Supplementary Online Content

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This supplementary material has been provided by the authors to give readers additional information about their work.

eMethods. Materials and Methods

Demographic and Clinical Characteristics of Participants

Participants were recruited from multi-center, randomized and open-labelled clinical trial. Briefly, all participants were taken into account to be included in the study if they met the following criteria: 1) aged from 18 to 45 years old; 2) Han Chinese descent; 3) fulfilled the DSM-IV diagnosis criteria for schizophrenia; 4) physically healthy with all laboratory tests (for example, measurement of blood pressure, ECG, liver and renal function within normal range); 5) total scores of PANSS more than 60, and at least three positive items scored more than 4. Patients with schizophrenia were excluded if 1) they were diagnosed with mental retardation or other cognitive disorders; 2) had a history of serious adverse reactions to the proposed treatments; 3) had a history of treatment resistance defined by the persistence of severe symptoms despite adequate trials of one of the proposed treatments or prior treatment with clozapine; 4) were pregnant or breast-feeding; 5) or had a serious and unstable medical condition. According to the study protocol, the first 2 weeks of treatment were spent on titration of drugs and the later 4 weeks were the maintenance period. Subjects were excluded if they experienced severe adverse effects anytime during these 6 weeks period. About 300 patients failed to complete 6 weeks' treatment due to severe side effects or significant worsening of symptoms. After quality controls, the study cohort consists of 3,023 subjects.

Whole Exome Sequencing (WES)

After matching for age, sex and antipsychotic treatment, a total of 337 subjects were selected for whole exome sequencing. Genomic DNA was purified from peripheral blood leucocytes. DNA

samples were prepared according to the Illumina Paired-End Sample Preparation Guide (http://supportres.illumina.com/documents/myillumina/e5af4eb5-6742-40c8-bcb1-d8b350bcb964/paired-end_sampleprep_guide_1005063_e.pdf). Targeted enrichment was performed with Agilent's SureSelect Human All Exon v.4 (Santa Clara, California, USA). Exon-enriched DNA libraries were sequenced on an Illumina HiSeq2000 at Axeq Technologies (http://www.axeq.com/), which produced 101bp paired-end reads. We used the standard pipeline that made use of the following tools: Burrow-Wheeler Alignment (BWA) [3] for aligning sequence reads to human genome reference sequence (UCSC hg19 as reference); Samtools [4] for sorting and indexing the aligned files; Picard (http://picard.sourceforge.net/) for sequence duplicate identification and removal; Genome Analysis Toolkit (GATK) [5] v2.7 for local realignment around small insertions and deletions, recalibration of base quality and variant calling by Unified Genotyper. KGGSeq (Li et al., 2013) was used to annotate variants (using RefGene hg19 as reference). It also predicted potentially deleterious non-synonymous variants using a logit model combining prediction scores from multiple functional prediction algorithms (such as SIFT, PolyPhen2, LRT, MutationTaster, MutationAssessor and FATHMM) as well as various conservation scores (PhyloP, GERP and SiPhy). KGGSeq yielded two flags on deleterious prediction: disease-causative and nondisease-causative. Variants that are predicted to be disease-causative by KGGSeq are referred to "damaging".

Genotyping was also performed in all 337 samples by using Infinium OmniZhongHua-8, which is Chinese-specific whole genome array from Illumina. It provides coverage of 77% of common variation (minor allele frequency (MAF) > 5%), 73% of intermediate variation (MAF > 2.5%), and 65% of rare variation (MAF > 1%) in the Chinese population at r2 ≥ 0.8. The SNP content are

optimized from all 3 HapMap phases and the 1kG. In addition, OmniZhongHua-8 allows profiling of > 875,000 markers per sample, delivering exceptionally high data quality for call rates (average > 99%), reproducibility (> 99.9%), and low sample repeat rates. The concordance rates of the sequence and GWAS genotypes were checked for evaluating the accuracy of variant calling. The concordance rate is over 99% for all samples.

Quality Control (QC) for WES

QC at the Read level:

Raw sequencing reads (FASTQ files) were subject to quality control by the FASTQC tool (http://www.bioinformatics.babraham.ac.uk/projects/fastqc/). Each base sequence quality, sequence duplication levels, GC bias and primer sequencing reads were evaluated.

QC at the genotype/variant level:

A series of filterings was applied to generate high-quality variants for subsequent analyses. Firstly, the GATK Variant Quality Score Recalibration (VQSR) approach was used to filter variants across all samples, variants with VQSLOD score (assigned by VQSR) <= 99.0 were removed. We excluded genotypes with genotyping quality score < 20, read depth < 8X or second most possible genotype with Phred < 30. Finally, variants with missing data in > 10% of samples, failing Hardy-Weinberg Equilibrium test (P < 0.00001) or becoming monomorphic due to removal of genotype by QC were removed from the downstream analysis.

QC at sample level:

We removed contaminated samples detected by VerifyBamID [6] . PLINK[7] was used to identify related individuals by evaluating their identity-by-state (IBD), pairs showing relatedness closer than first-cousin (IBD > 0.125) were identified. For each pair of related individuals, we discarded

the individual with lower genotype call rate. Samples with mismatched gender information were removed from the analysis. To ensure a homogenous study population, EIGENSOFT [8] was used to detect population stratification based on the principal component analysis of common variants (MAF > 5%).

Common variant association testing

A single variant test for association with treatment response was performed by logistic regression with age, sex, antipsychotic types and the first two principal components as covariates. We excluded variants with MAF < 5% and genotyping rate < 95%. The analyses were repeated for non-synonymous variants and damaging non-synonymous variants. Nominal p-value < 5×10^{-8} was used as the genome-wide significance threshold. Analyses were conducted in PLINK[7].

Targeted Sequencing

In the follow-up study, a total of 78 genes were sequenced in 1,999 subjects of the remaining cohort using targeted sequencing (Table S12). It consists of 34 genes involved in the top three gene sets (*reduced NMDA-mediated synaptic currents*, *reduced AMPA-mediated synaptic currents and Abnormal AMPA-mediated synaptic currents*), 3 candidate genes (*GRIN, GRM7* and *ZNF804A*) and additional 41 genes selected by investigator's interest based on the literature and other schizophrenia/pharmacogenetic candidates.

A two-step PCR reaction were used to construct the sequence library. Firstly, the target region sequences (i.e. the exons plus 2 bp of flanking regions) were conducted in a 15 μL reaction volume, consisting of 100 ng of genomic DNA template, 10ul primer pool mix, 5ul clean water and 2 X M_Enzyme MIX. PCRs were conducted as follows: 95°C for 3 min, 17 cycles of 98°C for 15sec and 60 °C for 4 min, followed by 10°C for 10 min. Next, the PCR products were

purificated by (0.4+0.6) X AMPure XP Beads. After that, the amplification was done using PCRs as following settings：95°C for 30 sec, 6 cycles of 98°C for 15 sec, 55 °C for 20 sec and 72 °C for 30s, followed by 72°C for 5 mi. Finally, the target library was obtained by 0.7 X AMPure XP Beads purification. The library was built using Hiseq3000/4000 PE Cluster Kit and HiSeq 3000/4000SBS Kit following the standard protocols of Illumina system. The DNA libraries were sequenced on Illumina HiSeq4000.

We used the standard pipeline that made use of the following tools: Burrow-Wheeler Alignment (BWA) [3] for aligning sequence reads to human genome reference sequence (UCSC hg19 as reference); Samtools[4] for sorting and indexing the aligned files; Picard (http://picard.sourceforge.net/) for sequence duplicate identification and removal; Genome Analysis Toolkit (GATK) [5] v3.5 for local realignment around small insertions and deletions, recalibration of base quality and variant calling by HaplotypeCaller. KGGSeq (Li et al., 2013) was used to annotate variants (using RefGene hg19 as reference) and predict deleteriousness of non-synonymous variants. We excluded genotypes with genotyping quality score < 20, read depth < 60X or second most possible genotype with Phred < 30. Finally, variants with missing data in > 10% of samples, failing Hardy-Weinberg Equilibrium test (P < 0.00001) or becoming monomorphic due to removal of genotype by QC were removed from the downstream analysis.

70 of 78 genes were successfully sequenced. After performing quality controls, 23 individuals with < 90% genotype rate and 34 subjects with high IBD/IBS (phi-hat>0.9) were removed; 22 subjects were regarded as outliers and removed from the analysis (outlier defined as 3 SD outside the mean total PANSS reduction rate). The final dataset contains 5,009 SNVs of 1,920 subjects.

Statistical analyses of gene-based and set-based tests were performed using RVTEST. Response (i.e. total PANSS reduction rate) was treated as quantitative trait in the CMC burden test, with sex, age, and antipsychotic type [typical/atypical] as covariates.

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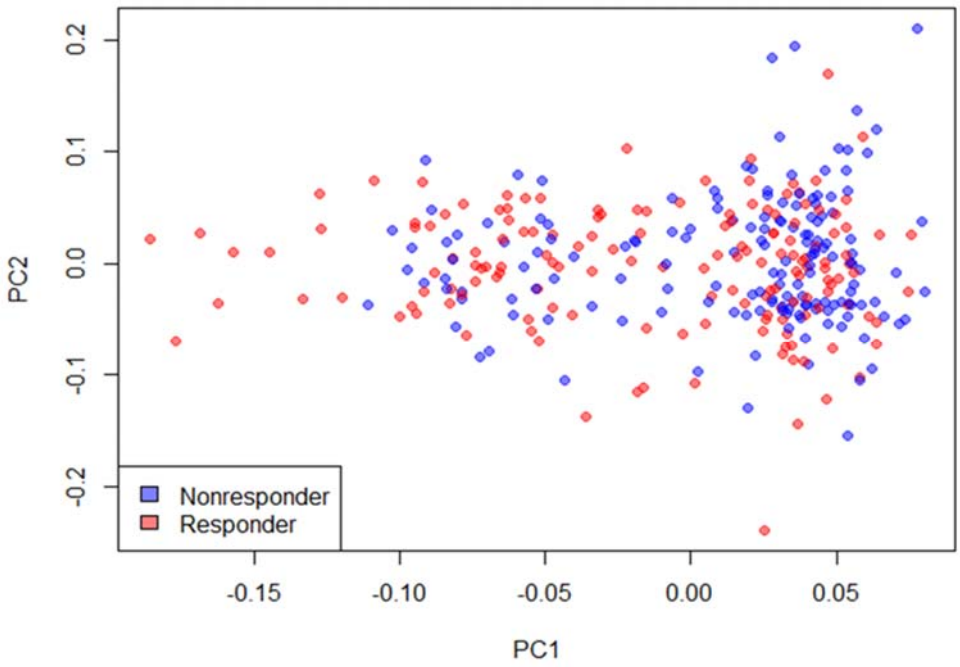
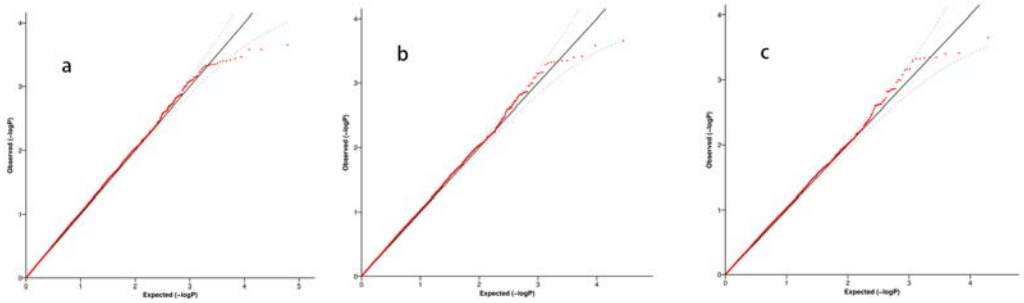


eFigure 1 The first two principal components of worst-responders (n=160) and best-responders (n=156) from PCA analysis result.



eFigure 2 Quantile-Quantile plot of genome-wide P values of single-variant (SNPs with MAF > 0.05) associations Note: We assessed association using logistic regression analysis with adjustment for age, sex, antipsychotic class, and the first two principal components. We display separate Q-Q plot for a) all exonic variants, b) non-synonymous variants, and c) damaging non-synonymous variants. 95% confidence intervals for the null hypothesis of no association are shown in dotted grey line. Genomic control lambda values are: All exonic variants $\lambda_{GC} = 1.03$; Non-synonymous variants only $\lambda_{GC} = 1.03$; Damaging non-synonymous variants only $\lambda_{GC} = 1.04$. a, All exonic variants; b, Non-synonymous variants only; c, Damaging-synonymous variants only.

eTable 1. Use of antipsychotics in the present study

	Drugs	N. of Individuals	Gender F:M	Age (years)	First-onset Ratio	Educational attainment (Months)
	Risperidone	514	291:223	30.29(10.6)	30.35%	9.83(3.21)
	Olanzapine	509	259:250	30.66(7.99)	29.08%	10.70(3.31)
	Quetiapine	496	247:249	31.10(7.81)	28.02%	10.27(3.26)
	Aripiprazole	502	247:255	31.40(7.89)	27.69%	10.47(3.20)
	Ziprasidone	506	253:253	30.69(8.08)	29.64%	10.44(3.53)
	Haloperidol	242	127:115	32.31(7.96)	30.58%	10.13(3.20)
	Perphenazine	254	125:129	31.82(8.03)	27.17%	9.89(2.93)
	Total	3023	1549:1474	31.20(7.96)	28.94%	10.41(3.29)
F/ χ^2			8.093	1.87	1.9126	1.40
p			0.231	0.0816	0.928	0.158

eTable 2. List of 175 pharmacogenetics associated genes selected as candidates

Candidate reviewed by Changasi								
CYP2D6	*CYP2C19*	*CYP1A2*	*CYP2C9*	*CYP3A4*	*CYP3A5*	*DRD2*	*DRD3*	*DRD4*
DRD1	*HTR2A*	*HTR7*	*ZNF804A*	*BDNF*	*ABCB1*	*NRXN1*	*HOMER-1*	
DrugBank candidate								
GABRP	*GABRD*	*ADRB2*	*CHRM2*	*CHRM4*	*ADRB1*	*HTR1A*	*CHRM5*	*ADRA2A*
CHRM1	*ADRB3*	*DRD2*	*GABRA1*	*GABRB1*	*GABRG2*	*ADRA2C*	*CHRM3*	*DRD1*
DRD4	*DRD5*	*HRH2*	*ADRA1D*	*HTR1D*	*HTR1B*	*HTR2A*	*HTR2C*	*GABRB3*
HTR1E	*GABRA5*	*GABRA3*	*HTR7*	*ADRA1A*	*HRH1*	*ADRA1B*	*DRD3*	*HTR2B*
HTR3A	*GABRA2*	*GABRB2*	*HTR5A*	*GABRA4*	*HTR6*	*CALM1*	*GABRE*	*GRIN2B*
GABRA6	*GABRG1*	*GABRG3*	*HRH4*	*GABRQ*	*ADRA2B*	*ABCB1*	*UGT1A9*	*CYP1A1*
CYP1A2	*CYP3A4*	*CYP2C8*	*CYP2D6*	*CYP2C9*	*CBR1*	*CYP2B6*	*CYP3A5*	*CYP3A7*
FMO3	*CYP2C18*	*CYP2C19*						
Cholinergic Receptor Genes								
CHRNA1	*CHRNA10*	*CHRNA2*	*CHRNA3*	*CHRNA4*	*CHRNA5*	*CHRNA6*	*CHRNA7*	*CHRNA9*
CHRNB1	*CHRNB2*	*CHRNB3*	*CHRNB4*	*CHRND*	*CHRNE*	*CHRNG*		
Dopamine Receptor Genes								
DRD1	*DRD2*	*DRD3*	*DRD4*	*DRD5*				
GABA Receptor Genes								
GABBR1	*GABBR2*	*GABRA1*	*GABRA2*	*GABRA3*	*GABRA4*	*GABRA5*	*GABRA6*	*GABRB1*
GABRB2	*GABRB3*	*GABRD*	*GABRE*	*GABRG1*	*GABRG2*	*GABRG3*	*GABRP*	*GABRQ*
GABRR1	*GABRR2*							
Glycine Receptor Genes								
GCOM1	*GLRA1*	*GLRA2*	*GLRA3*	*GLRB*	*GRIA1*	*GRIA2*	*GRIA3*	*GRIA4*

eTable 2 (continued). List of 175 pharmacogenetics associated genes selected as candidate

Ionotropic Glutamate Receptor Genes								
GRID1	*GRID2*	*GRIK1*	*GRIK2*	*GRIK3*	*GRIK4*	*GRIK5*	*GRIN1*	*GRIN2A*
GRIN2B	*GRIN2C*	*GRIN2D*	*GRIN3A*	*GRINA*				
Metabotropic Glutamate Receptor Genes								
GRM1	*GRM2*	*GRM3*	*GRM4*	*GRM5*	*GRM6*	*GRM7*	*GRM8*	
Serotonin Receptor Genes								
HTR1A	*HTR1B*	*HTR1D*	*HTR1E*	*HTR1F*	*HTR2A*	*HTR2C*	*HTR3A*	*HTR3B*
HTR3C	*HTR3D*	*HTR3E*	*HTR4*	*HTR5A*	*HTR6*	*HTR7*		
Ryanodine Receptor Genes								
RYR1	*RYR2*	*RYR3*						
CYP450 gene								
CYP1A1	*CYP1A2*	*CYP1B1*	*CYP2A6*	*CYP2A7*	*CYP2A13*	*CYP2B6*	*CYP2C8*	*CYP2C9*
CYP2C18	*CYP2C19*	*CYP2D6*	*CYP2E1*	*CYP2F1*	*CYP2J2*	*CYP2R1*	*CYP2S1*	*CYP2U1*
CYP2W1	*CYP3A4*	*CYP3A5*	*CYP3A7*	*CYP3A43*	*CYP4A11*	*CYP4A22*	*CYP4B1*	*CYP4F2*
CYP4F3	*CYP4F8*	*CYP4F11*	*CYP4F12*	*CYP4F22*	*CYP4V2*	*CYP4X1*	*CYP4Z1*	*CYP5A1*
CYP7A1	*CYP7B1*	*CYP8A1*	*CYP8B1*	*CYP11A1*	*CYP11B1*	*CYP11B2*	*CYP17A1*	*CYP19A1*
CYP20A1	*CYP21A2*	*CYP24A1*	*CYP26A1*	*CYP26B1*	*CYP26C1*	*CYP27A1*	*CYP27B1*	*CYP27C1*

Note: Data source includes a recent review paper on genetic of antipsychotic drug outcome by Changasi [15] (Abbreviation: candidate reviewed by Changasi) (n = 17), Drugbank information on drug targets/enzymes/transporters/carriers [16] (Abbreviation: DrugBank candidate) (n = 66), pharmacodynamics genes that encode for cholinergic receptor (Abbreviation: Cholinergic Receptor Genes) (n = 16), dopamine receptor (Abbreviation: dopamine Receptor Genes) (n = 5), GABA receptor (Abbreviation: GABA Receptor Genes) (n = 20), glycine receptor (Abbreviation: Gylcine Genes) (n = 9), ionotropic (Abbreviation: Ionotropic Glutamate Receptor Genes) (n = 14) and metabotropic (Abbreviation: Metabotropic Glutamate Receptor Genes) (n = 8) glutamate receptor, ryanodine receptor (Abbreviation: Ryanodine Receptor Genes) (n = 3) and serotonin receptor (Abbreviation: Serotonin Receptor Genes) (n = 16) and pharmacokinetic genes that encode for cytochrome P450 enzymes (Abbreviation: CYP450 gene) (n = 57).

eTable 3. Single variant based association results of the top 100 SNPs

CHR	SNP	BP (hg19)	A1	TEST	NMISS	OR	SE	L95	U95	STAT	P
14	rs13749	102514227	C	ADD	316	0.495	0.1962	0.337	0.7271	-3.584	0.000338
7	rs117074402	102950891	A	ADD	315	4.855	0.4422	2.041	11.55	3.574	0.000352
4	rs2347131	110791361	A	ADD	316	1.996	0.194	1.365	2.919	3.563	0.000367
4	rs2347132	110791413	T	ADD	316	1.996	0.194	1.365	2.919	3.563	0.000367
4	rs2347133	110791543	T	ADD	316	1.996	0.194	1.365	2.919	3.563	0.000367
12	rs10773127	125441359	C	ADD	316	2.324	0.2403	1.451	3.722	3.509	0.00045
11	rs11020845	94322352	T	ADD	316	0.5217	0.1866	0.3619	0.7521	-3.487	0.000489
11	rs11020846	94322353	A	ADD	316	0.5217	0.1866	0.3619	0.7521	-3.487	0.000489
1	rs2303307	85039955	A	ADD	316	0.4824	0.2097	0.3198	0.7277	-3.476	0.00051
5	rs2303138	96350710	A	ADD	316	0.5558	0.1696	0.3986	0.7749	-3.463	0.000534
14	rs229586	65263347	T	ADD	316	0.5104	0.1954	0.348	0.7485	-3.442	0.000577
14	rs731715	52182081	T	ADD	316	0.5437	0.1781	0.3834	0.7709	-3.421	0.000624
16	rs2235648	1836796	A	ADD	316	1.835	0.1779	1.295	2.601	3.413	0.000643
13	rs9554897	103383417	C	ADD	316	0.4372	0.2424	0.2719	0.7032	-3.413	0.000644
1	rs2994953	85031630	A	ADD	315	0.49	0.2091	0.3253	0.7382	-3.412	0.000646
8	rs16904753	133854970	G	ADD	316	3.309	0.3511	1.663	6.585	3.408	0.000654
8	rs16904774	133900495	A	ADD	316	3.309	0.3511	1.663	6.585	3.408	0.000654
13	rs9300756	103384824	G	ADD	314	0.4383	0.2424	0.2726	0.7049	-3.403	0.000667
1	rs2072035	175129946	C	ADD	310	0.5105	0.1979	0.3463	0.7524	-3.397	0.000681
3	rs6438869	124728626	A	ADD	316	0.552	0.1754	0.3914	0.7784	-3.389	0.000703
6	rs2296934	36931162	G	ADD	316	1.802	0.1742	1.28	2.535	3.379	0.000729
1	rs2292191	84944989	A	ADD	316	0.5	0.2056	0.3342	0.7482	-3.371	0.00075

eTable 3 (continued). Single variant based association results of the top 100 SNP

CHR	SNP	BP (hg19)	A1	TEST	NMISS	OR	SE	L95	U95	STAT	P
11	rs57607909	94326765	C	ADD	316	0.5323	0.1871	0.3689	0.7682	-3.369	0.000755
14	rs12893215	102463407	G	ADD	316	0.5099	0.2003	0.3444	0.755	-3.363	0.000771
14	rs8010870	102493761	G	ADD	316	0.5099	0.2003	0.3444	0.755	-3.363	0.000771
19	rs8100718	45016116	G	ADD	316	0.5382	0.1843	0.3751	0.7724	-3.361	0.000776
16	rs7201813	1664931	T	ADD	296	1.962	0.2007	1.324	2.908	3.359	0.000781
8	rs16893332	133906136	C	ADD	316	3.111	0.3379	1.604	6.034	3.359	0.000783
13	rs1218825	28009920	G	ADD	314	0.5492	0.1793	0.3865	0.7804	-3.343	0.000828
5	rs27044	96118852	G	ADD	316	0.563	0.1734	0.4007	0.7909	-3.313	0.000924
6	rs17625497	53883843	A	ADD	314	3.608	0.3875	1.688	7.71	3.311	0.000928
19	rs62104163	30021023	C	ADD	315	0.5294	0.1924	0.363	0.7719	-3.305	0.000949
16	rs9806826	1894912	T	ADD	313	0.5503	0.1812	0.3858	0.7849	-3.297	0.000978
7	rs1045012	98984354	C	ADD	316	0.1559	0.5686	0.05116	0.4752	-3.269	0.001081
14	rs17099370	62463129	G	ADD	316	0.5638	0.1759	0.3994	0.7958	-3.258	0.001121
16	rs8048410	1614097	A	ADD	316	1.751	0.172	1.25	2.453	3.257	0.001124
15	rs1607017	76726465	G	ADD	316	1.709	0.1645	1.238	2.359	3.257	0.001126
3	rs2259292	195501149	C	ADD	313	1.799	0.1805	1.263	2.563	3.254	0.001136
1	rs28391411	206239574	C	ADD	316	2.38	0.2671	1.41	4.017	3.245	0.001173
1	rs28602496	206239403	T	ADD	316	2.38	0.2671	1.41	4.017	3.245	0.001173
1	rs28639473	206239415	T	ADD	316	2.38	0.2671	1.41	4.017	3.245	0.001173
4	rs146127304	10542162	G	ADD	316	3.799	0.4117	1.695	8.514	3.242	0.001187
22	rs9619601	36700175	G	ADD	316	2.835	0.3218	1.509	5.327	3.238	0.001203
10	rs10825114	55582905	G	ADD	315	0.5426	0.1896	0.3742	0.7868	-3.225	0.00126

eTable 3 (continued). Single variant based association results of the top 100 SNP

CHR	SNP	BP (hg19)	A1	TEST	NMISS	OR	SE	L95	U95	STAT	P
16	rs1861759	50745583	G	ADD	316	0.3962	0.2876	0.2255	0.6962	-3.219	0.001285
16	rs57576928	84067004	T	ADD	316	0.5098	0.2108	0.3373	0.7706	-3.196	0.001393
20	rs11543239	34214173	A	ADD	316	0.1834	0.5313	0.06473	0.5195	-3.192	0.001411
20	rs11543244	34220755	T	ADD	316	0.1834	0.5313	0.06473	0.5195	-3.192	0.001411
19	rs78580402	900951	G	ADD	314	1.984	0.2148	1.302	3.023	3.19	0.001422
10	rs11016072	129901570	T	ADD	316	2.381	0.2726	1.395	4.063	3.182	0.001461
10	rs7083622	129903094	T	ADD	316	2.381	0.2726	1.395	4.063	3.182	0.001461
11	rs12277422	92623877	A	ADD	316	1.871	0.1972	1.271	2.754	3.176	0.001492
10	rs34750407	129899922	C	ADD	315	2.368	0.2725	1.388	4.039	3.163	0.001563
11	rs13941	62439569	G	ADD	316	0.3244	0.3561	0.1614	0.6519	-3.162	0.001569
3	rs1131199	112059768	C	ADD	316	0.5273	0.2027	0.3544	0.7844	-3.158	0.00159
5	rs2043112	38955796	A	ADD	314	1.684	0.1654	1.218	2.329	3.152	0.001621
15	rs41279212	34032131	A	ADD	316	0.4707	0.2391	0.2946	0.7521	-3.151	0.001625
9	rs10758145	32630472	C	ADD	316	1.74	0.176	1.233	2.457	3.148	0.001646
16	rs1742399	1962046	C	ADD	315	1.771	0.1817	1.241	2.529	3.147	0.001652
16	rs1657140	1962047	A	ADD	315	0.5731	0.177	0.4051	0.8108	-3.145	0.001663
12	rs4258464	125438523	C	ADD	316	2.277	0.2623	1.362	3.807	3.138	0.001701
12	rs4429156	125437019	T	ADD	316	2.277	0.2623	1.362	3.807	3.138	0.001701
12	rs4447263	125434580	C	ADD	316	2.277	0.2623	1.362	3.807	3.138	0.001701
12	rs4516060	125438516	T	ADD	316	2.277	0.2623	1.362	3.807	3.138	0.001701
2	rs3732111	10784491	G	ADD	315	0.5927	0.1671	0.4271	0.8224	-3.13	0.001748
2	rs2290075	239353001	T	ADD	316	3.044	0.3558	1.516	6.114	3.129	0.001753

eTable 3 (continued). Single variant based association results of the top 100 SNP

