</i>	Flatscher-Bader et al. (2005)
<i>CYP2E1</i>	Cytochrome p450, subfamily IIE	<i>10q26.3</i>	Lind et al. (2012)
<i>DDC</i>	Dopa decarboxylase	<i>7p12.1</i>	Pan et al. (2013)
<i>DKK2</i>	Dickkopf WNT signaling pathway inhibitor 2	<i>4q25</i>	Kalsi et al. (2010)

Gene symbol	Gene name	Location	References
<i>DLG2</i>	Disks large, Drosophila, homolog of, 2	<i>11q14.1</i>	Morozova et al. (2014)
<i>DPYSL2</i>	Dihydropyrimidinase-like 2	<i>8p21.2</i>	Taylor and Wang (2014)
<i>DRD2</i>	Dopamine receptor D2	<i>11q23.2</i>	Yang et al. (2008)
<i>DSCAML1</i>	Down syndrome cell adhesion molecule-like 1	<i>11q23.3</i>	Wang et al. (2011a)
<i>DTWD2</i>	DTW domain containing 2	<i>5q23.1</i>	Pan et al. (2013)
<i>EDIL3</i>	EGF (epidermal growth factor)-like repeats and discoidin I-like domains 3	<i>5q14.3</i>	Liu et al. (2006)
<i>EDNRB</i>	Endothelin receptor, type B	<i>13q22.3</i>	Wang et al. (2011a)
<i>EEF1G</i>	Eukaryotic translation elongation factor 1, gamma	<i>11q12.3</i>	Sokolov et al. (2003)
<i>EFNA5</i>	Ephrin-A5	<i>5q21.3</i>	Wang et al. (2012)
<i>ENO1</i>	Enolase 1	<i>1p36.23</i>	Guo et al. (2009)
<i>ENO3</i>	Enolase 3	<i>17p13.2</i>	Lind et al. (2012)
<i>ENPP2</i>	Ectonucleotide pyrophosphatase/phosphodiesterase 2	<i>8q24.12</i>	Liu et al. (2004); Manzardo et al. (2014)
<i>ETFA</i>	Electron-transfer-flavoprotein, alpha polypeptide	<i>15q24.3</i>	Flatscher-Bader et al. (2005)
<i>ETNPP1</i>	Ethanolamine-phosphate phospho-lyase	<i>4q25</i>	Manzardo et al. (2014)
<i>EV12A</i>	Ectropic viral integration site 2A	<i>17q11.2</i>	Manzardo et al. (2014)
<i>FGFR2</i>	Fibroblast growth factor receptor 2	<i>10q26.13</i>	Flatscher-Bader et al. (2010)
<i>FH</i>	Fumarate hydratase	<i>1q43</i>	Guo et al. (2009)
<i>FN1</i>	Fibronectin 1	<i>2q35</i>	Liu et al. (2004)
<i>FSIP2</i>	Fibrous sheath interacting protein 2	<i>2q32.1</i>	Wang et al. (2012)
<i>FZD9</i>	Frizzled class receptor 9	<i>7q11.23</i>	Mayfield et al. (2002)
<i>GABBR1</i>	GABA (gamma-aminobutyric acid) B receptor 1	<i>6p21.31</i>	Flatscher-Bader et al. (2005)
<i>GABRA1</i>	GABA (gamma-aminobutyric acid) receptor, alpha-1	<i>5q34</i>	Enoch (2008)
<i>GABRA2</i>	GABA (gamma-aminobutyric acid) receptor, alpha-2	<i>4p12</i>	Agrawal et al. (2006)
<i>GABRB1</i>	GABA (gamma-aminobutyric acid) receptor, beta-1	<i>4p12</i>	Liu et al. (2006)
<i>GABRG1</i>	GABA (gamma-aminobutyric acid) receptor, gamma-1	<i>4p12</i>	Enoch (2008)
<i>GABRG2</i>	GABA (gamma-aminobutyric acid) receptor, gamma-2	<i>5q34</i>	Zuo et al. (2011)
<i>GABRG3</i>	GABA (gamma-aminobutyric acid) receptor, gamma-3	<i>15q12</i>	Edenberg (2012)
<i>GAD1</i>	Glutamate decarboxylase 1	<i>2q31.1</i>	Zuo et al. (2011)
