Phillips JK, Goodchild AK, Dubey R, Sesiashvili E, Takeda M, Chalmers J, et al. Differential expression of catecholamine biosynthetic enzymes in the rat ventrolateral medulla. J Comp Neurol 2001;432:20–34.
Picazo O, Chuc-Meza E, Anaya-Martinez V, Jimenez I, Aceves J, Garcia-Ramirez M. 6-Hydroxydopamine lesion in thalamic reticular nucleus reduces anxiety behaviour in the rat. Behav Brain Res 2009;197:317–22.
Reyes BA, Van Bockstaele EJ. Divergent projections of catecholaminergic neurons in the nucleus of the solitary tract to limbic forebrain and medullary autonomic brain regions. Brain Res 2006;1117:69–79.
Rubin BS, Lenkowski JR, Schaeberle CM, Vandenberg LN, Ronsheim PM, Soto AM. Evidence of altered brain sexual differentiation in mice exposed perinatally to low, environmentally relevant levels of bisphenol A. Endocrinology 2006;147:3681–91.
Sajiki J, Takahashi K, Yonekubo J. Sensitive method for the determination of bisphenol-A in serum using two systems of high-performance liquid chromatography. J Chromatogr B Biomed Sci 1999;736:255–61.
Sajiki J, Miyamoto F, Fukata H, Mori C, Yonekubo J, Hayakawa K. Bisphenol A (BPA) and its source in foods in Japanese markets. Food Addit Contam 2007;24:103–12.
Schonfelder G, Wittfoht W, Hopp H, Talsness CE, Paul M, Chahoud I. Parent bisphenol A accumulation in the human maternal–fetal–placental unit. Environ Health Perspect 2002;110:703–7.
Shih JC, Chen K. Regulation of MAO-A and MAO-B gene expression. Curr Med Chem 2004;11:1995–2005.
Sun Y, Irie M, Kishikawa N, Wada M, Kuroda N, Nakashima K. Determination of bisphenol A in human breast milk by HPLC with column-switching and fluorescence detection. Biomed Chromatogr 2004;18:501–7.
Takayanagi S, Tokunaga T, Liu X, Okada H, Matsushima A, Shimohigashi Y. Endocrine disruptor bisphenol A strongly binds to human estrogen-related receptor gamma (ERRgamma) with high constitutive activity. Toxicol Lett 2006;167:95-105.
Tando S, Itoh K, Yaoi T, Ikeda J, Fujiwara Y, Fushiki S. Effects of pre- and neonatal exposure to bisphenol A on murine brain development. Brain Dev 2007;29:352–6.
Tanida T, Warita K, Ishihara K, Fukui S, Mitsuhashi T, Sugawara T, et al. Fetal and neonatal exposure to three typical environmental chemicals with different mechanisms of action: mixed exposure to phenol, phthalate, and dioxin cancels the effects of sole exposure on mouse midbrain dopaminergic nuclei. Toxicol Lett 2009;189:40–7.
Thiemann G, Watt CA, Ledent C, Molleman A, Hasenohrl RU. Modulation of anxiety by acute blockade and genetic deletion of the CB(1) cannabinoid receptor in mice together with biogenic amine changes in the forebrain. Behav Brain Res 2009;200:60–7.
Thorpe LW, Westlund KN, Kochersperger LM, Abell CW, Denney RM. Immunocytochemical localization of monoamine oxidases A and B in human peripheral tissues and brain. J Histochem Cytochem 1987;35:23–32.
Tian YH, Baek JH, Lee SY, Jang CG. Prenatal and postnatal exposure to bisphenol a induces anxiolytic behaviors and cognitive deficits in mice. Synapse 2010;64:432–9.
Tuchmann-Duplessis H, Auroux M, Haegel P. Illustrated human embryology. 1st ed. New York: Springer; 1974.
Vandenberg LN, Hauser R, Marcus M, Olea N, Welshons WV. Human exposure to bisphenol A (BPA). Reprod Toxicol 2007;24:139–77.
Vandenberg LN, Chahoud I, Heindel JJ, Padmanabhan V, Paumgartten FJ, Schoenfelder G. Urinary, circulating, and tissue biomonitoring studies indicate widespread exposure to bisphenol A. Environ Health Perspect 2010;118:1055–70.
Wetherill YB, Akingbemi BT, Kanno J, McLachlan JA, Nadal A, Sonnenschein C, et al. In vitro molecular mechanisms of bisphenol A action. Reprod Toxicol 2007;24:178–98.
Williams LM, Gatt JM, Schofield PR, Olivieri G, Peduto A, Gordon E. 'Negativity bias' in risk for depression and anxiety: brain–body fear circuitry correlates, 5-HTT-LPR and early life stress. Neuroimage 2009;47:804–14.
Wu MV, et al. Estrogen masculinizes neural pathways and sex-specific behaviors. Cell 2009;139:61–72.
Xu XH, Zhang J, Wang YM, Ye YP, Luo QQ. Perinatal exposure to bisphenol-A impairs learning-memory by concomitant down-regulation of N-methyl-D-aspartate receptors of hippocampus in male offspring mice. Horm Behav 2010;58:326–33.
Xu X, Tian D, Hong X, Chen L, Xie L. Sex-specific influence of exposure to bisphenol-A between adolescence and young adulthood on mouse behaviors. Neuropharmacology 2011;61:565–73.
Yaoi T, Itoh K, Nakamura K, Ogi H, Fujiwara Y, Fushiki S. Genome-wide analysis of epigenomic alterations in fetal mouse forebrain after exposure to low doses of bisphenol A. Biochem Biophys Res Commun 2008;376:563–7.
Yu C, Tai F, Song Z, Wu R, Zhang X, He F. Pubertal exposure to bisphenol A disrupts behavior in adult C57BL/6J mice. Environ Toxicol Pharmacol 2011;31:88–99.
Zagon A, Totterdell S, Jones RS. Direct projections from the ventrolateral medulla oblongata to the limbic forebrain: anterograde and retrograde tract-tracing studies in the rat. J Comp Neurol 1994;340:445–68.
Zarrindast MR, Naghdi-Sedeh N, Nasehi M, Sahraei H, Bahrami F, Asadi F. The effects of dopaminergic drugs in the ventral hippocampus of rats in the nicotine-induced anxiogenic-like response. Neurosci Lett 2010;475:156–60.
Zhang Z, Chen K, Shih JC, Teng CT. Estrogen-related receptors-stimulated monoamine oxidase B promoter activity is down-regulated by estrogen receptors. Mol Endocrinol 2006;20:1547–61.
Zhou R, Bai Y, Yang R, Zhu Y, Chi X, Li L, et al. Abnormal synaptic plasticity in basolateral amygdala may account for hyperactivity and attention-deficit in male rat exposed perinatally to low-dose bisphenol-A. Neuropharmacology 2011;60:789–98.