CHR	SNP	BP (hg19)	A1	TEST	NMISS	OR	SE	L95	U95	STAT	P
5	rs27529	96126308	G	ADD	314	1.721	0.174	1.224	2.421	3.122	0.001797
22	rs882753	50555635	T	ADD	315	1.978	0.219	1.288	3.039	3.115	0.001839
2	rs16844790	160968628	G	ADD	315	2.228	0.2577	1.344	3.692	3.109	0.001879
20	rs708973	3090848	G	ADD	316	2.063	0.2335	1.306	3.261	3.103	0.001918
14	rs3818188	102446161	A	ADD	315	1.734	0.1777	1.224	2.457	3.1	0.001938
7	rs17854665	99050039	A	ADD	316	0.1733	0.5663	0.0571	0.5257	-3.096	0.001964
7	rs34943973	99032517	A	ADD	316	0.1733	0.5663	0.0571	0.5257	-3.096	0.001964
19	rs1465723	45017249	C	ADD	316	2.215	0.2576	1.337	3.671	3.088	0.002016
13	rs3742300	53421432	C	ADD	316	0.5882	0.172	0.4199	0.8241	-3.085	0.002037
13	rs3742301	53422553	A	ADD	316	0.5882	0.172	0.4199	0.8241	-3.085	0.002037
21	rs2236694	43221555	A	ADD	316	1.964	0.2188	1.279	3.016	3.085	0.002037
12	rs80210207	70970293	C	ADD	316	0.3914	0.3041	0.2157	0.7104	-3.085	0.002039
9	rs61744789	101984093	C	ADD	315	3.47	0.4035	1.574	7.652	3.084	0.002044
10	rs2254174	72535007	C	ADD	316	0.5873	0.1728	0.4186	0.8241	-3.079	0.002076
5	rs1048307	168093522	A	ADD	315	0.5822	0.1759	0.4124	0.8217	-3.076	0.002095
22	rs2272838	50584201	C	ADD	316	1.748	0.1817	1.224	2.496	3.073	0.002119
10	rs7097319	52005153	G	ADD	302	0.5798	0.1779	0.4092	0.8217	-3.064	0.002184
9	rs10971047	32631369	T	ADD	316	1.771	0.1871	1.228	2.556	3.056	0.002245
19	rs16979130	44981516	T	ADD	316	2.201	0.2588	1.325	3.656	3.049	0.002299
15	rs56017612	43086885	C	ADD	316	0.225	0.4904	0.08605	0.5883	-3.042	0.002351
17	rs60994383	56247101	A	ADD	316	0.4751	0.2454	0.2937	0.7686	-3.033	0.002424
19	rs7951	6681991	A	ADD	316	2.346	0.2812	1.352	4.071	3.033	0.002425

eTable 3 (continued). Single variant based association results of the top 100 SNP

CHR	SNP	BP (hg19)	A1	TEST	NMISS	OR	SE	L95	U95	STAT	P
5	rs30187	96124330	C	ADD	316	1.689	0.1729	1.203	2.37	3.03	0.002442
4	rs3733227	83582211	C	ADD	315	1.678	0.1712	1.2	2.347	3.025	0.002489
22	rs2272836	50582550	A	ADD	316	1.764	0.1877	1.221	2.549	3.024	0.002491
19	rs7250872	1811603	T	ADD	316	0.5935	0.1731	0.4227	0.8332	-3.014	0.002579
22	rs2340601	50572473	A	ADD	315	1.73	0.1819	1.211	2.471	3.013	0.002584
22	rs9617018	50528916	T	ADD	316	1.826	0.2	1.234	2.703	3.011	0.002604
16	rs3765263	840378	A	ADD	316	1.676	0.1717	1.197	2.346	3.007	0.002637
22	rs738792	24121378	C	ADD	316	1.769	0.19	1.219	2.568	3.003	0.002672
11	rs1123991	4703165	C	ADD	316	0.5201	0.2182	0.3392	0.7977	-2.996	0.002735
11	rs7122644	6816875	A	ADD	316	0.5893	0.1766	0.4169	0.833	-2.995	0.002745
5	rs26653	96139250	G	ADD	316	1.677	0.1736	1.193	2.356	2.979	0.002895
19	rs1051738	10577843	A	ADD	316	0.4459	0.2712	0.2621	0.7587	-2.978	0.002898

eTable 4. The gene-based association results of rare variants using VT test, one-sided burden test and SKAT-O, top 100 genes are shown for each test

Gene	P (VT test)	Gene	P (burden)	Gene	P (SKAT-O)
KRT20	0.000488111	***EXOC6***	0.000606	***RDH16***	0.000883
EXOC6	0.000648659	***NTRK1***	0.001993	***FLRT1***	0.00109
BAZ2B	0.00106488	***SH3BP4***	0.00215	***SMCR7L***	0.001153
FBXO16	0.00162356	***RAB12***	0.002205	***CAPN3***	0.001161
TM4SF20	0.00172244	***FBXO16***	0.002244	***EXOC6***	0.001265
SH3BP4	0.00238541	***ROR2***	0.002799	***SLCO1B1***	0.001621
CCDC150	0.00254684	***SDF4***	0.003167	***CCR3***	0.001625
ROR2	0.00301334	***FNDC1***	0.003325	***FBXO16***	0.00176
TTC12	0.00328947	***ALPK3***	0.004684	***TRIM16***	0.001769
CNTNAP4	0.00344743	***MELK***	0.004839	***UBASH3B***	0.001909
KATNB1	0.00345168	***TTC12***	0.004979	***GAB2***	0.002059
SDF4	0.00434109	***ABAT***	0.004984	***NSD1***	0.002124
KCNIP2	0.00477002	***OR6C3***	0.005362	***AMBRA1***	0.002171
NTRK1	0.00483927	***TM4SF20***	0.00639	***TM4SF20***	0.002183
TNS1	0.00501074	***FAM3A***	0.006598	***ROBO2***	0.002372
FNDC1	0.00501612	***BAZ2B***	0.007191	***CPPED1***	0.002507
ATG2A	0.00608167	***IQSEC1***	0.007372	***GEMIN5***	0.002613
NUP210	0.0061296	***UNC79***	0.007499	***CSK***	0.002702
VAV2	0.00660689	***CHTOP***	0.007663	***TPST2***	0.002719
KANSL1L	0.00661626	***KANSL1L***	0.007782	***FERMT1***	0.00273
ZNF804A	0.00669216	***KALRN***	0.007887	***SETD1A***	0.002934
OR6C3	0.00688976	***KIF12***	0.008041	***POLR1B***	0.00301

eTable 4 (continued). The gene-based association results of rare variants using VT test, one-sided burden test and SKAT-O, top 100 genes are shown for each test

Gene	P (VT test)	Gene	P (burden)	Gene	P (SKAT-O)
IKBKAP	0.00689995	***SOS1***	0.00806	***HPS1***	0.003327
DNAH14	0.00692042	***SAMD11***	0.008088	***MRPS35***	0.003493
BLK	0.00724263	***DBR1***	0.008408	***CRELD2***	0.003506
KALRN	0.00745871	***BLK***	0.008469	***COG1***	0.003513
MELK	0.00749866	***XPNPEP2***	0.008573	***ZNF646***	0.003731
DSE	0.00806916	***SUSD4***	0.009241	***STAC2***	0.003781
SIGLEC15	0.00808781	***KATNB1***	0.009453	***TAL2***	0.003957
ALPK3	0.00832838	***UNC45B***	0.009466	***ATG4D***	0.004086
HPS1	0.00839832	***GLTPD1***	0.009715	***NPY4R***	0.004098
SLX4	0.00866873	***CAPS2***	0.010456	***CEP72***	0.004167
LRCH1	0.00881057	***PIK3R5***	0.010794	***AP1G2***	0.004501
SAMD11	0.00884397	***SIGLEC15***	0.010828	***NEUROD4***	0.004518
CAPS2	0.00896861	***ATMIN***	0.010963	***FGF22***	0.004533
CCDC24	0.00913242	***KCNIP2***	0.011227	***CDCA4***	0.004943
GLTPD1	0.00918033	***MYO9B***	0.011227	***GRIK4***	0.004955
SOS1	0.00972898	***NUP188***	0.01158	***SBNO1***	0.005023
MYO9B	0.00978337	***SEMA4C***	0.011599	***KIF9***	0.005023
TNFRSF10D	0.0101376	***DSE***	0.011657	***B4GALNT4***	0.005204
CEP72	0.0101818	***TNFRSF10D***	0.011676	***FAM151A***	0.005297
OR52E8	0.0105501	***HECTD4***	0.011696	***RSPH6A***	0.005397

eTable 4 (continued). The gene-based association results of rare variants using VT test, one-sided burden test and SKAT-O, top 100 genes are shown for each test

Gene	P (VT test)	Gene	P (burden)	Gene	P (SKATthe-O)
CAPN15	0.0106952	***CCDC24***	0.012142	***SH3BP4***	0.005397
PIK3R5	0.0109632	***TMEM143***	0.012335	***OR6T1***	0.005417
ITPKB	0.0109804	***ZNF804A***	0.012647	***RSAD2***	0.005494
SLC12A4	0.0112812	***LRP5L***	0.012856	***RARS2***	0.005628
EML6	0.0115037	***STON2***	0.013553	***FNDC1***	0.005816
TACC2	0.0118946	***IKBKAP***	0.01382	***ZBTB8B***	0.0059
CTC1	0.0121212	***PRAM1***	0.013848	***PHF2***	0.005904
C17orf64	0.0122699	***SBNO1***	0.014099	***SLC40A1***	0.005968
DBR1	0.0122699	***COL5A2***	0.014156	***CHD9***	0.006037
MYO10	0.0122915	***ADAM15***	0.014418	***SNAPC4***	0.006127
NUP188	0.0127389	***DAK***	0.014614	***GREB1***	0.006181
RNF157	0.012951	***FAM43A***	0.01566	***ABHD15***	0.006235
SBNO1	0.012975	***ZNF662***	0.016393	***WNK4***	0.00626
OR4D10	0.01322	***FAM3D***	0.016413	***KRT27***	0.006331
UNC79	0.0132701	***ACAN***	0.016509	***UNC45B***	0.006345
HYOU1	0.0133206	***GPR139***	0.016687	***ZNF83***	0.006359
PTPRF	0.0134486	***OR4M2***	0.016929	***CPZ***	0.006444
ATXN10	0.0135005	***CEP72***	0.017115	***SYNE1***	0.006461
SKIV2L2	0.0138751	***MR1***	0.017284	***COL8A1***	0.006491
AKAP5	0.0139581	***OR4D10***	0.017456	***C3orf67***	0.006505

eTable 4 (continued). The gene-based association results of rare variants using VT test, one-sided burden test and SKAT-O, top 100 genes are shown for each test

Gene	P (VT test)	Gene	P (burden)	Gene	P (SKAT-O)
DAK	0.014014	***LRCH1***	0.017522	***PFKL***	0.006553
ESYT2	0.0144778	***RUSC2***	0.01761	***CACTIN***	0.006558
ALDH9A1	0.0144928	***PALM2-AKAP2***	0.017767	***PDHA2***	0.006579
DLGAP4	0.014862	***SAMD3***	0.017789	***TANGO6***	0.006593
CCDC62	0.0154696	***STK33***	0.017834	***STXBP3***	0.006653
UNC45B	0.0155039	***GDF6***	0.017857	***ABHD5***	0.006687
HECTD4	0.0160367	***DUSP12***	0.018158	***DUOX2***	0.006853
SEMA4C	0.0161105	***CCDC30***	0.018519	***DTX2***	0.006886
ANKFY1	0.0161663	***KCNA5***	0.018543	***NTRK1***	0.007036
SLC19A2	0.016298	***KRR1***	0.018945	***FIGLA***	0.007087
SVIL	0.016317	***THEMIS***	0.019444	***PRAM1***	0.007127
DNAH3	0.0163743	***ANGPT4***	0.019663	***PCDH7***	0.007159
MRPS35	0.0163934	***INPP5J***	0.019691	***POC1A***	0.007203
ATMIN	0.0166865	***GLP2R***	0.019886	***FOSL2***	0.007204
ZNF215	0.0166865	***COX18***	0.020115	***KLHDC7A***	0.007269
SLC22A16	0.0168067	***POMT1***	0.020319	***MPHOSPH8***	0.007287
COX18	0.017199	***ZNF528***	0.020438	***TTC12***	0.007335
IQSEC1	0.018018	***ZNF609***	0.020468	***POMT1***	0.007572
PALM2-AKAP2	0.0185923	***ADHFE1***	0.02068	***ISM1***	0.007602
PRAM1	0.0186667	***C16orf11***	0.02068	***SH3BP2***	0.007722

eTable 4 (continued). The gene-based association results of rare variants using VT test, one-sided burden test and SKAT-O, top 100 genes are shown for each test

Gene	P (VT test)	Gene	P (burden)	Gene	P (SKAT-O)
RGS16	0.0188934	***PCDHA10***	0.020802	***TMEM200B***	0.007795
PADI3	0.0189189	***TNKS2***	0.021116	***LRCH1***	0.007901
ZMYND10	0.0190217	***CIB4***	0.021407	***RBFOX2***	0.007909
POMT1	0.0190736	***GPA33***	0.021407	***OR8B8***	0.007929
CAND2	0.0191781	***TM9SF4***	0.02144	***XIRP1***	0.008003
INPP5J	0.0192572	***IQGAP2***	0.021539	***ITSN2***	0.008008
KCNA5	0.0194175	***NRXN1***	0.021638	***MNT***	0.00808
GPA33	0.0196353	***FAM211A***	0.021773	***RAPGEF5***	0.008134
RUSC2	0.019774	***OR4Q3***	0.021875	***CNKSR3***	0.008211
KIF19	0.0199715	***OR52E8***	0.021909	***SPATS1***	0.008237
SLC7A9	0.0200286	***COX10***	0.022187	***LMOD2***	0.008282
ZNF768	0.0201439	***PRKD3***	0.022258	***TRIM3***	0.008316
C10orf120	0.0202899	***XPO6***	0.022258	***CCDC39***	0.008534
INO80	0.0203193	***CSK***	0.022364	***ZNF778***	0.00858
GPR139	0.0208955	***KIAA1009***	0.02269	***TAF2***	0.0086
COL5A2	0.0215054	***GEMIN4***	0.022801	***CD37***	0.008655
CDH3	0.0215716	***RNF151***	0.023217	***C19orf80***	0.008911
C5orf64	0.0217054	***TIE1***	0.023649	***CIB4***	0.008912

eTable 5. Nominally significant rare variant association (gene-based) results on candidate genes

Gene	Source	Variant(s)	Damaging non-synonymous				
			# var	**P (burden)**	**P (VT)**	**P (SKATO)**	**Allele count (Non/Res)**
GRID1	Ionotropic Glutamate Receptor Genes	p.P998S, p.A896V, rs150878754, p.D290N	4	**0.013**	**0.026**	**0.083**	4/0
ZNF804A	Candidate reviewed by_Changasi	rs139826553, rs78607324, p.T932N	3	**0.014**	**0.0067**	**0.012**	6/0
NRXN1	Candidate reviewed by Changasi	rs199701703, rs202006815, rs200935246, p.G263S, p.V179I, p.I100V, p.L804I, p.I754T,rs192069355, p.N274S, p.F150Y, p.T84K	12	**0.026**	**0.03**	**0.012**	12/4
CYP2J2	CYP450 gene	p.N300K, p.R158H, p.L126F	3	**0.043**	**0.028**	**0.062**	4/0
GABRA6	DrugBank andidate, GABA Receptor Genes	p.R84H, p.N128S, rs34907804	3	**0.047**	**0.057**	**0.052**	3/0
GRM7	Metabotropic Glutamate Receptor Genes	p.Q258H, p.P438T, p.Q577K	3	**0.049**	**0.04**	**0.22**	3/0

Abbreviation: # var, number of variants; P; P-value; Non, Non-responder; Res, Responder. Damaging variants are underlined. Nominal significant associations ($P < 0.05$) are given in bold.

eTable 6. Set-based association result of rare (MAF < 1%) damaging non-synymous variant in the 79 candidate gene sets

Gene set	Number of variants	allele count (Non/res)	raw P (burden test)	q value by histo method (pi0= 0.933544)	q value by BH method (pi0= 1)
reduced NMDA-mediated synaptic currents	49	42/19	0.0010143	0.04625231	0.04954485
reduced AMPA-mediated synaptic currents	43	36/14	0.0012543	0.04625231	0.04954485
abnormal AMPA-mediated synaptic currents	20	17/6	0.0120609	0.23748422	0.25438987
abnormal GABA-mediated receptor currents	55	43/24	0.0128805	0.23748422	0.25438987
abnormal long term depression	56	49/31	0.0303262	0.42450664	0.45472576
Long-term_potentiation	192	149/116	0.0405696	0.42450664	0.45472576
Long-term_depression	210	163/128	0.0478364	0.42450664	0.45472576
decreased synaptic glutamate release	33	26/14	0.0479007	0.42450664	0.45472576
REACTOME_GABA_A_RECEPTOR_ACTIVATION	16	15/7	0.0518042	0.42450664	0.45472576
abnormal synaptic transmission	104	80/60	0.0702003	0.49344139	0.52856773
abnormal paired-pulse inhibition	68	51/37	0.0790823	0.49344139	0.52856773
abnormal neurotransmitter level	31	26/16	0.0816229	0.49344139	0.52856773
decreased synaptic depression	52	37/25	0.0869795	0.49344139	0.52856773
absent long term depression	97	70/54	0.0946893	0.49880971	0.53431819
REACTOME_TRAFFICKING_OF_GLUR2_CONTAININ G_AMPA_RECEPTORS	20	13/7	0.101887	0.50094442	0.53660487
decreased prepulse inhibition	174	122/101	0.118789	0.54754305	0.58652069
REACTOME_GLUTAMATE_NEUROTRANSMITTER_R ELEASE_CYCLE	23	15/10	0.13055	0.55994319	0.59980355

eTable 6 (continued). Set-based association result of rare (MAF < 1%) damaging non-synymous variant in the 79 candidate gene sets

Gene set	Number of variants	allele count (Non/res)	raw P (burden test)	q value by histo method (pi0= 0.933544)	q value by BH method (pi0= 1)
Retrograde_endocannabinoid_signaling	300	210/183	0.139342	0.55994319	0.59980355
decreased excitatory postsynaptic current amplitude	58	42/32	0.147417	0.55994319	0.59980355
REACTOME_TRAFFICKING_OF_AMPA_RECEPTORS	50	35/26	0.151849	0.55994319	0.59980355
Serotonergic_synapse	307	216/193	0.216146	0.67587496	0.72398809
REACTOME_NEUROTRANSMITTER_RELEASE_CYCLE	73	49/41	0.22423	0.67587496	0.72398809
abnormal excitatory postsynaptic currents	316	218/198	0.235202	0.67587496	0.72398809
REACTOME_RAS_ACTIVATION_UOPN_CA2_INFUX_THROUGH_NMDA_RECEPTOR	55	43/36	0.255812	0.67587496	0.72398809
REACTOME_TRANSMISSION_ACROSS_CHEMICAL_SYNAPSES	447	305/283	0.257819	0.67587496	0.72398809
abnormal channel response	85	60/52	0.267005	0.67587496	0.72398809
REACTOME_ACTIVATION_OF_NMDA_RECEPTOR_UPON_GLUTAMATE_BINDING_AND_POSTSYNAPTIC_EVENTS	111	79/70	0.272692	0.67587496	0.72398809
REACTOME_GABA_RECEPTOR_ACTIVATION	104	70/61	0.27745	0.67587496	0.72398809
REACTOME_CREB_PHOSPHORYLATION_THROUGH_THE_ACTIVATION_OF_RAS	70	51/44	0.279722	0.67587496	0.72398809
REACTOME_INHIBITION_OF_VOLTAGE_GATED_CA2_CHANNELS_VIA_GBETA_GAMMA_SUBUNITS	16	12/9	0.284366	0.67587496	0.72398809

eTable 6 (continued). Set-based association result of rare (MAF < 1%) damaging non-synymous variant in the 79 candidate gene sets

Gene set	Number of variants	allele count (Non/res)	raw P (burden test)	q value by histo method (pi0= 0.933544)	q value by BH method (pi0= 1)
reduced long term depression	141	97/86	0.289811	0.67587496	0.72398809
REACTOME_NEUROTRANSMITTER_RECEPTOR_BINDING_AND_DOWNSTREAM_TRANSMISSION_IN_THE_POSTSYNAPTIC_CELL	317	220/204	0.293261	0.67587496	0.72398809
Dopaminergic_synapse	271	187/173	0.308275	0.68894792	0.73799167
REACTOME_POST_NMDA_RECEPTOR_ACTIVATION_EVENTS	102	73/67	0.355977	0.71971038	0.770944
REACTOME_UNBLOCKING_OF_NMDA_RECEPTOR_GLUTAMATE_BINDING_AND_ACTIVATION	52	37/33	0.370346	0.71971038	0.770944
Cholinergic_synapse	311	220/208	0.37777	0.71971038	0.770944
abnormal excitatory postsynaptic potential	219	147/139	0.388845	0.71971038	0.770944
REACTOME_GABA_SYNTHESIS_RELEASE_REUPTAKE_AND_DEGRADATION	26	17/16	0.403326	0.71971038	0.770944
abnormal miniature excitatory postsynaptic currents	270	177/168	0.409004	0.71971038	0.770944
reduced long term potentiation	380	238/227	0.416342	0.71971038	0.770944
abnormal synaptic dopamine release	32	24/22	0.420465	0.71971038	0.770944
REACTOME_INWARDLY_RECTIFYING_K_CHANNELS	37	27/25	0.443223	0.71971038	0.770944
abnormal inhibitory postsynaptic currents	159	116/111	0.44664	0.71971038	0.770944
REACTOME_VOLTAGE_GATED_POTASSIUM_CHANNELS	130	98/95	0.486099	0.71971038	0.770944

eTable 6 (continued). Set-based association result of rare (MAF < 1%) damaging non-synymous variant in the 79 candidate gene sets

Gene set	Number of variants	allele count (Non/res)	raw P (burden test)	q value by histo method (pi0= 0.933544)	q value by BH method (pi0= 1)
reduced long term depression	141	97/86	0.289811	0.67587496	0.72398809
abnormal prepulse inhibition	42	31/30	0.489138	0.71971038	0.770944
REACTOME_NOREPINEPHRINE_NEUROTRANSMITTER_RELEASE_CYCLE	12	4/8	0.708937	0.71971038	0.770944
REACTOME_TANDEM_PORE_DOMAIN_POTASSIUM_CHANNELS	21	8/16	0.722134	0.71971038	0.770944
decreased post-tetanic potentiation	32	18/20	0.733359	0.71971038	0.770944
REACTOME_GABA_B_RECEPTOR_ACTIVATION	82	48/51	0.735513	0.71971038	0.770944
REACTOME_HIGHLY_CALCIUM_PERMEABLE_POSTSYNAPTIC_NICOTINIC_ACETYLCHOLINE_RECEPTORS	38	22/26	0.738621	0.71971038	0.770944
abnormal long term potentiation	94	55/58	0.739286	0.71971038	0.770944
abnormal synaptic acetylcholine release	33	23/27	0.739834	0.71971038	0.770944
abnormal miniature endplate potential	178	117/134	0.739993	0.71971038	0.770944
decreased paired-pulse facilitation	43	24/30	0.741595	0.71971038	0.770944
REACTOME_ACETYLCHOLINE_BINDING_AND_DOWNSTREAM_EVENTS	49	28/32	0.743772	0.71971038	0.770944
REACTOME_CREB_PHOSPHORYLATION_THROUGH_THE_ACTIVATION_OF_CAMKII	44	31/31	0.744785	0.71971038	0.770944
enhanced long term potentiation	204	140/145	0.745396	0.71971038	0.770944

eTable 6 (continued). Set-based association result of rare (MAF < 1%) damaging non-synymous variant in the 79 candidate gene sets

Gene set	Number of variants	allele count (Non/res)	raw P (burden test)	q value by histo method (pi0= 0.933544)	q value by BH method (pi0= 1)
Neurotrophin_signaling_pathway	270	177/187	0.746169	0.71971038	0.770944
REACTOME_POTASSIUM_CHANNELS	208	142/149	0.74635	0.71971038	0.770944
enhanced paired-pulse facilitation	101	72/71	0.747037	0.71971038	0.770944
Synaptic_vesicle_cycle	167	111/113	0.748084	0.71971038	0.770944
REACTOME_ADENYLATE_CYCLASE_INHIBITORY_PATHWAY	66	36/42	0.749795	0.71971038	0.770944
abnormal miniature inhibitory postsynaptic currents	72	42/44	0.751976	0.71971038	0.770944
Glutamatergic_synapse	395	270/267	0.753088	0.71971038	0.770944
REACTOME_ACTIVATION_OF_KAINATE_RECEPTORS_UPON_GLUTAMATE_BINDING	57	41/51	0.753698	0.71971038	0.770944
abnormal CNS synaptic transmission	336	229/227	0.754792	0.71971038	0.770944
GABAergic_synapse	209	137/135	0.755213	0.71971038	0.770944
decreased neurotransmitter release	86	54/54	0.757449	0.71971038	0.770944
abnormal endplate potential	81	58/58	0.758989	0.71971038	0.770944
REACTOME_DOPAMINE_NEUROTRANSMITTER_RELEASE_CYCLE	17	7/10	0.759919	0.71971038	0.770944
REACTOME_ACETYLCHOLINE_NEUROTRANSMITTER_RELEASE_CYCLE	15	11/12	0.762093	0.71971038	0.770944
abnormal NMDA-mediated synaptic currents	28	15/16	0.763856	0.71971038	0.770944
abnormal PNS synaptic transmission	30	15/26	0.766586	0.71971038	0.770944
abnormal glutamate-mediated receptor currents	34	22/27	0.767735	0.71971038	0.770944

eTable 6 (continued). Set-based association result of rare (MAF < 1%) damaging non-synymous variant in the 79 candidate gene sets

Gene set	Number of variants	allele count (Non/res)	raw P (burden test)	q value by histo method (pi0= 0.933544)	q value by BH method (pi0= 1)
REACTOME_IONOTROPIC_ACTIVITY_OF_KAINATE_RECEPTORS	30	19/28	0.768246	0.71971038	0.770944
abnormal neurotransmitter secretion	37	22/29	0.768788	0.71971038	0.770944
increased prepulse inhibition	40	23/28	0.768811	0.71971038	0.770944
REACTOME_PRESYNAPTIC_NICOTINIC_ACETYLCHOLINE_RECEPTORS	42	23/30	0.769227	0.71971038	0.770944
increased synaptic depression	52	35/36	0.770944	0.71971038	0.770944
Retrograde_endocannabinoid_signaling	300	210/183	0.139342	0.55994319	0.59980355
decreased excitatory postsynaptic current amplitude	58	42/32	0.147417	0.55994319	0.59980355
REACTOME_TRAFFICKING_OF_AMPA_RECEPTORS	50	35/26	0.151849	0.55994319	0.59980355
Serotonergic_synapse	307	216/193	0.216146	0.67587496	0.72398809
REACTOME_NEUROTRANSMITTER_RELEASE_CYCLE	73	49/41	0.22423	0.67587496	0.72398809
abnormal excitatory postsynaptic currents	316	218/198	0.235202	0.67587496	0.72398809
REACTOME_RAS_ACTIVATION_UOPN_CA2_INFUX_THROUGH_NMDA_RECEPTOR	55	43/36	0.255812	0.67587496	0.72398809
REACTOME_TRANSMISSION_ACROSS_CHEMICAL_SYNAPSES	447	305/283	0.257819	0.67587496	0.72398809

eTable 6 (continued). Set-based association result of rare (MAF < 1%) damaging non-synymous variant in the 79 candidate gene sets

