Supplementary Methods

Subjects

Iceland. The Icelandic sample consisted of 589 cases with schizophrenia and 11,492 controls. Patients and controls were all Icelandic and were recruited from all over Iceland. Diagnoses were assigned according to Research Diagnostic Criteria (RDC)[1] through the use of the Schedule for Affective Disorders and Schizophrenia Lifetime Version (SADS-L)[2]. The 11,492 controls were recruited as a part of various genetic programs at deCODE and were not screened for psychiatric disorders. The breakdown of the control group into the various genetic programs is approximately: Type 2 diabetes 1150, Alzheimer's disease 150, Osteoarthritis 1350, Peripheral artery disease 550, Abdominal aortic aneurysm 150, Chronic obstructive pulmonary disease 250, Stroke 850, Osteoporosis 800, Coronary artery disease 2150, Hypertension 1050, Asthma 200, Sleep apnea 150, Age related macular degeneration 250, Polycystic ovary syndrome 100, Rheumatoid arthritis 150, Longevity 1200, Migraine 100, Prostate cancer 1200, Infectious diseases 1550, Anxiety 700, Colorectal cancer 800, Deep vein thrombosis 250, Restless leg syndrome 150, Addiction 2300, Breast cancer 1350, Atrial Fibrillation 850, Cataract 400, Population controls 500. Note that some of the individuals may have participated in more than one genetic program; however, their genotypes were counted only once.

Finland. The Finnish genome-wide typed sample consisted of 182 schizophrenia patients and 197 controls that had no medical history of schizophrenia. The controls were selected from among participants of the Health 2000 survey[3,4] and were matched with the cases with regard to age and sex. The schizophrenia patients were drawn from a nationwide collection of families with schizophrenia spectrum disorders. Two independent psychiatrists blind to family structures made a consensus diagnosis to give best-estimate lifetime diagnoses according to the criteria of Diagnostic and Statistical Manual of Mental Disorders, 4th edition (DSM-IV)[5-7]. Approximately half of the sample originated from an internal isolate of Finland (Kuusamo) having a 3.0% age-corrected lifetime risk for schizophrenia compared to 1.1% in the general population[6]. In addition, to test a selected set of individual markers, 287 cases, drawn from the remaining family sample not originating from the isolate, and 3,987 controls, drawn from the North Finnish Birth

Cohort 1966 (a longitudinal birth cohort of all individuals born in the two most Northern provinces in Finland in 1966[8]), and also not originating from the isolate, were used.

Scotland. The Scottish sample was comprised of 658 schizophrenia cases and 661 controls. All participants self-identified as born in the British Isles (95% in Scotland). All cases met DSM-IV and International Classification of Diseases, 10th revision (ICD-10) criteria for schizophrenia. Diagnosis was made by the Operational Criteria Checklist (OPCRIT)[9]. Controls were volunteers recruited through general practices in Scotland. Practice lists were screened for potentially suitable volunteers by age and sex and by exclusion of subjects with major mental illness or use of antipsychotic medication.

England. Samples from the English subjects (*N*=93) were drawn from the Maudsley Family Study of psychosis[10], the psychosis twin study[11], and the genetics and psychosis (GAP) study for which cases were derived from the Camberwell case register[12]. All controls were unrelated European Caucasians (*N*=88). Patients were interviewed with the SADS-L[1] or the Item Group Checklist (IGC) of the Schedule for Clinical Assessment in Neuropsychiatry (SCAN)[13] and only patients with an ICD-10 research diagnosis of schizophrenia were finally included as cases. The study received approval from the Ethics Committee of South London and the Maudsley Trust and after complete description of the study to the participants, written informed consent was obtained.

Italy. Diagnosis of the 84 Italian subjects was identical to that for the GAP sample (see **England**), using the IGC. Patients with a diagnosis of psychotic disorders (ICD-10, F20-F25) attending the South Verona CMHS were identified from the South Verona Psychiatric Case Register, and cases with ICD-10 research diagnosis of schizophrenia were finally included. The controls (*N*=89) were unrelated volunteers randomly selected from the general population of South Verona. The study received ethical approval and after complete description of the study to the participants, written informed consent was obtained.

Germany/Munich. The Munich sample consisted of 574 cases and 604 controls who were genome-wide typed and 303 cases and 1625 controls who were single-marker typed. All cases and controls were

Caucasian. Cases diagnosed with DSM-IV schizophrenia were ascertained from the Munich area in Germany. Detailed medical and psychiatric histories were collected, including a clinical interview using the Structured Clinical Interview for Axis I DSM-IV Disorders (SCID)[14]. Exclusion criteria included a history of head injury or neurological diseases. The controls were unrelated volunteers randomly selected from the general population of Munich. To exclude subjects with central neurological diseases and psychotic disorders or subjects who had first-degree relatives with psychotic disorders, several screenings were conducted before the volunteers were enrolled in the study.

Germany/Bonn. The Bonn sample was comprised of 483 patients and 367 controls who were genome-wide typed and 618 patients and 1550 controls who were single-marker typed. Patients were recruited from consecutive hospital admissions and were all of German descent. In patients, lifetime best estimate diagnoses according to DSM-IV criteria were based on multiple sources of information including structured interviews with the SCID[14] or SADS-L[1], the OPCRIT, medical records, and family history. Best estimate diagnoses were obtained from at least two experienced psychiatrists/psychologists. Genome-wide typed controls were derived from a German population-based cohort, Heinz Nixdorf Recall. The single-marker typed controls came from a population-based study in the Mannheim region. Ethical approval was obtained from the local Ethics Committees. All participants gave written informed consent.

The Netherlands. The follow-up set 1 Dutch sample consisted of 715 patients and 643 controls obtained from the University Medical Center Utrecht and an additional 2,991 control individuals collected by the Radboud University Nijmegen Medical Centre (RUNMC) in the Netherlands. In addition, 91 patients and 87 controls from the University Medical Center Utrecht were part of follow-up set 2. In-patients and out-patients were recruited from different psychiatric hospitals and institutions throughout the Netherlands, coordinated via academic hospitals in Amsterdam, Groningen, Maastricht and Utrecht. Detailed medical and psychiatric histories were collected, including the Comprehensive Assessment of Symptoms and History (CASH), an instrument for assessing diagnosis and psychopathology. Only patients with a DSM-IV diagnosis of schizophrenia were included as cases. The University Medical Center Utrecht controls were volunteers and were free of any psychiatric history. The RUNMC controls were collected as cancer and

control samples. As for SGENE-plus, STRUCTURE runs were carried out on the genome-wide typed samples and individuals with less than 90% estimated Caucasian ancestry were removed. Ethical approval was obtained from the local Ethics Committees (including the Institutional Review Board of Radboud University) and all participants gave written informed consent.

Denmark/Copenhagen. The Danish sample included 513 patients who had been recruited to the Danish Psychiatric Biobank from the psychiatric departments at the six hospitals in the Copenhagen region. All patients had been clinically diagnosed with schizophrenia according to ICD-10 (F20) without ever having received a diagnosis of mania or bipolar illness (F30-31). An experienced research- and consultant psychiatrist verified high reliability of the clinical diagnoses using OPCRIT. Eight hundred and eighty-eight healthy control subjects were recruited through the Danish Blood Donor Corps in the Copenhagen area. Apparent behavioral abnormality was an exclusion criterion and all individuals stated that they felt completely healthy and were able to discuss health related issues with a physician. An additional 451 population control samples from the Copenhagen area were recruited by the Danish Headache Center. The Danish Scientific Committees and the Danish Data Protection Agency approved the study and all the patients had given written informed consent prior to inclusion into the project.