RESEARCH ARTICLE

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Functional Genetic Variation at the *NRGN* Gene and Schizophrenia: Evidence From a Gene-Based Case–Control Study and Gene Expression Analysis

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Genome-wide association and follow-up studies have reported an association between schizophrenia and rs12807809 of the *NRGN* gene on chromosome 11q24.2. We investigated the association of five linkage disequilibrium-tagging SNPs and haplotypes that cover the *NRGN* gene with schizophrenia in a Japanese sample of 2,019 schizophrenia patients and 2,574 controls to determine whether rs12807809 is the most strongly associated variant for schizophrenia in the vicinity of the *NRGN* gene. We found that the rs12807809–rs12278912 haplotype of the *NRGN* gene was associated with schizophrenia (global $P = 0.0042$). The frequencies of the TG and TA haplotypes of rs12807809–rs12278912 in patients were higher (OR = 1.14, $P = 0.0019$) and lower (OR = 0.85, $P = 0.0053$), respectively, than in the controls. We did not detect any evidence of association of schizophrenia with any SNPs; however, two nominal associations of rs12278912 (OR = 1.10, $P = 0.057$) and rs2075713 (OR = 1.10, $P = 0.057$) were observed. Furthermore, we detected an association between the rs12807809–rs12278912 haplotype and *NRGN* expression in immortalized lymphoblasts derived from 45 HapMap JPT subjects ($z = 2.69$, $P = 0.007$) and confirmed

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the association in immortalized lymphoblasts derived from 42 patients with schizophrenia and 44 healthy controls ($z = 3.09$, $P = 0.002$). The expression of the high-risk TG haplotype was significantly lower than the protective TA haplotype. The expression was lower in patients with schizophrenia than in controls; however, this difference was not statistically significant. This study provides further evidence of the association of the *NRGN* gene with schizophrenia, and our results suggest that there is a link between the TG haplotype of rs12807809–rs12278912, decreased expression of *NRGN* and risk of developing schizophrenia.

Key words: schizophrenia; *neurogranin* (*NRGN*); single nucleotide polymorphism (SNP); genome-wide association study (GWAS); gene expression

INTRODUCTION

Schizophrenia is a common and complex psychiatric disease with strong genetic components. Schizophrenia has an estimated heritability of approximately 80% [Cardno and Gottesman, 2000; Tsuang, 2000], and many genes have been implicated in the pathogenesis of schizophrenia [Sun et al., 2008].

Genome-wide association studies (GWAS) of single nucleotide polymorphisms (SNPs) investigate thousands of DNA samples from patients and controls, and these studies are a powerful tool for identifying common risk factors in complex diseases. Stefansson et al. [2009] combined the samples (from 12,945 patients with schizophrenia and 34,591 controls) from three large GWAS (the SGENE-plus, the International Schizophrenia Consortium and the Molecular Genetics of Schizophrenia GWAS) and conducted follow-up studies in 4,999 patients and 15,555 controls from four sets of samples from Europe, including from the Netherlands, Denmark, Germany, Hungary, Norway, Russia, Sweden, Finland, and Spain. The authors detected several significant association signals. Seven markers gave P values smaller than the genome-wide significance threshold of approximately 1.6×10^{-7} in the combined samples: five markers, rs6913660, rs13219354, rs6932590, rs13211507, and rs3131296, which spanned the major histocompatibility complex (MHC) region on chromosome 6p21.3-22.1; a marker, rs12807809, located 3,457 bases upstream of the *neurogranin* (*NRGN*) gene on chromosome 11q24.2; and a marker, rs9960767, in intron 4 of the transcription factor 4 (*TCF4*) gene on chromosome 18q21.2. Of the seven SNPs, four SNPs, rs6913660, rs13219354, rs13211507, and rs9960767, were not polymorphic in the HapMap Japanese in Tokyo (JPT) samples. The minor allele frequencies (MAFs) for two SNPs, rs6932590 and rs3131296, were less than 5%. Because only one marker, rs12807809, in the *NRGN* gene was a common SNP in the HapMap JPT samples (MAF greater than 5%), we focused on this SNP and the *NRGN* gene in the present study.

The *NRGN* gene is the human homolog of the neuron-specific rat RC3/*neurogranin* gene. *NRGN* encodes a postsynaptic protein kinase substrate that binds calmodulin (CaM) in the absence of calcium and has been implicated in dendritic spine formation and synaptic plasticity [Baudier et al., 1991]. NRGN plays an important role in the Ca^{2+}–CaM signaling pathway [Hayashi, 2009]. Ca^{2+} influx-induced oxidation of NRGN leads to the postsynaptic activation of CaM-dependent protein kinase II (CaMKII) by CaM, which is associated with strengthened *N*-methyl-D-aspartate (NMDA) receptor signaling [Li et al., 1999]. Reduced NRGN activity may mediate the effects of NMDA hypofunction implicated in the pathophysiology of schizophrenia.

The *NRGN* gene spans 7.3 kb of genomic DNA and contains four exons [Martinez de Arrieta et al., 1997]. Part of exon 1 and exon 2 encode a 78-amino-acid protein, and exons 3 and 4 contain untranslated sequences. A thyroid hormone response element (TRE) has been identified in intron 1 [Martinez de Arrieta et al., 1999]. An association between the *NRGN* gene and schizophrenia has previously been reported in a small population of male Portuguese and Brazilians [Ruano et al., 2008], although the associated SNP in the study, rs7113041, was not tightly correlated with the genome-wide supported SNP, rs12807809 (HapMap CEU $r^2 = 0.07$, JPT $r^2 = 0.01$). In addition, two separate studies reported no association between the genetic variants of *NRGN* and schizophrenia in Bulgarian [Betcheva et al., 2009] and Chinese populations [Li et al., 2010]. The genome-wide supported SNP and other SNPs in the *NRGN* gene were not genotyped in the GWAS of schizophrenia in Japanese populations because of a difference in the genotyping chips used among the separate GWAS, which the Illumina HumanHap 300 or 550 BeadChips, Affymetrix Genome-Wide Human SNP Array 5.0 and Affymetrix GeneChip Mapping 100 K microarrays [Stefansson et al., 2009; Ikeda et al., 2011; Yamada et al., 2011] were used. Here, we first investigated the association between the *NRGN* gene and schizophrenia in a Japanese population using a gene-based approach to determine whether rs12807809 is the most strongly associated variant for schizophrenia near the *NRGN* gene. Second, we examined whether the associated haplotype of *NRGN* influenced *NRGN* expression in immortalized lymphoblasts derived from the HapMap JPT samples and our Japanese case–control samples.

