Supplementary Information for "Common Variants at *VRK2* and *TCF4* Conferring Risk of Schizophrenia"

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Subjects

Ascertainment and diagnosis information for groups not previously described is given below. All individuals provided written, informed consent for participation and approval was obtained from ethics committees at each location.

Belgium. The sample consisted of 521 patients and 341 controls collected in Leuven, Belgium. Following quality control, 510 patients and 341 controls were included. Of the patients finally included, 397 were diagnosed with schizophrenia and 113 were diagnosed with schizoaffective disorder. Patients were recruited from those in treatment at the University Psychiatric Centre of the Catholic University in Leuven and were diagnosed according to DSM-IV criteria by experienced psychiatrists. The control group consisted of unrelated, healthy Flemish individuals collected at the University Hospital Gasthuisberg in Leuven (1).

Denmark (Aarhus). The sample consisted of 909 patients clinically diagnosed with schizophrenia according to International Classification of Diseases, 10th revision (ICD-10) criteria, and 899 controls matched by birth cohort. Following quality-control (QC), there were 878 patients and 874 controls. All individuals were born in Denmark and obtained from the Danish Newborn Screening Biobank (www.ssi.dk).

Denmark (Copenhagen). Additional controls (*N* = 1,045) were derived from the Prospective Epidemiological Risk Factor (PERF study) (2).

Germany (Göttingen). The sample consisted of 1,014 patients and 1,144 controls from the Gottingen Research Association for Schizophrenia (GRAS) (3) project. Patients had a confirmed DSM-IV diagnosis of schizophrenia (~82%) or schizoaffective disorder (~18%). Controls were blood donors. The anonymized controls were 2.2% non-Caucasian; cases were proportionally matched for ethnicity.

Ireland. The Irish sample is part of the Wellcome Trust Case Control Consortium 2 investigation of common, complex genetic disorders. The case sample used in this study included 1,310 individuals recruited through community mental services and inpatient units in the Republic of Ireland and Northern Ireland. None of the individuals used here were included in the International Schizophrenia Consortium (ISC) genome-wide association (GWA) scan (4). Cases were interviewed by a psychiatrist or psychiatric nurse trained to use a structured clinical interview (Structured Clinical Interview for DSM-IV (SCID-P) (5); Schedule for Affective Disorders and Schizophrenia (Lifetime version; SADS-LB) (6); Schedule for Clinical Assessment in Neuropsychiatry (SCAN) for ICD-10 (7)). Diagnosis of a major psychotic disorder was made by the consensus lifetime best estimate method using DSM-IV criteria with all available information (interview, family or staff report and chart review). All cases were over 18 years of age, had four Irish grandparents and had been screened to exclude substance-induced psychotic disorder or psychosis due to a general medical condition. Cases were identified as meeting either narrow or broad diagnostic criteria. The narrow diagnostic group used here (*N* = 1,310) included Schizophrenia (*N* = 1,089), Schizoaffective Disorder (*N* = 219) and

Schizophreniform Disorder (*N* = 2). Controls (*N* =1,023), also not included in the ISC GWA study (4), were ascertained from the Irish GeneBank and represented blood donors from the Irish Blood Transfusion Service (IBTS). They met the same ethnicity criteria as cases but were not specifically screened for psychiatric illness. Individuals taking regular prescribed medication are excluded from blood donation in Ireland and donors are not financially remunerated, making it unlikely that patient or socially disadvantaged groups (which might have higher schizophrenia rates) were over-represented among control subjects.

Italy. The Italian sample consisted of 148 cases and 94 controls. Following quality control, there were 138 cases and 89 controls. Cases were ascertained as incident patients at the Department of Psychiatry, University of Rome-Tor Vergata. DSM-IV criteria for schizophrenia were verified using SCID-P interviews. Controls were healthy subjects with no history of either psychiatric illness or use of psychoactive medication.

Genotyping, quality control and imputation

deCODE Genetics and UCLA. The Netherlands 1 study group and Netherlands 2 controls were genotyped using Illumina genome-wide arrays as previously described (8). Samples were removed if they had yield < 98%, a discrepancy between reported and genotype-inferred sex, evidence of non-European ancestry or identity with a higher-yield sample already included in the study. Markers were excluded if they had case or control yield < 95%, control Hardy-Weinberg equilibrium $P < 1 \times 10^{-5}$ or a difference in allele frequency between typing centers with $P < 1 \times 10^{-5}$.

The Denmark/Aarhus 1, Denmark/Copenhagen, Germany/Bonn, Germany/Munich , Hungary, Italy, Norway, Russia and Sweden study groups, and the Belgium and Netherlands 2 cases, were single-track genotyped using Centaurus assays as previously described (8). Samples with yield < 90% were excluded, and the lower yield of each pair of duplicates was removed. Markers had control Hardy-Weinberg equilibrium *P* values > 0.001, and, in each group, yield in cases and controls was > 95%.

Belgium. Controls were genotyped and quality control was carried out as previously described (1).

CATIE. Individual genotypes were obtained from the NIMH Center for Collaborative Genetic Studies on Mental Disorders. Genotyping was previously described (9). All subjects had genotype yield > 96% and markers had MAF > 0.01, yield > 95% and control HWE *P* values > 1×10^{-6}. Individuals without self-reported ancestry only from Europe, discrepancy between reported and genotype-inferred sex, one of each pair of individuals determined by IBD estimation to be first or second degree relatives and outliers in the principal component analysis were removed.

Denmark/Aarhus 2. DNA was extracted from dried blood spots provided by the Danish Newborn Screening Biobank using the Extract-N-Amp Blood PCR kit (Sigma Aldrich), and whole-genome-amplification was performed using the RepliG kit (Qiagen) essentially as previously described (10). For each sample, whole-genome-amplification was performed in three separate reactions which were pooled before genotyping.

Samples with yield < 97% were excluded. SNPs included in this study had yield > 98% and Hardy Weinberg equilibrium *P* values > 0.05.

Finland. Data were subject to standard quality control procedures including: genotyping concordance with Sequencom MassArray for a selected set of SNPs, duplicate sample concordance, sample and SNP success rate thresholds of > 95%, Hardy-Weinberg equilibibrium *P* values > 1 x 10^{-6}, removal of heterozygosity outliers and related individuals (pi-hat cut off at 0.1).

Germany (Göttingen). Genotyping was carried out with SimpleProbes (TIB Molbiol) on a LightCycler480 (Roche). All markers had control Hardy-Weinberg equilibrium *P* values > 0.05 and genotyping yield was > 95% in both cases and controls.