Norway. The Norwegian sample included 114 patients who had been recruited to the TOP (Tematisk område psykoser) study at Oslo University Hospital-Ulleval from all the psychiatric hospitals in the Oslo area. The patients were diagnosed according to the SCID as having schizophrenia. The healthy control subjects (N=170) were randomly selected from statistical records of persons from the same catchment area as the patient groups. Only subjects born in Norway, all of Caucasian origin, were contacted by letter and invited to participate. All subjects had given written informed consent prior to inclusion into the project and the Norwegian Scientific-Ethical Committee and the Norwegian Data Protection Agency approved the study.

Russia. The sample from Moscow included 484 cases recruited from Moscow psychiatric clinics and 491 controls. All patients met the diagnosis of DSM-IV schizophrenia based on their Mini International

Neuropsychiatric Interview (M.I.N.I., version 5.0)[15] responses and medical records. Exclusion criteria were organic or neurological disorders. The controls were unrelated volunteers randomly selected from the general population of Moscow. All cases and controls were ethnic Russians. All subjects gave written informed consent for participation in the study.

Spain. The Santiago de Compostela (Galicia, NW Spain) sample consisted of 296 cases and 625 controls over 18 years of age. All cases were diagnosed as schizophrenic patients according to DSM-IV criteria by experienced psychiatrists. They were recruited at several psychiatric units of the Galician Mental Health Service from the Santiago de Compostela area, and signed written informed consent for the collection of DNA samples for use in genetic studies. Unscreened control samples were recruited through the Santiago de Compostela node of the Galician Blood Transfusion Centre. Drug consumers are excluded from blood donation and donors are not financially remunerated, limiting any bias associated to socially disadvantaged groups, which may present higher schizophrenia prevalence. The study was approved by the appropriate Ethics Committee (CEIC de Galicia). All samples, patients and controls, were Caucasian of Spanish descent.

The Valencia (East Spain) sample comprised 371 cases meeting the DSM-IV criteria for schizophrenia and 417 controls. Patients came from the Psychiatric In-patient Unit and the Out-patient Unit of the Valencia University Hospital and gave their written informed consent to participate in this study, which was approved by the Ethical Committee of the Medicine Faculty, University of Valencia. All patients had a minimum one-year evolution of the illness and were on antipsychotic treatment at evaluation time. Controls, matched by sex, were screened with a semi-structured interview to discard psychiatric records. All samples, patients and controls, were Caucasian of Spanish descent.

Hungary. Inpatients and outpatients with a DSM-IV diagnosis of schizophrenia (*N*=272) were enrolled in the study after written informed consent from two major psychiatric units in Budapest, Hungary (Department of Psychiatry and Psychotherapy, Semmelweis University and Szent János Hospital, Psychiatry Unit). Criteria for exclusion were severely disorganized behavior that prevented patient cooperation and meant a hindrance for testing, and severe comorbidity, such as neurological disorders, head trauma, mental

retardation, or substance-abuse. The DSM-IV diagnosis for schizophrenia excluding schizoaffective disorder was validated using the MINI 5.0 Neuropsychiatric Interview[16]. The Hungarian version of the Schedule for the Deficit Syndrome (SDS)[17] was completed for all patients, out of whom 154 met the criteria for the deficit-syndrome. The Positive and Negative Symptom Scale (PANSS)[18] was administered by trained staff members. Healthy controls (*N*=227) were recruited from the employees of Semmelweis University (Budapest, Hungary) and outpatients of the Department of Internal Medicine after screening for psychiatric disorders.

Sweden. The Swedish sample consisted of Caucasian patients (*N*=255) recruited from psychiatric clinics in northwestern Stockholm County. All patients had been clinically diagnosed according to DSM-III-R/DSM-IV diagnostic criteria based on interviews and record reviews. Control subjects (*N*=293) were all Caucasians and recruited either among subjects previously participating in biological psychiatric research at the Karolinska Institute or drawn from a representative register of the population in Stockholm County. Controls had been interviewed and none of them suffered from schizophrenia. All participants had given informed consent prior to inclusion in the project. The Ethical Committee of the Karolinska Hospital, the Stockholm Regional Ethical Committee and the Swedish Data Inspection Board approved the study.

Denmark/Aarhus. The Danish Aarhus sample consisted of 680 cases with schizophrenia and 1,110 controls. Of those, 444 cases, clinically diagnosed with schizophrenia according to ICD-10, and 610 controls (matched by birth cohort) came from the PKU Biobank (www.ssi.dk). The remainder of the sample consisted of 236 cases and 500 medical-student controls, both of Danish parentage three generations back. The additional 236 patients consisted of 193 incident cases and 43 cases ascertained from twin pairs, and were diagnosed with schizophrenia according to ICD-10-DCR and DSM-IV through the use of the SCAN interview and a best estimate procedure. As less DNA was available for the samples from the PKU Biobank, all of these samples were typed for only a subset of the follow-up markers. The study was approved by the Danish Data Protection Agency and the ethics committees in Denmark.

Supplementary Table 1. Top association results from SGENE-plus (2,663 cases / 13,498 controls)

