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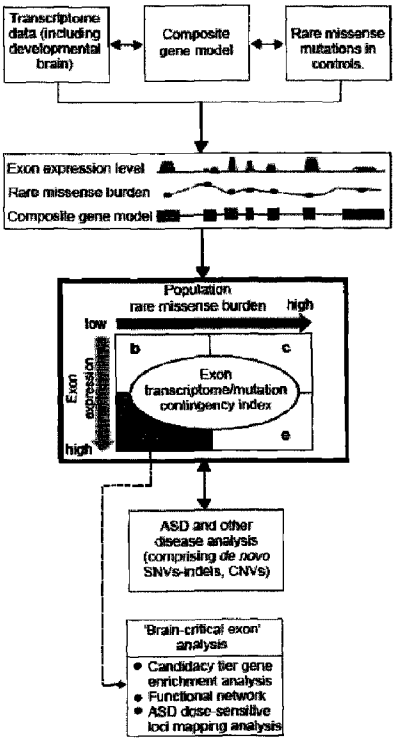

(57) Abrégé/Abstract:
A method of identifying a gene or genomic mutation that is linked to causality of a neuropsychiatric disorder is provided. The method comprises identifying exons which exhibit an expression level that is at least within the 75th percentile of exon expression levels within a nucleic acid-containing sample from a mammal having a neuropsychiatric disorder; comparing the sequence of each identified exon to the sequence of a corresponding exon from a healthy control to identify rare or de novo sequence mutations within the identified exon; calculating the burden of rare or de novo mutations within the exon; and determining the correlation between expression level of the identified exon and burden of de novo or rare mutations in the exon, wherein an inverse correlation indicates that the exon gene is linked to causality of the neuropsychiatric disorder.

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Les corrections suivantes sont faites en raison de l'article 109 des *Règles sur les brevets* et le brevet doit être lu tel que corrigé.

The following corrections are made pursuant to section 109 of the *Patent Rules* and the patent should read as corrected.

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(54) **Title**: METHOD OF DETERMINING DISEASE CAUSALITY OF GENOME MUTATIONS

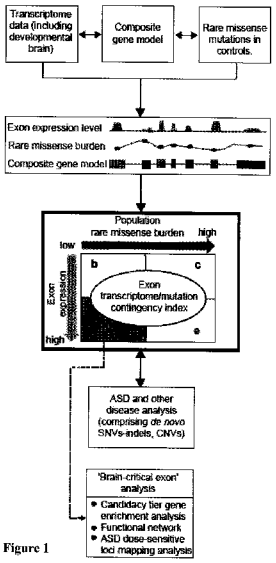

Figure 1

(57) **Abstract**: A method of identifying a gene or genomic mutation that is linked to causality of a neuropsychiatric disorder is provided. The method comprises identifying exons which exhibit an expression level that is at least within the 75th percentile of exon expression levels within a nucleic acid-containing sample from a mammal having a neuropsychiatric disorder; comparing the sequence of each identified exon to the sequence of a corresponding exon from a healthy control to identify rare or de novo sequence mutations within the identified exon; calculating the burden of rare or de novo mutations within the exon; and determining the correlation between expression level of the identified exon and burden of de novo or rare mutations in the exon, wherein an inverse correlation indicates that the exon gene is linked to causality of the neuropsychiatric disorder.

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METHOD OF DETERMINING DISEASE CAUSALITY OF GENOME MUTATIONS

Field of the Invention

[0001] The present invention relates generally to methods of identifying the significance of gene mutations, and more particularly, to a method of determining the disease causality associated with a genomic mutation.

Background of the Invention

[0002] Rare genomic variants are being revealed as preponderant genetic risk factors for neuropsychiatric conditions such as Autism Spectrum Disorder (ASD). ASD exhibits extensive clinical and genetic heterogeneity with high heritability (37-90%); for ~20% of affected individuals, an underlying genetic alteration is attributed as the cause. Chromosomal abnormalities, copy number variations (CNVs), smaller insertion/deletions (indels), single nucleotide variations (SNVs) and combinations thereof, have been described in ASD. Indeed, >100 ASD susceptibility genes of variable (and still largely undetermined) penetrance and expressivity are known, with several hundred others estimated to exist. A similar genetic architecture is also starting to emerge in other brain disorders such as schizophrenia (SZ), intellectual disability (ID) and epilepsy, and some genes are implicated across these disorders.

[0003] Proving causality of a particular DNA sequence variant(s) in a complex disorder such as ASD can be complicated by the exceptional rarity of mutations involved (often unique to individuals or families), and the rate of new mutation, which is often equal in controls. For example, the rate of *de novo* SNV-indels is similar (~1 per exome) between ASD-affected and -unaffected individuals (population controls or unaffected siblings). Regarding CNVs, a slightly increased burden of *de novo* events has been observed in ASD cases compared to family and population controls, but these deletions and duplications usually affect multiple genes complicating attempts in simple genotype-phenotype correlations. Through genotyping massive cohorts, there has been some progress identifying critical exons for clinical manifestation of ASD in the *NRXN, NRXN3* and *UTS2* genes. However, a more robust approach is needed to find those rare etiologic alterations amongst thousands of other variants generated in genome scanning experiments.

Summary of the Invention

[0004] It has now been determined that exons of genes harboring deleterious disease-related mutations were found to be significantly enriched in individuals having a neuropsychiatric disorder.

[0005] Accordingly, in aspects of the present invention, a method of identifying one or more genes or genome sequence mutations linked to causality of a neuropsychiatric disorder is provided. The method comprises the steps of:

i) identifying exons which exhibit an expression level that is greater than the 75th percentile of exon expression levels in nucleic acid from one or more individuals having a neuropsychiatric disorder;

ii) comparing the sequence of each identified exon to the sequence of a corresponding exon from a healthy control to identify rare or *de novo* sequence mutations within the identified exon;

iii) calculating the burden of rare or *de novo* mutations within the exon; and

iv) determining the correlation between expression level of the identified exon and burden of *de novo* or rare mutations in the exon, wherein an inverse correlation indicates that the exon gene and at least one of said sequence mutations is linked to causality of the neuropsychiatric disorder.

[0006] A computer system for conducting the method to determine genes linked to causality of a neuropsychiratric disorder, as well as a computer program product, comprising a tangible computer-readable medium carrying computer-usable instructions which, when executed by a processing unit of a computer, cause the processing unit to identify one or more genes linked to causality of a neuropsychiatric disorder using the above method, are also provided.

[0007] These and other aspects of the invention will be described in the detailed description by reference to the following figures.

Brief Description of the Figures

[0008] **Figure 1.** Assembling an exon transcriptome/mutation contingency index. A composite gene model was generated and used to integrate exon expression and rare missense mutation levels in controls. As a result an 'exon transcriptome/mutation contingency index' was generated. A 'critical exon' (d) was defined within the contingency index as one being highly-expressed relative to others, and at the same time being suppressed for the accumulation missense mutations in population controls (based on 75^{th} percentile thresholds from the data). Using this transcriptome/mutation contingency index, enrichment analyses were performed for genes implicated in ASD and other disorders. The entire set of 'critical exons' (3,955 in 1,744 genes) were further analyzed for functional enrichment and disease association testing.

[0009] **Figure 2.** Principal component analysis (PCA) to capture expression variability between brain samples. (A) Heatmap from principal component analysis showing temporal sample clustering captured by component 1 (PC1) loadings. The color gradient from red to blue represent the expression profile variation captured by the loadings. (B) Component 2 (PC2) loadings captures the variation within the prenatal (late prenatal) to early childhood samples.

[0010] **Figure 3.** Inverse correlation between burden of rare missense mutations and exon expression level. (A) Integration of exon expression level and rare missense mutation burden for *SCN2A*. (B) Genome-wide association between rare missense mutation burden and exon expression level in 11 human tissues (each in triplicate). (C) Exon expression level in 196 postmortem brain samples (controls) (from 13 male (M) and female (F) donors) in three developmental periods (prenatal (P), early childhood (E) and adult (A)) for 16 brain regions (11 neocortex regions (NCX), cerebellar cortex (CBC), hippocampus (HIP), Amygdala (AMY), mediodorsal nucleus of thalamus (MD), striatum (STR)). The spatio-temporal correlation coefficient shown in three panels was computed for genes reported to have *de novo* mutations (SNVs-indels) in ASD cases or unaffected siblings, ID and SZ. The last panel shows aggregate spatio-temporal correlation coefficient (average expression from samples for a developmental period) for genes ascertained in unaffected ASD siblings or in any of three disease subject groups.

[0011] **Figure 4.** Pearson correlation co-efficient between burden of rare missense and prenatal brain expression for known ASD genes *SHANK1*, *SHANK2*, *FMR1*, *AFF2(FMR2)*, and *SCN2A*. For these genes multiple independent ASD studies reported deletions (red square), duplications (blue square), point mutations (black triangle) or functional evidence from mouse (M) knockout studies.

[0012] **Figure 5.** Clustering of expression data. (A) The hierarchical clustering dendogram of replicates (A, B, C) for tissue types. The expression clustering for cerebellum and testis shows unique variance compared to the other tissues. (B) Principal component 1 (PC1) and 2 (PC2) plotted (for all replicates) for the tissue types capturing variance from their corresponding expression profile.

[0013] **Figure 6.** Distribution of conservation scores for gene exons reported to have *de novo* SNV/indel mutations in probands or siblings. phastCons and phyloP shows similar conservation patterns for both probands and siblings (mean PhastCons=0.566 and 0.563; phyloP=0.62 and 0.56, respectively). (A) PhastCons score histograms showing computed scores for exons of the gene reported to have *de novo* mutations in probands or siblings. (B) The distribution of phyloP showing minimum, maximum and average phyloP scores computed for each exon.

[0014] **Figure 7.** Distribution of rare missense mutations and age of the mutations for genes ascertained through probands or siblings. (A) Distribution of rare missense mutation burden for genes that harbor *de novo* mutations in probands and siblings (mean 0.0096 and 0.01, respectively). (B) All detected mutations (common and rare) reported in the exome sequencing database for the genes ascertained in probands or siblings, and mutation age (computed applying coalescent model (*9*)). (C) Only the rare missense mutations (<0.05 frequency) for genes ascertained through probands or siblings; these potentially deleterious mutations arose within the last 5,000 years.

[0015] **Figure 8.** Splicing code analysis of *de novo* SNVs. (A) The CDFs of code-predicted $\Delta\Psi$s for probands and unaffected siblings *de novo* mutations. Overall proband mutations do not have larger predicted $\Delta\Psi$s, and the K-S test does not reject the null hypothesis. (B) The ROC curve for discriminating probands from controls using code-predicted $\Delta\Psi$s; area under ROC curve (AUC) is nearly 0.5.

[0016] **Figure 9.** Highly expressed exons with *de novo* mutations. A) percentages of brain tissues that have high expression (>75th percentile) of the exons comprising *de novo* mutations that were ascertained in cases and unaffected siblings. B) box plots show the percentages of *de novo* mutations (for cases and unaffected siblings) that can be classified as critical exons (left) or tolerated exons (right) using all transcriptome samples. Each confidence interval represents the fraction of variability in the number of critical or tolerated exons obtained from different transcriptome samples (interquartile range (IQR) is between the first and third quartiles). C) the burden of rare missense mutations and expression in human developing brain of the *SLC6A1* gene, for which mutated exons have been reported in ASD cases. To capture the exon inclusion/exclusion event for the mutated exons in prenatal brain and adult brain, RT-PCR assays were designed considering various combinations of the flanking exons. Exclusion events

(defined by a line for an exon) were confirmed by Sanger sequencing (Table 5). Partial exclusion of exon 3 of the *SLC6A1* gene was also captured owing to the variable length of this exon in different isoforms.

[0017] **Figure 10A-C.** Validation of RNA-seq for *de novo* proband and sibling gene. Spatio-temporal association analysis where -log(P) value is represented by color intensities and the odds ratio (OR, 95% CI) on y-axis for genes reported to have *de novo* mutations in ASD probands (upward bar graph) and unaffected siblings (inverted bar graph) within three developmental time periods: (A) Prenatal, (B) early childhood and (C) adult samples. Similar to microarray data (Fig. 2A), we have observed strongest association within neocortex prenatal samples (Bonferroni corrected, $p < 7.8 \times 10^{-28}$; OR = 2.142).

[0018] **Figure 10D-E.** Classifying missense/LOF exons with de novo mutations in ASD proband and unaffected siblings: (D) box plots show the percentages of de novo mutations (for cases and unaffected siblings) that can be classified as critical exons (left) or tolerated exons (right) using all transcriptome samples. Each confidence interval represents the fraction of variability in the number of critical or tolerated exons obtained from different transcriptome samples (interquartile range (IQR) is between the first and third quartiles). (E) Applying 75th percentile cutoff on the transcriptome/mutation contingency index, we have computed the fraction of LOF that can be classified as 'critical' and 'tolerated' exons using all transcriptome samples. The confidence interval represents the fraction variability of 'critical' or 'tolerated' exons obtained from different transcriptome samples.

[0019] **Figure 11.** Exon skipping event for a loss of function (LOF) mutation reported in an unaffected sibling. Exon 17 (highlighted red) reported in sibling gene (*EPB41L3*) show frequent exclusion mostly in prenatal (P) and adult brains (A). The exclusion event was confirmed by Sanger sequencing.

[0020] **Figure 12.** Association between burden of rare missense mutations and expression (using 11 distinct human tissues, each with 3 replicates) for genes for nervous system disorders (per Online Mendelian Inheritance in Man (OMIM)). The phenotypes are classified (in OMIM) according to mode of inheritance (autosomal dominant/recessive). FET significance for each tissue replicate plotted where the –log(P) on left y-axis and odds ratio (OR) on right y-axis. Cerebellum replicates show the strongest association signals only for dominant nervous system disorder genes.

[0021] **Figure 13.** The association between burden of rare missense mutations and expression in various brain tissues for fragile X mental retardation protein targets (FMRP) and forkhead box P2

(FOXP2) targets. The plot shows significant association (-log(P) - Fisher exact test in y axis; odds ratio (OR) – in x-axis) for FMRP targets (color circles) but not for *FOXP2* targets that show evidence of positive selection (grey circles). Size of each circle represents the computed odds ratio.

[0022] **Figure 14.** Association of exon transcriptome and rare missense mutation burden using spatio-temporal expression for genes within *de novo* CNVs ascertained in ASD probands or controls. *De novo* losses/gains comprehensively ascertained in four earlier studies of ASD (AGP (stage 1 and 2), SSC1 and SSC2) were assayed in data from 16 brain regions of postmortem donors from three developmental periods (prenatal (P), early childhood (E), and adult (A)). The analysis plotted for 196 developing human brain samples (P-prenatal, E-early childhood, and A-adult) includes 11 neocortex (NCX) regions (Fig 4A), amygdala (AMY), cerebellar cortex (CBC), hippocampus (HIP), mediodorsal nucleus of the thalamus (MD) and striatum (STR).

[0023] **Figure 15.** Delineation and profiling of brain specific critical exons. (A) Association analysis of spatio-temporal expression for genes within *de novo* CNVs ascertained in four earlier studies of ASD (AGP (stage 1 and 2), SSC1 and SSC2) were assayed in data from 16 brain regions of postmortem donors from three developmental periods (prenatal (P), early childhood (E), and adult (A)). The plot shows spatio-temporal association results between exon expression level (11 neocortex regions) and burden of rare missense mutations for genes within *de novo* CNVs reported in ASD Probands and in controls (see Fig. 14 for amygdala, cerebellar cortex, hippocampus, mediodorsal nucleus of thalamus, and striatum transcriptome association results and RNA-Seq validation). (B) Brain specific 'critical exon' enrichment analysis on FMRP targets, PSP, ASD (autosomal dominant (AD), X-linked (XL)) and genes with *de novo* mutations represented by the vertical line and the *p*-values (FET; Benjamini Hochberg corrected) relative to the two corresponding backgrounds (entire RefSeq exons set (background 1) and highly brain expressed exons (background 2)). The empirical *p*-value was obtained from the permutation test for each background (10,000 random draw of equal number of exons). (C) A functional map of brain specific 'critical exons' by mapping enrichment significance as a network of gene sets (nodes), where edges represent mutual overlap between gene sets. The size of the node is proportional to the number of genes in each gene set, and the node color represents the significance (*p*-value) of overlap. Nodes that are functionally interconnected are similarly circled (implicated in previous ASD networks) into one major group and labeled with their corresponding function.

[0024] **Figure 16.** The RNA-seq validation for genes within *de novo* CNVs ascertained in ASD probands or controls. Applying 75th percentile cutoff (similar to microarray), the association significance (FET; left y-axis –log(P)) for three developmental periods (prenatal (P), early childhood (E), and adult

(A)) on 196 human brain samples. Bars illustrate -log(P) for genes within rare CNVs ascertained in AGP stage 1 and 2 controls. Similar to microarray, from RNA-seq analysis we observed the strongest association in neocortex from prenatal samples (FET, Bonferroni corrected, $p < 3.13 \times 10^{-11}$; OR=1.45).

[0025] **Figure 17.** *de novo*/rare single genic losses reported in AGP stage 1 and 2 and their association analysis. Spatio-temporal microarray analysis using human developmental brain for *de novo*/rare (<0.01 frequency) single gene losses (impacting coding sequence) exclusively identified in probands or controls. Significance with higher odds ratio (OR) was observed within genes ascertained for probands in prental neocortex samples.

[0026] **Figure 18.** Tissue-specific 'critical exons'. (A) Relative proportion of tissue-specific critical exons detected from 11 tissues. (B) Exon density distribution for genes containing 'brain-critical exons'. (C) Genes were scored based on the number of exons relative to mean number of tissue specific critical exons in the list. The plot shows exonic scores for the genes reported in – ASD (AD and X-linked), *de novo* SNVs, FMRP targets, and PSP.

[0027] **Figure 19.** Overlap of 'brain-critical exons' within the 16p11.2 deletion locus. (A) Overlapping 'brain-critical exons' for genes within the 16p11.2 locus and their corresponding exon score is plotted. The horizontal bars represent the recurrent breakpoint reported in DECIPHER database, the narrow critical region captured in a multiplex family with similar phenotypes. (B) Relative expression (2^(-dCt)) from quantitative real-time PCR (qRT-PCR) relative to ACTB (replicated with another housekeeping gene *MED13*) shows brain (adult cerebellum) specific higher expression of the identified 'brain-critical exons' in *SEZ6L2*, *ASPDH1*, *KCTD13*, and *PRRT2* within 11 different tissues, consistent with microarray expression intensities.

[0028] **Figure 20.** Genes from 3q29 and 17q21.31 loci containing 'brain-critical exons', and their expression profile from multiple tissues. (A) Within 3q29, recurrent micro-duplication/deletions are associated with syndromes. Genes containing critical exons from this locus are: discs large homolog 1 (*DLG1*) and phosphatidylinositol glycan anchor biosynthesis, class Z (*PIGZ*). *DLG1* is an ASD candidate gene within the locus and independent reports are emerging to establish *DLG1* as a primary candidate gene for 3q29 micro duplication/deletion syndrome. There is also emerging evidence for the potential role of *DLG1-4* in cognition and psychiatric disorder from mouse knockouts. A recent study on *PIGZ* knockout mouse experiment showed a significant increase of amyloid-β (Aβ) peptide (a molecule with pathological role for Alzheimer's disease). (B) Multiple brain specific critical exons (5 exons) within corticotropin-releasing hormone receptor 1 (*CRHR1*) gene and microtubule-associated protein tau

(*MAPT*) gene were detected within 17q21.31 deletion locus. Multiple lines of evidence suggest the role of corticotropin-releasing hormone receptor 1 (*CRHR1*) on neuropsychiatric disorders. *MAPT* is also a well-studied candidate gene for neuropsychiatric disorders.

[0029] **Figure 21.** Genes for neurofibromatosis 1 (NF1) microdeletion syndrome and 22q11.21 loci containing 'brain-critical exons' and their expression from multiple tissues. (A) The *NF1* micro-deletion syndrome involves two primary breakpoints with variable phenotypes. Both breakpoints affect coding sequence of *NF1* and RAB11 family interacting protein 4 (*RAB11FIP4*) genes and the cases also have intellectual disabilty as a common phenotypic manifestation. *NF1* is reported to be the primary candidate gene in the locus by multiple studies and in addition *RAB11FIP4* shown to be a candidate gene from gene expression analysis. (B) Within the 22q11.21 locus, four genes (armadillo repeat gene deleted in velocardiofacial syndrome (*ARVCF*), DGCR8 microprocessor complex subunit (*DGCR8*), zinc finger, DHHC-type containing 8 (*ZDHHC8*) and phosphatidylinositol 4-kinase, catalytic, alpha (*PI4KA*)) were found to have 'brain-critical exons'. All four genes within these loci implicated previously in multiple neuropsychiatric phenotype studies. *ARVCF, DGCR8, ZDHHC8* are the three well documented candidate genes.

[0030] **Figure 22** illustrates critical-exon enrichment analysis of prenatal pathogenic, VOUS and control samples from individuals with developmental delay.

[0031] **Figure 23** is a block diagram illustrating a processing system suitable for use in aspects of the invention.

Detailed Description of the Invention

[0032] A method of identifying a gene or genomic mutation that is linked to causality of a neuropsychiatric disorder is provided. The method comprises identifying exons which exhibit an expression level that is greater than the 75th percentile (third quartile) of exon expression levels in nucleic acid from one or more individuals having a neuropsychiatric disorder; comparing the sequence of each identified exon to the sequence of a corresponding exon from a healthy control to identify rare or *de novo* sequence mutations within the identified exon; calculating the burden of rare or *de novo* mutations within the exon; and determining the correlation between expression level of the identified exon and burden of *de novo* or rare

mutations in the exon, wherein an inverse correlation indicates that the exon gene is linked to causality of the neuropsychiatric disorder.

[0033] The term "neuropsychiatric disorder" is used herein to encompass Autism Spectrum Disorder (ASD), i.e. a disorder that results in developmental delay of an individual such as autism, Asperger's Disorder, Childhood Disintegrative Disorder, Pervasive Developmental Disorder-Not Otherwise Specified (PDD-NOS) and Rett Syndrome (APA DSM-IV 2000); schizophrenia (SZ), intellectual disability (ID), Fragile X syndrome, epilepsy and related nervous system disorders such as OMIM (*Online Mendelian Inheritance in Man)* nervous system disorders.

[0034] In the present method, nucleic acid from one or more individuals, e.g. humans, having a neuropsychiatric disorder of interest, a nucleic acid sample set, is studied and compared to corresponding nucleic acid control samples, i.e. nucleic acid samples from healthy individuals that do not have the neuropsychiatric disorder of interest. Nucleic acid from various biological samples may be studied. Preferred biological samples include brain samples, for example, neocortex, amygdala, cerebellar cortex, hippocampus, mediodorsal nucleus of the thalamus, and striatum. The samples may be obtained from any age group, including prenatal, child and adult samples.

[0035] The method comprises identifying exons within nucleic acid from one or more individuals (that have a selected neuropsychiatric disorder) that exhibit a high expression level relative to the expression of other exons within the sample, i.e. a high expression level is considered to be a level that is greater than the 75^{th} percentile of exon expression levels of all exons within the nucleic acid sample or data set.

[0036] Rare or *de novo* sequence mutations within exons exhibiting a high expression level are then identified by sequence comparison with corresponding control exon sequence, e.g. the nucleic acid sequence of a corresponding exon from a healthy control mammal that does not have the neuropsychiatric disorder of interest. Such sequence comparison is conducted using methods well-established in the art, and will preferably employ automated computer sequence comparison. Sequence mutations may include missense, frameshift, nonsense, splice-site variants and copy number variations (CNVs). "Rare" mutations are those which occur at a

frequency of less than 0.05. A mutation not possessed by either parent of a sample being analyzed is considered to be a "*de novo*" mutation.

[0037] Once rare and *de* novo mutations within a given exon are identified, the burden of rare and *de novo* mutations within the exon is calculated. Mutation burden is defined as the mutation count, e.g. of rare and *de novo* mutations, divided by the length of the exon. Low mutation burden is considered to be a mutation burden that is less than the 75^{th} percentile of a given sample or dataset.

[0038] The correlation between expression level of an exon that exhibits a high expression level, i.e. an expression level greater than the 75^{th} percentile of exon expression levels in the sample, and burden of rare and *de novo* mutations within the exon is then calculated. An inverse correlation between exon expression level and mutation burden indicates that at least one of the rare or *de novo* mutations is linked to causality of the neuropsychiatric disorder. It also provides an indication that the gene in which the subject exon exists is linked to causality of the neuropsychiatric disorder. Further analysis may be conducted to determine the mutation that is linked to causality of the neuropsychiatric disorder.

[0039] As one of skill in the art will appreciate, one or more of the steps of the present application may be carried out using an appropriate processing device, e.g. a computer. For example, the steps of identifying exons which exhibit an expression level that is greater than the 75^{th} percentile of exon expression levels within a sample, comparing the sequence of each identified exon to the sequence of a corresponding exon from a healthy control to identify sequence mutations, calculating the burden of rare or *de novo* mutations within the exon, and determining the correlation between expression level of the identified exon and burden of *de novo* or rare mutations in the exon, may each be conducted using a processing device or computer to analyze datasets of exons, conduct comparisons against controls and then to do calculations.

[0040] An appropriate processing device for use to conduct each step of the present method may include any suitable computer or microprocessor-based system, such as a desktop or laptop computer or a mobile wireless telecommunication computing device, such as a smartphone or tablet computer, which may receive data or information to be processed. The

computer or microprocessor-based system may be coupled to another device from which data/information to be processed in accordance with the claimed method, or such data/information may be obtained from a separate storage medium or network connection such as the Internet. An illustrative computer system in respect of which the methods herein described may be implemented is presented as a block diagram in Figure 23. The illustrative computer system is denoted generally by reference numeral 10 and includes a display 12, input devices in the form of keyboard 14 and pointing device 16, computer 18 and external devices 30. While pointing device is depicted as a mouse, it will be appreciated that other types of pointing device may also be used.

[0041] The computer may contain one or more processors or microprocessors, such as a central processing unit (CPU) 22. The CPU performs arithmetic calculations and control functions to execute software stored in an internal memory 26, preferably random access memory (RAM) and/or read only memory (ROM), and possibly additional memory 32. The additional memory may include, for example, mass memory storage, hard disk drives, optical disk drives (including CD and DVD drives), magnetic disk drives, magnetic tape drives (including LTO, DLT, DAT and DCC), flash drives, program cartridges and cartridge interfaces, removable memory chips such as EPROM or PROM, emerging storage media, such as holographic storage, or similar storage media as known in the art. This additional memory may be physically internal to the computer, external, or both. The computer system may also include other similar means for allowing computer programs or other instructions to be loaded. Such means can include, for example, a communications interface 34 which allows software and data to be transferred between the computer system and external systems and networks. Examples of communications interface include a modem, a network interface such as an Ethernet card, a wireless communication interface, or a serial or parallel communications port. Software and data transferred via communications interface are in the form of signals which can be electronic, acoustic, electromagnetic, optical or other signals capable of being received by communications interface. Multiple interfaces, of course, may be provided on a single computer system.

[0042] Input and output to and from the computer is administered by the input/output (I/O) interface 20. This I/O interface administers control of the display, keyboard, external devices and other such components of the computer system. The computer will generally

include a graphical processing unit (GPU) 24 useful for computational purposes as an adjunct to, or instead of, the CPU 22, for mathematical calculations.

[0043] The various components of the computer system are coupled to one another either directly or by coupling to suitable buses.

[0044] The methods described herein may be provided as computer program products comprising a tangible computer readable storage medium, such as non-volatile memory, having computer readable program code embodied therewith for executing the method. Thus, the non-volatile memory would contain instructions which, when executed by a processor, cause the computing device to execute the relevant method.

[0045] The above systems and methods may be implemented entirely in hardware, entirely in software, or by way of a combination of hardware and software. In a preferred embodiment, implementation is by way of software or a combination of hardware and software, which includes but is not limited to firmware, resident software, microcode, and the like. Furthermore, the above systems and methods may be implemented in the form of a computer program product accessible from a computer usable or computer readable medium providing program code for use by or in connection with a computer or any instruction execution system. In such embodiments, the computer program product may reside on a computer usable or computer readable medium in a computer such as the memory of the onboard computer system of the smartphone, or the memory of the computer, or on a computer usable or computer readable medium external to the onboard computer system of the smartphone or the computer, or on any combination thereof.

[0046] Thus, the present method advantageously provides a means of identifying disease causality in complex neuropsychiatric disorders that will aid in the diagnosis and treatment of such diseases. In particular, genes relevant to a neuropsychiatric disorder may be identified, including the related sequence mutation(s) within a pertinent exon of the particular disease-related gene. The identification of disease causality in this manner lends to the diagnosis of neuropsychiatric disorders, and provides a basis for developing treatments thereof by providing valid targets on which potential treatments may be based.

[0047] Embodiments of the present invention are described in the following specific examples which are not to be construed as limiting.

Example 1

MATERIALS AND METHODS

Burden of Rare Missense Mutations

[0048] Data from the Exome Sequence Project (ESP) (http://evs.gs.washington.edu/EVS/, downloaded February 2013) initiated by US National Health Heart, Lung and Blood Institute (NHLBI) was used to calculate the burden of rare missense mutations in human populations. The data was processed by computer to identify variants. Variants were obtained from 6,503 exomes (2,203 African Americans (AA) and 4,300 European Americans (EA)); each exome had a median sequence coverage of at least 100X (Fu et al. *Nature* **493**, 216-220 (2013); published online EpubJan 10 (10.1038/nature11690). We used the composite RefSeq gene annotation (which includes all exons from annotated isoforms) for our analysis and after excluding genes with no variant calls (3,267 genes), a total of 20,417 genes (including protein coding and pseudo genes) remained for analysis. The number of variants that passed quality control was 1,284,453 in EA exomes and 1,162,001 in AA exomes. Of these, the rare variants (<0.05 frequency) were 968,840 (75%) for EA and 600,174 (51%) for AA. The differences in rare variants between these two populations are highlighted in Fu et al. 2013. We computed (using a computer) the burden of rare missense mutation at the exon level for European populations using the genome analysis toolkit (GATK) variant annotation. Rare missense variants with a frequency <0.05 are a strong proxy for recent (mostly within the last 5,000-10,000 years) accelerated deleterious mutation events in humans. For any exons within the composite gene model (hg19) (Fig. 1), variants annotated as missense for any gene isoform were considered. We calculated a normalized burden of mutation from the rare missense count for each exon *e* in the EA data:

$$e_n = \frac{rare\ missense\ count}{|e_l|}$$

where e_n is the normalized exon burden and $|e_l|$ is the length of exon *e*.

Expression Data

A. Multiple Tissue Expression Data

[0049] We obtained expression data from the Affymetrix GeneChip Human Exon 1.0 ST array for 11 normal human tissues, each in triplicate (Gardina et al. *BMC genomics* **7**, 325 (2006)10.1186/1471-2164-7-325). Tissues included cerebellum, breast, heart, liver, muscle, kidney, thyroid, pancreas, prostate, spleen, and testis. Partek® Genomics Suite™ was used to compute core meta-probe set signal intensity from the raw .CEL. Exons were kept for analysis only if they were also covered in the exome sequencing project for variant calls. Probes prone to multiple hybridizations were excluded. The Robust Multi-array Average (RMA) algorithm (Irizarry et al. *Nucleic acids research* **31**, e15 (2003)) was used for background signal subtraction; normalization and the log2 expression value was computed for each exon. A total of 16,713 RefSeq genes (covering 141,224 exons) were surveyed in all 11 tissues. Using a threshold of $\log_2$-transformed intensity ≥ 6 to define expressivity (Sanders et al. *Nature* **485**, 237-241 (2012)), we detected 16,411 genes with at least one exon expressed for a tissue sample.

[0050] Hierarchical clustering with Euclidean distance is a method to detect overall variation among replicates. This method typically finds groups of genes with a similar expression pattern. Then, a dendogram can be constructed to illustrate the relationship between replicates. This approach demonstrated that the replicates were clustered strongly according to tissue type (Fig. 5A); testis and cerebellum showed similar expression patterns, different from the other tissues. We applied a second method - principal component analysis (PCA) - to capture overall variance among the tissues. PCA analysis also showed that tissues highly clustered by tissue type (Fig. 5B), with testis and cerebellum showing greater variance compared to other tissues.

B. Human Brain Microarray Data

[0051] The spatio-temporal expression profiles from developmental human brain used in this study were from the BrainSpan database (http://www.brainspan.org/static/download.html) (Sanders et al. 2012). The samples were chosen so that each developmental period comprised at least two age- and sex-matched donors (Table 1). The developmental periods were categorized into three groups: prenatal (8 post-conception weeks (pcw) to 21pcw), early childhood (4 months to 3 years) and adulthood (≥13 years). For each donor, we obtained expression data from at least

13 brain regions (Table 1 and 2). These included neocortex (NCX) (11 NCX regions includes orbital frontal cortex (OFC), dorsolateral prefrontal cortex (DFC), ventrolateral frontal cortex (VFC), medial prefrontal cortex (MFC), primary motor cortex (M1C), primary somatosensory cortex (S1C), posterior inferior parietal cortex (IPC), primary auditory cortx (A1C), posterior superior temporal cortex (STC), inferolateral temporal cortex (ITC), primary visual cortex (V1C)), amygdala (AMY), cerebellar cortex (CBC), hippocampus (HIP), mediodorsal nucleus of the thalamus (MD), and striatum (STR).

Table 1. Spatio-temporal Transcriptome (microarray and RNA-SEQ) data. Human development periods and sample brain tissues from 13 postmortem donors.

Age/ Period	Category	Male(M)	Female(F)	Analyzed Brain Region Nomenclature	
				M	F
8pcw/ Embryonic	Embryonic	13058	-	AMY,CGE,DFC,DTH,HIP,ITC,LGE,MFC,MGE,M1C-S1C,Ocx,OFC,PCx,STC,URL,VFC	-
13pcw/ Early Fetal	Prenatal	12820	12834	A1C,AMY,DFC,HIP,IPC,ITC,M1C,MFC,OFC,S1C,STC,STR,VFC	A1C,CB,DFC,HIP,IPC,ITC,M1C,MD,MFC,OFC,S1C,STC,STR,V1C,VFC
21pcw/Late Fetal	Prenatal	12886	12365	A1C,AMY,CBC,DFC,HIP,IPC,ITC,M1C,MD,MFC,OFC,S1C,STC,STR,V1C,VFC	A1C,AMY,CBC,DFC,HIP,IPC,ITC,M1C,MD,MFC,OFC,S1C,STC,STR,V1C,VFC
4-6Mo/ Early Infancy	Early Childhood	12296	12297	A1C,AMY,CBC,DFC,HIP,IPC,ITC,M1C,MD,MFC,OFC,S1C,STC,STR,V1C,VFC	A1C,AMY,CBC,DFC,HIP,IPC,ITC,M1C,MD,MFC,OFC,S1C,STC,STR,V1C,VFC
3Y/ Early Childhood	Early Childhood	12980	12836	A1C,AMY,CBC,DFC,HIP,IPC,ITC,M1C,MFC,OFC,S1C,STC,V1C,VFC	A1C,AMY,CBC,HIP,IPC,ITC,M1C,MD,S1C,STC,STR,V1C,VFC
13-15Y/ Adolescence	Adult	12299	12831	A1C,AMY,CBC,DFC,IPC,ITC,M1C,MD,MFC,OFC,S1C,STC,STR,V1C,VFC	A1C,AMY,CBC,DFC,HIP,IPC,ITC,M1C,MD,MFC,OFC,S1C,STC,STR,V1C,VFC
37-40Y/ Adulthood	Adult	12303	12304	A1C,AMY,DFC,HIP,IPC,ITC,M1C,MD,MFC,OFC,S1C,STC,STR,V1C,VFC,	A1C,AMY,DFC,HIP,IPC,ITC,M1C,MD,MFC,OFC,S1C,STC,STR,V1C,VFC

pcw = post-conceptional weeks; Mo = months; Y = years.

Table 2: Brain region ontology and nomenclature used in this study.

Brain Region Analysed	Region Name
AMY	amygdaloid complex
CGE	caudal ganglionic eminence
DFC	dorsolateral prefrontal cortex
DTH	dorsal thalamus
HIP	hippocampus
ITC	inferolateral temporal cortex

LGE	lateral ganglionic eminence
MFC	medial prefrontal cortex
MGE	medial ganglionic eminence
MIC-STC	primary motor-sensory cortex
Ocx	occipital neocortex
OFC	orbital frontal cortex
PCx	parietal neocortex
STC	posterior (caudal) superior temporal cortex
URL	upper (rostral) rhombic lip
VFC	ventrolateral prefrontal cortex
AIC	primary auditory cortex
IPC	posterior inferior parietal cortex
MIC	primary motor cortex
SIC	primary somatosensory cortex
STR	striatum
CB	cerebellum
MD	mediodorsal nucleus of thalamus
VIC	primary visual cortex
CBC	cerebellar cortex

[0052] RNA from 196 tissue samples from 13 post mortem donors were run on the Affymetrix GeneChip Human Exon 1.0 ST array platform. This data set surveyed 17,296 genes, comprising 230,881 exons, from which at least one exon was expressed (log_2-transformed signal intensity of $\geq$ 6) in at least one brain region. The quality control (QC) measures and the microarray data processing can be found at Kang et al. *Nature* 478, 483-489 (2011). We further applied quantile normalization across all samples. Exons without probes in the microarray, or if not covered in the NHLBI exome sequencing project, were also excluded. The 'loadings' of principle component analysis (PCA) are correlation coefficients between the principle component scores and the original variable, and reflect the importance of each variable in accounting for the variability in the principle component. We constructed a PCA box plot (Fig. 2) for the gene sets and loading vectors extracted from genome-wide spatio-temporal PCA analysis on 196 brain samples (with gene as object). It showed the greatest variation (captured as the first principal component (PC1) loadings) between prenatal (embryonic, early and late prenatal) and postnatal (early childhood and adult) transcriptomes. The second component (PC2) loadings captured variation between embryonic and early childhood expression of genes.

Our analysis from both PC1 and 2 shows CBC with highest variance among all brain regions analyzed.

C. Human Brain RNA Sequencing (RNA-seq) Data

[0053] We derived RNA sequencing (RNA-seq) data from the BrainSpan database. These data contained transcriptome profiles from the same 196 tissues from 13 postmortem donors as used in the microarray analysis. Method details for sequencing, alignment, quality control and expression quantification can be found in the BrainSpan Technical White Paper 2011 (http://www.brainspan.org/). The expression measures were provided for exons as reads per kilobase (kb) per million (RPKM) from mapped reads. We applied quantile normalization to the computed RPKM to reduce systematic bias across the samples. Exons were excluded if not covered in the exome sequencing project. RNA-seq data were used primarily to validate association significance (between exon expression level and burden of rare missense mutations) that we observed by microarray.

3. Candidacy Tier of Genes for Neuropsychiatric Phenotypes

A. *de novo* Single Nucleotide Variants (SNV) and Indels

[0054] To validate our analysis, a set of *de novo* mutations that are highly likely to give rise to the neurological conditions under study (i.e., ASD or other) were used. Hence, we curated 243 genes with 256 *de novo* mutations (nonsense, frameshift, splicing, missense) that are validated and predicted (using multiple algorithms) to be highly damaging, from nine whole genome/exome sequencing (WGS/WES) studies. These include 214 genes from ASD studies (*2, 4, 15-18*); 14 from a schizophrenia study (*7*); and 15 from intellectual disability studies (*6, 19*). We compiled 82 genes with 84 *de novo* possibly damaging exonic mutations from two large studies (*4, 15*) that used the Simon Simplex Collection (SSC). SSC is a phenotypically comprehensive resource of simplex pedigrees that consists of ASD probands and their unaffected siblings.

B. *de novo* Copy Number Variation (CNV)

[0055] We collected *de novo* CNVs from three published data sets *(3, 22, 23)* and one unpublished case-control set (Autism Genome Project (AGP) stage 2). AGP Stage 1 reported its

genome wide finding with validated rare/*de novo* CNVs using the Illumina 1M-single array (*3*). The ongoing stage 2 uses Illumina 1M-Duo. The total number of ASD cases used (stage 1 + 2 combined) was 2,446 and 2,640 controls. In the present analysis, we used 101 validated *de novo* CNVs from the cases, which encompass 886 unique genes. From stage 1 and 2 AGP population controls, we used genes within the rare CNVs (< 0.01 frequency) for our analysis (*3, 21*). In addition, we documented *de novo*/rare losses impacting coding sequences for a single gene exclusively in ASD Probands. Similarly, we ascertained rare single genic losses observed exclusively in controls (Table 3).

Table 3. AGP dataset (from stage 1 and 2) consists of losses impacting coding sequences for a single gene (*de novo*/rare).

AGP Stage 1 + 2	**Rare + *de novo* (Single Genic CNV Loss) genes.**
ASD Cases	153
Controls	148

[0056] We also curated genome wide *de novo* CNVs from two large well-studied SSC cohorts; SSC1 refers to 64 *de novo* CNVs (affecting 497 genes (*23*) and SSC2 refers to 75 *de novo* CNVs (affecting 993 genes) (*22*). A significantly increased *de novo* CNV burden is documented for ASD probands (*3, 22, 23*). For the SSC cohorts, there were not enough validated rare/*de novo* CNVs reported for unaffected siblings for meaningful statistical analysis.

C. OMIM Dominant and Recessive Phenotypic Genes for Nervous System

[0057] Online Mendelian Inheritance in Man (OMIM) is a continuously updated catalog of human genes and genetic disorders and traits. The database (http://omim.org/) is a compendium of human genes and phenotypic information. We used the MIM number notation to infer the mode of inheritance for all the genes in the Human Phenotype Ontology (HPO) database (harite.de/hudson/job/hpo.annotations.monthly/lastStableBuild/, accessed in April 2013). We only considered genes with HPO phenotype annotation derived from OMIM, as we could reliably infer the mode of inheritance for these. OMIM identifiers corresponding to official gene symbols were obtained from the Bioconductor package (version 2.8), available for R statistical software (version 2.15.3). Our analysis was primarily based on human phenotypes:

"abnormality of the nervous system" (HP:0000707) which includes 319 autosomal dominant genes, and 487 recessive genes.

D. FMRP and FOXP2 Target Genes

[0058] The loss of Fragile X mental retardation protein (FMRP) causes Fragile X Syndrome (FXS) which is the most common inherited form of intellectual disability. FXS is the leading monogenic cause of ASDs; approximately 50% of all FXS cases show autistic behavior. 842 gene products have been identified as FMRP targets. Multiple lines of evidence show a significant enrichment of mutations in FMRP target genes among ASD probands . The functional relevance of FMRP targets is also implicated within the context of ASD pathogenesis. The surplus of pathogenic mutations among FMRP targets for cases relative to controls implies that the targets are undergoing strong purifying selection.

[0059] In contrast to FMRP, a subset (Table 4) of genes targeted by Forkhead box P2 (FOXP2) protein show strong evidence of positive selection. *FOXP2* is a highly conserved gene implicated in human speech and language disorders. Its target genes have been curated from three studies (*40-42*) and Ayub et al. 2013 showed a subset of these (131 genes) to have strong positive selection properties only in the European population (as used in our analysis). These genes play important roles in the plasticity of the human developing brain.

Table 4. *FMRP* target genes; *FOXP2* gene targets show evidence of positive selection; and the reported ASD genes (autosomal dominant and X-linked).

Category (Positive/Purifying Selection)	Genes
FMR1 Targets Under Positive Selection	842
FOXP2 Targets Under Positive Selection	131
ASD (AD = autosomal dominant and XL = X-linked)	81

E. Genes for Post-synaptic Proteome (PSP)

[0060] Bayés et al. (*26*), isolated post-synaptic density from human neocortex and identified a large number of proteins, termed the post-synaptic proteome (PSP). They identified mutations within the PSP genes as the cause of 133 neurological and psychiatric diseases. Evidence from animal models (primate and rodent) also shows the importance of the PSP for nervous system disease and behavior. We used all experimentally identified human post-synaptic density genes in our analysis (Table 4).

F. Single Genes Associated with ASD

[0061] A list was curated from studies of ASD families of mutations with Mendelian inheritance (autosomal dominant (AD) or x-linked (XL))(*5*). This list consists of the best-studied *bona fide* ASD genes from multiple independent studies.

4. Analysis

A. Pearson Correlation

[0062] We used the Pearson correlation significance test for linear relationships between exonic expression and rare missense mutation burden. P-value < 0.05 (after Bonferroni multiple test correction) was the threshold for significance. Unless otherwise noted, the statistical analyses were performed using R statistical software, version 2.15 (http://www.r-project.org/). We applied the Wilcoxon association test (Bonferroni corrected) to quantify spatio-temporal expression differences for exons ascertained by virtue of mutation in probands and unaffected siblings.

B. Association

[0063] We tested the association between exon expression level and burden of rare missense mutation using Fisher's exact test (FET). The association was determined using a computer. To test the association, expression level was classified as high or low (above or below the 75^{th} percentile, respectively). The percentile was computed from expression data for all samples, separately either from microarray (11 tissues or spatio-temporal data from BrainSpan) or RNA sequencing. We used a similar procedure to classify the burden of rare missense mutations in EA data (Fig. 10). The association was tested for each tissue sample independently

and corrected for multiple tests whereby the observed *p*-value was multiplied by the number of samples.

C. Splicing Code

[0064] Previous analysis showed within neocortex regions 57.7% of genes (with at least one exon) showed the presence of differentially expressed exons in prenatal samples, whereas 9.1% and 0.7% of genes had differentially expressed exons in early childhood and adulthood samples, respectively. One mechanism to produce differential expression is through alternative splicing of exons. To analyze the implications of *de novo* SNVs (ascertained in proband and siblings) on alternative splicing patterns of affected genes, we ran the 'splicing code' (*20*) on the variants. We first mapped the *de novo* mutations onto canonical transcripts, and determined the target exon and its flanking introns and immediate neighboring exons. Then, we extracted all splicing code *cis* features for the mutation and the wildtype counterpart, passed them through the code, and computed the predicted change in inclusion of the target exon. Exon inclusion, denoted by 'percent spliced-in' (PSI Ψ), is defined as the fraction of times an exon is included in the final transcript. For each *de novo* mutation, the splicing code predicts a ΔΨ; if a mutation's ΔΨ is larger than 95% of ΔΨ for common polymorphisms (single nucleotide polymorphism database (dbSNP)), then it was deemed significant. The 'splicing code' analysis found only 73 *de novo* mutations (i.e. from probands and siblings) to pass the ΔΨ threshold of -0.01 (Table 10). The code-predicted ΔΨs showed no significant difference between *de novo* mutations of probands and siblings (Kolmogorov–Smirnov (K-S) test and AUC; Fig. 8).

[0065] Next, applying two additional normalizations, we analyzed whether expression of exons that can vary (according to developing time periods or across tissues) are the exons exclusively contributed to the association between spatio-temporal expression and burden of rare missense. For each gene (*g*), we computed differential expression by applying two transformations on each exon, $e_{d,i}$: 1) subtracting the exon expression e_i from the gene mean expression $e_{d,i} = e_i - \frac{1}{n}\sum_i^n g(e_i)$ and 2) subtracting the total expression from the gene median expression $e_{d,i} = e_i - \boldsymbol{median}(g(e))$. After applying both normalizations independently to the Brain-Span data, the association test for genes with *de novo* SNVs (as ascertained from proband or unaffected siblings) using spatio-temporal brain samples was not significant. This suggested

that these are not the only exons contributing to the association signal that is consistent with our 'splicing code' analysis.

D. Detection of 'Brain-Critical Exons'

[0066] We derived an algorithm to detect 'brain-critical exons', utilizing the multiple tissue microarray expression indices of an exon. Exons classified separately for each dataset into class *d* (for each dataset 75th percentile was used to construct contingency table in Fig. 1) were termed as 'critical exons' reflecting 'high' expression level and 'low' burden of rare missense mutation. To identify those exons specifically 'critical' in brain (or 'brain-critical exons'), we used the array matched (Affymetrix GeneChip Human Exon 1.0 ST) multiple tissue data set (ten non-brain tissue replicates). First, we identified all class *d* 'critical exons' from brain tissues (Brain-Span samples and cerebellum microarray replicates). From this exon set ***C***, we excluded exons that were not in class *d* for at least 10% of the brain samples for a given donor (BrainSpan data), or in a cerebellum replicate. Next, we excluded exons from set ***C*** that were in class *d* (for at least one tissue replicate) for ten other non-brain tissues. Therefore, after exclusions, set ***C'*** comprised exons with consistently high expression (above 75th percentile) and low burden of deleterious mutations, in brain tissue but not in other tissues. Similarly, we identified tissue-specific 'critical exons' from the other tissue types. We detected 15,872 tissue-specific critical exons, of which 3,955 were specific to brain (Fig. 18).