Gene set	Number of variants	allele count (Non/res)	raw P (burden test)	q value by histo method (pi0= 0.933544)	q value by BH method (pi0= 1)
abnormal channel response	85	60/52	0.267005	0.67587496	0.72398809
REACTOME_ACTIVATION_OF_NMDA_RECEPTOR_UPON_GLUTAMATE_BINDING_AND_POSTSYNAPTIC_EVENTS	111	79/70	0.272692	0.67587496	0.72398809
REACTOME_GABA_RECEPTOR_ACTIVATION	104	70/61	0.27745	0.67587496	0.72398809
REACTOME_CREB_PHOSPHORYLATION_THROUGH_THE_ACTIVATION_OF_RAS	70	51/44	0.279722	0.67587496	0.72398809
REACTOME_INHIBITION_OF_VOLTAGE_GATED_CA2_CHANNELS_VIA_GBETA_GAMMA_SUBUNITS	16	12/9	0.284366	0.67587496	0.72398809
reduced long term depression	141	97/86	0.289811	0.67587496	0.72398809
REACTOME_NEUROTRANSMITTER_RECEPTOR_BINDING_AND_DOWNSTREAM_TRANSMISSION_IN_THE_POSTSYNAPTIC_CELL	317	220/204	0.293261	0.67587496	0.72398809
Dopaminergic_synapse	271	187/173	0.308275	0.68894792	0.73799167
REACTOME_POST_NMDA_RECEPTOR_ACTIVATION_EVENTS	102	73/67	0.355977	0.71971038	0.770944
REACTOME_UNBLOCKING_OF_NMDA_RECEPTOR_GLUTAMATE_BINDING_AND_ACTIVATION	52	37/33	0.370346	0.71971038	0.770944
Cholinergic_synapse	311	220/208	0.37777	0.71971038	0.770944
abnormal excitatory postsynaptic potential	219	147/139	0.388845	0.71971038	0.770944

eTable 6 (continued). Set-based association result of rare (MAF < 1%) damaging non-synymous variant in the 79 candidate gene sets

Gene set	Number of variants	allele count (Non/res)	raw P (burden test)	q value by histo method (pi0= 0.933544)	q value by BH method (pi0= 1)
REACTOME_GABA_SYNTHESIS_RELEASE_REUPTAKE_AND_DEGRADATION	26	17/16	0.403326	0.71971038	0.770944
abnormal miniature excitatory postsynaptic currents	270	177/168	0.409004	0.71971038	0.770944
reduced long term potentiation	380	238/227	0.416342	0.71971038	0.770944
abnormal synaptic dopamine release	32	24/22	0.420465	0.71971038	0.770944
REACTOME_INWARDLY_RECTIFYING_K_CHANNELS	37	27/25	0.443223	0.71971038	0.770944
abnormal inhibitory postsynaptic currents	159	116/111	0.44664	0.71971038	0.770944
REACTOME_VOLTAGE_GATED_POTASSIUM_CHANNELS	130	98/95	0.486099	0.71971038	0.770944
abnormal prepulse inhibition	42	31/30	0.489138	0.71971038	0.770944
REACTOME_NOREPINEPHRINE_NEUROTRANSMITTER_RELEASE_CYCLE	12	4/8	0.708937	0.71971038	0.770944
REACTOME_TANDEM_PORE_DOMAIN_POTASSIUM_CHANNELS	21	8/16	0.722134	0.71971038	0.770944
decreased post-tetanic potentiation	32	18/20	0.733359	0.71971038	0.770944
REACTOME_GABA_B_RECEPTOR_ACTIVATION	82	48/51	0.735513	0.71971038	0.770944
REACTOME_HIGHLY_CALCIUM_PERMEABLE_POSTSYNAPTIC_NICOTINIC_ACETYLCHOLINE_RECEPTORS	38	22/26	0.738621	0.71971038	0.770944

eTable 6 (continued). Set-based association result of rare (MAF < 1%) damaging non-synymous variant in the 79 candidate gene sets

Gene set	Number of variants	allele count (Non/res)	raw P (burden test)	q value by histo method (pi0= 0.933544)	q value by BH method (pi0= 1)
abnormal long term potentiation	94	55/58	0.739286	0.71971038	0.770944
abnormal synaptic acetylcholine release	33	23/27	0.739834	0.71971038	0.770944
abnormal miniature endplate potential	178	117/134	0.739993	0.71971038	0.770944
decreased paired-pulse facilitation	43	24/30	0.741595	0.71971038	0.770944
REACTOME_ACETYLCHOLINE_BINDING_AND_DOWNSTREAM_EVENTS	49	28/32	0.743772	0.71971038	0.770944
REACTOME_CREB_PHOSPHORYLATION_THROUGH_THE_ACTIVATION_OF_CAMKII	44	31/31	0.744785	0.71971038	0.770944
enhanced long term potentiation	204	140/145	0.745396	0.71971038	0.770944
Neurotrophin_signaling_pathway	270	177/187	0.746169	0.71971038	0.770944
REACTOME_POTASSIUM_CHANNELS	208	142/149	0.74635	0.71971038	0.770944
enhanced paired-pulse facilitation	101	72/71	0.747037	0.71971038	0.770944
Synaptic_vesicle_cycle	167	111/113	0.748084	0.71971038	0.770944
REACTOME_ADENYLATE_CYCLASE_INHIBITORY_PATHWAY	66	36/42	0.749795	0.71971038	0.770944
abnormal miniature inhibitory postsynaptic currents	72	42/44	0.751976	0.71971038	0.770944
Glutamatergic_synapse	395	270/267	0.753088	0.71971038	0.770944
REACTOME_ACTIVATION_OF_KAINATE_RECEPTORS_UPON_GLUTAMATE_BINDING	57	41/51	0.753698	0.71971038	0.770944
abnormal CNS synaptic transmission	336	229/227	0.754792	0.71971038	0.770944

eTable 6 (continued). Set-based association result of rare (MAF < 1%) damaging non-synymous variant in the 79 candidate gene sets

Gene set	Number of variants	allele count (Non/res)	raw P (burden test)	q value by histo method (pi0= 0.933544)	q value by BH method (pi0= 1)
GABAergic_synapse	209	137/135	0.755213	0.71971038	0.770944
decreased neurotransmitter release	86	54/54	0.757449	0.71971038	0.770944
abnormal endplate potential	81	58/58	0.758989	0.71971038	0.770944
REACTOME_DOPAMINE_NEUROTRANSMITTER_RELEASE_CYCLE	17	7/10	0.759919	0.71971038	0.770944
REACTOME_ACETYLCHOLINE_NEUROTRANSMITTER_RELEASE_CYCLE	15	11/12	0.762093	0.71971038	0.770944
abnormal NMDA-mediated synaptic currents	28	15/16	0.763856	0.71971038	0.770944
abnormal PNS synaptic transmission	30	15/26	0.766586	0.71971038	0.770944
abnormal glutamate-mediated receptor currents	34	22/27	0.767735	0.71971038	0.770944
REACTOME_IONOTROPIC_ACTIVITY_OF_KAINATE_RECEPTORS	30	19/28	0.768246	0.71971038	0.770944
abnormal neurotransmitter secretion	37	22/29	0.768788	0.71971038	0.770944
increased prepulse inhibition	40	23/28	0.768811	0.71971038	0.770944
REACTOME_PRESYNAPTIC_NICOTINIC_ACETYLCHOLINE_RECEPTORS	42	23/30	0.769227	0.71971038	0.770944
increased synaptic depression	52	35/36	0.770944	0.71971038	0.770944

eTable 7. Information about variants identified in the reduced NMDA-mediated synaptic current in the discovery exome study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	MaxDBAltAF	num_non	num_re	Causal	Prediction_other
1	20998491	C/T	rs141985868	KIF17	missense	KIF17:NM_001122819(15Exons):exon12:c.G2662A:p.E888K&missense;KIF17:NM_020816(15Exons):exon12:c.G2662A:p.E888K&missense	0.003165	0.001134816	1	1	Y	A;B;C;D;E;F:0.0484:0.828:0.792
1	20998508	C/T	rs34232864	KIF17	missense	KIF17:NM_001122819(15Exons):exon12:c.G2645A:p.R882H&missense;KIF17:NM_020816(15Exons):exon12:c.G2645A:p.R882H&missense	0.001582	0.018155706	1	0	Y	A;G;B;C;D;E;F:0.0494:0.825:0.796
1	20998598	C/T	rs139517726	KIF17	missense	KIF17:NM_001122819(15Exons):exon12:c.G2555A:p.R852H&missense;KIF17:NM_020816(15Exons):exon12:c.G2555A:p.R852H&missense	0.001582	9.30E-04	1	0	Y	A;B;C;D;E;F:0.0484:0.828:0.792
1	21009211	C/A	NA	KIF17	missense	KIF17:NM_001122819(15Exons):exon11:c.G2398T:p.V800F&missense;KIF17:NM_020816(15Exons):exon11:c.G2398T:p.V800F&missense	0.001582	N	1	0	Y	A;B;C;D;E;F:0.0484:0.828:0.792
1	21009252	T/G	NA	KIF17	missense	KIF17:NM_001122819(15Exons):exon11:c.A2357C:p.Q786P&missense;KIF17:NM_020816(15Exons):exon11:c.A2357C:p.Q786P&missense	0.001582	N	1	0	Y	A;B;C;D;E;F:0.0484:0.828:0.792

eTable 7(continued). Information about variants identified in the reduced NMDA-mediated synaptic current in the discovery exome study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	MaxDBAltAF	num_non	num_re	Causal	Prediction_other
1	21011440	T/G	rs139742596	KIF17	missense	KIF17:NM_001122819(15Exons):exon10:c.A2093C:p.Q698P&missense;KIF17:NM_020816(15Exons):exon10:c.A2093C:p.Q698P&missense	0.004747	2.74E-04	2	1	Y	A;B;E;H;F;I:0.0287:0.885:0.676
1	21024922	G/A	NA	KIF17	stopgain	KIF17:NM_001122819(15Exons):exon6:c.C1183T:p.Q395*&stopgain;KIF17:NM_020816(15Exons):exon6:c.C1183T:p.Q395*&stopgain	0.001582	N	1	0	Y	B;D;H;F:0.0414:0.84:0.742
1	21031039	T/G	NA	KIF17	missense	KIF17:NM_001122819(15Exons):exon5:c.A1024C:p.N342H&missense;KIF17:NM_020816(15Exons):exon5:c.A1024C:p.N342H&missense	0.001582	N	0	1	Y	A;B;C;D;E;F:0.0484:0.828:0.792
1	21031266	G/A	NA	KIF17	missense	KIF17:NM_001122819(15Exons):exon5:c.C797T:p.S266L&missense;KIF17:NM_020816(15Exons):exon5:c.C797T:p.S266L&missense	0.001582	N	1	0	Y	A;B;C;D;E;F:0.0484:0.828:0.792
1	21040020	C/T	NA	KIF17	missense	KIF17:NM_001122819(15Exons):exon3:c.G407A:p.R136Q&missense;KIF17:NM_020816(15Exons):exon3:c.G407A:p.R136Q&missense	0.001582	N	0	1	Y	A;B;C;D;E;F:0.0484:0.828:0.792

eTable 7(continued). Information about variants identified in the reduced NMDA-mediated synaptic current in the discovery exome study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	MaxDBAltAF	num_non	num_re	Causal	Prediction_other
2	50280470	G/A	rs199701703	NRXN1	missense	NRXN1:NM_001135659(24Exons):exon22:c.C4187T:p.T1396M&missense; NRXN1:NM_004801(22Exons):exon20:c.C3977T:p.T1326M&missense;NRXN1:NM_138735(6Exons):exon4:c.C872T:p.T291M&missense	0.001582	N	1	0	Y	A;B;C;D;E;F:0.0484:0.828:0.792
2	50280477	T/A	rs202006815	NRXN1	missense	NRXN1:NM_001135659(24Exons):exon22:c.A4180T:p.T1394S&missense; NRXN1:NM_004801(22Exons):exon20:c.A3970T:p.T1324S&missense;NRXN1:NM_138735(6Exons):exon4:c.A865T:p.T289S&missense	0.006329	0.0014	4	0	Y	A;B;C;D;E;F:0.0484:0.828:0.792
2	50280526	C/G	rs200935246	NRXN1	missense	NRXN1:NM_001135659(24Exons):exon22:c.G4131C:p.E1377D&missense; NRXN1:NM_004801(22Exons):exon20:c.G3921C:p.E1307D&missense;NRXN1:NM_138735(6Exons):exon4:c.G816C:p.E272D&missense	0.001582	5.00E-04	1	0	Y	A;B;D;E;F:0.0385:0.859:0.732

eTable 7(continued). Information about variants identified in the reduced NMDA-mediated synaptic current in the discovery exome study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	MaxDBAltAF	num_non	num_re	Causal	Prediction_other
2	50280555	C/T	NA	NRXN1	missense	NRXN1:NM_001135659(24Exons):exon22:c.G4102A:p.G1368S&missense; NRXN1:NM_004801(22Exons):exon20:c.G3892A:p.G1298S&missense;NRXN1:NM_138735(6Exons):exon4:c.G787A:p.G263S&missense	0.001582	N	0	1	Y	A;B;C;D;E;F:0.0484:0.828:0.792
2	50318539	C/T	NA	NRXN1	missense	NRXN1:NM_001135659(24Exons):exon20:c.G3760A:p.V1254I&missense; NRXN1:NM_004801(22Exons):exon19:c.G3640A:p.V1214I&missense;NRXN1:NM_138735(6Exons):exon3:c.G535A:p.V179I&missense	0.001592	N	1	0	Y	A;D;E;H;I:0.0436:0.86:0.724
2	50464070	T/C	NA	NRXN1	missense	NRXN1:NM_001135659(24Exons):exon19:c.A3523G:p.I1175V&missense; NRXN1:NM_004801(22Exons):exon18:c.A3403G:p.I1135V&missense;NRXN1:NM_138735(6Exons):exon2:c.A298G:p.I100V&missense	0.001582	N	1	0	Y	A;B;C;D;E;F:0.0484:0.828:0.792

eTable 7(continued). Information about variants identified in the reduced NMDA-mediated synaptic current in the discovery exome study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	MaxDBAltAF	num_non	num_re	Causal	Prediction_other
2	50733720	G/T	NA	NRXN1	missense	NRXN1:NM_001135659(24Exons):exon14:c.C2530A:p.L844I&missense;NRXN1:NM_004801(22Exons):exon13:c.C2410A:p.L804I&missense	0.003165	N	2	0	Y	A;B;C;D;E;F:0.0484:0.828:0.792
2	50758451	A/G	NA	NRXN1	missense	NRXN1:NM_001135659(24Exons):exon12:c.T2381C:p.I794T&missense;NRXN1:NM_004801(22Exons):exon11:c.T2261C:p.I754T&missense	0.001582	N	1	0	Y	A;B;C;D;E;F:0.0484:0.828:0.792
2	50847168	G/C	rs192069355	NRXN1	missense	NRXN1:NM_001135659(24Exons):exon9:c.C1432G:p.L478V&missense;NRXN1:NM_004801(22Exons):exon8:c.C1312G:p.L438V&missense	0.001582	5.00E-04	0	1	Y	A;B;C;D;E;F:0.0484:0.828:0.792
2	51253559	T/C	NA	NRXN1	missense	NRXN1:NM_004801(22Exons):intronic2;NRXN1:NM_001135659(24Exons):exon3:c.A821G:p.N274S&missense	0.001592	N	0	1	Y	B;J;E;I:0.0312:0.928:0.884

eTable 7(continued). Information about variants identified in the reduced NMDA-mediated synaptic current in the discovery exome study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	MaxDBAltAF	num_non	num_re	Causal	Prediction_other
2	51254963	A/T	NA	NRXN1	missense	NRXN1:NM_001135659(24Exons):exon2:c.T449A:p.F150Y&missense;NRXN1:NM_004801(22Exons):exon2:c.T449A:p.F150Y&missense	0.001582	N	0	1	Y	A;B;C;D;E;F:0.0484:0.828:0.792
2	51255161	G/T	NA	NRXN1	missense	NRXN1:NM_001135659(24Exons):exon2:c.C251A:p.T84K&missense;NRXN1:NM_004801(22Exons):exon2:c.C251A:p.T84K&missense	0.001582	N	1	0	Y	A;D;E;F:0.0413:0.843:0.755
6	1.23E+08	A/T	NA	FABP7	missense	FABP7:NM_001446(4Exons):exon1:c.A1T:p.M1L&missense	0.001582	N	0	1	Y	A;D;E;F:0.0413:0.843:0.755
6	1.23E+08	G/C	NA	FABP7	missense	FABP7:NM_001446(4Exons):exon2:c.G140C:p.G47A&missense	0.001582	N	1	0	Y	A;B;C;D;E;F:0.0484:0.828:0.792
9	90266526	G/A	rs199940257	DAPK1	missense	DAPK1:NM_004938(26Exons):exon17:c.G1711A:p.D571N&missense	0.003165	4.74E-04	2	0	Y	A;D;E;F:0.0413:0.843:0.755
9	90272992	G/A	rs117269616	DAPK1	missense	DAPK1:NM_004938(26Exons):exon18:c.G1873A:p.V625M&missense	0.001582	8.68E-04	0	1	Y	A;B;C;D;E;F:0.0484:0.828:0.792
9	90321249	T/C	NA	DAPK1	missense	DAPK1:NM_004938(26Exons):exon26:c.T3263C:p.M1088T&missense	0.001582	N	0	1	Y	A;B;C;D;E;F:0.0484:0.828:0.792

eTable 7(continued). Information about variants identified in the reduced NMDA-mediated synaptic current in the discovery exome study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	MaxDBAltAF	num_non	num_re	Causal	Prediction_other
9	1.4E+08	G/A	NA	GRIN1	missense	GRIN1:NM_021569(19Exons):exon1:c.G14A:p.R5H&missense;GRIN1:NM_007327(20Exons):exon1:c.G14A:p.R5H&missense;GRIN1:NM_001185090(21Exons):exon1:c.G14A:p.R5H&missense;GRIN1:NM_001185091(20Exons):exon1:c.G14A:p.R5H&missense; GRIN1:NM_000832(19Exons):exon1:c.G14A:p.R5H&missense	0.001582	N	1	0	Y	A;G;B;D;H;F:0.0369:0.864:0.727
9	1.4E+08	T/C	NA	GRIN1	missense	GRIN1:NM_021569(19Exons):exon1:c.T86C:p.I29T&missense;GRIN1:NM_007327(20Exons):exon1:c.T86C:p.I29T&missense;GRIN1:NM_001185090(21Exons):exon1:c.T86C:p.I29T&missense;GRIN1:NM_001185091(20Exons):exon1:c.T86C:p.I29T&missense;GRIN1:NM_000832(19Exons):exon1:c.T86C:p.I29T&missense	0.001582	N	0	1	Y	A;B;C;D;H;F:0.0455:0.832:0.786

eTable 7(continued). Information about variants identified in the reduced NMDA-mediated synaptic current in the discovery exome study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	MaxDBAltAF	num_non	num_re	Causal	Prediction_other
9	1.4E+08	C/G	NA	GRIN1	missense	GRIN1:NM_021569(19Exons):exon5:c.C701G:p.A234G&missense;GRIN1:NM_007327(20Exons):exon5:c.C701G:p.A234G&missense;GRIN1:NM_001185090(21Exons):exon6:c.C764G:p.A255G&missense;GRIN1:NM_001185091(20Exons):exon6:c.C764G:p.A255G&missense;GRIN1:NM_000832(19Exons):exon5:c.C701G:p.A234G&missense	0.001582	N	1	0	Y	A;K;G;B;C;D;E;F:0.0405:0.851:0.764
9	1.4E+08	T/C	NA	GRIN1	missense	LRRC26:NM_001013653(2Exons):downstream+966;GRIN1:NM_021569(19Exons):3UTR+266;GRIN1:NM_007327(20Exons):3UTR+266;GRIN1:NM_001185090(21Exons):exon21:c.T2783C:p.I928T&missense;GRIN1:NM_001185091(20Exons):exon20:c.T2672C:p.I891T&missense;GRIN1:NM_000832(19Exons):exon19:c.T2609C:p.I870T&missense	0.001582	N	1	0	Y	A;D;F:0.039:0.846:0.75

eTable 7(continued). Information about variants identified in the reduced NMDA-mediated synaptic current in the discovery exome study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	MaxDBAltAF	num_non	num_re	Causal	Prediction_other
11	64428398	C/T	NA	NRXN2	missense	NRXN2:NM_138732(20Exons):exon9:c.G1919A:p.R640Q&missense;NRXN2:NM_015080(23Exons):exon10:c.G2012A:p.R671Q&missense	0.001582	N	1	0	Y	A;G;B;C;J;D;E;H;F:0.0283:0.944:0.891
11	64428458	C/A	NA	NRXN2	missense	NRXN2:NM_138732(20Exons):exon9:c.G1859T:p.R620L&missense;NRXN2:NM_015080(23Exons):exon10:c.G1952T:p.R651L&missense	0.001582	N	1	0	Y	A;K;G;B;C;D;E;H:0.0491:0.827:0.776
11	64434956	G/A	rs201258323	NRXN2	missense	NRXN2:NM_138732(20Exons):exon8:c.C1471T:p.R491C&missense;NRXN2:NM_015080(23Exons):exon9:c.C1564T:p.R522C&missense	0.001582	5.00E-04	0	1	Y	A;B;C;D;E;F:0.0484:0.828:0.792
11	64434997	C/T	rs140588352	NRXN2	missense	NRXN2:NM_138732(20Exons):exon8:c.G1430A:p.R477H&missense;NRXN2:NM_015080(23Exons):exon9:c.G1523A:p.R508H&missense	0.001582	0.006815084	1	0	Y	G;B;C;D;H:0.0541:0.817:0.783
11	64435078	T/A	rs139150995	NRXN2	missense	NRXN2:NM_138732(20Exons):exon8:c.A1349T:p.D450V&missense;NRXN2:NM_015080(23Exons):exon9:c.A1442T:p.D481V&missense	0.003165	2.20E-04	1	1	Y	K;B;J;D:0.028:0.942:0.879

eTable 7(continued). Information about variants identified in the reduced NMDA-mediated synaptic current in the discovery exome study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	MaxDBAltAF	num_non	num_re	Causal	Prediction_other
14	79175905	A/G	NA	NRXN3	missense	NRXN3:NR_073547(21Exons):ncRNA;NRXN3:NM_004796(17Exons):exon4:c.A448G:p.M150V&missense	0.001582	N	1	0	Y	B;C;D;F:0.0435:0.843:0.771
14	79423698	G/A	NA	NRXN3	missense	NRXN3:NR_073547(21Exons):ncRNA;NRXN3:NM_004796(17Exons):exon8:c.G1270A:p.A424T&missense	0.001582	N	0	1	Y	B;D;H;F:0.0414:0.84:0.742
14	79432407	A/G	NA	NRXN3	missense	NRXN3:NR_073547(21Exons):ncRNA;NRXN3:NM_004796(17Exons):exon9:c.A1316G:p.N439S&missense	0.001582	N	0	1	Y	B;D;H;F:0.0414:0.84:0.742
14	80164153	T/G	NA	NRXN3	missense	NRXN3:NR_073546(8Exons):ncRNA;NRXN3:NR_073547(21Exons):ncRNA;NRXN3:NM_001105250(7Exons):exon5:c.T872G:p.V291G&missense;NRXN3:NM_138970(6Exons):exon4:c.T782G:p.V261G&missense;NRXN3:NM_001272020(6Exons):exon4:c.T782G:p.V261G&missense;NRXN3:NM_004796(17Exons):exon15:c.T2678G:p.V893G&missense	0.001582	N	1	0	Y	G;B;C;D;E;F:0.0447:0.839:0.772

eTable 7(continued). Information about variants identified in the reduced NMDA-mediated synaptic current in the discovery exome study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	MaxDBAltAF	num_non	num_re	Causal	Prediction_other
14	80327583	A/T	NA	NRXN3	missense	NRXN3:NR_073546(8Exons):ncRNA;NRXN3:NR_073547(21Exons):ncRNA;NRXN3:NM_001105250(7Exons):intronic6;NRXN3:NM_138970(6Exons):intronic5;NRXN3:NM_004796(17Exons):intronic16;NRXN3:NM_001272020(6Exons):exon6:c.A1190T:p.D397V&missense	0.001582	N	1	0	Y	G;B;J;D;E;H;F:0.0311:0.938:0.89
16	9857416	A/T	NA	GRIN2A	missense	GRIN2A:NM_001134408(14Exons):intronic13;GRIN2A:NM_000833(14Exons):exon14:c.T3985A:p.F1329I&missense;GRIN2A:NM_001134407(13Exons):exon13:c.T3985A:p.F1329I&missense	0.001582	N	1	0	Y	B;C;D;F:0.0435:0.843:0.771
16	9858765	T/C	rs183029507	GRIN2A	missense	GRIN2A:NM_001134408(14Exons):exon13:c.A2636G:p.K879R&missense;GRIN2A:NM_000833(14Exons):exon14:c.A2636G:p.K879R&missense;GRIN2A:NM_001134407(13Exons):exon13:c.A2636G:p.K879R&missense	0.001582	0.0014	0	1	Y	G;B;C;D;E;F:0.0447:0.839:0.772

eTable 7(continued). Information about variants identified in the reduced NMDA-mediated synaptic current in the discovery exome study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	MaxDBAltAF	num_non	num_re	Causal	Prediction_other
16	9858774	A/G	rs199784503	GRIN2A	missense	GRIN2A:NM_001134408(14Exons):exon13:c.T2627C:p.I876T&missense; GRIN2A:NM_000833(14Exons):exon14:c.T2627C:p.I876T&missense;GRIN2A:NM_001134407(13Exons):exon13:c.T2627C:p.I876T&missense	0.004747	5.00E-04	2	1	Y	B;C;D;F:0.0435:0.843:0.771
16	9862818	C/A	NA	GRIN2A	missense	GRIN2A:NM_001134408(14Exons):exon12:c.G2485T:p.A829S&missense; GRIN2A:NM_000833(14Exons):exon13:c.G2485T:p.A829S&missense;GRIN2A:NM_001134407(13Exons):exon12:c.G2485T:p.A829S&missense	0.001582	N	1	0	Y	B;C;D;F:0.0435:0.843:0.771
16	9892139	C/G	rs76392464	GRIN2A	missense	GRIN2A:NM_001134408(14Exons):exon11:c.G2351C:p.G784A&missense; GRIN2A:NM_000833(14Exons):exon12:c.G2351C:p.G784A&missense;GRIN2A:NM_001134407(13Exons):exon11:c.G2351C:p.G784A&missense	0.001582	5.00E-04	1	0	Y	G;B;J;E;F:0.0313:0.934:0.89

eTable 7(continued). Information about variants identified in the reduced NMDA-mediated synaptic current in the discovery exome study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	MaxDBAltAF	num_non	num_re	Causal	Prediction_other
19	45975932	G/A	NA	FOSB	missense	FOSB:NM_006732(4Exons):exon4:c.G679A:p.E227K&missense;FOSB:NM_001114171(3Exons):exon3:c.G571A:p.E191K&missense	0.001582	N	1	0	Y	A;D;E;F:0.0413:0.843:0.755
22	51133230	C/T	NA	SHANK3	missense	SHANK3:NM_033517(22Exons):exon10:c.C1058T:p.A353V&missense	0.001582	N	1	0	Y	A;B;C;J;D;E;H;F;I:0.0247:0.949:0.88
22	51133409	C/T	NA	SHANK3	missense	SHANK3:NM_033517(22Exons):exon10:c.C1237T:p.R413W&missense	0.003165	N	1	1	Y	A;C;D:0.0555:0.805:0.804