Ireland. The samples from Ireland passing Affymetrix laboratory QC had their raw intensities renormalized within collections using CelQuantileNorm (see http://outmodedbonsai.sourceforge.net/). The normalized intensities were used to call genotypes with an updated version of the Chiamo software (see www.stats.ox.ac.uk/~marchini/software/gwas/chiamo.html) adapted for Affymetrix 6.0 SNP array data. Standard quality control measures were applied as part of the Wellcome Case Control Consortium 2 and have been published elsewhere (11). Briefly, in order to try to obtain the maximally powerful set of samples we calculated summary statistics of each individual's genotypes (heterozygosity, missingness, HapMap principal component scores) and probe intensities (the difference between the A and B channel intensity and the average X chromosomes intensity). Using a Bayesian mixture model we then clustered individuals on the basis of these statistics in order to identify individuals with outlying patterns of diversity. We excluded individuals with greater than 50% probability of assignment to the outlier class. To assess relatedness amongst study individuals we compared each individual with the 100 individuals they were most closely related to (on the basis of genome-wide levels of allele sharing) and used a hidden Markov Model (HMM) to decide, at each position in their genome, whether the two individuals shared 0, 1, or 2 chromosomes identical by descent. We obtained a set of individuals with IBD < 5% by iteratively removing one of each pair of putatively-related individuals. Imputation was carried out using IMPUTE2 (12). Details on the SNP quality control and imputation methodology have been published previously (13).

Spain. Genotyping was carried out as described previously (8). Samples had yield > 90% and one of each pair of duplicates was removed. SNPs had yield > 95% in cases and controls and control Hardy-Weinberg *P* values > 0.01.

United Kingdom. Genotyping and quality control have been described previously (14). Imputation was performed using Mach 1.0 (15) with the 1000 genomes-Sanger 2009-08 data release (http://www.sph.umich.edu/csg/yli/mach/download/1000G-Sanger-0908.html) as the reference source. Only SNPs with RSQR > 0.3 were retained. Tests for association were with a likelihood ratio test using mach2dat

(16). Note that imputed data were not available for the 'controls' derived from the 6 sets of non-psychiatric disorder cases reported by the WTCCC.

Note on potential population stratification

We controlled for potential population stratification in two ways. For the study groups collected from the United States and Finland (locations with the greatest population structure), association results were adjusted using principal components. For the remaining groups with genome-wide data, genomic control inflation factors were small (1.08, 1.05, 1.09 and 1.08 for the Netherlands 1, Denmark/Aarhus 2, Ireland and the UK, respectively) and were corrected for by using genomic control.

Table S1a. Schizophrenia case and control samples: GWAS and meta-analysis

	N cases	*N* controls	Sample description	Genotyping platform	Location of genotyping
SGENE-plus GWAS					
England	93	88	Stefansson *et al* (8)	Illumina 300K	deCODE Genetics
Finland, excl. Kuusamo	59	147	Stefansson *et al* (8)	Illumina 300K	deCODE Genetics
Finland, Kuusamo	123	50	Stefansson *et al* (8)	Illumina 300K	deCODE Genetics
Germany, Bonn	483	367	Stefansson *et al* (8)	Illumina 550K	University of Bonn
Germany, Munich	574	604	Stefansson *et al* (8)	Illumina 300K	deCODE Genetics, Duke University
Iceland	589	11492	Stefansson *et al* (8)	Illumina 300K	deCODE Genetics
Italy	84	89	Stefansson *et al* (8)	Illumina 300K	deCODE Genetics
Scotland, Aberdeen	658	661	Stefansson *et al* (8)	Illumina 300K/550K	deCODE Genetics, Duke University
Subtotal	2663	13498	-	-	-
2009 Collaboration (8)					
ISC, without Aberdeen	2602	2885	Purcell *et al* (4)	Affymetrix 500K/5.0/6.0	Broad Institute
MGS, European ancestry	2681	2653	Shi *et al* (17)	Affymetrix 6.0	Broad Institute
Subtotal	5283	5538	-	-	-
Total	7946	19036			

Shown are numbers of cases and controls following sample quality control.

Table S1b. Schizophrenia case and control samples: follow-up

	N cases	*N* controls	Sample description	Genotyping platform	Location of genotyping
Primary follow-up					
Belgium	510 (113)	341	this work	Centaurus/Illumina 370K	deCODE Genetics
CATIE	391	404	Sullivan *et al* (9)	Affymetrix 500K, 164K	Perlegen
Denmark, Aarhus 1	227	493	Stefansson *et al* (8)	Centaurus	deCODE Genetics
Denmark, Aarhus 2	878	874	this work	Illumina 610K	AROS A/S, Aarhus University
Denmark, Copenhagen	1324 (136)	2350	Stefansson *et al* (8) *(expanded),* t.w.	Centaurus	deCODE Genetics
Finland, excl. Kuusamo	287	3873	Stefansson *et al* (8)	Illumina 660K/370K	Sanger Institute, Broad Institute
Germany, Bonn	607	1534	Stefansson *et al (8)*	Centaurus	deCODE Genetics
Germany, Munich	303	1614	Stefansson *et al* (8)	Centaurus	deCODE Genetics
Hungary	241	214	Stefansson *et al* (8)	Centaurus	deCODE Genetics
Ireland	1310 (219)	1023	this work	Affymetrix 6.0	Affymetrix, Sanger Institute
Italy	138	89	this work	Centaurus	deCODE Genetics
Netherlands 1	693	3689	Stefansson *et al* (8)	Illumina 370K/550K	deCODE Genetics, UCLA
Netherlands 2	176	603	Stefansson *et al* (8) *(expanded)*	Centaurus/Illumina 370K	deCODE Genetics
Norway	228 (40)	293	Stefansson *et al* (8) *(expanded)*	Centaurus	deCODE Genetics
Russia	597 (28)	742	Stefansson *et al* (8) *(expanded)*	Centaurus	deCODE Genetics
Spain, Santiago	282	598	Stefansson *et al* (8)	Sequenom MassArray iPlex	Spanish National Genotyping Center
Spain, Valencia	323	398	Stefansson *et al* (8)	Sequenom MassArray iPlex	Spanish National Genotyping Center
Sweden	252	287	Stefansson *et al* (8)	Centaurus	deCODE Genetics
United Kingdom	479	2937	O'Donovan *et al* (14)	Affymetrix 500K	WTCCC Center
Subtotal	9246 (536)	22356	-	-	-
Secondary follow-up					
GRAS	1014 (180)	1144	this work	Roche LightCycler480	MPI of Experimental Medicine, Göttingen
Total	10260 (716)	23500			

Shown are numbers of cases and controls following sample quality control. For cases, the number of the total diagnosed with schizoaffective disorder (or persistent delusional disorder in the case of the Denmark, Copenhagen study) is given in parentheses. t.w, this work; UCLA, University of California at Los Angeles; WTCCC, Wellcome Trust Case Control Consortium; MPI, Max Planck Institute