SNP[Allele]	Chr	Position (Mb)	Gene	OR	*P* value
rs10812518[C]	9	27.0	*IFT74*	0.80	3.0×10^{-7}
rs12337896[A]	9	27.0	*IFT74*	0.80	3.7×10^{-7}
rs4974096[C]	3	51.4	*DOCK3*	0.51	2.3×10^{-6}
rs3804766[A]	3	51.4	*RBM15B*	0.52	2.4×10^{-6}
rs10758368[G]	9	36.3	*RNF38*	0.84	2.6×10^{-6}
rs12365860[C]	11	56.1	*OR8U8*	0.83	3.1×10^{-6}
rs2241785 [A]	3	51.4	*DOCK3*	1.88	3.4×10^{-6}
rs7863476[A]	9	26.9	*PLAA*	1.24	3.6×10^{-6}
rs12487468[A]	3	51.4	*DOCK3*	0.53	3.9×10^{-6}
rs7032756[C]	9	26.8	*C9orf82*	0.80	4.5×10^{-6}
rs1882411[C]	X	6.0	*NLGN4X*	1.16	5.2×10^{-6}
rs4687592[C]	3	51.6	*RAD54L2*	0.55	6.3×10^{-6}
rs3828395[C]	3	51.4	*DOCK3*	1.85	7.4×10^{-6}
rs747020[A]	1	32.5	*EIF3I*	0.70	8.2×10^{-6}
rs7868158[C]	9	26.9	*C9orf82*	1.23	9.9×10^{-6}
rs569919[C]	6	160.7	*SLC22A3*	0.83	1.3×10^{-5}
rs6470253[A]	8	125.7	*MTSS1*	0.85	1.3×10^{-5}
rs4275431[A]	1	163.2	*PBX1*	1.22	1.5×10^{-5}
rs2060833[C]	5	101.8	*SLCO6A1*	1.19	1.6×10^{-5}
rs12032332[A]	1	32.4	*IQCC*	0.71	1.6×10^{-5}
rs1275475 [A]	12	74.2	*KRR1*	1.32	1.6×10^{-5}
rs11746217[A]	5	101.8	*SLCO6A1*	1.19	1.7×10^{-5}
rs1562960[A]	5	101.8	*SLCO6A1*	0.84	1.7×10^{-5}
rs9327836[C]	5	101.7	*SLCO4C1*	0.84	2.2×10^{-5}
rs1018234[A]	6	160.7	*SLC22A3*	1.19	2.3×10^{-5}
rs7734926[C]	5	101.7	*SLCO4C1*	1.18	2.3×10^{-5}
rs4702[A]	15	89.2	*FURIN*	0.85	2.4×10^{-5}
rs1015195[C]	11	56.3	*OR9G4*	1.20	3.1×10^{-5}
rs1502844[C]	5	101.9	*SLCO6A1*	1.18	3.1×10^{-5}
rs1573182[C]	1	163.2	*PBX1*	0.83	3.2×10^{-5}
rs4745430[C]	9	77.5	-	0.85	3.8×10^{-5}
rs9611324[C]	22	39.1	*SGSM3*	0.82	3.9×10^{-5}
rs2283508[C]	16	16.2	*ABCC6*	1.17	4.0×10^{-5}
rs12484697[A]	22	39.1	*TNRC6B*	0.82	4.3×10^{-5}
rs4767658[C]	12	117.0	*FLJ20674*	1.17	4.3×10^{-5}
rs995703[G]	17	2.6	*GARNL4*	1.19	4.3×10^{-5}
rs241424[C]	6	32.9	*TAP2*	1.17	4.5×10^{-5}
rs11230864[C]	11	55.3	*OR5D13*	0.86	5.0×10^{-5}
rs2289136[C]	15	46.7	*FBN1*	1.24	5.1×10^{-5}
rs470113[A]	22	39.1	*TNRC6B*	1.21	5.4×10^{-5}
rs906517[C]	18	70.9	*ZNF407*	0.84	5.4×10^{-5}
rs1383102[C]	12	74.3	*KRR1*	0.76	5.4×10^{-5}
rs10123040[C]	9	36.3	*RNF38*	1.20	5.9×10^{-5}
rs1595796[C]	2	174.7	*OLA1*	1.18	6.4×10^{-5}
rs4264869[C]	4	40.0	*CHRNA9*	1.16	6.5×10^{-5}
rs2713831[G]	4	106.5	*PPA2*	0.85	6.6×10^{-5}
rs2512941[A]	11	55.5	*OR5F1*	1.17	6.9×10^{-5}
rs4799062[A]	18	75.4	*NFATC1*	1.47	6.9×10^{-5}
rs10948466[C]	6	49.0	-	1.17	7.1×10^{-5}
rs6848193[A]	4	182.9	-	1.16	7.4×10^{-5}

SNP[Allele]	Chr	Position (Mb)	Gene	OR	*P* value
rs4884665[C]	13	65.8	*PCDH9*	0.86	7.8×10^{-5}
rs658845[C]	11	56.1	*OR8U8*	0.84	8.0×10^{-5}
rs451391[A]	11	55.3	*OR5D18*	0.85	8.8×10^{-5}
rs10879771[A]	12	73.1	-	1.18	8.8×10^{-5}
rs1451526[A]	7	136.7	*DGKI*	0.83	8.8×10^{-5}
rs3099844[A]	6	31.6	*HCP5*	0.78	9.1×10^{-5}
rs1419070[A]	1	163.2	*PBX1*	1.19	9.3×10^{-5}
rs9316871[A]	13	21.8	-	1.20	9.4×10^{-5}
rs627933[C]	11	56.0	*OR8U8*	0.85	9.4×10^{-5}
rs7488514[C]	12	117.0	*FLJ20674*	0.86	9.9×10^{-5}
rs7035755[A]	9	26.9	*PLAA*	0.80	9.9×10^{-5}

Allelic ORs and *P* values based on the multiplicative model are shown. *P* values are adjusted using genomic control (see Methods). Position is based on NCBI build 36. Gene is the closest gene within 200 kb.

Supplementary Table 2. Top association results after combining top 1500 SGENE-plus markers with ISC and MGS