NOTE: MAF_dis: MAF (in our discovery sample); num_non: Count in Non-responder; num_re: Count in Responder; Causal: IsDiseaseCausal_predicted_by_KGGSeq; Prediction _other: Prediction_by_other_deleteriousness_prediction_tools; In the last column, prediction tools are labeled with letters: A-SIFT_score; B-MutationTaster_score; C- MutationAssessor_score; D-CADD_raw; E-GERP++_NR; F-phyloP100way_vertebrate; G-Polyphen2_HVAR_score; H-GERP++_RS; I-SiPhy_29way_logOdds; J-FATHMM_score; K-Polyphen2_HDIV_score

eTable 8. Information about variants identified in the reduced AMPA-mediated synaptic current in the discovery exome study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	MaxDBAltAF	num_non	num_re	Causal	Prediction _other
1	2.25E+08	C/T	ID15209	CNIH3	stopgain	CNIH3:NM_152495(6Exons):exon3:c.C193T:p.R65*&stopgain	0.001587	N	0	1	Y	A;D;E;F:0.0413:0.843:0.755
2	50280470	G/A	rs199701703	NRXN1	missense	NRXN1:NM_001135659(24Exons):exon22:c.C4187T:p.T1396M&missense;NRXN1:NM_004801(22Exons):exon20:c.C3977T:p.T1326M&missense;NRXN1:NM_138735(6Exons):exon4:c.C872T:p.T291M&missense	0.001582	N	1	0	Y	A;B;C;D;E;F:0.0484:0.828:0.792
2	50280477	T/A	rs202006815	NRXN1	missense	NRXN1:NM_001135659(24Exons):exon22:c.A4180T:p.T1394S&missense;NRXN1:NM_004801(22Exons):exon20:c.A3970T:p.T1324S&missense;NRXN1:NM_138735(6Exons):exon4:c.A865T:p.T289S&missense	0.006329	0.0014	4	0	Y	A;B;C;D;E;F:0.0484:0.828:0.792
2	50280526	C/G	rs200935246	NRXN1	missense	NRXN1:NM_001135659(24Exons):exon22:c.G4131C:p.E1377D&missense;NRXN1:NM_004801(22Exons):exon20:c.G3921C:p.E1307D&missense;NRXN1:NM_138735(6Exons):exon4:c.G816C:p.E272D&missense	0.001582	5.00E-04	1	0	Y	A;B;D;E;F:0.0385:0.859:0.732

eTable 8 (continued). Information about variants identified in the reduced AMPA-mediated synaptic current in the discovery exome study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	MaxDBAltAF	num_non	num_re	Causal	Prediction _other
2	50280555	C/T	ID19527	NRXN1	missense	NRXN1:NM_001135659(24Exons):exon22:c.G4102A:p.G1368S&missense;NRXN1:NM_004801(22Exons):exon20:c.G3892A:p.G1298S&missense;NRXN1:NM_138735(6Exons):exon4:c.G787A:p.G263S&missense	0.001582	N	0	1	Y	A;B;C;D;E;F:0.0484:0.828:0.792
2	50318539	C/T	ID19528	NRXN1	missense	NRXN1:NM_001135659(24Exons):exon20:c.G3760A:p.V1254I&missense;NRXN1:NM_004801(22Exons):exon19:c.G3640A:p.V1214I&missense;NRXN1:NM_138735(6Exons):exon3:c.G535A:p.V179I&missense	0.001592	N	1	0	Y	A;D;E;H;I:0.0436:0.86:0.724
2	50464070	T/C	ID19529	NRXN1	missense	NRXN1:NM_001135659(24Exons):exon19:c.A3523G:p.I1175V&missense;NRXN1:NM_004801(22Exons):exon18:c.A3403G:p.I1135V&missense;NRXN1:NM_138735(6Exons):exon2:c.A298G:p.I100V&missense	0.001582	N	1	0	Y	A;B;C;D;E;F:0.0484:0.828:0.792

eTable 8 (continued). Information about variants identified in the reduced AMPA-mediated synaptic current in the discovery exome study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	MaxDBAltAF	num_non	num_re	Causal	Prediction _other
2	50733720	G/T	ID19538	NRXN1	missense	NRXN1:NM_001135659(24Exons):exon14:c.C2530A:p.L844I&missense;NRXN1:NM_004801(22Exons):exon13:c.C2410A:p.L804I&missense	0.003165	N	2	0	Y	A;B;C;D;E;F:0.0484:0.828:0.792
2	50758451	A/G	ID19539	NRXN1	missense	NRXN1:NM_001135659(24Exons):exon12:c.T2381C:p.I794T&missense;NRXN1:NM_004801(22Exons):exon11:c.T2261C:p.I754T&missense	0.001582	N	1	0	Y	A;B;C;D;E;F:0.0484:0.828:0.792
2	50847168	G/C	rs192069355	NRXN1	missense	NRXN1:NM_001135659(24Exons):exon9:c.C1432G:p.L478V&missense;NRXN1:NM_004801(22Exons):exon8:c.C1312G:p.L438V&missense	0.001582	5.00E-04	0	1	Y	A;B;C;D;E;F:0.0484:0.828:0.792
2	51253559	T/C	ID19549	NRXN1	missense	NRXN1:NM_004801(22Exons):intronic2;NRXN1:NM_001135659(24Exons):exon3:c.A821G:p.N274S&missense	0.001592	N	0	1	Y	B;J;E;I:0.0312:0.928:0.884
2	51254963	A/T	ID19550	NRXN1	missense	NRXN1:NM_001135659(24Exons):exon2:c.T449A:p.F150Y&missense;NRXN1:NM_004801(22Exons):exon2:c.T449A:p.F150Y&missense	0.001582	N	0	1	Y	A;B;C;D;E;F:0.0484:0.828:0.792

eTable 8 (continued). Information about variants identified in the reduced AMPA-mediated synaptic current in the discovery exome study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	MaxDBAltAF	num_non	num_re	Causal	Prediction _other
2	51255161	G/T	ID19552	NRXN1	missense	NRXN1:NM_001135659(24Exons):exon2:c.C251A:p.T84K&missense;NRXN1:NM_004801(22Exons):exon2:c.C251A:p.T84K&missense	0.001582	N	1	0	Y	A;D;E;F:0.0413:0.843:0.755
3	1.24E+08	G/C	ID35831	KALRN	missense	KALRN:NM_001024660(60Exons):exon12:c.G2158C:p.E720Q&missense;KALRN:NM_003947(34Exons):exon12:c.G2158C:p.E720Q&missense	0.001582	N	1	0	Y	D;E;F:0.0344:0.859:0.721
3	1.24E+08	A/C	ID35832	KALRN	missense	KALRN:NM_001024660(60Exons):exon13:c.A2198C:p.H733P&missense;KALRN:NM_003947(34Exons):exon13:c.A2198C:p.H733P&missense	0.001582	N	1	0	Y	A;B;C;D;E;F:0.0484:0.828:0.792
3	1.24E+08	G/A	ID35837	KALRN	missense	KALRN:NM_007064(27Exons):exon2:c.G299A:p.R100Q&missense;KALRN:NM_001024660(60Exons):exon35:c.G5390A:p.R1797Q&missense	0.001582	1.16E-04	1	0	Y	B;C;D;F:0.0435:0.843:0.771
3	1.24E+08	T/C	ID35840	KALRN	missense	KALRN:NM_007064(27Exons):exon6:c.T722C:p.V241A&missense;KALRN:NM_001024660(60Exons):exon39:c.T5813C:p.V1938A&missense	0.001582	N	1	0	Y	A;B;C;D;E;F:0.0484:0.828:0.792

eTable 8 (continued). Information about variants identified in the reduced AMPA-mediated synaptic current in the discovery exome study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	MaxDBAltAF	num_non	num_re	Causal	Prediction _other
3	1.24E+08	C/T	rs143716563	KALRN	missense	KALRN:NM_007064(27Exons):exon16:c.C2054T:p.A685V&missense;KALRN:NM_001024660(60Exons):exon49:c.C7145T:p.A2382V&missense	0.003165	.	2	0	Y	A;K;B;J;E;H;F:0.0284:0.943:0.887
5	1.53E+08	C/G	ID52026	GRIA1	missense	GRIA1:NR_047578(14Exons):ncRNA;GRIA1:NM_001258023(16Exons):5UTR-112;GRIA1:NM_001258020(17Exons):5UTR-153052;GRIA1:NM_001258021(16Exons):exon2:c.C125G:p.P42R&missense;GRIA1:NM_001258022(16Exons):exon2:c.C125G:p.P42R&missense;GRIA1:NM_001114183(16Exons):exon2:c.C95G:p.P32R&missense;GRIA1:NM_001258019(15Exons):exon2:c.C95G:p.P32R&missense;GRIA1:NM_000827(16Exons):exon2:c.C95G:p.P32R&missense	0.001582	N	1	0	Y	A;G;B;C;D;E;H;F;I:0.047:0.83:0.789
7	31378294	C/T	ID62926	NEUROD6	missense	NEUROD6:NM_022728(2Exons):exon2:c.G589A:p.A197T&missense	0.001582	N	1	0	Y	LRT_score;J;E:0.0245:0.939:0.867

eTable 8 (continued). Information about variants identified in the reduced AMPA-mediated synaptic current in the discovery exome study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	MaxDBAltAF	num_non	num_re	Causal	Prediction _other
7	31378651	C/T	rs180839756	NEUROD6	missense	NEUROD6:NM_022728(2Exons):exon2:c.G232A:p.G78S&missense	0.001582	5.00E-04	0	1	Y	A;G;B;C;J;D;E;H;F:0.0283:0.944:0.891
7	31378712	C/G	ID62927	NEUROD6	missense	NEUROD6:NM_022728(2Exons):exon2:c.G171C:p.E57D&missense	0.001587	N	0	1	Y	A;G;B;C;J;D;E;H;F:0.0283:0.944:0.891
8	1.19E+08	G/A	rs188859975	EXT1	missense	EXT1:NM_000127(11Exons):exon6:c.C1457T:p.A486V&missense	0.003165	0.0018	2	0	Y	A;G;B;C;J;D;E;H;F:0.0283:0.944:0.891
8	1.19E+08	C/A	ID74202	EXT1	missense	EXT1:NM_000127(11Exons):exon1:c.G284T:p.G95V&missense	0.001582	N	0	1	Y	A;G;B;C;J;D;E;H;F:0.0283:0.944:0.891
9	1.4E+08	G/A	ID83395	GRIN1	missense	GRIN1:NM_021569(19Exons):exon1:c.G14A:p.R5H&missense;GRIN1:NM_007327(20Exons):exon1:c.G14A:p.R5H&missense;GRIN1:NM_001185090(21Exons):exon1:c.G14A:p.R5H&missense;GRIN1:NM_001185091(20Exons):exon1:c.G14A:p.R5H&missense;GRI	0.001582	N	1	0	Y	A;G;B;D;H;F:0.0369:0.864:0.727

						N1:NM_000832(19Exons):exon1:c.G14A:p.R5H&missense						

eTable 8 (continued). Information about variants identified in the reduced AMPA-mediated synaptic current in the discovery exome study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	MaxDBAltAF	num_non	num_re	Causal	Prediction _other
9	1.4E+08	T/C	ID83396	GRIN1	missense	GRIN1:NM_021569(19Exons):exon1:c.T86C:p.I29T&missense;GRIN1:NM_007327(20Exons):exon1:c.T86C:p.I29T&missense;GRIN1:NM_001185090(21Exons):exon1:c.T86C:p.I29T&missense;GRIN1:NM_001185091(20Exons):exon1:c.T86C:p.I29T&missense;GRIN1:NM_000832(19Exons):exon1:c.T86C:p.I29T&missense	0.001582	N	0	1	Y	A;B;C;D;H;F:0.0455:0.832:0.786
9	1.4E+08	C/G	ID83401	GRIN1	missense	GRIN1:NM_021569(19Exons):exon5:c.C701G:p.A234G&missense;GRIN1:NM_007327(20Exons):exon5:c.C701G:p.A234G&missense;GRIN1:NM_001185090(21Exons):exon6:c.C764G:p.A255G&missense;GRIN1:NM_001185091(20Exons):exon6:c.C764G:p.A255G&missense;GRIN1:NM_000832(19Exons):exon5:c.C701G:p.A234G&missense	0.001582	N	1	0	Y	A;K;G;B;C;D;E;F:0.0405:0.851:0.764

eTable 8 (continued). Information about variants identified in the reduced AMPA-mediated synaptic current in the discovery exome study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	MaxDBAltAF	num_non	num_re	Causal	Prediction _other
9	1.4E+08	T/C	ID83408	GRIN1	missense	LRRC26:NM_001013653(2Exons):downstream+966;GRIN1:NM_021569(19Exons):3UTR+266;GRIN1:NM_007327(20Exons):3UTR+266;GRIN1:NM_001185090(21Exons):exon21:c.T2783C:p.I928T&missense;GRIN1:NM_001185091(20Exons):exon20:c.T2672C:p.I891T&missense;GRIN1:NM_000832(19Exons):exon19:c.T2609C:p.I870T&missense	0.001582	N	1	0	Y	A;D;F:0.039:0.846:0.75
11	64428398	C/T	ID9628 5	NRXN 2	missense	NRXN2:NM_138732(20Exons):exon9:c.G1919A:p.R640Q&missense;NRXN2:NM_015080(23Exons):exon10:c.G2012A:p.R671Q&missense	0.001582	N	1	0	Y	A;G;B;C;J;D;E;H;F:0.0283:0.944:0.891
11	64428458	C/A	ID9628 6	NRXN 2	missense	NRXN2:NM_138732(20Exons):exon9:c.G1859T:p.R620L&missense;NRXN2:NM_015080(23Exons):exon10:c.G1952T:p.R651L&missense	0.001582	N	1	0	Y	A;K;G;B;C;D;E;H:0.0491:0.827:0.776

eTable 8 (continued). Information about variants identified in the reduced AMPA-mediated synaptic current in the discovery exome study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	MaxDBAltAF	num_non	num_re	Causal	Prediction _other
11	64434956	G/A	rs201258323	NRXN2	missense	NRXN2:NM_138732(20Exons):exon8:c.C1471T:p.R491C&missense;NRXN2:NM_015080(23Exons):exon9:c.C1564T:p.R522C&missense	0.001582	5.00E-04	0	1	Y	A;B;C;D;E;F:0.0484:0.828:0.792
11	64434997	C/T	rs140588352	NRXN2	missense	NRXN2:NM_138732(20Exons):exon8:c.G1430A:p.R477H&missense;NRXN2:NM_015080(23Exons):exon9:c.G1523A:p.R508H&missense	0.001582	0.006815	1	0	Y	G;B;C;D;H:0.0541:0.817:0.783
11	64435078	T/A	rs139150995	NRXN2	missense	NRXN2:NM_138732(20Exons):exon8:c.A1349T:p.D450V&missense;NRXN2:NM_015080(23Exons):exon9:c.A1442T:p.D481V&missense	0.003165	2.20E-04	1	1	Y	K;B;J;D:0.028:0.942:0.879
14	79175905	A/G	ID117003	NRXN3	missense	NRXN3:NR_073547(21Exons):ncRNA;NRXN3:NM_004796(17Exons):exon4:c.A448G:p.M150V&missense	0.001582	N	1	0	Y	B;C;D;F:0.0435:0.843:0.771
14	79423698	G/A	ID117004	NRXN3	missense	NRXN3:NR_073547(21Exons):ncRNA;NRXN3:NM_004796(17Exons):exon8:c.G1270A:p.A424T&missense	0.001582	N	0	1	Y	B;D;H;F:0.0414:0.84:0.742
14	79432407	A/G	ID1170	NRXN	missens	NRXN3:NR_073547(21Exons):ncRN	0.00158	N	0	1	Y	B;D;H;F:0.0414:0

			05	3	e	A;NRXN3:NM_004796(17Exons):exon9:c.A1316G:p.N439S&missense	2					.84:0.742

eTable 8 (continued). Information about variants identified in the reduced AMPA-mediated synaptic current in the discovery exome study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	MaxDBAltAF	num_non	num_re	Causal	Prediction _other
14	80164153	T/G	ID117007	NRXN3	missense	NRXN3:NR_073546(8Exons):ncRNA;NRXN3:NR_073547(21Exons):ncRNA;NRXN3:NM_001105250(7Exons):exon5:c.T872G:p.V291G&missense;NRXN3:NM_138970(6Exons):exon4:c.T782G:p.V261G&missense;NRXN3:NM_001272020(6Exons):exon4:c.T782G:p.V261G&missense;NRXN3:NM_004796(17Exons):exon15:c.T2678G:p.V893G&missense	0.001582	N	1	0	Y	G;B;C;D;E;F:0.0447:0.839:0.772
14	80327583	A/T	ID117011	NRXN3	missense	NRXN3:NR_073546(8Exons):ncRNA;NRXN3:NR_073547(21Exons):ncRNA;NRXN3:NM_001105250(7Exons):intronic6;NRXN3:NM_138970(6Exons):intronic5;NRXN3:NM_004796(17Exons):intronic16;NRXN3:NM_001272020(6Exons):exon6:c.A1190T:p.D397V&missense	0.001582	N	1	0	Y	G;B;J;D;E;H;F:0.0311:0.938:0.89

eTable 8 (continued). Information about variants identified in the reduced AMPA-mediated synaptic current in the discovery exome study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	MaxDBAltAF	num_non	num_re	Causal	Prediction _other
17	7097669	C/T	ID134394	DLG4	missense	DLG4:NM_001365(22Exons):exon14:c.G1576A:p.D526N&missense;DLG4:NM_001128827(20Exons):exon12:c.G1438A:p.D480N&missense	0.001582	N	0	1	Y	A;B;C;D;E;H;F:0.0432:0.844:0.773
19	54416185	C/G	rs185024703	CACNG7	missense	CACNG7:NM_031896(5Exons):exon1:c.C100G:p.L34V&missense	0.001582	5.00E-04	1	0	Y	A;B;C;D;E;F:0.0484:0.828:0.792
22	36960595	C/T	ID167064	CACNG2	missense	CACNG2:NM_006078(4Exons):exon4:c.G775A:p.G259S&missense	0.001582	N	1	0	Y	B;C;D;F:0.0435:0.843:0.771
22	51041880	C/T	ID169163	MAPK8IP2	missense	MAPK8IP2:NM_016431(10Exons):exon1:c.C319T:p.H107Y&missense;MAPK8IP2:NM_012324(12Exons):exon3:c.C400T:p.H134Y&missense	0.001582	N	1	0	Y	A;D;E;F:0.0413:0.843:0.755
22	51044133	C/T	ID169174	MAPK8IP2	missense	MAPK8IP2:NM_016431(10Exons):exon5:c.C1903T:p.R635W&missense;MAPK8IP2:NM_012324(12Exons):exon7:c.C1984T:p.R662W&missense	0.001582	N	1	0	Y	A;D;E;F:0.0413:0.843:0.755

NOTE:

MAF_dis: MAF (in our discovery sample); num_non: Count in Non-responder; num_re: Count in Responder; Causal: IsDiseaseCausal_predicted_by_KGGSeq; Prediction _other: Prediction_by_other_deleteriousness_prediction_tools;In the last column, prediction tools are labeled with letters: A-SIFT_score; B-MutationTaster_score; C- MutationAssessor_score; D-CADD_raw; E-GERP++_NR; F-phyloP100way_vertebrate; G-Polyphen2_HVAR_score; H-GERP++_RS; I-SiPhy_29way_logOdds; J-FATHMM_score; K-Polyphen2_HDIV_score

eTable 9. Information about variants identified in the abnormal AMPA-mediated synaptic current in the discovery exome study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	MaxDBAltAF	num_non	num_re	Causal	Prediction _other
4	1.58E+08	G/A	ID45267	GRIA2	missense	GRIA2:NM_001083620(16Exons):exon3:c.G172A:p.G58R&missense;GRIA2:NM_000826(16Exons):exon3:c.G313A:p.G105R&missense;GRIA2:NM_001083619(16Exons):exon3:c.G313A:p.G105R&missense	0.001582	N	1	0	Y	A;B;C;D;E;F:0.04484:0.828:0.792
4	1.58E+08	C/T	rs199654327	GRIA2	missense	GRIA2:NM_001083620(16Exons):exon4:c.C335T:p.S112L&missense;GRIA2:NM_000826(16Exons):exon4:c.C476T:p.S159L&missense;GRIA2:NM_001083619(16Exons):exon4:c.C476T:p.S159L&missense	0.001587	5.00E-04	1	0	Y	A;B;C;D;E;H;F:0.0432:0.844:0.773
9	1.4E+08	G/A	ID83395	GRIN1	missense	GRIN1:NM_021569(19Exons):exon1:c.G14A:p.R5H&missense;GRIN1:NM_007327(20Exons):exon1:c.G14A:p.R5H&missense;GRIN1:NM_001185090(21Exons):exon1:c.G14A:p.R5H&missense;GRIN1:NM_001185091(20Exons):exon1:c.G14A:p.R5H&missense;GRIN1:NM_000832(19Exons):exon1:c.G14A:p.R5H&missense	0.001582	N	1	0	Y	A;G;B;D;H;F:0.0369:0.864:0.727

eTable 9 (continued). Information about variants identified in the abnormal AMPA-mediated synaptic current in the discovery exome study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	MaxDBAltAF	num_non	num_re	Causal	Prediction _other
9	1.4E+08	T/C	ID83396	GRIN1	missense	GRIN1:NM_021569(19Exons):exon1:c.T86C:p.I29T&missense;GRIN1:NM_007327(20Exons):exon1:c.T86C:p.I29T&missense;GRIN1:NM_001185090(21Exons):exon1:c.T86C:p.I29T&missense;GRIN1:NM_001185091(20Exons):exon1:c.T86C:p.I29T&missense;GRIN1:NM_000832(19Exons):exon1:c.T86C:p.I29T&missense	0.001582	N	0	1	Y	A;B;C;D;H;F:0.0455:0.832:0.786
9	1.4E+08	C/G	ID83401	GRIN1	missense	GRIN1:NM_021569(19Exons):exon5:c.C701G:p.A234G&missense;GRIN1:NM_007327(20Exons):exon5:c.C701G:p.A234G&missense;GRIN1:NM_001185090(21Exons):exon6:c.C764G:p.A255G&missense;GRIN1:NM_001185091(20Exons):exon6:c.C764G:p.A255G&missense;GRIN1:NM_000832(19Exons):exon5:c.C701G:p.A234G&missense	0.001582	N	1	0	Y	A;K;G;B;C;D;E;F:0.0405:0.851:0.764

eTable 9 (continued). Information about variants identified in the abnormal AMPA-mediated synaptic current in the discovery exome study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	MaxDBAltAF	num_non	num_re	Causal	Prediction _other
9	1.4E+08	T/C	ID83408	GRIN1	missense	LRRC26:NM_001013653(2Exons):downstream+966;GRIN1:NM_021569(19Exons):3UTR+266;GRIN1:NM_007327(20Exons):3UTR+266;GRIN1:NM_001185090(21Exons):exon21:c.T2783C:p.I928T&missense;GRIN1:NM_001185091(20Exons):exon20:c.T2672C:p.I891T&missense;GRIN1:NM_000832(19Exons):exon19:c.T2609C:p.I870T&missense	0.001582	N	1	0	Y	A;D;F:0.039:0.846:0.75
11	1.06E+08	G/A	ID9949 8	GRIA4	missense	GRIA4:NR_046356(17Exons):ncRNA;GRIA4:NM_001112812(10Exons):exon3:c.G334A:p.A112T&missense;GRIA4:NM_001077243(17Exons):exon4:c.G334A:p.A112T&missense;GRIA4:NM_000829(17Exons):exon4:c.G334A:p.A112T&missense;GRIA4:NM_001077244(11Exons):exon4:c.G334A:p.A112T&missense	0.001582	N	1	0	Y	A;B;C;D;E;F:0.0484:0.828:0.792

eTable 9 (continued). Information about variants identified in the abnormal AMPA-mediated synaptic current in the discovery exome study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	MaxDBAltAF	num_non	num_re	Causal	Prediction _other
11	1.06E+08	G/A	ID99500	GRIA4	missense	GRIA4:NR_046356(17Exons):ncRNA;GRIA4:NM_001112812(10Exons):exon3:c.G458A:p.C153Y&missense;GRIA4:NM_001077243(17Exons):exon4:c.G458A:p.C153Y&missense;GRIA4:NM_000829(17Exons):exon4:c.G458A:p.C153Y&missense;GRIA4:NM_001077244(11Exons):exon4:c.G458A:p.C153Y&missense	0.001582	N	0	1	Y	A;D;E;F:0.0413:0.843:0.755
11	1.06E+08	A/G	ID99502	GRIA4	missense	GRIA4:NR_046356(17Exons):ncRNA;GRIA4:NM_001112812(10Exons):exon4:c.A569G:p.N190S&missense;GRIA4:NM_001077243(17Exons):exon5:c.A569G:p.N190S&missense;GRIA4:NM_000829(17Exons):exon5:c.A569G:p.N190S&missense;GRIA4:NM_001077244(11Exons):exon5:c.A569G:p.N190S&missense	0.001587	N	0	1	Y	B;D;E;F:0.0342:0.872:0.702

eTable 9 (continued). Information about variants identified in the abnormal AMPA-mediated synaptic current in the discovery exome study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	MaxDBAltAF	num_non	num_re	Causal	Prediction _other
11	1.06E+08	T/C	ID99505	GRIA4	missense	GRIA4:NR_046356(17Exons):ncRNA;GRIA4:NM_001112812(10Exons):exon5:c.T716C:p.I239T&missense;GRIA4:NM_001077243(17Exons):exon6:c.T716C:p.I239T&missense;GRIA4:NM_000829(17Exons):exon6:c.T716C:p.I239T&missense;GRIA4:NM_001077244(11Exons):exon6:c.T716C:p.I239T&missense	0.001592	N	1	0	Y	A;B;C;D;E;H;F:0.0432:0.844:0.773
11	1.06E+08	T/A	ID99512	GRIA4	missense	GRIA4:NR_046356(17Exons):ncRNA;GRIA4:NM_001077243(17Exons):exon13:c.T1849A:p.S617T&missense;GRIA4:NM_000829(17Exons):exon13:c.T1849A:p.S617T&missense	0.001582	N	0	1	Y	A;B;C;D;E;F:0.0484:0.828:0.792
12	13716186	C/T	ID102947	GRIN2B	missense	GRIN2B:NM_000834(13Exons):exon13:c.G3986A:p.R1329Q&missense	0.001582	N	1	0	Y	A;B;C;D;E;F:0.0484:0.828:0.792
12	13717061	G/T	ID102948	GRIN2B	missense	GRIN2B:NM_000834(13Exons):exon13:c.C3111A:p.D1037E&missense	0.001582	N	1	0	Y	K;B;E;F:0.0365:0.847:0.69
12	13717533	C/T	ID102949	GRIN2B	missense	GRIN2B:NM_000834(13Exons):exon13:c.G2639A:p.R880H&missense	0.003165	N	1	1	Y	A;D;E;F:0.0413:0.843:0.755

eTable 9 (continued). Information about variants identified in the abnormal AMPA-mediated synaptic current in the discovery exome study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	MaxDBAltAF	num_non	num_re	Causal	Prediction _other
14	64935238	A/T	ID115937	AKAP5	missense	AKAP5:NM_004857(2Exons):exon2:c.A126T:p.K42N&missense	0.001582	N	1	0	Y	A;G;B;J;D;E;H;F;I:0.0298:0.94:0.893
14	64935411	C/T	rs2230491	AKAP5	missense	AKAP5:NM_004857(2Exons):exon2:c.C299T:p.P100L&missense	0.004747	0.149651	3	0	Y	A;B;J;E:0.0316:0.929:0.891
14	64935674	C/T	ID115939	AKAP5	missense	AKAP5:NM_004857(2Exons):exon2:c.C562T:p.R188W&missense	0.001582	N	1	0	Y	A;B;E;H;F;I:0.0287:0.885:0.676
17	7097669	C/T	ID134394	DLG4	missense	DLG4:NM_001365(22Exons):exon14:c.G1576A:p.D526N&missense;DLG4:NM_001128827(20Exons):exon12:c.G1438A:p.D480N&missense	0.001582	N	0	1	Y	A;B;C;D;E;H;F:0.0432:0.844:0.773

eTable 9 (continued). Information about variants identified in the abnormal AMPA-mediated synaptic current in the discovery exome study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	MaxDBAltAF	num_non	num_re	Causal	Prediction _other
21	46596346	C/T	ID164351	ADARB1	missense	ADARB1:NR_027672(11Exons):ncRNA;ADARB1:NR_073200(13Exons):ncRNA;ADARB1:NR_027673(13Exons):ncRNA;ADARB1:NR_027674(12Exons):ncRNA;ADARB1:NM_001112(11Exons):exon4:c.C730T:p.R244C&missense;ADARB1:NM_015833(12Exons):exon4:c.C730T:p.R244C&missense;ADARB1:NM_015834(13Exons):exon4:c.C730T:p.R244C&missense;ADARB1:NM_001160230(12Exons):exon4:c.C730T:p.R244C&missense	0.001582	N	1	0	Y	A;B;C;D;E;H;F:0.0432:0.844:0.773
22	36960595	C/T	ID167064	CACNG2	missense	CACNG2:NM_006078(4Exons):exon4:c.G775A:p.G259S&missense	0.001582	N	1	0	Y	B;C;D;F:0.0435:0.843:0.771