Table S2. Association results in the previous schizophrenia meta-analysis (SGENE-plus+ISC+MGS), the primary follow-up set and the combined (discovery + primary follow-up) data set

					SGENE-plus + ISC + MGS (7,946 cases; 19,036 controls)		primary follow-up (9,246 cases; 22,356 controls)		SGENE-plus + ISC + MGS + primary follow-up (17,192 cases; 41,392 controls)		
Chr	Mb	SNP	Al	Freq	OR	*P* value	OR	*P* value	OR	*P* value	Close Genes
6	28.4	rs13211507	T	0.92	1.22	5.2×10^{-6}	1.21	1.1×10^{-7}	1.21	3.1×10^{-12}	*PGBD1*
6	27.4	rs6932590	T	0.78	1.15	5.6×10^{-7}	1.10	6.9×10^{-5}	1.12	4.6×10^{-10}	*PRSS16, FKSG83*
6	32.3	rs3131296	G	0.87	1.18	9.8×10^{-6}	1.14	1.4×10^{-5}	1.15	9.8×10^{-10}	*NOTCH4*
6	27.2	rs6913660	C	0.85	1.19	4.6×10^{-8}	1.09	0.00067	1.13	1.2×10^{-9}	*-, HIST1H2BJ*
18	51.3	rs9960767	C	0.056	1.27	1.8×10^{-6}	1.16	0.00025	1.20	4.2×10^{-9}	*TCF4*
2	58.1	rs2312147	C	0.61	1.11	3.7×10^{-6}	1.08	0.00024	1.09	6.2×10^{-9}	*-, VRK2*
18	50.9	rs4309482	A	0.58	1.10	7.1×10^{-5}	1.08	3.6×10^{-5}	1.09	1.1×10^{-8}	*CCDC68, TCF4*
11	124.1	rs12807809	T	0.83	1.16	2.3×10^{-6}	1.09	0.00057	1.12	1.5×10^{-8}	*SPA17 ,NRGN*
5	101.9	rs1502844	C	0.30	1.11	3.8×10^{-6}	1.06	0.0027	1.08	1.3×10^{-7}	*SLCO6A1 ,-*
8	89.3	rs6994019	T	0.25	1.12	1.0×10^{-5}	1.07	0.0017	1.09	1.7×10^{-7}	*MMP16*
11	112.9	rs6589386	C	0.61	1.10	1.3×10^{-5}	1.06	0.0026	1.08	2.7×10^{-7}	*DRD2, TMPRSS5*
10	104.7	rs1046778	T	0.67	1.11	4.5×10^{-5}	1.07	0.0020	1.08	6.0×10^{-7}	*AS3MT*
2	144.9	rs12991836	C	0.37	1.11	3.8×10^{-5}	1.06	0.0031	1.08	1.1×10^{-6}	*GTDC1, ZEB2*
16	29.9	rs4583255	T	0.56	1.10	2.5×10^{-5}	1.05	0.0072	1.07	1.9×10^{-6}	*TAOK2*
6	43.3	rs2273709	A	0.81	1.13	4.1×10^{-5}	1.07	0.0068	1.09	2.6×10^{-6}	*PARC*
11	30.3	rs1765142	A	0.64	1.12	1.4×10^{-5}	1.05	0.016	1.08	4.2×10^{-6}	*C11orf46, MPPED2*
5	76.2	rs2460508	G	0.45	1.10	9.2×10^{-5}	1.05	0.012	1.07	1.1×10^{-5}	*S100Z*
6	73.2	rs2789588	T	0.68	1.10	4.7×10^{-5}	1.05	0.026	1.07	1.6×10^{-5}	*RIMS1, KCNQ5*
9	120.4	rs1572299	A	0.49	1.12	3.1×10^{-6}	1.04	0.071	1.07	1.7×10^{-5}	-
16	4.5	rs3747600	A	0.28	1.12	3.2×10^{-6}	1.03	0.11	1.07	2.3×10^{-5}	*C16orf5*
5	113.5	rs1487222	A	0.41	1.11	7.3×10^{-6}	1.03	0.095	1.07	2.6×10^{-5}	-
6	32.4	rs2076537	C	0.59	1.14	5.5×10^{-5}	1.05	0.015	1.07	2.6×10^{-5}	*C6orf10*
1	53.5	rs5174	G	0.57	1.09	8.2×10^{-5}	1.04	0.039	1.06	3.4×10^{-5}	*LRP8*
9	26.9	rs7863476	A	0.19	1.16	6.3×10^{-7}	1.03	0.24	1.08	4.0×10^{-5}	*PLAA*
3	162.9	rs2063836	T	0.61	1.10	4.7×10^{-5}	1.04	0.060	1.06	4.5×10^{-5}	-
3	182.2	rs1010471	G	0.65	1.12	3.2×10^{-6}	1.03	0.17	1.06	5.0×10^{-5}	*FXR1*

Table S2 (cont). Association results in the previous schizophrenia meta-analysis (SGENE-plus+ISC+MGS), the primary follow-up set and the combined (discovery + primary follow-up) data set

					SGENE-plus + ISC + MGS (7,946 cases; 19,036 controls)		primary follow-up (9,246 cases; 22,356 controls)		SGENE-plus + ISC + MGS + primary follow-up (17,192 cases; 41,392 controls)		
Chr	Mb	SNP	Al	Freq	OR	*P* value	OR	*P* value	OR	*P* value	Close Genes
5	11.9	rs4466166	T	0.012	1.57	3.9×10^{-5}	1.17	0.054	1.29	8.9×10^{-5}	*CTNND2*
4	72.3	rs2579309	A	0.054	1.22	2.5×10^{-5}	1.05	0.20	1.12	0.00023	*SLC4A4*
7	110.9	rs38752	T	0.62	1.11	4.6×10^{-5}	1.03	0.20	1.06	0.00029	*IMMP2L*
11	55.3	rs11230864	T	0.37	1.10	3.9×10^{-5}	1.02	0.29	1.05	0.00053	*OR4C6, OR5D13*
12	1.5	rs3741976	G	0.36	1.10	8.8×10^{-5}	1.02	0.28	1.06	0.00082	*ERC1*
6	64.3	rs1744163	C	0.90	1.19	6.9×10^{-5}	1.03	0.43	1.09	0.0023	*PTP4A1*
6	31.2	rs3815087	T	0.19	1.12	6.7×10^{-5}	1.01	0.58	1.06	0.0030	*PSORS1C1*
22	18.3	rs7289747	C	0.063	1.22	9.6×10^{-6}	1.01	0.89	1.09	0.0032	*TXNRD2*
X	6.0	rs6639583	T	0.24	1.12	8.6×10^{-5}	1.01	0.73	1.06	0.019	*NLGN4X*
22	46.9	rs131137	A	0.57	1.11	9.3×10^{-5}	1.00	0.99	1.04	0.021	-
3	175.2	rs13078193	G	0.24	1.12	2.2×10^{-5}	0.99	0.56	1.04	0.027	*NLGN1*
22	26.1	rs5752534	C	0.73	1.11	5.6×10^{-5}	0.97	0.26	1.03	0.058	-
12	74.3	rs1383098	C	0.21	1.11	9.7×10^{-5}	0.97	0.15	1.03	0.14	*KRR1,-*

Mb, megabases based on NCBI Build 36; Al, allele; Freq, average control frequency in the SGENE-plus genome-wide typed data; Close genes, the RefSeq gene a SNP is located in or, if the SNP is not located in a gene, the closest RefSeq genes within 200 kb to either side.