MATERIALS AND METHODS

Subjects

Subjects for the genetic association analysis included 2,019 unrelated patients with schizophrenia (54.5% males, with a mean age ± SD of 44.7 ± 15.1 years) and 2,579 unrelated healthy controls (49.4% males, 45.4 ± 19.4 years). The mean age did not differ significantly between cases and controls ($P = 0.24$); however, the male to female ratio of the patients was significantly higher than in the controls ($P < 0.05$). Age and sex-matched subjects for *NRGN* expression analysis consisted of 42 patients with schizophrenia (58.1%, 38.4 ± 11.2 years) and 44 healthy subjects (56.8% males, 38.0 ± 11.4 years). These subjects were included in the genetic association analysis. All subjects used in both analyses were biologically unrelated, of Japanese ethnicity and were recruited from four geographical regions in Japan: Osaka, Aichi, Tokushima, and Tokyo [Yamaguchi-Kabata et al., 2008; Ohi et al., 2009]. Cases were recruited from outpatient and inpatient facilities at university hospitals and psychiatric hospitals. Each subject with schizophrenia had been diagnosed by at least two trained psychiatrists based on an unstructured clinical interview; diagnoses were made based on the

criteria of the fourth edition of the Diagnostic and Statistical Manual of Mental Disorders (DSM-IV). Controls were recruited through local advertisements. Psychiatrically healthy controls were evaluated using unstructured interviews to exclude individuals who had current or past contact with psychiatric services. Written informed consent was obtained for all subjects after the procedures had been fully explained. This study was carried out in accordance with the World Medical Association's Declaration of Helsinki and approved by the Research Ethical Committee of Osaka University, Fujita Health University, Nagoya University, Tokushima University and Juntendo University.

SNP Selection and SNP Genotyping

This study was designed to examine the association between the *NRGN* gene and schizophrenia by selectively tagging SNPs in the *NRGN* gene and flanking regions (±5 kb). We selected five tagging SNPs using the TAGGER algorithm (Paul de Bakker, http://www.broad.mit.edu/mpg/tagger) with the criteria of r^2 greater than 0.80 in "pair-wise tagging only" mode and an MAF greater than 5%, which was implemented in Haploview 4.2 using HapMap data release 27 Phase II + III, Feb 2009, on NCBI B36 assembly, dbSNP b126 [Japanese in Tokyo (JPT), Chr 11: 124,109,952.124,127,307]. The five tagging SNPs were rs1939214, rs12807809, rs12278912, rs2075713, and rs11219769. Markers are shown in Table I; orientation and alleles are reported on the genomic plus strand (rs12807809 is reported as T/C, as has been reported in previous GWAS [Stefansson et al., 2009]). Venous blood was collected from the subjects and genomic DNA was extracted from whole blood according to standard procedures. The SNPs were genotyped using the TaqMan 5′-exonuclease allelic discrimination assay (Applied Biosystems, Foster City, CA) as previously described [Hashimoto et al., 2006, 2007]. Detailed information on the PCR conditions is available upon request. Genotyping call rates were 98.9% (rs1939214), 98.5% (rs12807809), 99.3% (rs12278912), 99.3% (rs2075713), and 99.5% (rs11219769). No deviation from Hardy–Weinberg equilibrium (HWE) in the examined SNPs was detected in the patients with schizophrenia or healthy controls ($P > 0.05$). The positions of the five SNPs analyzed in the present study are shown in Figure 1.

Quantitative Measurement of *NRGN* Gene Expression

Isolation and immortalization procedures of lymphocytes from blood using the Epstein–Barr virus (EBV) were performed by SRL of Tokyo, Japan. Immortalized, patient-derived lymphocytes were grown in culture media supplemented with 20% fetal bovine serum. Total RNA was extracted from cell pellets using the RNeasy Mini Kit (Qiagen K.K., Tokyo, Japan). The total yield of RNA was determined by absorbance at 260 nm, and the quality of the RNA was determined using agarose gel electrophoresis.

According to the manufacturer's protocol, total RNA was treated with DNase to remove contaminating genomic DNA using DNase Treatment and Removal Reagents (Ambion, Austin, TX). Total RNA (10 μg) treated with DNase was used in a 50-μl reverse transcriptase reaction to synthesize cDNA with the SuperScript

TABLE I. Genotype and Allele Distributions for SNPs in the *NRGN* Gene Between Patients With Schizophrenia and Controls in a Japanese Population

Marker				SCZ (n = 2019)			CON (n = 2579)			Genotypic	MAF		Allelic	
SNP IDs (M)	Position[a]	M/m[b]	Gene	M/M	M/m	m/m	M/M	M/m	m/m	*P*-value (χ^2)	SCZ	CON	*P*-value (χ^2)	OR (95% CI)
rs1939214 (A)	124110500	A/G	5′	0.67	0.30	0.04	0.66	0.30	0.04	0.51 (1.3)	0.19	0.19	0.29 (1.1)	1.06 (0.95–1.18)
rs12807809 (T)[c]	124111495	T/C	5′	0.58	0.35	0.07	0.56	0.37	0.07	0.44 (1.6)	0.25	0.26	0.25 (1.3)	1.06 (0.96–1.16)
rs12278912 (G)[d]	124117369	G/A	Intron1	0.61	0.34	0.05	0.59	0.35	0.06	0.13 (4.1)	0.22	0.23	0.057 (3.6)	1.10 (1.00–1.22)
rs2075713 (A)	124123149	A/C	3′	0.65	0.31	0.04	0.62	0.33	0.05	0.17 (3.5)	0.20	0.21	0.057 (3.6)	1.10 (1.00–1.22)
rs11219769 (G)	124125357	G/T	3′	0.57	0.37	0.06	0.55	0.38	0.07	0.24 (2.8)	0.25	0.26	0.09 (2.8)	1.09 (0.99–1.19)

SCZ, patients with schizophrenia; CON, healthy controls; M, major allele; m, minor allele; MAF, minor allele frequency; OR, odds ratio.
[a]db SNP build 129.
[b]The first alleles shown are major alleles. All the alleles are represented according to the plus strand DNA sequence.
[c]The genome-wide supported SNP for schizophrenia [Stefansson et al., 2009].
[d]Because a high linkage disequilibrium between rs12278912 and rs7113041 [Ruano et al., 2008] was found in the HapMap JPT samples ($r^2 = 0.93$), rs12278912 was selected as the tagging SNP by the TAGGER program.