<i>GATA4</i>	GATA binding protein	<i>8p23.1</i>	Rietschel and Treutlein (2013)
<i>GFAP</i>	Glial fibrillary acidic protein	<i>17q21.31</i>	Liu et al. (2004)
<i>GJB6</i>	Gap junction protein, beta-6	<i>13q12.11</i>	Manzardo et al. (2014)

Gene symbol	Gene name	Location	References
<i>GKNI</i>	Gastrokine 1	2p13.3	Flatscher-Bader et al. (2005)
<i>GLDN</i>	Glionedin	15q21.2	Manzardo et al. (2014)
<i>GLUD1</i>	Glutamate dehydrogenase 1	10q23.2	Josslyn et al. (2010)
<i>GOSR1</i>	Golgi SNAP (NSF attachment protein) receptor complex member 1	17q11.2	Mayfield et al. (2002)
<i>GOT1</i>	Glutamate oxaloacetate transaminase, soluble	10q24.2	Lind et al. (2012)
<i>GPM6B</i>	Glycoprotein M6B	Xp22.2	Mayfield et al. (2002)
<i>GRB2</i>	Growth factor receptor-bound protein 2	17q25.1	Guo et al. (2009)
<i>GRIA1</i>	Glutamate receptor, ionotropic, AMPA (alpha-amino-3-hydroxy-5-methyl-4-isoxazole propionate) 1	5q33.2	Mayfield et al. (2013)
<i>GRIA4</i>	Glutamate receptor, ionotropic, AMPA (alpha-amino-3-hydroxy-5-methyl-4-isoxazole propionate) 4	11q22.3	Mayfield et al. (2013)
<i>GRIK3</i>	Glutamate receptor, ionotropic, kainate 3	1p34.3	Zuo et al. (2011)
<i>GRIN1</i>	Glutamate receptor, ionotropic, N-methyl-D-aspartate, subunit 1	9q34.3	Mayfield et al. (2013)
<i>GRIN2B</i>	Glutamate receptor, ionotropic, N-methyl-D-aspartate, subunit 2B	12p13.1	Mayfield et al. (2013)
<i>GRIN2C</i>	Glutamate receptor, ionotropic, N-methyl-D-aspartate, subunit 2C	17q25.1	Zuo et al. (2011)
<i>GRM8</i>	Glutamate receptor, metabotropic, 8	7q31.33	Chen et al. (2009)
<i>GSN</i>	Gelsolin	9q33.2	Kuo et al. (2006)
<i>HIP1</i>	Huntingtin-interacting protein 1	7q11.23	Heath et al. (2011)
<i>HLA-DRA</i>	Major histocompatibility complex, class II, DR alpha	6p21.32	Flatscher-Bader et al. (2005)
<i>HLA-DRB1</i>	Major histocompatibility complex, class II, DR beta 1	6p21.32	Flatscher-Bader et al. (2005)
<i>HLA-DRB4</i>	Major histocompatibility complex, class II, DR beta 4	6p21.3	Flatscher-Bader et al. (2005)
<i>HMGCR</i>	3-hydroxy-3-methylglutaryl-CoA reductase	5q13.3	Mayfield et al. (2002)
<i>HMOX1</i>	Heme oxygenase (decycling) 1	22q13.1	Mayfield et al. (2002)
<i>HSP90B1</i>	Heat-shock protein, 90-kDa, beta, 1	12q23.3	Guo et al. (2009)
<i>HSPA9</i>	Heat-shock 70-kDa protein 9	5q31.2	Guo et al. (2009)
<i>HTR1A</i>	5-hydroxytryptamine receptor 1A	5q12.3	Zuo et al. (2013b)
<i>HTR1B</i>	5-hydroxytryptamine receptor 1B	6q14.1	Cao et al. (2013)
<i>HTR3A</i>	5-hydroxytryptamine receptor 3A	11q23.2	Cao et al. (2013)
<i>HTR3B</i>	5-hydroxytryptamine receptor 3B	11q23.2	Cao et al. (2013)
<i>HTR7</i>	5-hydroxytryptamine receptor 7, adenylylate cyclase-coupled	10q23.31	Zlojutro et al. (2010)