NOTE: MAF_dis: MAF (in our discovery sample); num_non: Count in Non-responder; num_re: Count in Responder; Causal: IsDiseaseCausal_predicted_by_KGGSeq; Prediction _other: Prediction_by_other_deleteriousness_prediction_tools; In the last column, prediction tools are labeled with letters: A-SIFT_score; B-MutationTaster_score; C- MutationAssessor_score; D-CADD_raw; E-GERP++_NR; F-phyloP100way_vertebrate; G-Polyphen2_HVAR_score; H-GERP++_RS; I-SiPhy_29way_logOdds; J-FATHMM_score; K-Polyphen2_HDIV_score

eTable 10. Set-based association results on candidate gene-sets in the discovery exome on rare (MAF<0.01) synonymous variants

GeneSet	NVAR	Allele count (Non-re/ Re)	P
abnormal long term potentiation	98	91/64	0.030702
abnormal NMDA-mediated synaptic currents	33	30/16	0.056277
reduced long term potentiation	428	327/289	0.094891
enhanced paired-pulse facilitation	107	85/69	0.12
REACTOME_TANDEM_PORE_DOMAIN_POTASSIUM_CHANNELS	36	27/19	0.121212
increased prepulse inhibition	38	39/30	0.139535
abnormal AMPA-mediated synaptic currents	27	26/18	0.16
abnormal excitatory postsynaptic currents	355	275/250	0.196429
REACTOME_ACETYLCHOLINE_NEUROTRANSMITTER_RELEASE_CYCLE	19	13/10	0.25
REACTOME_IONOTROPIC_ACTIVITY_OF_KAINATE_RECEPTORS	27	21/19	0.268293
abnormal miniature endplate potential	136	109/97	0.277778
abnormal CNS synaptic transmission	417	295/283	0.30303
decreased prepulse inhibition	188	132/121	0.30303
decreased post-tetanic potentiation	41	28/23	0.3125
REACTOME_GABA_SYNTHESIS_RELEASE_REUPTAKE_AND_DEGRADATION	29	23/16	0.3125
abnormal long term depression	76	58/52	0.322581
abnormal synaptic dopamine release	35	25/20	0.470588

eTable 10 (continued). Set-based association results on candidate gene-sets in the discovery exome on rare (MAF<0.01) synonymous variants

GeneSet	NVAR	Allele count (Non-re/ Re)	P
abnormal glutamate-mediated receptor currents	51	34/33	0.538462
decreased paired-pulse facilitation	59	42/44	0.538462
REACTOME_DOPAMINE_NEUROTRANSMITTER_RELEASE_CYCLE	22	15/14	0.538462
REACTOME_NEUROTRANSMITTER_RELEASE_CYCLE	73	53/47	0.538462
decreased synaptic depression	74	52/56	0.583333
reduced long term depression	135	104/99	0.6
enhanced long term potentiation	205	152/148	0.6
decreased excitatory postsynaptic current amplitude	70	59/53	0.6
REACTOME_NEUROTRANSMITTER_RECEPTOR_BINDING_AND_DOWNSTREAM_TRANSMISSION_IN_THE_POSTSYNAPTIC_CELL	348	216/295	0.6
REACTOME_VOLTAGE_GATED_POTASSIUM_CHANNELS	144	106/97	0.6
REACTOME_POST_NMDA_RECEPTOR_ACTIVATION_EVENTS	106	79/88	0.666667
REACTOME_TRANSMISSION_ACROSS_CHEMICAL_SYNAPSES	480	310/391	0.666667
abnormal neurotransmitter level	41	26/35	0.714286
abnormal prepulse inhibition	37	23/26	0.714286
abnormal synaptic transmission	118	71/85	0.714286
decreased neurotransmitter release	101	67/69	0.714286

eTable 10 (continued). Set-based association results on candidate gene-sets in the discovery exome on rare (MAF<0.01) synonymous variants

GeneSet	NVAR	Allele count (Non-re/ Re)	P
abnormal miniature excitatory postsynaptic currents	306	221/216	0.714286
REACTOME_ACTIVATION_OF_KAINATE_RECEPTORS_UPON_GLUTAMATE_BINDING	66	45/61	0.714286
REACTOME_TRAFFICKING_OF_GLUR2_CONTAINING_AMPA_RECEPTORS	37	24/32	0.714286
absent long term depression	133	102/106	0.833333
reduced NMDA-mediated synaptic currents	66	41/57	0.833333
abnormal excitatory postsynaptic potential	271	196/209	0.833333
abnormal PNS synaptic transmission	29	20/20	0.833333
abnormal endplate potential	74	56/61	0.833333
abnormal GABA-mediated receptor currents	57	39/42	0.833333
decreased synaptic glutamate release	41	31/36	0.833333
abnormal paired-pulse inhibition	58	40/48	0.833333
abnormal synaptic acetylcholine release	30	20/24	0.833333
abnormal neurotransmitter secretion	46	31/28	0.833333
abnormal miniature inhibitory postsynaptic currents	81	56/63	0.833333
Cholinergic_synapse	406	264/315	0.833333
Dopaminergic_synapse	337	241/278	0.833333
Long-term_depression	227	165/186	0.833333
Neurotrophin_signaling_pathway	295	203/218	0.833333
Retrograde_endocannabinoid_signaling	357	250/268	0.833333

eTable 10 (continued). Set-based association results on candidate gene-sets in the discovery exome on rare (MAF<0.01) synonymous variants

GeneSet	NVAR	Allele count (Non-re/ Re)	P
REACTOME_ACETYLCHOLINE_BINDING_AND_DOWNSTREAM_EVENTS	35	18/28	0.833333
REACTOME_ACTIVATION_OF_NMDA_RECEPTOR_UPON_GLUTAMATE_BINDING_AND_POSTSYNAPTIC_EVENTS	113	84/94	0.833333
REACTOME_CREB_PHOSPHORYLATION_THROUGH_THE_ACTIVATION_OF_CAMKII	57	43/48	0.833333
REACTOME_CREB_PHOSPHORYLATION_THROUGH_THE_ACTIVATION_OF_RAS	84	68/74	0.833333
REACTOME_GABA_A_RECEPTOR_ACTIVATION	20	13/17	0.833333
REACTOME_GLUTAMATE_NEUROTRANSMITTER_RELEASE_CYCLE	28	17/17	0.833333
REACTOME_HIGHLY_CALCIUM_PERMEABLE_POSTSYNAPTIC_NICOTINIC_ACETYLCHOLINE_RECEPTORS	29	12/25	0.833333
REACTOME_INHIBITION_OF_VOLTAGE_GATED_CA2_CHANNELS_VIA_GBETA_GAMMA_SUBUNITS	40	16/36	0.833333
REACTOME_NOREPINEPHRINE_NEUROTRANSMITTER_RELEASE_CYCLE	14	6/9	0.833333
REACTOME_RAS_ACTIVATION_UOPN_CA2_INFUX_THROUGH_NMDA_RECEPTOR	61	51/51	0.833333
REACTOME_TRAFFICKING_OF_AMPA_RECEPTORS	57	32/47	0.833333
increased synaptic depression	55	38/37	1

eTable 10 (continued). Set-based association results on candidate gene-sets in the discovery exome on rare (MAF<0.01) synonymous variants

GeneSet	NVAR	Allele count (Non-re/ Re)	P
abnormal inhibitory postsynaptic currents	237	155/164	1
abnormal channel response	130	84/100	1
reduced AMPA-mediated synaptic currents	62	44/43	1
GABAergic_synapse	258	153/201	1
Glutamatergic_synapse	404	286/316	1
Long-term_potentiation	228	166/192	1
Serotonergic_synapse	327	247/257	1
Synaptic_vesicle_cycle	161	110/113	1
REACTOME_ADENYLATE_CYCLASE_INHIBITORY_PATHWAY	67	37/52	1
REACTOME_GABA_B_RECEPTOR_ACTIVATION	107	53/88	1
REACTOME_GABA_RECEPTOR_ACTIVATION	131	66/109	1
REACTOME_INWARDLY_RECTIFYING_K_CHANNELS	64	32/51	1
REACTOME_POTASSIUM_CHANNELS	274	187/186	1
REACTOME_PRESYNAPTIC_NICOTINIC_ACETYLCHOLINE_RECEPTORS	31	16/25	1
REACTOME_UNBLOCKING_OF_NMDA_RECEPTOR_GLUTAMATE_BINDING_AND_ACTIVATION	58	44/48	1

NOTE: Non-re/ Re : Non-responder/ Responder

eTable 11. Full list of genes selected for targeted sequencing

Gene	Reason of being selected	Sucessfully sequenced
ADARB1	gene member of abnormal AMPA	Yes
AKAP5	gene member of abnormal AMPA	Yes
APOC3	investigator's interest	No
ARC	gene member of abnormal AMPA	Yes
BRD2	investigator's interest	Yes
CACNG2	gene member of reduced AMPA, abnormal AMPA	Yes
CACNG7	gene member of reduced AMPA	Yes
CACNG8	gene member of abnormal AMPA	Yes
CCNE1	gene member of reduced NMDA	Yes
CCNE2	gene member of reduced NMDA	Yes
CNIH2	gene member of reduced AMPA, abnormal AMPA	Yes
CNIH3	gene member of reduced AMPA	Yes
CNR1	investigator's interest	Yes
COMT	investigator's interest	Yes
CYP1A2	investigator's interest	Yes
CYP2C19	investigator's interest	Yes
CYP2D6	investigator's interest	Yes
CYP2E1	investigator's interest	Yes
CYP3A4	investigator's interest	Yes
CYP3A5	investigator's interest	Yes
CYP3A7	investigator's interest	No

eTable 11 (continued). Full list of genes selected for targeted sequencing

Gene	Reason of being selected	Sucessfully sequenced
DAPK1	gene member of reduced NMDA	Yes
DBH	investigator's interest	Yes
DLG4	gene member of reduced AMPA, abnormal AMPA	Yes
DRD1	investigator's interest	Yes
DRD2	investigator's interest	Yes
DRD3	investigator's interest	Yes
DRD4	investigator's interest	Yes
EXT1	gene member of reduced AMPA	Yes
FABP7	gene member of reduced NMDA	Yes
FAT1	investigator's interest	No
FMO3	investigator's interest	Yes
FOSB	gene member of reduced NMDA	Yes
GHRL	investigator's interest	No
GNB3	investigator's interest	Yes
GRIA1	gene member of reduced AMPA	Yes
GRIA2	gene member of abnormal AMPA	Yes
GRIA4	gene member of abnormal AMPA	Yes
GRID1	Nominal p-value among candiate examined	No
GRIN1	gene member of reduced NMDA, reduced AMPA, abnormal AMPA	Yes
GRIN2A	gene member of reduced NMDA	Yes

eTable 11 (continued). Full list of genes selected for targeted sequencing

Gene	Reason of being selected	Sucessfully sequenced
GRIN2A	gene member of reduced NMDA	Yes
GRIN2B	gene member of abnormal AMPA	Yes
GRM3	investigator's interest	Yes
GRM7	Nominal p-value among candiate examined	No
HTR1A	investigator's interest	Yes
HTR2A	investigator's interest	Yes
HTR2C	investigator's interest	Yes
HTR3A	investigator's interest	Yes
HTR6	investigator's interest	Yes
HTR7	investigator's interest	Yes
KALRN	gene member of reduced AMPA	Yes
KIF17	gene member of reduced NMDA	Yes
LEP	investigator's interest	Yes
LEPR	investigator's interest	Yes
LPL	investigator's interest	Yes
MAPK8IP2	gene member of reduced AMPA	Yes
NEUROD6	gene member of reduced AMPA	Yes
NLGN3	gene member of reduced AMPA	Yes
NQO1	investigator's interest	Yes
NRXN1	gene member of reduced NMDA, reduced AMPA	Yes
NRXN2	gene member of reduced NMDA, reduced AMPA	Yes

eTable 11 (continued). Full list of genes selected for targeted sequencing

Gene	Reason of being selected	Sucessfully sequenced
NRXN3	gene member of reduced NMDA, reduced AMPA	Yes
PIWIL4	investigator's interest	No
PPARGC1A	investigator's interest	Yes
PPP1R9B	gene member of abnormal AMPA	No
ROBO2	investigator's interest	Yes
RPS6KA3	gene member of reduced AMPA	Yes
SHANK3	gene member of reduced NMDA	Yes
SLC1A1	investigator's interest	Yes
SLC1A2	investigator's interest	Yes
SLC1A3	investigator's interest	Yes
SLC6A3	investigator's interest	Yes
SLC6A4	investigator's interest	Yes
TPH1	investigator's interest	Yes
TPH2	investigator's interest	Yes
VPS35	gene member of reduced NMDA, reduced AMPA	Yes
ZNF804A	Nominal p-value among candiate examined	Yes

eTable 12. The gene-based association results of rare variants (damaging non-synonymous with MAF < 1%) using CMC burden test in follow-up study

Gene	N_INFORMATIVE	NumVar	NumPolyVar	NonRefSite	Pvalue
ADARB1	1920	9	9	9	0.296464
AKAP5	1920	7	7	16	0.0142277
ARC	1920	5	5	5	0.406692
BRD2	1920	21	21	57	0.193989
CACNG2	1920	2	2	2	0.412468
CACNG7	1920	3	3	10	0.853472
CACNG8	1920	2	2	2	0.0823758
CCNE1	1920	4	4	4	0.145463
CCNE2	1920	8	8	9	0.92912
CNIH2	1920	2	2	2	0.624458
CNIH3	1920	9	9	11	0.116095
CNR1	1920	13	13	19	0.681797
COMT	1920	8	8	11	0.092332
CYP1A2	1920	32	32	95	0.0377687
CYP2C19	1920	22	22	48	0.436555
CYP2D6	1920	30	30	74	0.899758
CYP2E1	1920	8	8	34	0.933459
CYP3A4	1920	11	11	16	0.160225
CYP3A5	1920	17	17	77	0.621241
CYP3A7	1920	12	12	19	0.679123
DAPK1	1920	34	34	59	0.358227
DBH	1920	34	34	72	0.269967

eTable 12 (continued). The gene-based association results of rare variants (damaging non-synonymous with MAF < 1%) using CMC burden test in follow-up study

Gene	N_INFORMATIVE	NumVar	NumPolyVar	NonRefSite	Pvalue
DLG4	1920	9	9	12	0.179597
DRD1	1920	5	5	6	0.708387
DRD2	1920	6	6	7	0.779242
DRD3	1920	7	7	9	0.364234
DRD4	1920	10	9	11	0.535634
EXT1	1920	16	16	27	0.493882
FABP7	1920	7	7	7	0.614972
FAT1	1920	151	149	371	0.317465
FMO3	1920	20	20	76	0.191115
FOSB	1920	9	9	9	0.225116
GHRL	1920	4	4	32	0.415558
GNB3	1920	15	15	17	0.984337
GRIA1	1920	11	11	14	0.964499
GRIA2	1920	10	10	21	0.59754
GRIA4	1920	16	16	20	0.366694
GRIN1	1920	6	6	7	0.885977
GRIN2A	1920	31	31	66	0.667686
GRIN2B	1920	10	10	15	0.852812
GRM3	1920	15	15	21	0.252392
HTR1A	1920	4	4	25	0.137462

eTable 12 (continued). The gene-based association results of rare variants (damaging non-synonymous with MAF < 1%) using CMC burden test in follow-up study

Gene	N_INFORMATIVE	NumVar	NumPolyVar	NonRefSite	Pvalue
HTR2A	1920	5	5	13	0.806531
HTR3A	1920	21	21	45	0.0525392
HTR6	1920	8	8	16	0.508206
HTR7	1920	9	8	25	0.959337
KALRN	1920	39	39	47	0.0721384
KIF17	1920	29	29	67	0.997782
LEP	1920	8	8	23	0.437189
LEPR	1920	15	15	16	0.998862
LPL	1920	13	13	13	0.117307
MAPK8IP2	1920	11	11	17	0.421053
NEUROD6	1920	9	9	12	0.87706
NQO1	1920	10	10	19	0.921827
NRXN1	1920	44	44	88	0.147845
NRXN2	1920	30	29	65	0.103387
NRXN3	1920	28	28	43	0.733983
PIWIL4	1920	21	20	34	0.174145
PPARGC1A	1920	31	30	30	0.945895
ROBO2	1920	32	32	49	0.222207
SHANK3	1920	24	24	37	0.385764
SLC1A1	1920	10	10	11	0.748195

eTable 12 (continued). The gene-based association results of rare variants (damaging non-synonymous with MAF < 1%) using CMC burden test in follow-up study

Gene	N_INFORMATIVE	NumVar	NumPolyVar	NonRefSite	Pvalue
SLC1A2	1920	14	14	20	0.642723
SLC1A3	1920	12	12	23	0.0239278
SLC6A3	1920	9	9	19	0.25645
SLC6A4	1920	9	9	22	0.344269
TPH1	1920	16	16	23	0.686267
TPH2	1920	18	18	35	0.821772
VPS35	1920	7	7	10	0.981706
ZNF804A	1920	19	19	45	0.979811

eTable 13. Information about variants identified in the reduced NMDA-mediated synaptic current in the follow-up study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	Causal _KGGSeq	Prediction _other
1	20991117	C/T	rs377443985	KIF17	missense	KIF17:NM_001122819(15Exons):exon15:c.G3047A:p.R1016H&missense;KIF17:NM_020816(15Exons):exon15:c.G3050A:p.R1017H&missense	0.0005149	Y	A;B;C;D;E;F:0.0484:0.828:0.792
1	20991243	G/A	rs376184055	KIF17	missense	KIF17:NM_001122819(15Exons):exon15:c.C2921T:p.S974L&missense;KIF17:NM_020816(15Exons):exon15:c.C2924T:p.S975L&missense	0.0002575	Y	A;B;C;D;E;H;F:0.0432:0.844:0.773
1	20996913	C/T	ID42	KIF17	splicing	KIF17:NM_001122819(15Exons):3splicing13+1;KIF17:NM_020816(15Exons):3splicing13+1	0.0007724	Y	B;D;H;F:0.0414:0.84:0.742
1	20998491	C/T	rs141985868	KIF17	missense	KIF17:NM_001122819(15Exons):exon12:c.G2662A:p.E888K&missense;KIF17:NM_020816(15Exons):exon12:c.G2662A:p.E888K&missense	0.001287	Y	A;B;C;D;E;F:0.0484:0.828:0.792
1	20998508	C/T	rs34232864	KIF17	missense	KIF17:NM_001122819(15Exons):exon12:c.G2645A:p.R882H&missense;KIF17:NM_020816(15Exons):exon12:c.G2645A:p.R882H&missense	0.0002575	Y	A;G;B;C;D;E;F:0.0494:0.825:0.796

eTable 13 (continued). Information about variants identified in the reduced NMDA-mediated synaptic current in the follow-up study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	Causal _KGGSeq	Prediction _other
1	20998568	T/A	rs113995871	KIF17	missense	KIF17:NM_001122819(15Exons):exon12:c.A2585T:p.E862V&missense;KIF17:NM_020816(15Exons):exon12:c.A2585T:p.E862V&missense	0.001287	Y	A;B;C;D;E;F:0.0484:0.828:0.792
1	20998598	C/T	rs139517726	KIF17	missense	KIF17:NM_001122819(15Exons):exon12:c.G2555A:p.R852H&missense;KIF17:NM_020816(15Exons):exon12:c.G2555A:p.R852H&missense	0.0002575	Y	A;B;C;D;E;F:0.0484:0.828:0.792
1	21009184	G/A	rs114545284	KIF17	missense	KIF17:NM_001122819(15Exons):exon11:c.C2425T:p.R809W&missense;KIF17:NM_020816(15Exons):exon11:c.C2425T:p.R809W&missense	0.0002575	Y	A;B;E;H;F;I:0.0287:0.885:0.676
1	21009232	C/T	rs200844482	KIF17	missense	KIF17:NM_001122819(15Exons):exon11:c.G2377A:p.G793R&missense;KIF17:NM_020816(15Exons):exon11:c.G2377A:p.G793R&missense	0.0002575	Y	A;B;C;D;E;F:0.0484:0.828:0.792
1	21009252	T/G	ID51	KIF17	missense	KIF17:NM_001122819(15Exons):exon11:c.A2357C:p.Q786P&missense;KIF17:NM_020816(15Exons):exon11:c.A2357C:p.Q786P&missense	0.0002575	Y	A;B;C;D;E;F:0.0484:0.828:0.792

eTable 13 (continued). Information about variants identified in the reduced NMDA-mediated synaptic current in the follow-up study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	Causal _KGGSeq	Prediction _other
1	21009286	C/A	rs116367430	KIF17	missense	KIF17:NM_001122819(15Exons):exon11:c.G2323T:p.D775Y&missense;KIF17:NM_020816(15Exons):exon11:c.G2323T:p.D775Y&missense	0.0002575	Y	A;B;C;D;E;F:0.0484:0.828:0.792
1	21009289	C/T	ID52	KIF17	missense	KIF17:NM_001122819(15Exons):exon11:c.G2320A:p.A774T&missense;KIF17:NM_020816(15Exons):exon11:c.G2320A:p.A774T&missense	0.0002575	Y	A;B;C;D;E;F:0.0484:0.828:0.792
1	21011440	T/G	rs139742596	KIF17	missense	KIF17:NM_001122819(15Exons):exon10:c.A2093C:p.Q698P&missense;KIF17:NM_020816(15Exons):exon10:c.A2093C:p.Q698P&missense	0.004797	Y	A;B;E;H;F;I:0.0287:0.885:0.676
1	21016692	C/T	rs186246358	KIF17	missense	KIF17:NM_001122819(15Exons):exon7:c.G1370A:p.R457Q&missense;KIF17:NM_020816(15Exons):exon7:c.G1370A:p.R457Q&missense	0.0002575	Y	B;C;H;I:0.0386:0.854:0.72
1	21016693	G/A	ID79	KIF17	missense	KIF17:NM_001122819(15Exons):exon7:c.C1369T:p.R457W&missense;KIF17:NM_020816(15Exons):exon7:c.C1369T:p.R457W&missense	0.0002575	Y	A;LRT_score;B;H;F:0.037:0.846:0.715

eTable 13 (continued). Information about variants identified in the reduced NMDA-mediated synaptic current in the follow-up study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	Causal _KGGSeq	Prediction _other
1	21016710	G/A	ID81	KIF17	missense	KIF17:NM_001122819(15Exons):exon7:c.C1352T:p.T451M&missense;KIF17:NM_020816(15Exons):exon7:c.C1352T:p.T451M&missense	0.0005149	Y	B;C;H;I:0.0386:0.854:0.72
1	21024892	C/T	rs199771446	KIF17	missense	KIF17:NM_001122819(15Exons):exon6:c.G1213A:p.E405K&missense;KIF17:NM_020816(15Exons):exon6:c.G1213A:p.E405K&missense	0.002317	Y	A;B;C;D;H;I:0.046:0.839:0.761
1	21024922	G/A	ID93	KIF17	stopgain	KIF17:NM_001122819(15Exons):exon6:c.C1183T:p.Q395*&stopgain;KIF17:NM_020816(15Exons):exon6:c.C1183T:p.Q395*&stopgain	0.0005149	Y	B;D;H;F:0.0414:0.84:0.742
1	21031011	C/T	rs374159508	KIF17	missense	KIF17:NM_001122819(15Exons):exon5:c.G1052A:p.R351H&missense;KIF17:NM_020816(15Exons):exon5:c.G1052A:p.R351H&missense	0.0002575	Y	A;B;C;D;E;F:0.0484:0.828:0.792
1	21031039	T/G	ID95	KIF17	missense	KIF17:NM_001122819(15Exons):exon5:c.A1024C:p.N342H&missense;KIF17:NM_020816(15Exons):exon5:c.A1024C:p.N342H&missense	0.0005149	Y	A;B;C;D;E;F:0.0484:0.828:0.792
1	21031159	C/T	rs142534674	KIF17	missense	KIF17:NM_001122819(15Exons):exon5:c.G904A:p.G302S&missense;KIF17:NM_020816(15Exons):exon5:c.G904A:p.G302S&missense	0.0002575	Y	A;B;C;D;E;F:0.0484:0.828:0.792

eTable 13 (continued). Information about variants identified in the reduced NMDA-mediated synaptic current in the follow-up study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	Causal _KGGSeq	Prediction _other
1	21031266	G/A	ID99	KIF17	missense	KIF17:NM_001122819(15Exons):exon5:c.C797T:p.S266L&missense;KIF17:NM_020816(15Exons):exon5:c.C797T:p.S266L&missense	0.0002575	Y	A;B;C;D;E;F:0.0484:0.828:0.792
1	21031326	C/T	ID101	KIF17	missense	KIF17:NM_001122819(15Exons):exon5:c.G737A:p.R246Q&missense;KIF17:NM_020816(15Exons):exon5:c.G737A:p.R246Q&missense	0.0002575	Y	A;B;C;D;E;F:0.0484:0.828:0.792
1	21031330	C/T	ID102	KIF17	missense	KIF17:NM_001122819(15Exons):exon5:c.G733A:p.E245K&missense;KIF17:NM_020816(15Exons):exon5:c.G733A:p.E245K&missense	0.0002575	Y	A;B;C;D;E;F:0.0484:0.828:0.792
1	21036173	G/A	ID109	KIF17	missense	KIF17:NM_001122819(15Exons):exon4:c.C629T:p.S210L&missense;KIF17:NM_020816(15Exons):exon4:c.C629T:p.S210L&missense	0.0002575	Y	A;B;C;D;E;F:0.0484:0.828:0.792
1	21036290	A/G	ID110	KIF17	missense	KIF17:NM_001122819(15Exons):exon4:c.T512C:p.V171A&missense;KIF17:NM_020816(15Exons):exon4:c.T512C:p.V171A&missense	0.0002575	Y	A;B;C;D;E;F:0.0484:0.828:0.792
1	21039972	C/T	ID113	KIF17	missense	KIF17:NM_001122819(15Exons):exon3:c.G455A:p.G152E&missense;KIF17:NM_020816(15Exons):exon3:c.G455A:p.G152E&missense	0.0002575	Y	A;C;D;F:0.0381:0.86:0.752
1	21039996	T/C	ID114	KIF17	missense	KIF17:NM_001122819(15Exons):exon3:c.A431G:p.N144S&missense;KIF17:NM_020816(15Exons):exon3:c.A431G:p.N144S&missense	0.0002575	Y	A;B;C;D;E;F:0.0484:0.828:0.792