[0067] A *de novo* mutation within one of these 'brain-critical exons' (or in other exons that can indirectly affect (truncate) such exons) could have an adverse effect on brain function while being relatively inconsequential in other tissues. Brain showed at least 2 fold more 'critical exons' compared to other tissues (except testis). We also observed a high number of 'testis-critical exons'. The functional enrichment analysis revealed that the genes corresponding to these 'brain-critical exons' are primarily associated with neuronal development, signaling networks and functions that regulate synapse development and plasticity. Next, for each gene (*g*), we assigned a score $S(g) = \frac{\#\ brain\ critical\ exon\ in\ (g)}{mean\ brain\ critical\ exon}$

where mean brain-critical exon was computed from all genes in the genome analyzed (Fig. 18).

E. 'Brain-Critical Exons' Enrichment Test

[0068] We assayed enrichment of brain-critical exons on candidate gene sets that are highly related to key biological processes in brain and ASD or other co-morbid disease pathogenesis. We first used the FET to identify the sets over-represented in two backgrounds: 1) all exons were compared (first background) to identify 'brain-critical exons' overlaps and 2) restricted the test only to highly (all exons expression above 75th percentile for a brain sample in developmental human brains) brain-expressed exons (second background). Although the second background tested a narrow hypothesis, this approach assumes a uniform gene sampling probability, which may not reflect accurately differences in gene exon density and composition. Therefore, we also used an empirical test comparing the percentage of genes with at least one critical exon that are also gene-set members versus the percentage obtained by random exon sampling (first background); this test was also performed sampling only from brain-expressed exons (second background).

[0069] Permutation analysis on FMRP targets, PSP, ASD (AD/XL) and *de novo* ASD genes was conducted by randomly drawn equal numbers of exons (i.e. 3,955 exons randomly drawn 10,000 times from two backgrounds: RefSeq background and second background with exons highly expressed and analysed the gene set enrichment under these premises. The empirical p-values were computed from 10,000 random draws and false discovery rate (FDR) was computed using the Benjamini-Hochberg method (*46*).

F. Reverse Transcription Polymerase Chain Reaction (RT-PCR) and quantitative RT-PCR (qRT-PCR)

[0070] The mRNA expression and alternative splicing events in selected genes were analyzed by RT-PCR and qRT-PCR. For detecting splicing events, primer pairs were designed to prime from the flanking exons (exons 3 to 12 of *SLC6A1* and exons 16 to 18 for *EPB41L3* gene) and different primers were combined to capture most possible exclusion events (for *SLC6A1*) (Table 5). Exclusion events were confirmed by Sanger sequencing. We used RNA samples (BD Biosciences) from whole adult (A) or fetal (F) human brains as templates for cDNA synthesis using Superscript III First strand Synthesis Supermix (Invitrogen). RT-PCR was performed using standard PCR conditions.

Table 5. Primer sequences for alternative splicing and for relative expression analysis by RT-PCR.

Target region	F	R	Inclusion[a]	Exclusion[b]	Detected[c]
SLC6A1 exon3-5	TGACATCGCACGTCCATCTG (SEQ ID NO: 1)	ACAGGTAGTAAATGGCCCAGG (SEQ ID NO: 2)	503bp	-	503bp, 371bp, 313bp, 181bp
SLC6A1 exon4-6	GAGCCTTCCTGATCCCCTAT (SEQ ID NO: 3)	ACTGTTTCCACGGCAGTGT (SEQ ID NO: 4)	252bp	-	252bp
SLC6A1 exon3-6	TGACATCGCACGTCCATCTG (SEQ ID NO: 1)	ACTGTTTCCACGGCAGTGT (SEQ ID NO: 4)	539bp	-	539bp, 407bp, 349bp, 217bp
SLC6A1 exon5-7	CGGCTGCTGTGCTATCATTC (SEQ ID NO: 5)	CAGCCAACACCCTTCCAGAT (SEQ ID NO: 6)	322bp	-	322bp
SLC6A1 exon4-7	GAGCCTTCCTGATCCCCTAT (SEQ ID NO: 3)	CAGCCAACACCCTTCCAGAT (SEQ ID NO: 6)	466bp	-	466bp
SLC6A1 exon7-9	GGCTGGATAAGCCAGGTCAG (SEQ ID NO: 7)	GGAAAGAGTTGTAGCTCCCGA (SEQ ID NO: 8)	330bp	-	330bp
SLC6A1 exon8-10	CCTGTTCTTCCGTGGAGTGA\(SEQ ID NO: 9)	CATGAAGCCCACGATGGAGA (SEQ ID NO: 10)	284bp	-	284bp
SLC6A1 exon7-10	GGCTGGATAAGCCAGGTCAG (SEQ ID NO: 11)	TACTCATCCACCAGGGCTGT (SEQ ID NO: 12)	628bp	-	628bp
EPB41L3 exon16-18	CCTCAACAGACACTGCCGTA (SEQ ID NO: 13)	GTCTCCCGCCGAGTAAGAAG (SEQ ID NO: 14)	395bp,	284bp, 272bp	395bp, 272bp

a - expected length in the longest isoform variant.
b - expected size of any known exclusion events (Refseq) in the region.
c - Figure 3C or Figure 12 RT-PCR detection bands length.

Table 6. Primer sequences for relative expression quantification using quantitative real-time PCR (qRT-PCR) of brain specific critical exons located within 16p11.2 CNVs.

Gene	qRT-PCR primers (F/R)
KCTD13_F	CCTCATCCCCATGGTGACATC (SEQ ID NO: 15)
KCTD13_R	TTACTGCGGTTGTGCAGGAG (SEQ ID NO: 16)
ASPHD1_F	GACTTTGTCTTCGCCCCAGA (SEQ ID NO: 17)
ASPHD1_R	CTACCATCAAGCCGTCCCTG (SEQ ID NO: 18)
SEZ6L2_F	TCCGACATTCTCACTTGCCA (SEQ ID NO: 19)
SEZ6L2_R	CCAGGGTCAGCACAAGTCAT (SEQ ID NO: 20)
PRRT2_F	GGACTGTTCTCTGCTGGGAC (SEQ ID NO: 21)
PRRT2_R	GTTCGGAACCAGTACTCGCC (SEQ ID NO: 22)
MED13_F	CCGCATCCTGATGTGTCTGA (SEQ ID NO: 23)
MED13_R	TTGCAGGTGGATACGTGACT (SEQ ID NO: 24)

[0071] For the quantification of 'brain-critical exons' by qRT-PCR, primers were designed to prime either from within the specific exon, or within the specific exon and the flanking exon (Table 6). All primers were first tested using RT-PCR with whole brain cDNA, -RT whole brain cDNA and non-target samples as templates. For validation of brain specific critical exon (Fig. 18) expression from selected genes, we used RNA from 11 human tissues (mammary gland, cerebellum, heart, kidney, liver, skeletal muscle, pancreas, prostate, spleen, thyroid and testis (BD Biosciences). DNase I-treated RNA was reverse-transcribed using Superscript III First strand Synthesis Supermix (Invitrogen). RT-PCR was performed under standard PCR conditions using 10 ng of cDNA as template. The qRT-PCR assay was performed using Brilliant III SYBR® Green PCR Master Mix (Agilent) in a total reaction volume of 15 µl, containing 10 ng of cDNA templates. The reactions were amplified using Mx3005P (Agilent). The expression of each gene of interest was normalized using *ACTB* or *MED13* (dCt) and presented as relative expression (2^(-dCt)). The primers were tested for their PCR efficiency by dilution standard curve and for specificity with melting curve analysis.

5. Pathway Enrichment Analysis

A. Construction of Gene Sets

[0072] Gene sets were derived from the manually curated gene ontology (GO) (R package, version 2.8.0), pathways from National Cancer Institute at the National Institutes of Health (NCI-NIH) (May 30th 2013), Kyoto Encyclopedia of Genes and Genomes (KEGG) (May 30th 2013) and Reactome (June 3rd, 2013); websites as previously described. For the analysis, term annotated with more than 1000 genes and fewer than 50 genes were excluded from GO, NCI, KEGG and Reactome, resulting in a total of 4,138 gene sets.

B. Gene Set Overrepresentation Analysis

[0073] To identify biologically meaningful pathways, an overrepresentation analysis was performed using the gene sets described above. FET determined the significance of the enrichment for a given pathway. The test evaluates the enrichment of genes in a pathway against a common background consisting of all the genes in the data set. We used FET to assess gene-set enrichment. After obtaining the null distribution of *P*-values, we computed FDR using the Benjamini-Hochberg procedure. A gene-set was considered to be significantly enriched when

FET $p < 1.0 \times 10^{-3}$ and FDR < 0.01. We used this cut-off to construct and visually represent a functional enrichment map (Fig 15C).

C. Permutation Test

[0074] We undertook a permutation test by randomly drawing equal number of exons (3,955) and re-analysis of the data under the null-hypothesis to reveal the strength of enrichment association with the gene list. If this procedure is performed a sufficient number of times, the resulting sets of *p*-values are presumed to be a reasonable approximation of the null distribution of the *p*-values, given a test statistic *t(observed)* and number of permutations *n* and the test statistics in permuted data t(i,permutation); $i = 1, \ldots n$; (n = 10,000 permutation).

$$P = \frac{\#(abs(t(i,permutation)) \geq abs(t(observed)))}{n}$$

Permutation was conducted for molecular pathway analysis randomly drawing an equal number of exons (equal to 'brain-critical exons' 3,955) from RefSeq genes and enrichment analysis was done on GO, NCI, KEGG and Reactome gene sets. The empirical *P*-value was not significant after the permutation test.

D. Visualization of Functional Enrichment Map

[0075] We represented gene sets that were significantly enriched with 'brain-critical exons' (described above) by constructing a network where each gene-set is a node, and the edges represent gene overlap between sets. The Cytoscape network software v.2.8.3 (*47*) and the plugin "Enrichment Map" (*48, 49*) were used to construct and visualize the network. The node size is proportional to the total number of genes in the respective gene set. After constructing the enrichment map, the nodes were colored according to the *p*-value obtained from FET. The functional gene-set clusters were manually identified and annotated, and highlighted by shaded ovals/circles, representing groups of gene sets that are highly overlapping. Ovals/circles highlighted blue represents functional pathways implicated in previous ASD or other neuropsychiatric disorders literature; GTPase signaling, ERBB-NGF signaling pathways, neuronal synapse , higher cognitive functions, voltage-gated channel, neuron projection and

axonogenesis, synaptic vesicle, brain development, neuron differentiation and mitogen-activated protein kinase (MAPK) cascade.

RESULTS

[0076] We sought to exploit transcriptome maps of human developing brain coupled with data from population genetics studies about mutational burden to examine the impact of genetic variants in ASD and other neuropsychiatric disorders (Fig. 1 and Fig. 2). Exome sequencing has revealed an excess of damaging variants arising over the past 5,000 years among individuals of European ancestry, but how this relates to gene expression in developing human brain or to disease is little understood. Our initial examination of a few *bona fide* ASD risk genes (*SHANK1, SHANK2, FMR1, AFF2, SCN2A*) in control sample data revealed an inverse correlation between the burden of rare missense mutations (defined as the number of rare missense variants divided by the exon length) and the expression levels for individual exons in prenatal brain (Fig. 3A and Fig. 4).

[0077] We then hypothesized that due to adverse functional consequences, the accumulation of potentially deleterious mutations is suppressed for 'critical exons' demonstrating higher expression in brain. We undertook to test whether dysregulation of the expression of such critical exons caused by rare mutations was more likely to cause disease than other exons where recent mutational burden was relaxed regardless of gene expression. We classified exons in two ways to construct an exon transcriptome/mutation contingency index: (i) exon expression levels were discretized into high and low classes (above or below 75^{th} percentile of the entire data, respectively) and (ii) rare missense mutation burden was defined as the number of rare missense variants divided by the exon length and defined as high or low in the same manner (Fig. 1). With expression data from 11 human tissues (each in triplicate (Fig. 5)) including 16,713 RefSeq genes, we tested genome-wide association between the burden of rare missense mutations and exonic expression; brain cerebellum showed a striking association (Fisher's exact test (FET), Bonferroni corrected, $p < 2.53 \times 10^{-67}$) (Fig. 3B).

[0078] To examine the relevance of our observations in relation to disease, we tested whether genes found (by sequencing or microarrays) in selected datasets to carry *de novo* mutations (SNV/indel or CNV, respectively) predicted to be deleterious, exhibit a similar inverse

correlation with spatio-temporal exonic expression. From whole exome or genome sequence datasets of index cases of ASD, SZ or ID, we collected 243 genes containing 256 *de novo* mutations predicted to be deleterious. For the ASD cases from the Simon's Simplex Collection (SSC), equivalent sequence data exists for unaffected sibling controls, identifying 82 genes with *de novo* exonic mutations. Exon expression data was obtained from both microarrays and RNA-sequencing of 196 normal human brain tissue samples.

[0079] Our initial analysis between the ASD case and sibling genes showed identical conservation scores and no significant difference in the distribution of the burden of rare missense mutations (Fig. 6-7). In addition, when we tested if the *de novo* mutations in these gene induce aberrant-splicing pattern using the 'splicing code' (*20*), again no significant difference was found (Fig. 8). However, the inverse correlation was found to be strikingly significant within spatio-temporal brain microarray-based transcriptome datasets (i.e. from control samples) for genes with *de novo* mutations ascertained in ASD probands (Spearman's Correlation Test, Bonferroni corrected; $p < 2.0 \times 10^{-16}$). No association was detected for genes ascertained through unaffected siblings (Fig. 3C). We also observed a similar pattern of inverse correlation for ID and SZ *de novo* mutated genes (Fig. 3C). Applying a 75th percentile contingency index, the strongest association of genes in ASD cases (FET, Bonferroni corrected; $p < 1.13 \times 10^{-38}$; OR=2.40) was observed for the expression levels in prenatal neocortex samples (Fig 9A); no association was observed in any brain expression data within ASD siblings genes. The association for the ASD case genes was validated using RNA-sequencing transcriptome data (Fig. 10).

[0080] When restricting the analysis only to exons with *de novo* mutations ascertained from ASD cases and siblings, we observed significant differences in expression pattern with respect to high and low rare missense mutation burden (Fig. 9B), predominantly for prenatal samples (Wilcoxon test, Bonferroni corrected; $p < 6.06 \times 10^{-40}$). In one example, reverse transcription-polymerase chain reaction (RT-PCR) confirmed the inverse correlation of missense burden and expression level of exons 5 and 9 in *SLC6A1* (for which *de novo* mutations are reported in ASD probands) including evidence that these are not subject to splicing in normal prenatal or adult brain (Fig. 9C). However, the exons with *de novo* mutations found in unaffected

siblings have a different non-specific pattern (Fig 9B and 11). We confirmed that exons prone to differential usage do not represent a significant determinant driving our association signal.

[0081] When restricting our analysis to exons with de novo mutations ascertained in ASD cases and in siblings without ASD, 37.3% and 32.2% of the 196 brain samples, respectively, showed high expression (above the 75th percentile) (Fig. 9A). The presence of a roughly equal rate of de novo mutations in cases and siblings within these exons that are highly expressed in the brain makes it difficult to distinguish actual mutational effects. However, when we applied our transcriptome-mutation contingency index, a difference was found (predominantly for prenatal transcriptome samples), whereby 116 of 256 (45%) exons affected by de novo mutation in cases and 24 of 84 (28%) exons affected by de novo mutation in unaffected siblings were classified as critical exons. In contrast, a twofold excess of de novo mutations classified as 'tolerated' was found in siblings (Figure. 10D). Considering loss-of-function mutations only, the enrichment was threefold for critical exons in cases (Figure. 10E).

[0082] Building from our ASD, ID and SZ findings, we also tested a more general grouping of genes involved in brain disorders (termed nervous system abnormalities in the Online Mendelian Inheritance for Man) for a similar inverse correlation with exon expression. A positive association was observed ($p < 1.2 \times 10^{-9}$; OR = 1.73) in cerebellum (amongst 11 tissues examined) for autosomal dominant disease genes (Fig. 12). Further analysis revealed an association in genes under purifying selection (Fig. 13).

[0083] For CNV analysis, we used *de novo* calls from the Autism Genome Project (AGP) Consortium (Stage 1 *(3)* and 2 *(21)* and two independent SSC cohorts (SSC1 and SSC2) *(22, 23)*. The combined AGP stage 1 and 2 data (2,446 ASD cases and 2,640 controls), included 101 *de novo* validated CNVs (losses and gains) (affecting 886 genes in cases and 544 genes in controls). The SSC cohort data included 64 *de novo* calls (affecting 497 genes) in SSC1 and 75 *de novo* CNVs (affecting 993 genes) from SSC2. As with our findings for *de novo* SNV/indel mutations, we observed striking associations between microarray-based expression and rare missense burden in control spatio-temporal brain tissues for genes ascertained through *de novo* CNVs in ASD cases (Fig 14 and 15A). The strongest association was found for prenatal neocortex samples (FET, Bonferroni corrected, $p < 8.06 \times 10^{-16}$; OR=1.47). The lack of significant

association for CNVs ascertained in controls implies that only *de novo* CNVs from cases harbor genes enriched with exons that follow the correlation principal between expression and rare missense burden. We also validated the association using RNA-sequencing transcriptomes for all three CNV data sets (Fig. 16).

[0084] Since these *de novo* CNVs typically encompass more than one gene (average: AGP= 9 genes; SSC1= 8 genes; SSC2= 13 genes) a core of dose-sensitive genes are producing the signals. We further restricted the analysis to CNVs involving single gene losses, and observed overall higher odds ratios for those ascertained in cases than in controls (Fig. 17), reminiscent of what was observed using the *de novo* SNV and indel data.

[0085] To develop a resource for potential discovery of neuronal disease genes, we applied the inverse correlation framework to multiple transcriptome datasets and identified 3,955 'critical exons' (from 1,744 unique genes) with high expression specific to brain and low rare mutation burden (2-fold greater expression in brain over that of most other tissues - testis being the exception and similar to brain) (Fig. 18 and Table 7). Such exons are present in most transcripts of their respective genes and functional or splicing mutations in these regions may be manifest as various disorders of the brain. For example, *RBFOX1* and its downstream regulatory targets *ATP2B1* and *GRIN1* are identified in this brain-specific critical exon dataset and this pathway has recently been found to be dysregulated in ASD. Moreover, *SHANK1, SHANK2, NRXN2, NRXN3, SCN2A, FMR1, AFF2* and *AUTS2* genes, known to confer risk of ASD are also found to be enriched with brain-specific critical exons (transcriptome data were not available for *NRXN1* and *SHANK3*).

[0086] We analyzed biological pathways using the FET to look for potential enrichment (considering two backgrounds, first, entire RefSeq exons and second, only brain expressed exons) of the 3,955 critical exons in candidacy tier datasets comprised of Fragile X mental retardation protein (FMRP) targets, the post-synaptic proteome (PSP), *bona fide* ASD risk genes (autosomal dominant (AD) and X-linked (XL)), and genes affected by predicted deleterious *de novo* mutations from ASD trio studies. Indeed, highly significant enrichment of critical exons was detected for the FMRP targets: 41.8% (Bonferroni corrected FET; $p < 2.91 \times 10^{-157}$, OR=9.52), PSP: 28.11% ($p < 7.190 \times 10^{-54}$; OR=4.43), ASD (AD/XL): 34.56% ($p < 3.40 \times 10^{-}$

[11]; OR=6.08) and *de novo* mutation genes in ASD probands: 25.5%($p < 7.73 \times 10^{-13}$; OR=3.31)(Fig. 15B). Empirical p-values from 10,000 permutations (from both background) also showed significance after correction for Benjamini-Hochberg false discovery rate (FDR). As a negative control, we analyzed an equal number of exons (3,955) that are enriched for rare missense mutations (tolerated in control brain tissues) and highly expressed in brain. Enrichment re-analysis showed no significance after conducting permutation tests on two backgrounds (Table 8).

Table 8: Enrichment Analysis for Exons Highly Enriched with Burden of Rare Missense

Equal number of exons were analysed (3955 exons) where burden of rare missense mutation is high. Following is the Fisher's Exact Test and empirical significance (using two background) of enrichment after 10,000 permutation for FMRP, Post-synaptic Proteome, ASD (AD,XL) and *de*

Gene Categories	Background	FET *P*	Empirical *P* (10,000 Permutation)	Empirical *P (Corrected)*
FMRP	Refseq	6.70E-05	1	1
FMRP	Brain Expressed	0.000677025	1	1
Post-Synaptic Proteome	Refseq	0.03616252	0.97	1
Post-Synaptic Proteome	Brain Expressed	0.454409035	0.99	1
ASD(AD,XL)	Refseq	0.801966304	0.73	1
ASD(AD,XL)	Brain Expressed	0.887460535	1	1
SNV	Refseq	2.33E-06	0.5	1
SNV	Brain Expressed	0.000677025	0.99	1

[0087] We examined the 1,744 genes encompassing these 3,955 critical exons for enrichment in specific functional or biological pathways (stringent cutoffs of $p < 1.0 \times 10^{-3}$; FDR of <0.01). Gene sets were downloaded from multiple databases: gene ontology (GO), pathways from the National Cancer Institute at the National Institutes of Health (NCI-NIH), Kyoto Encyclopedia of Genes and Genomes (KEGG) and Reactome. FET was used to determine the significance of the enrichment for a given pathway. The test evaluated the enrichment of genes in a pathway against a common background consisting of all the genes in the data set. From the null distribution of *p*-values, FDR was computed using the Benjamini-Hochberg procedure. A gene-set was considered to be significantly enriched when FET $p < 1.0 \times 10\text{-}3$ and FDR < 0.01. The results revealed a modular network involving neuronal synapse regulation, neuron differentiation, signaling complexes and synaptic vesicles (Fig. 15C, Table 9). These findings, which were generated without prior knowledge of ASD disease genes, overlap with results obtained using other datasets derived from known ASD genes.

[0088] We speculate that these 1,744 genes represent high priority candidates to be susceptibility loci for ASD and/or related disorders. Of these, 518 (29.7%) genes have already been implicated as candidate genes for neuropsychiatric diseases (Table 7). We therefore examined whether our brain-specific critical exon index might help to differentiate the specific etiological gene(s) from mere bystanders co-located within genomic CNV loci that are well documented to be involved in ASD. At the 16p11.2 CNV (~600kb encompassing 29 genes) four genes (*PRRT2, SEZ6L2, ASPHD1, KCTD13*) were identified harboring critical exons (Fig. 19); three of these have been implicated within the smallest region of overlap identified by atypical cases with smaller deletions (Fig. 19). All four genes are implicated through functional and large phenotypic analyses to be relevant to ASD or other neuropsychiatric phenotypes. Our analysis identified other candidate genes for neuronal phenotypes from disease loci: 3q29 micro-duplication/deletion (*PIGZ, DLG1*), 17q21.31 micro-deletion syndrome (*CRHR1, MAPT*), 17q11.2-NF1 micro-deletion syndrome (*NF1, RAB11FIP4*) and 22q11.2 micro-duplication/deletion syndrome (*ARVCF, DGCR8, ZDHHC8, PI4KA*) (Fig. 20 and 21).

[0089] The development of our exon transcriptome/mutation contingency index provides a new approach to prioritize putative mutations for subsequent clinical- and functional-genetic analyses. Applying this strategy has already allowed us to add unprecedented specificity and clarity to re-analysis of mutation data, helping to redefine the genes, sites within genes, and molecular pathways involved in the disease processes. Our studies of ASD have yielded the most significant data so far, most likely because of the greater maturity of datasets available for this disorder. From an evolutionary perspective, there seems to be selective pressure for specific neuronal genes (our data suggests at least 1,744 of them) to maintain the integrity of particular exons (3,955). Our data indicates that as mutations are identified and proven, through functional studies, to be etiologic for brain disorders – e.g. for ASD, they will be found to have arisen in genes having the properties we have identified here. Moreover, the impact of upstream mutations that lead to some form of alteration of the 'critical exon', as well as more subtle mutations, with direct and indirect effects of modifier genes can also now be modeled within this framework. Ultimately, exploiting this new understanding of the role of the brain transcriptome in modulating mutational impact will facilitate more accurate genotype and phenotype studies in ASD and related disorders.

Table 7. Gene List That are Enriched with 'Brain-Critical Exons'.

Gene	egID	name	Chr	Enrichment Overlap	Exon_score	KLF13	
SEPT4	5414	septin 4	17	Postsynaptic Proteome	1.322882427	OTUD7A 1.7638	
SEPT8	23176	septin 8	5	Postsynaptic Proteome	0.440960809	LOC100288637	pseudo gene
ABCA2	20	ATP-binding cassette, sub-family A (ABC1), member 2	9	FMRP Target	5.732490518	MTMR10	
ABCA3	21	ATP-binding cassette, sub-family A (ABC1), member 3	16	FMRP Target	1.763843236	MIR211	ncRNA
ABCC5	10057	ATP-binding cassette, sub-family C (CFTR/MRP), member 5	3	---	0.881921618	FAN1 0.8819	
ABCC8	6833	ATP-binding cassette, sub-family C (CFTR/MRP), member 8	11	---	3.527686473	CHRNA7	
ABCG2	9429	ATP-binding cassette, sub-family G (WHITE), member 2	4	---	0.881921618	LOC283710	
ABCG4	64137	ATP-binding cassette, sub-family G (WHITE), member 4	11	---	1.763843236	ARHGAP11B	
ACAP3	116983	ArfGAP with coiled-coil, ankyrin repeat and PH domains 3	1	---	0.440960809	TRPM1	
ACSL6	23305	acyl-CoA synthetase long-chain family member 6	5	Postsynaptic Proteome	2.645764855		
ADAM11	4185	ADAM metallopeptidase domain 11	17	---	2.645764855		
ADAM22	53616	ADAM metallopeptidase domain 22	7	---	6.614412137		
ADAMTS16	170690	ADAM metallopeptidase with thrombospondin type 1 motif, 16	5	---	0.440960809		
ADAMTS18	170692	ADAM metallopeptidase with thrombospondin type 1 motif, 18	16	---	3.527686473		
ADCY8	114	adenylate cyclase 8 (brain)	8	---	0.881921618		
ADD1	118	adducin 1 (alpha)	4	FMRP Target,Postsynaptic Proteome	0.440960809		
ADD3	120	adducin 3 (gamma)	10	Postsynaptic Proteome	0.440960809		
AFG3L1P	172	AFG3 ATPase family member 3-like 1 (S. cerevisiae), pseudogene	16	---	0.440960809		
AFTPH	54812	aftiphilin	2	---	0.440960809		
AGPAT4	56895	1-acylglycerol-3-phosphate O-acyltransferase 4	6	---	0.440960809		
AHI1	54806	Abelson helper integration site 1	6	---	2.204804046		
AJAP1	55966	adherens junctions associated protein 1	1	---	0.440960809		
AKAP10	11216	A kinase (PRKA) anchor protein 10	17	---	0.440960809		
ALS2	57679	amyotrophic lateral sclerosis 2 (juvenile)	2	FMRP Target	4.8505689		
AMER2	219287	APC membrane recruitment protein 2	13	---	0.440960809		
AMIGO1	57463	adhesion molecule with Ig-like domain 1	1	---	0.440960809		
AMPH	273	amphiphysin	7	FMRP Target,Postsynaptic Proteome	2.645764855		
ANGEL2	90806	angel homolog 2 (Drosophila)	1	---	0.881921618		
ANK1	286	ankyrin 1, erythrocytic	8	FMRP Target,Postsynaptic Proteome	8.378255373		
ANK3	288	ankyrin 3, node of Ranvier (ankyrin G)	10	denovo SNV,FMRP Target,Postsynaptic Proteome	1.322882427		
ANKRD13B	124930	ankyrin repeat domain 13B	17	---	0.440960809		
ANKRD17	26057	ankyrin repeat domain 17	4	FMRP Target	0.440960809		
ANKRD26	22852	ankyrin repeat domain 26	10	---	0.440960809		
ANKRD6	22881	ankyrin repeat domain 6	6	---	0.440960809		
ANKS6	203286	ankyrin repeat and sterile alpha motif domain containing 6	9	---	0.440960809		
ANKZF1	55139	ankyrin repeat and zinc finger domain containing 1	2	---	0.881921618		
ANLN	54443	anillin, actin binding protein	7	---	0.881921618		
ANO4	121601	anoctamin 4	12	---	1.322882427		
ANP32E	81611	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E	1	---	0.881921618		
AP3M2	10947	adaptor-related protein complex 3, mu 2 subunit	8	---	0.440960809		
AP4B1	10717	adaptor-related protein complex 4, beta 1 subunit	1	---	0.440960809		
APBA1	320	amyloid beta (A4) precursor protein-binding, family A, member 1	9	FMRP Target	1.322882427		
APBB1	322	amyloid beta (A4) precursor protein-binding, family B, member 1 (Fe65)	11	FMRP Target	0.440960809		
AQP4	361	aquaporin 4	18	Postsynaptic Proteome	0.440960809		
AQR	9716	aquarius homolog (mouse)	15	---	0.440960809		
ARGLU1	55082	arginine and glutamate rich 1	13	---	0.881921618		
ARHGAP22	58504	Rho GTPase activating protein 22	10	---	0.440960809		
ARHGAP26	23092	Rho GTPase activating protein 26	5	---	1.322882427		
ARHGAP29	9411	Rho GTPase activating protein 29	1	---	0.440960809		
ARHGAP44	9912	Rho GTPase activating protein 44	17	FMRP Target	3.086725664		
ARHGDIG	398	Rho GDP dissociation inhibitor (GDI) gamma	16	---	0.440960809		
ARHGEF11	9826	Rho guanine nucleotide exchange factor (GEF) 11	1	FMRP Target	0.440960809		
ARHGEF4	50649	Rho guanine nucleotide exchange factor (GEF) 4	2	FMRP Target	0.440960809		
ARHGEF7	8874	Rho guanine nucleotide exchange factor (GEF) 7	13	FMRP Target	0.881921618		

ARID4A	5926	AT rich interactive domain 4A (RBP1-like)	14	---	0.881921618
ARID4B	51742	AT rich interactive domain 4B (RBP1-like)	1	---	0.440960809
ARMC8	25852	armadillo repeat containing 8	3	---	0.440960809
ARPP21	10777	cAMP-regulated phosphoprotein, 21kDa	3	FMRP Target	0.881921618
ARVCF	421	armadillo repeat gene deleted in velocardiofacial syndrome	22	FMRP Target	0.881921618
ASIC2	40	acid-sensing (proton-gated) ion channel 2	17	FMRP Target	0.440960809
ASPHD1	253982	aspartate beta-hydroxylase domain containing 1	16	---	0.440960809
ASPHD2	57168	aspartate beta-hydroxylase domain containing 2	22	---	0.440960809
ASTN2	23245	astrotactin 2	9	---	2.204804046
ATP2C1	27032	ATPase, Ca++ transporting, type 2C, member 1	3	---	0.881921618
ATXN3	4287	ataxin 3	14	---	0.440960809
ATXN7L3B	552889	ataxin 7-like 3B	12	---	0.440960809
AVIL	10677	advillin	12	---	0.440960809
BARHL2	343472	BarH-like homeobox 2	1	---	0.440960809
BCAN	63827	brevican	1	FMRP Target,Postsynaptic Proteome	1.322882427
BCAS1	8537	breast carcinoma amplified sequence 1	20	Postsynaptic Proteome	0.881921618
BCL2L2	599	BCL2-like 2	14	---	0.440960809
BCL2L2-PABPN	1E+08	BCL2L2-PABPN1 readthrough	14	---	0.440960809
BEGAIN	57596	brain-enriched guanylate kinase-associated	14	---	0.440960809
BEND6	221336	BEN domain containing 6	6	---	0.881921618
BIN1	274	bridging integrator 1	2	Postsynaptic Proteome	0.440960809
BMPER	168667	BMP binding endothelial regulator	7	---	0.440960809
BRD9	65980	bromodomain containing 9	5	---	0.440960809
BRSK2	9024	BR serine/threonine kinase 2	11	FMRP Target	0.440960809
BRWD3	254065	bromodomain and WD repeat domain containing 3	X	---	2.204804046
BSN	8927	bassoon presynaptic cytomatrix protein	3	FMRP Target,Postsynaptic Proteome	1.322882427
BTBD9	114781	BTB (POZ) domain containing 9	6	---	0.440960809
BTN2A2	10385	butyrophilin, subfamily 2, member A2	6	---	0.440960809
C10orf35	219738	chromosome 10 open reading frame 35	10	Postsynaptic Proteome	0.440960809
C11orf30	56946	chromosome 11 open reading frame 30	11	---	0.440960809
C12orf29	91298	chromosome 12 open reading frame 29	12	---	0.440960809
C12orf76	400073	chromosome 12 open reading frame 76	12	---	0.440960809
C14orf132	56967	chromosome 14 open reading frame 132	14	---	0.440960809
C14orf37	145407	chromosome 14 open reading frame 37	14	---	0.440960809
C15orf27	123591	chromosome 15 open reading frame 27	15	---	2.204804046
C17orf85	55421	chromosome 17 open reading frame 85	17	---	0.440960809
C1orf126	200197	TMEM51 antisense RNA 1	1	---	0.440960809
C1orf51	148523	chromosome 1 open reading frame 51	1	---	0.440960809
C1QTNF3	114899	C1q and tumor necrosis factor related protein 3	5	---	0.440960809
1QTNF3-AMAC	1E+08	C1QTNF3-AMACR readthrough	5	---	0.440960809
C20orf112	140688	chromosome 20 open reading frame 112	20	---	0.440960809
C2CD5	9847	C2 calcium-dependent domain containing 5	12	---	2.204804046
C4orf21	55345	chromosome 4 open reading frame 21	4	---	0.881921618
C5orf45	51149	chromosome 5 open reading frame 45	5	---	0.440960809
C8orf34	116328	chromosome 8 open reading frame 34	8	---	0.440960809
C8orf46	254778	chromosome 8 open reading frame 46	8	---	0.440960809
C9orf72	203228	chromosome 9 open reading frame 72	9	---	0.440960809
CA10	56934	carbonic anhydrase X	17	---	1.763843236
CA11	770	carbonic anhydrase XI	19	---	1.322882427
CA8	767	carbonic anhydrase VIII	8	---	0.440960809
CABP1	9478	calcium binding protein 1	12	---	0.440960809
CACNA1D	776	calcium channel, voltage-dependent, L type, alpha 1D subunit	3	denovo SNV	6.173451327
CACNA1G	8913	calcium channel, voltage-dependent, T type, alpha 1G subunit	17	FMRP Target	7.496333755
CACNA2D2	9254	calcium channel, voltage-dependent, alpha 2/delta subunit 2	3	---	3.527686473
CACNG2	10369	calcium channel, voltage-dependent, gamma subunit 2	22	---	1.322882427
CADPS2	93664	Ca++-dependent secretion activator 2	7	---	2.645764855
CALB2	794	calbindin 2	16	---	0.881921618
CAMK2G	818	calcium/calmodulin-dependent protein kinase II gamma	10	Postsynaptic Proteome	1.322882427
CAMKK1	84254	calcium/calmodulin-dependent protein kinase kinase 1, alpha	17	Postsynaptic Proteome	1.763843236
CAND1	55832	cullin-associated and neddylation-dissociated 1	12	FMRP Target,Postsynaptic Proteome	0.440960809
CAPRIN2	65981	caprin family member 2	12	---	1.322882427
CASKIN1	57524	CASK interacting protein 1	16	FMRP Target,Postsynaptic Proteome	2.204804046
CATSPER2	117155	cation channel, sperm associated 2	15	---	0.440960809
CBLN1	869	cerebellin 1 precursor	16	---	0.881921618
CCBL1	883	cysteine conjugate-beta lyase, cytoplasmic	9	---	0.440960809
CCDC111	201973	coiled-coil domain containing 111	4	---	0.440960809
CCDC115	84317	coiled-coil domain containing 115	2	---	0.440960809
CCDC132	55610	coiled-coil domain containing 132	7	---	0.440960809

CCDC136	64753	coiled-coil domain containing 136	7	---	0.440960809
CCNG2	901	cyclin G2	4	---	0.440960809
CCNJL	79616	cyclin J-like	5	---	0.440960809
CCSAP	126731	centriole, cilia and spindle-associated protein	1	---	0.440960809
CDH10	1008	cadherin 10, type 2 (T2-cadherin)	5	---	1.763843236
CDH18	1016	cadherin 18, type 2	5	---	4.8505689
CDH20	28316	cadherin 20, type 2	18	---	0.881921618
CDH22	64405	cadherin 22, type 2	20	---	1.763843236
CDH23	64072	cadherin-related 23	10	---	3.086725664
CDH24	64403	cadherin 24, type 2	14	---	0.440960809
CDH7	1005	cadherin 7, type 2	18	---	1.322882427
CDHR3	222256	cadherin-related family member 3	7	---	0.440960809
CDIP1	29965	cell death-inducing p53 target 1	16	---	0.440960809
CDK8	1024	cyclin-dependent kinase 8	13	---	0.440960809
CDON	50937	cell adhesion associated, oncogene regulated	11	---	1.763843236
CDR2L	30850	cerebellar degeneration-related protein 2-like	17	---	0.440960809
CDS1	1040	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 1	4	---	2.645764855
CDYL2	124359	chromodomain protein, Y-like 2	16	---	0.881921618
CECR2	27443	cat eye syndrome chromosome region, candidate 2	22	---	0.440960809
CELF4	56853	CUGBP, Elav-like family member 4	18	---	2.645764855
CELF6	60677	CUGBP, Elav-like family member 6	15	---	0.440960809
CELSR2	1952	cadherin, EGF LAG seven-pass G-type receptor 2	1	FMRP Target	0.440960809
CELSR3	1951	cadherin, EGF LAG seven-pass G-type receptor 3	3	FMRP Target	3.527686473
CENPT	80152	centromere protein T	16	---	0.440960809
CEP120	153241	centrosomal protein 120kDa	5	---	0.440960809
CEP192	55125	centrosomal protein 192kDa	18	---	0.440960809
CEP95	90799	centrosomal protein 95kDa	17	---	0.440960809
CERCAM	51148	cerebral endothelial cell adhesion molecule	9	---	0.440960809
CERKL	375298	ceramide kinase-like	2	---	0.881921618
CERS5	91012	ceramide synthase 5	12	---	0.881921618
CHD6	84181	chromodomain helicase DNA binding protein 6	20	FMRP Target	1.322882427
CHRD	8646	chordin	3	---	2.645764855
CHRNB3	1142	cholinergic receptor, nicotinic, beta 3 (neuronal)	8	---	0.440960809
CIC	23152	capicua homolog (Drosophila)	19	denovo SNV,FMRP Target	0.440960809
CIT	11113	citron (rho-interacting, serine/threonine kinase 21)	12	FMRP Target,Postsynaptic Proteome	2.204804046
CLCN6	1185	chloride channel, voltage-sensitive 6	1	---	0.440960809
CLIP2	7461	CAP-GLY domain containing linker protein 2	7	Postsynaptic Proteome	0.440960809
CLK4	57396	CDC-like kinase 4	5	---	1.763843236
CLSTN3	9746	calsyntenin 3	12	---	0.881921618
CLUHP3	1E+08	clustered mitochondria (cluA/CLU1) homolog pseudogene 3	16	---	0.440960809
CNDP1	84735	carnosine dipeptidase 1 (metallopeptidase M20 family)	18	---	0.881921618
CNOT2	4848	CCR4-NOT transcription complex, subunit 2	12	---	0.440960809
CNOT6	57472	CCR4-NOT transcription complex, subunit 6	5	---	0.440960809
CNTN4	152330	contactin 4	3	---	1.322882427
CNTN6	27255	contactin 6	3	---	2.645764855
CNTNAP1	8506	contactin associated protein 1	17	Postsynaptic Proteome	6.173451327
CNTNAP4	85445	contactin associated protein-like 4	16	---	4.8505689
COA5	493753	cytochrome c oxidase assembly factor 5	2	---	0.440960809
COL13A1	1305	collagen, type XIII, alpha 1	10	---	0.881921618
COL19A1	1310	collagen, type XIX, alpha 1	6	---	3.527686473
COL27A1	85301	collagen, type XXVII, alpha 1	9	---	1.763843236
CPLX1	10815	complexin 1	4	FMRP Target	0.440960809
CPLX2	10814	complexin 2	5	FMRP Target	0.881921618
CPLX3	594855	complexin 3	15	---	0.440960809
CPNE6	9362	copine VI (neuronal)	14	---	3.086725664
CPNE9	151835	copine family member IX	3	---	0.881921618
CRAMP1L	57585	Crm, cramped-like (Drosophila)	16	---	0.881921618
CRB1	23418	crumbs homolog 1 (Drosophila)	1	---	0.881921618
CRHR1	1394	corticotropin releasing hormone receptor 1	17	---	2.204804046
CRTAM	56253	cytotoxic and regulatory T cell molecule	11	---	0.440960809
CRTC1	23373	CREB regulated transcription coactivator 1	19	FMRP Target	0.440960809
CRY1	1407	cryptochrome 1 (photolyase-like)	12	---	0.440960809
CSMD1	64478	CUB and Sushi multiple domains 1	8	---	2.645764855
CSPG5	10675	chondroitin sulfate proteoglycan 5 (neuroglycan C)	3	---	0.440960809
CSTF3	1479	cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kDa	11	---	0.440960809
CTPS2	56474	CTP synthase 2	X	---	0.440960809
CTTNBP2	83992	cortactin binding protein 2	7	denovo SNV	0.440960809
CUL9	23113	cullin 9	6	FMRP Target	0.440960809
CWC27	10283	CWC27 spliceosome-associated protein homolog (S. cerevisiae)	5	---	0.881921618
CWF19L2	143884	CWF19-like 2, cell cycle control (S. pombe)	11	---	0.881921618
CXorf23	256643	chromosome X open reading frame 23	X	---	1.322882427
CXXC1	30827	CXXC finger protein 1	18	---	0.440960809

CYP26B1	56603	cytochrome P450, family 26, subfamily B, polypeptide 1	2	---	0.440960809
CYP46A1	10858	cytochrome P450, family 46, subfamily A, polypeptide 1	14	---	0.440960809
DAAM1	23002	dishevelled associated activator of morphogenesis 1	14	---	0.440960809
DAB1	1600	disabled homolog 1 (Drosophila)	1	---	1.322882427
DAB2IP	153090	DAB2 interacting protein	9	FMRP Target	1.763843236
DACT1	51339	dapper, antagonist of beta-catenin, homolog 1 (Xenopus laevis)	14	---	1.322882427
DCAF8	50717	DDB1 and CUL4 associated factor 8	1	---	0.440960809
DCTN1	1639	dynactin 1	2	FMRP Target,Postsynaptic Proteome	0.440960809
DDX26B	203522	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26B	X	---	0.440960809
DEF8	54849	differentially expressed in FDCP 8 homolog (mouse)	16	---	0.440960809
DEPDC5	9681	DEP domain containing 5	22	---	0.881921618
DGCR8	54487	DiGeorge syndrome critical region gene 8	22	---	0.881921618
DGKB	1607	diacylglycerol kinase, beta 90kDa	7	---	0.881921618
DGKD	8527	diacylglycerol kinase, delta 130kDa	2	---	0.440960809
DGKG	1608	diacylglycerol kinase, gamma 90kDa	3	---	1.763843236
DGKI	9162	diacylglycerol kinase, iota	7	---	2.645764855
DISP2	85455	dispatched homolog 2 (Drosophila)	15	FMRP Target	0.440960809
DIXDC1	85458	DIX domain containing 1	11	---	2.204804046
DLGAP4	22839	discs, large (Drosophila) homolog-associated protein 4	20	FMRP Target	0.440960809
DLK2	65989	delta-like 2 homolog (Drosophila)	6	---	0.440960809
DNAJB2	3300	DnaJ (Hsp40) homolog, subfamily B, member 2	2	---	0.440960809
DNAJC17	55192	DnaJ (Hsp40) homolog, subfamily C, member 17	15	---	0.440960809
DNMT3A	1788	DNA (cytosine-5-)-methyltransferase 3 alpha	2	denovo SNV	0.440960809
DOPEY2	9980	dopey family member 2	21	FMRP Target	1.763843236
DPF3	8110	D4, zinc and double PHD fingers, family 3	14	---	0.440960809
DTNA	1837	dystrobrevin, alpha	18	FMRP Target	0.440960809
DVL2	1856	dishevelled, dsh homolog 2 (Drosophila)	17	---	0.440960809
E4F1	1877	E4F transcription factor 1	16	---	0.440960809
ECE2	9718	endothelin converting enzyme 2	3	---	1.322882427
EHMT1	79813	euchromatic histone-lysine N-methyltransferase 1	9	FMRP Target,ASD-AD/XL	0.440960809
EIF4E3	317649	eukaryotic translation initiation factor 4E family member 3	3	---	0.440960809
ELAVL1	1994	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R)	19	---	0.440960809
ELMO1	9844	engulfment and cell motility 1	7	---	0.440960809
ELMO2	63916	engulfment and cell motility 2	20	FMRP Target,Postsynaptic Proteome	0.440960809
ELMOD1	55531	ELMO/CED-12 domain containing 1	11	---	2.204804046
ELOVL4	6785	ELOVL fatty acid elongase 4	6	---	0.881921618
ELP4	26610	elongator acetyltransferase complex subunit 4	11	---	0.440960809
EML5	161436	echinoderm microtubule associated protein like 5	14	---	8.378255373
EOMES	8320	eomesodermin	3	---	0.881921618
EP400	57634	E1A binding protein p400	12	FMRP Target	0.440960809
EPB41	2035	erythrocyte membrane protein band 4.1 (elliptocytosis 1, RH-linked)	1	Postsynaptic Proteome	0.881921618
EPB41L4B	54566	erythrocyte membrane protein band 4.1 like 4B	9	---	0.440960809
EPB41L5	57669	erythrocyte membrane protein band 4.1 like 5	2	---	0.440960809
EPHA6	285220	EPH receptor A6	3	---	0.881921618
EPHA7	2045	EPH receptor A7	6	---	1.322882427
EPHB1	2047	EPH receptor B1	3	---	1.322882427
ERC1	23085	ELKS/RAB6-interacting/CAST family member 1	12	Postsynaptic Proteome	1.763843236
ERCC6	2074	excision repair cross-complementing rodent repair deficiency, complementation group 6	10	---	1.322882427
ERP44	23071	endoplasmic reticulum protein 44	9	---	0.440960809
ESYT3	83850	extended synaptotagmin-like protein 3	3	---	0.440960809
EXOSC10	5394	exosome component 10	1	---	0.440960809
EZH1	2145	enhancer of zeste homolog 1 (Drosophila)	17	---	0.440960809
FAM120C	54954	family with sequence similarity 120C	X	---	0.440960809
FAM126B	285172	family with sequence similarity 126, member B	2	---	0.881921618
FAM131B	9715	family with sequence similarity 131, member B	7	---	1.322882427
FAM135A	57579	family with sequence similarity 135, member A	6	---	0.440960809
FAM188A	80013	family with sequence similarity 188, member A	10	---	0.440960809
FAM193A	8603	family with sequence similarity 193, member A	4	---	0.440960809
FAM19A5	25817	family with sequence similarity 19 (chemokine (C-C motif)-like), member A5	22	---	0.440960809
FAM5C	339479	family with sequence similarity 5, member C	1	---	0.440960809
FAM73B	84895	family with sequence similarity 73, member B	9	---	0.440960809
FAM98B	283742	family with sequence similarity 98, member B	15	---	0.440960809
FAN1	22909	FANCD2/FANCI-associated nuclease 1	15	---	0.881921618
FAT2	2196	FAT tumor suppressor homolog 2 (Drosophila)	5	FMRP Target	5.291529709
FAXC	84553	failed axon connections homolog (Drosophila)	6	---	0.881921618
FBXL14	144699	F-box and leucine-rich repeat protein 14	12	---	0.440960809
FBXL16	146330	F-box and leucine-rich repeat protein 16	16	FMRP Target	0.440960809
FBXO16	157574	F-box protein 16	8	---	0.440960809
FBXO27	126433	F-box protein 27	19	---	0.881921618