			SGENE-plus (2,663 cases / 13,498 controls)		ISC (2,602 cases / 2,885 controls)		MGS (2,681 cases / 2,653 controls)		Combined (7,946 cases / 19,036 controls)		
SNP[allele]	Chr	Mb	OR (95% CI)	*P* value	OR (95% CI)	*P* value	OR (95% CI)	*P* value	OR (95% CI)	*P* value	Gene
rs6913660[C][1,39]	6	27.2	1.22 (1.10,1.36)	0.00024	1.26 (1.11,1.42)	0.00040	1.13 (1.02,1.25)	0.017	1.19 (1.12,1.27)	4.6×10^{-8}	*HIST1H2BJ*
rs13219354[T][2,39]	6	27.3	1.25 (1.11,1.42)	0.00043	1.26 (1.11,1.42)	0.00040	1.14 (1.01,1.29)	0.036	1.21 (1.13,1.30)	1.4×10^{-7}	*PRSS16*
rs7776351[C]	6	27.8	1.16 (1.06,1.26)	0.0017	1.19 (1.08,1.30)	0.00027	1.10 (1.01,1.21)	0.028	1.15 (1.09,1.21)	2.3×10^{-7}	*HIST1H2BL*
rs6932590[T][3,39]	6	27.4	1.15 (1.05,1.26)	0.0024	1.14 (1.04,1.26)	0.0071	1.15 (1.05,1.26)	0.0034	1.15 (1.09,1.21)	5.6×10^{-7}	*PRSS16*
rs7863476[A]	9	26.9	1.24 (1.13,1.36)	3.6×10^{-6}	1.12 (1.00,1.27)	0.058	1.10 (0.99,1.21)	0.065	1.16 (1.09,1.23)	6.3×10^{-7}	*PLAA*
rs10812518[T]	9	27.0	1.26 (1.15,1.37)	3.0×10^{-7}	1.11 (1.00,1.23)	0.049	1.05 (0.96,1.15)	0.31	1.14 (1.08,1.21)	1.5×10^{-6}	*IFT74*
rs9960767[C][4,39]	18	51.3	1.30 (1.11,1.51)	0.0011	1.35 (1.12,1.63)	0.0017	1.18 (0.99,1.39)	0.061	1.27 (1.15,1.40)	1.8×10^{-6}	*TCF4*
rs12807809[T]	11	124.1	1.19 (1.08,1.32)	0.00045	1.14 (1.00,1.30)	0.057	1.15 (1.03,1.27)	0.0092	1.16 (1.09,1.24)	2.3×10^{-6}	*NRGN*
rs1572299[A][5,39]	9	120.4	1.12 (1.04,1.21)	0.0026	1.08 (0.98,1.20)	0.11	1.14 (1.05,1.23)	0.0011	1.12 (1.07,1.17)	3.1×10^{-6}	-
rs1010471[G][6,39]	3	182.2	1.12 (1.04,1.21)	0.0032	1.12 (1.03,1.23)	0.011	1.11 (1.03,1.20)	0.0099	1.12 (1.07,1.17)	3.2×10^{-6}	*FXR1*
rs3747600[A]	16	4.5	1.14 (1.05,1.23)	0.0021	1.09 (1.00,1.19)	0.049	1.14 (1.05,1.24)	0.0028	1.12 (1.07,1.18)	3.2×10^{-6}	*C16orf5*
rs2312147[C][7,39]	2	58.1	1.16 (1.08,1.26)	0.00013	1.09 (1.00,1.18)	0.043	1.09 (1.01,1.18)	0.035	1.11 (1.06,1.17)	3.7×10^{-6}	*VRK2*
rs1502844[C]	5	101.9	1.18 (1.09,1.28)	3.1×10^{-5}	1.06 (0.98,1.15)	0.14	1.10 (1.01,1.19)	0.021	1.11 (1.06,1.17)	3.8×10^{-6}	*SLCO6A1*
rs13211507[T][8,39]	6	28.4	1.24 (1.08,1.42)	0.0027	1.39 (1.17,1.66)	0.00026	1.11 (0.97,1.27)	0.13	1.22 (1.12,1.33)	5.2×10^{-6}	*PGBD1*
rs1487222[A][9,39]	5	113.5	1.12 (1.04,1.20)	0.0033	1.12 (1.04,1.21)	0.0045	1.08 (1.00,1.17)	0.048	1.11 (1.06,1.16)	7.3×10^{-6}	-
rs17594721[G][10,39]	18	51.2	1.42 (1.15,1.76)	0.0012	1.28 (0.97,1.70)	0.080	1.32 (1.07,1.63)	0.0099	1.35 (1.18,1.54)	8.4×10^{-6}	*TCF4*
rs7289747[C]	22	18.3	1.29 (1.11,1.48)	0.00056	1.17 (1.00,1.37)	0.055	1.20 (1.02,1.42)	0.028	1.22 (1.12,1.34)	9.6×10^{-6}	*TXNRD2*
rs3131296[G][11,39]	6	32.3	1.21 (1.08,1.36)	0.0011	1.31 (1.11,1.54)	0.0013	1.09 (0.97,1.22)	0.14	1.18 (1.10,1.27)	9.8×10^{-6}	*NOTCH4*
rs6994019[T]	8	89.3	1.16 (1.07,1.26)	0.00061	1.11 (1.02,1.21)	0.022	1.09 (1.00,1.18)	0.058	1.12 (1.06,1.17)	1.0×10^{-5}	*MMP16*
rs11682175[C][12,39]	2	57.8	1.14 (1.05,1.22)	0.00074	1.07 (0.97,1.18)	0.16	1.11 (1.02,1.19)	0.010	1.11 (1.06,1.16)	1.2×10^{-5}	-
rs2160567[C]	16	4.5	1.14 (1.05,1.23)	0.0016	1.06 (0.98,1.16)	0.16	1.13 (1.04,1.23)	0.0033	1.11 (1.06,1.17)	1.3×10^{-5}	*HMOX2*
rs6589386[C][13,39]	11	112.9	1.14 (1.06,1.23)	0.00074	1.08 (1.00,1.17)	0.044	1.09 (1.01,1.17)	0.033	1.10 (1.06,1.15)	1.3×10^{-5}	*DRD2*
rs1765142[A][14,39]	11	30.3	1.14 (1.05,1.23)	0.0013	1.14 (1.03,1.27)	0.014	1.08 (1.00,1.17)	0.061	1.12 (1.06,1.17)	1.4×10^{-5}	*C11orf46*
rs13078193[G][15,39]	3	175.2	1.14 (1.05,1.24)	0.0015	1.17 (1.05,1.31)	0.0056	1.07 (0.98,1.17)	0.14	1.12 (1.06,1.19)	2.2×10^{-5}	*NLGN1*
rs13198474[G][16,39]	6	26.0	1.36 (1.16,1.58)	0.00013	1.16 (0.99,1.35)	0.060	1.13 (0.98,1.30)	0.095	1.20 (1.10,1.31)	2.5×10^{-5}	*SLC17A3*
rs2579309[A][17,39]	4	72.3	1.30 (1.12,1.51)	0.00053	1.21 (1.03,1.42)	0.021	1.13 (0.96,1.33)	0.15	1.22 (1.11,1.33)	2.5×10^{-5}	*SLC4A4*
rs4583255[T][18,39]	16	29.9	1.15 (1.06,1.23)	0.00035	1.05 (0.97,1.13)	0.26	1.11 (1.02,1.19)	0.011	1.10 (1.05,1.15)	2.5×10^{-5}	*TAOK2*
rs149990[G][19,39]	6	28.1	1.21 (1.07,1.36)	0.0026	1.24 (1.10,1.41)	0.00050	1.05 (0.94,1.18)	0.38	1.16 (1.08,1.24)	2.6×10^{-5}	*ZNF165*
rs10967704[G][20,39]	9	27.1	1.18 (1.08,1.29)	0.00042	1.11 (0.99,1.26)	0.081	1.09 (0.99,1.21)	0.086	1.13 (1.07,1.20)	3.5×10^{-5}	*TEK*
rs12991836[C]	2	144.9	1.13 (1.05,1.22)	0.0020	1.05 (0.95,1.16)	0.37	1.12 (1.04,1.21)	0.0045	1.11 (1.05,1.16)	3.8×10^{-5}	*ZEB2*
rs11230864[T][21,39]	11	55.3	1.17 (1.08,1.26)	5.0×10^{-5}	1.07 (0.98,1.16)	0.12	1.06 (0.98,1.15)	0.16	1.10 (1.05,1.15)	3.9×10^{-5}	*OR5D13*
rs4466166[T][22,39]	5	11.9	1.88 (1.29,2.75)	0.0010	1.73 (1.19,2.52)	0.0044	1.21 (0.85,1.74)	0.29	1.57 (1.27,1.95)	3.9×10^{-5}	*CTNND2*