<i>IFRD1</i>	Interferon-related developmental regulator 1	7q31.1	Liu et al. (2006)
<i>IGF1</i>	Insulin-like growth factor I	12q23.2	Hill et al. (2004)

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<i>IGF1R</i>	Insulin-like growth factor 1 receptor	15q26.3	Liu et al. (2004)
<i>IGF2R</i>	Insulin-like growth factor II receptor	6q25.3	Morozova et al. (2014)
<i>IKBKB</i>	Inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta	8q11.21	Flatscher-Bader et al. (2005)
<i>IKZF1</i>	Ikaros family zinc finger 1	7p12.2	Flatscher-Bader et al. (2005)
<i>IL10RA</i>	Interleukin 10 receptor, alpha	11q23.3	Mayfield et al. (2002)
<i>IMPA2</i>	Myo-Inositol monophosphatase 2	18p11.21	Morozova et al. (2014)
<i>INADL</i>	InaD-like	1p31.3	Heath et al. (2011)
<i>IPO11</i>	Importin 11	5q12.1	Zuo et al. (2013b)
<i>ITGA2</i>	Integrin, alpha-2	5q11.2	Manzardo et al. (2014)
<i>ITGAV</i>	Integrin, alpha-V	2q32.1	Flatscher-Bader et al. (2010)
<i>ITPKA</i>	Inositol 1,4,5-trisphosphate 3-kinase A	15q15.1	Flatscher-Bader et al. (2005)
<i>KCNB2</i>	Potassium channel, voltage-gated, Shab-related subfamily, member 2	8q13.3	Pan et al. (2013)
<i>KCNE3</i>	Potassium channel, voltage-gated, Isk-related subfamily, member 2	11q13.4	Flatscher-Bader et al. (2005)
<i>KCNIP1</i>	Potassium channel-interacting protein 1	5q31.1	Morozova et al. (2012)
<i>KCNJ6</i>	Potassium channel, inwardly rectifying, subfamily j, member 6	21q22.13	Kang et al. (2012)
<i>KCNJ10</i>	Potassium channel, inwardly rectifying, subfamily j, member 6	11q24.3	Lewohl et al. (2000)
<i>KDM4C</i>	Lysine (K)-specific demethylase 4C	9p24.1	Wang et al. (2012)
<i>KIAA0040</i>	Uncharacterized protein	1q25.1	Zuo et al. (2012)
<i>KLK6</i>	Kallikrein-related peptidase 6	19q13.41	Manzardo et al. (2014)
<i>LAMP1</i>	Lysosomal-associated membrane protein 1	13q34	Flatscher-Bader et al. (2005)
<i>LAMP2</i>	Lysosomal-associated membrane protein 2	Xq24	Liu et al. (2006)
<i>LDHB</i>	Lactate dehydrogenase B	12p12.1	Guo et al. (2009)
<i>LGR5</i>	Leucine-rich repeat-containing G protein-coupled receptor 5	12q21.1	Manzardo et al. (2014)
<i>LIMS1</i>	LIM and senescent cell antigen-like domains 1	2q12.3	Mayfield et al. (2002)
<i>LMO1</i>	LIM domain only 1	11p15.4	Kapoor et al. (2013)
<i>LPIN1</i>	Lipin 1	2p25.1	Flatscher-Bader et al. (2005)
<i>LPXN</i>	Leupaxin	11q12.1	Flatscher-Bader et al. (2005)
<i>LRP2</i>	Low density lipoprotein receptor-related protein 2	2q31.1	Manzardo et al. (2014)
<i>LRRN1</i>	Leucine rich repeats neuronal 1	3p26.2	Wetherill et al. (2014)
<i>LTF</i>	Lactotransferrin	3p21.31	Mayfield et al. (2002)