FBXO9	26268	F-box protein 9	6	---	0.440960809
FBXW11	23291	F-box and WD repeat domain containing 11	5	---	0.440960809
FER	2241	fer (fps/fes related) tyrosine kinase	5	---	0.440960809
FGF17	8822	fibroblast growth factor 17	8	---	0.440960809
FGF5	2250	fibroblast growth factor 5	4	---	0.440960809
FGFR2	2263	fibroblast growth factor receptor 2	10	ASD-AD/XL	0.440960809
FIG4	9896	FIG4 homolog, SAC1 lipid phosphatase domain containing (S. cerevisiae)	6	---	0.440960809
FLT3	2322	fms-related tyrosine kinase 3	13	---	3.086725664
FNBP4	23360	formin binding protein 4	11	---	0.440960809
FOXN2	3344	forkhead box N2	2	---	0.440960809
FRMD5	84978	FERM domain containing 5	15	---	0.440960809
FSTL4	23105	follistatin-like 4	5	---	1.322882427
FUBP3	8939	far upstream element (FUSE) binding protein 3	9	---	0.440960809
FUT8	2530	fucosyltransferase 8 (alpha (1,6) fucosyltransferase)	14	---	0.440960809
FZR1	51343	fizzy/cell division cycle 20 related 1 (Drosophila)	19	---	0.440960809
GABRA1	2554	gamma-aminobutyric acid (GABA) A receptor, alpha 1	5	Postsynaptic Proteome	3.968647282
GABRA6	2559	gamma-aminobutyric acid (GABA) A receptor, alpha 6	5	---	2.204804046
GABRB1	2560	gamma-aminobutyric acid (GABA) A receptor, beta 1	4	---	0.881921618
GABRD	2563	gamma-aminobutyric acid (GABA) A receptor, delta	1	---	1.763843236
GABRG1	2565	gamma-aminobutyric acid (GABA) A receptor, gamma 1	4	---	0.440960809
GAD1	2571	glutamate decarboxylase 1 (brain, 67kDa)	2	---	2.645764855
GAD2	2572	glutamate decarboxylase 2 (pancreatic islets and brain, 65kDa)	10	---	3.527686473
GALNT13	114805	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 13 (GalNAc-T13)	2	---	2.204804046
GALNT5	11227	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 5 (GalNAc-T5)	2	---	0.881921618
GALNT9	50614	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 9 (GalNAc-T9)	12	---	0.440960809
GAN	8139	gigaxonin	16	---	0.881921618
GARNL3	84253	GTPase activating Rap/RanGAP domain-like 3	9	FMRP Target	5.291529709
GEMIN7	79760	gem (nuclear organelle) associated protein 7	19	---	0.440960809
GFAP	2670	glial fibrillary acidic protein	17	Postsynaptic Proteome	1.322882427
GFOD1	54438	glucose-fructose oxidoreductase domain containing 1	6	---	0.440960809
GIGYF2	26058	GRB10 interacting GYF protein 2	2	---	0.440960809
GIT2	9815	G protein-coupled receptor kinase interacting ArfGAP 2	12	---	0.440960809
GLCE	26035	glucuronic acid epimerase	15	---	0.440960809
GLMN	11146	glomulin, FKBP associated protein	1	---	0.440960809
GLRA2	2742	glycine receptor, alpha 2	X	---	1.322882427
GLT25D2	23127	glycosyltransferase 25 domain containing 2	1	---	1.763843236
GNB3	2784	guanine nucleotide binding protein (G protein), beta polypeptide 3	12	---	0.440960809
GNB5	10681	guanine nucleotide binding protein (G protein), beta 5	15	---	0.440960809
GNL1	2794	guanine nucleotide binding protein-like 1	6	Postsynaptic Proteome	0.440960809
GPR158	57512	G protein-coupled receptor 158	10	FMRP Target,Postsynaptic Proteome	2.645764855
GPR158-AS1	1E+08	GPR158 antisense RNA 1	10	---	0.440960809
GPR180	160897	G protein-coupled receptor 180	13	---	0.440960809
GPR37L1	9283	G protein-coupled receptor 37 like 1	1	---	0.440960809
GPR52	9293	G protein-coupled receptor 52	1	---	0.440960809
GPR83	10888	G protein-coupled receptor 83	11	---	1.322882427
GPR98	84059	G protein-coupled receptor 98	5	denovo SNV	2.204804046
GPRASP1	9737	G protein-coupled receptor associated sorting protein 1	X	---	0.440960809
GPRASP2	114928	G protein-coupled receptor associated sorting protein 2	X	---	0.440960809
GRAMD1B	57476	GRAM domain containing 1B	11	FMRP Target	1.322882427
GRIA4	2893	glutamate receptor, ionotropic, AMPA 4	11	---	3.968647282
GRID2	2895	glutamate receptor, ionotropic, delta 2	4	---	2.204804046
GRIK1	2897	glutamate receptor, ionotropic, kainate 1	21	---	0.440960809
GRIK2	2898	glutamate receptor, ionotropic, kainate 2	6	---	3.968647282
GRIN1	2902	glutamate receptor, ionotropic, N-methyl D-aspartate 1	9	FMRP Target,Postsynaptic Proteome	0.440960809
GRIN2A	2903	glutamate receptor, ionotropic, N-methyl D-aspartate 2A	16	FMRP Target	2.645764855
GRIN2C	2905	glutamate receptor, ionotropic, N-methyl D-aspartate 2C	17	---	3.086725664
GRM1	2911	glutamate receptor, metabotropic 1	6	---	1.763843236
GRM4	2914	glutamate receptor, metabotropic 4	6	FMRP Target	0.440960809
GTF2H4	2968	general transcription factor IIH, polypeptide 4, 52kDa	6	---	0.881921618
GUSBP4	375513	glucuronidase, beta pseudogene 4	6	---	0.440960809
HABP4	22927	hyaluronan binding protein 4	9	---	0.440960809
HACE1	57531	HECT domain and ankyrin repeat containing E3 ubiquitin protein ligase 1	6	---	0.881921618
HAPLN2	60484	hyaluronan and proteoglycan link protein 2	1	Postsynaptic Proteome	0.440960809
HAUS3	79441	HAUS augmin-like complex, subunit 3	4	---	0.881921618
HECTD4	283450	HECT domain containing E3 ubiquitin protein ligase 4	12	---	1.322882427
HINFP	25988	histone H4 transcription factor	11	---	0.440960809
HMGCLL1	54511	3-hydroxymethyl-3-methylglutaryl-CoA lyase-like 1	6	---	0.881921618
HNRNPR	10236	heterogeneous nuclear ribonucleoprotein R	1	---	0.440960809

HPCA	3208	hippocalcin	1	—	0.440960809
HPCAL4	51440	hippocalcin like 4	1	—	0.440960809
HR	55806	hair growth associated	8	—	0.881921618
HRH3	11255	histamine receptor H3	20	—	0.440960809
HS3ST1	9957	heparan sulfate (glucosamine) 3-O-sulfotransferase 1	4	—	0.440960809
HSF4	3299	heat shock transcription factor 4	16	—	0.440960809
IDUA	3425	iduronidase, alpha-L-	4	—	0.440960809
IGSF21	84966	immunoglobin superfamily, member 21	1	Postsynaptic Proteome	0.881921618
IGSF8	93185	immunoglobulin superfamily, member 8	1	Postsynaptic Proteome	0.440960809
IKBKAP	8518	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase complex-associated protein	9	—	0.440960809
IL16	3603	interleukin 16	15	—	1.322882427
INPP5F	22876	inositol polyphosphate-5-phosphatase F	10	—	3.086725664
INTS4	92105	integrator complex subunit 4	11	—	0.440960809
ITPR1	3708	inositol 1,4,5-trisphosphate receptor, type 1	3	FMRP Target	5.291529709
JARID2	3720	jumonji, AT rich interactive domain 2	6	—	0.440960809
JMJD1C	221037	jumonji domain containing 1C	10	—	0.881921618
JMJD7	1E+08	jumonji domain containing 7	15	—	0.440960809
MJD7-PLA2G4	8681	JMJD7-PLA2G4B readthrough	15	—	1.763843236
JMY	133746	junction mediating and regulatory protein, p53 cofactor	5	—	0.440960809
JPH3	57338	junctophilin 3	16	FMRP Target	0.881921618
KANSL2	54934	KAT8 regulatory NSL complex subunit 2	12	—	0.440960809
KAT2A	2648	K(lysine) acetyltransferase 2A	17	—	0.440960809
KBTBD3	143879	kelch repeat and BTB (POZ) domain containing 3	11	—	0.440960809
KCNA2	3737	potassium voltage-gated channel, shaker-related subfamily, member 2	1	FMRP Target	1.322882427
KCNAB1	7881	potassium voltage-gated channel, shaker-related subfamily, beta member 1	3	—	2.204804046
KCNAB3	9196	potassium voltage-gated channel, shaker-related subfamily, beta member 3	17	—	1.322882427
KCNC3	3748	potassium voltage-gated channel, Shaw-related subfamily, member 3	19	FMRP Target	0.440960809
KCND3	3752	potassium voltage-gated channel, Shal-related subfamily, member 3	1	—	0.440960809
KCNH1	3756	potassium voltage-gated channel, subfamily H (eag-related), member 1	1	FMRP Target	3.527686473
KCNIP4	80333	Kv channel interacting protein 4	4	—	1.763843236
KCNJ6	3763	potassium inwardly-rectifying channel, subfamily J, member 6	21	—	0.881921618
KCNK1	3775	potassium channel, subfamily K, member 1	1	—	0.881921618
KCNK10	54207	potassium channel, subfamily K, member 10	14	—	0.440960809
KCNK12	56660	potassium channel, subfamily K, member 12	2	—	0.440960809
KCNK9	51305	potassium channel, subfamily K, member 9	8	—	0.881921618
KCTD6	200845	potassium channel tetramerisation domain containing 6	3	—	0.440960809
KCTD8	386617	potassium channel tetramerisation domain containing 8	4	Postsynaptic Proteome	0.440960809
KDM2B	84678	lysine (K)-specific demethylase 2B	12	—	0.440960809
KDM4C	23081	lysine (K)-specific demethylase 4C	9	—	1.763843236
KIAA0319	9856	KIAA0319	6	—	0.440960809
KIAA0513	9764	KIAA0513	16	—	2.645764855
KIAA0895L	653319	KIAA0895-like	16	—	0.881921618
KIAA1109	84162	KIAA1109	4	FMRP Target	0.881921618
KIAA1199	57214	KIAA1199	15	—	0.440960809
KIAA1324L	222223	KIAA1324-like	7	—	1.763843236
KIAA1456	57604	KIAA1456	8	—	0.440960809
KIAA1704	55425	KIAA1704	13	—	0.440960809
KIFC2	90990	kinesin family member C2	8	FMRP Target	1.322882427
KIN	22944	KIN, antigenic determinant of recA protein homolog (mouse)	10	—	0.440960809
KLC2	64837	kinesin light chain 2	11	Postsynaptic Proteome	0.440960809
KLHL18	23276	kelch-like family member 18	3	—	0.440960809
KLHL3	26249	kelch-like family member 3	5	—	1.322882427
KNDC1	85442	kinase non-catalytic C-lobe domain (KIND) containing 1	10	FMRP Target	1.322882427
KRIT1	889	KRIT1, ankyrin repeat containing	7	—	0.440960809
KRT222	125113	keratin 222	17	—	1.322882427
KSR2	283455	kinase suppressor of ras 2	12	—	0.881921618
L1CAM	3897	L1 cell adhesion molecule	X	Postsynaptic Proteome,ASD-AD/XL	3.527686473
LAS1L	81887	LAS1-like (S. cerevisiae)	X	—	0.440960809
LATS1	9113	LATS, large tumor suppressor, homolog 1 (Drosophila)	6	—	0.440960809
LCOR	84458	ligand dependent nuclear receptor corepressor	10	—	0.440960809
LDLRAD3	143458	low density lipoprotein receptor class A domain containing 3	11	—	0.440960809
LEMD3	23592	LEM domain containing 3	12	—	0.440960809
LENG8	114823	leukocyte receptor cluster (LRC) member 8	19	—	0.440960809
LENG9	94059	leukocyte receptor cluster (LRC) member 9	19	—	0.440960809
LEO1	123169	Leo1, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	15	—	0.881921618
LGI1	9211	leucine-rich, glioma inactivated 1	10	—	1.763843236
LGI3	203190	leucine-rich repeat LGI family, member 3	8	—	1.322882427
LHFPL4	375323	lipoma HMGIC fusion partner-like 4	3	FMRP Target	0.440960809
LIN7C	55327	lin-7 homolog C (C. elegans)	11	Postsynaptic Proteome	0.440960809
LIX1	167410	Lix1 homolog (chicken)	5	—	0.440960809

LLGL1	3996	lethal giant larvae homolog 1 (Drosophila)	17	denovo SNV,FMRP Target,Postsynaptic Proteome	0.440960809
LMAN1L	79748	lectin, mannose-binding, 1 like	15	---	0.440960809
LMNB1	4001	lamin B1	5	---	0.440960809
LMTK2	22853	lemur tyrosine kinase 2	7	FMRP Target	0.881921618
.OC100379224	1E+08	uncharacterized LOC100379224	19	---	0.440960809
LONRF2	164832	LON peptidase N-terminal domain and ring finger 2	2	---	0.881921618
LRCH1	23143	leucine-rich repeats and calponin homology (CH) domain containing 1	13	---	0.881921618
LRCH2	57631	leucine-rich repeats and calponin homology (CH) domain containing 2	X	---	0.881921618
LRP1B	53353	low density lipoprotein receptor-related protein 1B	2	---	10.14209861
LRRTM3	347731	leucine rich repeat transmembrane neuronal 3	10	---	0.881921618
LSS	4047	lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)	21	---	0.881921618
LUC7L	55692	LUC7-like (S. cerevisiae)	16	---	0.881921618
LY6G5B	58496	lymphocyte antigen 6 complex, locus G5B	6	---	0.440960809
LYST	1130	lysosomal trafficking regulator	1	---	0.881921618
MACROD2	140733	MACRO domain containing 2	20	---	0.440960809
MADD	8567	MAP-kinase activating death domain	11	denovo SNV,FMRP Target	0.881921618
MAG	4099	myelin associated glycoprotein	19	---	0.440960809
MAGEE1	57692	melanoma antigen family E, 1	X	---	0.440960809
MAGI3	260425	membrane associated guanylate kinase, WW and PDZ domain containing 3	1	---	0.440960809
MAGOHB	55110	mago-nashi homolog B (Drosophila)	12	---	0.440960809
MAML3	55534	mastermind-like 3 (Drosophila)	4	---	0.440960809
MAP2K5	5607	mitogen-activated protein kinase kinase 5	15	---	0.440960809
MAP3K10	4294	mitogen-activated protein kinase kinase kinase 10	19	---	0.440960809
MAP4K2	5871	mitogen-activated protein kinase kinase kinase kinase 2	11	---	1.763843236
MAP6D1	79929	MAP6 domain containing 1	3	Postsynaptic Proteome	0.440960809
MAP7D2	256714	MAP7 domain containing 2	X	---	0.440960809
MAPK4	5596	mitogen-activated protein kinase 4	18	FMRP Target	0.440960809
MAPK8IP3	23162	mitogen-activated protein kinase 8 interacting protein 3	16	FMRP Target	3.527686473
MAPK9	5601	mitogen-activated protein kinase 9	5	---	1.322882427
MAPT	4137	microtubule-associated protein tau	17	Postsynaptic Proteome	0.440960809
MARK1	4139	MAP/microtubule affinity-regulating kinase 1	1	---	1.763843236
MBTPS2	51360	membrane-bound transcription factor peptidase, site 2	X	---	1.322882427
MCF2L	23263	MCF.2 cell line derived transforming sequence-like	13	---	2.645764855
MCF2L2	23101	MCF.2 cell line derived transforming sequence-like 2	3	---	2.204804046
MCTP1	79772	multiple C2 domains, transmembrane 1	5	---	1.763843236
MCU	90550	mitochondrial calcium uniporter	10	---	0.440960809
MDGA1	266727	MAM domain containing glycosylphosphatidylinositol anchor 1	6	---	2.645764855
MDN1	23195	MDN1, midasin homolog (yeast)	6	denovo SNV	3.086725664
MED12L	116931	mediator complex subunit 12-like	3	---	1.763843236
MED13L	23389	mediator complex subunit 13-like	12	denovo SNV,FMRP Target	0.440960809
MEGF10	84466	multiple EGF-like-domains 10	5	---	3.968647282
MEGF11	84465	multiple EGF-like-domains 11	15	denovo SNV	2.204804046
METTL10	399818	methyltransferase like 10	10	---	0.440960809
METTL21D	79609	methyltransferase like 21D	14	---	0.440960809
MGARP	84709	mitochondria-localized glutamic acid-rich protein	4	---	0.440960809
MGAT3	4248	mannosyl (beta-1,4-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase	22	---	0.440960809
MGAT4A	11320	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme A	2	---	0.440960809
MGAT5B	146664	mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-glucosaminyltransferase, isozyme B	17	FMRP Target	0.440960809
MID1	4281	midline 1 (Opitz/BBB syndrome)	X	ASD-AD/XL	0.440960809
MINK1	50488	misshapen-like kinase 1	17	FMRP Target,Postsynaptic Proteome	0.440960809
MMP24	10893	matrix metallopeptidase 24 (membrane-inserted)	20	FMRP Target	1.763843236
MMS19	64210	MMS19 nucleotide excision repair homolog (S. cerevisiae)	10	---	0.440960809
MOG	4340	myelin oligodendrocyte glycoprotein	6	Postsynaptic Proteome	1.322882427
MORN1	79906	MORN repeat containing 1	1	---	0.440960809
MPHOSPH6	10200	M-phase phosphoprotein 6	16	---	0.440960809
MPHOSPH9	10198	M-phase phosphoprotein 9	12	---	0.440960809
MREG	55686	melanoregulin	2	---	0.440960809
MRPL50	54534	mitochondrial ribosomal protein L50	9	---	0.440960809
MSANTD4	84437	Myb/SANT-like DNA-binding domain containing 4 with coiled-coils	11	---	0.440960809
MSH2	4436	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)	2	---	0.440960809
MTERFD2	130916	MTERF domain containing 2	2	---	0.440960809
MTUS1	57509	microtubule associated tumor suppressor 1	8	---	0.440960809
MUM1	84939	melanoma associated antigen (mutated) 1	19	---	0.440960809
MYO15A	51168	myosin XVA	17	---	0.440960809
MYT1	4661	myelin transcription factor 1	20	---	6.173451327
NAA38	51691	N(alpha)-acetyltransferase 38, NatC auxiliary subunit	7	---	0.440960809

NAB1	4664	NGFI-A binding protein 1 (EGR1 binding protein 1)	2	---	0.440960809
NALCN	259232	sodium leak channel, non-selective	13	---	9.7011378
NAP1L2	4674	nucleosome assembly protein 1-like 2	X	---	0.440960809
NAP1L5	266812	nucleosome assembly protein 1-like 5	4	---	0.440960809
NCOA7	135112	nuclear receptor coactivator 7	6	---	1.322882427
NDP	4693	Norrie disease (pseudoglioma)	X	ASD-AD/XL	0.440960809
NDRG2	57447	NDRG family member 2	14	FMRP Target	0.440960809
NDRG4	65009	NDRG family member 4	16	FMRP Target	0.440960809
NEFH	4744	neurofilament, heavy polypeptide	22	Postsynaptic Proteome	0.440960809
NEGR1	257194	neuronal growth regulator 1	1	Postsynaptic Proteome	0.440960809
NEK1	4750	NIMA-related kinase 1	4	---	0.440960809
NEURL4	84461	neuralized homolog 4 (Drosophila)	17	FMRP Target	0.440960809
NEUROD2	4761	neuronal differentiation 2	17	---	0.440960809
NEUROD6	63974	neuronal differentiation 6	7	---	0.440960809
NINL	22981	ninein-like	20	---	0.440960809
NIPA1	123606	non imprinted in Prader-Willi/Angelman syndrome 1	15	---	0.440960809
NIPAL3	57185	NIPA-like domain containing 3	1	---	0.881921618
NKAIN1	79570	Na+/K+ transporting ATPase interacting 1	1	---	0.440960809
NKIRAS1	28512	NFKB inhibitor interacting Ras-like 1	3	---	0.440960809
NKTR	4820	natural killer-tumor recognition sequence	3	---	0.881921618
NOL4	8715	nucleolar protein 4	18	---	0.881921618
NOP58	51602	NOP58 ribonucleoprotein	2	---	0.440960809
NPAS3	64067	neuronal PAS domain protein 3	14	---	0.440960809
NPAT	4863	nuclear protein, ataxia-telangiectasia locus	11	---	0.440960809
NPFFR1	64106	neuropeptide FF receptor 1	10	---	0.440960809
NPM2	10361	nucleophosmin/nucleoplasmin 2	8	---	0.440960809
NPPA-AS1	1E+08	NPPA antisense RNA 1	1	---	0.440960809
NPR2	4882	natriuretic peptide receptor B/guanylate cyclase B (atrionatriuretic peptide receptor B)	9	---	1.763843236
NPTX1	4884	neuronal pentraxin I	17	---	1.763843236
NR1D1	9572	nuclear receptor subfamily 1, group D, member 1	17	---	0.440960809
NRIP2	83714	nuclear receptor interacting protein 2	12	---	0.881921618
NRSN1	140767	neurensin 1	6	---	0.440960809
NRXN3	9369	neurexin 3	14	FMRP Target	3.968647282
NSD1	64324	nuclear receptor binding SET domain protein 1	5	FMRP Target,ASD-AD/XL	0.440960809
NSG1	27065	neuron specific gene family member 1	4	---	0.440960809
NUAK1	9891	NUAK family, SNF1-like kinase, 1	12	denovo SNV	0.440960809
NXPH3	11248	neurexophilin 3	17	---	0.440960809
OLFM3	118427	olfactomedin 3	1	---	1.763843236
OSBP2	23762	oxysterol binding protein 2	22	---	0.440960809
OSBPL2	9885	oxysterol binding protein-like 2	20	---	0.440960809
OSBPL7	114881	oxysterol binding protein-like 7	17	---	0.440960809
OTUD7A	161725	OTU domain containing 7A	15	---	1.763843236
P2RX7	5027	purinergic receptor P2X, ligand-gated ion channel, 7	12	---	0.881921618
P4HTM	54681	prolyl 4-hydroxylase, transmembrane (endoplasmic reticulum)	3	---	0.440960809
PAAF1	80227	proteasomal ATPase-associated factor 1	11	---	0.440960809
PACSIN1	29993	protein kinase C and casein kinase substrate in neurons 1	6	Postsynaptic Proteome	1.322882427
PAGR1	79447	PAXIP1 associated glutamate-rich protein 1	16	---	0.440960809
PAK1	5058	p21 protein (Cdc42/Rac)-activated kinase 1	11	Postsynaptic Proteome	0.440960809
PANK4	55229	pantothenate kinase 4	1	---	0.440960809
PAPD5	64282	PAP associated domain containing 5	16	---	0.440960809
PAPL	390928	iron/zinc purple acid phosphatase-like protein	19	---	0.440960809
PAQR6	79957	progestin and adipoQ receptor family member VI	1	---	0.881921618
PARD6A	50855	par-6 partitioning defective 6 homolog alpha (C. elegans)	16	---	0.440960809
PARP2	10038	poly (ADP-ribose) polymerase 2	14	---	0.440960809
PAXIP1	22976	PAX interacting (with transcription-activation domain) protein 1	7	---	2.204804046
PCBP3	54039	poly(rC) binding protein 3	21	---	1.322882427
PCF11	51585	PCF11, cleavage and polyadenylation factor subunit, homolog (S. cerevisiae)	11	---	0.440960809
PCIF1	63935	PDX1 C-terminal inhibiting factor 1	20	---	0.881921618
PCYOX1L	78991	prenylcysteine oxidase 1 like	5	---	0.440960809
PDE1A	5136	phosphodiesterase 1A, calmodulin-dependent	2	---	0.440960809
PDE3B	5140	phosphodiesterase 3B, cGMP-inhibited	11	---	0.440960809
PDIA2	64714	protein disulfide isomerase family A, member 2	16	---	0.440960809
PELI3	246330	pellino E3 ubiquitin protein ligase family member 3	11	---	0.440960809
PER3	8863	period circadian clock 3	1	---	1.763843236
PGBD5	79605	piggyBac transposable element derived 5	1	---	1.322882427
PHF21A	51317	PHD finger protein 21A	11	---	0.440960809
PHTF1	10745	putative homeodomain transcription factor 1	1	---	0.881921618
PI4KA	5297	phosphatidylinositol 4-kinase, catalytic, alpha	22	FMRP Target,Postsynaptic Proteome	0.881921618
PIGZ	80235	phosphatidylinositol glycan anchor biosynthesis, class Z	3	---	0.440960809
PITPNM1	9600	phosphatidylinositol transfer protein, membrane-associated 1	11	FMRP Target	0.881921618

PITPNM3	83394	PITPNM family member 3	17	---	1.763843236
PKD1	5310	polycystic kidney disease 1 (autosomal dominant)	16	FMRP Target	0.440960809
PLA2G4B	1E+08	phospholipase A2, group IVB (cytosolic)	15	---	1.322882427
PLCB4	5332	phospholipase C, beta 4	20	---	4.409608091
PLCG1	5335	phospholipase C, gamma 1	20	---	1.322882427
PLCL2	23228	phospholipase C-like 2	3	---	0.440960809
PLD5	200150	phospholipase D family, member 5	1	---	1.322882427
PLEKHA6	22874	pleckstrin homology domain containing, family A member 6	1	---	0.440960809
PLEKHB1	58473	pleckstrin homology domain containing, family B (evectins) member 1	11	---	0.440960809
PLEKHG5	57449	pleckstrin homology domain containing, family G (with RhoGef domain) member 5	1	---	2.645764855
PLXNA3	55558	plexin A3	X	---	1.763843236
PLXNB3	5365	plexin B3	X	---	0.440960809
PMP2	5375	peripheral myelin protein 2	8	---	1.322882427
PMVK	10654	phosphomevalonate kinase	1	---	0.440960809
POGZ	23126	pogo transposable element with ZNF domain	1	denovo SNV	0.440960809
POLA1	5422	polymerase (DNA directed), alpha 1, catalytic subunit	X	---	0.440960809
POLE	5426	polymerase (DNA directed), epsilon, catalytic subunit	12	---	3.527686473
POLR3A	11128	polymerase (RNA) III (DNA directed) polypeptide A, 155kDa	10	---	0.440960809
POLR3F	10621	polymerase (RNA) III (DNA directed) polypeptide F, 39 kDa	20	---	0.440960809
PPARGC1B	133522	peroxisome proliferator-activated receptor gamma, coactivator 1 beta	5	---	0.440960809
PPFIA1	8500	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1	11	Postsynaptic Proteome	0.440960809
PPFIA3	8541	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 3	19	FMRP Target,Postsynaptic Proteome	1.763843236
PPIP5K1	9677	diphosphoinositol pentakisphosphate kinase 1	15	---	0.440960809
PPP1R16B	26051	protein phosphatase 1, regulatory subunit 16B	20	---	0.881921618
PPP2R2C	5522	protein phosphatase 2, regulatory subunit B, gamma	4	FMRP Target	2.645764855
PRDM15	63977	PR domain containing 15	21	---	0.440960809
PRKCE	5581	protein kinase C, epsilon	2	FMRP Target	0.881921618
PRKCG	5582	protein kinase C, gamma	19	FMRP Target,Postsynaptic Proteome	2.645764855
PRMT7	54496	protein arginine methyltransferase 7	16	---	0.440960809
PRMT8	56341	protein arginine methyltransferase 8	12	---	0.881921618
PROSAPIP1	9762	ProSAPiP1 protein	20	FMRP Target	0.881921618
PRPF18	8559	PRP18 pre-mRNA processing factor 18 homolog (S. cerevisiae)	10	---	0.440960809
PRPF38B	55119	PRP38 pre-mRNA processing factor 38 (yeast) domain containing B	1	---	0.440960809
PRPF39	55015	PRP39 pre-mRNA processing factor 39 homolog (S. cerevisiae)	14	---	0.440960809
PRPF6	24148	PRP6 pre-mRNA processing factor 6 homolog (S. cerevisiae)	20	---	0.440960809
PRR3	80742	proline rich 3	6	---	0.440960809
PRRT1	80863	proline-rich transmembrane protein 1	6	---	0.440960809
PRUNE2	158471	prune homolog 2 (Drosophila)	9	---	1.322882427
PSD2	84249	pleckstrin and Sec7 domain containing 2	5	---	2.204804046
PTCHD1	139411	patched domain containing 1	X	ASD-AD/XL	0.440960809
PTK2	5747	protein tyrosine kinase 2	8	FMRP Target	0.440960809
PTK2B	2185	PTK2B protein tyrosine kinase 2 beta	8	FMRP Target,Postsynaptic Proteome	0.440960809
PTPRN	5798	protein tyrosine phosphatase, receptor type, N	2	---	2.204804046
PTPRR	5801	protein tyrosine phosphatase, receptor type, R	12	---	3.527686473
PTPRS	5802	protein tyrosine phosphatase, receptor type, S	19	FMRP Target,Postsynaptic Proteome	0.440960809
PUM2	23369	pumilio homolog 2 (Drosophila)	2	FMRP Target	0.440960809
PVALB	5816	parvalbumin	22	---	0.440960809
QSOX2	169714	quiescin Q6 sulfhydryl oxidase 2	9	---	0.440960809
RAB11FIP4	84440	RAB11 family interacting protein 4 (class II)	17	---	0.440960809
RAB26	25837	RAB26, member RAS oncogene family	16	---	0.881921618
RAB37	326624	RAB37, member RAS oncogene family	17	---	1.763843236
RAB39B	116442	RAB39B, member RAS oncogene family	X	denovo SNV,ASD-AD/XL	0.440960809
RALGDS	5900	ral guanine nucleotide dissociation stimulator	9	FMRP Target	0.881921618
RALGPS1	9649	Ral GEF with PH domain and SH3 binding motif 1	9	---	0.881921618
RALYL	138046	RALY RNA binding protein-like	8	---	0.440960809
RAP1GAP2	23108	RAP1 GTPase activating protein 2	17	FMRP Target	1.322882427
RAPGEF4	11069	Rap guanine nucleotide exchange factor (GEF) 4	2	FMRP Target,Postsynaptic Proteome	5.732490518
RAPGEF6	51735	Rap guanine nucleotide exchange factor (GEF) 6	5	---	1.322882427
RASGEF1A	221002	RasGEF domain family, member 1A	10	---	0.440960809
RASGEF1C	255426	RasGEF domain family, member 1C	5	---	0.881921618
RASGRF1	5923	Ras protein-specific guanine nucleotide-releasing factor 1	15	FMRP Target	4.8505689
RASGRP1	10125	RAS guanyl releasing protein 1 (calcium and DAG-regulated)	15	FMRP Target	3.527686473
RBFOX1	54715	RNA binding protein, fox-1 homolog (C. elegans) 1	16	---	0.881921618
RBM15	64783	RNA binding motif protein 15	1	---	0.440960809

RBM39	9584	RNA binding motif protein 39	20	---	0.440960809
RCAN2	10231	regulator of calcineurin 2	6	---	0.440960809
RCOR3	55758	REST corepressor 3	1	---	0.440960809
RDH13	112724	retinol dehydrogenase 13 (all-trans/9-cis)	19	---	0.440960809
REC8	9985	REC8 homolog (yeast)	14	---	0.440960809
RELL2	285613	RELT-like 2	5	---	0.440960809
RELN	5649	reelin	7	FMRP Target	3.968647282
REV1	51455	REV1, polymerase (DNA directed)	2	---	1.322882427
REV3L	5980	REV3-like, polymerase (DNA directed), zeta, catalytic subunit	6	FMRP Target	0.881921618
RFTN2	130132	raftlin family member 2	2	---	0.440960809
RFX3	5991	regulatory factor X, 3 (influences HLA class II expression)	9	---	0.881921618
RGS11	8786	regulator of G-protein signaling 11	16	---	0.881921618
RGS12	6002	regulator of G-protein signaling 12	4	---	0.440960809
RGS8	85397	regulator of G-protein signaling 8	1	---	0.881921618
RHBDL1	9028	rhomboid, veinlet-like 1 (Drosophila)	16	---	0.881921618
RIMS2	9699	regulating synaptic membrane exocytosis 2	8	---	5.291529709
RIMS3	9783	regulating synaptic membrane exocytosis 3	1	---	0.881921618
RIT2	6014	Ras-like without CAAX 2	18	---	0.881921618
RNF112	7732	ring finger protein 112	17	---	1.322882427
RNF182	221687	ring finger protein 182	6	---	0.440960809
RPH3A	22895	rabphilin 3A homolog (mouse)	12	FMRP Target,Postsynaptic Proteome	3.086725664
RPRD2	23248	regulation of nuclear pre-mRNA domain containing 2	1	FMRP Target	0.440960809
RPS6KA5	9252	ribosomal protein S6 kinase, 90kDa, polypeptide 5	14	---	1.763843236
RPS6KL1	83694	ribosomal protein S6 kinase-like 1	14	---	0.440960809
RSBN1	54665	round spermatid basic protein 1	1	---	0.440960809
RTEL1	51750	regulator of telomere elongation helicase 1	20	---	0.440960809
TEL1-TNFRSF6	1E+08	RTEL1-TNFRSF6B readthrough (non-protein coding)	20	---	0.440960809
SALL2	6297	sal-like 2 (Drosophila)	14	FMRP Target	0.440960809
SAMD14	201191	sterile alpha motif domain containing 14	17	---	0.881921618
SART3	9733	squamous cell carcinoma antigen recognized by T cells 3	12	---	0.440960809
SCN1A	6323	sodium channel, voltage-gated, type I, alpha subunit	2	ASD-AD/XL	4.8505689
SCN2B	6327	sodium channel, voltage-gated, type II, beta subunit	11	---	0.440960809
SCN4B	6330	sodium channel, voltage-gated, type IV, beta subunit	11	---	0.881921618
SDCCAG8	10806	serologically defined colon cancer antigen 8	1	---	0.440960809
SEC24B	10427	SEC24 family, member B (S. cerevisiae)	4	---	0.440960809
SEC31B	25956	SEC31 homolog B (S. cerevisiae)	10	---	1.763843236
SEL1L3	23231	sel-1 suppressor of lin-12-like 3 (C. elegans)	4	---	0.440960809
SEMA4F	10505	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4F	2	---	0.881921618
SEMA6A	57556	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A	5	---	1.322882427
SENP7	57337	SUMO1/sentrin specific peptidase 7	3	---	1.322882427
SERGEF	26297	secretion regulating guanine nucleotide exchange factor	11	---	0.440960809
SEZ6	124925	seizure related 6 homolog (mouse)	17	---	2.204804046
SEZ6L2	26470	seizure related 6 homolog (mouse)-like 2	16	FMRP Target	1.763843236
SGTB	54557	small glutamine-rich tetratricopeptide repeat (TPR)-containing, beta	5	---	0.440960809
SH3D21	79729	SH3 domain containing 21	1	---	0.440960809
SH3GL2	6456	SH3-domain GRB2-like 2	9	Postsynaptic Proteome	1.322882427
SH3GLB2	56904	SH3-domain GRB2-like endophilin B2	9	Postsynaptic Proteome	0.881921618
SHF	90525	Src homology 2 domain containing F	15	---	0.440960809
SHISA6	388336	shisa homolog 6 (Xenopus laevis)	17	---	1.322882427
SHPRH	257218	SNF2 histone linker PHD RING helicase, E3 ubiquitin protein ligase	6	---	2.645764855
SIPA1L1	26037	signal-induced proliferation-associated 1 like 1	14	FMRP Target	1.322882427
SLC12A2	6558	solute carrier family 12 (sodium/potassium/chloride transporters), member 2	5	---	0.440960809
SLC12A5	57468	solute carrier family 12 (potassium/chloride transporter), member 5	20	FMRP Target	6.173451327
SLC17A7	57030	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 7	19	FMRP Target	3.968647282
SLC1A6	6511	solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6	19	---	0.881921618
SLC22A15	55356	solute carrier family 22, member 15	1	---	1.322882427
SLC23A2	9962	solute carrier family 23 (nucleobase transporters), member 2	20	---	0.440960809
SLC24A2	25769	solute carrier family 24 (sodium/potassium/calcium exchanger), member 2	9	FMRP Target	2.204804046
SLC24A3	57419	solute carrier family 24 (sodium/potassium/calcium exchanger), member 3	20	---	0.440960809
SLC25A27	9481	solute carrier family 25, member 27	6	---	1.763843236
SLC26A10	65012	solute carrier family 26, member 10	12	---	0.440960809
SLC26A5	375611	solute carrier family 26, member 5 (prestin)	7	denovo SNV	0.440960809
SLC32A1	140679	solute carrier family 32 (GABA vesicular transporter), member 1	20	---	0.440960809
SLC4A10	57282	solute carrier family 4, sodium bicarbonate transporter, member 10	2	---	7.496333755
SLC4A8	9498	solute carrier family 4, sodium bicarbonate cotransporter, member 8	12	FMRP Target	0.881921618
SLC6A1	6529	solute carrier family 6 (neurotransmitter transporter, GABA), member 1	3	denovo SNV,FMRP Target	0.440960809
SLC6A7	6534	solute carrier family 6 (neurotransmitter transporter, L-proline), member 7	5	---	1.763843236
SLC7A14	57709	solute carrier family 7 (orphan transporter), member 14	3	---	1.322882427
SLC9A5	6553	solute carrier family 9, subfamily A (NHE5, cation proton antiporter 5), member 5	16	---	0.440960809

SLCO1A2	6579	solute carrier organic anion transporter family, member 1A2	12	---	0.881921618
SLITRK3	22865	SLIT and NTRK-like family, member 3	3	---	0.440960809
SLITRK5	26050	SLIT and NTRK-like family, member 5	13	FMRP Target	0.440960809
SLX4	84464	SLX4 structure-specific endonuclease subunit homolog (S. cerevisiae)	16	---	0.440960809
SMARCAD1	56916	SWI/SNF-related, matrix-associated actin-dependent regulator of chromatin, subfamily a, containing DEAD/H box 1	4	---	1.322882427
SMC1A	8243	structural maintenance of chromosomes 1A	X	ASD-AD/XL	0.440960809
SMG1	23049	smg-1 homolog, phosphatidylinositol 3-kinase-related kinase (C. elegans)	16	FMRP Target	0.440960809
SNCAIP	9627	synuclein, alpha interacting protein	5	---	1.322882427
SNTG1	54212	syntrophin, gamma 1	8	---	0.440960809
SNX25	83891	sorting nexin 25	4	---	1.763843236
SOGA1	140710	suppressor of glucose, autophagy associated 1	20	FMRP Target	2.204804046
SOGA2	23255	SOGA family member 2	18	FMRP Target	1.763843236
SORL1	6653	sortilin-related receptor, L(DLR class) A repeats containing	11	FMRP Target	0.440960809
SPIN3	169981	spindlin family, member 3	X	---	0.440960809
SPOCK2	9806	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 2	10	---	0.440960809
SPOCK3	50859	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 3	4	---	0.440960809
SPRYD3	84926	SPRY domain containing 3	12	---	0.440960809
SPTAN1	6709	spectrin, alpha, non-erythrocytic 1	9	FMRP Target,Postsynaptic Proteome	0.440960809
SPTBN2	6712	spectrin, beta, non-erythrocytic 2	11	FMRP Target,Postsynaptic Proteome	2.204804046
SPTBN4	57731	spectrin, beta, non-erythrocytic 4	19	Postsynaptic Proteome	2.645764855
SRCIN1	80725	SRC kinase signaling inhibitor 1	17	FMRP Target	1.763843236
SRRM4	84530	serine/arginine repetitive matrix 4	12	---	0.881921618
SRSF11	9295	serine/arginine-rich splicing factor 11	1	---	0.440960809
SRSF7	6432	serine/arginine-rich splicing factor 7	2	---	0.440960809
SS18L1	26039	synovial sarcoma translocation gene on chromosome 18-like 1	20	---	0.440960809
SSTR2	6752	somatostatin receptor 2	17	---	0.440960809
ST18	9705	suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein)	8	---	5.291529709
ST8SIA1	6489	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 1	12	---	0.440960809
ST8SIA3	51046	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 3	18	---	1.763843236
ST8SIA5	29906	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 5	18	---	1.763843236
STAMBPL1	57559	STAM binding protein-like 1	10	---	0.440960809
STARD4	134429	StAR-related lipid transfer (START) domain containing 4	5	---	0.881921618
STRC	161497	stereocilin	15	---	0.440960809
STRIP1	85369	striatin interacting protein 1	1	---	0.440960809
STX16	8675	syntaxin 16	20	---	0.440960809
STX1A	6804	syntaxin 1A (brain)	7	Postsynaptic Proteome	0.440960809
STXBP5	134957	syntaxin binding protein 5 (tomosyn)	6	FMRP Target	2.645764855
STXBP5-AS1	729178	STXBP5 antisense RNA 1	6	---	0.440960809
SULT4A1	25830	sulfotransferase family 4A, member 1	22	---	2.204804046
SUPT3H	8464	suppressor of Ty 3 homolog (S. cerevisiae)	6	---	0.440960809
SUPT7L	9913	suppressor of Ty 7 (S. cerevisiae)-like	2	---	0.440960809
SUV420H2	84787	suppressor of variegation 4-20 homolog 2 (Drosophila)	19	---	0.440960809
SV2B	9899	synaptic vesicle glycoprotein 2B	15	denovo SNV,FMRP Target	2.645764855
SYBU	55638	syntabulin (syntaxin-interacting)	8	---	0.440960809
SYN1	6853	synapsin I	X	FMRP Target,Postsynaptic Proteome,ASD-AD/XL	3.527686473
SYN2	6854	synapsin II	3	Postsynaptic Proteome	0.440960809
SYN3	8224	synapsin III	22	Postsynaptic Proteome	3.086725664
SYNDIG1	79953	synapse differentiation inducing 1	20	---	0.440960809
SYNE1	23345	spectrin repeat containing, nuclear envelope 1	6	denovo SNV,FMRP Target	14.11074589
SYNGR1	9145	synaptogyrin 1	22	FMRP Target	0.440960809
SYNPR	132204	synaptoporin	3	---	0.881921618
SYP	6855	synaptophysin	X	Postsynaptic Proteome	0.440960809
SYT12	91683	synaptotagmin XII	11	---	0.440960809
SYT13	57586	synaptotagmin XIII	11	---	0.881921618
SYT14	255928	synaptotagmin XIV	1	---	1.763843236
SYT2	127833	synaptotagmin II	1	---	1.763843236
SYT3	84258	synaptotagmin III	19	---	0.440960809
SYT9	143425	synaptotagmin IX	11	---	1.322882427
TAF1C	9013	TATA box binding protein (TBP)-associated factor, RNA polymerase I, C, 110kDa	16	---	0.440960809
TAF2	6873	TAF2 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 150kDa	8	---	0.440960809
TAOK3	51347	TAO kinase 3	12	---	0.440960809
TARBP1	6894	TAR (HIV-1) RNA binding protein 1	1	---	2.645764855
TBC1D9B	23061	TBC1 domain family, member 9B (with GRAM domain)	5	FMRP Target	0.440960809
TBCK	93627	TBC1 domain containing kinase	4	---	0.440960809
TCEAL2	140597	transcription elongation factor A (SII)-like 2	X	---	0.440960809
TCF4	6925	transcription factor 4	18	FMRP Target	0.440960809

TDRKH	11022	tudor and KH domain containing	1	---	0.440960809
TEF	7008	thyrotrophic embryonic factor	22	FMRP Target	0.881921618
TELO2	9894	TEL2, telomere maintenance 2, homolog (S. cerevisiae)	16	---	0.440960809
TENM1	10178	teneurin transmembrane protein 1	X	---	9.260176991
THAP10	56906	THAP domain containing 10	15	---	0.440960809
THUMPD2	80745	THUMP domain containing 2	2	---	0.440960809
TIAM1	7074	T-cell lymphoma invasion and metastasis 1	21	FMRP Target	5.291529709
TIAM2	26230	T-cell lymphoma invasion and metastasis 2	6	---	0.440960809
TLE2	7089	transducin-like enhancer of split 2 (E(sp1) homolog, Drosophila)	19	---	1.763843236
TLL1	7092	tolloid-like 1	4	---	3.086725664
TM2D3	80213	TM2 domain containing 3	15	---	0.440960809
TMC2	117532	transmembrane channel-like 2	20	---	0.440960809
TMCC2	9911	transmembrane and coiled-coil domain family 2	1	---	0.440960809
TMEFF2	23671	transmembrane protein with EGF-like and two follistatin-like domains 2	2	---	0.440960809
TMEM132A	54972	transmembrane protein 132A	11	FMRP Target	0.881921618
TMEM175	84286	transmembrane protein 175	4	---	0.440960809
TMEM180	79847	transmembrane protein 180	10	---	0.440960809
TMEM200B	399474	transmembrane protein 200B	1	---	0.440960809
TMEM25	84866	transmembrane protein 25	11	---	0.440960809
TMEM50B	757	transmembrane protein 50B	21	---	0.440960809
TMEM74	157753	transmembrane protein 74	8	---	0.440960809
TMTC2	160335	transmembrane and tetratricopeptide repeat containing 2	12	---	0.440960809
TNK2	10188	tyrosine kinase, non-receptor, 2	3	FMRP Target	0.881921618
TNRC6A	27327	trinucleotide repeat containing 6A	16	---	0.440960809
TNRC6C	57690	trinucleotide repeat containing 6C	17	---	0.440960809
TOP3A	7156	topoisomerase (DNA) III alpha	17	---	0.440960809
TPCN1	53373	two pore segment channel 1	12	---	0.440960809
TRAPPC11	60684	trafficking protein particle complex 11	4	---	0.881921618
TRIM23	373	tripartite motif containing 23	5	---	0.440960809
TRIM3	10612	tripartite motif containing 3	11	FMRP Target,Postsynaptic Proteome	0.881921618
TRIM46	80128	tripartite motif containing 46	1	---	0.881921618
TRIM67	440730	tripartite motif containing 67	1	---	0.440960809
TRNAU1AP	54952	tRNA selenocysteine 1 associated protein 1	1	---	0.440960809
TRO	7216	trophinin	X	FMRP Target	0.440960809
TRPC3	7222	transient receptor potential cation channel, subfamily C, member 3	4	---	0.881921618
TRPM2	7226	transient receptor potential cation channel, subfamily M, member 2	21	---	0.881921618
TRPM3	80036	transient receptor potential cation channel, subfamily M, member 3	9	FMRP Target	0.440960809
TRRAP	8295	transformation/transcription domain-associated protein	7	denovo SNV,FMRP Target	0.881921618
TSC1	7248	tuberous sclerosis 1	9	ASD-AD/XL	0.881921618
TSEN2	80746	tRNA splicing endonuclease 2 homolog (S. cerevisiae)	3	---	0.440960809
TTC21B	79809	tetratricopeptide repeat domain 21B	2	---	0.881921618
TTC39B	158219	tetratricopeptide repeat domain 39B	9	---	0.881921618
TUBB3	10381	tubulin, beta 3 class III	16	FMRP Target,Postsynaptic Proteome	0.440960809
TUBGCP6	85378	tubulin, gamma complex associated protein 6	22	---	0.881921618
TYRO3	7301	TYRO3 protein tyrosine kinase	15	---	0.440960809
UBTD2	92181	ubiquitin domain containing 2	5	---	0.440960809
UBTF	7343	upstream binding transcription factor, RNA polymerase I	17	---	0.440960809
UNC5C	8633	unc-5 homolog C (C. elegans)	4	---	0.881921618
UNC80	285175	unc-80 homolog (C. elegans)	2	---	2.645764855
USP20	10868	ubiquitin specific peptidase 20	9	---	0.440960809
USP21	27005	ubiquitin specific peptidase 21	1	---	0.440960809
USP33	23032	ubiquitin specific peptidase 33	1	---	0.881921618
USP45	85015	ubiquitin specific peptidase 45	6	---	0.440960809
USP46	64854	ubiquitin specific peptidase 46	4	denovo SNV	0.440960809
USP48	84196	ubiquitin specific peptidase 48	1	---	0.881921618
USP9Y	8287	ubiquitin specific peptidase 9, Y-linked	Y	---	4.409608091
UTP23	84294	UTP23, small subunit (SSU) processome component, homolog (yeast)	8	---	0.440960809
UXS1	80146	UDP-glucuronate decarboxylase 1	2	---	0.440960809
VPS18	57617	vacuolar protein sorting 18 homolog (S. cerevisiae)	15	---	0.440960809
VPS33B	26276	vacuolar protein sorting 33 homolog B (yeast)	15	---	0.440960809
VPS54	51542	vacuolar protein sorting 54 homolog (S. cerevisiae)	2	---	0.881921618
VSX1	30813	visual system homeobox 1	20	---	0.440960809
VWC2	375567	von Willebrand factor C domain containing 2	7	---	0.881921618
WDR19	57728	WD repeat domain 19	4	---	0.440960809
WDR27	253769	WD repeat domain 27	6	---	0.881921618
WDR67	93594	WD repeat domain 67	8	---	0.881921618
WDSUB1	151525	WD repeat, sterile alpha motif and U-box domain containing 1	2	---	0.440960809
WHSC1L1	54904	Wolf-Hirschhorn syndrome candidate 1-like 1	8	---	2.645764855
WRAP73	49856	WD repeat containing, antisense to TP73	1	---	0.440960809
WSCD1	23302	WSC domain containing 1	17	---	0.881921618
WSCD2	9671	WSC domain containing 2	12	---	1.322882427