			SGENE-plus (2,663 cases / 13,498 controls)		ISC (2,602 cases / 2,885 controls)		MGS (2,681 cases / 2,653 controls)		Combined (7,946 cases / 19,036 controls)		
SNP[allele]	Chr	Mb	OR (95% CI)	*P* value	OR (95% CI)	*P* value	OR (95% CI)	*P* value	OR (95% CI)	*P* value	Gene
rs2273709[A][23,39]	6	43.3	1.15(1.05,1.27)	0.0032	1.18(1.04,1.33)	0.0076	1.08(0.98,1.19)	0.11	1.13(1.07,1.20)	$4.2x10^{-5}$	*PARC*
rs1046778[T][24,39]	10	104.7	1.14 (1.05,1.23)	0.0015	1.06 (0.97,1.17)	0.20	1.11 (1.02,1.21)	0.013	1.11 (1.05,1.16)	$4.5x10^{-5}$	*AS3MT*
rs38752[T][25,39]	7	110.9	1.13 (1.04,1.22)	0.0032	1.04 (0.95,1.14)	0.35	1.13 (1.04,1.23)	0.0026	1.11 (1.05,1.16)	$4.6x10^{-5}$	*IMMP2L*
rs2063836[T][26,39]	3	162.9	1.13 (1.04,1.22)	0.0024	1.07 (0.98,1.16)	0.11	1.10 (1.02,1.19)	0.017	1.10 (1.05,1.15)	$4.7x10^{-5}$	-
rs2789588[T][27,39]	6	73.2	1.13 (1.04,1.22)	0.0026	1.08 (0.99,1.18)	0.084	1.10 (1.01,1.20)	0.023	1.10 (1.05,1.16)	$4.7x10^{-5}$	*RIMS1*
rs6914964[A][28,39]	6	43.3	1.25 (1.10,1.42)	0.00056	1.21 (1.04,1.42)	0.017	1.08 (0.95,1.23)	0.23	1.18 (1.09,1.27)	$5.4x10^{-5}$	*SRF*
rs2076537[C][29]	6	32.4	1.13 (1.05,1.23)	0.0016	1.14 (1.03,1.27)	0.012	-	-	1.14 (1.07,1.21)	$5.5x10^{-5}$	*C6orf10*
rs5752534[C]	22	26.1	1.15 (1.06,1.26)	0.0012	1.09 (1.00,1.19)	0.054	1.08 (0.99,1.18)	0.073	1.11 (1.05,1.17)	$5.6x10^{-5}$	-
rs3815087[T][30,39]	6	31.2	1.20 (1.09,1.31)	0.00013	1.09 (0.99,1.21)	0.077	1.06 (0.96,1.17)	0.22	1.12 (1.06,1.18)	$6.7x10^{-5}$	*PSORS1C1*
rs1324087[C]	6	25.9	1.20 (1.06,1.36)	0.0029	1.14 (0.99,1.31)	0.063	1.13 (1.00,1.28)	0.043	1.16 (1.08,1.25)	$6.9x10^{-5}$	*SLC17A3*
rs1744163[C][31,39]	6	64.3	1.26 (1.10,1.43)	0.00064	1.19 (0.99,1.43)	0.070	1.12 (0.97,1.28)	0.13	1.19 (1.09,1.29)	$6.9x10^{-5}$	*PTP4A1*
rs4309482[A][32,39]	18	50.9	1.14 (1.06,1.23)	0.00076	1.05 (0.97,1.14)	0.24	1.10 (1.01,1.19)	0.022	1.10 (1.05,1.15)	$7.1x10^{-5}$	*CCDC68*
rs3130544[C]	6	31.2	1.25 (1.11,1.41)	0.00033	1.22 (1.04,1.42)	0.013	1.05 (0.94,1.19)	0.38	1.16 (1.08,1.25)	$8.2x10^{-5}$	*C6orf15*
rs5174[G][33,39]	1	53.5	1.13 (1.05,1.22)	0.0013	1.02 (0.94,1.10)	0.66	1.13 (1.05,1.22)	0.0019	1.09 (1.05,1.14)	$8.2x10^{-5}$	*LRP8*
rs6639583[T][34]	X	6.0	1.11 (1.04,1.18)	0.0011	1.17 (1.02,1.34)	0.023	-	-	1.12 (1.06,1.18)	$8.6x10^{-5}$	*NLGN4X*
rs7745603[C]	6	27.2	1.18 (1.07,1.30)	0.00067	-	-	1.11 (1.01,1.21)	0.030	1.14 (1.07,1.22)	$8.7x10^{-5}$	*HIST1H2BJ*
rs3741976[G][35,39]	12	1.5	1.15 (1.06,1.24)	0.00053	1.01 (0.91,1.12)	0.84	1.12 (1.03,1.21)	0.0083	1.10 (1.05,1.16)	$8.8x10^{-5}$	*ERC1*
rs1882411[C][40]	X	6.0	1.16 (1.09,1.23)	$5.2x10^{-6}$	1.09 (0.97,1.22)	0.14	0.99 (0.90,1.08)	0.83	1.10 (1.05,1.15)	$9.1x10^{-5}$	*NLGN4X*
rs953280[A]	5	101.9	1.12 (1.04,1.22)	0.0031	1.08 (0.99,1.17)	0.068	1.08 (1.00,1.17)	0.049	1.10 (1.05,1.15)	$9.1x10^{-5}$	*SLCO6A1*
rs2460508[G][36,39]	5	76.2	1.14 (1.06,1.23)	0.00068	1.08 (0.98,1.19)	0.14	1.07 (0.99,1.16)	0.088	1.10 (1.05,1.15)	$9.2x10^{-5}$	*S100Z*
rs131137[A][37,39]	22	46.9	1.15 (1.07,1.24)	0.00030	1.15 (1.03,1.28)	0.015	1.03 (0.93,1.13)	0.59	1.11 (1.05,1.17)	$9.3x10^{-5}$	-
rs1383098[C][38,39]	12	74.3	1.16 (1.06,1.27)	0.0016	1.17 (1.06,1.29)	0.0018	1.02 (0.93,1.12)	0.65	1.11 (1.06,1.18)	$9.7x10^{-5}$	*KRR1*

Results for markers from the SGENE-plus top 1500 having *P* values < 1×10^{-4} after combination with ISC and MGS. Samples from Aberdeen are included in SGENE-plus but excluded from ISC. Position (Mb) is from NCBI build 36. Combined results may vary between the three companion papers in this issue for reasons including which group the Aberdeen samples were used in, the way in which *Z* scores were combined, and whether imputation or surrogates were used. [1]rs4452638 in ISC (HapMap r^2=0.866) [2]rs4452638 in ISC (HapMap r^2=1) [3]rs3800307 in ISC (HapMap r^2=0.843) [4]rs10401120 in ISC (HapMap r^2=0.867) [5]rs11789399 in ISC (HapMap r^2=1) [6]rs9810292 in ISC (HapMap r^2=0.959) [7]rs2678910 in ISC (HapMap r^2=0.967) [8]rs13214023 in ISC (HapMap r^2=0.915) [9]rs2974486 in ISC (HapMap r^2=0.966) [10]rs8092679 in ISC (HapMap r^2=1) [11]rs1150753 in ISC (HapMap r^2=1) [12]rs13011472 in ISC (HapMap r^2=0.868) [13]rs4936278 in ISC (HapMap r^2=1) [14]rs1235089 in ISC (HapMap r^2=0.804) [15]rs7647044 in ISC (HapMap r^2=1) [16]rs13220395 in ISC (HapMap r^2=1) [17]rs1814082 in ISC (HapMap r^2=1) [18]rs4283241 in ISC (HapMap r^2=1) [19]rs202906 in ISC (HapMap r^2=1) [20]rs1591355 in ISC (HapMap r^2=1) [21]rs2512730 in ISC (HapMap r^2=0.826) [22]rs4702830 in ISC (HapMap r^2=1) [23]rs6938026 in ISC (HapMap r^2=0.953) [24]rs7897654 in ISC (HapMap r^2=1) [25]rs7810543 in ISC (HapMap r^2=0.929) [26]rs1399898 in ISC (HapMap r^2=1) [27]rs9360557 in ISC (HapMap r^2=1) [28]rs16896344 in ISC (HapMap r^2=1) [29]rs2273019 in ISC (HapMap r^2=1) [30]rs9263715 in ISC (HapMap r^2=1) [31]rs1681967 in ISC (HapMap r^2=1) [32]rs4131791 in ISC (HapMap r^2=1) [33]rs5177 in ISC (HapMap r^2=1) [34]rs11798625 in ISC (HapMap r^2=0.852) [35]rs739971 in ISC (HapMap r^2=0.965) [36]rs12697859 in ISC (HapMap r^2=0.904) [37]rs135614 in ISC (HapMap r^2=0.931) [38]rs1627431 in ISC (HapMap r^2=0.948) [39]imputed using MACH 1.0 in MGS [40]imputed using PLINK in MGS