Table S3. Association of rs2312147[C] with schizophrenia by study group

Study Group	*N* cases	*N* con	Freq	OR (95% CI)	*P* value
SGENE-plus					
England	93	88	0.568	1.38 (0.90,2.11)	0.13
Finland,excl Kuusamo	59	147	0.619	1.40 (0.88,2.22)	0.15
Finland, Kuusamo	123	50	0.660	0.88 (0.53,1.46)	0.61
Germany, Bonn	483	367	0.583	1.29 (1.06,1.58)	0.013
Germany, Munich	574	604	0.607	1.07 (0.91,1.27)	0.41
Iceland	589	11492	0.653	1.18 (1.03,1.35)	0.021
Italy	84	89	0.556	1.73 (1.11,2.70)	0.016
Scotland	658	661	0.622	1.07 (0.90,1.26)	0.44
2009 Collaboration					
ISC[1]	NA	NA	NA	1.09 (1.00,1.18)	0.043
MGS[2]	NA	NA	NA	1.09 (1.01,1.18)	0.035
Primary Follow-up					
Belgium	506	340	0.600	1.20 (0.98,1.47)	0.072
CATIE[3]	380	392	0.591	1.06 (0.85,1.32)	0.62
Denmark, Aarhus 1	226	474	0.636	1.01 (0.80,1.28)	0.90
Denmark, Aarhus 2	877	871	0.602	1.07 (0.93,1.23)	0.37
Denmark, Copenhagen	1300	2338	0.615	1.07 (0.97,1.18)	0.19
Finland, excl. Kuusamo	287	3873	0.631	1.02 (0.85,1.24)	0.81
Germany, Bonn	603	1526	0.613	1.03 (0.90,1.19)	0.63
Germany, Munich	300	1602	0.608	0.93 (0.78,1.11)	0.42
Hungary	239	214	0.596	1.07 (0.82,1.39)	0.64
Ireland[2]	1310	1023	0.623	1.12 (0.99,1.27)	0.076
Italy	137	89	0.618	1.04 (0.71,1.54)	0.83
Netherlands 1	692	3684	0.610	1.12 (0.99,1.26)	0.083
Netherlands 2	176	603	0.623	1.11 (0.87,1.43)	0.39
Norway	225	280	0.662	0.90 (0.69,1.16)	0.41
Russia	595	737	0.577	1.15 (0.98,1.34)	0.079
Spain, Santiago	282	597	0.654	1.20 (0.96,1.48)	0.10
Spain, Valencia	320	397	0.657	0.97 (0.78,1.20)	0.77
Sweden	251	287	0.622	1.08 (0.84,1.38)	0.55
United Kingdom[2]	479	2937	NA	1.14 (0.98,1.32)	0.083
Secondary Follow-up					
GRAS	993	1141	0.600	1.10 (0.97,1.24)	0.13

Freq, control frequency [1] rs2678910 (HapMap CEU r^2=0.967) [2]imputed [3]rs1518395 (HapMap CEU r^2=0.967)

Table S4. Association of rs4309482[A] with schizophrenia by study group

Study Group	*N* cases	*N* con	Freq	OR (95% CI)	*P* value
SGENE-plus					
England	93	88	0.602	1.07 (0.70,1.63)	0.76
Finland, excl Kuusamo	58	147	0.497	1.12 (0.73,1.74)	0.60
Finland, Kuusamo	123	50	0.530	1.54 (0.94,2.51)	0.086
Germany, Bonn	483	367	0.601	1.15 (0.94,1.41)	0.18
Germany, Munich	574	602	0.578	1.23 (1.04,1.46)	0.015
Iceland	589	11483	0.586	1.08 (0.95,1.23)	0.26
Italy	84	88	0.682	0.72 (0.46,1.13)	0.15
Scotland	658	661	0.568	1.19 (1.01,1.39)	0.039
2009 Collaboration					
ISC[1]	NA	NA	NA	1.05 (0.97,1.14)	0.24
MGS[2]	NA	NA	NA	1.10 (1.01,1.19)	0.022
Primary follow-up					
Belgium	507	340	0.591	0.96 (0.79,1.17)	0.70
CATIE[1]	384	394	0.574	1.10 (0.88,1.37)	0.40
Denmark, Aarhus 1	223	476	0.576	1.08 (0.86,1.36)	0.51
Denmark, Aarhus 2	878	872	0.562	1.22 (1.06,1.40)	0.0045
Denmark, Copenhagen	1276	2258	0.582	1.06 (0.96,1.17)	0.24
Finland, excl. Kuusamo	287	3863	0.556	1.08 (0.90,1.29)	0.39
Germany, Bonn	591	1510	0.610	0.95 (0.82,1.08)	0.42
Germany, Munich	290	1556	0.578	1.24 (1.03,1.49)	0.02
Hungary	232	211	0.628	1.02 (0.77,1.33)	0.91
Ireland[2]	1310	1023	0.582	1.08 (0.96,1.22)	0.21
Italy	137	89	0.567	1.33 (0.90,1.95)	0.15
Netherlands 1	693	3675	0.571	1.15 (1.02,1.30)	0.025
Netherlands 2	174	603	0.575	1.14 (0.89,1.45)	0.30
Norway	225	282	0.567	1.06 (0.83,1.37)	0.63
Russia	589	733	0.583	1.13 (0.97,1.32)	0.12
Spain, Santiago	281	595	0.601	0.98 (0.80,1.20)	0.85
Spain, Valencia	322	398	0.652	1.03 (0.83,1.28)	0.80
Sweden	251	284	0.570	1.04 (0.81,1.32)	0.76
United Kingdom[2]	479	2937	NA	1.09 (0.94,1.26)	0.25
Secondary follow-up					
GRAS	991	1141	0.592	1.06 (0.94,1.20)	0.34