eTable 13 (continued). Information about variants identified in the reduced NMDA-mediated synaptic current in the follow-up study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	Causal _KGGSeq	Prediction _other
1	21040020	C/T	ID116	KIF17	missense	KIF17:NM_001122819(15Exons):exon3:c.G407A:p.R136Q&missense;KIF17:NM_020816(15Exons):exon3:c.G407A:p.R136Q&missense	0.0005149	Y	A;B;C;D;E;F:0.0484:0.828:0.792
11	64375368	T/A	ID2445	NRXN2	missense	NRXN2:NM_138732(20Exons):exon20:c.A4229T:p.E1410V&missense;NRXN2:NM_015080(23Exons):exon23:c.A4439T:p.E1480V&missense;NRXN2:NM_138734(7Exons):exon7:c.A1301T:p.E434V&missense	0.0002575	Y	A;D;H:0.0506:0.84:0.741
11	64375369	C/A	ID2446	NRXN2	stopgain	NRXN2:NM_138732(20Exons):exon20:c.G4228T:p.E1410*&stopgain;NRXN2:NM_015080(23Exons):exon23:c.G4438T:p.E1480*&stopgain;NRXN2:NM_138734(7Exons):exon7:c.G1300T:p.E434*&stopgain	0.0002575	Y	A;B;D;F:0.0324:0.877:0.706
11	64375399	G/A	ID2448	NRXN2	missense	NRXN2:NM_138732(20Exons):exon20:c.C4198T:p.R1400C&missense;NRXN2:NM_015080(23Exons):exon23:c.C4408T:p.R1470C&missense;NRXN2:NM_138734(7Exons):exon7:c.C1270T:p.R424C&missense	0.0002575	Y	A;G;B;F:0.0385:0.849:0.732

eTable 13 (continued). Information about variants identified in the reduced NMDA-mediated synaptic current in the follow-up study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	Causal _KGGSeq	Prediction _other
11	64390305	T/C	ID2463	NRXN2	missense	NRXN2:NM_138732(20Exons):exon18:c.A3883G:p.I1295V&missense;NRXN2:NM_015080(23Exons):exon21:c.A4093G:p.I1365V&missense;NRXN2:NM_138734(7Exons):exon5:c.A955G:p.I319V&missense	0.0005149	Y	K;G;B;C;D;H:0.0478:0.829:0.769
11	64390433	G/A	rs375639642	NRXN2	missense	NRXN2:NM_138732(20Exons):exon18:c.C3755T:p.A1252V&missense;NRXN2:NM_015080(23Exons):exon21:c.C3965T:p.A1322V&missense;NRXN2:NM_138734(7Exons):exon5:c.C827T:p.A276V&missense	0.0002575	Y	A;D;E;F:0.0413:0.843:0.755
11	64398035	G/A	ID2473	NRXN2	missense	NRXN2:NM_138732(20Exons):exon17:c.C3476T:p.T1159I&missense;NRXN2:NM_015080(23Exons):exon19:c.C3596T:p.T1199I&missense;NRXN2:NM_138734(7Exons):exon3:c.C458T:p.T153I&missense	0.0002575	Y	A;D;E;F:0.0413:0.843:0.755
11	64402807	C/T	ID2475	NRXN2	missense	NRXN2:NM_138732(20Exons):exon16:c.G3401A:p.R1134Q&missense;NRXN2:NM_015080(23Exons):exon18:c.G3521A:p.R1174Q&missense;NRXN2:NM_138734(7Exons):exon2:c.G383A:p.R128Q&missense	0.0005149	Y	A;D;E;F:0.0413:0.843:0.755

eTable 13 (continued). Information about variants identified in the reduced NMDA-mediated synaptic current in the follow-up study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	Causal _KGGSeq	Prediction _other
11	64402864	T/C	rs3701080 57	NRXN2	missense	NRXN2:NM_138732(20Exons):exon16:c.A3 344G:p.N1115S&missense;NRXN2:NM_015 080(23Exons):exon18:c.A3464G:p.N1155S& missense;NRXN2:NM_138734(7Exons):exon 2:c.A326G:p.N109S&missense	0.0005149	Y	A;B;J;F:0.0313:0. 936:0.894
11	64415766	C/T	ID2482	NRXN2	missense	NRXN2:NM_138732(20Exons):exon15:c.G3 208A:p.V1070I&missense;NRXN2:NM_0150 80(23Exons):exon17:c.G3328A:p.V1110I&mi ssense	0.0002575	Y	B;C;D;F:0.0435:0 .843:0.771
11	64416245	C/T	ID2486	NRXN2	missense	NRXN2:NM_138732(20Exons):exon14:c.G3 124A:p.A1042T&missense;NRXN2:NM_015 080(23Exons):exon16:c.G3244A:p.A1082T& missense	0.0002575	Y	A;B;C;D;E;F:0.04 84:0.828:0.792
11	64418931	T/C	ID2494	NRXN2	missense	NRXN2:NM_138732(20Exons):exon12:c.A2 594G:p.E865G&missense;NRXN2:NM_0150 80(23Exons):exon14:c.A2714G:p.E905G&mi ssense	0.0002575	Y	A;B;C;D;E;F:0.04 84:0.828:0.792
11	64428001	G/A	ID2522	NRXN2	missense	NRXN2:NM_138732(20Exons):exon10:c.C20 99T:p.T700M&missense;NRXN2:NM_01508 0(23Exons):exon11:c.C2192T:p.T731M&miss ense	0.0002575	Y	A;B;C;D;E;F:0.04 84:0.828:0.792

eTable 13 (continued). Information about variants identified in the reduced NMDA-mediated synaptic current in the follow-up study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	Causal _KGGSeq	Prediction _other
11	64428239	C/T	rs72927004	NRXN2	missense	NRXN2:NM_138732(20Exons):exon9:c.G2078A:p.R693Q&missense;NRXN2:NM_015080(23Exons):exon10:c.G2171A:p.R724Q&missense	0.0007724	Y	G;B;D;F:0.0309:0.881:0.696
11	64428252	C/T	ID2523	NRXN2	missense	NRXN2:NM_138732(20Exons):exon9:c.G2065A:p.G689S&missense;NRXN2:NM_015080(23Exons):exon10:c.G2158A:p.G720S&missense	0.0002575	Y	A;B;C;D;E;F:0.0484:0.828:0.792
11	64428287	C/A	ID2524	NRXN2	missense	NRXN2:NM_138732(20Exons):exon9:c.G2030T:p.G677V&missense;NRXN2:NM_015080(23Exons):exon10:c.G2123T:p.G708V&missense	0.0002575	Y	A;B;C;D;E;F:0.0484:0.828:0.792
11	64428398	C/T	ID2526	NRXN2	missense	NRXN2:NM_138732(20Exons):exon9:c.G1919A:p.R640Q&missense;NRXN2:NM_015080(23Exons):exon10:c.G2012A:p.R671Q&missense	0.0002575	Y	A;G;B;C;J;D;E;H;F:0.0283:0.944:0.891
11	64428447	C/G	ID2527	NRXN2	missense	NRXN2:NM_138732(20Exons):exon9:c.G1870C:p.V624L&missense;NRXN2:NM_015080(23Exons):exon10:c.G1963C:p.V655L&missense	0.0005149	Y	A;B;C;D;E;F:0.0484:0.828:0.792

eTable 13 (continued). Information about variants identified in the reduced NMDA-mediated synaptic current in the follow-up study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	Causal _KGGSeq	Prediction _other
11	64428458	C/A	ID2528	NRXN2	missense	NRXN2:NM_138732(20Exons):exon9:c.G1859T:p.R620L&missense;NRXN2:NM_015080(23Exons):exon10:c.G1952T:p.R651L&missense	0.0002575	Y	A;K;G;B;C;D;E;H:0.0491:0.827:0.776
11	64428501	C/A	ID2529	NRXN2	missense	NRXN2:NM_138732(20Exons):exon9:c.G1816T:p.V606L&missense;NRXN2:NM_015080(23Exons):exon10:c.G1909T:p.V637L&missense	0.0002575	Y	A;D;H:0.0506:0.84:0.741
11	64434956	G/A	rs201258323	NRXN2	missense	NRXN2:NM_138732(20Exons):exon8:c.C1471T:p.R491C&missense;NRXN2:NM_015080(23Exons):exon9:c.C1564T:p.R522C&missense	0.0002575	Y	A;B;C;D;E;F:0.0484:0.828:0.792
11	64434980	T/C	ID2534	NRXN2	missense	NRXN2:NM_138732(20Exons):exon8:c.A1447G:p.T483A&missense;NRXN2:NM_015080(23Exons):exon9:c.A1540G:p.T514A&missense	0.0002575	Y	A;LRT_score;B;E;H;F:0.0325:0.867:0.686
11	64434997	C/T	rs140588352	NRXN2	missense	NRXN2:NM_138732(20Exons):exon8:c.G1430A:p.R477H&missense;NRXN2:NM_015080(23Exons):exon9:c.G1523A:p.R508H&missense	0.0002575	Y	G;B;C;D;H:0.0541:0.817:0.783

eTable 13 (continued). Information about variants identified in the reduced NMDA-mediated synaptic current in the follow-up study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	Causal _KGGSeq	Prediction _other
11	64435006	G/A	rs200334993	NRXN2	missense	NRXN2:NM_138732(20Exons):exon8:c.C1421T:p.A474V&missense;NRXN2:NM_015080(23Exons):exon9:c.C1514T:p.A505V&missense	0.0007724	Y	K;B;D;F:0.0325:0.873:0.687
11	64435078	T/A	rs376239889	NRXN2	missense	NRXN2:NM_138732(20Exons):exon8:c.A1349T:p.D450V&missense;NRXN2:NM_015080(23Exons):exon9:c.A1442T:p.D481V&missense	0.001287	Y	K;B;J;D:0.028:0.942:0.879
11	64436045	G/A	ID2537	NRXN2	missense	NRXN2:NM_138732(20Exons):exon7:c.C1136T:p.T379I&missense;NRXN2:NM_015080(23Exons):exon8:c.C1229T:p.T410I&missense	0.00027	Y	B;C;D;F:0.0435:0.843:0.771
11	64457922	C/A	ID2554	NRXN2	missense	NRXN2:NM_138732(20Exons):intronic4;NRXN2:NM_015080(23Exons):exon5:c.G805T:p.G269W&missense	0.0002575	Y	A;D;E;F:0.0413:0.843:0.755
11	64480473	G/C	ID2571	NRXN2	missense	NRXN2:NM_138732(20Exons):exon2:c.C699G:p.H233Q&missense;NRXN2:NM_015080(23Exons):exon2:c.C699G:p.H233Q&missense	0.006959	Y	A;B;C;J;F:0.0275:0.943:0.89
11	64480595	C/T	ID2575	NRXN2	missense	NRXN2:NM_138732(20Exons):exon2:c.G577A:p.G193S&missense;NRXN2:NM_015080(23Exons):exon2:c.G577A:p.G193S&missense	0.0002584	Y	B;J:0.023:0.938:0.858

eTable 13 (continued). Information about variants identified in the reduced NMDA-mediated synaptic current in the follow-up study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	Causal _KGGSeq	Prediction _other
11	64480718	C/T	ID2578	NRXN2	missense	NRXN2:NM_138732(20Exons):exon2:c.G454A:p.V152M&missense;NRXN2:NM_015080(23Exons):exon2:c.G454A:p.V152M&missense	0.000258	Y	A;B;C;D;E;H;F:0.0432:0.844:0.773
11	64480829	C/A	ID2580	NRXN2	missense	NRXN2:NM_138732(20Exons):exon2:c.G343T:p.V115L&missense;NRXN2:NM_015080(23Exons):exon2:c.G343T:p.V115L&missense	0.000258	Y	B;D;H;F;I:0.0292:0.883:0.683
14	79175584	C/T	ID2990	NRXN3	missense	NRXN3:NR_073547(21Exons):ncRNA;NRXN3:NM_004796(17Exons):exon4:c.C127T:p.R43C&missense	0.0002575	Y	B;D;H;F:0.0414:0.84:0.742
14	79175600	G/A	ID2991	NRXN3	missense	NRXN3:NR_073547(21Exons):ncRNA;NRXN3:NM_004796(17Exons):exon4:c.G143A:p.R48H&missense	0.0002575	Y	B;D;H;F:0.0414:0.84:0.742
14	79175723	A/G	ID2994	NRXN3	missense	NRXN3:NR_073547(21Exons):ncRNA;NRXN3:NM_004796(17Exons):exon4:c.A266G:p.K89R&missense	0.0002575	Y	G;B;C;E;H;F;I:0.0411:0.848:0.763
14	79175765	G/T	rs199543320	NRXN3	missense	NRXN3:NR_073547(21Exons):ncRNA;NRXN3:NM_004796(17Exons):exon4:c.G308T:p.R103L&missense	0.0002575	Y	B;C;D;F:0.0435:0.843:0.771
14	79175899	C/T	ID2995	NRXN3	missense	NRXN3:NR_073547(21Exons):ncRNA;NRXN3:NM_004796(17Exons):exon4:c.C442T:p.L148F&missense	0.0002575	Y	B;D;H;F:0.0414:0.84:0.742

eTable 13 (continued). Information about variants identified in the reduced NMDA-mediated synaptic current in the follow-up study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	Causal _KGGSeq	Prediction _other
14	79175905	A/G	ID2996	NRXN3	missense	NRXN3:NR_073547(21Exons):ncRNA;NRXN3:NM_004796(17Exons):exon4:c.A448G:p.M150V&missense	0.0002575	Y	B;C;D;F:0.0435:0.843:0.771
14	79181440	G/A	ID2998	NRXN3	missense	NRXN3:NR_073547(21Exons):ncRNA;NRXN3:NM_004796(17Exons):exon5:c.G883A:p.D295N&missense	0.0002575	Y	B;D;H;F:0.0414:0.84:0.742
14	79270043	G/A	ID3000	NRXN3	missense	NRXN3:NR_073547(21Exons):ncRNA;NRXN3:NM_004796(17Exons):exon6:c.G1006A:p.V336M&missense	0.0002575	Y	B;D;H;F:0.0414:0.84:0.742
14	79270103	G/A	ID3001	NRXN3	missense	NRXN3:NR_073547(21Exons):ncRNA;NRXN3:NM_004796(17Exons):exon6:c.G1066A:p.D356N&missense	0.0002575	Y	B;D;H;F:0.0414:0.84:0.742
14	79423698	G/A	ID3017	NRXN3	missense	NRXN3:NR_073547(21Exons):ncRNA;NRXN3:NM_004796(17Exons):exon8:c.G1270A:p.A424T&missense	0.0002575	Y	B;D;H;F:0.0414:0.84:0.742
14	79432407	A/G	ID3018	NRXN3	missense	NRXN3:NR_073547(21Exons):ncRNA;NRXN3:NM_004796(17Exons):exon9:c.A1316G:p.N439S&missense	0.0002575	Y	B;D;H;F:0.0414:0.84:0.742
14	79432508	A/G	ID3020	NRXN3	missense	NRXN3:NR_073547(21Exons):ncRNA;NRXN3:NM_004796(17Exons):exon9:c.A1417G:p.I473V&missense	0.000516	Y	B;D;H;F:0.0414:0.84:0.742

eTable 13 (continued). Information about variants identified in the reduced NMDA-mediated synaptic current in the follow-up study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	Causal _KGGSeq	Prediction _other
14	79433612	C/T	ID3030	NRXN3	missense	NRXN3:NR_073547(21Exons):ncRNA;NRXN3:NM_004796(17Exons):exon10:c.C1720T:p.R574C&missense	0.0002575	Y	B;D;H;F:0.0414:0.84:0.742
14	79433613	G/A	rs140528152	NRXN3	missense	NRXN3:NR_073547(21Exons):ncRNA;NRXN3:NM_004796(17Exons):exon10:c.G1721A:p.R574H&missense	0.001545	Y	B;D;H;F:0.0414:0.84:0.742
14	79433645	G/A	rs186034014	NRXN3	missense	NRXN3:NR_073547(21Exons):ncRNA;NRXN3:NM_004796(17Exons):exon10:c.G1753A:p.V585I&missense	0.0002575	Y	B;D;H;F:0.0414:0.84:0.742
14	79434660	G/A	rs151072919	NRXN3	missense	NRXN3:NR_073547(21Exons):ncRNA;NRXN3:NM_004796(17Exons):exon11:c.G1994A:p.R665Q&missense	0.00206	Y	B;D;H;F:0.0414:0.84:0.742
14	79454415	A/G	ID3035	NRXN3	missense	NRXN3:NR_073547(21Exons):ncRNA;NRXN3:NM_004796(17Exons):exon12:c.A2074G:p.M692V&missense	0.0002575	Y	B;J;E;H;F:0.0339:0.929:0.895

eTable 13 (continued). Information about variants identified in the reduced NMDA-mediated synaptic current in the follow-up study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	Causal _KGGSeq	Prediction _other
14	80130283	T/C	ID3041	NRXN3	missense	NRXN3:NR_073546(8Exons):ncRNA;NRXN3:NR_073547(21Exons):ncRNA;NRXN3:NM_001105250(7Exons):exon3:c.T592C:p.Y198H&missense;NRXN3:NM_138970(6Exons):exon3:c.T592C:p.Y198H&missense;NRXN3:NM_001272020(6Exons):exon3:c.T592C:p.Y198H&missense;NRXN3:NM_004796(17Exons):exon14:c.T2488C:p.Y830H&missense	0.0005149	Y	B;C;D;F:0.0435:0.843:0.771
14	80158519	A/T	ID3044	NRXN3	missense	NRXN3:NR_073546(8Exons):ncRNA;NRXN3:NR_073547(21Exons):ncRNA;NRXN3:NM_138970(6Exons):intronic3;NRXN3:NM_001272020(6Exons):intronic3;NRXN3:NM_004796(17Exons):intronic14;NRXN3:NM_001105250(7Exons):exon4:c.A605T:p.N202I&missense	0.0002575	Y	G;B;J;D;E;H;F:0.0311:0.938:0.89

eTable 13 (continued). Information about variants identified in the reduced NMDA-mediated synaptic current in the follow-up study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	Causal _KGGSeq	Prediction _other
14	80164026	G/C	ID3048	NRXN3	missense	NRXN3:NR_073546(8Exons):ncRNA;NRXN3:NR_073547(21Exons):ncRNA;NRXN3:NM_001105250(7Exons):exon5:c.G745C:p.D249H&missense;NRXN3:NM_138970(6Exons):exon4:c.G655C:p.D219H&missense;NRXN3:NM_001272020(6Exons):exon4:c.G655C:p.D219H&missense;NRXN3:NM_004796(17Exons):exon15:c.G2551C:p.D851H&missense	0.0002575	Y	B;C;D;F:0.0435:0.843:0.771
14	80164153	T/G	ID3051	NRXN3	missense	NRXN3:NR_073546(8Exons):ncRNA;NRXN3:NR_073547(21Exons):ncRNA;NRXN3:NM_001105250(7Exons):exon5:c.T872G:p.V291G&missense;NRXN3:NM_138970(6Exons):exon4:c.T782G:p.V261G&missense;NRXN3:NM_001272020(6Exons):exon4:c.T782G:p.V261G&missense;NRXN3:NM_004796(17Exons):exon15:c.T2678G:p.V893G&missense	0.0002575	Y	G;B;C;D;E;F:0.0447:0.839:0.772

eTable 13 (continued). Information about variants identified in the reduced NMDA-mediated synaptic current in the follow-up study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	Causal _KGGSeq	Prediction _other
14	80164252	G/A	rs144373051	NRXN3	missense	NRXN3:NR_073546(8Exons):ncRNA;NRXN3:NR_073547(21Exons):ncRNA;NRXN3:NM_001105250(7Exons):exon5:c.G971A:p.R324H&missense;NRXN3:NM_138970(6Exons):exon4:c.G881A:p.R294H&missense;NRXN3:NM_001272020(6Exons):exon4:c.G881A:p.R294H&missense;NRXN3:NM_004796(17Exons):exon15:c.G2777A:p.R926H&missense	0.0002575	Y	G;C;J;D;E;H;F:0.026:0.945:0.881
14	80327436	T/C	ID3061	NRXN3	missense	NRXN3:NR_073546(8Exons):ncRNA;NRXN3:NR_073547(21Exons):ncRNA;NRXN3:NM_001105250(7Exons):intronic6;NRXN3:NM_138970(6Exons):intronic5;NRXN3:NM_004796(17Exons):intronic16;NRXN3:NM_001272020(6Exons):exon6:c.T1043C:p.I348T&missense	0.0002667	Y	B;D;H;F:0.0414:0.84:0.742
14	80327477	C/T	ID3064	NRXN3	missense	NRXN3:NR_073546(8Exons):ncRNA;NRXN3:NR_073547(21Exons):ncRNA;NRXN3:NM_001105250(7Exons):intronic6;NRXN3:NM_138970(6Exons):intronic5;NRXN3:NM_004796(17Exons):intronic16;NRXN3:NM_001272020(6Exons):exon6:c.C1084T:p.R362C&missense	0.0002814	Y	B;D;H;F:0.0414:0.84:0.742

eTable 13 (continued). Information about variants identified in the reduced NMDA-mediated synaptic current in the follow-up study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	Causal _KGGSeq	Prediction _other
14	80327547	G/A	ID3067	NRXN3	missense	NRXN3:NR_073546(8Exons):ncRNA;NRXN3:NR_073547(21Exons):ncRNA;NRXN3:NM_001105250(7Exons):intronic6;NRXN3:NM_138970(6Exons):intronic5;NRXN3:NM_004796(17Exons):intronic16;NRXN3:NM_001272020(6Exons):exon6:c.G1154A:p.C385Y&missense	0.000258	Y	G;B;J;D;E;H;F:0.0311:0.938:0.89
14	80327583	A/T	ID3068	NRXN3	missense	NRXN3:NR_073546(8Exons):ncRNA;NRXN3:NR_073547(21Exons):ncRNA;NRXN3:NM_001105250(7Exons):intronic6;NRXN3:NM_138970(6Exons):intronic5;NRXN3:NM_004796(17Exons):intronic16;NRXN3:NM_001272020(6Exons):exon6:c.A1190T:p.D397V&missense	0.0002576	Y	G;B;J;D;E;H;F:0.0311:0.938:0.89
14	80328078	C/T	ID3071	NRXN3	missense	NRXN3:NR_073546(8Exons):ncRNA;NRXN3:NR_073547(21Exons):ncRNA;NRXN3:NM_001105250(7Exons):exon7:c.C1151T:p.T384I&missense;NRXN3:NM_138970(6Exons):exon6:c.C1070T:p.T357I&missense;NRXN3:NM_001272020(6Exons):exon6:c.C1685T:p.T562I&missense;NRXN3:NM_004796(17Exons):exon17:c.C2957T:p.T986I&missense	0.0005152	Y	G;B;C;J;H;F:0.0261:0.946:0.88

eTable 13 (continued). Information about variants identified in the reduced NMDA-mediated synaptic current in the follow-up study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	Causal _KGGSeq	Prediction _other
14	80328207	A/C	ID3073	NRXN3	missense	NRXN3:NR_073546(8Exons):ncRNA;NRXN3:NR_073547(21Exons):ncRNA;NRXN3:NM_001105250(7Exons):exon7:c.A1280C:p.N427T&missense;NRXN3:NM_138970(6Exons):exon6:c.A1199C:p.N400T&missense;NRXN3:NM_001272020(6Exons):exon6:c.A1814C:p.N605T&missense;NRXN3:NM_004796(17Exons):exon17:c.A3086C:p.N1029T&missense	0.0002576	Y	G;B;C;J;E;H;F:0.0331:0.934:0.901
16	10031817	G/T	rs148511104	GRIN2A	missense	GRIN2A:NM_001134408(14Exons):exon3:c.C1006A:p.P336T&missense;GRIN2A:NM_000833(14Exons):exon4:c.C1006A:p.P336T&missense;GRIN2A:NM_001134407(13Exons):exon3:c.C1006A:p.P336T&missense	0.0002576	Y	B;D;H;F:0.0414:0.84:0.742
16	10031829	G/C	ID3206	GRIN2A	missense	GRIN2A:NM_001134408(14Exons):exon3:c.C994G:p.H332D&missense;GRIN2A:NM_000833(14Exons):exon4:c.C994G:p.H332D&missense;GRIN2A:NM_001134407(13Exons):exon3:c.C994G:p.H332D&missense	0.0002575	Y	B;D;E;F:0.0342:0.872:0.702

eTable 13 (continued). Information about variants identified in the reduced NMDA-mediated synaptic current in the follow-up study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	Causal _KGGSeq	Prediction _other
16	10031919	C/T	ID3207	GRIN2A	missense	GRIN2A:NM_001134408(14Exons):exon3:c.G904A:p.A302T&missense;GRIN2A:NM_000833(14Exons):exon4:c.G904A:p.A302T&missense;GRIN2A:NM_001134407(13Exons):exon3:c.G904A:p.A302T&missense	0.0002575	Y	B;C;D;F:0.0435:0.843:0.771
16	10032221	T/C	ID3211	GRIN2A	missense	GRIN2A:NM_001134408(14Exons):exon3:c.A602G:p.Q201R&missense;GRIN2A:NM_000833(14Exons):exon4:c.A602G:p.Q201R&missense;GRIN2A:NM_001134407(13Exons):exon3:c.A602G:p.Q201R&missense	0.0002575	Y	B;C;D;F:0.0435:0.843:0.771
16	10274027	C/T	ID3238	GRIN2A	missense	GRIN2A:NM_001134408(14Exons):exon2:c.G242A:p.S81N&missense;GRIN2A:NM_000833(14Exons):exon3:c.G242A:p.S81N&missense;GRIN2A:NM_001134407(13Exons):exon2:c.G242A:p.S81N&missense	0.0002575	Y	B;C;D;F:0.0435:0.843:0.771
16	10274090	G/A	ID3240	GRIN2A	missense	GRIN2A:NM_001134408(14Exons):exon2:c.C179T:p.A60V&missense;GRIN2A:NM_000833(14Exons):exon3:c.C179T:p.A60V&missense;GRIN2A:NM_001134407(13Exons):exon2:c.C179T:p.A60V&missense	0.0002575	Y	B;D;E;F;I:0.0296:0.882:0.686