Supplementary Table 3. Association results for top markers after SGENE-plus, ISC and MGS combination in four follow-up sets and together with the discovery set

				Follow-up set 1 (715 cases / 3,634 controls)		Follow-up set 2 (3,330 cases / 6,892 controls)		Follow-up set 3 (287 cases / 3,987 controls)		Follow-up set 4 (667 cases / 1,042 controls)		All follow-up (4,999 cases / 15,555 controls)		All follow-up + SGENE-plus, ISC and MGS (12,945 cases / 34,591 controls)	
SNP[allele]	Chr	Mb	Gene	OR	*P* val	OR	*P* val	OR	*P* val	OR	*P* val	OR	*P* val	OR	*P* val
rs2312147[C][1,12]	2	58.1	*VRK2*	1.11	0.084	1.05	0.10	1.06	0.51	1.07	0.35	1.07	0.012	1.09	$3.2x10^{-7}$
rs1010471[G][2,12]	3	182.2	*FXR1*	1.04	0.57	1.04	0.28	0.95	0.62	1.06	0.39	1.03	0.21	1.08	$1.6x10^{-5}$
rs1502844[C]	5	101.9	*SLCO6A1*	1.11	0.097	1.07	0.039	0.96	0.68	0.98	0.80	1.06	0.035	1.09	$1.1x10^{-6}$
rs1487222[A][3,12]	5	113.5	-	1.04	0.49	1.01	0.79	0.91	0.30	1.11	0.15	1.02	0.47	1.07	0.00010
rs6913660[C][4,12]	**6**	**27.2**	***HIST1H2BJ***	**1.16**	**0.062**	**1.09**	**0.036**	**1.50**	**0.016**	**1.02**	**0.88**	**1.11**	**0.0021**	**1.15**	$\mathbf{1.1x10^{-9}}$
rs13219354[T][5,12]	**6**	**27.3**	***PRSS16***	**1.15**	**0.11**	**1.18**	**0.0026**	**1.37**	**0.10**	**-**	**-**	**1.19**	**0.00022**	**1.20**	$\mathbf{1.3x10^{-10}}$
rs6932590[T][6,12]	**6**	**27.4**	***PRSS16***	**1.20**	**0.0082**	**1.16**	**0.00020**	**1.23**	**0.16**	**1.15**	**0.091**	**1.17**	$\mathbf{4.9x10^{-7}}$	**1.16**	$\mathbf{1.4x10^{-12}}$
rs7776351[C]	6	27.8	*HIST1H2BL*	0.95	0.48	1.08	0.041	1.20	0.12	0.94	0.46	1.04	0.17	1.10	$1.5x10^{-6}$
rs13211507[T][7,12]	**6**	**28.4**	***PGBD1***	**1.13**	**0.21**	**1.37**	$\mathbf{6.9x10^{-7}}$	**1.39**	**0.22**	**0.90**	**0.56**	**1.27**	$\mathbf{3.1x10^{-6}}$	**1.24**	$\mathbf{8.3x10^{-11}}$
rs3131296[G][8,12]	**6**	**32.3**	***NOTCH4***	**1.14**	**0.14**	**1.21**	**0.00015**	**1.34**	**0.061**	**1.17**	**0.20**	**1.20**	$\mathbf{5.3x10^{-6}}$	**1.19**	$\mathbf{2.3x10^{-10}}$
rs7863476[A]	9	26.9	*PLAA*	1.00	0.98	1.02	0.62	0.86	0.14	1.13	0.17	1.01	0.67	1.09	$7.9x10^{-5}$
rs10812518[T]	9	27.0	*IFT74*	1.01	0.89	1.01	0.81	0.89	0.24	1.09	0.30	1.01	0.80	1.08	0.00021
rs1572299[A][9,12]	9	120.4	-	0.94	0.28	1.09	0.0078	0.97	0.75	1.04	0.56	1.05	0.086	1.08	$4.4x10^{-6}$
rs12807809[T]	**11**	**124.1**	***NRGN***	**1.10**	**0.22**	**1.11**	**0.014**	**1.24**	**0.082**	**1.25**	**0.029**	**1.13**	**0.00022**	**1.15**	$\mathbf{2.4x10^{-9}}$
rs3747600[A]	16	4.5	*C16orf5*	1.02	0.73	1.00	0.92	1.17	0.13	0.96	0.58	1.01	0.66	1.07	0.00014
rs17594721[G][10,12]	18	51.2	*TCF4*	1.28	0.15	1.19	0.073	1.29	0.34	1.17	0.30	1.21	0.0079	1.28	$4.3x10^{-7}$
rs9960767[C][11,12]	**18**	**51.3**	***TCF4***	**1.27**	**0.044**	**1.20**	**0.0084**	**1.46**	**0.021**	**1.00**	**1.0**	**1.20**	**0.00044**	**1.23**	$\mathbf{4.1x10^{-9}}$
rs7289747[C]	22	18.3	*TXNRD2*	1.20	0.12	0.83	0.0097	1.12	0.49	1.04	0.81	0.95	0.36	1.10	0.0053

Results, including follow-up, for markers from the SGENE-plus top 1500 having *P* values < $1x10^{-5}$ after combination with ISC and MGS. *P* values for follow-up set 1 are adjusted using genomic control. Gene is the closest gene within 200 kb. Bold indicates markers that are genome-wide significant in the combined data. One marker, rs13219354, did not produce adequately separated clusters in follow-up set 4. [1] rs2678910 in ISC (HapMap CEU r^2=0.967) [2] rs9810292 in ISC (HapMap CEU r^2=0.959) [3]rs2974486 in ISC (HapMap CEU r^2=0.966) [4]rs4452638 in ISC (HapMap CEU r^2=0.866) [5]rs4452638 in ISC (HapMap CEU r^2=1) [6]rs3800307 in ISC (HapMap CEU r^2=0.843) [7]rs13214023 in ISC (HapMap CEU r^2=0.915) [8]rs1150753 in ISC (HapMap CEU r^2=1) [9]rs11789399 in ISC (HapMap CEU r^2=1) [10]rs8092679 in ISC (HapMap CEU r^2=1) [11]rs10401120 in ISC (HapMap CEU r^2=0.867) [12]imputed using MACH 1.0 in MGS