Freq, control frequency [1]rs4131791 (HapMap CEU r^2=1.0) [2]imputed

Table S5. Association of rs13211507[T] with schizophrenia by study group

Study Group	*N* cases	*N* con	Freq	OR (95% CI)	*P* value
SGENE-plus					
England	93	88	0.898	1.30 (0.63,2.67)	0.48
Finland, excl Kuusamo	59	147	0.959	1.63 (0.47,5.69)	0.44
Finland, Kuusamo	123	50	0.960	2.01 (0.48,8.32)	0.34
Germany, Bonn	483	367	0.909	1.33 (0.92,1.91)	0.13
Germany, Munich	574	604	0.917	1.41 (1.02,1.95)	0.036
Iceland	589	11492	0.932	1.02 (0.79,1.32)	0.86
Italy	84	89	0.944	1.94 (0.66,5.74)	0.23
Scotland	658	661	0.870	1.24 (0.97,1.58)	0.091
2009 Collaboration					
ISC[1]	NA	NA	NA	1.39 (1.17,1.66)	0.00026
MGS[2]	NA	NA	NA	1.11 (0.97,1.27)	0.13
Primary follow-up					
Belgium	505	341	0.915	1.37 (0.95,1.99)	0.093
CATIE[3]	386	400	0.910	1.19 (0.81,1.74)	0.39
Denmark, Aarhus 1	223	484	0.892	1.23 (0.85,1.80)	0.27
Denmark, Aarhus 2	878	874	0.911	0.97 (0.77,1.23)	0.81
Denmark, Copenhagen	1310	2327	0.899	1.27 (1.07,1.50)	0.0053
Finland, excl. Kuusamo	287	3872	0.966	1.33 (0.68,2.62)	0.41
Germany, Bonn	597	1522	0.913	1.26 (0.98,1.62)	0.071
Germany, Munich	302	1604	0.919	1.89 (1.30,2.76)	0.00088
Hungary	239	213	0.939	1.35 (0.75,2.41)	0.32
Ireland[2]	1310	1023	0.898	1.24 (1.00,1.55)	0.048
Italy	138	89	0.972	0.97 (0.31,3.00)	0.96
Netherlands 1	693	3689	0.896	1.13 (0.93,1.39)	0.23
Netherlands 2	175	603	0.883	1.97 (1.28,3.05)	0.0022
Norway	226	286	0.911	1.38 (0.87,2.19)	0.18
Russia	593	736	0.957	1.16 (0.78,1.72)	0.46
Spain, Santiago	282	597	0.955	0.87 (0.55,1.39)	0.57
Spain, Valencia	323	398	0.969	0.96 (0.53,1.74)	0.91
Sweden	249	283	0.935	1.59 (0.92,2.73)	0.094
United Kingdom[2]	479	2937	NA	1.04 (0.83,1.30)	0.73
Secondary follow-up					
GRAS	991	1141	0.906	1.34 (1.08,1.67)	0.0089

Freq, control frequency [1]rs13214023 (HapMap CEU r^2=0.915) [2]imputed [3]rs10484399 (HapMap CEU r^2=1.0)

Table S6. Association of rs3131296[G] with schizophrenia by study group

Study Group	*N* cases	*N* con	Freq	OR (95% CI)	*P* value
SGENE-plus					
England	92	88	0.841	1.26 (0.70,2.28)	0.44
Finland, excl Kuusamo	59	147	0.854	2.72 (1.26,5.85)	0.011
Finland, Kuusamo	123	50	0.910	1.64 (0.65,4.13)	0.30
Germany, Bonn	481	367	0.860	1.30 (0.97,1.76)	0.080
Germany, Munich	574	604	0.877	1.03 (0.80,1.33)	0.82
Iceland	589	11489	0.913	0.98 (0.78,1.23)	0.85
Italy	84	89	0.904	0.88 (0.43,1.79)	0.72
Scotland	658	661	0.806	1.48 (1.20,1.84)	0.00031
2009 Collaboration					
ISC[1]	NA	NA	NA	1.31 (1.11,1.54)	0.0013
MGS[2]	NA	NA	NA	1.09 (0.97,1.22)	0.14
Primary follow-up					
Belgium	503	339	0.888	1.09 (0.80,1.50)	0.57
CATIE[1]	390	402	0.884	1.19 (0.84,1.68)	0.34
Denmark, Aarhus 1	227	489	0.863	1.08 (0.78,1.51)	0.63
Denmark, Aarhus 2	873	871	0.874	0.99 (0.81,1.22)	0.94
Denmark, Copenhagen	1322	2321	0.862	1.17 (1.02,1.35)	0.028
Finland, excl. Kuusamo	287	3854	0.896	1.45 (0.98,2.15)	0.067
Germany, Bonn	603	1520	0.875	1.05 (0.85,1.28)	0.67
Germany, Munich	301	1604	0.870	1.43 (1.08,1.89)	0.013
Hungary	241	212	0.882	1.30 (0.85,1.99)	0.23
Ireland[2]	1310	1023	0.853	1.20 (1.00,1.45)	0.046
Italy	136	89	0.888	1.59 (0.83,3.06)	0.16
Netherlands 1	690	3657	0.860	1.14 (0.95,1.36)	0.15
Netherlands 2	175	598	0.851	1.22 (0.86,1.72)	0.27
Norway	226	291	0.880	0.91 (0.63,1.32)	0.62
Russia	595	735	0.891	1.28 (0.99,1.65)	0.065
Spain, Santiago	282	598	0.904	1.05 (0.74,1.48)	0.79
Spain, Valencia	322	398	0.898	1.29 (0.90,1.85)	0.17
Sweden	251	284	0.849	1.37 (0.96,1.95)	0.085
United Kingdom[2]	479	2937	NA	0.92 (0.76,1.12)	0.41
Secondary follow-up					
GRAS	993	1141	0.865	1.28 (1.07,1.54)	0.0080