<i>MAG</i>	Myelin-associated glycoprotein	19q13.12	Mayfield et al. (2002); Manzardo et al. (2014)

Gene symbol	Gene name	Location	References
<i>MAOA</i>	Monoamine oxidase A	<i>Xp11.3</i>	Tikkanen et al. (2009)
<i>MAPT</i>	Microtubule-associated protein tau	<i>17q21.31</i>	Flatscher-Bader et al. (2005)
<i>MAX</i>	MAX protein	<i>14q23.3</i>	Morozova et al. (2014)
<i>MBP</i>	Myelin basic protein	<i>18q23</i>	Liu et al. (2004); Manzardo et al. (2014)
<i>MCM5</i>	Minichromosome maintenance complex component 5	<i>22q13.3</i>	Liu et al. (2006)
<i>MDK</i>	Midkine	<i>11p11.2</i>	Flatscher-Bader et al. (2005)
<i>MGST1</i>	Glutathione S-transferase, microsomal, 1	<i>12p12.3</i>	Liu et al. (2007)
<i>MOBP</i>	Myelin-associated oligodendrocyte basic protein	<i>3p21.33</i>	Mayfield et al. (2002)
<i>MOG</i>	Myelin-oligodendrocyte glycoprotein	<i>6p22.1</i>	Liu et al. (2004); Manzardo et al. (2014)
<i>MPDZ</i>	Multiple PDZ (PSD95, Dlg1, & ZO-1) domain protein	<i>9p23</i>	Zhao et al. (2012)
<i>MTIL</i>	metallothionein 1 L	<i>16q12.2</i>	Mayfield et al. (2002)
<i>MUS81</i>	MUS81 structure-specific endonuclease subunit	<i>11q13.1</i>	Flatscher-Bader et al. (2005)
<i>MYT1L</i>	Myelin transcription factor 1-like	<i>2p25.3</i>	Liu et al. (2004)
<i>NALCN</i>	Sodium leak channel, non-selective	<i>13q33.1</i>	Wetherill et al. (2014)
<i>NCAM1</i>	Cell adhesion molecule, neural, 1	<i>11q23.2</i>	Yang et al. (2008)
<i>NDUFA1</i>	NADH (nicotinamide adenine dinucleotide) dehydrogenase (ubiquinone) 1	<i>Xq24</i>	Flatscher-Bader et al. (2005)
<i>NDUFA11</i>	NADH (nicotinamide adenine dinucleotide) dehydrogenase 1 alpha subcomplex, 11	<i>19p13.3</i>	Liu et al. (2006)
<i>NDST4</i>	N-deacetylase/N-sulfotransferase 4	<i>4q26</i>	Pan et al. (2013)
<i>NFKB1</i>	Nuclear factor kappa-B, subunit 1	<i>4q24</i>	Morozova et al. (2014)
<i>NKAIN1</i>	Na+/K+ transporting ATPase interacting 1	<i>1p35.2</i>	Zuo et al. (2013a)
<i>NKAIN2</i>	Na+/K+ transporting ATPase-interacting 2	<i>6q22.31</i>	Wang et al. (2011a)
<i>NPAS3</i>	Neuronal PAS (Per-Amt-Sim) domain protein 3	<i>14q13.1</i>	Morozova et al. (2012)
<i>NPY</i>	Neuropeptide Y	<i>7p15.3</i>	Kauhanen et al. (2000); Mayfield et al. (2002)
<i>NPY1R</i>	Neuropeptide Y receptor Y1	<i>4q32.2</i>	Zuo et al. (2011)
<i>NPY2R</i>	Neuropeptide Y receptor Y2	<i>4q32.1</i>	Zhao et al. (2012)
<i>NPY5R</i>	Neuropeptide Y receptor Y5	<i>4q32.2</i>	Wetherill et al. (2008)
<i>NR4A2</i>	Nuclear receptor subfamily 4, group A, member 2	<i>2q24.1</i>	Pan et al. (2013)
<i>NRD1</i>	Nardilysin	<i>1p32.3</i>	Wang et al. (2011b)
<i>NRXN3</i>	Neurexin 3	<i>14q24.3-q31</i>	Hishimoto et al. (2007)