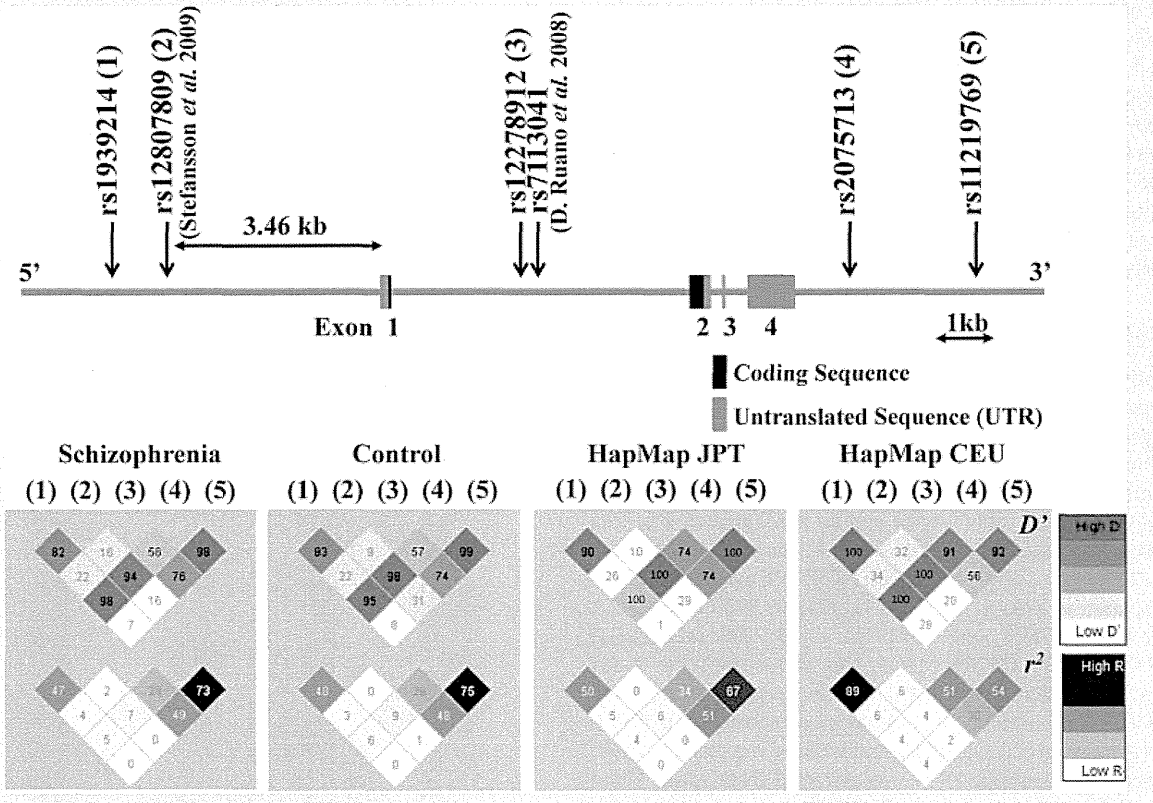

FIG. 1. The genomic structure of *NRGN*, including the locations of the five tagging SNPs studied and linkage disequilibrium of these SNPs in the patient, control, HapMap JPT, and CEU groups. Based on an entry in the Entrez Gene database (National Center for Biotechnology Information), the genomic structure of *NRGN* is shown above. The locations of the SNPs analyzed in this study are indicated by arrows, with numbers indicated in parentheses. The numbers indicated in parentheses refer to the numbering of the SNPs in the linkage disequilibrium (LD) diagram. The distances of exons–introns and intermarkers are drawn to scale. The LDs between pairwise SNPs are shown using the D′ (upper) and r^2 (lower) values at the bottom of the map of the gene structure separately for cases, controls, the HapMap JPT samples and the HapMap CEU samples. High levels of LD are represented by black (D′ and r^2) coloring, with increasing color intensity from 0 to 100, as shown by color bars.

First-Strand Synthesis System for RT-PCR (Invitrogen, Carlsbad, CA) according to the manufacturer's protocol. Detailed information on the PCR conditions is available upon request.

To measure mRNA expression levels of housekeeping (β-*actin*) and *NRGN* genes, we used the Pre-Developed TaqMan Assay Reagent kit (Applied Biosystems). Primer information (gene name: assay ID, transcript ID, target region) is as follows; *NRGN*: Hs00382922_m1, NM_001126181.1 and NM_006176.2, Exon1-2; β-actin: 4326315E, NM_001101, no region indicated (Applied Biosystems). Expression levels of these genes were measured by quantitative real-time reverse transcriptase polymerase chain reaction (qRT-PCR) using an ABI Prism 7900 Sequence Detection System (Applied Biosystems) with a 384-well format as previously described [Yamamori et al., 2011; Yasuda et al., 2011]. PCR data were obtained using Sequence Detector software (SDS version 2.1; Applied Biosystems) and quantified using a standard curve. This software plotted the real-time fluorescence intensity and selected the threshold within the linear phase of the amplicon profile. The software plotted a standard curve of the cycle at threshold C_t, which is where the fluorescence generated within a reaction crossed the threshold, versus the quantity of RNA. All samples were measured using a single plate per target gene, and their C_t values were in the linear range of the standard curve. The quantity of each sample was predicted by C_t values. The qRT-PCR reaction was performed in triplicate, and the expression level of the gene was taken as the average of three independent measurements. Standard curves were obtained using serial dilutions (1:4) of pooled complementary DNA prepared from 300 ng total RNA derived from immortalized lymphocytes. The standard curves of β-*actin* and *NRGN* showed that these genes were expressed in immortalized lymphocytes. In each experiment for β-*actin* and *NRGN*, the R^2 value of the standard curve was >0.99, and no-template control assays resulted in no detectable signal. The individual expression levels of the *NRGN* gene were normalized to the housekeeping gene (raw target gene expression level divided by raw housekeeping gene expression level) and were used for statistical analysis.

Haplotype Associated With *NRGN* Expression (eQTL)

To identify whether the haplotypes in *NRGN* associated with schizophrenia may be expression quantitative trait loci (eQTL), we analyzed *NRGN* expression in two datasets of lymphoblast-derived HapMap JPT samples and in the Japanese case–control samples. For the HapMap JPT samples, we extracted genotypes and *NRGN* lymphoblastoid expression data from the HapMap JPT samples (n = 45) deposited in GeneVar (http://www.sanger.ac.uk/humgen/genevar/ [Stranger et al., 2007]). For the Japanese case–control samples, we used our genotypes and *NRGN* lymphoblastoid expression data obtained using the method described above.

Statistical Analyses

We performed power calculations using the Power Calculator for Two-Stage Association Studies (http://www.sph.umich.edu/csg/abecasis/CaTS/ [Skol et al., 2006]). The power estimate was based on an allele frequency of 0.83 at rs12807809, an odds ratio of 1.19, which was indicated by Stefansson et al. [2009], a prevalence of 0.01, and an alpha level of 0.05 using a multiplicative model.

Differences in clinical characteristics between patients and controls or between genotypes were analyzed using χ^2 tests for sex and the Mann–Whitney *U*-test for age using PASW Statistics 18.0 software (SPSS Japan, Inc., Tokyo, Japan). Deviation from HWE was tested separately in test cases and controls using χ^2 tests for goodness of fit using SNPAlyze V5.1.1 Pro software (DYNACOM, Yokohama, Japan). The allelic and genotypic distributions of *NRGN* polymorphisms between patients and controls were analyzed using χ^2 tests with SNPAlyze V5.1.1 Pro software. The number of effective independent SNPs assayed was estimated to correct for multiple testing by the spectral decomposition method of Nyholt using the SNPSpD software [Nyholt, 2004]. The effective number of independent marker loci was 4.13 and corrected *P*-value for allelic and genotypic associations was set at $P < 0.012$. Pairwise linkage disequilibrium (LD) analyses expressed by D′ and r^2 were applied to detect the intermarker relationships in each group using Haploview 4.2 software (http://www.broad.mit.edu/mpg/haploview/contact.php). Haplotype frequencies were estimated using the method of maximum likelihood with genotyping data using the expectation–maximization (EM) algorithm from SNPAlyze V5.1.1 Pro software. Rare haplotypes detected in less than 3% of patients and controls were excluded from the haplotypic association analysis, as previously described [Ohi et al., 2009, 2010]. We performed 10,000 permutations for significance tests to determine empirical significance using a 2×2 contingency table approach. We used a 2- to 5-window fashion analysis. Since Bonferroni correction for multiple testing is considered to be too conservative to apply to genetic association analyses [Nyholt, 2001], method of Nyholt [Nyholt, 2004] for allelic and genotypic associations and permutation tests [Dudbridge, 2003] for haplotypic associations are considered to be appropriate for these analyses.