Freq, control frequency [1]rs1150753 (HapMap CEU r^2=0.94) [2]imputed

Table S7. Association of rs12807809[T] with schizophrenia by study group

Study Group	*N* cases	*N* con	Freq	OR (95% CI)	*P* value
SGENE-plus					
England	93	88	0.835	0.91 (1.58,0.53)	0.75
Finland/Helsinki	59	147	0.854	1.02 (0.55,1.88)	0.96
Finland/Kuusamo	123	50	0.820	1.28 (0.67,2.46)	0.46
Germany/Bonn	483	367	0.804	1.13 (0.88,1.46)	0.33
Germany/Munich	574	604	0.814	1.15 (0.93,1.43)	0.20
Iceland	589	11491	0.813	1.30 (1.09,1.55)	0.0030
Italy	83	89	0.860	1.13 (0.60,2.13)	0.71
Scotland	658	661	0.826	1.19 (0.96,1.48)	0.12
2009 Collaboration					
ISC	NA	NA	NA	1.14 (1.00,1.30)	0.057
MGS	NA	NA	NA	1.15 (1.03,1.27)	0.0092
Primary follow-up					
Belgium	509	340	0.824	1.15 (0.89,1.49)	0.30
CATIE[1]	386	404	0.816	1.24 (0.93,1.65)	0.14
Denmark, Aarhus 1	225	487	0.803	1.27 (0.95,1.70)	0.11
Denmark, Aarhus 2	878	871	0.825	0.92 (0.77,1.10)	0.36
Denmark, Copenhagen	1316	2339	0.817	1.03 (0.91,1.17)	0.60
Finland, excl. Kuusamo	287	3871	0.827	1.23 (0.96,1.59)	0.10
Germany, Bonn	601	1529	0.814	1.09 (0.92,1.30)	0.33
Germany, Munich	302	1609	0.831	1.31 (1.03,1.68)	0.03
Hungary	237	214	0.848	1.07 (0.74,1.55)	0.72
Ireland	1310	1023	0.830	1.02 (0.87,1.20)	0.83
Italy	138	89	0.815	1.52 (0.90, 2.55)	0.11
Netherlands 1	693	3687	0.818	1.10 (0.94,1.29)	0.23
Netherlands 2	176	603	0.818	0.96 (0.71,1.31)	0.80
Norway	226	289	0.825	1.24 (0.88,1.73)	0.21
Russia	592	738	0.846	1.05 (0.85,1.29)	0.68
Spain, Santiago	282	598	0.839	1.29 (0.97,1.72)	0.077
Spain, Valencia	322	397	0.821	1.21 (0.92,1.61)	0.18
Sweden	252	285	0.798	1.34 (0.98,1.83)	0.067
United Kingdom[2]	479	2937	NA	0.97 (0.77,1.21)	0.77
Secondary follow-up					
GRAS	989	1141	0.818	1.16 (0.99,1.37)	0.063

Freq, control frequency [1]rs1939214 (HapMap CEU r^2=0.943) [2]imputed

Table S8. Association of rs9960767[C] with schizophrenia by study group

Study Group	*N* cases	*N* con	Freq	OR (95% CI)	*P* value
SGENE-plus					
England	93	88	0.051	1.51 (0.64,3.56)	0.35
Finland, excl Kuusamo	59	147	0.044	2.22 (0.94,5.27)	0.070
Finland, Kuusamo	123	49	0.051	1.74 (0.64,4.71)	0.28
Germany, Bonn	483	366	0.048	1.56 (1.02,2.37)	0.040
Germany, Munich	574	604	0.067	1.11 (0.81,1.54)	0.52
Iceland	589	11475	0.050	1.30 (0.99,1.70)	0.059
Italy	84	88	0.091	0.43 (0.18,1.07)	0.069
Scotland	658	661	0.042	1.40 (0.97,2.03)	0.069
2009 Collaboration					
ISC[1]	NA	NA	NA	1.35 (1.12,1.63)	0.0017
MGS[2]	NA	NA	NA	1.18 (0.99,1.39)	0.061
Primary follow-up					
Belgium	506	341	0.062	1.18 (0.80,1.75)	0.39
CATIE[3]	391	404	0.032	1.63 (0.93,2.85)	0.087
Denmark, Aarhus 1	220	489	0.054	1.19 (0.74,1.91)	0.48
Denmark, Aarhus 2	878	874	0.064	0.84 (0.63,1.13)	0.25
Denmark, Copenhagen	1289	2320	0.053	1.07 (0.87,1.32)	0.52
Finland, excl. Kuusamo	287	3866	0.060	1.61 (1.15,2.25)	0.0057
Germany, Bonn	603	1517	0.055	1.20 (0.91,1.59)	0.19
Germany, Munich	301	1597	0.051	1.40 (0.98,2.02)	0.066
Hungary	237	213	0.045	1.76 (1.01,3.08)	0.048
Ireland[2]	1310	1023	0.038	1.21 (0.89,1.64)	0.23
Italy	134	89	0.146	0.79 (0.45,1.39)	0.41
Netherlands 1	692	3681	0.062	1.30 (1.03,1.64)	0.027
Netherlands 2	176	603	0.059	1.17 (0.72,1.90)	0.53
Norway	227	290	0.050	1.44 (0.86,2.42)	0.17
Russia	594	740	0.057	0.88 (0.63,1.24)	0.48
Spain, Santiago	282	596	0.098	0.95 (0.68,1.34)	0.78
Spain, Valencia	323	398	0.094	0.98 (0.69,1.41)	0.93
Sweden	252	285	0.044	1.83 (1.10,3.05)	0.02
United Kingdom[2]	479	2937	NA	1.10 (0.80,1.52)	0.54
Secondary follow-up					
GRAS	991	1141	0.056	1.09 (0.85,1.41)	0.50

Freq, control frequency [1]rs10401120 (HapMap CEU r^2=0.867) [2]imputed [3]rs17511755 (HapMap CEU r^2=0.737)