<i>NSMAF</i>	Neutral sphingomyelinase activation-associated factor	<i>8q12.1</i>	Liu et al. (2004)

Gene symbol	Gene name	Location	References
<i>NTRK2</i>	Neurotrophic tyrosine kinase, receptor, type 2	8q21.33	Mayfield et al. (2002)
<i>OMG</i>	Oligodendrocyte-myelin glycoprotein	17q11.2	Hill et al. (2004)
<i>OPRD1</i>	Opioid receptor, delta-1	1p35.3	Ashenhurst et al. (2012); Zhang et al. (2008)
<i>OPRM1</i>	Opioid receptor, mu-1	6q25.2	Ray and Hutchison (2004)
<i>OR51L1</i>	Olfactory receptor, family 51, subfamily L, member 1	11p15.4	Wetherill et al. (2014)
<i>PARK7</i>	Parkinson protein 7	1p36.23	Guo et al. (2009)
<i>PARP1</i>	Poly(ADP-ribose) polymerase 1	1q42.12	Mayfield et al. (2002)
<i>PARP4</i>	Poly(ADP-ribose) polymerase 4	13q12.12	Mayfield et al. (2002)
<i>PDHB</i>	pyruvate dehydrogenase, beta polypeptide	3p14.3	Guo et al. (2009)
<i>PDI4.3</i>	Protein disulfide isomerase, family A, member 3	15q15.3	Morozova et al. (2014)
<i>PDYN</i>	Prodynorphin	20p13	Williams et al. (2007)
<i>PEA15</i>	Phosphoprotein enriched in astrocytes, 15-kDa	1q23.2	Liu et al. (2007)
<i>PEBP1</i>	Phosphatidylethanolamine-binding protein 1	12q24.23	Manzardo et al. (2014)
<i>PGM2L1</i>	Phosphoglucosaminase 2-like 1	11q13.4	Flatscher-Bader et al. (2005)
<i>PHF3</i>	PHD (plant homeodomain) finger protein 3	6q12	Zuo et al. (2011)
<i>PIBF1</i>	Progesterone-induced blocking factor 1	13q22.1	Flatscher-Bader et al. (2005)
<i>PIEZO2</i>	Piezo-type mechanosensitive ion channel component 2	18p11.22	Manzardo et al. (2014)
<i>PIPOX</i>	Pipelicolic acid oxidase	17q11.2	Flatscher-Bader et al. (2005)
<i>PKN1</i>	Protein kinase N1	19p13.12	Guo et al. (2009)
<i>PKNOX2</i>	PBX(pre-B-cell leukemia homeobox)/knotted 1 homeobox 2	11q24.2	Bierut et al. (2010)
<i>PLA2G1B</i>	Phospholipase A2, group IB (pancreas)	12q24.31	Mayfield et al. (2002)
<i>PLCLI</i>	Phospholipase C-like 1	2q33.1	Kapoor et al. (2013)
<i>PLPI</i>	Proteolipid protein 1	Xq22.2	Mayfield et al. (2002)
<i>PML</i>	Promyelocytic leukemia	15q24.1	Flatscher-Bader et al. (2005)
<i>PMP22</i>	Peripheral myelin protein 22	17p12	Liu et al. (2004); Manzardo et al. (2014)
<i>POLD2</i>	Polymerase (DNA-directed), delta 2, regulatory subunit	7p13	Flatscher-Bader et al. (2005)
<i>POMC</i>	Proopiomelanocortin	2p23.3	Zuo et al. (2011)
<i>PPAN</i>	Peter pan, Drosophila, homolog of	19p13.2	Flatscher-Bader et al. (2005)
<i>PRDX6</i>	Peroxiredoxin 6	1q25.1	Guo et al. (2009)
<i>PRKCA</i>	Protein kinase C, alpha	17q24.2	Morozova et al. (2014)
<i>PSMB2</i>	Proteasome subunit, beta type, 2	1p34.3	Liu et al. (2006)

Gene symbol	Gene name	Location	References
<i>PTP4A1</i>	Protein-tyrosine phosphatase, type 4A, 1	6q12	Zuo et al. (2009)