WWC3	55841	WWC family member 3	X	denovo SNV	0.440960809
XKR6	286046	XK, Kell blood group complex subunit-related family, member 6	8	---	0.440960809
YPEL4	219539	yippee-like 4 (Drosophila)	11	---	0.881921618
ZBTB41	360023	zinc finger and BTB domain containing 41	1	denovo SNV	0.881921618
ZCCHC12	170261	zinc finger, CCHC domain containing 12	X	---	0.440960809
ZDHHC8	29801	zinc finger, DHHC-type containing 8	22	---	0.440960809
ZFAND1	79752	zinc finger, AN1-type domain 1	8	---	0.440960809
ZFHX2	85446	zinc finger homeobox 2	14	FMRP Target	0.440960809
ZFP1	162239	ZFP1 zinc finger protein	16	---	0.440960809
ZFP112	7771	zinc finger protein 112 homolog (mouse)	19	---	0.440960809
ZFP30	22835	ZFP30 zinc finger protein	19	---	0.440960809
ZFPM2	23414	zinc finger protein, FOG family member 2	8	---	0.440960809
ZFYVE16	9765	zinc finger, FYVE domain containing 16	5	---	0.440960809
ZFYVE27	118813	zinc finger, FYVE domain containing 27	10	---	0.881921618
ZFYVE28	57732	zinc finger, FYVE domain containing 28	4	---	1.322882427
ZIC1	7545	Zic family member 1	3	---	0.881921618
ZIC2	7546	Zic family member 2	13	---	0.440960809
ZIC3	7547	Zic family member 3	X	---	0.440960809
ZIC4	84107	Zic family member 4	3	---	1.322882427
ZMYND11	10771	zinc finger, MYND-type containing 11	10	denovo SNV	0.440960809
ZNF133	7692	zinc finger protein 133	20	---	0.440960809
ZNF136	7695	zinc finger protein 136	19	---	0.440960809
ZNF138	7697	zinc finger protein 138	7	---	0.440960809
ZNF175	7728	zinc finger protein 175	19	---	0.440960809
ZNF211	10520	zinc finger protein 211	19	---	0.440960809
ZNF224	7767	zinc finger protein 224	19	---	0.440960809
ZNF236	7776	zinc finger protein 236	18	---	0.440960809
ZNF238	10472	zinc finger and BTB domain containing 18	1	FMRP Target	0.440960809
ZNF25	219749	zinc finger protein 25	10	---	0.440960809
ZNF250	58500	zinc finger protein 250	8	---	0.440960809
ZNF256	10172	zinc finger protein 256	19	---	0.440960809
ZNF280D	54816	zinc finger protein 280D	15	---	0.440960809
ZNF287	57336	zinc finger protein 287	17	---	0.440960809
ZNF335	63925	zinc finger protein 335	20	denovo SNV	0.440960809
ZNF343	79175	zinc finger protein 343	20	---	0.440960809
ZNF365	22891	zinc finger protein 365	10	FMRP Target	0.440960809
ZNF385D	79750	zinc finger protein 385D	3	---	0.440960809
ZNF418	147686	zinc finger protein 418	19	---	0.440960809
ZNF461	92283	zinc finger protein 461	19	---	0.881921618
ZNF471	57573	zinc finger protein 471	19	---	0.440960809
ZNF483	158399	zinc finger protein 483	9	---	0.881921618
ZNF490	57474	zinc finger protein 490	19	---	0.440960809
ZNF493	284443	zinc finger protein 493	19	---	0.440960809
ZNF521	25925	zinc finger protein 521	18	FMRP Target	1.763843236
ZNF528	84436	zinc finger protein 528	19	---	0.440960809
ZNF529	57711	zinc finger protein 529	19	---	0.440960809
ZNF536	9745	zinc finger protein 536	19	FMRP Target	1.322882427
ZNF540	163255	zinc finger protein 540	19	---	1.763843236
ZNF566	84924	zinc finger protein 566	19	---	0.440960809
ZNF568	374900	zinc finger protein 568	19	---	0.440960809
ZNF585A	199704	zinc finger protein 585A	19	---	0.440960809
ZNF589	51385	zinc finger protein 589	3	---	0.440960809
ZNF605	1E+08	zinc finger protein 605	12	---	0.440960809
ZNF702P	79986	zinc finger protein 702, pseudogene	19	---	0.881921618
ZNF738	148203	zinc finger protein 738	19	---	0.440960809
ZNF740	283337	zinc finger protein 740	12	---	0.440960809
ZNF75A	7627	zinc finger protein 75a	16	---	0.440960809
ZNF764	92595	zinc finger protein 764	16	---	0.440960809
ZNF767	79970	zinc finger family member 767	7	---	1.322882427
ZNF778	197320	zinc finger protein 778	16	---	0.440960809
ZNF793	390927	zinc finger protein 793	19	---	0.440960809
ZNF85	7639	zinc finger protein 85	19	---	0.440960809
ZP2	7783	zona pellucida glycoprotein 2 (sperm receptor)	16	---	3.968647282
ZSWIM8	23053	zinc finger, SWIM-type containing 8	10	---	0.440960809
SEPT3	55964	septin 3	22	FMRP Target,Postsynaptic Proteome	3.086725664
SEP15	9403	15 kDa selenoprotein	1	---	0.440960809
AAK1	22848	AP2 associated kinase 1	2	FMRP Target,Postsynaptic Proteome	0.440960809
ABCD2	225	ATP-binding cassette, sub-family D (ALD), member 2	12	---	0.440960809
ABI2	10152	abl-interactor 2	2	Postsynaptic Proteome	0.881921618
ACACA	31	acetyl-CoA carboxylase alpha	17	---	0.440960809
ACBD3	64746	acyl-CoA binding domain containing 3	1	---	0.440960809

ACSL3	2181	acyl-CoA synthetase long-chain family member 3	2	Postsynaptic Proteome	0.440960809
ACTL6B	51412	actin-like 6B	7	---	1.322882427
ADAM23	8745	ADAM metallopeptidase domain 23	2	---	0.881921618
ADARB1	104	adenosine deaminase, RNA-specific, B1	21	FMRP Target	0.881921618
ADCY1	107	adenylate cyclase 1 (brain)	7	FMRP Target	1.322882427
ADCYAP1R1	117	adenylate cyclase activating polypeptide 1 (pituitary) receptor type I	7	---	2.645764855
ADD2	119	adducin 2 (beta)	2	Postsynaptic Proteome	2.204804046
AEBP2	121536	AE binding protein 2	12	---	0.440960809
AES	166	amino-terminal enhancer of split	19	---	0.881921618
AFF2	2334	AF4/FMR2 family, member 2	X	ASD-AD/XL	0.881921618
AGAP1	116987	ArfGAP with GTPase domain, ankyrin repeat and PH domain 1	2	FMRP Target	0.440960809
AGAP2	116986	ArfGAP with GTPase domain, ankyrin repeat and PH domain 2	12	FMRP Target,Postsynaptic Proteome	0.881921618
AGAP3	116988	ArfGAP with GTPase domain, ankyrin repeat and PH domain 3	7	FMRP Target	0.440960809
AGTPBP1	23287	ATP/GTP binding protein 1	9	FMRP Target	1.322882427
AKAP11	11215	A kinase (PRKA) anchor protein 11	13	---	0.881921618
AKAP9	10142	A kinase (PRKA) anchor protein (yotiao) 9	7	FMRP Target	0.440960809
AKD1	221264	adenylate kinase domain containing 1	6	---	0.440960809
AKT3	10000	v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)	1	FMRP Target	2.645764855
AMZ2	51321	archaelysin family metallopeptidase 2	17	---	0.440960809
ANAPC5	51433	anaphase promoting complex subunit 5	12	---	0.440960809
ANK2	287	ankyrin 2, neuronal	4	denovo SNV,FMRP Target,Postsynaptic Proteome	0.881921618
ANKRD12	23253	ankyrin repeat domain 12	18	---	1.322882427
ANKRD13C	81573	ankyrin repeat domain 13C	1	---	0.440960809
ANKS1B	56899	ankyrin repeat and sterile alpha motif domain containing 1B	12	Postsynaptic Proteome	3.968647282
ANO10	55129	anoctamin 10	3	---	0.881921618
AP1G1	164	adaptor-related protein complex 1, gamma 1 subunit	16	---	0.440960809
AP1S1	1174	adaptor-related protein complex 1, sigma 1 subunit	7	Postsynaptic Proteome	0.440960809
AP3B1	8546	adaptor-related protein complex 3, beta 1 subunit	5	---	0.881921618
AP3B2	8120	adaptor-related protein complex 3, beta 2 subunit	15	denovo SNV,Postsynaptic Proteome	2.645764855
AP5M1	55745	adaptor-related protein complex 5, mu 1 subunit	14	---	0.440960809
APBA2	321	amyloid beta (A4) precursor protein-binding, family A, member 2	15	---	0.440960809
APBB2	323	amyloid beta (A4) precursor protein-binding, family B, member 2	4	---	0.440960809
APC	324	adenomatous polyposis coli	5	FMRP Target	3.527686473
APLP1	333	amyloid beta (A4) precursor-like protein 1	19	FMRP Target	0.881921618
APLP2	334	amyloid beta (A4) precursor-like protein 2	11	---	0.440960809
APOO	79135	apolipoprotein O	X	---	0.440960809
APP	351	amyloid beta (A4) precursor protein	21	FMRP Target	0.440960809
APPL1	26060	adaptor protein, phosphotyrosine interaction, PH domain and leucine zipper containing 1	3	---	0.881921618
RHGAP19-SLIT	1E+08	ARHGAP19-SLIT1 readthrough	10	---	0.440960809
ARHGAP33	115703	Rho GTPase activating protein 33	19	FMRP Target	0.440960809
ARHGEF25	115557	Rho guanine nucleotide exchange factor (GEF) 25	12	---	0.440960809
ARL1	400	ADP-ribosylation factor-like 1	12	---	0.440960809
ARL8A	127829	ADP-ribosylation factor-like 8A	1	---	0.440960809
ARMC9	80210	armadillo repeat containing 9	2	---	0.440960809
ARMCX5	64860	armadillo repeat containing, X-linked 5	X	---	0.881921618
RMCX5-GPRAS	1E+08	ARMCX5-GPRASP2 readthrough	X	---	0.440960809
ARNT2	9915	aryl-hydrocarbon receptor nuclear translocator 2	15	FMRP Target	1.322882427
ASAP1	50807	ArfGAP with SH3 domain, ankyrin repeat and PH domain 1	8	---	1.322882427
ASB3	51130	ankyrin repeat and SOCS box containing 3	2	---	0.440960809
ASIC1	41	acid-sensing (proton-gated) ion channel 1	12	---	0.440960809
ASTN1	460	astrotactin 1	1	---	2.204804046
ASXL1	171023	additional sex combs like 1 (Drosophila)	20	---	0.440960809
ATCAY	85300	ataxia, cerebellar, Cayman type	19	---	1.763843236
ATF2	1386	activating transcription factor 2	2	---	0.881921618
ATG4C	84938	autophagy related 4C, cysteine peptidase	1	---	0.881921618
ATL1	51062	atlastin GTPase 1	14	Postsynaptic Proteome	1.322882427
ATP1B2	482	ATPase, Na+/K+ transporting, beta 2 polypeptide	17	Postsynaptic Proteome	0.881921618
ATP2B1	490	ATPase, Ca++ transporting, plasma membrane 1	12	Postsynaptic Proteome	0.440960809
ATP2B2	491	ATPase, Ca++ transporting, plasma membrane 2	3	FMRP Target,Postsynaptic Proteome	0.881921618
ATP2B3	492	ATPase, Ca++ transporting, plasma membrane 3	X	Postsynaptic Proteome	0.440960809
ATP6V1G2	534	ATPase, H+ transporting, lysosomal 13kDa, V1 subunit G2	6	Postsynaptic Proteome	0.440960809
P6V1G2-DDX3	1E+08	ATP6V1G2-DDX39B readthrough (non-protein coding)	6	---	0.440960809
ATP8A1	10396	ATPase, aminophospholipid transporter (APLT), class I, type 8A, member 1	4	Postsynaptic Proteome	0.440960809
ATP8A2	51761	ATPase, aminophospholipid transporter, class I, type 8A, member 2	13	---	0.440960809
ATRN	8455	attractin	20	---	0.440960809
ATRNL1	26033	attractin-like 1	10	---	3.527686473

ATXN1	6310	ataxin 1	6	FMRP Target	0.440960809
ATXN2	6311	ataxin 2	12	---	1.322882427
AUTS2	26053	autism susceptibility candidate 2	7	FMRP Target	0.440960809
B3GAT1	27087	beta-1,3-glucuronyltransferase 1 (glucuronosyltransferase P)	11	FMRP Target	0.881921618
B4GALNT1	2583	beta-1,4-N-acetyl-galactosaminyl transferase 1	12	---	0.440960809
B4GALNT4	338707	beta-1,4-N-acetyl-galactosaminyl transferase 4	11	---	0.881921618
B4GALT6	9331	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 6	18	---	0.440960809
BAALC	79870	brain and acute leukemia, cytoplasmic	8	---	0.440960809
BAI1	575	brain-specific angiogenesis inhibitor 1	8	FMRP Target	0.440960809
BAI2	576	brain-specific angiogenesis inhibitor 2	1	FMRP Target	3.968647282
BAI3	577	brain-specific angiogenesis inhibitor 3	6	---	4.8505689
BAZ2B	29994	bromodomain adjacent to zinc finger domain, 2B	2	---	0.881921618
BBS7	55212	Bardet-Biedl syndrome 7	4	---	0.440960809
BCAS3	54828	breast carcinoma amplified sequence 3	17	---	0.440960809
BCL11A	53335	B-cell CLL/lymphoma 11A (zinc finger protein)	2	denovo SNV	0.440960809
BDP1	55814	B double prime 1, subunit of RNA polymerase III transcription initiation factor IIIB	5	---	0.881921618
BIVM	54841	basic, immunoglobulin-like variable motif containing	13	---	0.881921618
BIVM-ERCC5	1E+08	BIVM-ERCC5 readthrough	13	---	0.881921618
BLCAP	10904	bladder cancer associated protein	20	---	0.440960809
BMPR2	659	bone morphogenetic protein receptor, type II (serine/threonine kinase)	2	FMRP Target	0.440960809
BPTF	2186	bromodomain PHD finger transcription factor	17	FMRP Target	0.881921618
BRD8	10902	bromodomain containing 8	5	---	0.440960809
BRSK1	84446	BR serine/threonine kinase 1	19	FMRP Target,Postsynaptic Proteome	3.086725664
BRWD1	54014	bromodomain and WD repeat domain containing 1	21	denovo SNV	0.440960809
BSDC1	55108	BSD domain containing 1	1	---	0.440960809
BTBD1	53339	BTB (POZ) domain containing 1	15	---	0.440960809
BTBD10	84280	BTB (POZ) domain containing 10	11	---	1.322882427
BTRC	8945	beta-transducin repeat containing E3 ubiquitin protein ligase	10	---	0.440960809
C14orf2	9556	chromosome 14 open reading frame 2	14	---	0.440960809
C18orf32	497661	chromosome 18 open reading frame 32	18	---	0.440960809
C1orf61	10485	chromosome 1 open reading frame 61	1	---	1.322882427
C20orf24	55969	chromosome 20 open reading frame 24	20	---	0.440960809
C20orf27	54976	chromosome 20 open reading frame 27	20	---	0.440960809
C3orf17	25871	chromosome 3 open reading frame 17	3	---	0.881921618
C5orf42	65250	chromosome 5 open reading frame 42	5	---	0.440960809
CACHD1	57685	cache domain containing 1	1	---	0.881921618
CACNA1A	773	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit	19	FMRP Target	1.322882427
CACNA1B	774	calcium channel, voltage-dependent, N type, alpha 1B subunit	9	FMRP Target	1.322882427
CACNA1E	777	calcium channel, voltage-dependent, R type, alpha 1E subunit	1	denovo SNV,FMRP Target	3.527686473
CACNA2D1	781	calcium channel, voltage-dependent, alpha 2/delta subunit 1	7	Postsynaptic Proteome	0.881921618
CACNB3	784	calcium channel, voltage-dependent, beta 3 subunit	12	FMRP Target	3.086725664
CACNB4	785	calcium channel, voltage-dependent, beta 4 subunit	2	Postsynaptic Proteome	3.527686473
CACNG7	59284	calcium channel, voltage-dependent, gamma subunit 7	19	---	1.322882427
CADM1	23705	cell adhesion molecule 1	11	---	0.440960809
CADM3	57863	cell adhesion molecule 3	1	---	1.322882427
CADM4	199731	cell adhesion molecule 4	19	---	1.322882427
CADPS	8618	Ca++-dependent secretion activator	3	FMRP Target,Postsynaptic Proteome	3.086725664
CALN1	83698	calneuron 1	7	---	0.440960809
CAMK2B	816	calcium/calmodulin-dependent protein kinase II beta	7	FMRP Target,Postsynaptic Proteome	0.440960809
CAMK4	814	calcium/calmodulin-dependent protein kinase IV	5	---	1.322882427
CAMKK2	10645	calcium/calmodulin-dependent protein kinase kinase 2, beta	12	FMRP Target	0.440960809
CAMKV	79012	CaM kinase-like vesicle-associated	3	Postsynaptic Proteome	1.763843236
CAMSAP1	157922	calmodulin regulated spectrin-associated protein 1	9	FMRP Target	0.881921618
CAMSAP2	23271	calmodulin regulated spectrin-associated protein family, member 2	1	FMRP Target	0.440960809
CAMTA1	23261	calmodulin binding transcription activator 1	1	FMRP Target	0.881921618
CASD1	64921	CAS1 domain containing 1	7	---	0.881921618
CASK	8573	calcium/calmodulin-dependent serine protein kinase (MAGUK family)	X	denovo SNV,Postsynaptic Proteome,ASD-AD/XL	3.086725664
CBX1	10951	chromobox homolog 1	17	---	0.440960809
CCAR1	55749	cell division cycle and apoptosis regulator 1	10	---	0.440960809
CCDC6	8030	coiled-coil domain containing 6	10	---	0.440960809
CCDC88A	55704	coiled-coil domain containing 88A	2	---	1.322882427
CCDC92	80212	coiled-coil domain containing 92	12	---	0.440960809
CCNC	892	cyclin C	6	---	0.881921618
CCNT2	905	cyclin T2	2	---	0.881921618
CCNY	219771	cyclin Y	10	---	0.440960809
CCP110	9738	centriolar coiled coil protein 110kDa	16	---	0.440960809
CD200	4345	CD200 molecule	3	---	0.440960809

CDC42BPA	8476	CDC42 binding protein kinase alpha (DMPK-like)	1	FMRP Target,Postsynaptic Proteome	0.881921618
CDC42BPB	9578	CDC42 binding protein kinase beta (DMPK-like)	14	denovo SNV,FMRP Target,Postsynaptic Proteome	0.881921618
CDC5L	988	cell division cycle 5-like	6	---	0.440960809
CDK13	8621	cyclin-dependent kinase 13	7	---	0.881921618
CDK14	5218	cyclin-dependent kinase 14	7	---	0.440960809
CDK17	5128	cyclin-dependent kinase 17	12	FMRP Target	1.322882427
CDK5R1	8851	cyclin-dependent kinase 5, regulatory subunit 1 (p35)	17	FMRP Target	0.440960809
CDKL5	6792	cyclin-dependent kinase-like 5	X	FMRP Target,ASD-AD/XL	1.322882427
CELF3	11189	CUGBP, Elav-like family member 3	1	---	5.732490518
CELF5	60680	CUGBP, Elav-like family member 5	19	FMRP Target	1.322882427
CEP170	9859	centrosomal protein 170kDa	1	---	0.440960809
CERS6	253782	ceramide synthase 6	2	---	0.440960809
CFL1	1072	cofilin 1 (non-muscle)	11	Postsynaptic Proteome	0.440960809
CHD2	1106	chromodomain helicase DNA binding protein 2	15	denovo SNV	0.440960809
CHD3	1107	chromodomain helicase DNA binding protein 3	17	denovo SNV,FMRP Target	0.440960809
CHD9	80205	chromodomain helicase DNA binding protein 9	16	---	0.440960809
CHL1	10752	cell adhesion molecule with homology to L1CAM (close homolog of L1)	3	---	2.204804046
CHM	1121	choroideremia (Rab escort protein 1)	X	---	0.440960809
CHN1	1123	chimerin 1	2	FMRP Target	0.440960809
CHRNB2	1141	cholinergic receptor, nicotinic, beta 2 (neuronal)	1	---	0.881921618
CHST10	9486	carbohydrate sulfotransferase 10	2	---	0.881921618
CKAP5	9793	cytoskeleton associated protein 5	11	FMRP Target,Postsynaptic Proteome	0.440960809
CLASP1	23332	cytoplasmic linker associated protein 1	2	FMRP Target	0.881921618
CLASP2	23122	cytoplasmic linker associated protein 2	3	FMRP Target,Postsynaptic Proteome	0.440960809
CLCN3	1182	chloride channel, voltage-sensitive 3	4	FMRP Target	0.440960809
CLIP3	25999	CAP-GLY domain containing linker protein 3	19	FMRP Target	0.881921618
CLTC	1213	clathrin, heavy chain (Hc)	17	FMRP Target,Postsynaptic Proteome	0.440960809
CLVS1	157807	clavesin 1	8	---	0.881921618
CMC2	56942	COX assembly mitochondrial protein 2 homolog (S. cerevisiae)	16	---	0.440960809
CNIH2	254263	cornichon homolog 2 (Drosophila)	11	---	2.645764855
CNKSR2	22866	connector enhancer of kinase suppressor of Ras 2	X	---	6.173451327
CNTN1	1272	contactin 1	12	Postsynaptic Proteome	1.763843236
CNTN2	6900	contactin 2 (axonal)	1	Postsynaptic Proteome	0.881921618
CNTNAP2	26047	contactin associated protein-like 2	7	ASD-AD/XL	1.763843236
CNTNAP5	129684	contactin associated protein-like 5	2	---	0.440960809
CORO2B	10391	coronin, actin binding protein, 2B	15	Postsynaptic Proteome	4.409608091
CPD	1362	carboxypeptidase D	17	---	0.440960809
CPT1C	126129	carnitine palmitoyltransferase 1C	19	FMRP Target	1.763843236
CRMP1	1400	collapsin response mediator protein 1	4	FMRP Target,Postsynaptic Proteome	2.204804046
CSRNP3	80034	cysteine-serine-rich nuclear protein 3	2	---	1.322882427
CTIF	9811	CBP80/20-dependent translation initiation factor	18	---	0.881921618
CTNNB1	1499	catenin (cadherin-associated protein), beta 1, 88kDa	3	denovo SNV,FMRP Target,Postsynaptic Proteome	0.440960809
CTNND2	1501	catenin (cadherin-associated protein), delta 2	5	FMRP Target,Postsynaptic Proteome	1.763843236
DAGLA	747	diacylglycerol lipase, alpha	11	FMRP Target	0.440960809
DBC1	1620	deleted in bladder cancer 1	9	FMRP Target	0.881921618
DCAF17	80067	DDB1 and CUL4 associated factor 17	2	---	0.440960809
DCC	1630	deleted in colorectal carcinoma	18	---	0.440960809
DCLK1	9201	doublecortin-like kinase 1	13	FMRP Target,Postsynaptic Proteome	0.881921618
DCLK2	166614	doublecortin-like kinase 2	4	---	2.204804046
DCTN2	10540	dynactin 2 (p50)	12	Postsynaptic Proteome	0.440960809
DCUN1D4	23142	DCN1, defective in cullin neddylation 1, domain containing 4 (S. cerevisiae)	4	---	0.440960809
DDX42	11325	DEAD (Asp-Glu-Ala-Asp) box polypeptide 42	17	---	0.440960809
DDX6	1656	DEAD (Asp-Glu-Ala-Asp) box helicase 6	11	---	0.440960809
DEAF1	10522	DEAF1 transcription factor	11	denovo SNV	0.881921618
DENND4A	10260	DENN/MADD domain containing 4A	15	---	0.881921618
DENND5B	160518	DENN/MADD domain containing 5B	12	---	0.440960809
DGKH	160851	diacylglycerol kinase, eta	13	---	0.440960809
DHX36	170506	DEAH (Asp-Glu-Ala-His) box polypeptide 36	3	---	0.440960809
DICER1	23405	dicer 1, ribonuclease type III	14	denovo SNV,FMRP Target	0.440960809
DIRAS2	54769	DIRAS family, GTP-binding RAS-like 2	9	FMRP Target	0.440960809
DLG1	1739	discs, large homolog 1 (Drosophila)	3	Postsynaptic Proteome	0.440960809

DLG2	1740	discs, large homolog 2 (Drosophila)	11	FMRP Target,Postsynaptic Proteome	2.204804046
DLG3	1741	discs, large homolog 3 (Drosophila)	X	Postsynaptic Proteome	0.881921618
DLG4	1742	discs, large homolog 4 (Drosophila)	17	FMRP Target,Postsynaptic Proteome	3.086725664
DLGAP1	9229	discs, large (Drosophila) homolog-associated protein 1	18	FMRP Target,Postsynaptic Proteome	7.055372946
DMTF1	9988	cyclin D binding myb-like transcription factor 1	7	---	0.440960809
DMXL1	1657	Dmx-like 1	5	---	0.440960809
DMXL2	23312	Dmx-like 2	15	FMRP Target,Postsynaptic Proteome	2.204804046
DNAJC6	9829	DnaJ (Hsp40) homolog, subfamily C, member 6	1	FMRP Target	3.968647282
DNAJC7	7266	DnaJ (Hsp40) homolog, subfamily C, member 7	17	---	0.881921618
DNER	92737	delta/notch-like EGF repeat containing	2	---	1.763843236
DNM1	1759	dynamin 1	9	FMRP Target,Postsynaptic Proteome	1.763843236
DNMT1	1786	DNA (cytosine-5-)-methyltransferase 1	19	---	0.440960809
DOCK3	1795	dedicator of cytokinesis 3	3	FMRP Target	4.8505689
DOCK4	9732	dedicator of cytokinesis 4	7	FMRP Target	1.763843236
DOCK9	23348	dedicator of cytokinesis 9	13	FMRP Target,Postsynaptic Proteome	2.204804046
DOK6	220164	docking protein 6	18	---	0.440960809
DOPEY1	23033	dopey family member 1	6	FMRP Target	0.440960809
DPF1	8193	D4, zinc and double PHD fingers family 1	19	---	0.881921618
DPP10	57628	dipeptidyl-peptidase 10 (non-functional)	2	---	2.204804046
DPP6	1804	dipeptidyl-peptidase 6	7	---	2.204804046
DPYSL2	1808	dihydropyrimidinase-like 2	8	FMRP Target,Postsynaptic Proteome	0.440960809
DPYSL3	1809	dihydropyrimidinase-like 3	5	Postsynaptic Proteome	0.440960809
DPYSL5	56896	dihydropyrimidinase-like 5	2	---	1.322882427
DRG1	4733	developmentally regulated GTP binding protein 1	22	---	0.440960809
DROSHA	29102	drosha, ribonuclease type III	5	---	0.881921618
DTNB	1838	dystrobrevin, beta	2	---	0.440960809
DTX3	196403	deltex homolog 3 (Drosophila)	12	---	0.440960809
DUSP11	8446	dual specificity phosphatase 11 (RNA/RNP complex 1-interacting)	2	---	0.440960809
DYNC1H1	1778	dynein, cytoplasmic 1, heavy chain 1	14	denovo SNV,FMRP Target,Postsynaptic Proteome	0.440960809
DYNC1LI2	1783	dynein, cytoplasmic 1, light intermediate chain 2	16	Postsynaptic Proteome	0.440960809
DYRK1A	1859	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A	21	denovo SNV	0.440960809
DZIP3	9666	DAZ interacting protein 3, zinc finger	3	---	0.440960809
EBAG9	9166	estrogen receptor binding site associated, antigen, 9	8	denovo SNV	0.881921618
EDIL3	10085	EGF-like repeats and discoidin I-like domains 3	5	---	0.440960809
EFHA2	286097	EF-hand domain family, member A2	8	---	0.881921618
EFR3B	22979	EFR3 homolog B (S. cerevisiae)	2	---	3.527686473
EHBP1	23301	EH domain binding protein 1	2	---	0.440960809
EIF2B5	8893	eukaryotic translation initiation factor 2B, subunit 5 epsilon, 82kDa	3	---	0.440960809
EIF4A2	1974	eukaryotic translation initiation factor 4A2	3	Postsynaptic Proteome	0.440960809
EIF4G2	1982	eukaryotic translation initiation factor 4 gamma, 2	11	FMRP Target	0.440960809
EIF4G3	8672	eukaryotic translation initiation factor 4 gamma, 3	1	FMRP Target	0.881921618
EIF6	3692	eukaryotic translation initiation factor 6	20	---	0.440960809
ELAVL3	1995	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 3 (Hu antigen C)	19	---	1.763843236
ELAVL4	1996	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 4	1	---	1.763843236
ELK4	2005	ELK4, ETS-domain protein (SRF accessory protein 1)	1	---	0.440960809
EMC4	51234	ER membrane protein complex subunit 4	15	---	0.440960809
ENAH	55740	enabled homolog (Drosophila)	1	---	0.440960809
ENO2	2026	enolase 2 (gamma, neuronal)	12	Postsynaptic Proteome	0.881921618
ENOX1	55068	ecto-NOX disulfide-thiol exchanger 1	13	---	0.440960809
ENY2	56943	enhancer of yellow 2 homolog (Drosophila)	8	---	0.881921618
EPB41L1	2036	erythrocyte membrane protein band 4.1-like 1	20	FMRP Target,Postsynaptic Proteome	0.440960809
EPB41L3	23136	erythrocyte membrane protein band 4.1-like 3	18	Postsynaptic Proteome	1.322882427
EPC2	26122	enhancer of polycomb homolog 2 (Drosophila)	2	---	0.881921618
EPHB2	2048	EPH receptor B2	1	denovo SNV	0.440960809
ERC2	26059	ELKS/RAB6-interacting/CAST family member 2	3	Postsynaptic Proteome	1.763843236
ERCC3	2071	excision repair cross-complementing rodent repair deficiency, complementation group 3	2	---	0.440960809
ERGIC2	51290	ERGIC and golgi 2	12	---	0.440960809
ERH	2079	enhancer of rudimentary homolog (Drosophila)	14	---	0.440960809
ETV1	2115	ets variant 1	7	---	0.440960809
EVL	51466	Enah/Vasp-like	14	Postsynaptic Proteome	0.440960809
EXOC1	55763	exocyst complex component 1	4	Postsynaptic Proteome	0.440960809

EXOC2	55770	exocyst complex component 2	6	Postsynaptic Proteome	0.881921618
EXT2	2132	exostosin 2	11	---	0.440960809
FADS2	9415	fatty acid desaturase 2	11	---	0.440960809
FAIM2	23017	Fas apoptotic inhibitory molecule 2	12	---	0.440960809
FAM120A	23196	family with sequence similarity 120A	9	FMRP Target	0.440960809
FAM13B	51306	family with sequence similarity 13, member B	5	---	0.440960809
FAM160A2	84067	family with sequence similarity 160, member A2	11	FMRP Target	0.440960809
FAM168A	23201	family with sequence similarity 168, member A	11	---	0.440960809
FAM171A2	284069	family with sequence similarity 171, member A2	17	---	0.881921618
FAM171B	165215	family with sequence similarity 171, member B	2	FMRP Target	1.763843236
FAM179B	23116	family with sequence similarity 179, member B	14	FMRP Target	0.440960809
FAM199X	139231	family with sequence similarity 199, X-linked	X	---	0.440960809
FAM216A	29902	family with sequence similarity 216, member A	12	---	0.881921618
FAM217B	63939	family with sequence similarity 217, member B	20	---	0.440960809
FAM228B	375190	family with sequence similarity 228, member B	2	---	0.881921618
FAM5B	57795	family with sequence similarity 5, member B	1	FMRP Target	0.440960809
FANCL	55120	Fanconi anemia, complementation group L	2	---	0.440960809
FBRSL1	57666	fibrosin-like 1	12	---	0.440960809
FBXL20	84961	F-box and leucine-rich repeat protein 20	17	---	0.440960809
FBXL3	26224	F-box and leucine-rich repeat protein 3	13	---	0.440960809
FBXO11	80204	F-box protein 11	2	---	0.440960809
FBXO3	26273	F-box protein 3	11	---	0.440960809
FBXW7	55294	F-box and WD repeat domain containing 7, E3 ubiquitin protein ligase	4	---	0.440960809
FEZ1	9638	fasciculation and elongation protein zeta 1 (zygin I)	11	---	3.086725664
FGF14	2259	fibroblast growth factor 14	13	---	0.440960809
FMN2	56776	formin 2	1	Postsynaptic Proteome	2.204804046
FMNL2	114793	formin-like 2	2	Postsynaptic Proteome	2.204804046
FMR1	2332	fragile X mental retardation 1	X	ASD-AD/XL	0.440960809
FN1	2335	fibronectin 1	2	---	0.440960809
FQCAD	54914	focadhesin	9	---	0.440960809
FOXJ3	22887	forkhead box J3	1	---	0.881921618
FOXK2	3607	forkhead box K2	17	FMRP Target	0.440960809
FOXP1	27086	forkhead box P1	3	ASD-AD/XL	1.322882427
FRS2	10818	fibroblast growth factor receptor substrate 2	12	---	0.440960809
FRY	10129	furry homolog (Drosophila)	13	FMRP Target	0.440960809
FSD1	79187	fibronectin type III and SPRY domain containing 1	19	Postsynaptic Proteome	0.440960809
FUT9	10690	fucosyltransferase 9 (alpha (1,3) fucosyltransferase)	6	---	0.440960809
FXYD7	53822	FXYD domain containing ion transport regulator 7	19	---	0.440960809
FZD3	7976	frizzled family receptor 3	8	---	0.881921618
G3BP2	9908	GTPase activating protein (SH3 domain) binding protein 2	4	---	0.881921618
GABBR1	2550	gamma-aminobutyric acid (GABA) B receptor, 1	6	FMRP Target	4.409608091
GABBR2	9568	gamma-aminobutyric acid (GABA) B receptor, 2	9	FMRP Target,Postsynaptic Proteome	3.086725664
GABRA2	2555	gamma-aminobutyric acid (GABA) A receptor, alpha 2	4	---	1.322882427
GABRA3	2556	gamma-aminobutyric acid (GABA) A receptor, alpha 3	X	---	1.322882427
GABRB2	2561	gamma-aminobutyric acid (GABA) A receptor, beta 2	5	---	0.440960809
GABRB3	2562	gamma-aminobutyric acid (GABA) A receptor, beta 3	15	---	1.322882427
GABRG2	2566	gamma-aminobutyric acid (GABA) A receptor, gamma 2	5	---	3.086725664
GAP43	2596	growth associated protein 43	3	Postsynaptic Proteome	0.440960809
GDAP1L1	78997	ganglioside induced differentiation associated protein 1-like 1	20	---	2.204804046
GDPD1	284161	glycerophosphodiester phosphodiesterase domain containing 1	17	---	0.881921618
GHITM	27069	growth hormone inducible transmembrane protein	10	---	0.440960809
GLCCI1	113263	glucocorticoid induced transcript 1	7	---	0.440960809
GLRB	2743	glycine receptor, beta	4	---	0.440960809
GMFB	2764	glia maturation factor, beta	14	---	0.440960809
GNAI1	2770	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 1	7	---	0.881921618
GNAL	2774	guanine nucleotide binding protein (G protein), alpha activating activity polypeptide, olfactory type	18	FMRP Target	0.881921618
GNAO1	2775	guanine nucleotide binding protein (G protein), alpha activating activity polypeptide O	16	FMRP Target,Postsynaptic Proteome	1.322882427
GNAZ	2781	guanine nucleotide binding protein (G protein), alpha z polypeptide	22	FMRP Target,Postsynaptic Proteome	0.440960809
GNPDA2	132789	glucosamine-6-phosphate deaminase 2	4	---	0.440960809
GNPTAB	79158	N-acetylglucosamine-1-phosphate transferase, alpha and beta subunits	12	---	0.440960809
GOLM1	51280	golgi membrane protein 1	9	---	0.440960809
GPM6A	2823	glycoprotein M6A	4	FMRP Target	0.881921618
GPM6B	2824	glycoprotein M6B	X	---	0.881921618
GPR107	57720	G protein-coupled receptor 107	9	---	0.440960809
GPR75-ASB3	1E+08	GPR75-ASB3 readthrough	2	---	0.440960809

GRIA1	2890	glutamate receptor, ionotropic, AMPA 1	5	Postsynaptic Proteome	1.763843236
GRIA2	2891	glutamate receptor, ionotropic, AMPA 2	4	Postsynaptic Proteome	4.8505689
GRIA3	2892	glutamate receptor, ionotropic, AMPA 3	X	Postsynaptic Proteome,ASD-AD/XL	2.204804046
GRID1	2894	glutamate receptor, ionotropic, delta 1	10	---	0.440960809
GRIK5	2901	glutamate receptor, ionotropic, kainate 5	19	FMRP Target	1.322882427
GRIN2B	2904	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	12	FMRP Target	0.881921618
GRM3	2913	glutamate receptor, metabotropic 3	7	---	1.322882427
GRM5	2915	glutamate receptor, metabotropic 5	11	FMRP Target	0.440960809
GSTA4	2941	glutathione S-transferase alpha 4	6	---	0.440960809
GTPBP10	85865	GTP-binding protein 10 (putative)	7	---	0.440960809
HAUS2	55142	HAUS augmin-like complex, subunit 2	15	---	0.440960809
HCN1	348980	hyperpolarization activated cyclic nucleotide-gated potassium channel 1	5	---	0.440960809
HDAC2	3066	histone deacetylase 2	6	---	0.881921618
HECTD2	143279	HECT domain containing E3 ubiquitin protein ligase 2	10	---	0.881921618
HECW1	23072	HECT, C2 and WW domain containing E3 ubiquitin protein ligase 1	7	---	0.881921618
HERC1	8925	HECT and RLD domain containing E3 ubiquitin protein ligase family member 1	15	FMRP Target	0.881921618
HERC3	8916	HECT and RLD domain containing E3 ubiquitin protein ligase 3	4	---	0.881921618
HERPUD2	64224	HERPUD family member 2	7	---	0.440960809
HIPK1	204851	homeodomain interacting protein kinase 1	1	FMRP Target	0.881921618
HIPK2	28996	homeodomain interacting protein kinase 2	7	FMRP Target	0.440960809
HIST1H2BC	8347	histone cluster 1, H2bc	6	---	0.440960809
HIST1H4E	8367	histone cluster 1, H4e	6	---	0.440960809
HIVEP2	3097	human immunodeficiency virus type I enhancer binding protein 2	6	denovo SNV,FMRP Target	0.881921618
HMG20A	10363	high mobility group 20A	15	---	0.881921618
HMGCR	3156	3-hydroxy-3-methylglutaryl-CoA reductase	5	---	0.440960809
HMP19	51617	HMP19 protein	5	---	0.440960809
HNRNPA0	10949	heterogeneous nuclear ribonucleoprotein A0	5	---	0.440960809
HNRNPH3	3189	heterogeneous nuclear ribonucleoprotein H3 (2H9)	10	---	0.440960809
HOOK3	84376	hook homolog 3 (Drosophila)	8	---	0.440960809
HP1BP3	50809	heterochromatin protein 1, binding protein 3	1	---	0.440960809
ICA1L	130026	islet cell autoantigen 1,69kDa-like	2	---	1.763843236
IFT46	56912	intraflagellar transport 46 homolog (Chlamydomonas)	11	---	0.440960809
IGFBP7	3490	insulin-like growth factor binding protein 7	4	---	0.440960809
INPP4A	3631	inositol polyphosphate-4-phosphatase, type I, 107kDa	2	FMRP Target	0.440960809
INTS3	65123	integrator complex subunit 3	1	---	0.881921618
INTU	27152	inturned planar cell polarity effector homolog (Drosophila)	4	---	0.881921618
IRX2	153572	iroquois homeobox 2	5	---	0.440960809
ITFG1	81533	integrin alpha FG-GAP repeat containing 1	16	---	0.440960809
ITM2C	81618	integral membrane protein 2C	2	---	0.881921618
ITSN1	6453	intersectin 1 (SH3 domain protein)	21	FMRP Target,Postsynaptic Proteome	0.881921618
IWS1	55677	IWS1 homolog (S. cerevisiae)	2	---	0.440960809
JAK2	3717	Janus kinase 2	9	---	0.440960809
JAKMIP2	9832	janus kinase and microtubule interacting protein 2	5	---	2.204804046
JAM2	58494	junctional adhesion molecule 2	21	---	0.440960809
JPH4	84502	junctophilin 4	14	FMRP Target	0.440960809
KALRN	8997	kalirin, RhoGEF kinase	3	FMRP Target	1.763843236
KAT6B	23522	K(lysine) acetyltransferase 6B	10	---	0.440960809
KCND2	3751	potassium voltage-gated channel, Shal-related subfamily, member 2	7	FMRP Target	0.440960809
KCNH7	90134	potassium voltage-gated channel, subfamily H (eag-related), member 7	2	FMRP Target	0.440960809
KCNIP1	30820	Kv channel interacting protein 1	5	---	2.204804046
KCNMB4	27345	potassium large conductance calcium-activated channel, subfamily M, beta member 4	12	---	0.440960809
KCNN1	3780	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 1	19	---	0.440960809
KCNN2	3781	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 2	5	---	0.440960809
KCNQ2	3785	potassium voltage-gated channel, KQT-like subfamily, member 2	20	FMRP Target	0.881921618
KCNQ3	3786	potassium voltage-gated channel, KQT-like subfamily, member 3	8	denovo SNV,FMRP Target	2.645764855
KCTD13	253980	potassium channel tetramerisation domain containing 13	16	---	0.440960809
KCTD3	51133	potassium channel tetramerisation domain containing 3	1	---	0.440960809
KHDRBS2	202559	KH domain containing, RNA binding, signal transduction associated 2	6	---	0.440960809
KHDRBS3	10656	KH domain containing, RNA binding, signal transduction associated 3	8	---	0.440960809
KIAA0408	9729	KIAA0408	6	Postsynaptic Proteome	0.881921618
KIAA0430	9665	KIAA0430	16	FMRP Target	0.440960809
KIAA0930	23313	KIAA0930	22	---	0.440960809
KIAA1033	23325	KIAA1033	12	---	0.440960809
KIAA1191	57179	KIAA1191	5	---	0.440960809
KIAA1468	57614	KIAA1468	18	---	0.440960809
KIAA1598	57698	KIAA1598	10	---	1.322882427
KIAA1841	84542	KIAA1841	2	---	0.881921618

KIF1A	547	kinesin family member 1A	2	FMRP Target,Postsynaptic Proteome	2.645764855
KIF1B	23095	kinesin family member 1B	1	FMRP Target	0.440960809
KIF21A	55605	kinesin family member 21A	12	FMRP Target,Postsynaptic Proteome	1.763843236
KIF2A	3796	kinesin heavy chain member 2A	5	Postsynaptic Proteome	0.440960809
KIF3A	11127	kinesin family member 3A	5	---	2.204804046
KIF3C	3797	kinesin family member 3C	2	FMRP Target	2.204804046
KIF5A	3798	kinesin family member 5A	12	FMRP Target,Postsynaptic Proteome	5.291529709
KIF5B	3799	kinesin family member 5B	10	Postsynaptic Proteome	1.322882427
KIF5C	3800	kinesin family member 5C	2	FMRP Target,Postsynaptic Proteome	3.086725664
KIFAP3	22920	kinesin-associated protein 3	1	---	1.763843236
KLHL2	11275	kelch-like family member 2	4	---	0.440960809
KLHL24	54800	kelch-like family member 24	3	---	0.440960809
KLHL32	114792	kelch-like family member 32	6	---	0.440960809
KLHL5	51088	kelch-like family member 5	4	---	0.440960809
KLHL8	57563	kelch-like family member 8	4	---	0.440960809
KPNA3	3839	karyopherin alpha 3 (importin alpha 4)	13	---	0.440960809
KREMEN2	79412	kringle containing transmembrane protein 2	16	---	0.440960809
LANCL1	10314	LanC lantibiotic synthetase component C-like 1 (bacterial)	2	---	0.440960809
LGALSL	29094	lectin, galactoside-binding-like	2	---	0.440960809
LIMK1	3984	LIM domain kinase 1	7	---	0.881921618
LMBR1	64327	limb region 1 homolog (mouse)	7	---	0.440960809
LMBRD1	55788	LMBR1 domain containing 1	6	---	0.440960809
LOC100131825	1E+08	uncharacterized LOC100131825	1	---	0.881921618
LPHN1	22859	latrophilin 1	19	FMRP Target,Postsynaptic Proteome	2.645764855
LPHN3	23284	latrophilin 3	4	FMRP Target	5.732490518
LPPR2	64748	lipid phosphate phosphatase-related protein type 2	19	---	0.440960809
LRCH3	84859	leucine-rich repeats and calponin homology (CH) domain containing 3	3	---	0.881921618
LRRC40	55631	leucine rich repeat containing 40	1	---	0.440960809
LRRC7	57554	leucine rich repeat containing 7	1	FMRP Target,Postsynaptic Proteome	5.732490518
LRRFIP2	9209	leucine rich repeat (in FLII) interacting protein 2	3	---	0.440960809
LRRTM4	80059	leucine rich repeat transmembrane neuronal 4	2	---	0.440960809
LSAMP	4045	limbic system-associated membrane protein	3	Postsynaptic Proteome	0.881921618
LTN1	26046	listerin E3 ubiquitin protein ligase 1	21	---	0.440960809
LY6H	4062	lymphocyte antigen 6 complex, locus H	8	---	0.440960809
LYPLAL1	127018	lysophospholipase-like 1	1	---	0.440960809
MACF1	23499	microtubule-actin crosslinking factor 1	1	FMRP Target,Postsynaptic Proteome	0.440960809
MAGI1	9223	membrane associated guanylate kinase, WW and PDZ domain containing 1	3	---	0.881921618
MAGI2	9863	membrane associated guanylate kinase, WW and PDZ domain containing 2	7	FMRP Target	1.322882427
MANEAL	149175	mannosidase, endo-alpha-like	1	---	0.440960809
MAP1A	4130	microtubule-associated protein 1A	15	FMRP Target,Postsynaptic Proteome	0.881921618
MAP2	4133	microtubule-associated protein 2	2	FMRP Target,Postsynaptic Proteome	2.645764855
MAP3K12	7786	mitogen-activated protein kinase kinase kinase 12	12	FMRP Target	0.440960809
MAP4	4134	microtubule-associated protein 4	3	denovo SNV,FMRP Target,Postsynaptic Proteome	0.440960809
MAP4K3	8491	mitogen-activated protein kinase kinase kinase kinase 3	2	---	0.440960809
MAP4K4	9448	mitogen-activated protein kinase kinase kinase kinase 4	2	FMRP Target	2.204804046
MAP4K5	11183	mitogen-activated protein kinase kinase kinase kinase 5	14	---	1.322882427
MAPK1	5594	mitogen-activated protein kinase 1	22	FMRP Target	0.440960809
MAPK10	5602	mitogen-activated protein kinase 10	4	---	2.645764855
MAPK8	5599	mitogen-activated protein kinase 8	10	---	0.440960809
MAPK8IP1	9479	mitogen-activated protein kinase 8 interacting protein 1	11	FMRP Target	0.440960809
MAPRE3	22924	microtubule-associated protein, RP/EB family, member 3	2	Postsynaptic Proteome	0.440960809
MARCH8	8933	family with sequence similarity 127, member A	X	---	0.881921618
MARK4	57787	MAP/microtubule affinity-regulating kinase 4	19	---	0.440960809
MAST1	22983	microtubule associated serine/threonine kinase 1	19	FMRP Target	2.645764855
MBD5	55777	methyl-CpG binding domain protein 5	2	denovo SNV,FMRP Target,ASD-AD/XL	0.440960809
MBOAT2	129642	membrane bound O-acyltransferase domain containing 2	2	---	3.086725664
MEA1	4201	male-enhanced antigen 1	6	---	0.440960809
MEGF8	1954	multiple EGF-like-domains 8	19	---	0.440960809
METTL21A	151194	methyltransferase like 21A	2	---	0.440960809
MIR497HG	1E+08	mir-497-195 cluster host gene (non-protein coding)	17	---	0.440960809