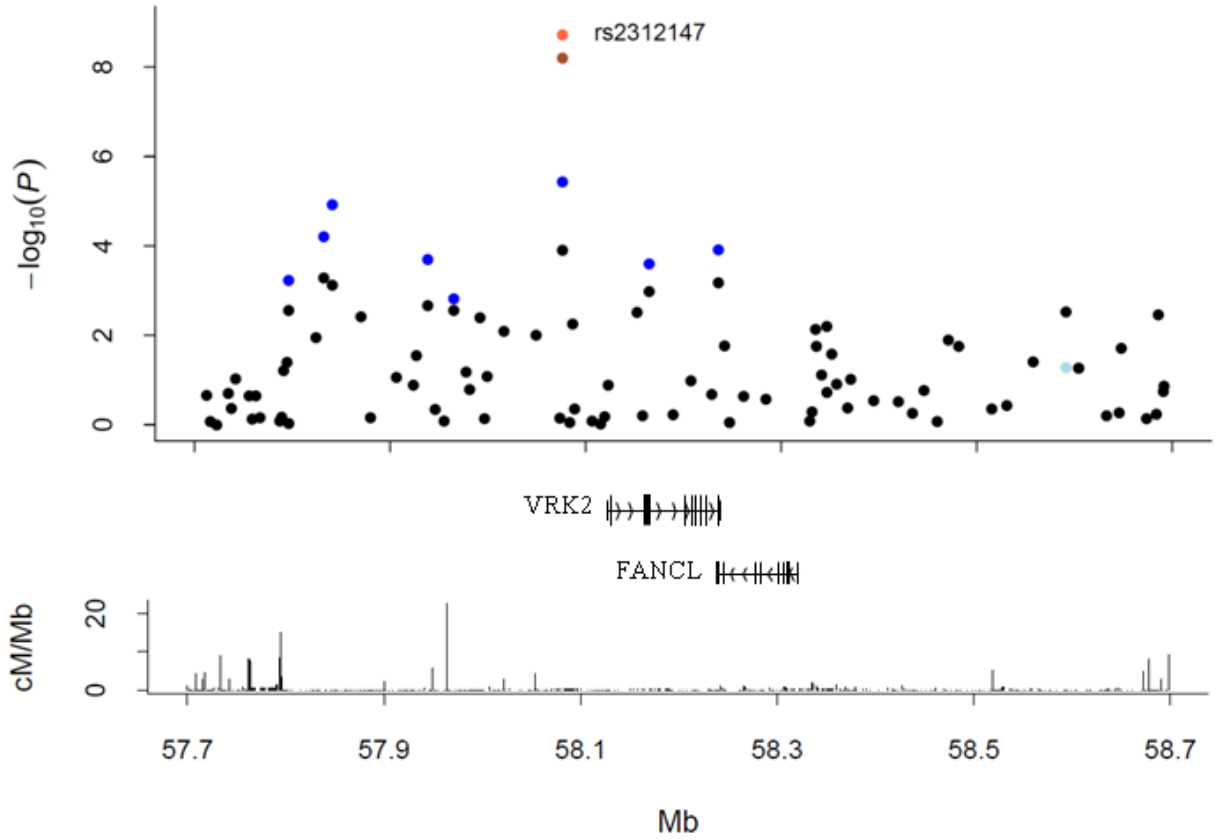

Figure S1. Association results and structure of the 2p15.1 region. Top, association results for SGENE-plus (black), SGENE-plus+MGS+ISC (blue, with darker blue indicating SGENE-plus r^2 with rs2312147 > 0.3), SGENE-plus+MGS+ISC+primary follow-up (brown), and SGENE-plus+MGS+ISC+all follow-up (red). Middle, location of genes in the region. Bottom, estimated recombination rate in the HapMap CEU sample.

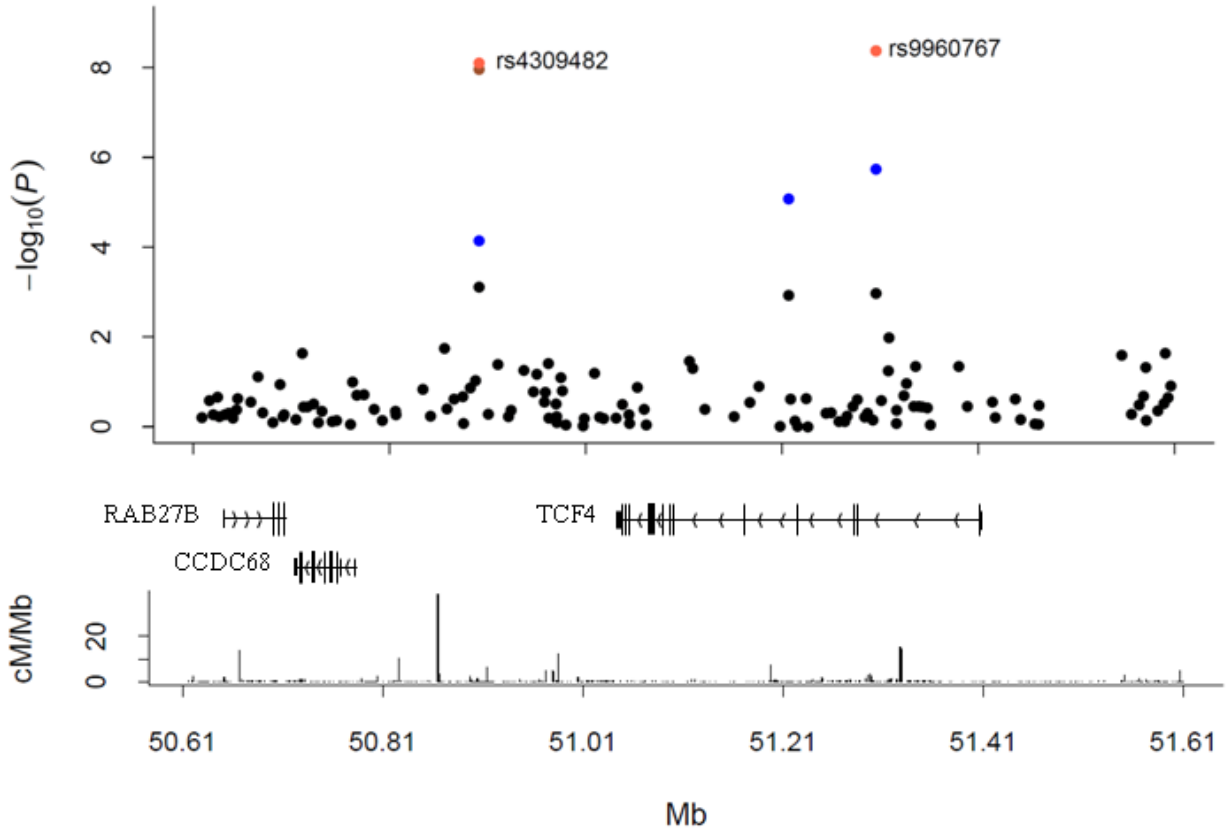

Figure S2. Association results and structure of the 18q21.2 region. Top, association results for SGENE-plus (black) SGENE-plus+MGS+ISC (blue, all having SGENE-plus $r^2 > 0.3$ with rs4309482 or rs9960767), SGENE-plus+MGS+ISC+primary follow-up (brown), and SGENE-plus+MGS+ISC+all follow-up (red). Middle, location of genes in the region. Bottom, estimated recombination rate in the HapMap CEU sample.