The difference in expression levels between Japanese patients with schizophrenia and controls was analyzed using linear regression in PASW Statistics 18.0 software. Age and sex, which may influence gene expression, were corrected for in the expression analysis. HPlus (http://qge.fhcrc.org/hplus) is a software application for estimating haplotype frequencies and inferring individual haplotypes based on EM and progressive ligation (PL) algorithms [Li et al., 2003], and most significantly assessing haplotypic associations with various types of phenotypes using linear regression. Differences of expression levels among haplotypes were analyzed using linear regression in HPlus software. Each genotype was treated as the number of major alleles (0, 1, and 2) in the expression analysis. For the joint haplotype analysis in HPlus software, each haplotype was tested against the reference haplotype (equal to most frequent haplotype) using linear regression. As age and sex were not available for the HapMap samples, these confounding factors were not corrected for in the expression analysis. Expression levels in Japanese cases, control samples and in the combined samples were corrected for age and sex in the analyses. We applied a Bonferroni correction in expression analysis (three tests). The significance level for statistical tests was set at two-tailed $P < 0.05$.

RESULTS

Genetic Association Analysis

Our study size of 2,019 cases and 2,579 controls had sufficient power (>80%) to detect a genetic effect at ORs of 1.19 or greater for rs12807809 when the allele frequency was 0.83, as described in previous GWAS (SGENE-plus) [Stefansson et al., 2009].

The genotype and allele frequencies of five tagging SNPs located in the *NRGN* gene and flanking regions are summarized in Table I. There was no allelic or genotypic association with schizophrenia for any of the five SNPs (uncorrected $P > 0.05$). However, nominal differences in allele frequencies between patients and controls were observed in rs12278912 ($\chi^2 = 3.6$, $P = 0.057$, corrected $P = 0.24$) and rs2075713 ($\chi^2 = 3.6$, $P = 0.057$, corrected $P = 0.24$). The major allele frequencies of both SNPs were higher in patients than in controls. Consistent with previous GWAS [Stefansson et al., 2009], the frequency of the major T allele of rs12807809 was higher in patients (75.4%) than in controls (74.4%) in our Japanese population, although the results did not reach statistical significance [$\chi^2 = 1.3$, $P = 0.25$, OR (95% confidence interval (CI)) = 1.06 (0.96–1.16)].

We focused on haplotypic association between patients with schizophrenia and healthy subjects using a 2- to 5-window fashion analysis. Haplotype analysis showed a significant association with schizophrenia (rs12807809–rs12278912, $\chi^2 = 13.1$, global $P = 0.0042$) (Supplementary Table I). The frequency of the major TG haplotype of rs12807809–rs12278912 was higher in patients (62%) than in controls (58%) [$\chi^2 = 9.4$, $P = 0.0019$, OR (95% CI) = 1.14 (1.05–1.24)] (Table II). On the other hand, the frequency of the TA haplotype of rs12807809–rs12278912 was lower in patients (14%) than in controls (16%) [$\chi^2 = 7.3$, $P = 0.0053$, OR (95% CI) = 0.85 (0.76–0.96)] (Table II). There was no haplotypic association with schizophrenia for any other haplotypes. These findings suggest that the major TG haplotype of rs12807809–rs12278912 may be related to an increased risk of schizophrenia, and the TA haplotype may have a protective role against the susceptibility to schizophrenia. These results of allelic, genotypic, or haplotypic associations were not affected by excluding 86 samples used for expression analyses (data not shown).

TABLE II. Differences in the rs12807809–rs12278912 Haplotype Between Patients With Schizophrenia and Healthy Subjects

Haplotype rs12807809[a]–rs12278912[b]	Frequency Patients	Frequency Controls	Individual P (χ^2)	OR (95%CI)	Global P (χ^2)
					0.0042 (13.1)
TG	0.62	0.58	**0.0019 (9.4)**	1.14 (1.05–1.24)	
CG	0.17	0.18	0.07 (3.4)	0.90 (0.81–1.01)	
TA	0.14	0.16	**0.0053 (7.3)**	0.85 (0.76–0.96)	
CA	0.08	0.08	0.57 (0.3)	1.05 (0.90–1.22)	

Significant P values are shown as bold-faced and underlined type.
[a]The genome-wide supported SNP for schizophrenia [Stefansson et al., 2009].
[b]Because a high linkage disequilibrium between rs12278912 and rs7113041 [Ruano et al., 2008] was found in the HapMap JPT samples ($r^2 = 0.93$), rs12278912 was selected as the tagging SNP by the TAGGER program.

The LD relationships between the markers are provided in Figure 1. The LD pattern observed in our controls was similar to our patients and the JPT HapMap samples; however, it was different from that of the CEU HapMap samples. The strengths of the LD patterns of rs1939214–rs12807809 and rs12278912–rs2075713–rs11219769 were different between Japanese populations and the CEU HapMap samples. The low LD pattern of rs12807809–rs12278912 was similar among the groups ($D' < 0.50$, $r^2 < 0.10$).

NRGN Gene Expression Analysis

The *NRGN* expression level was lower in patients with schizophrenia ($n = 42$, mean $\pm$ SD, 0.86 ± 0.58) than in controls ($n = 44$, 1.00 ± 0.75). However, the results did not reach statistical significance ($r = -0.14$, beta $= -0.11$, SE $= 0.14$, $t = -0.97$, $P = 0.34$).

Based on the results from the genetic association analysis, we investigated whether the rs12807809–rs12278912 haplotype of the *NRGN* gene was an eQTL in two datasets. The rs12807809–rs12278912 haplotype related to schizophrenia was significantly associated with *NRGN* expression in healthy HapMap JPT samples. The *NRGN* gene expression of the high-risk TG haplotype of rs12807809–rs12278912 was significantly lower than that of the protective TA haplotype ($z = 2.69$, $P = 0.007$). We confirmed that the rs12807809–rs12278912 haplotype was significantly associated with *NRGN* expression normalized to the β-*actin* expression in the controls and combined samples (Fig. 2 and Table III, control samples: $z = 2.30$, $P = 0.021$, combined samples: $z = 3.09$, $P = 0.002$). The association occurred in the same direction among the HapMap JPT, control, and combined samples. In case samples, the expression level of rs12807809–rs12278912 was lower in samples with the high-risk TG haplotype than in those with the protective TA haplotype, although the result did not reach statistical significance ($z = 1.49$, $P = 0.14$). The association in the HapMap JPT and combined samples remained significant after correction for multiple tests (HapMap JPT samples: corrected $P = 0.021$, combined samples: corrected $P = 0.006$). However, there was no significant association after applying the correction in control samples (corrected $P = 0.063$).