Supplementary Table 4. Association results by study group

SNP[allele]	Study group (*N* cases / *N* controls)	Frequency		OR (95% CI)	*P* value
		Cases	Controls		
rs6913660[C]					
(I^2=0%)	**SGENE-plus**				
	England (93/88)	0.844	0.818	1.20 (0.69,2.09)	0.51
	Finland/Helsinki (59/147)	0.958	0.912	2.19 (0.87,5.54)	0.097
	Finland/Kuusamo (123/50)	0.959	0.920	2.05 (0.74,5.70)	0.17
	Germany/Bonn (483/367)	0.847	0.822	1.20 (0.92,1.56)	0.18
	Germany/Munich (574/602)	0.858	0.823	1.30 (1.04,1.63)	0.024
	Iceland (589/11483)	0.896	0.879	1.18 (0.96,1.45)	0.11
	Italy (84/89)	0.869	0.826	1.40 (0.77,2.55)	0.27
	Scotland (658/660)	0.826	0.808	1.13 (0.92,1.39)	0.24
	All (2663/13486)	-	-	1.22 (1.10,1.36)	0.00023
	Follow-up				
	Set 1				
	Netherlands (715/3633)	0.831	0.809	1.16 (0.99,1.35)	0.062
	Set 2				
	Denmark/Aarhus (667/1099)	0.826	0.820	1.04 (0.87,1.24)	0.66
	Denmark/Copenhagen (510/1328)	0.835	0.822	1.10 (0.90,1.33)	0.35
	Germany/Bonn (616/1527)	0.846	0.826	1.16 (0.97,1.38)	0.11
	Germany/Munich (301/1603)	0.839	0.826	1.10 (0.87,1.39)	0.43
	Hungary (270/221)	0.874	0.846	1.26 (0.88,1.81)	0.21
	Netherlands (91/86)	0.863	0.843	1.17 (0.65,2.11)	0.60
	Norway (109/167)	0.849	0.841	1.06 (0.66,1.70)	0.82
	Russia (480/480)	0.873	0.871	1.02 (0.78,1.33)	0.89
	Sweden (254/292)	0.892	0.890	1.01 (0.69,1.48)	0.94
	Set 3				
	Finland (270/3984)	0.935	0.906	1.50 (1.08,2.10)	0.016
	Set 4				
	Spain/Santiago (278/602)	0.867	0.876	0.92 (0.68,1.24)	0.59
	Spain/Valencia (345/406)	0.867	0.853	1.12 (0.83,1.50)	0.46
	All follow-up (4906/15428)	-	-	1.11 (1.04,1.19)	0.0021
rs13219354[T]					
(I^2=17%)	**SGENE-plus**				
	England (88/82)	0.915	0.884	1.41 (0.69,2.87)	0.35
	Finland/Helsinki (58/147)	0.974	0.942	2.31 (0.72,7.39)	0.16
	Finland/Kuusamo (122/50)	0.980	0.920	4.16 (1.29,13.44)	0.017
	Germany/Bonn (483/367)	0.901	0.881	1.22 (0.89,1.67)	0.22
	Germany/Munich (551/600)	0.916	0.881	1.47 (1.11,1.94)	0.0070
	Iceland (587/11404)	0.917	0.911	1.08 (0.86,1.36)	0.50
	Italy (84/89)	0.964	0.899	3.04 (1.23,7.51)	0.016
	Scotland (657/660)	0.877	0.864	1.13 (0.89,1.43)	0.31
	All (2630/13399)	-	-	1.25 (1.11,1.42)	0.00043
	Follow-up				
	Set 1				
	Netherlands (714/3634)	0.881	0.865	1.15 (0.97,1.38)	0.11
	Set 2				
	Denmark/Aarhus (229/490)	0.895	0.870	1.27 (0.90,1.80)	0.18
	Denmark/Copenhagen (503/1323)	0.889	0.879	1.10 (0.87,1.38)	0.42

SNP[allele]	Study group (*N* cases / *N* controls)	Frequency		OR (95% CI)	*P* value
		Cases	Controls		
	Germany/Bonn (615/1534)	0.903	0.886	1.20 (0.96,1.49)	0.10
	Germany/Munich (303/1610)	0.914	0.892	1.29 (0.96,1.73)	0.097
	Hungary (260/224)	0.942	0.897	1.87 (1.17,3.00)	0.0095
	Netherlands (91/86)	0.896	0.930	0.64 (0.30,1.36)	0.25
	Norway (114/164)	0.899	0.896	1.03 (0.59,1.80)	0.92
	Russia (478/482)	0.928	0.926	1.02 (0.72,1.44)	0.90
	Sweden (254/293)	0.935	0.918	1.28 (0.81,2.03)	0.28
	Set 3				
	Finland (287/3985)	0.953	0.937	1.37 (0.94,2.00)	0.10
	All follow-up (3848/13825)	-	-	1.19 (1.08,1.30)	0.00022
rs6932590[T]					
(I^2=0%)	**SGENE-plus**				
	England (91/87)	0.753	0.741	1.06 (0.66,1.72)	0.81
	Finland/Helsinki (59/147)	0.949	0.874	2.69 (1.18,6.11)	0.018
	Finland/Kuusamo (121/50)	0.930	0.900	1.47 (0.62,3.50)	0.38
	Germany/Bonn (483/366)	0.785	0.742	1.27 (1.01,1.60)	0.045
	Germany/Munich (571/604)	0.774	0.741	1.20 (0.99,1.45)	0.067
	Iceland (584/11394)	0.848	0.836	1.10 (0.92,1.31)	0.30
	Italy (83/88)	0.765	0.699	1.40 (0.86,2.29)	0.17
	Scotland (656/661)	0.742	0.736	1.03 (0.86,1.23)	0.75
	All (2648/13397)	-	-	1.15 (1.05,1.26)	0.0024
	Follow-up				
	Set 1				
	Netherlands (715/3630)	0.773	0.738	1.20 (1.05,1.38)	0.0082
	Set 2				
	Denmark/Aarhus (341/627)	0.762	0.761	1.01 (0.81,1.26)	0.93
	Denmark/Copenhagen (495/1309)	0.784	0.764	1.12 (0.94,1.34)	0.20
	Germany/Bonn (589/1501)	0.777	0.750	1.16 (0.99,1.36)	0.066
	Germany/Munich (282/1600)	0.809	0.759	1.34 (1.08,1.67)	0.0087
	Hungary (264/222)	0.803	0.764	1.26 (0.93,1.72)	0.14
	Netherlands (89/85)	0.781	0.765	1.10 (0.66,1.81)	0.72
	Norway (108/154)	0.833	0.802	1.23 (0.79,1.94)	0.36
	Russia (463/471)	0.822	0.798	1.17 (0.92,1.47)	0.20
	Sweden (254/285)	0.862	0.842	1.17 (0.84,1.64)	0.35
	Set 3				
	Finland (286/3981)	0.909	0.891	1.23 (0.92,1.63)	0.16
	Set 4				
	Spain/Santiago (288/607)	0.764	0.747	1.10 (0.87,1.38)	0.44
	Spain/Valencia (355/401)	0.730	0.692	1.20 (0.96,1.50)	0.11
	All follow-up (4529/14873)	-	-	1.17 (1.10,1.25)	4.9×10^{-7}
rs13211507[T]					
(I^2=0%)	**SGENE-plus**				
	England (93/88)	0.919	0.898	1.30 (0.63,2.67)	0.48
	Finland/Helsinki (59/147)	0.975	0.959	1.63 (0.47,5.69)	0.44
	Finland/Kuusamo (123/50)	0.980	0.960	2.01 (0.48,8.32)	0.34
	Germany/Bonn (483/367)	0.930	0.909	1.33 (0.92,1.91)	0.13
	Germany/Munich (574/604)	0.940	0.917	1.41 (1.02,1.95)	0.036
	Iceland (589/11492)	0.934	0.932	1.02 (0.79,1.32)	0.86
	Italy (84/89)	0.970	0.944	1.94 (0.66,5.74)	0.23