eTable 13 (continued). Information about variants identified in the reduced NMDA-mediated synaptic current in the follow-up study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	Causal _KGGSeq	Prediction _other
16	10274189	G/A	rs367543129	GRIN2A	missense	GRIN2A:NM_001134408(14Exons):exon2:c.C80T:p.A27V&missense;GRIN2A:NM_000833(14Exons):exon3:c.C80T:p.A27V&missense;GRIN2A:NM_001134407(13Exons):exon2:c.C80T:p.A27V&missense	0.0007724	Y	B;C;D;F:0.0435:0.843:0.771
16	46694511	G/A	ID3243	VPS35	missense	VPS35:NM_018206(17Exons):exon17:c.C2264T:p.P755L&missense	0.0002575	Y	A;G;B;C;J;D;E;H;F:0.0283:0.944:0.891
16	46696993	C/A	ID3252	VPS35	missense	VPS35:NM_018206(17Exons):exon14:c.G1729T:p.A577S&missense	0.0002575	Y	A;D;E;F:0.0413:0.843:0.755
16	46705646	G/A	ID3255	VPS35	missense	VPS35:NM_018206(17Exons):exon12:c.C1495T:p.R499C&missense	0.0002575	Y	A;G;B;C;J;D;E;H;F:0.0283:0.944:0.891
16	46706251	A/G	ID3257	VPS35	missense	VPS35:NM_018206(17Exons):exon11:c.T1294C:p.S432P&missense	0.0002575	Y	A;G;B;C;J;D;E;H;F:0.0283:0.944:0.891
16	46710558	C/T	ID3272	VPS35	missense	VPS35:NM_018206(17Exons):exon8:c.G851A:p.R284Q&missense	0.0005149	Y	B;J;F;I:0.0287:0.937:0.881
16	46716039	C/T	rs193077277	VPS35	missense	VPS35:NM_018206(17Exons):exon3:c.G151A:p.G51S&missense	0.0007728	Y	B;D;H;F:0.0414:0.84:0.742
16	46717518	G/C	ID3287	VPS35	missense	VPS35:NM_018206(17Exons):exon2:c.C4G:p.P2A&missense	0.0002575	Y	A;D;E;F:0.0413:0.843:0.755

eTable 13 (continued). Information about variants identified in the reduced NMDA-mediated synaptic current in the follow-up study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	Causal _KGGSeq	Prediction _other
16	9857034	T/C	ID3119	GRIN2A	missense	GRIN2A:NM_001134408(14Exons):3UTR+177;GRIN2A:NM_000833(14Exons):exon14:c.A4367G:p.K1456R&missense;GRIN2A:NM_001134407(13Exons):exon13:c.A4367G:p.K1456R&missense	0.0002575	Y	B;C;D;F:0.0435:0.843:0.771
16	9857071	C/A	ID3121	GRIN2A	missense	GRIN2A:NM_001134408(14Exons):3UTR+140;GRIN2A:NM_000833(14Exons):exon14:c.G4330T:p.V1444F&missense;GRIN2A:NM_001134407(13Exons):exon13:c.G4330T:p.V1444F&missense	0.0005149	Y	B;C;D;F:0.0435:0.843:0.771
16	9857391	G/C	ID3124	GRIN2A	missense	GRIN2A:NM_001134408(14Exons):intronic13;GRIN2A:NM_000833(14Exons):exon14:c.C4010G:p.S1337W&missense;GRIN2A:NM_001134407(13Exons):exon13:c.C4010G:p.S1337W&missense	0.0002575	Y	G;LRT_score;B;D;E;H;F:0.0311:0.883:0.683
16	9857416	A/T	ID3125	GRIN2A	missense	GRIN2A:NM_001134408(14Exons):intronic13;GRIN2A:NM_000833(14Exons):exon14:c.T3985A:p.F1329I&missense;GRIN2A:NM_001134407(13Exons):exon13:c.T3985A:p.F1329I&missense	0.000258	Y	B;C;D;F:0.0435:0.843:0.771

eTable 13 (continued). Information about variants identified in the reduced NMDA-mediated synaptic current in the follow-up study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	Causal _KGGSeq	Prediction _other
16	9857830	A/C	ID3133	GRIN2A	missense	GRIN2A:NM_001134408(14Exons):exon13:c.T3571G:p.F1191V&missense;GRIN2A:NM_000833(14Exons):exon14:c.T3571G:p.F1191V&missense;GRIN2A:NM_001134407(13Exons):exon13:c.T3571G:p.F1191V&missense	0.0002575	Y	B;D;E;H;F:0.0336:0.865:0.712
16	9857976	G/C	ID3135	GRIN2A	missense	GRIN2A:NM_001134408(14Exons):exon13:c.C3425G:p.P1142R&missense;GRIN2A:NM_000833(14Exons):exon14:c.C3425G:p.P1142R&missense;GRIN2A:NM_001134407(13Exons):exon13:c.C3425G:p.P1142R&missense	0.0002577	Y	G;B;C;E;H;F;I:0.0411:0.848:0.763
16	9858103	C/T	ID3136	GRIN2A	missense	GRIN2A:NM_001134408(14Exons):exon13:c.G3298A:p.E1100K&missense;GRIN2A:NM_000833(14Exons):exon14:c.G3298A:p.E1100K&missense;GRIN2A:NM_001134407(13Exons):exon13:c.G3298A:p.E1100K&missense	0.0002575	Y	B;C;D;F:0.0435:0.843:0.771
16	9858162	T/A	ID3137	GRIN2A	missense	GRIN2A:NM_001134408(14Exons):exon13:c.A3239T:p.H1080L&missense;GRIN2A:NM_000833(14Exons):exon14:c.A3239T:p.H1080L&missense;GRIN2A:NM_001134407(13Exons):exon13:c.A3239T:p.H1080L&missense	0.0002575	Y	B;D;E;F:0.0342:0.872:0.702

eTable 13 (continued). Information about variants identified in the reduced NMDA-mediated synaptic current in the follow-up study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	Causal _KGGSeq	Prediction _other
16	9858195	G/A	ID3138	GRIN2A	missense	GRIN2A:NM_001134408(14Exons):exon13:c.C3206T:p.T1069M&missense;GRIN2A:NM_000833(14Exons):exon14:c.C3206T:p.T1069M&missense;GRIN2A:NM_001134407(13Exons):exon13:c.C3206T:p.T1069M&missense	0.0002575	Y	B;C;D;F:0.0435:0.843:0.771
16	9858202	G/A	ID3139	GRIN2A	missense	GRIN2A:NM_001134408(14Exons):exon13:c.C3199T:p.R1067W&missense;GRIN2A:NM_000833(14Exons):exon14:c.C3199T:p.R1067W&missense;GRIN2A:NM_001134407(13Exons):exon13:c.C3199T:p.R1067W&missense	0.0002575	Y	G;B;C;E;F:0.0455:0.829:0.783
16	9858403	C/T	ID3142	GRIN2A	missense	GRIN2A:NM_001134408(14Exons):exon13:c.G2998A:p.V1000M&missense;GRIN2A:NM_000833(14Exons):exon14:c.G2998A:p.V1000M&missense;GRIN2A:NM_001134407(13Exons):exon13:c.G2998A:p.V1000M&missense	0.0002575	Y	B;C;D;F:0.0435:0.843:0.771
16	9858642	C/G	ID3143	GRIN2A	missense	GRIN2A:NM_001134408(14Exons):exon13:c.G2759C:p.R920T&missense;GRIN2A:NM_000833(14Exons):exon14:c.G2759C:p.R920T&missense;GRIN2A:NM_001134407(13Exons):exon13:c.G2759C:p.R920T&missense	0.0002575	Y	B;C;D;F:0.0435:0.843:0.771

eTable 13 (continued). Information about variants identified in the reduced NMDA-mediated synaptic current in the follow-up study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	Causal _KGGSeq	Prediction _other
16	9858751	C/T	ID3144	GRIN2A	missense	GRIN2A:NM_001134408(14Exons):exon13:c.G2650A:p.D884N&missense;GRIN2A:NM_000833(14Exons):exon14:c.G2650A:p.D884N&missense;GRIN2A:NM_001134407(13Exons):exon13:c.G2650A:p.D884N&missense	0.0005149	Y	B;C;D;F:0.0435:0.843:0.771
16	9858765	T/C	rs183029507	GRIN2A	missense	GRIN2A:NM_001134408(14Exons):exon13:c.A2636G:p.K879R&missense;GRIN2A:NM_000833(14Exons):exon14:c.A2636G:p.K879R&missense;GRIN2A:NM_001134407(13Exons):exon13:c.A2636G:p.K879R&missense	0.002317	Y	G;B;C;D;E;F:0.0447:0.839:0.772
16	9858774	A/G	rs199784503	GRIN2A	missense	GRIN2A:NM_001134408(14Exons):exon13:c.T2627C:p.I876T&missense;GRIN2A:NM_000833(14Exons):exon14:c.T2627C:p.I876T&missense;GRIN2A:NM_001134407(13Exons):exon13:c.T2627C:p.I876T&missense	0.005664	Y	B;C;D;F:0.0435:0.843:0.771
16	9862737	G/C	rs201072838	GRIN2A	missense	GRIN2A:NM_001134408(14Exons):exon12:c.C2566G:p.R856G&missense;GRIN2A:NM_000833(14Exons):exon13:c.C2566G:p.R856G&missense;GRIN2A:NM_001134407(13Exons):exon12:c.C2566G:p.R856G&missense	0.0007724	Y	B;C;D;F:0.0435:0.843:0.771

eTable 13 (continued). Information about variants identified in the reduced NMDA-mediated synaptic current in the follow-up study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	Causal _KGGSeq	Prediction _other
16	9862818	C/A	ID3150	GRIN2A	missense	GRIN2A:NM_001134408(14Exons):exon12:c.G2485T:p.A829S&missense;GRIN2A:NM_000833(14Exons):exon13:c.G2485T:p.A829S&missense;GRIN2A:NM_001134407(13Exons):exon12:c.G2485T:p.A829S&missense	0.0002575	Y	B;C;D;F:0.0435:0.843:0.771
16	9892139	C/G	rs76392464	GRIN2A	missense	GRIN2A:NM_001134408(14Exons):exon11:c.G2351C:p.G784A&missense;GRIN2A:NM_000833(14Exons):exon12:c.G2351C:p.G784A&missense;GRIN2A:NM_001134407(13Exons):exon11:c.G2351C:p.G784A&missense	0.0002575	Y	G;B;J;E;F:0.0313:0.934:0.89
16	9923450	A/G	ID3167	GRIN2A	missense	GRIN2A:NM_001134408(14Exons):exon9:c.T1837C:p.F613L&missense;GRIN2A:NM_000833(14Exons):exon10:c.T1837C:p.F613L&missense;GRIN2A:NM_001134407(13Exons):exon9:c.T1837C:p.F613L&missense	0.0002575	Y	G;B;C;J;D;E;H;F:0.0288:0.942:0.888
16	9923507	G/A	rs367543140	GRIN2A	missense	GRIN2A:NM_001134408(14Exons):exon9:c.C1780T:p.P594S&missense;GRIN2A:NM_000833(14Exons):exon10:c.C1780T:p.P594S&missense;GRIN2A:NM_001134407(13Exons):exon9:c.C1780T:p.P594S&missense	0.0005149	Y	G;B;J;D;E;H;F:0.0311:0.938:0.89

eTable 13 (continued). Information about variants identified in the reduced NMDA-mediated synaptic current in the follow-up study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	Causal _KGGSeq	Prediction _other
16	9928058	T/A	ID3172	GRIN2A	missense	GRIN2A:NM_001134408(14Exons):exon8:c.A1681T:p.M561L&missense;GRIN2A:NM_000833(14Exons):exon9:c.A1681T:p.M561L&missense;GRIN2A:NM_001134407(13Exons):exon8:c.A1681T:p.M561L&missense	0.0002575	Y	B;J;F:0.0352:0.926:0.895
16	9934949	A/T	ID3196	GRIN2A	missense	GRIN2A:NM_001134408(14Exons):exon6:c.T1341A:p.N447K&missense;GRIN2A:NM_000833(14Exons):exon7:c.T1341A:p.N447K&missense;GRIN2A:NM_001134407(13Exons):exon6:c.T1341A:p.N447K&missense	0.0005149	Y	B;C;E;I:0.0411:0.84:0.733
16	9943670	G/A	ID3198	GRIN2A	missense	GRIN2A:NM_001134408(14Exons):exon5:c.C1271T:p.P424L&missense;GRIN2A:NM_000833(14Exons):exon6:c.C1271T:p.P424L&missense;GRIN2A:NM_001134407(13Exons):exon5:c.C1271T:p.P424L&missense	0.0002575	Y	B;C;D;F:0.0435:0.843:0.771
16	9984907	T/G	ID3200	GRIN2A	missense	GRIN2A:NM_001134408(14Exons):exon4:c.A1058C:p.E353A&missense;GRIN2A:NM_000833(14Exons):exon5:c.A1058C:p.E353A&missense;GRIN2A:NM_001134407(13Exons):exon4:c.A1058C:p.E353A&missense	0.0002575	Y	B;D;H;F:0.0414:0.84:0.742
19	30303652	G/A	ID3498	CCNE1	missense	CCNE1:NM_001238(12Exons):exon3:c.G80A:p.R27H&missense	0.0002575	Y	A;B;C;D;E;F:0.0484:0.828:0.792

eTable 13 (continued). Information about variants identified in the reduced NMDA-mediated synaptic current in the follow-up study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	Causal _KGGSeq	Prediction _other
19	30303901	T/C	ID3501	CCNE1	missense	CCNE1:NM_001238(12Exons):exon4:c.T137C:p.M46T&missense	0.0002575	Y	B;D;H;F:0.0414:0.84:0.742
19	30312636	A/G	rs149261350	CCNE1	missense	CCNE1:NM_001238(12Exons):exon8:c.A617G:p.Y206C&missense	0.0002575	Y	A;B;C;D;E;F:0.0484:0.828:0.792
19	30314658	C/T	ID3520	CCNE1	stopgain	CCNE1:NM_001238(12Exons):exon12:c.C1207T:p.Q403*&stopgain	0.0002575	Y	B;D;H;F:0.0414:0.84:0.742
19	45971874	C/A	ID3526	FOSB	missense	FOSB:NM_006732(4Exons):exon1:c.C30A:p.D10E&missense;FOSB:NM_001114171(3Exons):exon1:c.C30A:p.D10E&missense	0.0002575	Y	C;D;E;F:0.042:0.839:0.776
19	45971902	T/A	ID3527	FOSB	missense	FOSB:NM_006732(4Exons):exon1:c.T58A:p.S20T&missense;FOSB:NM_001114171(3Exons):exon1:c.T58A:p.S20T&missense	0.0002575	Y	A;B;C;D;E;F:0.0484:0.828:0.792
19	45974059	C/T	rs199733739	FOSB	missense	FOSB:NM_006732(4Exons):exon2:c.C299T:p.P100L&missense;FOSB:NM_001114171(3Exons):exon2:c.C299T:p.P100L&missense	0.0002575	Y	A;B;C;D;E;H:0.056:0.812:0.793
19	45974106	G/A	rs143780767	FOSB	missense	FOSB:NM_006732(4Exons):exon2:c.G346A:p.G116R&missense;FOSB:NM_001114171(3Exons):exon2:c.G346A:p.G116R&missense	0.0002575	Y	B;D;E;F;I:0.0296:0.882:0.686
19	45974182	G/A	ID3535	FOSB	missense	FOSB:NM_006732(4Exons):exon2:c.G422A:p.R141Q&missense;FOSB:NM_001114171(3Exons):exon2:c.G422A:p.R141Q&missense	0.0002575	Y	A;B;C;D;E;F:0.0484:0.828:0.792

eTable 13 (continued). Information about variants identified in the reduced NMDA-mediated synaptic current in the follow-up study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	Causal _KGGSeq	Prediction _other
19	45974196	C/G	ID3536	FOSB	missense	FOSB:NM_006732(4Exons):exon2:c.C436G:p.R146G&missense;FOSB:NM_001114171(3Exons):exon2:c.C436G:p.R146G&missense	0.0002575	Y	A;B;C;D;H;F:0.0455:0.832:0.786
19	45975932	G/A	ID3549	FOSB	missense	FOSB:NM_006732(4Exons):exon4:c.G679A:p.E227K&missense;FOSB:NM_001114171(3Exons):exon3:c.G571A:p.E191K&missense	0.0002575	Y	A;D;E;F:0.0413:0.843:0.755
19	45976191	C/T	ID3555	FOSB	missense	FOSB:NM_006732(4Exons):exon4:c.C938T:p.A313V&missense;FOSB:NM_001114171(3Exons):exon3:c.C830T:p.A277V&missense	0.0002575	Y	A;B;J;D;E;H:0.0322:0.938:0.895
19	45976196	G/T	ID3556	FOSB	missense	FOSB:NM_006732(4Exons):exon4:c.G943T:p.A315S&missense;FOSB:NM_001114171(3Exons):exon3:c.G835T:p.A279S&missense	0.0002575	Y	A;B;D;E;F:0.0385:0.859:0.732
2	50280445	T/G	ID270	NRXN1	missense	NRXN1:NM_001135659(24Exons):exon22:c.A4212C:p.R1404S&missense;NRXN1:NM_004801(22Exons):exon20:c.A4002C:p.R1334S&missense;NRXN1:NM_138735(6Exons):exon4:c.A897C:p.R299S&missense	0.0002576	Y	A;B;C;D;E;F:0.0484:0.828:0.792
2	50280470	G/A	rs199701703	NRXN1	missense	NRXN1:NM_001135659(24Exons):exon22:c.C4187T:p.T1396M&missense;NRXN1:NM_004801(22Exons):exon20:c.C3977T:p.T1326M&missense;NRXN1:NM_138735(6Exons):exon4:c.C872T:p.T291M&missense	0.0005149	Y	A;B;C;D;E;F:0.0484:0.828:0.792

eTable 13 (continued). Information about variants identified in the reduced NMDA-mediated synaptic current in the follow-up study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	Causal _KGGSeq	Prediction _other
2	50280477	T/A	rs2020068 15	NRXN1	missense	NRXN1:NM_001135659(24Exons):exon22:c. A4180T:p.T1394S&missense;NRXN1:NM_0 04801(22Exons):exon20:c.A3970T:p.T1324S &missense;NRXN1:NM_138735(6Exons):ex on4:c.A865T:p.T289S&missense	0.005664	Y	A;B;C;D;E;F:0.04 84:0.828:0.792
2	50280526	C/G	rs2009352 46	NRXN1	missense	NRXN1:NM_001135659(24Exons):exon22:c. G4131C:p.E1377D&missense;NRXN1:NM_0 04801(22Exons):exon20:c.G3921C:p.E1307D &missense;NRXN1:NM_138735(6Exons):ex on4:c.G816C:p.E272D&missense	0.001287	Y	A;B;D;E;F:0.0385 :0.859:0.732
2	50280545	G/A	ID272	NRXN1	missense	NRXN1:NM_001135659(24Exons):exon22:c. C4112T:p.P1371L&missense;NRXN1:NM_0 04801(22Exons):exon20:c.C3902T:p.P1301L &missense;NRXN1:NM_138735(6Exons):ex on4:c.C797T:p.P266L&missense	0.0002576	Y	A;B;C;D;E;F:0.04 84:0.828:0.792
2	50280555	C/T	ID273	NRXN1	missense	NRXN1:NM_001135659(24Exons):exon22:c. G4102A:p.G1368S&missense;NRXN1:NM_0 04801(22Exons):exon20:c.G3892A:p.G1298S &missense;NRXN1:NM_138735(6Exons):ex on4:c.G787A:p.G263S&missense	0.0002576	Y	A;B;C;D;E;F:0.04 84:0.828:0.792

eTable 13 (continued). Information about variants identified in the reduced NMDA-mediated synaptic current in the follow-up study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	Causal _KGGSeq	Prediction _other
2	50280645	A/G	ID274	NRXN1	missense	NRXN1:NM_001135659(24Exons):exon22:c.T4012C:p.S1338P&missense;NRXN1:NM_004801(22Exons):exon20:c.T3802C:p.S1268P&missense;NRXN1:NM_138735(6Exons):exon4:c.T697C:p.S233P&missense	0.0002587	Y	A;B;C;D;E;F:0.0484:0.828:0.792
2	50282126	C/G	ID278	NRXN1	missense	NRXN1:NM_004801(22Exons):intronic19;NRXN1:NM_138735(6Exons):intronic3;NRXN1:NM_001135659(24Exons):exon21:c.G3895C:p.G1299R&missense	0.0002575	Y	A;G;B;C;J;D;E;H;F:0.0283:0.944:0.891
2	50318539	C/T	ID282	NRXN1	missense	NRXN1:NM_001135659(24Exons):exon20:c.G3760A:p.V1254I&missense;NRXN1:NM_004801(22Exons):exon19:c.G3640A:p.V1214I&missense;NRXN1:NM_138735(6Exons):exon3:c.G535A:p.V179I&missense	0.0002575	Y	A;D;E;H;I:0.0436:0.86:0.724
2	50464070	T/C	ID285	NRXN1	missense	NRXN1:NM_001135659(24Exons):exon19:c.A3523G:p.I1175V&missense;NRXN1:NM_004801(22Exons):exon18:c.A3403G:p.I1135V&missense;NRXN1:NM_138735(6Exons):exon2:c.A298G:p.I100V&missense	0.00103	Y	A;B;C;D;E;F:0.0484:0.828:0.792

eTable 13 (continued). Information about variants identified in the reduced NMDA-mediated synaptic current in the follow-up study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	Causal _KGGSeq	Prediction _other
2	50573850	C/G	ID287	NRXN1	missense	NRXN1:NM_001135659(24Exons):intronic18 ;NRXN1:NM_004801(22Exons):intronic17;N RXN1:NM_138735(6Exons):exon1:c.G238C: p.A80P&missense	0.0002583	Y	A;B;C;D;E;H;F:0. 0432:0.844:0.773
2	50573937	C/T	rs2016983 70	NRXN1	missense	NRXN1:NM_001135659(24Exons):intronic18 ;NRXN1:NM_004801(22Exons):intronic17;N RXN1:NM_138735(6Exons):exon1:c.G151A: p.A51T&missense	0.0002612	Y	A;B;C;D;E;H;F:0. 0432:0.844:0.773
2	50692685	A/G	ID297	NRXN1	missense	NRXN1:NM_001135659(24Exons):exon18:c. T3379C:p.C1127R&missense;NRXN1:NM_0 04801(22Exons):exon17:c.T3259C:p.C1087R &missense	0.0002575	Y	A;B;C;D;E;F:0.04 84:0.828:0.792
2	50699586	C/G	ID304	NRXN1	missense	NRXN1:NM_001135659(24Exons):exon17:c. G3214C:p.A1072P&missense;NRXN1:NM_0 04801(22Exons):exon16:c.G3094C:p.A1032P &missense	0.0002595	Y	B;D;H;F:0.0414:0 .84:0.742
2	50723070	C/A	ID308	NRXN1	missense	NRXN1:NM_001135659(24Exons):exon16:c. G3163T:p.A1055S&missense;NRXN1:NM_0 04801(22Exons):exon15:c.G3043T:p.A1015S &missense	0.0005149	Y	B;D;F:0.0397:0.8 42:0.734

eTable 13 (continued). Information about variants identified in the reduced NMDA-mediated synaptic current in the follow-up study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	Causal _KGGSeq	Prediction _other
2	50724568	G/A	ID316	NRXN1	missense	NRXN1:NM_001135659(24Exons):exon15:c.C2902T:p.H968Y&missense;NRXN1:NM_004801(22Exons):exon14:c.C2782T:p.H928Y&missense	0.0002575	Y	A;B;C;D;E;F:0.0484:0.828:0.792
2	50733642	C/T	ID320	NRXN1	missense	NRXN1:NM_001135659(24Exons):exon14:c.G2608A:p.A870T&missense;NRXN1:NM_004801(22Exons):exon13:c.G2488A:p.A830T&missense	0.0002599	Y	B;D;H;F:0.0414:0.84:0.742
2	50733684	G/A	ID321	NRXN1	missense	NRXN1:NM_001135659(24Exons):exon14:c.C2566T:p.R856W&missense;NRXN1:NM_004801(22Exons):exon13:c.C2446T:p.R816W&missense	0.0002599	Y	A;B;C;D;E;F:0.0484:0.828:0.792
2	50733720	G/T	ID322	NRXN1	missense	NRXN1:NM_001135659(24Exons):exon14:c.C2530A:p.L844I&missense;NRXN1:NM_004801(22Exons):exon13:c.C2410A:p.L804I&missense	0.001299	Y	A;B;C;D;E;F:0.0484:0.828:0.792
2	50758389	G/A	rs201387857	NRXN1	missense	NRXN1:NM_001135659(24Exons):exon12:c.C2443T:p.R815C&missense;NRXN1:NM_004801(22Exons):exon11:c.C2323T:p.R775C&missense	0.0002575	Y	A;B;C;D;E;F:0.0484:0.828:0.792

eTable 13 (continued). Information about variants identified in the reduced NMDA-mediated synaptic current in the follow-up study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	Causal _KGGSeq	Prediction _other
2	50758451	A/G	ID330	NRXN1	missense	NRXN1:NM_001135659(24Exons):exon12:c.T2381C:p.I794T&missense;NRXN1:NM_004801(22Exons):exon11:c.T2261C:p.I754T&missense	0.0007724	Y	A;B;C;D;E;F:0.0484:0.828:0.792
2	50758482	A/C	ID331	NRXN1	missense	NRXN1:NM_001135659(24Exons):exon12:c.T2350G:p.L784V&missense;NRXN1:NM_004801(22Exons):exon11:c.T2230G:p.L744V&missense	0.0002575	Y	A;B;C;D;E;F:0.0484:0.828:0.792
2	50765424	C/T	ID333	NRXN1	missense	NRXN1:NM_001135659(24Exons):exon11:c.G2230A:p.G744R&missense;NRXN1:NM_004801(22Exons):exon10:c.G2110A:p.G704R&missense	0.0007724	Y	A;B;C;D;E;F:0.0484:0.828:0.792
2	50765565	G/A	rs200844126	NRXN1	missense	NRXN1:NM_001135659(24Exons):exon11:c.C2089T:p.R697W&missense;NRXN1:NM_004801(22Exons):exon10:c.C1969T:p.R657W&missense	0.0002575	Y	A;G;B;C;J;D;E;H;F:0.0283:0.944:0.891
2	50765756	G/A	rs201530175	NRXN1	missense	NRXN1:NM_001135659(24Exons):exon11:c.C1898T:p.T633M&missense;NRXN1:NM_004801(22Exons):exon10:c.C1778T:p.T593M&missense	0.0005149	Y	A;B;C;D;E;F:0.0484:0.828:0.792

eTable 13 (continued). Information about variants identified in the reduced NMDA-mediated synaptic current in the follow-up study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	Causal _KGGSeq	Prediction _other
2	50779802	A/G	ID338	NRXN1	missense	NRXN1:NM_001135659(24Exons):exon10:c.T1802C:p.I601T&missense;NRXN1:NM_004801(22Exons):exon9:c.T1682C:p.I561T&missense	0.0002579	Y	A;B;D;E;F:0.0385:0.859:0.732
2	50779857	T/C	ID339	NRXN1	missense	NRXN1:NM_001135659(24Exons):exon10:c.A1747G:p.I583V&missense;NRXN1:NM_004801(22Exons):exon9:c.A1627G:p.I543V&missense	0.0002579	Y	B;D;E;F:0.0342:0.872:0.702
2	50780027	G/A	ID341	NRXN1	missense	NRXN1:NM_001135659(24Exons):exon10:c.C1577T:p.T526I&missense;NRXN1:NM_004801(22Exons):exon9:c.C1457T:p.T486I&missense	0.0002579	Y	A;B;C;D;E;F:0.0484:0.828:0.792
2	50780102	G/A	ID342	NRXN1	missense	NRXN1:NM_001135659(24Exons):exon10:c.C1502T:p.P501L&missense;NRXN1:NM_004801(22Exons):exon9:c.C1382T:p.P461L&missense	0.0002579	Y	A;G;B;C;J;D;E;H;F:0.0283:0.944:0.891
2	50780163	C/T	ID343	NRXN1	missense	NRXN1:NM_001135659(24Exons):exon10:c.G1441A:p.V481I&missense;NRXN1:NM_004801(22Exons):exon9:c.G1321A:p.V441I&missense	0.0002579	Y	A;B;C;D;E;F:0.0484:0.828:0.792