<i>PTPRD</i>	Protein-tyrosine phosphatase, receptor-type, delta	9p23	Morozova et al. (2012)
<i>PURA</i>	Purine-rich element-binding protein A	5q31.2	Liu et al. (2004)
<i>QDPR</i>	Quinoid dihydropteridine reductase	4p15.32	Joslyn et al. (2010); Yu et al. (2008)
<i>RAB1A</i>	RAS-associated protein RAB1	2p14	Guo et al. (2009)
<i>RAB11B</i>	RAB11B, member RAS oncogene family	19p13.2	Mayfield et al. (2002)
<i>RAB3A</i>	RAS-associated protein RAB3A	19p13.11	Guo et al. (2009)
<i>RANBP3L</i>	RAN (Ras-related nuclear protein) Binding Protein 3-like	5p13.2	Manzardo et al. (2014)
<i>RASGRP3</i>	RAS guanyl nucleotide-releasing protein 3	2p22.3	Manzardo et al. (2014)
<i>RGS8</i>	Regulator of G protein signaling 8	1q25.3	Flatscher-Bader et al. (2005)
<i>RHOA</i>	RAS homolog gene family, member A	3p21.31	Flatscher-Bader et al. (2010)
<i>RHOB</i>	RAS homolog gene family, member B	2p24.1	Flatscher-Bader et al. (2010)
<i>RPE</i>	Ribulose 5-phosphate 3-epimerase	2q34	Flatscher-Bader et al. (2005)
<i>RPL22</i>	Ribosomal protein L22	1p36.31	Flatscher-Bader et al. (2005)
<i>RPS29</i>	Ribosomal protein S29	14q21.3	Flatscher-Bader et al. (2005)
<i>RPS6KA5</i>	Ribosomal protein S6 kinase, 90 kDa, polypeptide 5	14q22.11	Flatscher-Bader et al. (2005)
<i>RTN1</i>	Reticulon 1	14q23.1	Mayfield et al. (2002)
<i>RTN4</i>	Reticulon 4	2p16.1	Liu et al. (2007)
<i>SAMHD1</i>	SAM (sterile alpha-motif) domain and HD (Huntington disease) domain 1	20q11.23	Flatscher-Bader et al. (2005)
<i>SCD</i>	Stearoyl-CoA desaturase	10q24.31	Liu et al. (2006)
<i>SDC2</i>	Syndecan 2	8q22.1	Mayfield et al. (2002)
<i>SEMA3E</i>	Sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3E	7q21.11	Kerner et al. (2011)
<i>SEMA5A</i>	Semaphorin 5A	5p15.31	Wang et al. (2011b)
<i>SERINC2</i>	Serine incorporator 2	1p35.2	Zuo et al. (2013a)
<i>SERTAD3</i>	SERTA (SEI-1, RBT1, TARA) domain containing 3	19q13.2	Flatscher-Bader et al. (2005)
<i>SESN2</i>	Sestrin 2	1p35.3	Flatscher-Bader et al. (2005)
<i>SGOL1</i>	Shugoshin-like 1	3p24.3	Pan et al. (2013)
<i>SHC3</i>	SHC (Src homology 2 domain containing) transforming protein 3	9q22.1	Morozova et al. (2014)
<i>SI</i>	Sucrase-isomaltase (alpha-glucosidase)	3q26.1	Guo et al. (2009)
<i>SLC1A3</i>	Solute carrier family 1 (glial high affinity glutamate transporter), member 3	5p13.2	Flatscher-Bader et al. (2005)

Gene symbol	Gene name	Location	References
<i>SLC12A2</i>	Solute carrier family 12 (sodium/potassium/chloride transporter), member 2	5q23.3	Liu et al. (2006)
<i>SLC30A5</i>	Solute carrier family 30 (zinc transporter), member 5	5q13.1-q13.2	Hill et al. (2004); Flatscher-Bader et al. (2005)