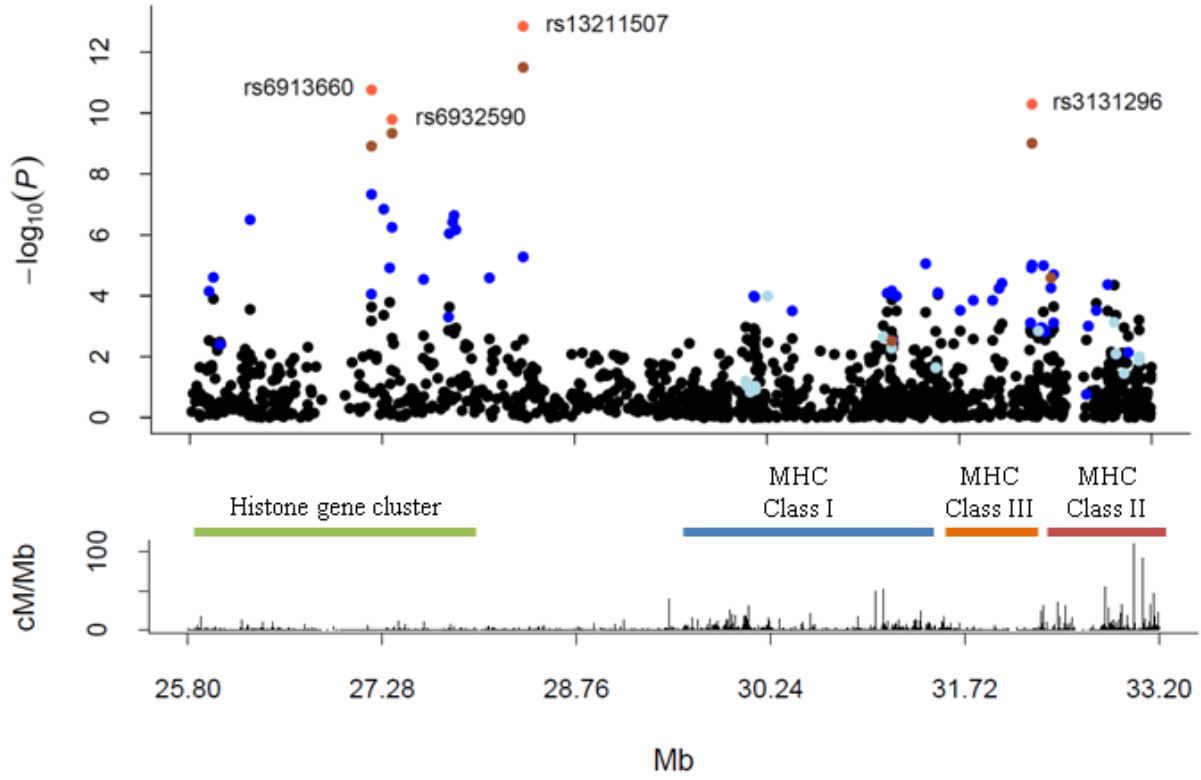

Figure S3. Association results and structure of the MHC region. Top, association results for SGENE-plus (black), SGENE-plus+MGS+ISC (blue, with darker blue indicating SGENE-plus $r^2 > 0.3$ with a SNP that was followed-up), SGENE-plus+MGS+ISC+primary follow-up (brown), and SGENE-plus+MGS+ISC+all follow-up (red). Middle, location of four gene clusters in the region. Bottom, estimated recombination rate in the HapMap CEU sample.

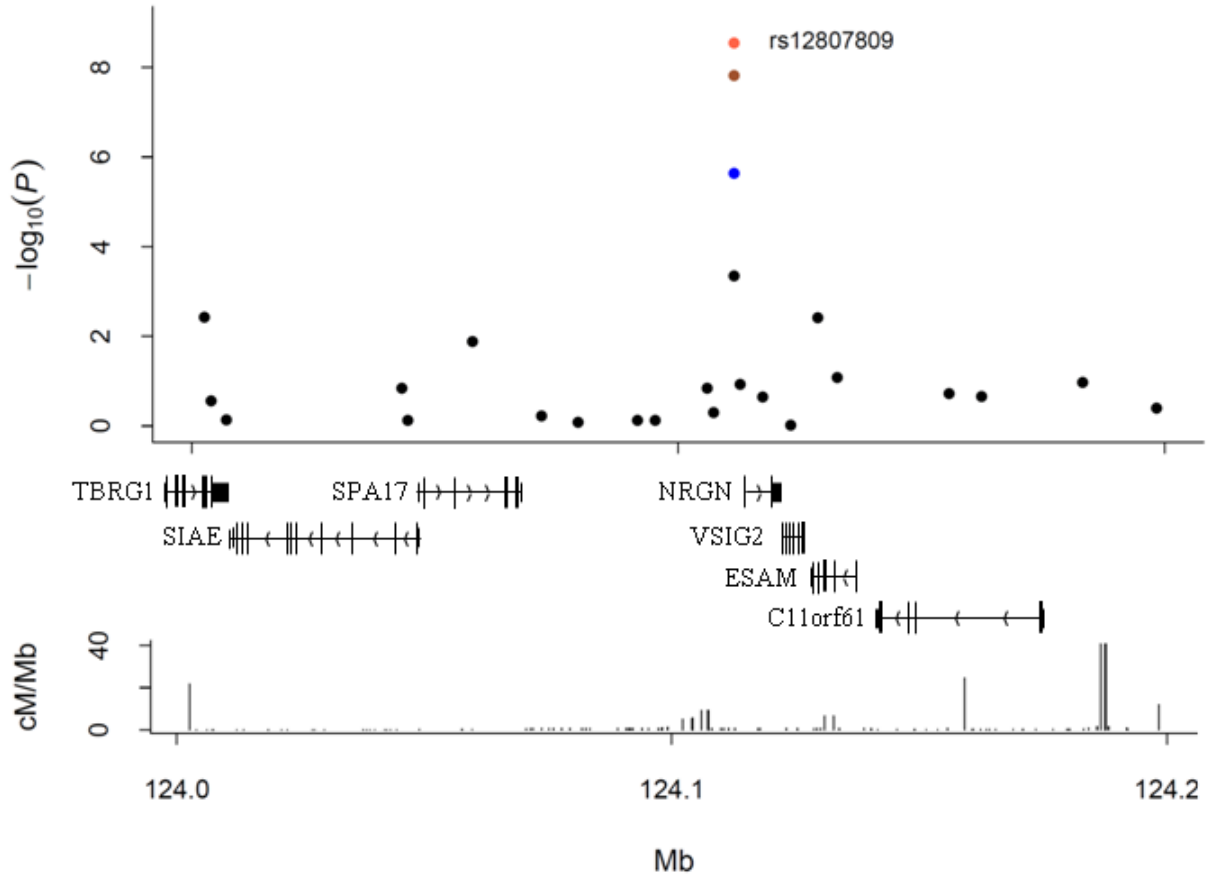

Figure S4. Association results and structure of the region. Top, association results for SGENE-plus (black), SGENE-plus+MGS+ISC (blue), SGENE-plus+MGS+ISC+primary follow-up (brown), and SGENE-plus+MGS+ISC+all follow-up (red). Middle, location of genes in the region. Bottom, estimated recombination rate in the HapMap CEU sample.

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