DISCUSSION

In this study, we provided evidence that haplotypes, including the genome-wide-screen-supported SNP of the *NRGN* gene, were associated with an increased risk of schizophrenia. Our in silico analysis showed that the high-risk rs12807809–rs12278912 haplotype of the *NRGN* gene may be associated with a low expression level of the *NRGN* gene in lymphoblasts derived from the HapMap JPT samples. We confirmed the association between the haplotype and *NRGN* expression in the combined case–control samples. Our results suggest that the schizophrenia-associated haplotype at the

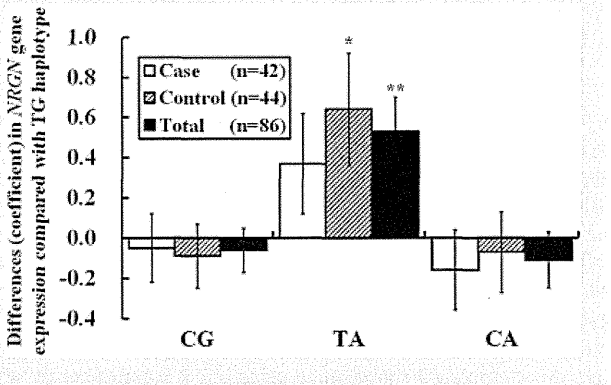

FIG. 2. The association between the rs12807809–rs12278912 haplotype of the *NRGN* gene and *NRGN* expression in lymphoblasts. Expression of the protective TA haplotype of rs12807809–rs12278912 was significantly higher than that of the high-risk TG haplotype in controls and combined case–control samples. The error bars represent standard errors of the coefficient. Estimated frequencies of each haplotype were as follows—TG haplotype: Case, 69%; Control, 61%; Total, 65%; CG haplotype: Case, 16%; Control, 20%; Total, 18%; TA haplotype: Case, 7%; Control, 11%; Total, 9%; CA haplotype: Case, 8%; Control, 9%; Total, 8%. *$P < 0.05$, **$P < 0.01$.

NRGN gene may be a functional variant, and the results support an association between the *NRGN* gene and schizophrenia.

This report is the first investigation of the association of tagging SNPs and haplotypes covering the *NRGN* gene with schizophrenia. To our knowledge, five genetic studies have investigated whether the *NRGN* gene is implicated in schizophrenia. A genome-wide linkage study has shown that the chromosomal region 11q23.3-24 including the *NRGN* gene is linked to schizophrenia in British and Icelandic populations [Gurling et al., 2001]. Subsequently, an association study determined that rs7113041, which displays high LD with rs12278912 and is located on intron 1 in the *NRGN* gene, is related to the risk of developing schizophrenia in male subjects of Portuguese origin [Ruano et al., 2008]. In addition, three GWAS and follow-up studies have shown that rs12807809 is associated with schizophrenia in large European samples [Stefansson et al., 2009]. However, two studies reported no association between *NRGN* and schizophrenia in Bulgarian or Chinese populations [Betcheva et al., 2009; Li et al., 2010]. In the present study, we determined that the rs12807809–rs12278912 haplotype is associated with an increased risk of schizophrenia in a Japanese population. However, there were no significant associations between any SNP, including rs12807809 and rs12278912, and schizophrenia in the population. The inconsistency of association among the previous studies and the present study might result from ethnic differences or type I or II errors for the different sample sizes: Portuguese, 315 cases, 295 controls and 73 trios [Ruano et al., 2008]; European Caucasian, 12,945 cases and 34,591 controls [Stefansson et al., 2009]; Japanese, 2,019 cases and 2,579 controls (present study); Bulgarian, 185 cases and 184 controls [Betcheva et al., 2009]; and Chinese, 2,496 cases and 5,184 controls [Li et al., 2010]. In addition, the SNPs investigated in each study were different. Ruano et al. [2008] and Betcheva et al. [2009] examined rs7113041, which has high LD with rs12278912 but not with rs12807809, whereas Stefansson et al. [2009] and Li et al. [2010] examined rs12807809 but not rs12278912. However, none of these studies examined haplotypes for the *NRGN* gene. Because the rs12807809–rs12278912 haplotype may be the most significant genetic variant in this region, further study is required to confirm the association between the rs12807809–rs12278912 haplotype and schizophrenia in other populations.

Differences in the relative *NRGN* expression levels between patients with schizophrenia and healthy subjects were not demonstrated. This result may be due to the small sample sizes in this study, which may have resulted in the failure to identify a modest difference in *NRGN* expression in this complex disease. We determined that the major TG haplotypic and the TA haplotypic frequencies of rs12807809–rs12278912 were higher and lower, respectively, in patients with schizophrenia than in healthy controls. In addition to these findings, we found that *NRGN* gene expression of the high-risk TG haplotype was significantly lower than that of the protective TA haplotype in lymphoblasts derived from our Japanese case–control subjects as well as the JPT HapMap sample. The low LD patterns of rs12807809–rs12278912 were similar across populations. This region may be vulnerable to recombination. Combinations of the TG and TA of rs12807809–rs12278912 could play an important role in the pathogenesis of schizophrenia. In this study, gene expression data derived from lymphoblasts raised the possibility that the rs12807809–rs12278912 haplotype may be a functional variant of *NRGN*. Further biological studies of the function of rs12807809–rs12278912 are required to verify the expression results.

Smith et al. [2011] analyzed *NRGN* expression in several brain tissues derived from a dataset of at least 130 individuals of European ancestry. However, they showed that neither the genome-wide supported SNP nor any individually correlated SNPs were associated with *NRGN* expression. They did not examine any association between haplotype and *NRGN* expression. There are several challenges in investigating expression findings in the postmortem

TABLE III. The Association Between the rs12807809–rs12278912 Haplotype and mRNA Expression

Haplotypes	Frequency	Coefficient	SE	CI	*P*-value (Z-score)
Schizophrenia ($n=42$)					
TG	0.69	0 (ref)	—	—	—
CG	0.16	−0.05	0.17	(−0.39–0.29)	0.76 (−0.30)
TA	0.07	0.37	0.25	(−0.12–0.86)	0.14 (1.49)
CA	0.08	−0.16	0.20	(−0.55–0.24)	0.43 (−0.78)
Healthy control (n = 44)					
TG	0.61	0 (ref)	—	—	—
CG	0.20	−0.09	0.16	(−0.39–0.22)	0.58 (−0.55)
TA	0.11	0.64	0.28	(0.09–1.18)	**0.021 (2.30)**
CA	0.09	−0.07	0.20	(−0.46–0.32)	0.73 (−0.34)
Total subjects (n = 86)					
TG	0.65	0 (ref)	—	—	—
CG	0.18	−0.06	0.11	(−0.28–0.15)	0.57 (−0.57)
TA	0.09	0.53	0.17	(0.19–0.87)	**0.002 (3.09)**
CA	0.08	−0.11	0.14	(−0.39–0.17)	0.45 (−0.75)