MLL	4297	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila)	11	FMRP Target	0.881921618
MLL2	8085	myeloid/lymphoid or mixed-lineage leukemia 2	12	FMRP Target	0.440960809
MLL3	58508	myeloid/lymphoid or mixed-lineage leukemia 3	7	denovo SNV,FMRP Target	0.440960809
MLL5	55904	myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, Drosophila)	7	denovo SNV,FMRP Target	0.440960809
MLST8	64223	MTOR associated protein, LST8 homolog (S. cerevisiae)	16	---	0.440960809
MMP16	4325	matrix metallopeptidase 16 (membrane-inserted)	8	---	0.881921618
MON2	23041	MON2 homolog (S. cerevisiae)	12	FMRP Target	0.440960809
MPDZ	8777	multiple PDZ domain protein	9	---	0.881921618
MPP6	51678	membrane protein, palmitoylated 6 (MAGUK p55 subfamily member 6)	7	denovo SNV	0.881921618
MRPS21	54460	mitochondrial ribosomal protein S21	1	---	0.440960809
MRPS30	10884	mitochondrial ribosomal protein S30	5	---	0.440960809
SANTD3-TMEF	1E+08	MSANTD3-TMEFF1 readthrough	9	---	0.881921618
MTA3	57504	metastasis associated 1 family, member 3	2	---	0.440960809
MTHFD1L	25902	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like	6	---	0.440960809
MTMR9	66036	myotubularin related protein 9	8	denovo SNV	0.440960809
MTPAP	55149	mitochondrial poly(A) polymerase	10	---	0.440960809
MTSS1L	92154	metastasis suppressor 1-like	16	FMRP Target	0.440960809
MYCBP2	23077	MYC binding protein 2, E3 ubiquitin protein ligase	13	FMRP Target	0.881921618
MYH10	4628	myosin, heavy chain 10, non-muscle	17	FMRP Target,Postsynaptic Proteome	0.440960809
MYO5A	4644	myosin VA (heavy chain 12, myoxin)	15	FMRP Target,Postsynaptic Proteome	4.8505689
MYT1L	23040	myelin transcription factor 1-like	2	FMRP Target	4.409608091
N4BP2L2	10443	NEDD4 binding protein 2-like 2	13	---	0.440960809
NAE1	8883	NEDD8 activating enzyme E1 subunit 1	16	---	0.440960809
NAPB	63908	N-ethylmaleimide-sensitive factor attachment protein, beta	20	Postsynaptic Proteome	1.322882427
NAV2	89797	neuron navigator 2	11	denovo SNV,FMRP Target	0.440960809
NAV3	89795	neuron navigator 3	12	FMRP Target	2.204804046
NBAS	51594	neuroblastoma amplified sequence	2	---	0.440960809
NBEA	26960	neurobeachin	13	FMRP Target	3.968647282
NCAM1	4684	neural cell adhesion molecule 1	11	FMRP Target,Postsynaptic Proteome	0.881921618
NCAM2	4685	neural cell adhesion molecule 2	21	Postsynaptic Proteome	0.881921618
NCAN	1463	neurocan	19	FMRP Target,Postsynaptic Proteome	2.645764855
NCBP1	4686	nuclear cap binding protein subunit 1, 80kDa	9	---	0.440960809
NCDN	23154	neurochondrin	1	FMRP Target,Postsynaptic Proteome	1.763843236
NCKAP1	10787	NCK-associated protein 1	2	denovo SNV,FMRP Target,Postsynaptic Proteome	0.881921618
NCOA1	8648	nuclear receptor coactivator 1	2	FMRP Target	1.322882427
NCOA2	10499	nuclear receptor coactivator 2	8	FMRP Target	0.440960809
NCOA6	23054	nuclear receptor coactivator 6	20	FMRP Target	0.440960809
NCOR1	9611	nuclear receptor corepressor 1	17	FMRP Target	0.440960809
NCS1	23413	neuronal calcium sensor 1	9	FMRP Target	2.204804046
NDFIP1	80762	Nedd4 family interacting protein 1	5	---	0.881921618
NDRG3	57446	NDRG family member 3	20	---	0.440960809
NDST3	9348	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 3	4	---	0.440960809
NDUFA6	4700	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6, 14kDa	22	---	0.440960809
NEDD4L	23327	neural precursor cell expressed, developmentally down-regulated 4-like, E3 ubiquitin protein ligase	18	---	0.440960809
NEFL	4747	neurofilament, light polypeptide	8	Postsynaptic Proteome	0.440960809
NEFM	4741	neurofilament, medium polypeptide	8	Postsynaptic Proteome	0.440960809
NELL2	4753	NEL-like 2 (chicken)	12	---	3.086725664
NEMF	9147	nuclear export mediator factor	14	---	0.440960809
NEO1	4756	neogenin 1	15	---	0.881921618
NETO2	81831	neuropilin (NRP) and tolloid (TLL)-like 2	16	---	0.881921618
NF1	4763	neurofibromin 1	17	denovo SNV,FMRP Target,ASD-AD/XL	0.881921618
NF2	4771	neurofibromin 2 (merlin)	22	---	1.763843236
NFASC	23114	neurofascin	1	Postsynaptic Proteome	1.763843236
NFAT5	10725	nuclear factor of activated T-cells 5, tonicity-responsive	16	---	0.440960809
NKAIN2	154215	Na+/K+ transporting ATPase interacting 2	6	---	1.763843236
NKAIN3	286183	Na+/K+ transporting ATPase interacting 3	8	---	0.440960809
NLGN1	22871	neuroligin 1	3	denovo SNV	0.440960809
NLGN2	57555	neuroligin 2	17	FMRP Target,Postsynaptic Proteome	0.440960809
NLGN3	54413	neuroligin 3	X	FMRP Target,ASD-AD/XL	2.645764855
NLGN4X	57502	neuroligin 4, X-linked	X	ASD-AD/XL	0.440960809
NLK	51701	nemo-like kinase	17	---	0.881921618
NMNAT2	23057	nicotinamide nucleotide adenylyltransferase 2	1	---	0.440960809

NNAT	4826	neuronatin	20	---	0.440960809
NOVA1	4857	neuro-oncological ventral antigen 1	14	---	0.440960809
NOVA2	4858	neuro-oncological ventral antigen 2	19	---	0.440960809
NPTN	27020	neuroplastin	15	Postsynaptic Proteome	0.440960809
NRBP1	29959	nuclear receptor binding protein 1	2	---	0.440960809
NRCAM	4897	neuronal cell adhesion molecule	7	Postsynaptic Proteome	6.173451327
NRD1	4898	nardilysin (N-arginine dibasic convertase)	1	---	0.440960809
NRSN2	80023	neurensin 2	20	---	0.440960809
NRXN2	9379	neurexin 2	11	FMRP Target	1.322882427
NSF	4905	N-ethylmaleimide-sensitive factor	17	FMRP Target,Postsynaptic Proteome	0.440960809
NTM	50863	neurotrimin	11	---	0.440960809
NTRK2	4915	neurotrophic tyrosine kinase, receptor, type 2	9	FMRP Target	0.440960809
NTRK3	4916	neurotrophic tyrosine kinase, receptor, type 3	15	FMRP Target	0.881921618
NUDT3	11165	nudix (nucleoside diphosphate linked moiety X)-type motif 3	6	---	0.881921618
NUFIP1	26747	nuclear fragile X mental retardation protein interacting protein 1	13	---	0.440960809
NUFIP2	57532	nuclear fragile X mental retardation protein interacting protein 2	17	---	0.440960809
NUP133	55746	nucleoporin 133kDa	1	---	0.440960809
NUP153	9972	nucleoporin 153kDa	6	---	0.440960809
NUP93	9688	nucleoporin 93kDa	16	---	0.440960809
OCIAD1	54940	OCIA domain containing 1	4	---	0.440960809
OGFRL1	79627	opioid growth factor receptor-like 1	6	---	0.440960809
OLFM1	10439	olfactomedin 1	9	FMRP Target	1.322882427
OLFM2	93145	olfactomedin 2	19	---	0.440960809
OPCML	4978	opioid binding protein/cell adhesion molecule-like	11	Postsynaptic Proteome	2.204804046
OPHN1	4983	oligophrenin 1	X	ASD-AD/XL	0.440960809
OSBP	5007	oxysterol binding protein	11	---	0.440960809
OSBPL6	114880	oxysterol binding protein-like 6	2	---	0.440960809
OSBPL8	114882	oxysterol binding protein-like 8	12	---	0.881921618
OTUB1	55611	OTU domain, ubiquitin aldehyde binding 1	11	---	0.440960809
OTUD6B	51633	OTU domain containing 6B	8	---	0.440960809
PACS1	55690	phosphofurin acidic cluster sorting protein 1	11	FMRP Target,Postsynaptic Proteome	0.440960809
PAK3	5063	p21 protein (Cdc42/Rac)-activated kinase 3	X	---	0.440960809
PAK7	57144	p21 protein (Cdc42/Rac)-activated kinase 7	20	---	0.440960809
PALM	5064	paralemmin	19	Postsynaptic Proteome	0.440960809
PAPSS1	9061	3'-phosphoadenosine 5'-phosphosulfate synthase 1	4	---	0.440960809
PAX6	5080	paired box 6	11	---	0.881921618
PCCA	5095	propionyl CoA carboxylase, alpha polypeptide	13	---	0.440960809
PCDH9	5101	protocadherin 9	13	FMRP Target	0.440960809
PCDHGC3	5098	protocadherin gamma subfamily C, 3	5	FMRP Target	0.440960809
PCGF3	10336	polycomb group ring finger 3	4	---	0.440960809
PCLO	27445	piccolo presynaptic cytomatrix protein	7	FMRP Target,Postsynaptic Proteome	0.881921618
PCNXL2	80003	pecanex-like 2 (Drosophila)	1	FMRP Target	0.440960809
PDE4B	5142	phosphodiesterase 4B, cAMP-specific	1	FMRP Target	0.440960809
PDP1	54704	pyruvate dehyrogenase phosphatase catalytic subunit 1	8	---	0.440960809
PDS5A	23244	PDS5, regulator of cohesion maintenance, homolog A (S. cerevisiae)	4	---	0.440960809
PDS5B	23047	PDS5, regulator of cohesion maintenance, homolog B (S. cerevisiae)	13	FMRP Target	2.204804046
PDXP	57026	pyridoxal (pyridoxine, vitamin B6) phosphatase	22	---	0.440960809
PDZD4	57595	PDZ domain containing 4	X	---	1.763843236
PEA15	8682	phosphoprotein enriched in astrocytes 15	1	Postsynaptic Proteome	0.440960809
PEG10	23089	paternally expressed 10	7	---	0.440960809
PEG3	5178	paternally expressed 3	19	FMRP Target	0.440960809
PEX1	5189	peroxisomal biogenesis factor 1	7	---	0.440960809
PGAP1	80055	post-GPI attachment to proteins 1	2	---	1.322882427
PGM2L1	283209	phosphoglucomutase 2-like 1	11	FMRP Target	3.086725664
PHACTR3	116154	phosphatase and actin regulator 3	20	---	0.881921618
PHF14	9678	PHD finger protein 14	7	---	1.763843236
PHKB	5257	phosphorylase kinase, beta	16	---	0.440960809
PHYHIP	9796	phytanoyl-CoA 2-hydroxylase interacting protein	8	FMRP Target	0.440960809
PHYHIPL	84457	phytanoyl-CoA 2-hydroxylase interacting protein-like	10	---	0.440960809
PIGY	84992	phosphatidylinositol glycan anchor biosynthesis, class Y	4	---	0.440960809
PIK3C3	5289	phosphatidylinositol 3-kinase, catalytic subunit type 3	18	---	0.440960809
PIK3R2	5296	phosphoinositide-3-kinase, regulatory subunit 2 (beta)	19	---	0.440960809
PIP4K2B	8396	phosphatidylinositol-5-phosphate 4-kinase, type II, beta	17	Postsynaptic Proteome	1.322882427
PIP5K1C	23396	phosphatidylinositol-4-phosphate 5-kinase, type I, gamma	19	FMRP Target	0.440960809
PITPNA	5306	phosphatidylinositol transfer protein, alpha	17	---	0.440960809
PITPNC1	26207	phosphatidylinositol transfer protein, cytoplasmic 1	17	---	0.440960809
PLCB1	23236	phospholipase C, beta 1 (phosphoinositide-specific)	20	FMRP Target,Postsynaptic Proteome	1.322882427
PLK2	10769	polo-like kinase 2	5	---	0.440960809

PLXDC2	84898	plexin domain containing 2	10	---	0.440960809
PMPCB	9512	peptidase (mitochondrial processing) beta	7	---	0.440960809
POLB	5423	polymerase (DNA directed), beta	8	---	0.440960809
POU2F1	5451	POU class 2 homeobox 1	1	---	0.440960809
PPFIA2	8499	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 2	12	Postsynaptic Proteome	4.8505689
PPID	5481	peptidylprolyl isomerase D	4	---	0.440960809
PPME1	51400	protein phosphatase methylesterase 1	11	---	0.881921618
PPP1R11	6992	protein phosphatase 1, regulatory (inhibitor) subunit 11	6	---	0.440960809
PPP1R12A	4659	protein phosphatase 1, regulatory subunit 12A	12	Postsynaptic Proteome	0.440960809
PPP1R9B	84687	protein phosphatase 1, regulatory subunit 9B	17	FMRP Target,Postsynaptic Proteome	0.440960809
PPP2CA	5515	protein phosphatase 2, catalytic subunit, alpha isozyme	5	---	0.440960809
PPP2R2B	5521	protein phosphatase 2, regulatory subunit B, beta	5	---	7.055372946
PPP2R2D	55844	protein phosphatase 2, regulatory subunit B, delta	10	---	0.440960809
PPP2R5B	5526	protein phosphatase 2, regulatory subunit B', beta	11	FMRP Target	0.881921618
PPP3CA	5530	protein phosphatase 3, catalytic subunit, alpha isozyme	4	FMRP Target,Postsynaptic Proteome	0.440960809
PPP3R1	5534	protein phosphatase 3, regulatory subunit B, alpha	2	---	0.440960809
PPP6R2	9701	protein phosphatase 6, regulatory subunit 2	22	FMRP Target	0.440960809
PRDM10	56980	PR domain containing 10	11	---	1.322882427
PRDM2	7799	PR domain containing 2, with ZNF domain	1	---	0.440960809
PRDX3	10935	peroxiredoxin 3	10	---	0.440960809
PREP	5550	prolyl endopeptidase	6	---	0.440960809
PREX2	80243	phosphatidylinositol-3,4,5-trisphosphate-dependent Rac exchange factor 2	8	FMRP Target	0.881921618
PRKACB	5567	protein kinase, cAMP-dependent, catalytic, beta	1	FMRP Target	1.322882427
PRKAG2	51422	protein kinase, AMP-activated, gamma 2 non-catalytic subunit	7	---	0.440960809
PRKAR2B	5577	protein kinase, cAMP-dependent, regulatory, type II, beta	7	Postsynaptic Proteome	0.440960809
PROSER1	80209	proline and serine rich 1	13	---	1.322882427
PRPF31	26121	PRP31 pre-mRNA processing factor 31 homolog (S. cerevisiae)	19	---	0.440960809
PRRC2C	23215	proline-rich coiled-coil 2C	1	FMRP Target	0.881921618
PRRT2	112476	proline-rich transmembrane protein 2	16	---	0.440960809
PRTFDC1	56952	phosphoribosyl transferase domain containing 1	10	---	0.440960809
PSD	5662	pleckstrin and Sec7 domain containing	10	FMRP Target	0.440960809
PSEN1	5663	presenilin 1	14	denovo SNV	0.440960809
PSIP1	11168	PC4 and SFRS1 interacting protein 1	9	---	0.440960809
PSME3	10197	proteasome (prosome, macropain) activator subunit 3 (PA28 gamma; Ki)	17	---	0.440960809
PSPC1	55269	paraspeckle component 1	13	---	0.881921618
PTN	5764	pleiotrophin	7	---	0.440960809
PTPN13	5783	protein tyrosine phosphatase, non-receptor type 13 (APO-1/CD95 (Fas)-associated phosphatase)	4	---	0.440960809
PTPN5	84867	protein tyrosine phosphatase, non-receptor type 5 (striatum-enriched)	11	FMRP Target	0.440960809
PTPRA	5786	protein tyrosine phosphatase, receptor type, A	20	---	0.881921618
PTPRD	5789	protein tyrosine phosphatase, receptor type, D	9	FMRP Target,Postsynaptic Proteome	1.763843236
PTPRG-AS1	1E+08	PTPRG antisense RNA 1	3	---	1.322882427
PTPRZ1	5803	protein tyrosine phosphatase, receptor-type, Z polypeptide 1	7	Postsynaptic Proteome	5.291529709
PYURF	1E+08	PIGY upstream reading frame	4	---	0.440960809
QSER1	79832	glutamine and serine rich 1	11	---	0.440960809
R3HDM1	23518	R3H domain containing 1	2	FMRP Target	1.322882427
R3HDM2	22864	R3H domain containing 2	12	FMRP Target	1.322882427
RAB15	376267	RAB15, member RAS oncogene family	14	Postsynaptic Proteome	1.322882427
RAB1A	5861	RAB1A, member RAS oncogene family	2	Postsynaptic Proteome	0.440960809
RAB3A	5864	RAB3A, member RAS oncogene family	19	Postsynaptic Proteome	0.881921618
RAB3C	115827	RAB3C, member RAS oncogene family	5	---	1.322882427
RAB3GAP2	25782	RAB3 GTPase activating protein subunit 2 (non-catalytic)	1	Postsynaptic Proteome	1.322882427
RAB5A	5868	RAB5A, member RAS oncogene family	3	---	0.440960809
RAB6B	51560	RAB6B, member RAS oncogene family	3	Postsynaptic Proteome	1.763843236
RABGAP1L	9910	RAB GTPase activating protein 1-like	1	---	0.440960809
RALGAPA1	253959	Ral GTPase activating protein, alpha subunit 1 (catalytic)	14	FMRP Target	0.440960809
RALGAPB	57148	Ral GTPase activating protein, beta subunit (non-catalytic)	20	FMRP Target	0.440960809
RAP1GDS1	5910	RAP1, GTP-GDP dissociation stimulator 1	4	Postsynaptic Proteome	0.440960809
RAP2A	5911	RAP2A, member of RAS oncogene family	13	---	0.440960809
RAPGEF2	9693	Rap guanine nucleotide exchange factor (GEF) 2	4	FMRP Target,Postsynaptic Proteome	0.440960809
RB1	5925	retinoblastoma 1	13	---	0.440960809
RCBTB1	55213	regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 1	13	---	0.440960809
REEP2	51308	receptor accessory protein 2	5	---	1.763843236
REEP5	7905	receptor accessory protein 5	5	---	0.440960809
REPS1	85021	RALBP1 associated Eps domain containing 1	6	---	0.881921618
RFC1	5981	replication factor C (activator 1) 1, 145kDa	4	---	0.440960809
RFWD2	64326	ring finger and WD repeat domain 2, E3 ubiquitin protein ligase	1	---	0.440960809

RGS7	6000	regulator of G-protein signaling 7	1	Postsynaptic Proteome	1.763843236
RHOT1	55288	ras homolog family member T1	17	---	2.204804046
RICTOR	253260	RPTOR independent companion of MTOR, complex 2	5	---	0.881921618
RIF1	55183	RAP1 interacting factor homolog (yeast)	2	---	0.440960809
RIMS1	22999	regulating synaptic membrane exocytosis 1	6	denovo SNV,Postsynaptic Proteome	0.881921618
RLF	6018	rearranged L-myc fusion	1	---	0.440960809
RNF145	153830	ring finger protein 145	5	---	0.881921618
RNF146	81847	ring finger protein 146	6	---	0.440960809
RNF165	494470	ring finger protein 165	18	---	0.440960809
RNFT2	84900	ring finger protein, transmembrane 2	12	---	0.440960809
RNGTT	8732	RNA guanylyltransferase and 5'-phosphatase	6	---	0.881921618
RPAIN	84268	RPA interacting protein	17	---	1.322882427
RPAP3	79657	RNA polymerase II associated protein 3	12	---	0.440960809
RPL17-C18orf3	1E+08	RPL17-C18orf32 readthrough	18	---	0.881921618
RPRD1A	55197	regulation of nuclear pre-mRNA domain containing 1A	18	---	0.881921618
RPS10-NUDT3	1E+08	RPS10-NUDT3 readthrough	6	---	0.881921618
RTF1	23168	Rtf1, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	15	---	0.440960809
RTN1	6252	reticulon 1	14	FMRP Target,Postsynaptic Proteome	0.881921618
RUFY2	55680	RUN and FYVE domain containing 2	10	---	0.440960809
RUFY3	22902	RUN and FYVE domain containing 3	4	Postsynaptic Proteome	0.881921618
RUNDC3A	10900	RUN domain containing 3A	17	---	3.968647282
RUNDC3B	154661	RUN domain containing 3B	7	---	0.881921618
RUNX1T1	862	runt-related transcription factor 1; translocated to, 1 (cyclin D-related)	8	---	0.881921618
RUSC1	23623	RUN and SH3 domain containing 1	1	FMRP Target	0.440960809
RYBP	23429	RING1 and YY1 binding protein	3	---	0.440960809
SAR1A	56681	SAR1 homolog A (S. cerevisiae)	10	---	0.440960809
SATB2	23314	SATB homeobox 2	2	ASD-AD/XL	1.322882427
SBF2	81846	SET binding factor 2	11	---	0.440960809
SCAI	286205	suppressor of cancer cell invasion	9	Postsynaptic Proteome	0.440960809
SCAPER	49855	S-phase cyclin A-associated protein in the ER	15	---	0.440960809
SCG3	29106	secretogranin III	15	---	1.322882427
SCN2A	6326	sodium channel, voltage-gated, type II, alpha subunit	2	denovo SNV,FMRP Target	4.8505689
SCN3A	6328	sodium channel, voltage-gated, type III, alpha subunit	2	---	0.440960809
SCN3B	55800	sodium channel, voltage-gated, type III, beta subunit	11	---	0.440960809
SCN8A	6334	sodium channel, voltage gated, type VIII, alpha subunit	12	FMRP Target	0.881921618
SCRN3	79634	secernin 3	2	---	0.881921618
SDC3	9672	syndecan 3	1	---	0.440960809
SEC31A	22872	SEC31 homolog A (S. cerevisiae)	4	---	0.440960809
SEC62	7095	SEC62 homolog (S. cerevisiae)	3	---	0.440960809
SECISBP2L	9728	SECIS binding protein 2-like	15	FMRP Target	0.440960809
SENP6	26054	SUMO1/sentrin specific peptidase 6	6	---	0.440960809
SERF2	10169	small EDRK-rich factor 2	15	---	0.440960809
ERF2-C15ORF6	1E+08	SERF2-C15orf63 readthrough	15	---	0.440960809
SEZ6L	23544	seizure related 6 homolog (mouse)-like	22	---	1.322882427
SF3B1	23451	splicing factor 3b, subunit 1, 155kDa	2	---	0.440960809
SFPQ	6421	splicing factor proline/glutamine-rich	1	---	0.440960809
SGIP1	84251	SH3-domain GRB2-like (endophilin) interacting protein 1	1	FMRP Target,Postsynaptic Proteome	1.763843236
SGK196	84197	protein kinase-like protein SgK196	8	---	0.440960809
SHANK1	50944	SH3 and multiple ankyrin repeat domains 1	19	FMRP Target,Postsynaptic Proteome	1.763843236
SHANK2	22941	SH3 and multiple ankyrin repeat domains 2	11	FMRP Target,Postsynaptic Proteome,ASD-AD/XL	0.440960809
SHC3	53358	SHC (Src homology 2 domain containing) transforming protein 3	9	---	0.881921618
SLAIN1	122060	SLAIN motif family, member 1	13	---	1.322882427
SLBP	7884	stem-loop binding protein	4	---	0.440960809
SLC22A17	51310	solute carrier family 22, member 17	14	FMRP Target	0.881921618
SLC25A40	55972	solute carrier family 25, member 40	7	---	0.440960809
SLC30A9	10463	solute carrier family 30 (zinc transporter), member 9	4	---	0.881921618
SLC36A4	120103	solute carrier family 36 (proton/amino acid symporter), member 4	11	---	0.440960809
SLC4A7	9497	solute carrier family 4, sodium bicarbonate cotransporter, member 7	3	---	1.763843236
SLC6A15	55117	solute carrier family 6 (neutral amino acid transporter), member 15	12	---	1.763843236
SLC9A6	10479	solute carrier family 9, subfamily A (NHE6, cation proton antiporter 6), member 6	X	ASD-AD/XL	0.440960809
SLIT1	6585	slit homolog 1 (Drosophila)	10	---	2.204804046
SLK	9748	STE20-like kinase	10	denovo SNV	0.440960809
SMAD4	4089	SMAD family member 4	18	---	0.440960809
SMARCA2	6595	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	9	FMRP Target	0.440960809
SMARCD3	6604	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3	7	---	0.440960809
SMG7	9887	smg-7 homolog, nonsense mediated mRNA decay factor (C. elegans)	1	---	0.440960809

SNAP25	6616	synaptosomal-associated protein, 25kDa	20	FMRP Target,Postsynaptic Proteome	2.645764855
SNAPC3	6619	small nuclear RNA activating complex, polypeptide 3, 50kDa	9	---	0.440960809
SNCA	6622	synuclein, alpha (non A4 component of amyloid precursor)	4	---	0.881921618
SNCB	6620	synuclein, beta	5	---	0.881921618
SNX14	57231	sorting nexin 14	6	---	0.440960809
SNX2	6643	sorting nexin 2	5	---	0.440960809
SNX27	81609	sorting nexin family member 27	1	Postsynaptic Proteome	0.440960809
SOGA3	387104	SOGA family member 3	6	---	0.881921618
SORBS2	8470	sorbin and SH3 domain containing 2	4	FMRP Target,Postsynaptic Proteome	0.440960809
SORT1	6272	sortilin 1	1	FMRP Target	0.440960809
SOS1	6654	son of sevenless homolog 1 (Drosophila)	2	---	0.440960809
SOS2	6655	son of sevenless homolog 2 (Drosophila)	14	---	0.440960809
SOX2	6657	SRY (sex determining region Y)-box 2	3	---	0.440960809
SPAG9	9043	sperm associated antigen 9	17	FMRP Target	0.881921618
SPAST	6683	spastin	2	---	0.440960809
SPNS1	83985	spinster homolog 1 (Drosophila)	16	---	0.440960809
SRGAP3	9901	SLIT-ROBO Rho GTPase activating protein 3	3	denovo SNV,FMRP Target	3.527686473
SRI	6717	sorcin	7	Postsynaptic Proteome	0.440960809
SRSF9	8683	serine/arginine-rich splicing factor 9	12	---	0.440960809
ST6GAL2	84620	ST6 beta-galactosamide alpha-2,6-sialyltranferase 2	2	---	0.881921618
STAM2	10254	signal transducing adaptor molecule (SH3 domain and ITAM motif) 2	2	---	0.881921618
STAU1	6780	staufen, RNA binding protein, homolog 1 (Drosophila)	20	---	0.440960809
STK19	8859	serine/threonine kinase 19	6	---	0.440960809
STK32C	282974	serine/threonine kinase 32C	10	---	0.440960809
STK39	27347	serine threonine kinase 39	2	---	0.440960809
STMN1	3925	stathmin 1	1	---	0.440960809
STMN2	11075	stathmin-like 2	8	---	0.881921618
STMN3	50861	stathmin-like 3	20	---	0.440960809
STMN4	81551	stathmin-like 4	8	---	1.322882427
STRN4	29888	striatin, calmodulin binding protein 4	19	FMRP Target	1.322882427
STX1B	112755	syntaxin 1B	16	Postsynaptic Proteome	0.440960809
STX6	10228	syntaxin 6	1	---	0.440960809
STXBP1	6812	syntaxin binding protein 1	9	FMRP Target,Postsynaptic Proteome	1.763843236
SUV420H1	51111	suppressor of variegation 4-20 homolog 1 (Drosophila)	11	denovo SNV	0.440960809
SV2A	9900	synaptic vesicle glycoprotein 2A	1	FMRP Target	3.527686473
SYNJ1	8867	synaptojanin 1	21	FMRP Target,Postsynaptic Proteome	0.881921618
SYT1	6857	synaptotagmin I	12	FMRP Target,Postsynaptic Proteome	3.968647282
SYT11	23208	synaptotagmin XI	1	---	0.881921618
SYT4	6860	synaptotagmin IV	18	---	0.881921618
SYT5	6861	synaptotagmin V	19	Postsynaptic Proteome	0.881921618
TAB2	23118	TGF-beta activated kinase 1/MAP3K7 binding protein 2	6	---	0.440960809
TAF15	8148	TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 68kDa	17	---	0.440960809
TAGLN3	29114	transgelin 3	3	Postsynaptic Proteome	1.322882427
TBC1D19	55296	TBC1 domain family, member 19	4	---	0.881921618
TBC1D5	9779	TBC1 domain family, member 5	3	---	0.440960809
TBCEL	219899	tubulin folding cofactor E-like	11	---	0.440960809
TBRG1	84897	transforming growth factor beta regulator 1	11	---	0.440960809
TCEB2	6923	transcription elongation factor B (SIII), polypeptide 2 (18kDa, elongin B)	16	---	0.440960809
TCF12	6938	transcription factor 12	15	---	0.440960809
TCTN1	79600	tectonic family member 1	12	---	0.440960809
TFDP1	7027	transcription factor Dp-1	13	---	0.440960809
TGIF2-C20orf2	1E+08	TGIF2-C20orf24 readthrough	20	---	0.440960809
THOC7	80145	THO complex 7 homolog (Drosophila)	3	---	0.440960809
THRA	7067	thyroid hormone receptor, alpha	17	FMRP Target	0.440960809
TLK1	9874	tousled-like kinase 1	2	---	0.881921618
TMEFF1	8577	transmembrane protein with EGF-like and two follistatin-like domains 1	9	---	0.881921618
TMEM116	89894	transmembrane protein 116	12	---	0.440960809
TMEM130	222865	transmembrane protein 130	7	---	0.440960809
TMEM135	65084	transmembrane protein 135	11	---	0.440960809
TMEM14C	51522	transmembrane protein 14C	6	---	0.440960809
TMEM170A	124491	transmembrane protein 170A	16	---	0.440960809
MEM189-UBE2	387522	TMEM189-UBE2V1 readthrough	20	---	0.440960809
TMEM196	256130	transmembrane protein 196	7	---	0.440960809
TMEM241	85019	transmembrane protein 241	18	---	0.440960809
TMEM30A	55754	transmembrane protein 30A	6	---	0.440960809
TMEM59L	25789	transmembrane protein 59-like	19	---	0.440960809
TMEM9B	56674	TMEM9 domain family, member B	11	---	0.440960809

TNIK	23043	TRAF2 and NCK interacting kinase	3	FMRP Target	0.881921618
TNKS2	80351	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase 2	10	---	0.440960809
TNPO2	30000	transportin 2	19	FMRP Target	0.440960809
TNR	7143	tenascin R	1	Postsynaptic Proteome	1.322882427
TOP2B	7155	topoisomerase (DNA) II beta 180kDa	3	---	0.881921618
TP53BP1	7158	tumor protein p53 binding protein 1	15	---	0.440960809
TPD52L2	7165	tumor protein D52-like 2	20	---	1.763843236
TPGS2	25941	tubulin polyglutamylase complex subunit 2	18	---	1.322882427
TRA2A	29896	transformer 2 alpha homolog (Drosophila)	7	---	0.440960809
TRAK2	66008	trafficking protein, kinesin binding 2	2	FMRP Target	0.440960809
TRAPPC10	7109	trafficking protein particle complex 10	21	FMRP Target	0.440960809
TRAPPC12	51112	trafficking protein particle complex 12	2	---	0.440960809
TRAPPC8	22878	trafficking protein particle complex 8	18	---	0.440960809
TRIM33	51592	tripartite motif containing 33	1	---	0.440960809
TRIM8	81603	tripartite motif containing 8	10	---	0.440960809
TRIM9	114088	tripartite motif containing 9	14	FMRP Target	1.763843236
TRIO	7204	trio Rho guanine nucleotide exchange factor	5	denovo SNV,FMRP Target	1.322882427
TRIP12	9320	thyroid hormone receptor interactor 12	2	denovo SNV,FMRP Target	0.440960809
TRPC1	7220	transient receptor potential cation channel, subfamily C, member 1	3	---	0.440960809
TRPC4AP	26133	transient receptor potential cation channel, subfamily C, member 4 associated protein	20	FMRP Target	0.440960809
TSPAN5	10098	tetraspanin 5	4	---	0.440960809
TSPYL4	23270	TSPY-like 4	6	FMRP Target	0.440960809
TTC33	23548	tetratricopeptide repeat domain 33	5	---	0.440960809
TTC37	9652	tetratricopeptide repeat domain 37	5	---	0.440960809
TTLL11	158135	tubulin tyrosine ligase-like family, member 11	9	---	0.440960809
TTLL7	79739	tubulin tyrosine ligase-like family, member 7	1	FMRP Target	1.763843236
TUB	7275	tubby homolog (mouse)	11	---	0.440960809
TUBB2A	7280	tubulin, beta 2A class IIa	6	Postsynaptic Proteome	0.440960809
TUBB2B	347733	tubulin, beta 2B class IIb	6	Postsynaptic Proteome	0.881921618
TULP4	56995	tubby like protein 4	6	FMRP Target	0.440960809
TUSC3	7991	tumor suppressor candidate 3	8	---	0.440960809
UBAP2L	9898	ubiquitin associated protein 2-like	1	FMRP Target	0.440960809
UBE2K	3093	ubiquitin-conjugating enzyme E2K	4	---	0.440960809
UBE2O	63893	ubiquitin-conjugating enzyme E2O	17	FMRP Target	0.440960809
UBE2V1	7335	ubiquitin-conjugating enzyme E2 variant 1	20	---	1.322882427
UBP1	7342	upstream binding protein 1 (LBP-1a)	3	---	0.440960809
UBQLN1	29979	ubiquilin 1	9	FMRP Target	0.440960809
UCK1	83549	uridine-cytidine kinase 1	9	---	0.881921618
ULK2	9706	unc-51-like kinase 2 (C. elegans)	17	FMRP Target	0.440960809
UNC79	57578	unc-79 homolog (C. elegans)	14	---	3.968647282
UPF3B	65109	UPF3 regulator of nonsense transcripts homolog B (yeast)	X	ASD-AD/XL	0.440960809
URI1	8725	URI1, prefoldin-like chaperone	19	---	0.440960809
USP16	10600	ubiquitin specific peptidase 16	21	---	0.440960809
USP31	57478	ubiquitin specific peptidase 31	16	---	0.440960809
USP32	84669	ubiquitin specific peptidase 32	17	FMRP Target	0.440960809
USP34	9736	ubiquitin specific peptidase 34	2	FMRP Target	0.440960809
UTP18	51096	UTP18 small subunit (SSU) processome component homolog (yeast)	17	---	0.440960809
VAMP2	6844	vesicle-associated membrane protein 2 (synaptobrevin 2)	17	FMRP Target,Postsynaptic Proteome	0.881921618
VAPB	9217	VAMP (vesicle-associated membrane protein)-associated protein B and C	20	Postsynaptic Proteome	0.440960809
VAT1L	57687	vesicle amine transport protein 1 homolog (T. californica)-like	16	---	0.440960809
VOPP1	81552	vesicular, overexpressed in cancer, prosurvival protein 1	7	---	0.440960809
VPS13C	54832	vacuolar protein sorting 13 homolog C (S. cerevisiae)	15	---	0.440960809
VPS29	51699	vacuolar protein sorting 29 homolog (S. cerevisiae)	12	---	0.440960809
VPS37A	137492	vacuolar protein sorting 37 homolog A (S. cerevisiae)	8	---	0.440960809
VPS41	27072	vacuolar protein sorting 41 homolog (S. cerevisiae)	7	FMRP Target	0.440960809
VPS53	55275	vacuolar protein sorting 53 homolog (S. cerevisiae)	17	---	1.322882427
WASF1	8936	WAS protein family, member 1	6	FMRP Target,Postsynaptic Proteome	0.881921618
WASF3	10810	WAS protein family, member 3	13	Postsynaptic Proteome	1.763843236
WASL	8976	Wiskott-Aldrich syndrome-like	7	Postsynaptic Proteome	0.440960809
WDFY3	23001	WD repeat and FYVE domain containing 3	4	denovo SNV,FMRP Target	0.881921618
WDR17	116966	WD repeat domain 17	4	---	2.645764855
WDR41	55255	WD repeat domain 41	5	---	0.440960809
WDR47	22911	WD repeat domain 47	1	---	0.440960809
WDR7	23335	WD repeat domain 7	18	Postsynaptic Proteome	2.645764855
XPO7	23039	exportin 7	8	FMRP Target	1.322882427
XRCC1	7515	X-ray repair complementing defective repair in Chinese hamster cells 1	19	---	0.440960809
XYLT1	64131	xylosyltransferase I	16	---	0.440960809
YEATS2	55689	YEATS domain containing 2	3	---	0.881921618
YLPM1	56252	YLP motif containing 1	14	---	0.440960809
YME1L1	10730	YME1-like 1 (S. cerevisiae)	10	---	0.440960809

YTHDC2	64848	YTH domain containing 2	5	---	0.440960809
YTHDF1	54915	YTH domain family, member 1	20	---	0.440960809
YTHDF2	51441	YTH domain family, member 2	1	---	0.440960809
YY1	7528	YY1 transcription factor	14	denovo SNV	0.440960809
ZC2HC1A	51101	zinc finger, C2HC-type containing 1A	8	---	0.881921618
ZC3H15	55854	zinc finger CCCH-type containing 15	2	---	0.881921618
ZDHHC17	23390	zinc finger, DHHC-type containing 17	12	---	1.322882427
ZDHHC21	340481	zinc finger, DHHC-type containing 21	9	---	0.440960809
ZDHHC4	55146	zinc finger, DHHC-type containing 4	7	---	0.881921618
ZEB1	6935	zinc finger E-box binding homeobox 1	10	---	0.440960809
ZFC3H1	196441	zinc finger, C3H1-type containing	12	---	0.440960809
ZFYVE9	9372	zinc finger, FYVE domain containing 9	1	---	0.440960809
ZIM2	23619	zinc finger, imprinted 2	19	---	0.440960809
ZMYM2	7750	zinc finger, MYM-type 2	13	---	0.440960809
ZMYM4	9202	zinc finger, MYM-type 4	1	---	1.322882427
ZMYND8	23613	zinc finger, MYND-type containing 8	20	---	0.440960809
ZNF362	149076	zinc finger protein 362	1	---	0.440960809
ZNF382	84911	zinc finger protein 382	19	---	0.440960809
ZNF532	55205	zinc finger protein 532	18	---	0.440960809
ZNF721	170960	zinc finger protein 721	4	---	0.440960809

Table 9. Enrichment Statistics for 'Brain-Critical Exons'.

Gene Set ID	Corresponding Pathway Name	P_Value	Discovery Rate (FDR)
GO:0035637	GO: MULTICELLULAR ORGANISMAL SIGNALING	1.37E-53	3.57E-50
GO:0019226	GO: TRANSMISSION OF NERVE IMPULSE	1.58E-52	2.06E-49
GO:0045202	GO: SYNAPSE	1.10E-51	9.55E-49
GO:0043005	GO: NEURON PROJECTION	1.82E-50	1.18E-47
GO:0007268	GO: SYNAPTIC TRANSMISSION	1.44E-49	7.52E-47
GO:0044456	GO: SYNAPSE PART	3.50E-42	1.52E-39
GO:0048666	GO: NEURON DEVELOPMENT	2.81E-33	1.05E-30
GO:0031175	GO: NEURON PROJECTION DEVELOPMENT	1.18E-32	3.84E-30
GO:0048699	GO: GENERATION OF NEURONS	4.62E-32	1.34E-29
GO:0030182	GO: NEURON DIFFERENTIATION	1.19E-31	3.11E-29
GO:0030425	GO: DENDRITE	2.38E-30	5.65E-28
GO:0030030	GO: CELL PROJECTION ORGANIZATION	8.77E-30	1.91E-27
GO:0030424	GO: AXON	2.74E-29	5.50E-27
GO:0048667	GO: CELL MORPHOGENESIS INVOLVED IN NEURON DIFFERENTIATION	3.78E-29	7.03E-27
GO:0048812	GO: NEURON PROJECTION MORPHOGENESIS	1.55E-28	2.70E-26
REACT:NEURONAL SYSTEM	REACT: NEURONAL SYSTEM	1.91E-28	3.11E-26
GO:0044463	GO: CELL PROJECTION PART	2.75E-26	4.21E-24
GO:0048858	GO: CELL PROJECTION MORPHOGENESIS	3.82E-26	5.53E-24
REACT:TRANSMISSION ACROSS CHEMICAL SYNAPSES	REACT: TRANSMISSION ACROSS CHEMICAL SYNAPSES	9.94E-26	1.36E-23
GO:0097060	GO: SYNAPTIC MEMBRANE	1.08E-25	1.41E-23
GO:0007409	GO: AXONOGENESIS	2.10E-25	2.61E-23
GO:0000904	GO: CELL MORPHOGENESIS INVOLVED IN DIFFERENTIATION	2.47E-25	2.93E-23
GO:0032990	GO: CELL PART MORPHOGENESIS	2.92E-25	3.31E-23
GO:0030054	GO: CELL JUNCTION	3.91E-22	4.25E-20
GO:0000902	GO: CELL MORPHOGENESIS	9.52E-22	9.93E-20
GO:0050804	GO: REGULATION OF SYNAPTIC TRANSMISSION	3.58E-20	3.59E-18
GO:0045211	GO: POSTSYNAPTIC MEMBRANE	4.97E-20	4.80E-18
GO:0051969	GO: REGULATION OF TRANSMISSION OF NERVE IMPULSE	1.16E-19	1.08E-17
GO:0032989	GO: CELLULAR COMPONENT MORPHOGENESIS	3.98E-19	3.58E-17
GO:0022836	GO: GATED CHANNEL ACTIVITY	6.77E-19	5.89E-17
GO:0006836	GO: NEUROTRANSMITTER TRANSPORT	1.01E-18	8.54E-17
REACT:AXON GUIDANCE	REACT: AXON GUIDANCE	1.81E-18	1.48E-16
GO:0031644	GO: REGULATION OF NEUROLOGICAL SYSTEM PROCESS	3.93E-18	3.10E-16
GO:0007411	GO: AXON GUIDANCE	2.37E-17	1.82E-15
GO:0033267	GO: AXON PART	3.66E-17	2.73E-15
GO:0005216	GO: ION CHANNEL ACTIVITY	6.35E-17	4.55E-15
GO:0043197	GO: DENDRITIC SPINE	6.63E-17	4.55E-15
GO:0044309	GO: NEURON SPINE	6.63E-17	4.55E-15
GO:0022838	GO: SUBSTRATE-SPECIFIC CHANNEL ACTIVITY	9.68E-17	6.48E-15
GO:0042391	GO: REGULATION OF MEMBRANE POTENTIAL	1.23E-16	8.01E-15
REACT:NEUROTRANSMITTER RECEPTOR BINDING AND DOWNSTREAM TRANSMISSION IN THE POSTSYNAPTIC CELL	REACT: NEUROTRANSMITTER RECEPTOR BINDING AND DOWNSTREAM TRANSMISSION IN THE POSTSYNAPTIC CELL	5.05E-16	3.21E-14
GO:0014069	GO: POSTSYNAPTIC DENSITY	7.77E-16	4.71E-14
GO:0044327	GO: DENDRITIC SPINE HEAD	7.77E-16	4.71E-14
GO:0015267	GO: CHANNEL ACTIVITY	1.87E-15	1.08E-13
GO:0022803	GO: PASSIVE TRANSMEMBRANE TRANSPORTER ACTIVITY	1.87E-15	1.08E-13
KEGG:HSA04723	KEGG: RETROGRADE ENDOCANNABINOID SIGNALING	4.84E-15	2.74E-13
GO:0001505	GO: REGULATION OF NEUROTRANSMITTER LEVELS	5.55E-15	3.08E-13
REACT:DEVELOPMENTAL BIOLOGY	REACT: DEVELOPMENTAL BIOLOGY	1.14E-14	6.17E-13
GO:0030695	GO: GTPASE REGULATOR ACTIVITY	1.83E-14	9.72E-13
GO:0030136	GO: CLATHRIN-COATED VESICLE	3.18E-14	1.66E-12
KEGG:HSA05033	KEGG: NICOTINE ADDICTION	3.51E-14	1.80E-12
GO:0060589	GO: NUCLEOSIDE-TRIPHOSPHATASE REGULATOR ACTIVITY	3.86E-14	1.93E-12
GO:0010975	GO: REGULATION OF NEURON PROJECTION DEVELOPMENT	1.07E-13	5.25E-12