<i>SLC5A11</i>	Solute carrier family 5 (sodium/glucose cotransporter), member 11	16p12.1	Manzardo et al. (2014)
<i>SLC6A4</i>	Solute carrier family 6 (neurotransmitter transporter, serotonin), member 4	17q11.2	Feinn et al. (2005)
<i>SMARCA5</i>	SWI/SNF (switch/sucrose nonfermentable) related, matrix associated, actin dependent regulator of chromatin, subfamily A, member 5	4q31.21	Liu et al. (2006)
<i>SMPD2</i>	Sphingomyelin phosphodiesterase 2, neutral membrane	6q21	Liu et al. (2004)
<i>SMPDL3A</i>	Sphingomyelin phosphodiesterase, acid-like, 3A	6q22.31	Liu et al. (2004)
<i>SMPDL3B</i>	Sphingomyelin phosphodiesterase, acid-like, 3B	1p35.3	Liu et al. (2004)
<i>SNCA</i>	Synuclein, alpha	4q22.1	Bönsch et al. (2005)
<i>SOC1</i>	Suppressor of cytokine signaling 1	16p13.13	Guo et al. (2009)
<i>SOX9</i>	SRY (sex determining region Y)-box 9	17q24.3	Mayfield et al. (2002)
<i>SPARC</i>	Secreted protein, acidic, cysteine-rich	5q33.1	Flatscher-Bader et al. (2010)
<i>SPOCK1</i>	Sparc/osteonectin, CWCV (cys-trp-cys-val) and kazal-like domains proteoglycan (testican) 1	5q31.2	Liu et al. (2006)
<i>SPPI</i>	Secreted phosphoprotein 1	4q22.1	Manzardo et al. (2014)
<i>SRSF10</i>	Splicing factor, serine/arginine-rich, 10	1p36.11	Flatscher-Bader et al. (2005)
<i>ST18</i>	Suppression of tumorigenicity 18, zinc finger	8q11.23	Manzardo et al. (2014)
<i>STXBP2</i>	Syntaxin binding protein 2	19p13.2	Mayfield et al. (2002)
<i>SYN2</i>	Synapsin II	3p25.2	Mayfield et al. (2002)
<i>SYT1</i>	Synaptotagmin 1	12q21.2	Flatscher-Bader et al. (2005)
<i>TACR3</i>	Tachykinin receptor 3	4q24	Foroud et al. (2008)
<i>TAS2R16</i>	Taste receptor, type 2, Member 16	7q31.32	Hinrichs et al. (2006)
<i>TAS2R38</i>	Taste receptor, type 2, Member 38	7q34	Wang et al. (2007)
<i>TF</i>	Transferrin	3q22.1	Liu et al. (2004)
<i>TGFB1</i>	Transforming growth factor, beta-1	19q13.2	Mayfield et al. (2002)
<i>THRB</i>	Thyroid hormone receptor, beta	3p24.2	Mayfield et al. (2002)
<i>THSD7B</i>	Thrombospondin, type I, domain containing 7B	2q22.1	Wang et al. (2011b)
<i>TIMM10B</i>	Translocase of inner mitochondrial membrane 10 homolog B (yeast)	11p15.4	Flatscher-Bader et al. (2005)
<i>TIMP1</i>	TIMP (human tissue inhibitor of metalloproteinase) Metalloproteinase Inhibitor 1	Xp11.23	Mayfield et al. (2002)

Gene symbol	Gene name	Location	References
<i>TIMP2</i>	Tissue inhibitor of metalloproteinase 2	<i>17q25.3</i>	Liu et al. (2006)
<i>TIMP3</i>	Tissue inhibitor of metalloproteinase 3	<i>22q12.3</i>	Flatscher-Bader et al. (2005)
<i>TIPARP</i>	TCDD (tetrachlorodibenzo-p-dioxin)-inducible poly(ADP-ribose) polymerase	<i>3q25.31</i>	Wang et al. (2011a)