eTable 13 (continued). Information about variants identified in the reduced NMDA-mediated synaptic current in the follow-up study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	Causal _KGGSeq	Prediction _other
2	50847168	G/C	rs192069355	NRXN1	missense	NRXN1:NM_001135659(24Exons):exon9:c.C1432G:p.L478V&missense;NRXN1:NM_004801(22Exons):exon8:c.C1312G:p.L438V&missense	0.0005149	Y	A;B;C;D;E;F:0.04484:0.828:0.792
2	50847192	C/T	ID344	NRXN1	missense	NRXN1:NM_001135659(24Exons):exon9:c.G1408A:p.V470I&missense;NRXN1:NM_004801(22Exons):exon8:c.G1288A:p.V430I&missense	0.0002575	Y	A;G;B;C;E;H;F;I:0.0486:0.826:0.795
2	51253559	T/C	ID365	NRXN1	missense	NRXN1:NM_004801(22Exons):intronic2;NRXN1:NM_001135659(24Exons):exon3:c.A821G:p.N274S&missense	0.00103	Y	B;J;E;I:0.0312:0.928:0.884
2	51254796	C/G	ID373	NRXN1	missense	NRXN1:NM_001135659(24Exons):exon2:c.G616C:p.D206H&missense;NRXN1:NM_004801(22Exons):exon2:c.G616C:p.D206H&missense	0.0002575	Y	G;B;C;D;E;F:0.04047:0.839:0.772
2	51254801	A/T	ID375	NRXN1	missense	NRXN1:NM_001135659(24Exons):exon2:c.T611A:p.L204Q&missense;NRXN1:NM_004801(22Exons):exon2:c.T611A:p.L204Q&missense	0.00103	Y	B;C;E;H;F;I:0.04445:0.826:0.782

eTable 13 (continued). Information about variants identified in the reduced NMDA-mediated synaptic current in the follow-up study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	Causal _KGGSeq	Prediction _other
2	51254843	T/C	rs200792504	NRXN1	missense	NRXN1:NM_001135659(24Exons):exon2:c.A569G:p.N190S&missense;NRXN1:NM_004801(22Exons):exon2:c.A569G:p.N190S&missense	0.0002575	Y	A;B;C;D;E;F:0.0484:0.828:0.792
2	51254933	G/A	rs371517584	NRXN1	missense	NRXN1:NM_001135659(24Exons):exon2:c.C479T:p.P160L&missense;NRXN1:NM_004801(22Exons):exon2:c.C479T:p.P160L&missense	0.0002575	Y	A;B;C;D;E;F:0.0484:0.828:0.792
2	51254957	C/A	ID377	NRXN1	missense	NRXN1:NM_001135659(24Exons):exon2:c.G455T:p.G152V&missense;NRXN1:NM_004801(22Exons):exon2:c.G455T:p.G152V&missense	0.0002575	Y	C;D;H;I:0.0488:0.826:0.778
2	51254963	A/T	ID378	NRXN1	missense	NRXN1:NM_001135659(24Exons):exon2:c.T449A:p.F150Y&missense;NRXN1:NM_004801(22Exons):exon2:c.T449A:p.F150Y&missense	0.0002575	Y	A;B;C;D;E;F:0.0484:0.828:0.792
2	51254966	A/G	ID379	NRXN1	missense	NRXN1:NM_001135659(24Exons):exon2:c.T446C:p.V149A&missense;NRXN1:NM_004801(22Exons):exon2:c.T446C:p.V149A&missense	0.0005149	Y	A;B;C;D;E;F:0.0484:0.828:0.792

eTable 13 (continued). Information about variants identified in the reduced NMDA-mediated synaptic current in the follow-up study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	Causal _KGGSeq	Prediction _other
2	51255129	T/C	ID382	NRXN1	missense	NRXN1:NM_001135659(24Exons):exon2:c.A283G:p.I95V&missense;NRXN1:NM_004801(22Exons):exon2:c.A283G:p.I95V&missense	0.0005149	Y	A;B;C;D;E;F:0.04 84:0.828:0.792
2	51255161	G/T	ID384	NRXN1	missense	NRXN1:NM_001135659(24Exons):exon2:c.C251A:p.T84K&missense;NRXN1:NM_004801(22Exons):exon2:c.C251A:p.T84K&missense	0.0002575	Y	A;D;E;F:0.0413:0 .843:0.755
2	51255311	G/T	ID385	NRXN1	missense	NRXN1:NM_001135659(24Exons):exon2:c.C101A:p.P34Q&missense;NRXN1:NM_004801(22Exons):exon2:c.C101A:p.P34Q&missense	0.0002575	Y	G;B;C;E;H;I:0.04 96:0.825:0.766
2	51255384	C/T	ID386	NRXN1	missense	NRXN1:NM_001135659(24Exons):exon2:c.G28A:p.G10S&missense;NRXN1:NM_004801(22Exons):exon2:c.G28A:p.G10S&missense	0.0002575	Y	B;C;D;F:0.0435:0 .843:0.771
22	51113650	A/G	ID3913	SHANK3	missense	SHANK3:NM_033517(22Exons):exon2:c.A238G:p.N80D&missense	0.0005149	Y	A;D;F:0.039:0.84 6:0.75
22	51117284	G/A	ID3923	SHANK3	missense	SHANK3:NM_033517(22Exons):exon5:c.G536A:p.R179H&missense	0.0002575	Y	A;B;C;D;E;F:0.04 84:0.828:0.792
22	51117307	G/A	ID3925	SHANK3	missense	SHANK3:NM_033517(22Exons):exon5:c.G559A:p.V187M&missense	0.0002575	Y	A;K;B;D;E;F:0.03 49:0.874:0.696

eTable 13 (continued). Information about variants identified in the reduced NMDA-mediated synaptic current in the follow-up study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	Causal _KGGSeq	Prediction _other
22	51133230	C/T	ID3943	SHANK3	missense	SHANK3:NM_033517(22Exons):exon10:c.C1058T:p.A353V&missense	0.000266	Y	A;B;C;J;D;E;H;F;I:0.0247:0.949:0.88
22	51133347	C/T	ID3944	SHANK3	missense	SHANK3:NM_033517(22Exons):exon10:c.C1175T:p.S392L&missense	0.0002658	Y	A;B;C;J;D;E;H;F;I:0.0247:0.949:0.88
22	51133409	C/T	ID3946	SHANK3	missense	SHANK3:NM_033517(22Exons):exon10:c.C1237T:p.R413W&missense	0.0005322	Y	A;C;D:0.0555:0.805:0.804
22	51143179	C/G	ID3974	SHANK3	missense	SHANK3:NM_033517(22Exons):exon15:c.C1743G:p.I581M&missense	0.0002575	Y	A;C;D;E;I:0.0455:0.835:0.771
22	51144506	C/T	ID3980	SHANK3	missense	SHANK3:NM_033517(22Exons):exon17:c.C1994T:p.P665L&missense	0.0002575	Y	A;B;C;J;D;E;H;F;I:0.0247:0.949:0.88
22	51153371	G/A	rs61729471	SHANK3	missense	SHANK3:NM_033517(22Exons):exon19:c.G2119A:p.A707T&missense	0.00103	Y	A;D;E;H;F:0.036:0.861:0.732
22	51153377	G/C	ID3993	SHANK3	missense	SHANK3:NM_033517(22Exons):exon19:c.G2125C:p.E709Q&missense	0.0005149	Y	B;D;H;F;I:0.0292:0.883:0.683
22	51153389	C/T	ID3994	SHANK3	missense	SHANK3:NM_033517(22Exons):exon19:c.C2137T:p.R713W&missense	0.0002575	Y	A;D;E;F:0.0413:0.843:0.755
22	51153390	G/A	ID3995	SHANK3	missense	SHANK3:NM_033517(22Exons):exon19:c.G2138A:p.R713Q&missense	0.0002575	Y	A;D;E;F:0.0413:0.843:0.755

eTable 13 (continued). Information about variants identified in the reduced NMDA-mediated synaptic current in the follow-up study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	Causal _KGGSeq	Prediction _other
22	51153417	G/A	ID3996	SHANK3	missense	SHANK3:NM_033517(22Exons):exon19:c.G2165A:p.R722K&missense	0.0002575	Y	A;G;J;D;F:0.0267:0.944:0.882
22	51153461	C/G	ID3997	SHANK3	missense	SHANK3:NM_033517(22Exons):exon19:c.C2209G:p.P737A&missense	0.0005149	Y	G;B;J;F:0.0314:0.936:0.89
22	51158740	C/T	ID4006	SHANK3	missense	SHANK3:NM_033517(22Exons):exon21:c.C2437T:p.P813S&missense	0.0002575	Y	A;B;C;D;E;H;F:0.0432:0.844:0.773
22	51158852	G/C	ID4008	SHANK3	missense	SHANK3:NM_033517(22Exons):exon21:c.G2549C:p.G850A&missense	0.0005155	Y	B;D;H;F:0.0414:0.84:0.742
22	51158984	C/T	ID4014	SHANK3	missense	SHANK3:NM_033517(22Exons):exon21:c.C2681T:p.P894L&missense	0.0005152	Y	G;B;E;F:0.0351:0.86:0.712
22	51159850	A/G	ID4024	SHANK3	missense	SHANK3:NM_033517(22Exons):exon21:c.A3547G:p.S1183G&missense	0.0002575	Y	A;G;B;C;J;D;E;H;F:0.0283:0.944:0.891
22	51159952	C/T	ID4025	SHANK3	missense	SHANK3:NM_033517(22Exons):exon21:c.C3649T:p.R1217C&missense	0.0005149	Y	A;B;D;F:0.0324:0.877:0.706
22	51160049	C/T	ID4031	SHANK3	missense	SHANK3:NM_033517(22Exons):exon21:c.C3746T:p.P1249L&missense	0.00103	Y	A;G;B;C;E;H:0.0558:0.807:0.789
22	51160268	C/T	ID4035	SHANK3	missense	SHANK3:NM_033517(22Exons):exon21:c.C3965T:p.P1322L&missense	0.0005149	Y	K;G;B;C;E;H;F;I:0.0421:0.84:0.768
22	51160786	C/T	ID4042	SHANK3	missense	SHANK3:NM_033517(22Exons):exon21:c.C4483T:p.R1495C&missense	0.0002575	Y	A;B;C;D;E;F:0.0484:0.828:0.792

eTable 13 (continued). Information about variants identified in the reduced NMDA-mediated synaptic current in the follow-up study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	Causal _KGGSeq	Prediction _other
22	51160801	G/A	ID4043	SHANK3	missense	SHANK3:NM_033517(22Exons):exon21:c.G4498A:p.E1500K&missense	0.0002575	Y	G;B;J;E;H;F;I:0.0355:0.933:0.895
22	51169682	C/T	ID4054	SHANK3	missense	SHANK3:NM_033517(22Exons):exon22:c.C5096T:p.T1699M&missense	0.0002604	Y	A;G;B;C;J;D;E;H;F:0.0283:0.944:0.891
6	1.23E+08	A/T	ID1492	FABP7	missense	FABP7:NM_001446(4Exons):exon1:c.A1T:p.M1L&missense	0.0002575	Y	A;D;E;F:0.0413:0.843:0.755
6	1.23E+08	G/C	ID1498	FABP7	missense	FABP7:NM_001446(4Exons):exon2:c.G140C:p.G47A&missense	0.0002575	Y	A;B;C;D;E;F:0.0484:0.828:0.792
6	1.23E+08	T/A	ID1499	FABP7	missense	FABP7:NM_001446(4Exons):exon2:c.T152A:p.V51D&missense	0.0002575	Y	A;K;G;B;C;D;E;F:0.0405:0.851:0.764
6	1.23E+08	A/T	ID1500	FABP7	missense	FABP7:NM_001446(4Exons):exon2:c.A154T:p.I52F&missense	0.0002575	Y	A;B;C;D;E;F:0.0484:0.828:0.792
6	1.23E+08	A/G	ID1501	FABP7	missense	FABP7:NM_001446(4Exons):exon2:c.A233G:p.D78G&missense	0.0002575	Y	A;K;G;B;D;E;H;F:0.0345:0.869:0.722
6	1.23E+08	G/A	ID1502	FABP7	missense	FABP7:NM_001446(4Exons):exon3:c.G322A:p.E108K&missense	0.0002575	Y	A;B;C;D;E;F:0.0484:0.828:0.792
6	1.23E+08	C/T	ID1504	FABP7	missense	FABP7:NM_001446(4Exons):exon4:c.C352T:p.L118F&missense	0.0002575	Y	A;B;C;D;E;F:0.0484:0.828:0.792

eTable 13 (continued). Information about variants identified in the reduced NMDA-mediated synaptic current in the follow-up study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	Causal _KGGSeq	Prediction _other
8	95893921	A/G	ID1790	CCNE2	missense	CCNE2:NM_057749(12Exons):exon12:c.T1154C:p.V385A&missense	0.0002575	Y	B;C;E;H;I:0.0521:0.802:0.786
8	95895020	T/C	ID1797	CCNE2	missense	CCNE2:NM_057749(12Exons):exon10:c.A932G:p.K311R&missense	0.0002575	Y	C;E;F:0.0424:0.828:0.781
8	95897302	A/G	ID1802	CCNE2	missense	CCNE2:NM_057749(12Exons):exon9:c.T824C:p.I275T&missense	0.0002575	Y	A;B;C;D;E;F:0.0484:0.828:0.792
8	95897368	A/G	ID1803	CCNE2	missense	CCNE2:NM_057749(12Exons):exon9:c.T758C:p.V253A&missense	0.0002575	Y	A;B;C;D;E;F:0.0484:0.828:0.792
8	95897785	T/G	ID1807	CCNE2	missense	CCNE2:NM_057749(12Exons):exon8:c.A602C:p.E201A&missense	0.0005149	Y	A;B;C;D;E;F:0.0484:0.828:0.792
8	95905121	G/A	ID1813	CCNE2	missense	CCNE2:NM_057749(12Exons):exon5:c.C242T:p.T81I&missense	0.0002575	Y	A;B;C;D;E;F:0.0484:0.828:0.792
8	95906334	C/T	ID1816	CCNE2	missense	CCNE2:NM_057749(12Exons):exon3:c.G28A:p.A10T&missense	0.0002575	Y	G;B;C;D;E;F:0.0447:0.839:0.772
8	95906449	T/C	ID1819	CCNE2	missense	CCNE2:NM_057749(12Exons):exon2:c.A1G:p.M1V&missense	0.0002575	Y	A;D;E;F:0.0413:0.843:0.755

eTable 13 (continued). Information about variants identified in the reduced NMDA-mediated synaptic current in the follow-up study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	Causal _KGGSeq	Prediction _other
9	1.4E+08	T/C	ID2142	GRIN1	missense	GRIN1:NM_021569(19Exons):exon1:c.T86C:p.I29T&missense;GRIN1:NM_007327(20Exons):exon1:c.T86C:p.I29T&missense;GRIN1:NM_001185090(21Exons):exon1:c.T86C:p.I29T&missense;GRIN1:NM_001185091(20Exons):exon1:c.T86C:p.I29T&missense;GRIN1:NM_000832(19Exons):exon1:c.T86C:p.I29T&missense	0.0002575	Y	A;B;C;D;H;F:0.0455:0.832:0.786
9	1.4E+08	G/A	ID2145	GRIN1	missense	GRIN1:NM_021569(19Exons):exon2:c.G371A:p.R124H&missense;GRIN1:NM_007327(20Exons):exon2:c.G371A:p.R124H&missense;GRIN1:NM_001185090(21Exons):exon2:c.G371A:p.R124H&missense;GRIN1:NM_001185091(20Exons):exon2:c.G371A:p.R124H&missense;GRIN1:NM_000832(19Exons):exon2:c.G371A:p.R124H&missense	0.0002575	Y	A;B;C;D;E;F:0.0484:0.828:0.792

eTable 13 (continued). Information about variants identified in the reduced NMDA-mediated synaptic current in the follow-up study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	Causal _KGGSeq	Prediction _other
9	1.4E+08	C/G	ID2160	GRIN1	missense	GRIN1:NM_021569(19Exons):exon5:c.C701G:p.A234G&missense;GRIN1:NM_007327(20Exons):exon5:c.C701G:p.A234G&missense;GRIN1:NM_001185090(21Exons):exon6:c.C764G:p.A255G&missense;GRIN1:NM_001185091(20Exons):exon6:c.C764G:p.A255G&missense;GRIN1:NM_000832(19Exons):exon5:c.C701G:p.A234G&missense	0.0002575	Y	A;K;G;B;C;D;E;F:0.0405:0.851:0.764
9	1.4E+08	C/T	ID2169	GRIN1	missense	GRIN1:NM_021569(19Exons):exon7:c.C1109T:p.T370I&missense;GRIN1:NM_007327(20Exons):exon7:c.C1109T:p.T370I&missense;GRIN1:NM_001185090(21Exons):exon8:c.C1172T:p.T391I&missense;GRIN1:NM_001185091(20Exons):exon8:c.C1172T:p.T391I&missense;GRIN1:NM_000832(19Exons):exon7:c.C1109T:p.T370I&missense	0.0002603	Y	A;B;E;F:0.0391:0.836:0.739

eTable 13 (continued). Information about variants identified in the reduced NMDA-mediated synaptic current in the follow-up study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	Causal _KGGSeq	Prediction _other
9	1.4E+08	G/C	ID2197	GRIN1	missense	GRIN1:NM_021569(19Exons):exon13:c.G1780C:p.E594Q&missense;GRIN1:NM_007327(20Exons):exon13:c.G1780C:p.E594Q&missense;GRIN1:NM_001185090(21Exons):exon14:c.G1843C:p.E615Q&missense;GRIN1:NM_001185091(20Exons):exon14:c.G1843C:p.E615Q&missense;GRIN1:NM_000832(19Exons):exon13:c.G1780C:p.E594Q&missense	0.0002687	Y	A;G;B;J;D;F:0.0327:0.938:0.896
9	1.4E+08	T/C	ID2213	GRIN1	missense	LRRC26:NM_001013653(2Exons):downstream+966;GRIN1:NM_021569(19Exons):3UTR+266;GRIN1:NM_007327(20Exons):3UTR+266;GRIN1:NM_001185090(21Exons):exon21:c.T2783C:p.I928T&missense;GRIN1:NM_001185091(20Exons):exon20:c.T2672C:p.I891T&missense;GRIN1:NM_000832(19Exons):exon19:c.T2609C:p.I870T&missense	0.0005149	Y	A;D;F:0.039:0.846:0.75
9	90114017	G/A	ID1937	DAPK1	missense	DAPK1:NM_004938(26Exons):exon2:c.G25A:p.V9M&missense	0.0002575	Y	G;B;C;D;E;H:0.0506:0.825:0.773
9	90219880	C/T	ID1938	DAPK1	missense	DAPK1:NM_004938(26Exons):exon3:c.C74T:p.A25V&missense	0.0002575	Y	A;G;B;C;J;D;E;H;F:0.0283:0.944:0.891

eTable 13 (continued). Information about variants identified in the reduced NMDA-mediated synaptic current in the follow-up study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	Causal _KGGSeq	Prediction _other
9	90220066	C/T	ID1940	DAPK1	missense	DAPK1:NM_004938(26Exons):exon3:c.C260T:p.T87M&missense	0.0005149	Y	A;B;C;E;H;F;I:0.0412:0.846:0.768
9	90254375	T/C	ID1951	DAPK1	missense	DAPK1:NM_004938(26Exons):exon5:c.T530C:p.I177T&missense	0.0002577	Y	A;G;B;J;D;E;F;I:0.0268:0.946:0.88
9	90255314	C/T	ID1957	DAPK1	missense	DAPK1:NM_004938(26Exons):exon8:c.C731T:p.T244I&missense	0.0002575	Y	A;G;J;D;F:0.0267:0.944:0.882
9	90256957	C/T	ID1962	DAPK1	missense	DAPK1:NM_004938(26Exons):exon10:c.C902T:p.A301V&missense	0.0002575	Y	A;B;C;D;E;F:0.0484:0.828:0.792
9	90258343	C/A	ID1970	DAPK1	missense	DAPK1:NM_004938(26Exons):exon11:c.C971A:p.S324Y&missense	0.0002575	Y	A;B;C;D;E;F:0.0484:0.828:0.792
9	90258376	A/T	ID1971	DAPK1	missense	DAPK1:NM_004938(26Exons):exon11:c.A1004T:p.D335V&missense	0.0005155	Y	A;B;C;D;E;F:0.0484:0.828:0.792
9	90258378	A/G	ID1972	DAPK1	missense	DAPK1:NM_004938(26Exons):exon11:c.A1006G:p.T336A&missense	0.0002575	Y	A;B;C;D;E;F:0.0484:0.828:0.792
9	90262235	G/A	rs12343465	DAPK1	missense	DAPK1:NM_004938(26Exons):exon14:c.G1246A:p.V416I&missense	0.0002576	Y	B;D;E;F:0.0342:0.872:0.702
9	90264892	A/C	ID1996	DAPK1	missense	DAPK1:NM_004938(26Exons):exon16:c.A1485C:p.K495N&missense	0.0005149	Y	K;B;D;E;H;F:0.0346:0.865:0.698
9	90264917	G/A	rs372895478	DAPK1	missense	DAPK1:NM_004938(26Exons):exon16:c.G1510A:p.V504M&missense	0.0002575	Y	A;B;C;D;E;F:0.0484:0.828:0.792

eTable 13 (continued). Information about variants identified in the reduced NMDA-mediated synaptic current in the follow-up study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	Causal _KGGSeq	Prediction _other
9	90266442	G/A	ID1999	DAPK1	missense	DAPK1:NM_004938(26Exons):exon17:c.G1627A:p.D543N&missense	0.0005149	Y	G;LRT_score;B;C;H;F;I:0.0389:0.853:0.749
9	90266526	G/A	rs199940257	DAPK1	missense	DAPK1:NM_004938(26Exons):exon17:c.G1711A:p.D571N&missense	0.002832	Y	A;D;E;F:0.0413:0.843:0.755
9	90266544	G/A	rs369647209	DAPK1	missense	DAPK1:NM_004938(26Exons):exon17:c.G1729A:p.G577S&missense	0.0002575	Y	A;B;C;D;E;F:0.0484:0.828:0.792
9	90266619	A/G	ID2002	DAPK1	missense	DAPK1:NM_004938(26Exons):exon17:c.A1804G:p.N602D&missense	0.0002575	Y	A;K;E;H;F:0.0343:0.866:0.704
9	90272992	G/A	rs117269616	DAPK1	missense	DAPK1:NM_004938(26Exons):exon18:c.G1873A:p.V625M&missense	0.00309	Y	A;B;C;D;E;F:0.0484:0.828:0.792
9	90296353	G/A	ID2011	DAPK1	missense	DAPK1:NM_004938(26Exons):exon20:c.G2036A:p.R679Q&missense	0.0005149	Y	A;B;C;D;E;F:0.0484:0.828:0.792
9	90296355	C/T	ID2012	DAPK1	missense	DAPK1:NM_004938(26Exons):exon20:c.C2038T:p.P680S&missense	0.0002575	Y	A;B;C;D;E;F:0.0484:0.828:0.792
9	90311939	G/A	ID2020	DAPK1	missense	DAPK1:NM_004938(26Exons):exon22:c.G2431A:p.V811M&missense	0.0002575	Y	A;B;C;D;E;F:0.0484:0.828:0.792
9	90317947	T/G	ID2028	DAPK1	missense	DAPK1:NM_004938(26Exons):exon25:c.T2875G:p.C959G&missense	0.0002575	Y	A;B;C;D;E;H;F:0.0432:0.844:0.773
9	90321218	G/A	ID2035	DAPK1	missense	DAPK1:NM_004938(26Exons):exon26:c.G3232A:p.V1078M&missense	0.0002575	Y	A;B;C;D;E;H;F:0.0432:0.844:0.773

eTable 13 (continued). Information about variants identified in the reduced NMDA-mediated synaptic current in the follow-up study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	Causal _KGGSeq	Prediction _other
9	90321249	T/C	ID2036	DAPK1	missense	DAPK1:NM_004938(26Exons):exon26:c.T3263C:p.M1088T&missense	0.0002575	Y	A;B;C;D;E;F:0.0484:0.828:0.792
9	90321263	C/T	ID2037	DAPK1	missense	DAPK1:NM_004938(26Exons):exon26:c.C3277T:p.R1093W&missense	0.0002575	Y	A;B;C;D;E;F:0.0484:0.828:0.792
9	90321357	T/C	ID2042	DAPK1	missense	DAPK1:NM_004938(26Exons):exon26:c.T3371C:p.M1124T&missense	0.0005149	Y	A;B;E;H;F;I:0.0287:0.885:0.676
9	90321480	C/T	rs201991862	DAPK1	missense	DAPK1:NM_004938(26Exons):exon26:c.C3494T:p.A1165V&missense	0.0002575	Y	A;B;C;D;E;H;F:0.0432:0.844:0.773
9	90321510	A/G	ID2045	DAPK1	missense	DAPK1:NM_004938(26Exons):exon26:c.A3524G:p.K1175R&missense	0.0005149	Y	A;B;E;F:0.0391:0.836:0.739
9	90321582	G/A	ID2047	DAPK1	missense	DAPK1:NM_004938(26Exons):exon26:c.G3596A:p.R1199H&missense	0.0002575	Y	A;B;C;D;E;F:0.0484:0.828:0.792
9	90321802	G/T	rs56169226	DAPK1	missense	DAPK1:NM_004938(26Exons):exon26:c.G3816T:p.M1272I&missense	0.0002576	Y	A;B;C;D;E;F:0.0484:0.828:0.792
9	90321833	A/G	ID2050	DAPK1	missense	DAPK1:NM_004938(26Exons):exon26:c.A3847G:p.M1283V&missense	0.0002575	Y	B;J;E;H:0.0301:0.93:0.886
9	90322005	T/G	ID2051	DAPK1	missense	DAPK1:NM_004938(26Exons):exon26:c.T4019G:p.V1340G&missense	0.0002575	Y	A;B;C;D;E;H;F:0.0432:0.844:0.773
9	90322028	G/A	ID2052	DAPK1	missense	DAPK1:NM_004938(26Exons):exon26:c.G4042A:p.G1348R&missense	0.0002575	Y	A;G;D;E;F:0.04:0.856:0.738
9	90322121	A/G	ID2054	DAPK1	missense	DAPK1:NM_004938(26Exons):exon26:c.A4135G:p.K1379E&missense	0.0002575	Y	A;B;C;D;E;F:0.0484:0.828:0.792

eTable 13 (continued). Information about variants identified in the reduced NMDA-mediated synaptic current in the follow-up study

CHR	POS	REF/ ALT	rsID	Gene	Variant	RefGeneFeatures	MAF_dis	Causal _KGGSeq	Prediction _other
9	90322220	G/T	ID2056	DAPK1	missense	DAPK1:NM_004938(26Exons):exon26:c.G4234T:p.A1412S&missense	0.0002575	Y	A;D;E;F:0.0413:0.843:0.755

eTable 14. Set-based association results on the 3 candidate gene-sets in the follow-upd study on rare (MAF<0.01) synonymous variants in CMC burden test

Gene Set	NumVar	NumPolyVar	NonRefSite	Pvalue
abnormal AMPA-mediated synaptic currents	138	138	273	0.44231
reduced AMPA-mediated synaptic currents	263	251	561	0.71572
reduced NMDA-mediated synaptic currents	271	271	502	0.992278

eTable 15. Burden of rare allele (damaging nonsyn with MAF < 0.01) in follow-up by median splitting, with subjects with lower PANSS were treated as "less responsiver".

Gene Set	# var	Allele count (Nonresponder/Responder)
Reduced NMDA-mediated synaptic currents	261	260/225
Reduced AMPA-mediated synaptic currents	231	199/181
Abnormal AMPA-mediated synaptic currents	78	61/50