GO:0031344	GO: REGULATION OF CELL PROJECTION ORGANIZATION	1.13E-13	5.45E-12
REACT:L1CAM INTERACTIONS	REACT: L1CAM INTERACTIONS	1.51E-13	7.14E-12
KEGG:HSA04724	KEGG: GLUTAMATERGIC SYNAPSE	1.59E-13	7.39E-12
GO:0050808	GO: SYNAPSE ORGANIZATION	2.28E-13	1.04E-11
GO:0005261	GO: CATION CHANNEL ACTIVITY	3.50E-13	1.57E-11
GO:0051960	GO: REGULATION OF NERVOUS SYSTEM DEVELOPMENT	7.57E-13	3.35E-11
GO:0044297	GO: CELL BODY	8.70E-13	3.78E-11
GO:0046873	GO: METAL ION TRANSMEMBRANE TRANSPORTER ACTIVITY	9.44E-13	4.03E-11
GO:0030135	GO: COATED VESICLE	1.37E-12	5.76E-11
GO:0045664	GO: REGULATION OF NEURON DIFFERENTIATION	3.41E-12	1.41E-10
REACT:INTERACTION BETWEEN L1 AND ANKYRINS	REACT: INTERACTION BETWEEN L1 AND ANKYRINS	4.16E-12	1.70E-10
GO:0005083	GO: SMALL GTPASE REGULATOR ACTIVITY	4.59E-12	1.84E-10
GO:0034702	GO: ION CHANNEL COMPLEX	5.68E-12	2.24E-10
REACT:ACTIVATION OF NMDA RECEPTOR UPON GLUTAMATE BINDING AND POSTSYNAPTIC EVENTS	REACT: ACTIVATION OF NMDA RECEPTOR UPON GLUTAMATE BINDING AND POSTSYNAPTIC EVENTS	8.02E-12	3.12E-10
GO:0043025	GO: NEURONAL CELL BODY	9.30E-12	3.57E-10
GO:0015075	GO: ION TRANSMEMBRANE TRANSPORTER ACTIVITY	1.61E-11	6.07E-10
GO:0007010	GO: CYTOSKELETON ORGANIZATION	1.88E-11	7.00E-10
GO:0007611	GO: LEARNING OR MEMORY	2.23E-11	8.19E-10
GO:0050890	GO: COGNITION	3.17E-11	1.15E-09
GO:0008092	GO: CYTOSKELETAL PROTEIN BINDING	3.28E-11	1.17E-09
GO:0050767	GO: REGULATION OF NEUROGENESIS	3.42E-11	1.21E-09
KEGG:HSA04727	KEGG: GABAERGIC SYNAPSE	5.33E-11	1.85E-09
GO:0016192	GO: VESICLE-MEDIATED TRANSPORT	5.98E-11	2.05E-09
RECEPTOR, GLUTAMATE BINDING AND ACTIVATION	REACT: UNBLOCKING OF NMDA RECEPTOR, GLUTAMATE BINDING AND ACTIVATION	6.78E-11	2.30E-09
GO:0015276	GO: LIGAND-GATED ION CHANNEL ACTIVITY	8.50E-11	2.81E-09
GO:0022834	GO: LIGAND-GATED CHANNEL ACTIVITY	8.50E-11	2.81E-09
KEGG:HSA04728	KEGG: DOPAMINERGIC SYNAPSE	5.23E-10	1.70E-08
GO:0005244	GO: VOLTAGE-GATED ION CHANNEL ACTIVITY	7.70E-10	2.45E-08
GO:0022832	GO: VOLTAGE-GATED CHANNEL ACTIVITY	7.70E-10	2.45E-08
GO:0007417	GO: CENTRAL NERVOUS SYSTEM DEVELOPMENT	1.65E-09	5.18E-08
GO:0030662	GO: COATED VESICLE MEMBRANE	2.03E-09	6.30E-08
GO:0016358	GO: DENDRITE DEVELOPMENT	3.12E-09	9.58E-08
GO:0034703	GO: CATION CHANNEL COMPLEX	4.90E-09	1.49E-07
GO:0030659	GO: CYTOPLASMIC VESICLE MEMBRANE	6.23E-09	1.87E-07
GO:0060284	GO: REGULATION OF CELL DEVELOPMENT	6.32E-09	1.87E-07
GO:0031252	GO: CELL LEADING EDGE	6.63E-09	1.93E-07
GO:0015085	GO: CALCIUM ION TRANSMEMBRANE TRANSPORTER ACTIVITY	6.67E-09	1.93E-07
GO:0005543	GO: PHOSPHOLIPID BINDING	7.66E-09	2.20E-07
REACT:NEUROTRANSMITTER RELEASE CYCLE	REACT: NEUROTRANSMITTER RELEASE CYCLE	7.76E-09	2.20E-07
REACT:POST NMDA RECEPTOR ACTIVATION EVENTS	REACT: POST NMDA RECEPTOR ACTIVATION EVENTS	8.11E-09	2.27E-07
GO:0001508	GO: REGULATION OF ACTION POTENTIAL	8.99E-09	2.49E-07
GO:0012506	GO: VESICLE MEMBRANE	1.12E-08	3.07E-07
REACT:GABA SYNTHESIS, RELEASE, REUPTAKE AND DEGRADATION	REACT: GABA SYNTHESIS, RELEASE, REUPTAKE AND DEGRADATION	1.18E-08	3.21E-07
GO:0016773	GO: PHOSPHOTRANSFERASE ACTIVITY, ALCOHOL GROUP AS ACCEPTOR	1.30E-08	3.48E-07
GO:0003001	GO: GENERATION OF A SIGNAL INVOLVED IN CELL-CELL SIGNALING	1.40E-08	3.70E-07
GO:0023061	GO: SIGNAL RELEASE	1.40E-08	3.70E-07
GO:0007017	GO: MICROTUBULE-BASED PROCESS	1.98E-08	5.16E-07
GO:0016301	GO: KINASE ACTIVITY	2.11E-08	5.45E-07
GO:0022843	GO: VOLTAGE-GATED CATION CHANNEL ACTIVITY	2.22E-08	5.64E-07
GO:0016772	GO: TRANSFERASE ACTIVITY, TRANSFERRING PHOSPHORUS-CONTAINING GROUPS	2.23E-08	5.64E-07
GO:0010769	GO: REGULATION OF CELL MORPHOGENESIS INVOLVED IN DIFFERENTIATION	2.37E-08	5.95E-07
GO:0004672	GO: PROTEIN KINASE ACTIVITY	2.53E-08	6.29E-07

GO:0022890	GO: INORGANIC CATION TRANSMEMBRANE TRANSPORTER ACTIVITY	2.77E-08	6.81E-07
GO:0017124	GO: SH3 DOMAIN BINDING	2.79E-08	6.81E-07
GO:0072509	GO: DIVALENT INORGANIC CATION TRANSMEMBRANE TRANSPORTER ACTIVITY	3.44E-08	8.30E-07
KEGG:HSA04713	KEGG: CIRCADIAN ENTRAINMENT	3.88E-08	9.29E-07
GO:0015630	GO: MICROTUBULE CYTOSKELETON	4.73E-08	1.12E-06
GO:0006811	GO: ION TRANSPORT	5.05E-08	1.19E-06
GO:0008324	GO: CATION TRANSMEMBRANE TRANSPORTER ACTIVITY	5.63E-08	1.31E-06
KEGG:HSA05032	KEGG: MORPHINE ADDICTION	5.93E-08	1.37E-06
GO:0030234	GO: ENZYME REGULATOR ACTIVITY	5.97E-08	1.37E-06
GO:0022892	GO: SUBSTRATE-SPECIFIC TRANSPORTER ACTIVITY	6.53E-08	1.48E-06
GO:0022857	GO: TRANSMEMBRANE TRANSPORTER ACTIVITY	6.98E-08	1.57E-06
GO:0022891	GO: SUBSTRATE-SPECIFIC TRANSMEMBRANE TRANSPORTER ACTIVITY	7.38E-08	1.65E-06
GO:0051056	GO: REGULATION OF SMALL GTPASE MEDIATED SIGNAL TRANSDUCTION	8.88E-08	1.96E-06
GO:0034220	GO: ION TRANSMEMBRANE TRANSPORT	1.01E-07	2.21E-06
GO:0004674	GO: PROTEIN SERINE/THREONINE KINASE ACTIVITY	1.02E-07	2.22E-06
GO:0044057	GO: REGULATION OF SYSTEM PROCESS	1.08E-07	2.32E-06
GO:0019904	GO: PROTEIN DOMAIN SPECIFIC BINDING	1.35E-07	2.89E-06
GO:0005516	GO: CALMODULIN BINDING	1.75E-07	3.71E-06
GO:0060627	GO: REGULATION OF VESICLE-MEDIATED TRANSPORT	1.93E-07	4.07E-06
GO:0030001	GO: METAL ION TRANSPORT	2.09E-07	4.36E-06
REACT:GLUTAMATE NEUROTRANSMITTER RELEASE CYCLE	REACT: GLUTAMATE NEUROTRANSMITTER RELEASE CYCLE	2.39E-07	4.95E-06
KEGG:HSA04010	KEGG: MAPK SIGNALING PATHWAY	2.69E-07	5.52E-06
KEGG:HSA04720	KEGG: LONG-TERM POTENTIATION	2.80E-07	5.71E-06
GO:0006873	GO: CELLULAR ION HOMEOSTASIS	3.14E-07	6.36E-06
GO:0006935	GO: CHEMOTAXIS	3.48E-07	6.92E-06
GO:0042330	GO: TAXIS	3.48E-07	6.92E-06
GO:0022604	GO: REGULATION OF CELL MORPHOGENESIS	4.06E-07	8.01E-06
REACT:RAS ACTIVATION UOPN CA2+ INFUX THROUGH NMDA RECEPTOR	REACT: RAS ACTIVATION UOPN CA2+ INFUX THROUGH NMDA RECEPTOR	5.31E-07	1.04E-05
GO:0044433	GO: CYTOPLASMIC VESICLE PART	5.32E-07	1.04E-05
GO:0005085	GO: GUANYL-NUCLEOTIDE EXCHANGE FACTOR ACTIVITY	6.13E-07	1.19E-05
GO:0032409	GO: REGULATION OF TRANSPORTER ACTIVITY	6.63E-07	1.27E-05
GO:0008022	GO: PROTEIN C-TERMINUS BINDING	6.84E-07	1.30E-05
GO:0007420	GO: BRAIN DEVELOPMENT	9.18E-07	1.74E-05
GO:0007610	GO: BEHAVIOR	1.08E-06	2.03E-05
GO:0016023	GO: CYTOPLASMIC MEMBRANE-BOUNDED VESICLE	1.15E-06	2.14E-05
GO:0048011	GO: NERVE GROWTH FACTOR RECEPTOR SIGNALING PATHWAY	1.30E-06	2.41E-05
GO:0006184	GO: GTP CATABOLIC PROCESS	1.31E-06	2.41E-05
GO:1901069	GO: GUANOSINE-CONTAINING COMPOUND CATABOLIC PROCESS	1.45E-06	2.64E-05
REACT:CREB PHOSPHORYLATION THROUGH THE ACTIVATION OF CAMKII	REACT: CREB PHOSPHORYLATION THROUGH THE ACTIVATION OF CAMKII	1.61E-06	2.92E-05
GO:0051049	GO: REGULATION OF TRANSPORT	1.73E-06	3.11E-05
GO:0006887	GO: EXOCYTOSIS	1.75E-06	3.12E-05
GO:0034765	GO: REGULATION OF ION TRANSMEMBRANE TRANSPORT	1.93E-06	3.43E-05
GO:0022898	GO: REGULATION OF TRANSMEMBRANE TRANSPORTER ACTIVITY	2.03E-06	3.59E-05
GO:0031988	GO: MEMBRANE-BOUNDED VESICLE	2.29E-06	3.99E-05
GO:0006152	GO: PURINE NUCLEOSIDE CATABOLIC PROCESS	2.31E-06	3.99E-05
GO:0046130	GO: PURINE RIBONUCLEOSIDE CATABOLIC PROCESS	2.31E-06	3.99E-05
GO:0050801	GO: ION HOMEOSTASIS	2.33E-06	4.00E-05
GO:0044087	GO: REGULATION OF CELLULAR COMPONENT BIOGENESIS	2.78E-06	4.73E-05
GO:0042454	GO: RIBONUCLEOSIDE CATABOLIC PROCESS	2.80E-06	4.74E-05
KEGG:HSA04721	KEGG: SYNAPTIC VESICLE CYCLE	2.84E-06	4.75E-05
GO:0043087	GO: REGULATION OF GTPASE ACTIVITY	2.84E-06	4.75E-05
GO:0007626	GO: LOCOMOTORY BEHAVIOR	2.87E-06	4.77E-05
KEGG:HSA04911	KEGG: INSULIN SECRETION	3.35E-06	5.53E-05
GO:0006813	GO: POTASSIUM ION TRANSPORT	3.38E-06	5.55E-05
GO:0031982	GO: VESICLE	3.57E-06	5.82E-05
GO:0055082	GO: CELLULAR CHEMICAL HOMEOSTASIS	3.61E-06	5.84E-05
GO:0033124	GO: REGULATION OF GTP CATABOLIC PROCESS	3.63E-06	5.84E-05
GO:0032940	GO: SECRETION BY CELL	3.73E-06	5.97E-05

NCI:HNF3BPATHWAY	NCI: FOXA2 AND FOXA3 TRANSCRIPTION FACTOR NETWORKS	3.97E-06	6.30E-05
GO:0046039	GO: GTP METABOLIC PROCESS	3.98E-06	6.30E-05
GO:0030027	GO: LAMELLIPODIUM	4.05E-06	6.37E-05
GO:0019725	GO: CELLULAR HOMEOSTASIS	5.03E-06	7.86E-05
GO:0031410	GO: CYTOPLASMIC VESICLE	5.33E-06	8.27E-05
KEGG:HSA04730	KEGG: LONG-TERM DEPRESSION	5.61E-06	8.65E-05
GO:0030036	GO: ACTIN CYTOSKELETON ORGANIZATION	5.67E-06	8.70E-05
REACT:G-PROTEIN MEDIATED EVENTS	REACT: G-PROTEIN MEDIATED EVENTS	5.86E-06	8.94E-05
GO:0007264	GO: SMALL GTPASE MEDIATED SIGNAL TRANSDUCTION	6.50E-06	9.86E-05
GO:0015631	GO: TUBULIN BINDING	7.29E-06	0.000109835
GO:0031346	GO: POSITIVE REGULATION OF CELL PROJECTION ORGANIZATION	7.36E-06	0.000110268
ACTIVATION OF AMPA RECEPTORS AND SYNAPTIC PLASTICITY	REACT: GLUTAMATE BINDING, ACTIVATION OF AMPA RECEPTORS AND SYNAPTIC PLASTICITY	7.61E-06	0.000112746
REACT:TRAFFICKING OF AMPA RECEPTORS	REACT: TRAFFICKING OF AMPA RECEPTORS	7.61E-06	0.000112746
GO:0009164	GO: NUCLEOSIDE CATABOLIC PROCESS	8.66E-06	0.000127663
GO:0016568	GO: CHROMATIN MODIFICATION	9.17E-06	0.000134355
GO:1901068	GO: GUANOSINE-CONTAINING COMPOUND METABOLIC PROCESS	9.47E-06	0.000137987
REACT:OPIOID SIGNALLING	REACT: OPIOID SIGNALLING	9.96E-06	0.000144283
GO:0006812	GO: CATION TRANSPORT	1.09E-05	0.000156825
GO:0043269	GO: REGULATION OF ION TRANSPORT	1.14E-05	0.00016343
GO:0009203	GO: RIBONUCLEOSIDE TRIPHOSPHATE CATABOLIC PROCESS	1.22E-05	0.00017331
GO:0009207	GO: PURINE RIBONUCLEOSIDE TRIPHOSPHATE CATABOLIC PROCESS	1.22E-05	0.00017331
REACT:ION CHANNEL TRANSPORT	REACT: ION CHANNEL TRANSPORT	1.24E-05	0.000174564
GO:0009146	GO: PURINE NUCLEOSIDE TRIPHOSPHATE CATABOLIC PROCESS	1.32E-05	0.0001852
GO:0046578	GO: REGULATION OF RAS PROTEIN SIGNAL TRANSDUCTION	1.37E-05	0.000191337
GO:0042278	GO: PURINE NUCLEOSIDE METABOLIC PROCESS	1.48E-05	0.000204684
REACT:CREB PHOSPHORYLATION THROUGH THE ACTIVATION OF RAS	REACT: CREB PHOSPHORYLATION THROUGH THE ACTIVATION OF RAS	1.49E-05	0.000205325
GO:0009199	GO: RIBONUCLEOSIDE TRIPHOSPHATE METABOLIC PROCESS	1.52E-05	0.000208472
GO:0009154	GO: PURINE RIBONUCLEOTIDE CATABOLIC PROCESS	1.66E-05	0.00022676
REACT:GABA RECEPTOR ACTIVATION	REACT: GABA RECEPTOR ACTIVATION	1.69E-05	0.000229161
GO:0009143	GO: NUCLEOSIDE TRIPHOSPHATE CATABOLIC PROCESS	1.79E-05	0.000240761
GO:0009261	GO: RIBONUCLEOTIDE CATABOLIC PROCESS	1.79E-05	0.000240761
REACT:PLC BETA MEDIATED EVENTS	REACT: PLC BETA MEDIATED EVENTS	2.18E-05	0.000291428
GO:0046128	GO: PURINE RIBONUCLEOSIDE METABOLIC PROCESS	2.21E-05	0.000293784
REACT:REGULATION OF INSULIN SECRETION	REACT: REGULATION OF INSULIN SECRETION	2.34E-05	0.00031001
GO:0051020	GO: GTPASE BINDING	2.98E-05	0.000392492
REACT:INTEGRATION OF ENERGY METABOLISM	REACT: INTEGRATION OF ENERGY METABOLISM	3.01E-05	0.000394406
GO:0005815	GO: MICROTUBULE ORGANIZING CENTER	3.29E-05	0.000429007
GO:0009119	GO: RIBONUCLEOSIDE METABOLIC PROCESS	3.39E-05	0.000439692
GO:0009205	GO: PURINE RIBONUCLEOSIDE TRIPHOSPHATE METABOLIC PROCESS	3.47E-05	0.000447379
GO:0016569	GO: COVALENT CHROMATIN MODIFICATION	3.59E-05	0.000460764
KEGG:HSA04725	KEGG: CHOLINERGIC SYNAPSE	3.72E-05	0.00047592
GO:0051276	GO: CHROMOSOME ORGANIZATION	3.96E-05	0.000503895
GO:0030811	GO: REGULATION OF NUCLEOTIDE CATABOLIC PROCESS	4.06E-05	0.000511547
GO:0033121	GO: REGULATION OF PURINE NUCLEOTIDE CATABOLIC PROCESS	4.06E-05	0.000511547
GO:0009116	GO: NUCLEOSIDE METABOLIC PROCESS	4.18E-05	0.000523634
GO:0009141	GO: NUCLEOSIDE TRIPHOSPHATE METABOLIC PROCESS	4.25E-05	0.000529008
GO:0016570	GO: HISTONE MODIFICATION	4.26E-05	0.000529008
GO:0000226	GO: MICROTUBULE CYTOSKELETON ORGANIZATION	4.34E-05	0.000536008
REACT:EFFECTS OF PIP2 HYDROLYSIS	REACT: EFFECTS OF PIP2 HYDROLYSIS	4.43E-05	0.00054221
REACT:LIGAND-GATED ION CHANNEL TRANSPORT	REACT: LIGAND-GATED ION CHANNEL TRANSPORT	4.43E-05	0.00054221
GO:0009144	GO: PURINE NUCLEOSIDE TRIPHOSPHATE METABOLIC PROCESS	4.54E-05	0.000550902
GO:0006325	GO: CHROMATIN ORGANIZATION	4.54E-05	0.000550902
GO:0030029	GO: ACTIN FILAMENT-BASED PROCESS	4.64E-05	0.000560673
GO:0005096	GO: GTPASE ACTIVATOR ACTIVITY	4.95E-05	0.000594632
KEGG:HSA05031	KEGG: AMPHETAMINE ADDICTION	5.68E-05	0.000679265
GO:0008289	GO: LIPID BINDING	5.78E-05	0.000688646
GO:0005938	GO: CELL CORTEX	5.91E-05	0.000701073

GO:0043547	GO: POSITIVE REGULATION OF GTPASE ACTIVITY	6.57E-05	0.000775779
GO:0008047	GO: ENZYME ACTIVATOR ACTIVITY	7.53E-05	0.000884642
GO:0051130	GO: POSITIVE REGULATION OF CELLULAR COMPONENT ORGANIZATION	8.17E-05	0.000955398
GO:0005874	GO: MICROTUBULE	8.70E-05	0.001012401
GO:0035023	GO: REGULATION OF RHO PROTEIN SIGNAL TRANSDUCTION	9.19E-05	0.001064728
GO:0007155	GO: CELL ADHESION	9.23E-05	0.001064728
GO:0007254	GO: JNK CASCADE	9.55E-05	0.001097636
REACT:POTASSIUM CHANNELS	REACT: POTASSIUM CHANNELS	9.95E-05	0.001138391
GO:0022610	GO: BIOLOGICAL ADHESION	0.000101185	0.001152361
GO:0009259	GO: RIBONUCLEOTIDE METABOLIC PROCESS	0.00010384	0.001177458
GO:0030900	GO: FOREBRAIN DEVELOPMENT	0.000104312	0.001177683
GO:0032535	GO: REGULATION OF CELLULAR COMPONENT SIZE	0.000107885	0.001208639
REACT:BOTULINUM NEUROTOXICITY	REACT: BOTULINUM NEUROTOXICITY	0.00010798	0.001208639
GO:0051493	GO: REGULATION OF CYTOSKELETON ORGANIZATION	0.000114458	0.001275665
GO:0030902	GO: HINDBRAIN DEVELOPMENT	0.000116481	0.001287214
GO:0005875	GO: MICROTUBULE ASSOCIATED COMPLEX	0.000116481	0.001287214
NCI:DNAPK_PATHWAY	NCI: DNA-PK PATHWAY IN NONHOMOLOGOUS END JOINING	0.00011724	0.001290131
GO:0015081	GO: SODIUM ION TRANSMEMBRANE TRANSPORTER ACTIVITY	0.000121396	0.001327411
GO:0032318	GO: REGULATION OF RAS GTPASE ACTIVITY	0.000121645	0.001327411
REACT:SIGNALLING BY NGF	REACT: SIGNALLING BY NGF	0.000127402	0.00138444
GO:0009150	GO: PURINE RIBONUCLEOTIDE METABOLIC PROCESS	0.000134935	0.001460211
GO:0006195	GO: PURINE NUCLEOTIDE CATABOLIC PROCESS	0.000142236	0.001532862
GO:0017016	GO: RAS GTPASE BINDING	0.000160926	0.001727135
REACT:NRAGE SIGNALS DEATH THROUGH JNK	REACT: NRAGE SIGNALS DEATH THROUGH JNK	0.000169824	0.001815163
KEGG:HSA04360	KEGG: AXON GUIDANCE	0.000178591	0.001901083
GO:0072523	GO: PURINE-CONTAINING COMPOUND CATABOLIC PROCESS	0.000182265	0.001932303
GO:0005267	GO: POTASSIUM CHANNEL ACTIVITY	0.000185339	0.001956935
GO:0015079	GO: POTASSIUM ION TRANSMEMBRANE TRANSPORTER ACTIVITY	0.000208113	0.002188542
GO:0010959	GO: REGULATION OF METAL ION TRANSPORT	0.000215199	0.002253971
GO:0005769	GO: EARLY ENDOSOME	0.000224066	0.002337462
GO:0015672	GO: MONOVALENT INORGANIC CATION TRANSPORT	0.000233196	0.002423007
GO:0046903	GO: SECRETION	0.000267792	0.002771438
GO:0044431	GO: GOLGI APPARATUS PART	0.000271465	0.002798339
GO:2000026	GO: REGULATION OF MULTICELLULAR ORGANISMAL DEVELOPMENT	0.000276448	0.002838485
GO:0007018	GO: MICROTUBULE-BASED MOVEMENT	0.00028254	0.002889663
GO:0000139	GO: GOLGI MEMBRANE	0.000287059	0.002924412
GO:0006816	GO: CALCIUM ION TRANSPORT	0.000301146	0.003055983
NCI:CERAMIDE_PATHWAY	NCI: CERAMIDE SIGNALING PATHWAY	0.000310861	0.003113653
NCI:ECADHERIN_STABILIZATION_PATHWAY	NCI: STABILIZATION AND EXPANSION OF THE E-CADHERIN ADHERENS JUNCTION	0.000310861	0.003113653
GO:0051403	GO: STRESS-ACTIVATED MAPK CASCADE	0.000312235	0.003113653
GO:0009166	GO: NUCLEOTIDE CATABOLIC PROCESS	0.000312302	0.003113653
REACT:RHO GTPASE CYCLE	REACT: RHO GTPASE CYCLE	0.000314529	0.003113653
REACT:SIGNALING BY RHO GTPASES	REACT: SIGNALING BY RHO GTPASES	0.000314529	0.003113653
GO:0046777	GO: PROTEIN AUTOPHOSPHORYLATION	0.000315186	0.003113653
KEGG:HSA04726	KEGG: SEROTONERGIC SYNAPSE	0.000321417	0.003163231
GO:0070838	GO: DIVALENT METAL ION TRANSPORT	0.000328008	0.003215958
REACT:NETRIN-1 SIGNALING	REACT: NETRIN-1 SIGNALING	0.000336475	0.003286619
REACT:DAG AND IP3 SIGNALING	REACT: DAG AND IP3 SIGNALING	0.000356189	0.003466199
GO:0000165	GO: MAPK CASCADE	0.000377961	0.003664393
KEGG:HSA04070	KEGG: PHOSPHATIDYLINOSITOL SIGNALING SYSTEM	0.000414143	0.004000314
GO:0031098	GO: STRESS-ACTIVATED PROTEIN KINASE SIGNALING CASCADE	0.000416778	0.004010916
GO:0046434	GO: ORGANOPHOSPHATE CATABOLIC PROCESS	0.00042693	0.004093501
GO:0072511	GO: DIVALENT INORGANIC CATION TRANSPORT	0.000454942	0.004346113
GO:1901292	GO: NUCLEOSIDE PHOSPHATE CATABOLIC PROCESS	0.000466275	0.004421989
GO:0009894	GO: REGULATION OF CATABOLIC PROCESS	0.000466276	0.004421989
REACT:SIGNALING BY ROBO RECEPTOR	REACT: SIGNALING BY ROBO RECEPTOR	0.000474995	0.00448836
GO:0007173	GO: EPIDERMAL GROWTH FACTOR RECEPTOR SIGNALING PATHWAY	0.000492641	0.004621614
GO:0038127	GO: ERBB SIGNALING PATHWAY	0.000492641	0.004621614
GO:0008509	GO: ANION TRANSMEMBRANE TRANSPORTER ACTIVITY	0.000500989	0.004683079
GO:0048878	GO: CHEMICAL HOMEOSTASIS	0.000511012	0.004759714
GO:0044270	GO: CELLULAR NITROGEN COMPOUND CATABOLIC PROCESS	0.000519978	0.004825991

BIOCARTA_CK1_PATHWAY	BIOCARTA_CK1_PATHWAY	0.000522052	0.004828054
GO:0046700	GO: HETEROCYCLE CATABOLIC PROCESS	0.000544721	0.005019898
BIOCARTA_NOS1_PATHWAY	BIOCARTA_NOS1_PATHWAY	0.000560981	0.005151541
REACT:NCAM SIGNALING FOR NEURITE OUT-GROWTH	REACT: NCAM SIGNALING FOR NEURITE OUT-GROWTH	0.000567474	0.005192881
GO:0044451	GO: NUCLEOPLASM PART	0.000571801	0.005214189
GO:0015077	GO: MONOVALENT INORGANIC CATION TRANSMEMBRANE TRANSPORTER ACTIVITY	0.000604003	0.005488643
REACT:EGFR INTERACTS WITH PHOSPHOLIPASE C-GAMMA	REACT: EGFR INTERACTS WITH PHOSPHOLIPASE C-GAMMA	0.000624877	0.005639033
REACT:PLC-GAMMA1 SIGNALLING	REACT: PLC-GAMMA1 SIGNALLING	0.000624877	0.005639033
GO:0070647	GO: PROTEIN MODIFICATION BY SMALL PROTEIN CONJUGATION OR REMOVAL	0.000649747	0.005843238
GO:0016337	GO: CELL-CELL ADHESION	0.00066052	0.005919715
GO:0006897	GO: ENDOCYTOSIS	0.000709382	0.006335853
GO:0031267	GO: SMALL GTPASE BINDING	0.000739687	0.006571117
NCI:CMYB_PATHWAY	NCI: C-MYB TRANSCRIPTION FACTOR NETWORK	0.000740762	0.006571117
GO:0007265	GO: RAS PROTEIN SIGNAL TRANSDUCTION	0.000764132	0.006755444
GO:1900542	GO: REGULATION OF PURINE NUCLEOTIDE METABOLIC PROCESS	0.000783452	0.00688989
GO:0006403	GO: RNA LOCALIZATION	0.000784623	0.00688989
GO:0015103	GO: INORGANIC ANION TRANSMEMBRANE TRANSPORTER ACTIVITY	0.000809701	0.007056794
GO:0034655	GO: NUCLEOBASE-CONTAINING COMPOUND CATABOLIC PROCESS	0.000810321	0.007056794
REACT:PLCG1 EVENTS IN ERBB2 SIGNALING	REACT: PLCG1 EVENTS IN ERBB2 SIGNALING	0.000811748	0.007056794
KEGG:HSA04020	KEGG: CALCIUM SIGNALING PATHWAY	0.000848082	0.007348163
GO:0007169	GO: TRANSMEMBRANE RECEPTOR PROTEIN TYROSINE KINASE SIGNALING PATHWAY	0.000915052	0.007902169
GO:0019900	GO: KINASE BINDING	0.000940112	0.008089539
GO:1901136	GO: CARBOHYDRATE DERIVATIVE CATABOLIC PROCESS	0.000942952	0.008089539
GO:0006140	GO: REGULATION OF NUCLEOTIDE METABOLIC PROCESS	0.000955856	0.00817335
GO:0022603	GO: REGULATION OF ANATOMICAL STRUCTURE MORPHOGENESIS	0.000997789	0.008504031
NCI:RAPID_GR_PATHWAY	NCI: RAPID GLUCOCORTICOID SIGNALING	0.001061012	0.00901342
GO:0008154	GO: ACTIN POLYMERIZATION OR DEPOLYMERIZATION	0.001076557	0.009115782
GO:0021537	GO: TELENCEPHALON DEVELOPMENT	0.001127815	0.009518908
KEGG:HSA05014	KEGG: AMYOTROPHIC LATERAL SCLEROSIS (ALS)	0.001163057	0.009753221
REACT:PHOSPHOLIPASE C-MEDIATED CASCADE	REACT: PHOSPHOLIPASE C-MEDIATED CASCADE	0.001163057	0.009753221
GO:0005509	GO: CALCIUM ION BINDING	0.001190331	0.009949944

Table 10. Splicing Code Prediction of Significant ΔΨ or dPSI(< -0.01) for Exons Reported to Have *de novo* Mutations in Cases and Siblings.

Chr	Pos (hg19)	Strand	Variant	Gene	dPSI	CDS	Exon/-Intron	Splice site distance	Target exon	Gene description	Conserved	LIB_GERP++	Cases/Sibling
chr14	103434646	-	G/A	CDC42BPB	-0.882208	c.2290G>A	16	50	CDSexon	CDC42 binding protein kinase beta (DMPK-like)	366;Name=lod=41	3.19	case
chr11	34107924	+	C/T	CAPRIN1	-0.864494	c.1195C>T	11	37	CDSexon	cell cycle associated protein 1	548;Name=lod=226	5.57	case
chr11	22276997	+	C/T	ANO5	-0.842105	c.1261C>T	13	72	CDSexon	anoctamin 5	479;Name=lod=118	4.76	case
chr13	20235898	+	C/T	MPHOSPH8	-0.831742	c.1852C>T	8	-61	CDSexon	M-phase phosphoprotein 8		-5.16	case
chr9	95027326	-	C/A	IARS	-0.813624	c.1585C>A	16	80	CDSexon	isoleucyl-tRNA synthetase	597;Name=lod=355	4.72	sibling
chr6	52878774	-	G/A	ICK	-0.803551	c.838G>A	10	7	CDSexon	intestinal cell (MAK-like) kinase	501;Name=lod=145	2.82	sibling
chr1	229783350	+	G/T	URB2	-0.785288	c.4000G>T	7	-94	CDSexon	URB2 ribosome biogenesis 2 homolog (S. cerevisiae)	433;Name=lod=77	5.01	case
chr2	166210819	+	G/T	SCN2A	-0.751802	c.3037G>T	17	-118	CDSexon	sodium channel, voltage-gated, type II, alpha subunit	600;Name=lod=365	5.15	case
chr3	9490270	+	C/T	SETD5	-0.746878	c.2302C>T	16	45	CDSexon	SET domain containing 5	639;Name=lod=525		case
chr9	95277357	-	G/A	ECM2	-0.720592	c.610G>A	4	129	CDSexon	extracellular matrix protein 2, female organ and adipocyte specific		4.34	case
chr2	166201379	+	C/A	SCN2A	-0.696137	c.2877C>A	16	43	CDSexon	sodium channel, voltage-gated, type II, alpha subunit	677;Name=lod=750	3.89	case
chr8	61484622	+	C/T	RAB2A	-0.690189	c.136C>T	3	-18	CDSexon	RAB2A, member RAS oncogene family	581;Name=lod=306	5.4	case
chr7	151842339	-	G/T	MLL3	-0.655967	c.14073G>T	54	42	CDSexon	na		-6.76	case
chr6	153075412	+	T/A	VIP	-0.597364	c.219T>A	3	12	CDSexon	vasoactive intestinal peptide	443;Name=lod=84	1.55	case
chr4	39900030	-	G/T	PDS5A	-0.554932	c.1749G>T	16	-22	CDSexon	PDS5, regulator of cohesion maintenance, homolog A (S. cerevisiae)	556;Name=lod=242		sibling
chr1	115280664	-	G/A	CSDE1	-0.497058	c.367G>A	4	30	CDSexon	cold shock domain containing E1, RNA-binding	711;Name=lod=1031	4.58	case
chrX	20193403	-	G/C	RPS6KA3	-0.486833	c.1106G>C	14	4	CDSexon	ribosomal protein S6 kinase, 90kDa, polypeptide 3	665;Name=lod=673	4.32	case
chr4	114232545	+	C/T	ANK2	-0.477584	c.2683C>T	24	11	CDSexon	ankyrin 2, neuronal	443;Name=lod=84	2.83	case
chr18	44603833	+	G/C	KATNAL2	-0.464204	c.995+1G>C	-12	1	CDSexon	katanin p60 subunit A-like 2	419;Name=lod=67		case
chr1	169096506	+	C/T	ATP1B1	-0.431529	c.427C>T	5	-45	CDSexon	ATPase, Na+/K+ transporting, beta 1		2.36	case
chr4	85719152	-	T/A	WDFY3	-0.395202	c.2932T>A	18	-4	CDSexon	WD repeat and FYVE domain containing 3	524;Name=lod=180	5.32	case
chr10	129183053	+	G/C	DOCK1	-0.355606	c.3745-1G>C	-37	-1	CDSexon	dedicator of cytokinesis 1	425;Name=lod=71		sibling
chr3	9786691	+	G/A	BRPF1	-0.302156	c.2921-1G>A	-9	-1	CDSexon	bromodomain and PHD finger containing, 1	640;Name=lod=533		case
chr18	5398076	-	G/A	EPB41L3	-0.298613	c.2416G>A	17	-57	CDSexon	erythrocyte membrane protein band 4.1-like 3	618;Name=lod=432	2.54	sibling
chr10	293337	+	G/A	ZMYND11	-0.29616	c.1159-1G>A	-11	-1	CDSexon	zinc finger, MYND-type containing 11	638;Name=lod=520		case
chr16	57095444	+	G/T	NLRC5	-0.237041	c.4070+1G>T	-31	1	CDSexon	NLR family, CARD domain containing 5	340;Name=lod=32		case
chr3	54921984	+	A/G	CACNA2D3	-0.222493	c.2057-2A>G	-23	-2	CDSexon	calcium channel, voltage-dependent, alpha 2/delta subunit 3	534;Name=lod=197		case
chr2	183791570	-	C/A	NCKAP1	-0.21943	c.3262C>A	31	-27	CDSexon	NCK-associated protein 1	661;Name=lod=650	5.01	case
chr11	9111272	-	C/A	SCUBE2	-0.212271	c.238C>A	2	-19	CDSexon	signal peptide, CUB domain, EGF-like 2	625;Name=lod=464	4.41	case
chr8	144659231	-	C/T	NAPRT1	-0.192919	c.684+1C>T	-5	1	CDSexon	phosphoribosyltransferase domain containing 1	381;Name=lod=47		case
chr11	67938481	-	C/T	SUV420H1	-0.174944	c.977+1C>T	-9	1	CDSexon	suppressor of variegation 4-20 homolog 1 (Drosophila)	449;Name=lod=89		case
chr1	61553905	+	C/T	NFIA	-0.163101	c.247C>T	3	-85	CDSexon	nuclear factor I/A	739;Name=lod=1349	5.7	case

chr2	230701696	-	G/A	TRIP12	-0.149057	c.1012G>A	5	5	CDSexon	thyroid hormone receptor interactor 12	687;Name=lod=823	5.7	case
chr2	225376218	-	C/A	CUL3	-0.107103	c.736C>A	6	82	CDSexon	cullin 3	759;Name=lod=1624	5.51	case
chr9	36375929	-	A/G	RNF38	-0.102421	c.356+2A>G	-3	2	CDSexon	ring finger protein 38	740;Name=lod=1358		case
chr3	100015120	+	G/C	TBC1D23	-0.094528	c.876+1G>C	-8	1	CDSexon	TBC1 domain family, member 23	640;Name=lod=534		case
chr6	35378934	+	G/A	PPARD	-0.093836	c.70G>A	4	61	5pCDSexon	peroxisome proliferator-activated receptor delta	652;Name=lod=595	3.46	sibling
chr1	23236941	+	C/T	EPHB2	-0.092702	c.2572C>T	14	-67	CDSexon	EPH receptor B2	676;Name=lod=743	4.59	case
chr2	170042308	-	G/A	LRP2	-0.091028	c.9550G>A	50	222	CDSexon	low density lipoprotein receptor-related protein 2	562;Name=lod=256	5.62	case
chr12	53608241	-	T/A	RARG	-0.08532	c.625T>A	6	-12	CDSexon	retinoic acid receptor, gamma	544;Name=lod=217	4.26	case
chr7	31609423	+	G/C	CCDC129	-0.083088	c.386G>C	5	1	CDSexon	coiled-coil domain containing 129	481;Name=lod=120		sibling
chr11	102593283	-	G/A	MMP8	-0.073614	c.224G>A	2	122	CDSexon	matrix metallopeptidase 8 (neutrophil collagenase)	349;Name=lod=35	5.14	case
chr1	240964755	-	C/T	RGS7	-0.070916	c.1413C>T	17	-1	CDSexon	regulator of G-protein signaling 7	596;Name=lod=351		sibling
chr15	66198459	-	G/A	MEGF11	-0.068597	c.2731G>A	21	21	CDSexon	multiple EGF-like-domains 11	598;Name=lod=359	3.14	case
chr7	50611651	-	C/T	DDC	-0.051272	c.133C>T	2	-69	5pCDSexon	dopa decarboxylase (aromatic L-amino acid decarboxylase)		-11.1	sibling
chr2	162275553	+	A/C	TBR1	-0.050543	c.1120A>C	4	9	CDSexon	T-box, brain, 1	569;Name=lod=273	5.4	case
chr15	93518170	+	A/G	CHD2	-0.050324	c.2567A>G	20	11	CDSexon	chromodomain helicase DNA binding protein 2	551;Name=lod=232	5.13	case
chrX	12828150	+	G/A	PRPS2	-0.047336	c.424G>A	4	-10	CDSexon	phosphoribosyl pyrophosphate synthetase 2	479;Name=lod=118	4.46	sibling
chr5	176715871	+	C/G	NSD1	-0.043699	c.6203C>G	21	-52	CDSexon	nuclear receptor binding SET domain protein 1	634;Name=lod=501	5.29	sibling
chr7	21737764	+	A/G	DNAH11	-0.041451	c.6134A>G	37	68	CDSexon	dynein, axonemal, heavy chain 11	615;Name=lod=420		case
chr9	139636334	-	G/A	LCN10	-0.04029	c.256G>A	2	-2	CDSexon	lipocalin 10			case
chr3	53764493	+	C/G	CACNA1D	-0.039392	c.2306C>G	17	-25	CDSexon	calcium channel, voltage-dependent, L type, alpha 1D subunit	657;Name=lod=621	4.91	case
chr9	139636334	-	G/A	LCN6	-0.038889	c.*19G>A	8	-2	3pUTRexon	lipocalin 6			case
chr9	95782633	+	A/G	FGD3	-0.037646	c.1421A>G	13	-35	CDSexon	FYVE, RhoGEF and PH domain containing 3	537;Name=lod=203	4.12	case
chr4	8620162	+	C/T	CPZ	-0.036628	c.1510C>T	10	-7	CDSexon	carboxypeptidase Z	389;Name=lod=51	4.63	case
chr1	36367118	+	C/T	EIF2C1	-0.036596	c.1064C>T	9	-44	CDSexon	na	603;Name=lod=378	4.2	case
chr17	5286429	+	C/T	RABEP1	-0.030378	c.2500C>T	18	-13	3pCDSexon	rabaptin, RAB GTPase binding effector protein 1	516;Name=lod=167	1.28	sibling
chr10	112359556	+	C/T	SMC3	-0.029273	c.2413C>T	21	15	CDSexon	structural maintenance of chromosomes 3	584;Name=lod=316	5.1	case
chr11	113631634	-	G/A	ZW10	-0.028343	c.247G>A	3	7	CDSexon	zw10 kinetochore protein	561;Name=lod=254	3.87	sibling
chr3	62356982	-	G/A	FEZF2	-0.024484	c.1030G>A	4	43	CDSexon	FEZ family zinc finger 2	708;Name=lod=1006	2.65	case
chr11	64974022	+	G/A	CAPN1	-0.024396	c.1442G>A	12	-89	CDSexon	calpain 1, (mu/I) large subunit	567;Name=lod=268		sibling
chr3	11067472	+	C/T	SLC6A1	-0.022118	c.863C>T	9	-14	CDSexon	solute carrier family 6 (neurotransmitter transporter), member 1	510;Name=lod=157	4.55	case
chrX	8522080	-	G/T	KAL1	-0.021476	c.1267G>T	9	60	CDSexon	Kallmann syndrome 1 sequence			case
chr22	19127459	-	T/C	DGCR14	-0.021358	c.479T>C	4	79	CDSexon	DiGeorge syndrome critical region gene 14	577;Name=lod=294	4.5	case
chr3	48621941	-	G/T	COL7A1	-0.019809	c.4096G>T	35	-24	CDSexon	collagen, type VII, alpha 1			case
chr17	556648	-	G/A	VPS53	-0.019287	c.491G>A	7	3	CDSexon	vacuolar protein sorting 53 homolog (S. cerevisiae)	593;Name=lod=343	5.71	sibling
chr4	77038831	-	G/T	NUP54	-0.018403	c.1381G>T	11	-15	CDSexon	nucleoporin 54kDa	541;Name=lod=211		case
chr1	120298147	-	A/G	HMGCS2	-0.017795	c.1090A>G	6	74	CDSexon	3-hydroxy-3-methylglutaryl-CoA synthase 2 (mitochondrial)	473;Name=lod=112	5.35	sibling
chr17	18140835	+	C/T	LLGL1	-0.01657	c.1652C>T	14	-41	CDSexon	lethal giant larvae homolog 1 (Drosophila)		1.35	case
chr16	66434715	+	C/T	CDH5	-0.015905	c.1633C>T	11	-42	CDSexon	cadherin 5, type 2 (vascular endothelium)	352;Name=lod=36	4.9	case
chr7	135122938	-	C/T	CNOT4	-0.014752	c.142C>T	2	-33	5pCDSexon	CCR4-NOT transcription complex, subunit 4	734;Name=lod=1286	5.52	case
chr12	57594563	+	A/G	LRP1	-0.014581	c.10190A>G	64	36	CDSexon	low density lipoprotein receptor-related protein 1	617;Name=lod=428	4.7	case
chr12	51090925	+	C/T	DIP2B	-0.014328	c.2015C>T	17	34	CDSexon	DIP2 disco-interacting protein 2 homolog B (Drosophila)	455;Name=lod=94	5.01	sibling

CLAIMS

1. A method of detecting a critical exon associated with a disease in a nucleic acid sample from one or more mammals having the disease, comprising the steps of:

i) detecting exons within target genes in the nucleic acid sample which exhibit an expression level greater than the 75th percentile of exon expression levels in the target genes using nucleic acid primers that target exons within target genes;

ii) detecting rare mutations which occur at a frequency of less than 0.05 or de novo sequence mutations not possessed by either parent of the nucleic acid sample within each exon detected in step i) and determining the burden of mutation of each exon by dividing the number of mutations in each exon by the length of the exon; and

iii) identifying an exon as a critical exon associated with the disease when the burden of mutation of the exon is less than the 75th percentile of mutations in the exon and inversely correlates with the exon expression level, wherein the disease is a neuropsychiatric disorder.

2. The method of claim 1, wherein the neuropsychiatric disorder is selected from Autism Spectral disorder (ASD), schizophrenia (SZ), intellectual disability (ID), Fragile X syndrome, epilepsy and related nervous disorders.

3. The method of claim 2, wherein the ASD is selected from the group of autism, Asperger's Disorder, Childhood Disintegrative Disorder, Pervasive Developmental Disorder-Not Otherwise Specified and Rett Syndrome.

4. The method of claim 1, wherein the nucleic acid sample is selected from neocortex, amygdala, cerebellar cortex, hippocampus, mediodorsal nucleus of the thalamus, and striatum.

5. The method of claim 4, wherein the sample is a cerebellar cortex sample.

6. The method of claim 1, wherein the sample is a prenatal, child or adult sample.

7. The method of claim 1, wherein the rare or de novo mutations are selected from the group of missense, frameshift, nonsense, splice-site variants and copy number variations.

8. The method of claim 7, wherein the mutations are missense mutations.

9. The method of claim 1, wherein the target gene is selected from one or more of the Fragile X mental retardation (FMRP) gene, Forkhead box P2 (FOXP2) gene, post-synaptic proteome (PSP) gene and an autism spectral disorder (ASD) gene.

Date reçue / Date received 2021-11-08

10. The method of claim 1, wherein one or more primer pairs utilized to determine exon expression levels in step i) are selected from the group consisting of: TGACATCGCACGTCCATCTG (SEQ ID NO: 1) and ACAGGTAGTAAATGGCCCAGG (SEQ ID NO: 2); GAGCCTTCCTGATCCCCTAT (SEQ ID NO: 3) and ACTGTTTCCACGGCAGTGT (SEQ ID NO: 4); TGACATCGCACGTCCATCTG (SEQ ID NO: 1) and ACTGTTTCCACGGCAGTGT (SEQ ID NO: 4); CGGCTGCTGTGCTATCATTC (SEQ ID NO: 5) and CAGCCAACACCCTTCCAGAT (SEQ ID NO: 6); GAGCCTTCCTGATCCCCTAT (SEQ ID NO: 3) and CAGCCAACACCCTTCCAGAT (SEQ ID NO: 6); GGCTGGATAAGCCAGGTCAG (SEQ ID NO: 7) and GGAAAGAGTTGTAGCTCCCGA (SEQ ID NO: 8); CCTGTTCTTCCGTGGAGTGA\(SEQ ID NO: 9) and CATGAAGCCCACGATGGAGA (SEQ ID NO: 10); GGCTGGATAAGCCAGGTCAG (SEQ ID NO: 11) and TACTCATCCACCAGGGCTGT (SEQ ID NO: 12); CCTCAACAGACACTGCCGTA (SEQ ID NO: 13) and GTCTCCCGCCGAGTAAGAAG (SEQ ID NO: 14); CCTCATCCCCATGGTGACATC (SEQ ID NO: 15) and TTACTGCGGTTGTGCAGGAG (SEQ ID NO: 16); GACTTTGTCTTCGCCCCAGA (SEQ ID NO: 17) and CTACCATCAAGCCGTCCCTG (SEQ ID NO: 18); TCCGACATTCTCACTTGCCA (SEQ ID NO: 19) and CCAGGGTCAGCACAAGTCAT (SEQ ID NO: 20); GGACTGTTCTCTGCTGGGAC (SEQ ID NO: 21) and GTTCGGAACCAGTACTCGCC (SEQ ID NO: 22); and CCGCATCCTGATGTGTCTGA (SEQ ID NO: 23) and TTGCAGGTGGATACGTGACT (SEQ ID NO: 24).