<i>TKT</i>	Transketolase	<i>3p21.1</i>	Liu et al. (2006)
<i>TMED10</i>	Transmembrane emp24-like trafficking protein 10 (yeast)	<i>14q24.3</i>	Mayfield et al. (2002)
<i>TMEM63A</i>	Transmembrane protein 63A	<i>1q42.12</i>	Manzardo et al. (2014)
<i>TMEM108</i>	Transmembrane protein 108	<i>3q22.1</i>	Heath et al. (2011)
<i>TMX1</i>	Thioredoxin-related transmembrane protein 1	<i>14q22.1</i>	Flatscher-Bader et al. (2005)
<i>TPH1</i>	Triosephosphate isomerase 1	<i>12p13.31</i>	Liu et al. (2006)
<i>TSPAN7</i>	Tetraspanin 7	<i>Xp11.4</i>	Liu et al. (2007)
<i>TTC12</i>	Tetratricopeptide repeat domain-containing protein 12	<i>11q23.2</i>	Yang et al. (2008)
<i>TXN</i>	Thioredoxin	<i>9q31.3</i>	Flatscher-Bader et al. (2005)
<i>TUBGCP2</i>	Tubulin, gamma complex associated protein 2	<i>10q26.3</i>	Mayfield et al. (2002)
<i>TULP1</i>	Tubby like protein 1	<i>6p21.31</i>	Mayfield et al. (2002)
<i>UBP1</i>	Upstream binding protein 1	<i>3p22.3</i>	Flatscher-Bader et al. (2005)
<i>UGT8</i>	Uridine diphosphate glycosyltransferase 8	<i>4q26</i>	Manzardo et al. (2014)
<i>ULK2</i>	Unc51-like kinase 2	<i>17p11.2</i>	Liu et al. (2006)
<i>UPP1</i>	Uridine phosphorylase 1	<i>7p12.3</i>	Flatscher-Bader et al. (2005)
<i>UQCRC2</i>	Ubiquinol-cytochrome c reductase core protein II	<i>16p12.2</i>	Liu et al. (2006)
<i>UQCRCF1</i>	Ubiquinol-cytochrome C reductase, Rieske iron-sulfur polypeptide 1	<i>19q12</i>	Liu et al. (2006)
<i>UROD</i>	Uroporphyrinogen decarboxylase	<i>1p34.1</i>	Flatscher-Bader et al. (2005)
<i>USH2A</i>	Usher syndrome, type IIA	<i>1q41</i>	Morozova et al. (2012)
<i>UTP20</i>	Small subunit (SSU) processome component, homolog (yeast)	<i>12q23.2</i>	Kapoor et al. (2014)
<i>VAMP3</i>	Vesicle-associated membrane protein 3	<i>1p36.23</i>	Mayfield et al. (2002)
<i>VCP</i>	Valosin-containing protein	<i>9p13.3</i>	Guo et al. (2009)
<i>WASF1</i>	Wiskott-Aldrich syndrome protein family, member 1	<i>6q21</i>	Flatscher-Bader et al. (2005)
<i>WIF1</i>	WNT (wingless-type MMTV integration site family) inhibitory factor 1	<i>12q14.3</i>	Manzardo et al. (2014)
<i>XRCC5</i>	X-ray repair, complementing defective, in Chinese hamster cells 5 (double-strand-break rejoining)	<i>2q35</i>	Joslyn et al. (2010); Yu et al. (2008)
<i>ZBTB11</i>	Zinc finger and BTB domain containing 11	<i>3q12.3</i>	Flatscher-Bader et al. (2005)
<i>ZBTB49</i>	Zinc finger and BTB domain containing 49	<i>4p16.3</i>	Flatscher-Bader et al. (2005)

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<i>ZNF24</i>	Zinc finger protein 24	<i>18q12.2</i>	Flatscher-Bader et al. (2005)
<i>ZSCAN32</i>	Zinc finger and SCAN domain containing 32	<i>16p13.3</i>	Flatscher-Bader et al. (2005)