Joint Association Analysis (the reference haplotype is the most frequent haplotype).
For the joint haplotype test, several haplotypes were tested against the reference haplotype.
Significant *P* values are shown as bold-faced and underlined type.

brain: (1) the choice of an appropriate brain region for investigation; (2) the heterogeneity of cell types within brain tissue; (3) the reliance on relatively small samples; and (4) the impact of cause of death and/or postdeath handling of the tissues on gene expression [Marcotte et al., 2003]. Thus, the use of postmortem brain tissue is compounded by a range of confounding factors (age, race, gender, different microarray platforms, and analysis methods) and may be the cause of the relative lack of gene/transcript-level consistency among expression studies. To overcome some of these problems, several groups have considered the use of lymphoblasts rather than the postmortem brain [Matigian et al., 2008; Slonimsky et al., 2010; Yamamori et al., 2011; Yasuda et al., 2011]. Lymphoblasts are useful for schizophrenia researchers because blood-based tissue (lymphoblasts) can be obtained with ease from living subjects, which allows larger case–control studies with optimal matching of key variables (age, sex, and race). In addition, immortalized lymphoblasts in culture are considered an effective tool for studying cells in the absence of the effect of antipsychotic treatments and duration of illness, both of which could mask the genetic differences in RNA expression. Thus, lymphoblasts could be good tool to investigate the impact of a gene in the absence of the impact of any confounding factors. On the other hand, there were some demerits of using lymphoblasts. In immortalized lymphocytes, it might be difficult to observe the effects of genes on their neuron-specific functions, for example, the effects of genes on glutamate and dopamine release and on the formation of synaptic vesicles. When isolation and immortalization procedures of lymphocytes from blood were performed or immortalized lymphocytes were grown in culture media, a genetic mutation might be inserted into genomic DNA in the cultured lymphoblasts and alter DNA sequences. It remains still controversial whether immortalized lymphocytes are an appropriate alternative to neuronal tissue, because there was a little evidence of analysis using immortalized lymphocytes from patients with schizophrenia. In this study, the difference in the association of gene expression with genetic variants between previous study and present study could be explained by the difference in the gene expression profile between immortalized lymphoblast and postmortem brain tissue. Other possible factors contributing to differences in association between studies could be a difference in the SNPs and haplotypes investigated or ethnic differences between Japanese and Caucasian populations.

Smith et al. [2011] performed mutation searches of all four exons of *NRGN* gene in 14 Caucasian subjects with schizophrenia and of the cording exons of *NRGN* gene in 1,113 Bulgarians individuals, 699 of whom had schizophrenia. However, they did not find any novel common polymorphism in the region. Thus, we did not perform a systematic mutation search in this study because there has been no novel common genetic variant in the region. If we perform sequencing and find a novel rare polymorphism, we cannot analyze association between the rare polymorphism and gene expression for only a small number of individuals with rare variant. A genetic variant, particularly a SNP not listed in the HapMap database, that is likely to be more strongly associated with schizophrenia may exist in the rs12807809–rs12278912 haplotype region. Sequencing the entire gene in individuals with risk haplotype in comparison with the protective haplotype carriers with larger sample sizes could provide further information underlying the genomic mechanism for this risk haplotype.

There are several limitations to interpreting our results. Because a number of statistical analyses supported the association of the *NRGN* gene and schizophrenia, such as genotypic and allelic associations for five SNPs (total 5×2), haplotype analysis using a window fashion analysis (total 10) and expression analysis for three individual haplotypes (total 3×4), a correction for multiple testing should be considered. In this study, the overall number of genetic association tests was 32; however, not all tests were independent, and several hypotheses were included. Thus, Bonferroni correction, a method to correct for multiple independent tests for one hypothesis, might not be appropriate. The consensus how to correct such multiple testing has not been reached in this research field. Thus, we applied SNPSpD correction for genotypic and allelic association analysis, permutation method for haplotype analysis and Bonferroni correction for expression analysis (three tests). However, even though we applied these methods of correcting such multiple testing, they might cause false positive results. We did not control for geographical variation of control origin because there is little possibility for ethnic/genetic difference among four geographical regions for feature of homogeneous race in Japan [Yamaguchi-Kabata et al., 2008]. Our significant results may be derived from sample bias owing to population stratification and non-sex-matched samples. In the present study, our results support an association between the *NRGN* gene and schizophrenia. We suggest that the functional haplotype of the *NRGN* gene, which is associated with *NRGN* expression, could be related to the pathogenesis of schizophrenia.

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REFERENCES

Baudier J, Deloulme JC, Van Dorsselaer A, Black D, Matthes HW. 1991. Purification and characterization of a brain-specific protein kinase C substrate, neurogranin (p17). Identification of a consensus amino acid sequence between neurogranin and neuromodulin (GAP43) that corresponds to the protein kinase C phosphorylation site and the calmodulin-binding domain. J Biol Chem 266(1):229–237.

Betcheva ET, Mushiroda T, Takahashi A, Kubo M, Karachanak SK, Zaharieva IT, Vazharova RV, Dimova II, Milanova VK, Tolev T, Kirov G, Owen MJ, O'Donovan MC, Kamatani N, Nakamura Y, Toncheva DI. 2009. Case-control association study of 59 candidate genes reveals the DRD2 SNP rs6277 (C957T) as the only susceptibility factor for schizophrenia in the Bulgarian population. J Hum Genet 54(2):98–107.

Cardno AG, Gottesman II. 2000. Twin studies of schizophrenia: From bow-and-arrow concordances to star wars Mx and functional genomics. Am J Med Genet 97(1):12–17.

Dudbridge F. 2003. Pedigree disequilibrium tests for multilocus haplotypes. Genet Epidemiol 25(2):115–121.

Gurling HM, Kalsi G, Brynjolfson J, Sigmundsson T, Sherrington R, Mankoo BS, Read T, Murphy P, Blaveri E, McQuillin A, Petursson H, Curtis D. 2001. Genomewide genetic linkage analysis confirms the presence of susceptibility loci for schizophrenia, on chromosomes 1q32.2, 5q33.2, and 8p21-22 and provides support for linkage to schizophrenia, on chromosomes 11q23.3-24 and 20q12.1-11.23. Am J Hum Genet 68(3):661–673.

Hashimoto R, Numakawa T, Ohnishi T, Kumamaru E, Yagasaki Y, Ishimoto T, Mori T, Nemoto K, Adachi N, Izumi A, Chiba S, Noguchi H, Suzuki T, Iwata N, Ozaki N, Taguchi T, Kamiya A, Kosuga A, Tatsumi M, Kamijima K, Weinberger DR, Sawa A, Kunugi H. 2006. Impact of the DISC1 Ser704Cys polymorphism on risk for major depression, brain morphology and ERK signaling. Hum Mol Genet 15(20):3024–3033.