Date reçue / Date received 2021-11-08

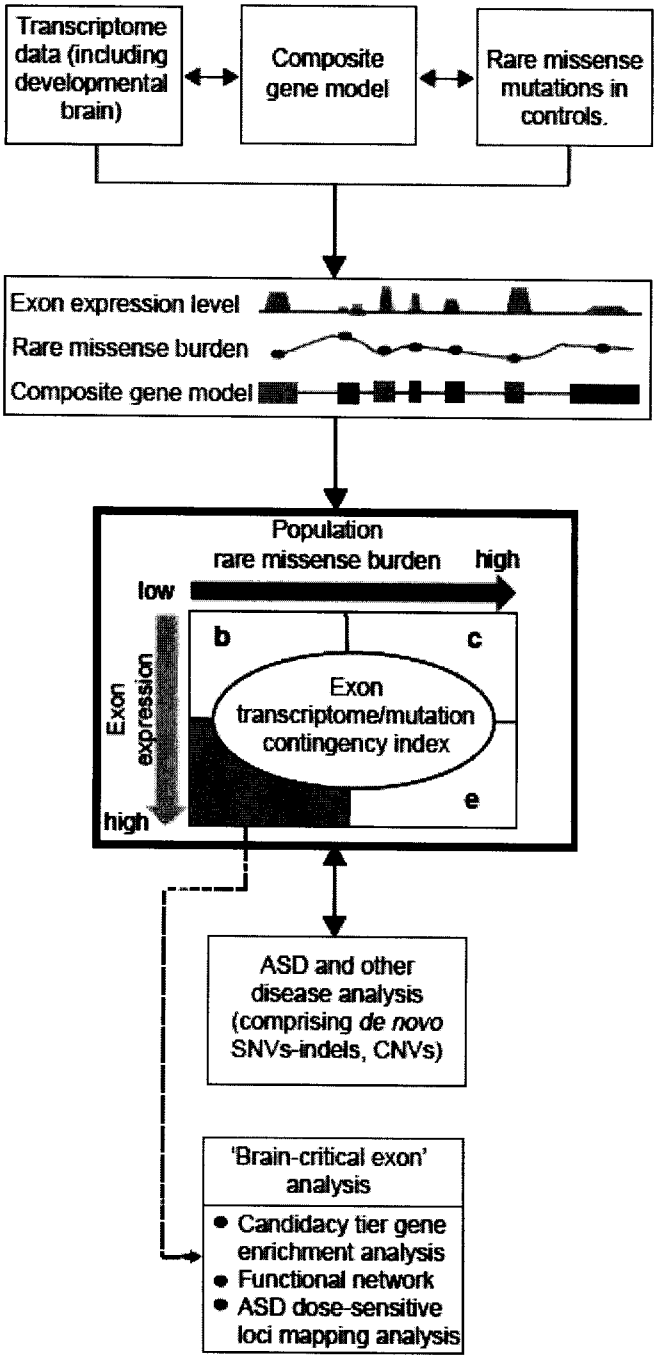

Transcriptome data (including developmental brain)
Composite gene model
Rare missense mutations in controls.
Exon expression level
Rare missense burden
Composite gene model
Population
rare missense burden
high
low
Exon expression
high
b
c
Exon transcriptome/mutation contingency index
e
ASD and other disease analysis (comprising de novo SNVs-indels, CNVs)
'Brain-critical exon' analysis
Candidacy tier gene enrichment analysis
Functional network
ASD dose-sensitive loci mapping analysis

Figure 1

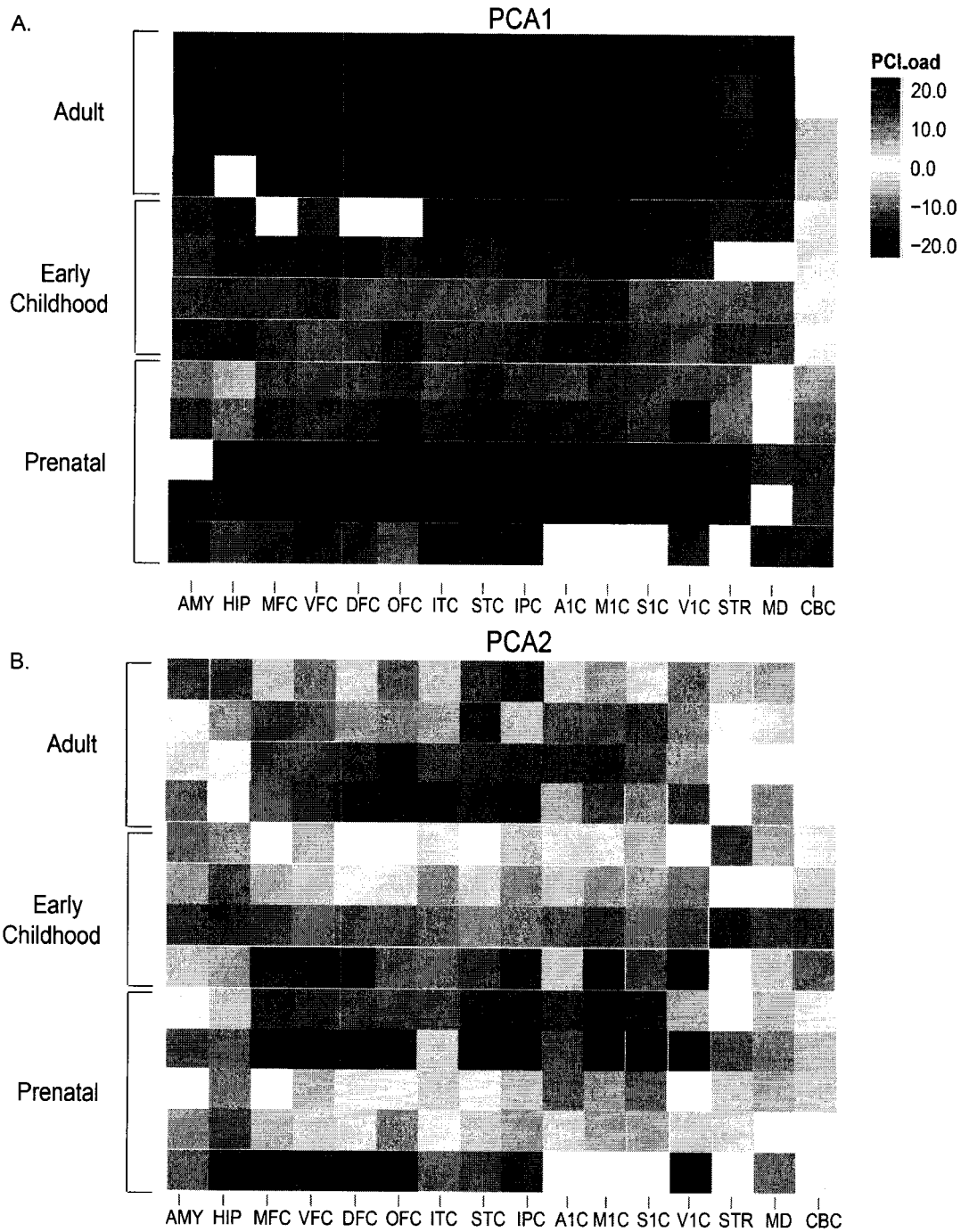

A.
PCA1
Adult
Early Childhood
Prenatal
PCl.oad
20.0
10.0
0.0
−10.0
−20.0
AMY HIP MFC VFC DFC OFC ITC STC IPC A1C M1C S1C V1C STR MD CBC
B.
PCA2
Adult
Early Childhood
Prenatal
AMY HIP MFC VFC DFC OFC ITC STC IPC A1C M1C S1C V1C STR MD CBC

Figure 2

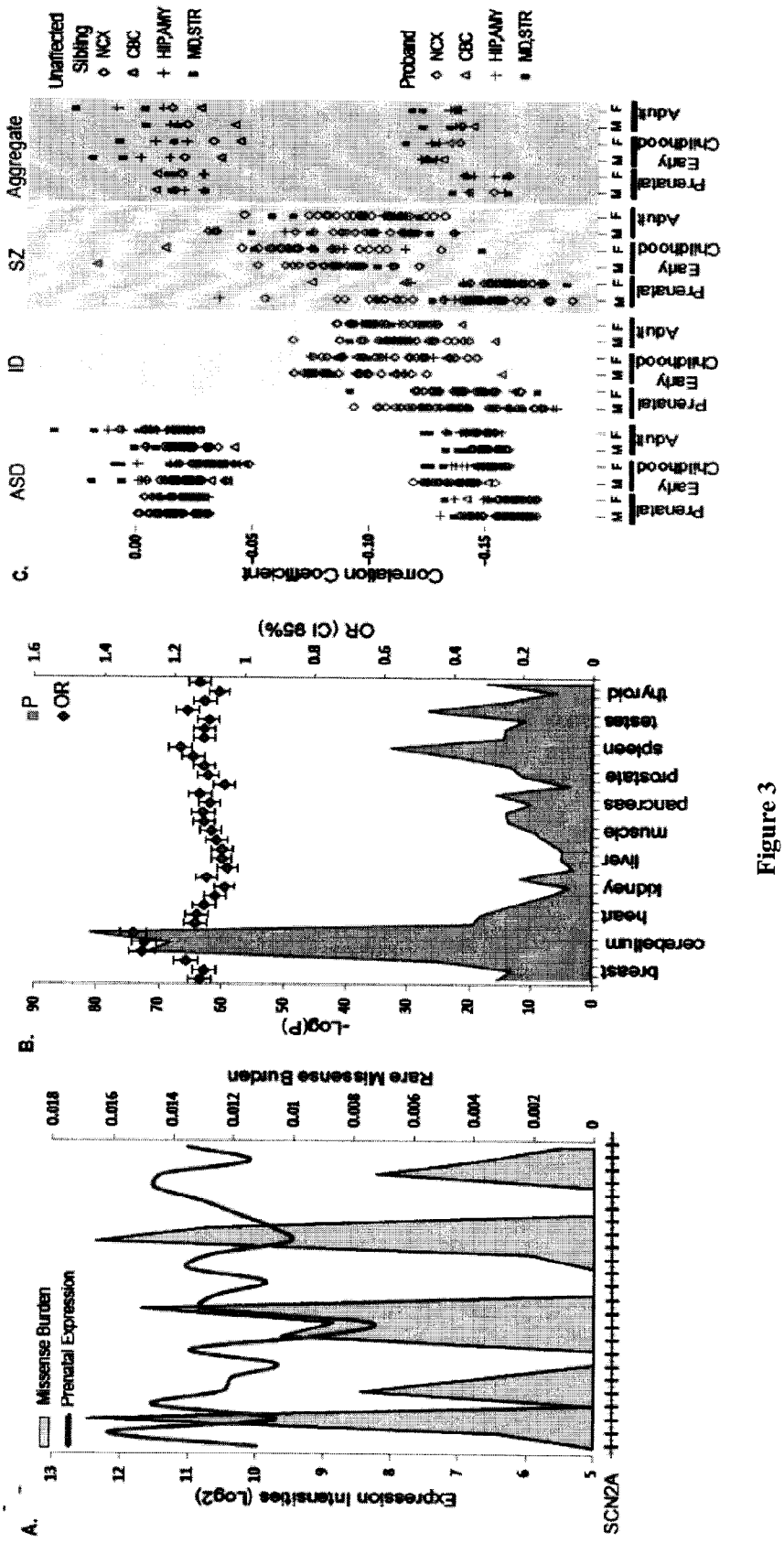

A.
Missense Burden
Prenatal Expression
Expression Intensities (Log2)
Rare Missense Burden
SCN2A
B.
-Log(P)
OR (CI 95%)
P
OR
breast
cerebellum
heart
kidney
liver
muscle
pancreas
prostate
spleen
testes
thyroid
C.
Correlation Coefficient
ASD
ID
SZ
Aggregate
Unaffected Sibling
Proband
NCX
CBC
HIP,AMY
MD,STR
Prenatal
Early Childhood
Adult

Figure 3

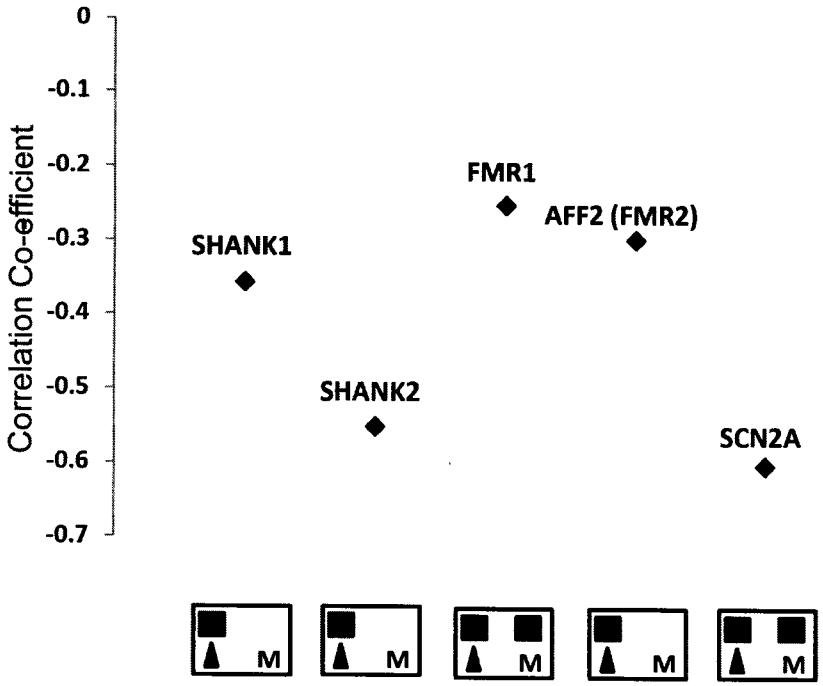
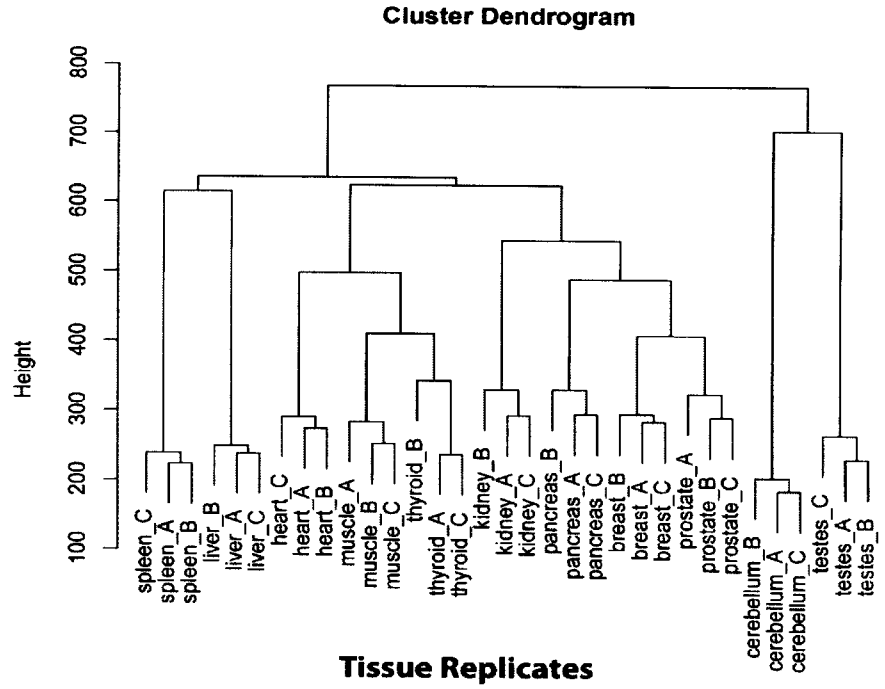

0
-0.1
-0.2
-0.3
-0.4
-0.5
-0.6
-0.7
Correlation Co-efficient
SHANK1
SHANK2
FMR1
AFF2 (FMR2)
SCN2A
M
M
M
M
M

Figure 4

A.



Tissue Replicates

B.

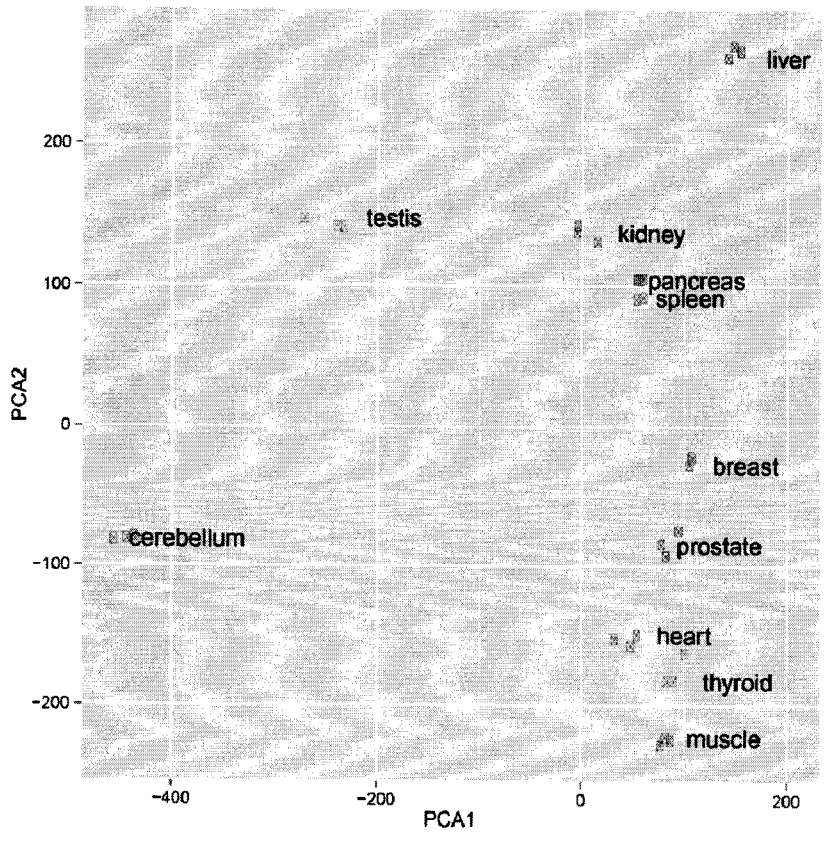


Figure 5

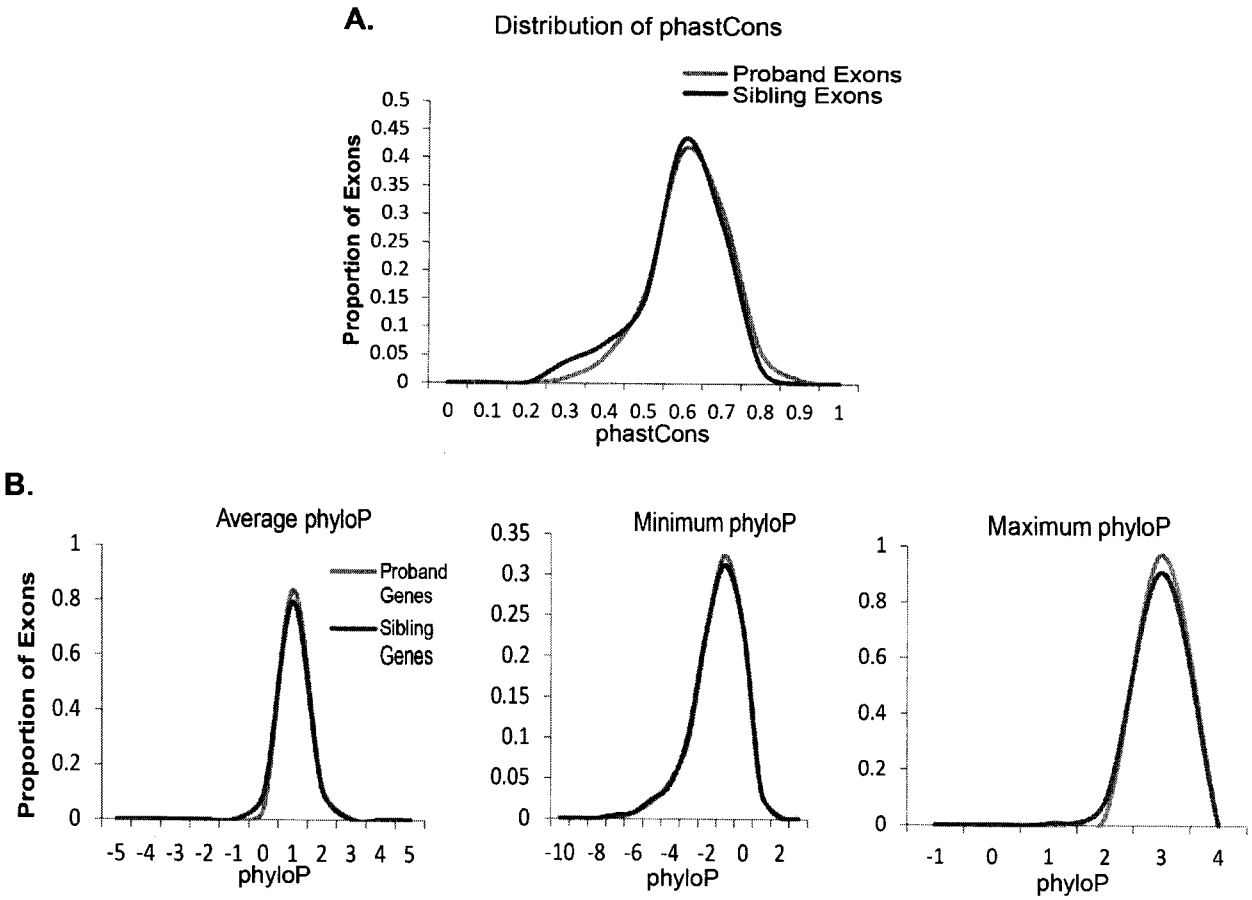

A.
Distribution of phastCons
Proband Exons
Sibling Exons
Proportion of Exons
0.5
0.45
0.4
0.35
0.3
0.25
0.2
0.15
0.1
0.05
0
0 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9 1
phastCons
B.
Average phyloP
Proband Genes
Sibling Genes
Proportion of Exons
1
0.8
0.6
0.4
0.2
0
-5 -4 -3 -2 -1 0 1 2 3 4 5
phyloP
Minimum phyloP
0.35
0.3
0.25
0.2
0.15
0.1
0.05
0
-10 -8 -6 -4 -2 0 2
phyloP
Maximum phyloP
1
0.8
0.6
0.4
0.2
0
-1 0 1 2 3 4
phyloP

Figure 6

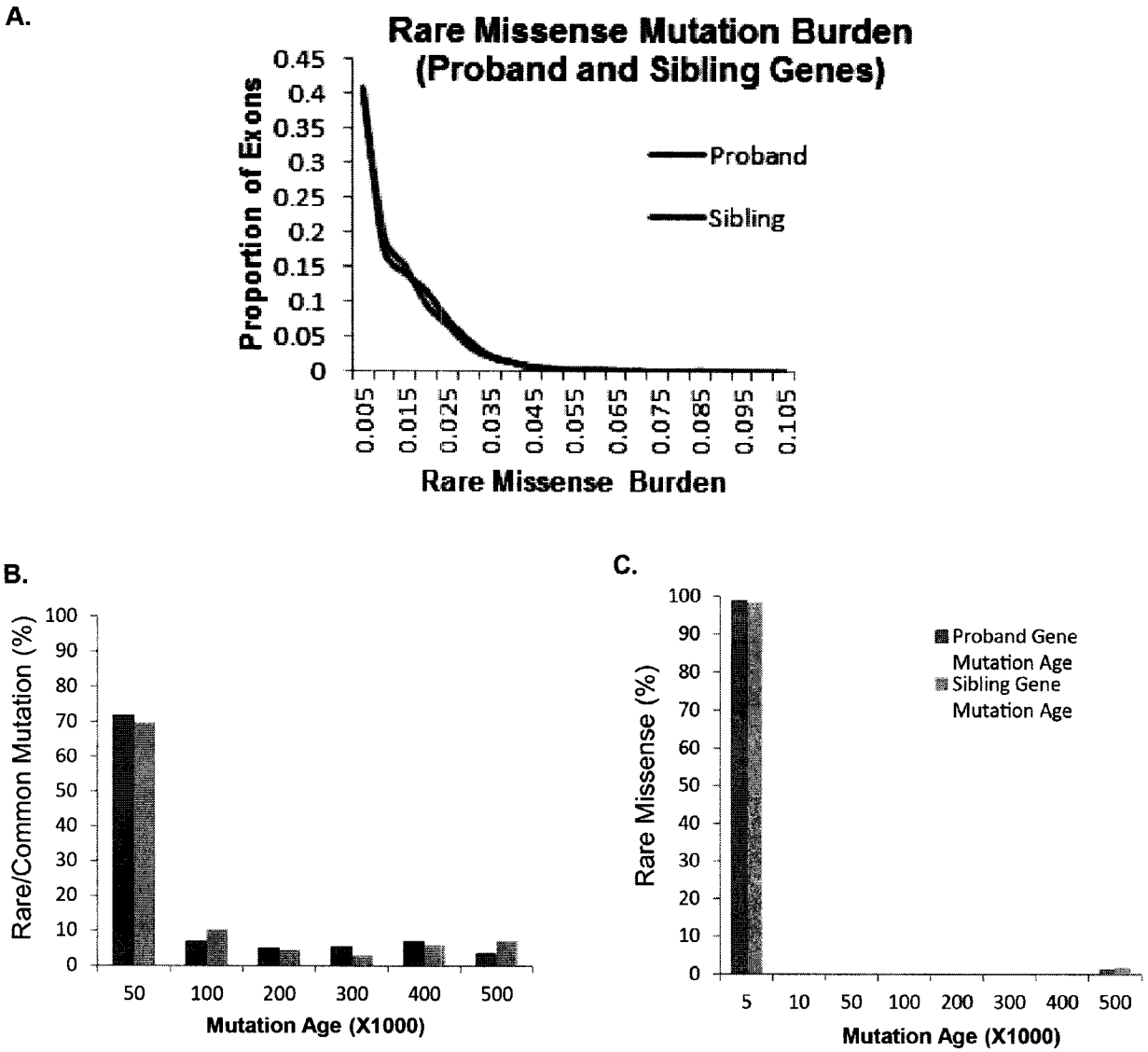

A.
Rare Missense Mutation Burden
(Proband and Sibling Genes)
Proportion of Exons
0.45
0.4
0.35
0.3
0.25
0.2
0.15
0.1
0.05
0
Proband
Sibling
0.005
0.015
0.025
0.035
0.045
0.055
0.065
0.075
0.085
0.095
0.105
Rare Missense Burden
B.
Rare/Common Mutation (%)
100
90
80
70
60
50
40
30
20
10
0
50
100
200
300
400
500
Mutation Age (X1000)
C.
Rare Missense (%)
100
90
80
70
60
50
40
30
20
10
0
Proband Gene Mutation Age
Sibling Gene Mutation Age
5
10
50
100
200
300
400
500
Mutation Age (X1000)

Figure 7

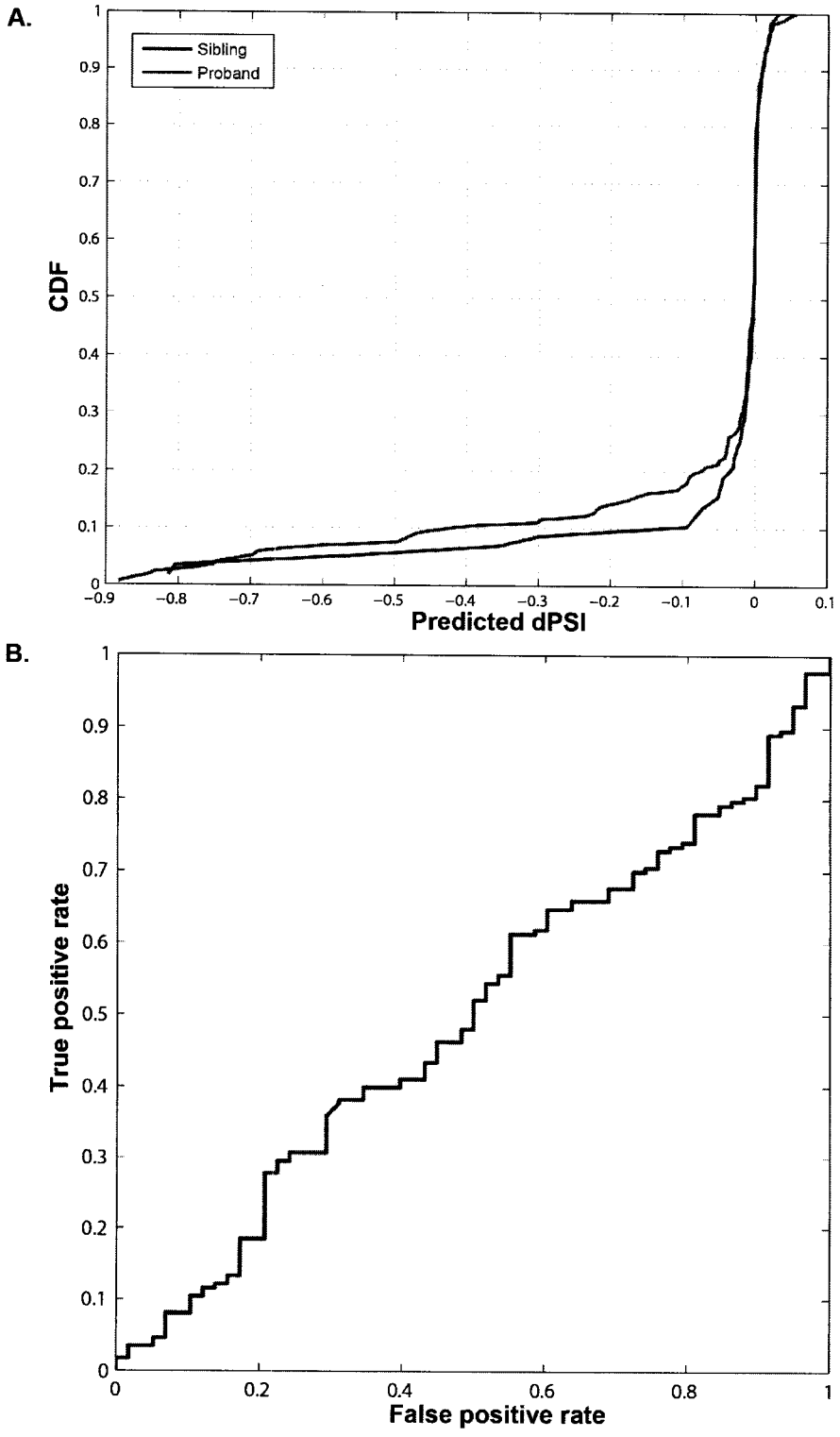

A.
Sibling
Proband
CDF
Predicted dPSI
B.
True positive rate
False positive rate

Figure 8

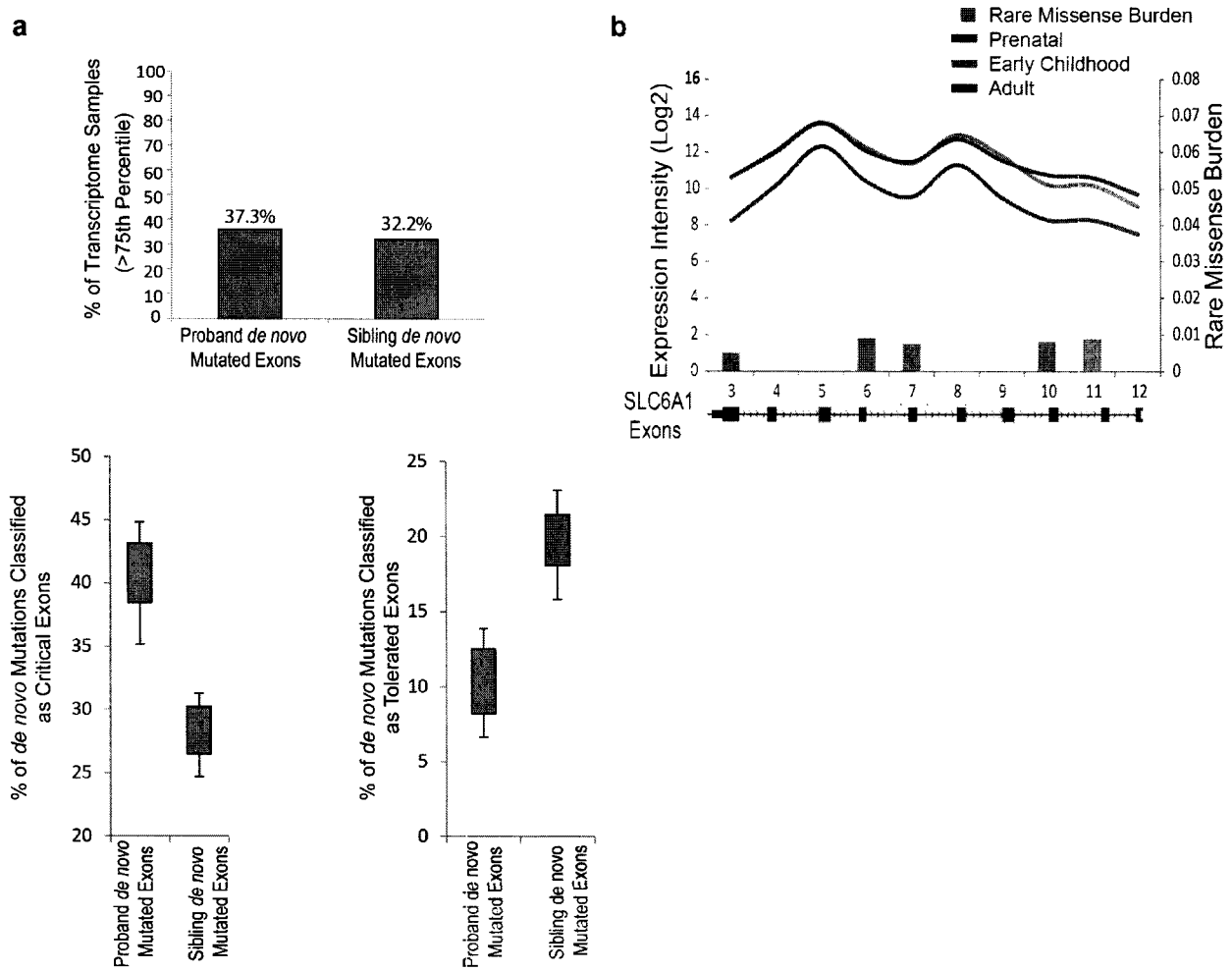

a
% of Transcriptome Samples (>75th Percentile)
37.3%
32.2%
Proband de novo Mutated Exons
Sibling de novo Mutated Exons
b
Rare Missense Burden
Prenatal
Early Childhood
Adult
Expression Intensity (Log2)
Rare Missense Burden
SLC6A1 Exons
% of de novo Mutations Classified as Critical Exons
% of de novo Mutations Classified as Tolerated Exons
Proband de novo Mutated Exons
Sibling de novo Mutated Exons

Figure 9

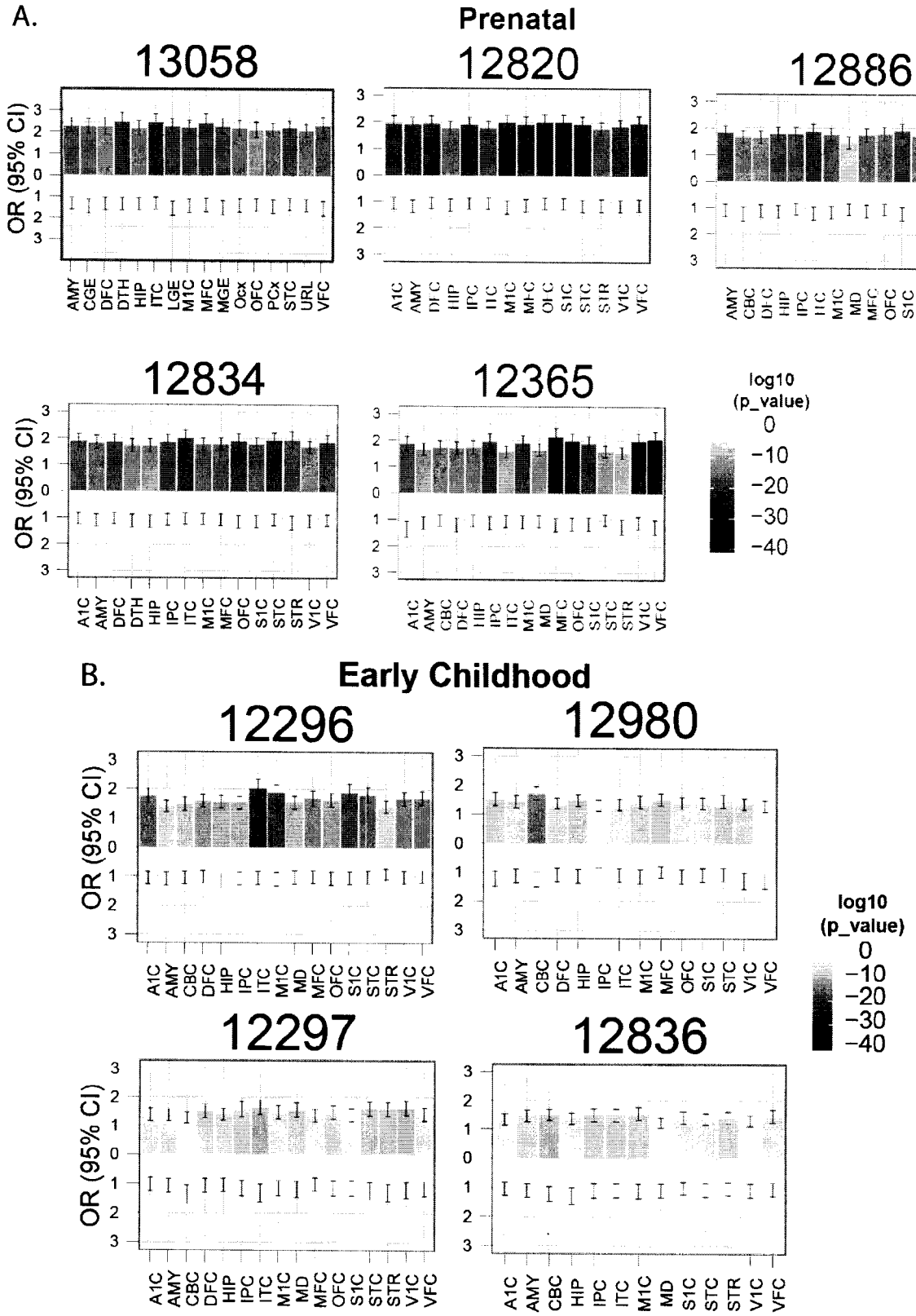

A.
Prenatal
13058
12820
12886
12834
12365
OR (95% CI)
log10 (p_value)
0
−10
−20
−30
−40
AMY CGE DFC DTH HIP ITC LGE M1C MFC MGE Ocx OFC PCx STC URL VFC
A1C AMY DFC HIP IPC ITC M1C MFC OFC S1C STC STR V1C VFC
AMY CBC DFC HIP IPC ITC M1C MD MFC OFC S1C STC STR V1C VFC
A1C AMY DFC DTH HIP IPC ITC M1C MFC OFC S1C STC STR V1C VFC
A1C AMY CBC DFC HIP IPC ITC M1C MD MFC OFC S1C STC STR V1C VFC
B.
Early Childhood
12296
12980
12297
12836
A1C AMY CBC DFC HIP IPC ITC M1C MD MFC OFC S1C STC STR V1C VFC
A1C AMY CBC DFC HIP IPC ITC M1C MFC OFC S1C STC V1C VFC
A1C AMY CBC DFC HIP IPC ITC M1C MD MFC OFC S1C STC STR V1C VFC
A1C AMY CBC HIP IPC ITC M1C MD S1C STC STR V1C VFC

Figure 10

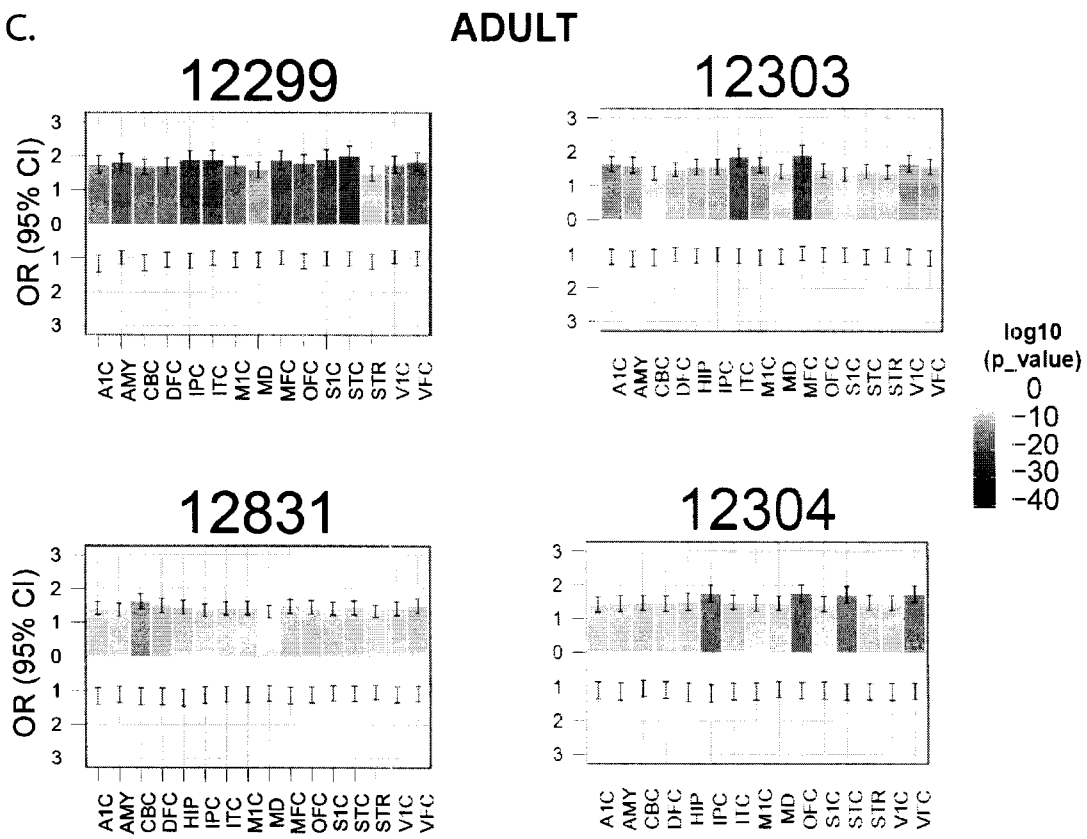


Figure 10 cont'd

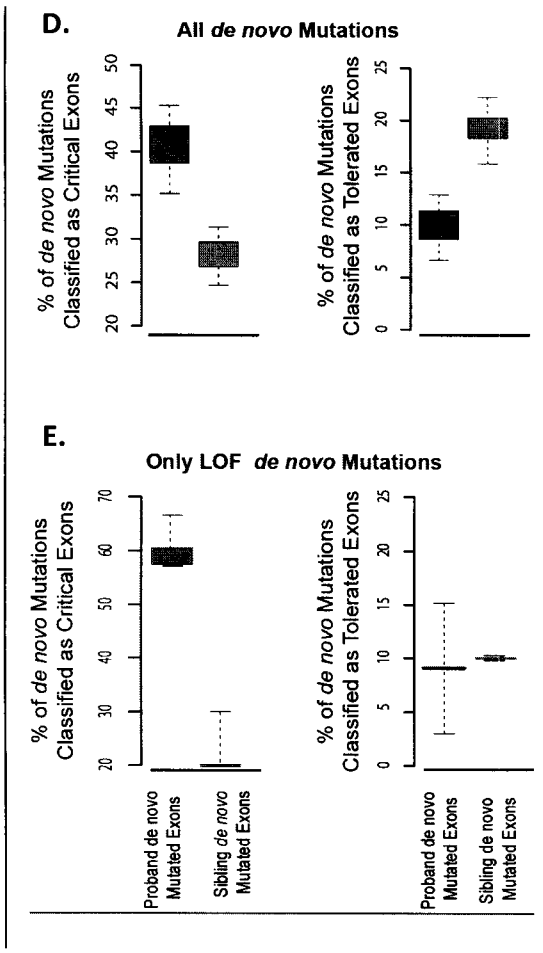


Figure 10 cont'd

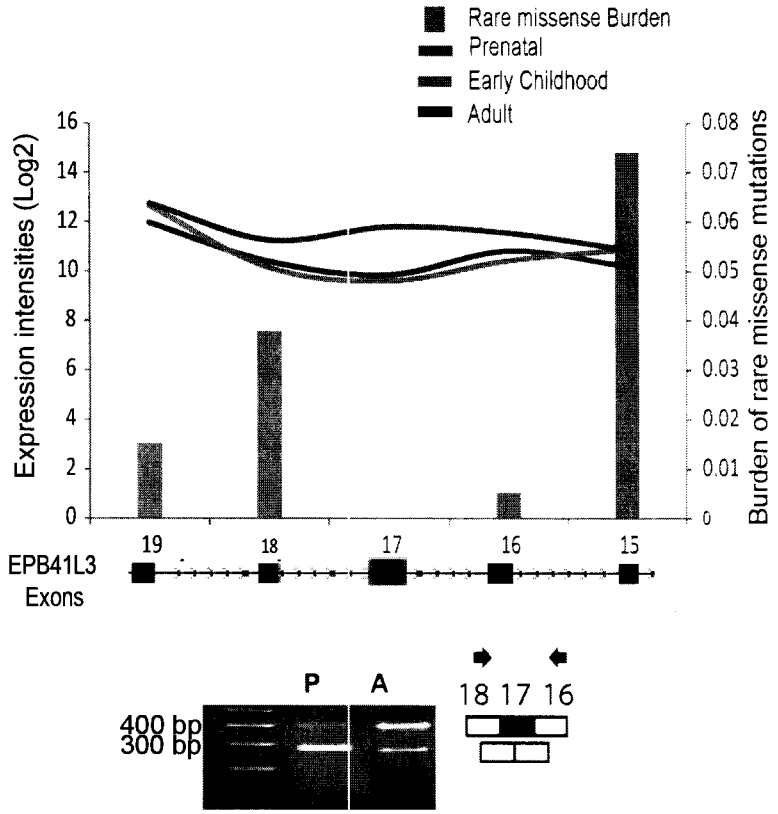

Rare missense Burden
Prenatal
Early Childhood
Adult
Expression intensities (Log2)
Burden of rare missense mutations
EPB41L3
Exons
19
18
17
16
15
P
A
18 17 16
400 bp
300 bp

Figure 11

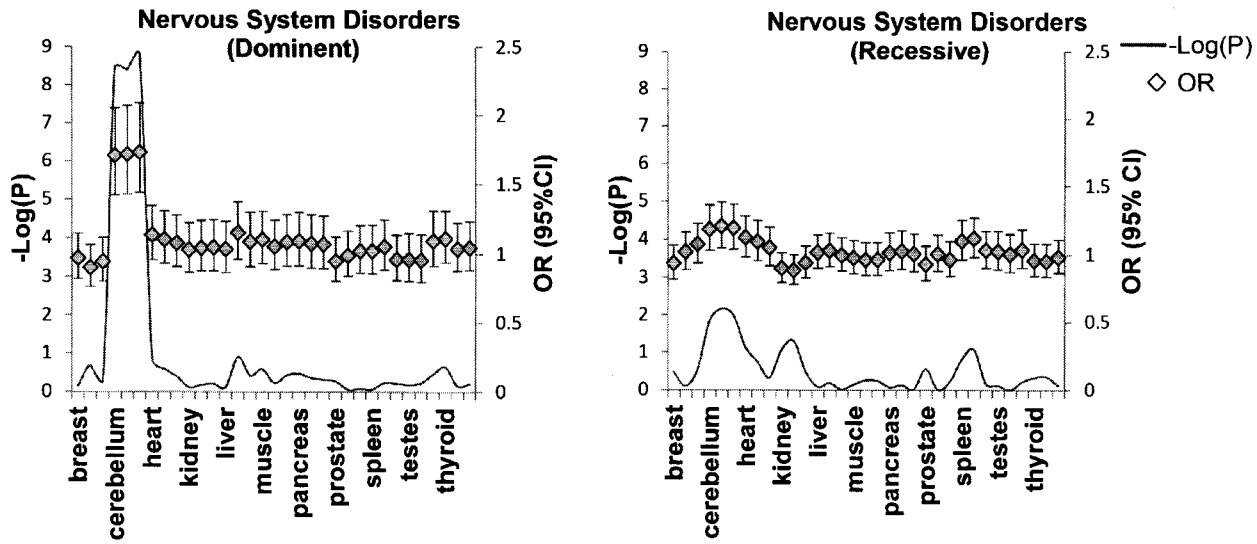

Nervous System Disorders
(Dominent)
-Log(P)
OR (95%CI)
breast
cerebellum
heart
kidney
liver
muscle
pancreas
prostate
spleen
testes
thyroid
Nervous System Disorders
(Recessive)
-Log(P)
OR
OR (95% CI)

Figure 12

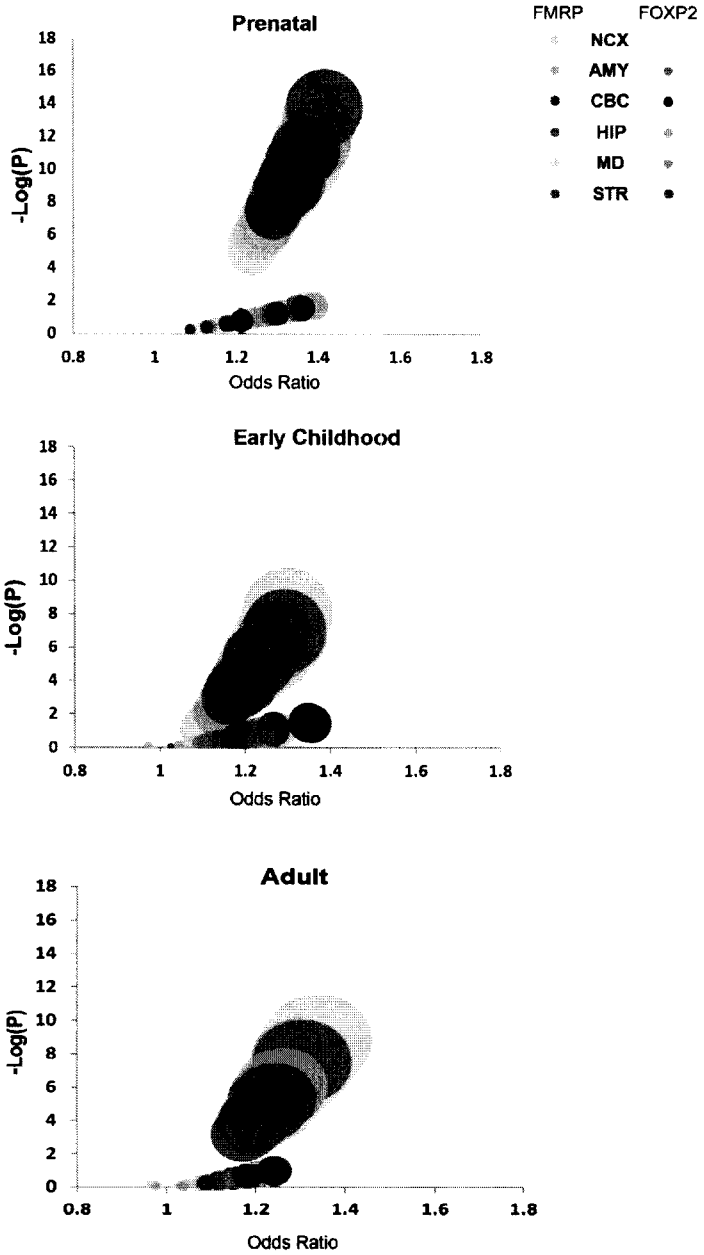

Prenatal
Early Childhood
Adult
-Log(P)
Odds Ratio
FMRP
FOXP2
NCX
AMY
CBC
HIP
MD
STR

Figure 13

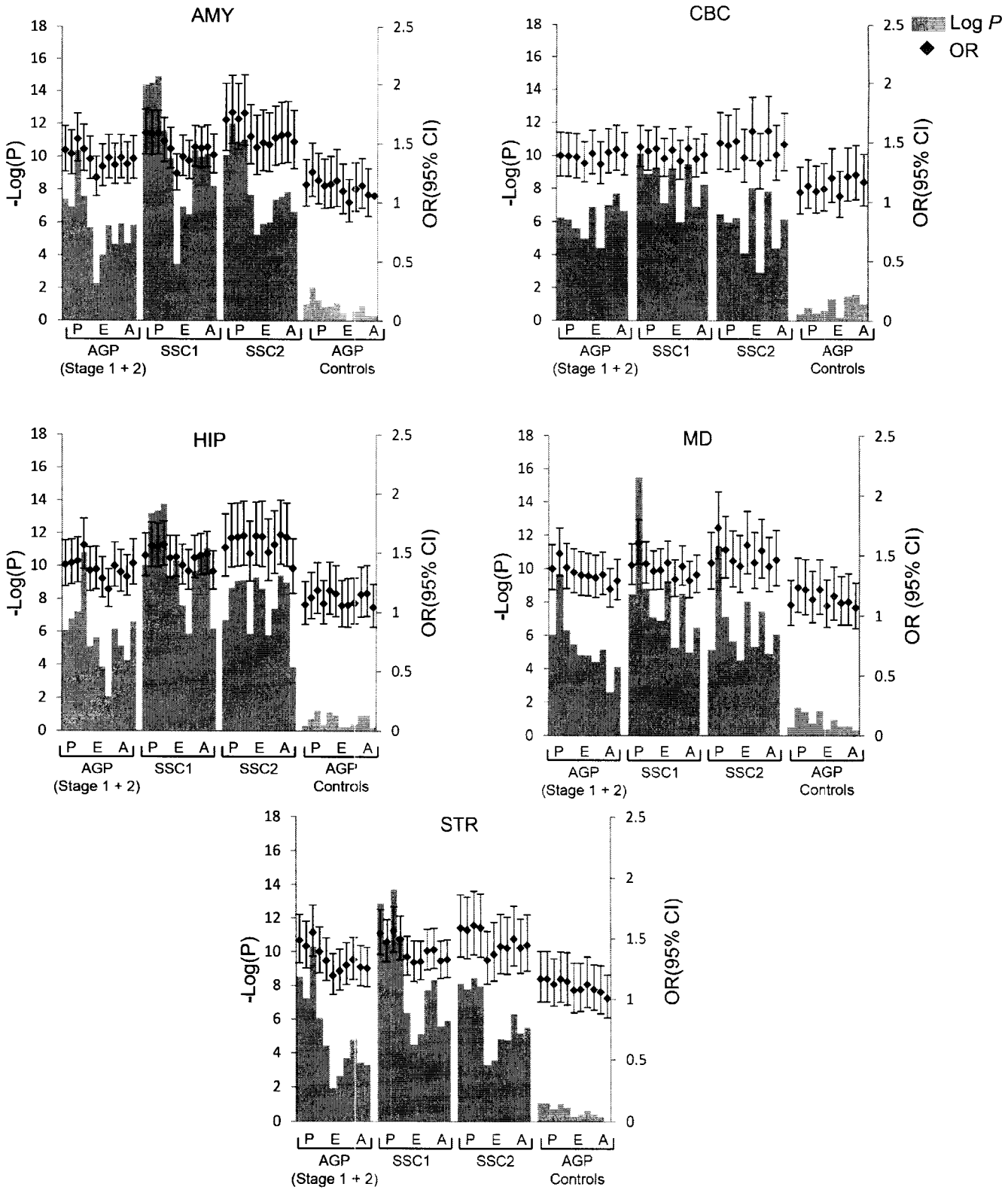

AMY
CBC
HIP
MD
STR
Log P
OR
-Log(P)
OR(95% CI)
OR (95% CI)
P E A
AGP (Stage 1 + 2)
SSC1
SSC2
AGP Controls

Figure 14

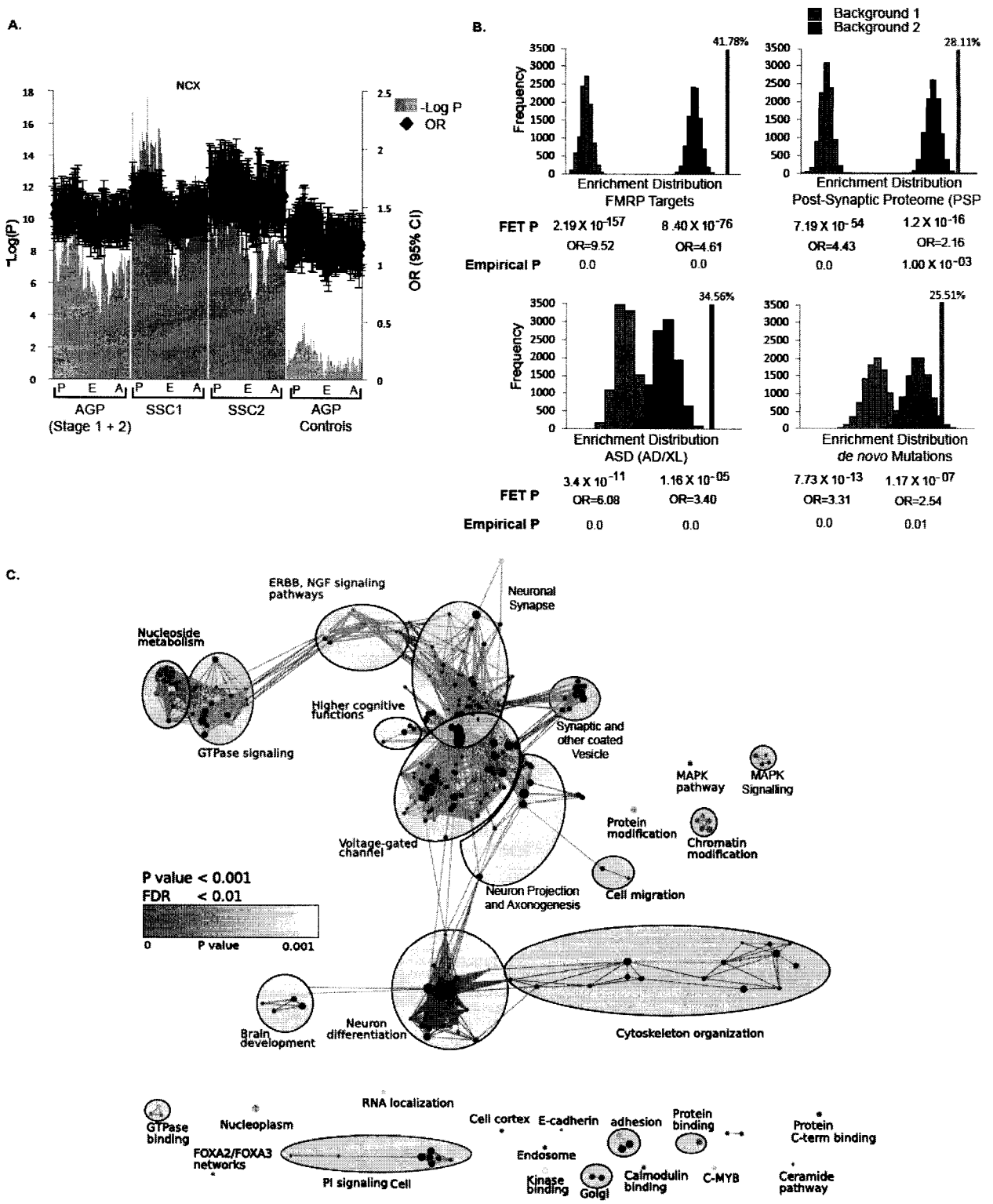

A.
NCX
-Log P
OR
-Log(P)
OR (95% CI)
P E A
AGP (Stage 1 + 2)
SSC1
SSC2
AGP Controls
B.
Background 1
Background 2
Frequency
41.78%
Enrichment Distribution FMRP Targets
28.11%
Enrichment Distribution Post-Synaptic Proteome (PSP
FET P
2.19 X 10-157
OR=9.52
8.40 X 10-76
OR=4.61
7.19 X 10-54
OR=4.43
1.2 X 10-16
OR=2.16
Empirical P
0.0
0.0
0.0
1.00 X 10-03
34.56%
Enrichment Distribution ASD (AD/XL)
25.51%
Enrichment Distribution de novo Mutations
3.4 X 10-11
OR=6.08
1.16 X 10-05
OR=3.40
7.73 X 10-13
OR=3.31
1.17 X 10-07
OR=2.54
0.0
0.0
0.0
0.01
C.
ERBB, NGF signaling pathways
Neuronal Synapse
Nucleoside metabolism
Higher cognitive functions
GTPase signaling
Synaptic and other coated Vesicle
MAPK pathway
MAPK Signalling
Protein modification
Chromatin modification
Voltage-gated channel
Cell migration
Neuron Projection and Axonogenesis
P value < 0.001
FDR < 0.01
0
P value
0.001
Brain development
Neuron differentiation
Cytoskeleton organization
RNA localization
GTPase binding
Nucleoplasm
Cell cortex
E-cadherin
adhesion
Protein binding
Protein C-term binding
FOXA2/FOXA3 networks
PI signaling
Cell
Endosome
Kinase binding
Golgi
Calmodulin binding
C-MYB
Ceramide pathway

Figure 15

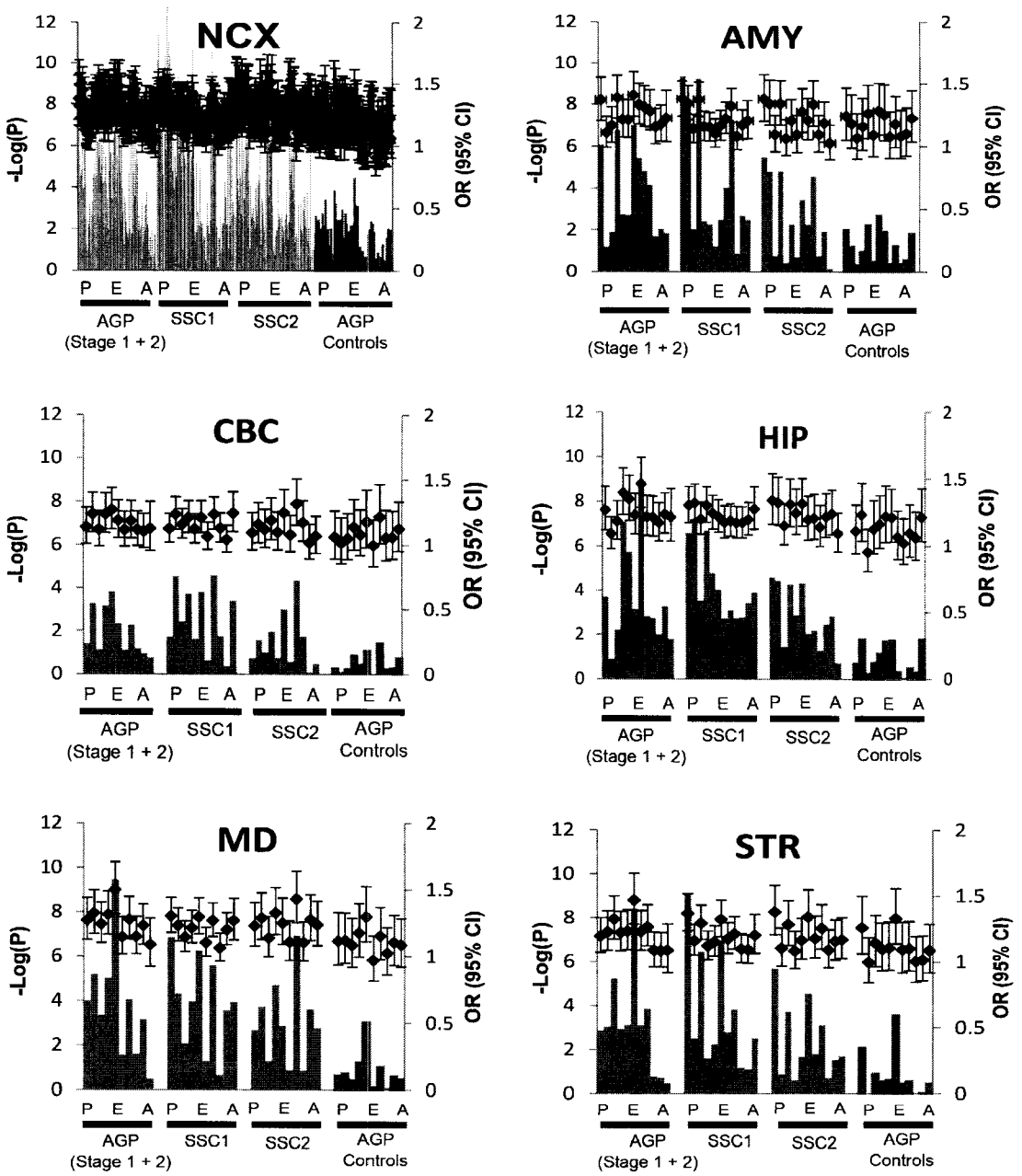

NCX
AMY
CBC
HIP
MD
STR
-Log(P)
OR (95% CI)
P E A P E A P E A P E A
AGP (Stage 1 + 2)
SSC1
SSC2
AGP Controls

Figure 16

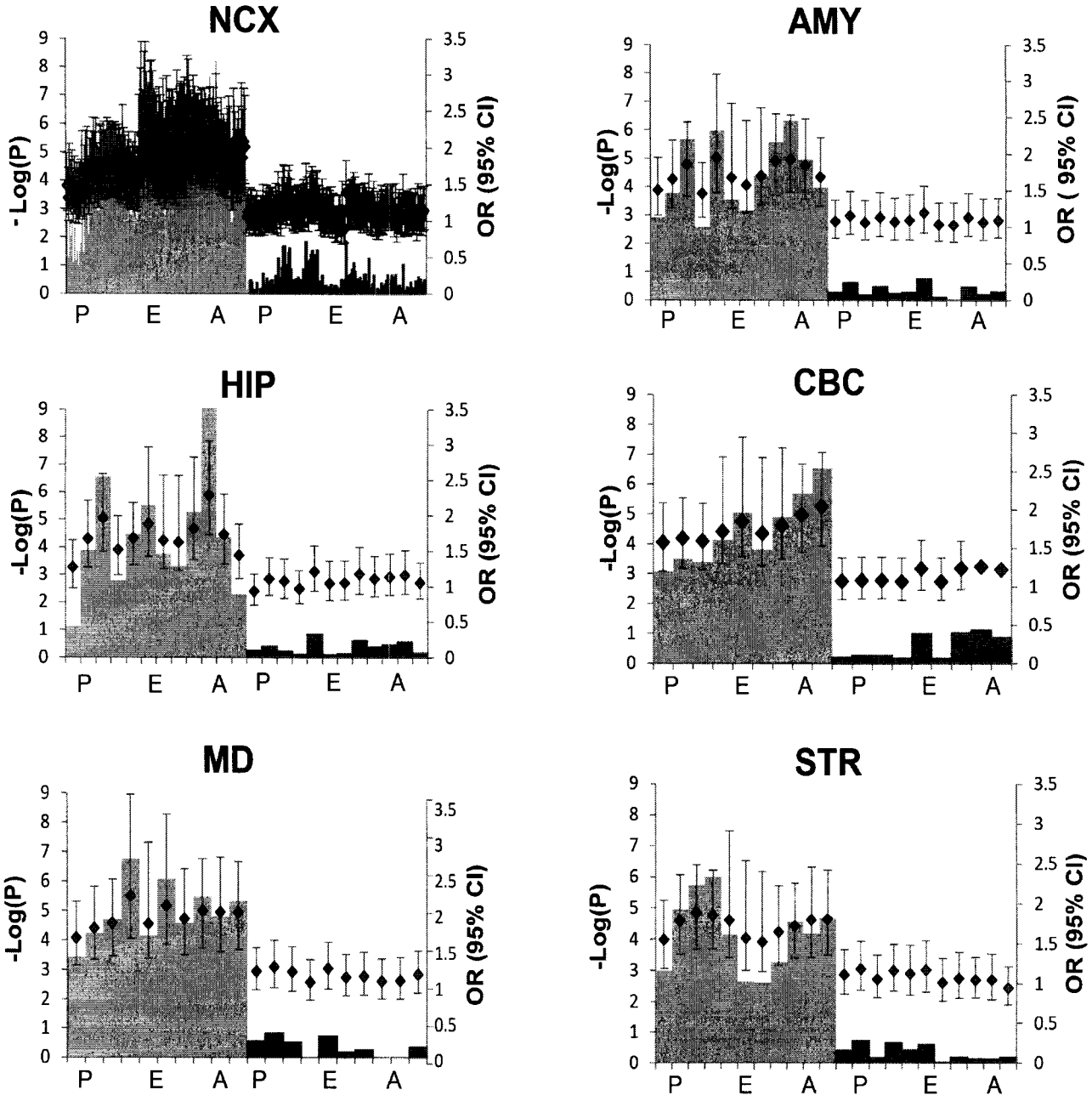


Figure 17

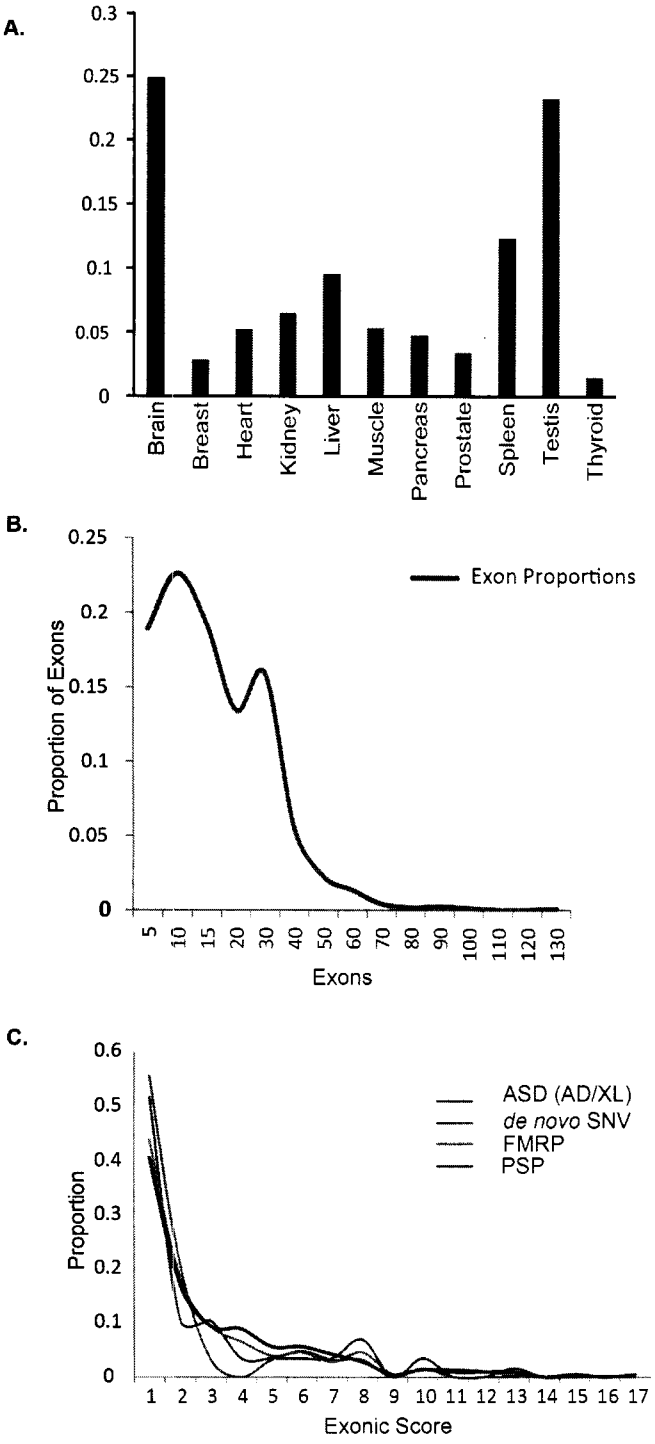

A.
0.3
0.25
0.2
0.15
0.1
0.05
0
Brain
Breast
Heart
Kidney
Liver
Muscle
Pancreas
Prostate
Spleen
Testis
Thyroid
B.
0.25
0.2
0.15
0.1
0.05
0
Proportion of Exons
Exon Proportions
5
10
15
20
30
40
50
60
70
80
90
100
110
120
130
Exons
C.
0.6
0.5
0.4
0.3
0.2
0.1
0
Proportion
ASD (AD/XL)
de novo SNV
FMRP
PSP
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17
Exonic Score

Figure 18

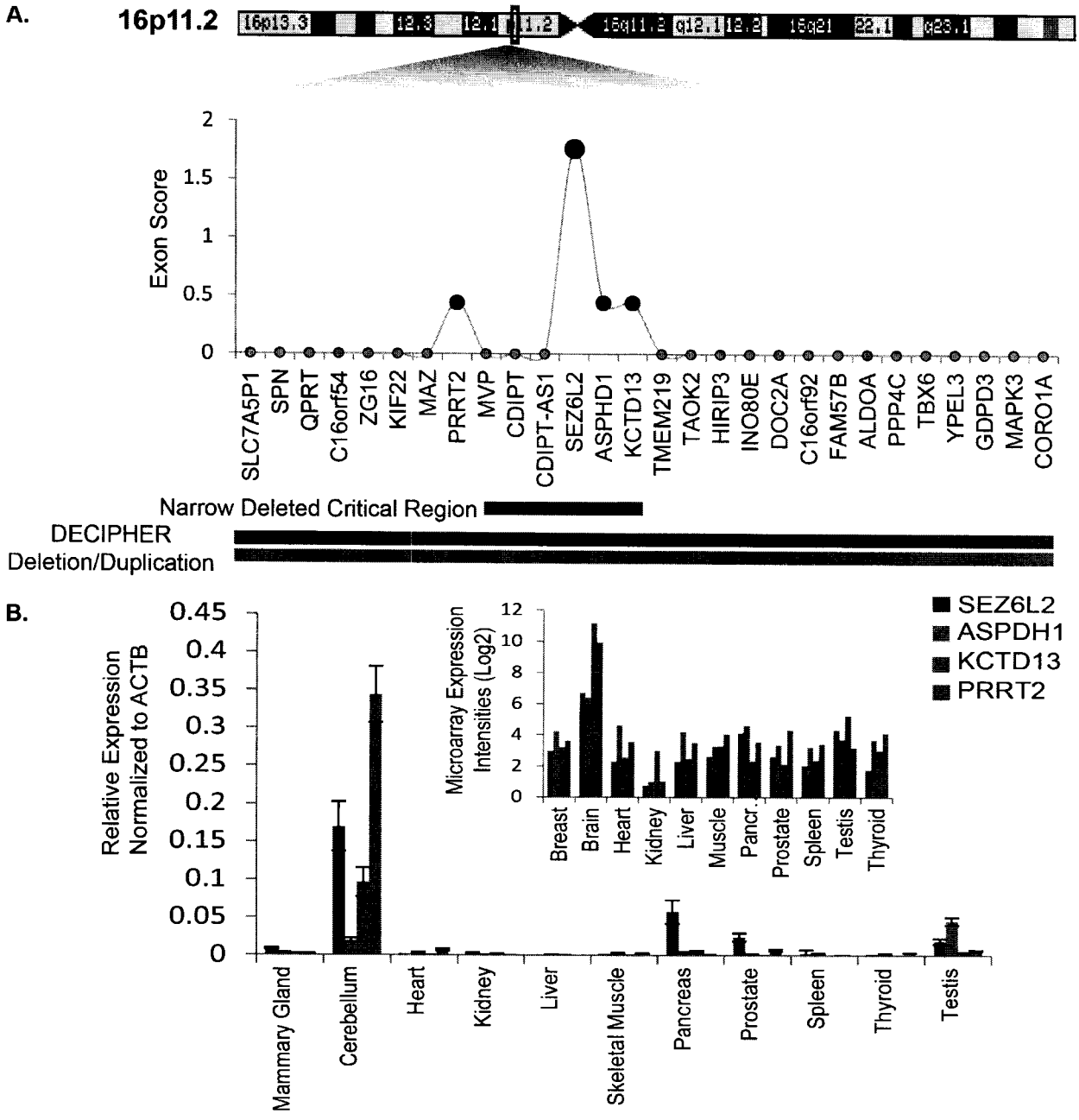

A.
16p11.2
Exon Score
SLC7A5P1
SPN
QPRT
C16orf54
ZG16
KIF22
MAZ
PRRT2
MVP
CDIPT
CDIPT-AS1
SEZ6L2
ASPHD1
KCTD13
TMEM219
TAOK2
HIRIP3
INO80E
DOC2A
C16orf92
FAM57B
ALDOA
PPP4C
TBX6
YPEL3
GDPD3
MAPK3
CORO1A
Narrow Deleted Critical Region
DECIPHER
Deletion/Duplication
B.
Relative Expression
Normalized to ACTB
Microarray Expression
Intensities (Log2)
SEZ6L2
ASPDH1
KCTD13
PRRT2
Breast
Brain
Heart
Kidney
Liver
Muscle
Pancr.
Prostate
Spleen
Testis
Thyroid
Mammary Gland
Cerebellum
Heart
Kidney
Liver
Skeletal Muscle
Pancreas
Prostate
Spleen
Thyroid
Testis

Figure 19

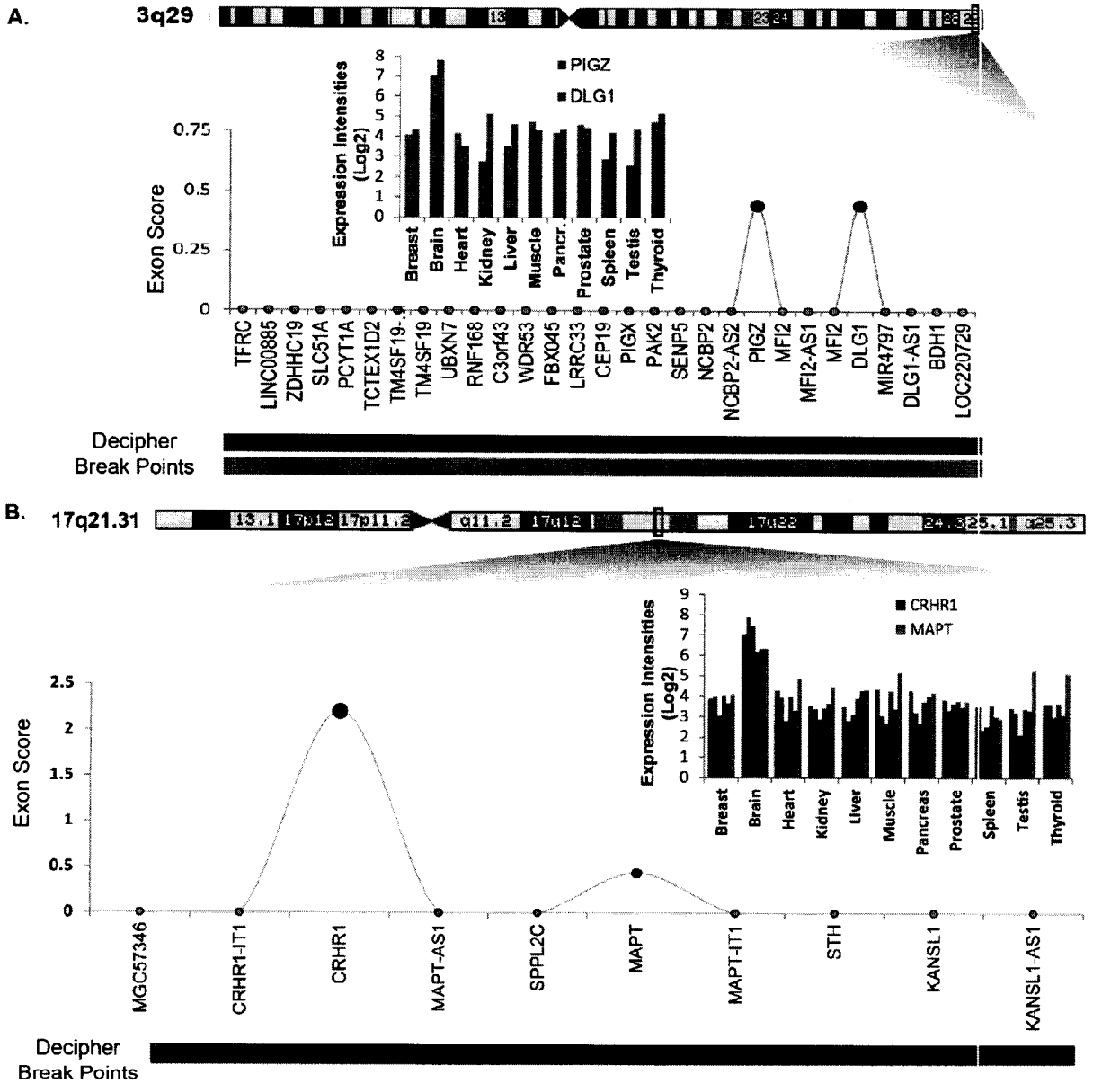

A.
3q29
Expression Intensities (Log2)
PIGZ
DLG1
Exon Score
Breast
Brain
Heart
Kidney
Liver
Muscle
Pancr.
Prostate
Spleen
Testis
Thyroid
TFRC
LINC00885
ZDHHC19
SLC51A
PCYT1A
TCTEX1D2
TM4SF19
UBXN7
RNF168
C3orf43
WDR53
FBXO45
LRRC33
CEP19
PIGX
PAK2
SENP5
NCBP2
NCBP2-AS2
PIGZ
MFI2
MFI2-AS1
MFI2
DLG1
MIR4797
DLG1-AS1
BDH1
LOC220729
Decipher
Break Points
B.
17q21.31
CRHR1
MAPT
Exon Score
MGC57346
CRHR1-IT1
CRHR1
MAPT-AS1
SPPL2C
MAPT
MAPT-IT1
STH
KANSL1
KANSL1-AS1
Decipher
Break Points

Figure 20

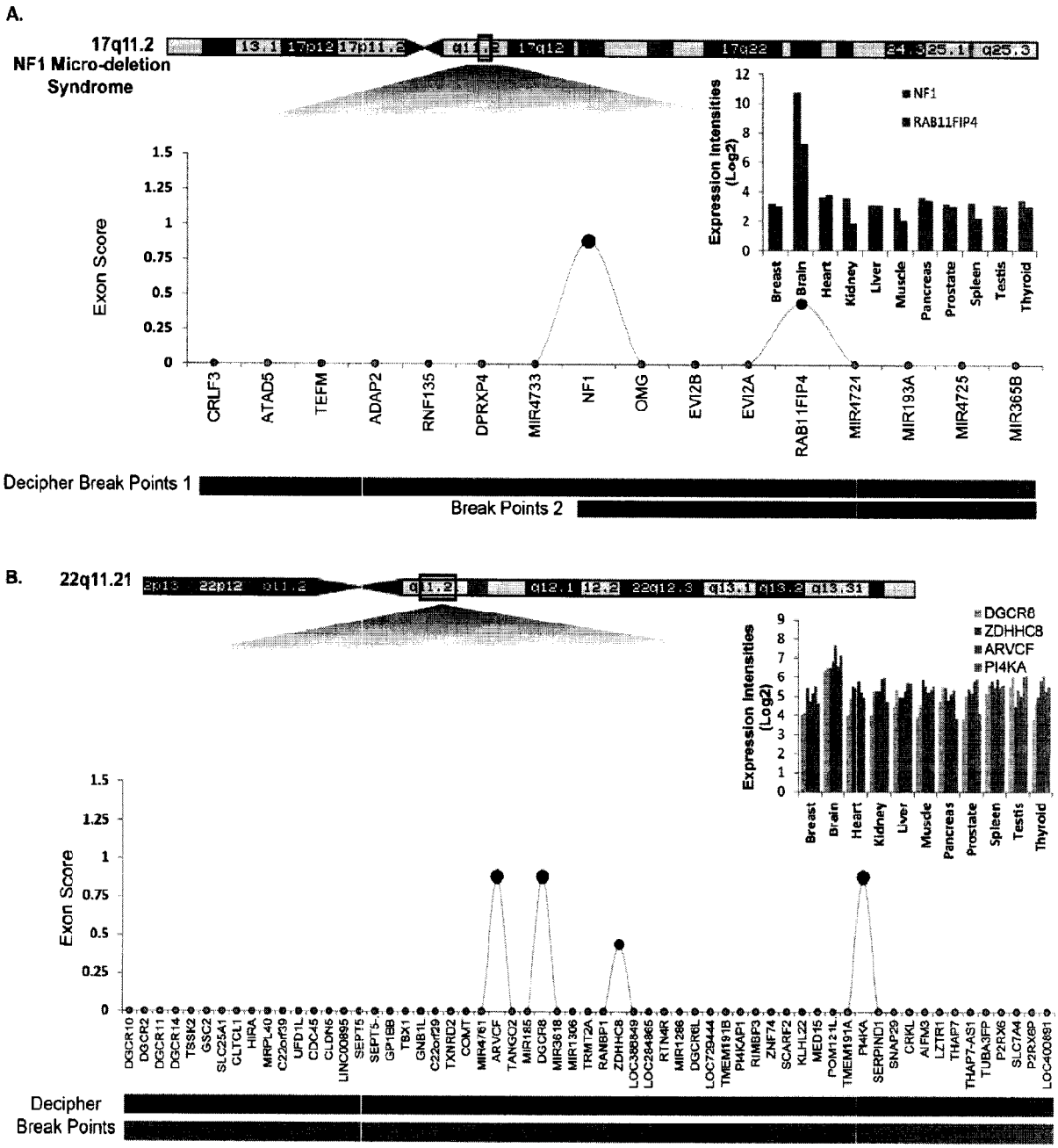

A.
17q11.2
NF1 Micro-deletion Syndrome
Exon Score
Expression Intensities (Log2)
NF1
RAB11FIP4
Breast
Brain
Heart
Kidney
Liver
Muscle
Pancreas
Prostate
Spleen
Testis
Thyroid
CRLF3
ATAD5
TEFM
ADAP2
RNF135
DPRXP4
MIR4733
NF1
OMG
EVI2B
EVI2A
RAB11FIP4
MIR4724
MIR193A
MIR4725
MIR365B
Decipher Break Points 1
Break Points 2
B.
22q11.21
DGCR6
ZDHHC8
ARVCF
PI4KA
Exon Score
Expression Intensities (Log2)
Decipher Break Points

Figure 21

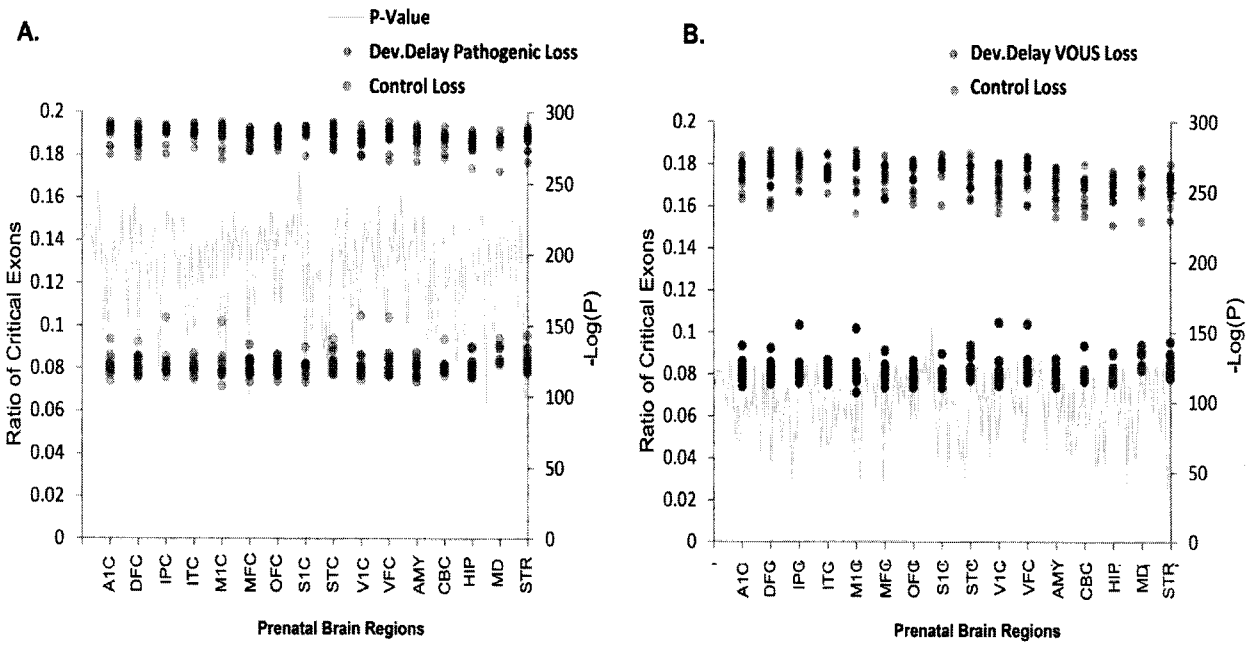

A.
P-Value
Dev.Delay Pathogenic Loss
Control Loss
Ratio of Critical Exons
-Log(P)
A1C DFC IPC ITC M1C MFC OFC S1C STC V1C VFC AMY CBC HIP MD STR
Prenatal Brain Regions
B.
Dev.Delay VOUS Loss
Control Loss
Ratio of Critical Exons
-Log(P)
A1C DFG IPG ITG M1G MFG OFG S1G STG V1C VFC AMY CBC HIP MD STR
Prenatal Brain Regions

Figure 22

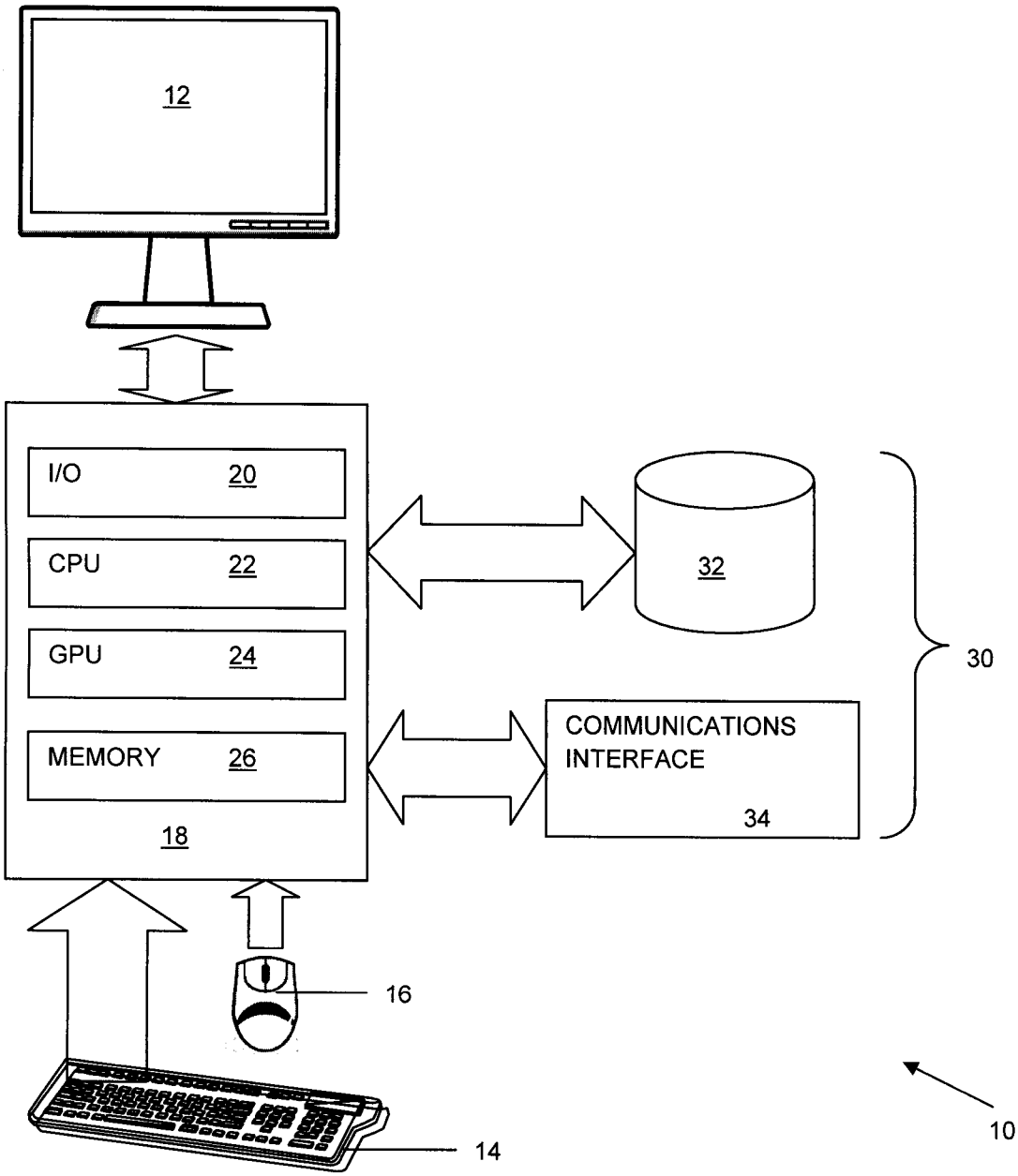
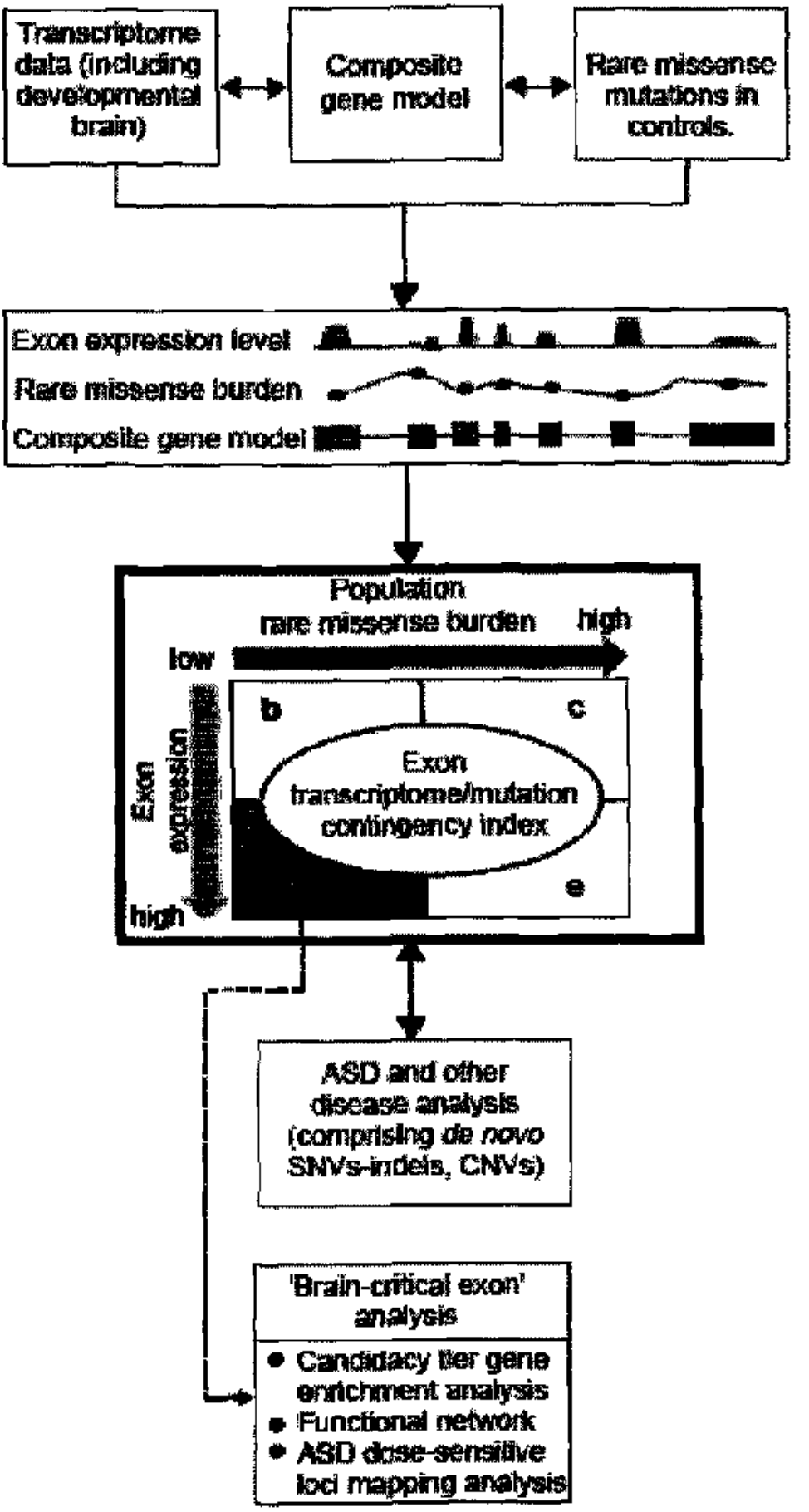

12
I/O 20
CPU 22
GPU 24
MEMORY 26
18
32
COMMUNICATIONS INTERFACE
34
30
16
14
10

Figure 23


Transcriptome data (including developmental brain)
Composite gene model
Rare missense mutations in controls.
Exon expression level
Rare missense burden
Composite gene model
Population
rare missense burden
high
low
Exon expression
high
b
c
Exon transcriptome/mutation contingency index
e
ASD and other disease analysis (comprising de novo SNVs-indels, CNVs)
'Brain-critical exon' analysis
Candidacy tier gene enrichment analysis
Functional network
ASD dose-sensitive loci mapping analysis