Hashimoto R, Hashimoto H, Shintani N, Chiba S, Hattori S, Okada T, Nakajima M, Tanaka K, Kawagishi N, Nemoto K, Mori T, Ohnishi T, Noguchi H, Hori H, Suzuki T, Iwata N, Ozaki N, Nakabayashi T, Saitoh O, Kosuga A, Tatsumi M, Kamijima K, Weinberger DR, Kunugi H, Baba A. 2007. Pituitary adenylate cyclase-activating polypeptide is associated with schizophrenia. Mol Psychiatry 12(11):1026–1032.

Hayashi Y. 2009. Long-term potentiation: Two pathways meet at neurogranin. EMBO J 28(19):2859–2860.

Ikeda M, Aleksic B, Kinoshita Y, Okochi T, Kawashima K, Kushima I, Ito Y, Nakamura Y, Kishi T, Okumura T, Fukuo Y, Williams HJ, Hamshere ML, Ivanov D, Inada T, Suzuki M, Hashimoto R, Ujike H, Takeda M, Craddock N, Kaibuchi K, Owen MJ, Ozaki N, O'Donovan MC, Iwata N. 2011. Genome-wide association study of schizophrenia in a Japanese population. Biol Psychiatry 69(5):472–478.

Li J, Pak JH, Huang FL, Huang KP. 1999. N-methyl-D-aspartate induces neurogranin/RC3 oxidation in rat brain slices. J Biol Chem 274(3): 1294–1300.

Li SS, Khalid N, Carlson C, Zhao LP. 2003. Estimating haplotype frequencies and standard errors for multiple single nucleotide polymorphisms. Biostatistics 4(4):513–522.

Li T, Li Z, Chen P, Zhao Q, Wang T, Huang K, Li J, Li Y, Liu J, Zeng Z, Feng G, He L, Shi Y. 2010. Common variants in major histocompatibility complex region and TCF4 gene are significantly associated with schizophrenia in Han Chinese. Biol Psychiatry 68(7):671–673.

Marcotte ER, Srivastava LK, Quirion R. 2003. cDNA microarray and proteomic approaches in the study of brain diseases: Focus on schizophrenia and Alzheimer's disease. Pharmacol Ther 100(1):63–74.

Martinez de Arrieta C, Perez Jurado L, Bernal J, Coloma A. 1997. Structure, organization, and chromosomal mapping of the human neurogranin gene (NRGN). Genomics 41(2):243–249.

Martinez de Arrieta C, Morte B, Coloma A, Bernal J. 1999. The human RC3 gene homolog, NRGN contains a thyroid hormone-responsive element located in the first intron. Endocrinology 140(1):335–343.

Matigian NA, McCurdy RD, Feron F, Perry C, Smith H, Filippich C, McLean D, McGrath J, Mackay-Sim A, Mowry B, Hayward NK. 2008. Fibroblast and lymphoblast gene expression profiles in schizophrenia: Are non-neural cells informative? PLoS ONE 3(6):e2412.

Nyholt DR. 2001. Genetic case-control association studies—Correcting for multiple testing. Hum Genet 109(5):564–567.

Nyholt DR. 2004. A simple correction for multiple testing for single-nucleotide polymorphisms in linkage disequilibrium with each other. Am J Hum Genet 74(4):765–769.

Ohi K, Hashimoto R, Yasuda Y, Yoshida T, Takahashi H, Iike N, Fukumoto M, et al. 2009. Association study of the G72 gene with schizophrenia in a Japanese population: A multicenter study. Schizophr Res 109(1–3): 80–85.

Ohi K, Hashimoto R, Yasuda Y, Yoshida T, Takahashi H, Iike N, Iwase M, et al. 2010. The chitinase 3-like 1 gene and schizophrenia: Evidence from a multi-center case-control study and meta-analysis. Schizophr Res 116(2–3):126–132.

Ruano D, Aulchenko YS, Macedo A, Soares MJ, Valente J, Azevedo MH, Hutz MH, Gama CS, Lobato MI, Belmonte-de-Abreu P, Goodman AB, Pato C, Heutink P, Palha JA. 2008. Association of the gene encoding neurogranin with schizophrenia in males. J Psychiatr Res 42(2):125–133.

Skol AD, Scott LJ, Abecasis GR, Boehnke M. 2006. Joint analysis is more efficient than replication-based analysis for two-stage genome-wide association studies. Nat Genet 38(2):209–213.

Slonimsky A, Levy I, Kohn Y, Rigbi A, Ben-Asher E, Lancet D, Agam G, Lerer B. 2010. Lymphoblast and brain expression of AHI1 and the novel primate-specific gene, C6orf217, in schizophrenia and bipolar disorder. Schizophr Res 120(1–3):159–166.

Smith RL, Knight D, Williams H, Dwyer S, Richards A, Kirov G, O'Donovan MC, Owen MJ. 2011. Analysis of neurogranin (NRGN) in schizophrenia. Am J Med Genet Part B 156B(5):532–535.

Stefansson H, Ophoff RA, Steinberg S, Andreassen OA, Cichon S, Rujescu D, Werge T, et al. 2009. Common variants conferring risk of schizophrenia. Nature 460(7256):744–747.

Stranger BE, Nica AC, Forrest MS, Dimas A, Bird CP, Beazley C, Ingle CE, Dunning M, Flicek P, Koller D, Montgomery S, Tavare S, Deloukas P, Dermitzakis ET. 2007. Population genomics of human gene expression. Nat Genet 39(10):1217–1224.

Sun J, Kuo PH, Riley BP, Kendler KS, Zhao Z. 2008. Candidate genes for schizophrenia: A survey of association studies and gene ranking. Am J Med Genet Part B 147B(7):1173–1181.

Tsuang M. 2000. Schizophrenia: Genes and environment. Biol Psychiatry 47(3):210–220.

Yamada K, Iwayama Y, Hattori E, Iwamoto K, Toyota T, Ohnishi T, Ohba H, Maekawa M, Kato T, Yoshikawa T. 2011. Genome-wide association study of schizophrenia in Japanese population. PLoS ONE 6(6):e20468.

Yamaguchi-Kabata Y, Nakazono K, Takahashi A, Saito S, Hosono N, Kubo M, Nakamura Y, Kamatani N. 2008. Japanese population structure, based on SNP genotypes from 7003 individuals compared to other ethnic groups: Effects on population-based association studies. Am J Hum Genet 83(4):445–456.

Yamamori H, Hashimoto R, Verrall L, Yasuda Y, Ohi K, Fukumoto M, Umeda-Yano S, Ito A, Takeda M. 2011. Dysbindin-1 and NRG-1 gene expression in immortalized lymphocytes from patients with schizophrenia. J Hum Genet 56(7):478–483.

Yasuda Y, Hashimoto R, Yamamori H, Ohi K, Fukumoto M, Umeda-Yano S, Mohri I, Ito A, Taniike M, Takeda M. 2011. Gene expression analysis in lymphoblasts derived from patients with autism spectrum disorder. Mol Autism 2(1):9.