SNP[allele]	Study group (*N* cases / *N* controls)	Frequency		OR (95% CI)	*P* value
		Cases	Controls		
	Scotland (658/661)	0.892	0.870	1.24 (0.97,1.58)	0.091
	All (2663/13498)	-	-	1.24 (1.08,1.42)	0.0027
	Follow-up				
	Set 1				
	Netherlands (715/3634)	0.906	0.895	1.13 (0.93,1.38)	0.21
	Set 2				
	Denmark/Aarhus (337/640)	0.918	0.892	1.36 (0.99,1.88)	0.061
	Denmark/Copenhagen (506/1324)	0.920	0.903	1.24 (0.96,1.60)	0.11
	Germany/Bonn (606/1537)	0.928	0.912	1.24 (0.97,1.59)	0.089
	Germany/Munich (302/1614)	0.955	0.919	1.90 (1.30,2.76)	0.00085
	Hungary (266/224)	0.949	0.935	1.29 (0.75,2.22)	0.35
	Netherlands2 (90/86)	0.928	0.948	0.71 (0.30,1.69)	0.44
	Norway (112/164)	0.933	0.902	1.51 (0.80,2.82)	0.20
	Russia (480/478)	0.972	0.948	1.91 (1.20,3.04)	0.0067
	Sweden (252/288)	0.956	0.936	1.50 (0.88,2.57)	0.13
	Set 3				
	Finland (287/3986)	0.976	0.967	1.39 (0.82,2.33)	0.22
	Set 4				
	Spain/Santiago (296/624)	0.951	0.955	0.91 (0.58,1.45)	0.70
	Spain/Valencia (366/413)	0.964	0.969	0.88 (0.51,1.53)	0.66
	All follow-up (4615/15012)	-	-	1.27 (1.15,1.40)	3.1×10^{-6}
rs3131296[G]					
(I^2=18%)	**SGENE-plus**				
	England (92/88)	0.870	0.841	1.26 (0.70,2.28)	0.44
	Finland/Helsinki (59/147)	0.941	0.854	2.72 (1.26,5.85)	0.011
	Finland/Kuusamo (123/50)	0.943	0.910	1.64 (0.65,4.13)	0.30
	Germany/Bonn (481/367)	0.889	0.860	1.30 (0.97,1.76)	0.080
	Germany/Munich (574/604)	0.881	0.877	1.03 (0.80,1.33)	0.82
	Iceland (589/11489)	0.911	0.913	0.98 (0.78,1.23)	0.85
	Italy (84/89)	0.893	0.904	0.88 (0.43,1.79)	0.72
	Scotland (658/661)	0.860	0.806	1.48 (1.20,1.84)	0.00031
	All (2660/13495)	-	-	1.21 (1.08,1.36)	0.0011
	Follow-up				
	Set 1				
	Netherlands (712/3603)	0.874	0.859	1.14 (0.96,1.36)	0.14
	Set 2				
	Denmark/Aarhus (236/496)	0.871	0.865	1.05 (0.76,1.46)	0.76
	Denmark/Copenhagen (511/1330)	0.891	0.861	1.32 (1.06,1.65)	0.014
	Germany/Bonn (612/1534)	0.879	0.875	1.04 (0.85,1.28)	0.68
	Germany/Munich (301/1614)	0.905	0.869	1.44 (1.09,1.90)	0.011
	Hungary (263/220)	0.907	0.877	1.36 (0.90,2.05)	0.14
	Netherlands (90/86)	0.867	0.884	0.86 (0.45,1.61)	0.63
	Norway (111/167)	0.869	0.871	0.98 (0.59,1.63)	0.95
	Russia (480/482)	0.907	0.881	1.33 (0.99,1.77)	0.058
	Sweden (254/290)	0.886	0.848	1.39 (0.98,1.97)	0.069
	Set 3				
	Finland (272/3964)	0.921	0.897	1.34 (0.99,1.83)	0.061
	Set 4				
	Spain/Santiago (295/620)	0.907	0.902	1.06 (0.76,1.48)	0.73

SNP[allele]	Study group (*N* cases / *N* controls)	Frequency		OR (95% CI)	*P* value
		Cases	Controls		
	Spain/Valencia (359/411)	0.921	0.899	1.30 (0.92,1.85)	0.14
	All follow-up (4496/14817)	-	-	1.20 (1.11,1.30)	$5.3x10^{-6}$
rs12807809[T]					
(I^2=0%)	**SGENE-plus**				
	England (93/88)	0.823	0.835	0.91 (0.53,1.58)	0.75
	Finland/Helsinki (59/147)	0.856	0.854	1.02 (0.55,1.88)	0.96
	Finland/Kuusamo (123/50)	0.854	0.820	1.28 (0.67,2.46)	0.46
	Germany/Bonn (483/367)	0.823	0.804	1.13 (0.88,1.46)	0.33
	Germany/Munich (574/604)	0.834	0.814	1.15 (0.93,1.43)	0.20
	Iceland (589/11491)	0.850	0.813	1.30 (1.09,1.55)	0.0030
	Italy (83/89)	0.873	0.860	1.13 (0.60,2.13)	0.71
	Scotland (658/661)	0.850	0.826	1.19 (0.96,1.48)	0.12
	All (2662/13497)	-	-	1.19 (1.08,1.32)	0.00045
	Follow-up				
	Set 1				
	Netherlands (714/3631)	0.833	0.819	1.10 (0.94,1.29)	0.22
	Set 2				
	Denmark/Aarhus (344/642)	0.837	0.805	1.25 (0.98,1.59)	0.072
	Denmark/Copenhagen (513/1331)	0.813	0.822	0.94 (0.78,1.13)	0.50
	Germany/Bonn (610/1542)	0.829	0.814	1.11 (0.93,1.32)	0.24
	Germany/Munich (302/1620)	0.866	0.830	1.32 (1.03,1.69)	0.026
	Hungary (259/225)	0.867	0.856	1.10 (0.76,1.58)	0.61
	Netherlands (91/87)	0.802	0.828	0.84 (0.49,1.44)	0.54
	Norway (111/164)	0.860	0.808	1.46 (0.92,2.33)	0.11
	Russia (456/457)	0.830	0.833	0.98 (0.77,1.25)	0.88
	Sweden (255/290)	0.841	0.798	1.34 (0.98,1.83)	0.066
	Set 3				
	Finland (272/3985)	0.857	0.828	1.24 (0.97,1.58)	0.082
	Set 4				
	Spain/Santiago (287/615)	0.871	0.839	1.30 (0.98,1.72)	0.073
	Spain/Valencia (337/404)	0.847	0.822	1.20 (0.91,1.58)	0.19
	All follow-up (4551/14993)	-	-	1.13 (1.06,1.21)	0.00022
rs9960767[C]					
(I^2=8%)	**SGENE-plus**				
	England (93/88)	0.075	0.051	1.51 (0.64,3.56)	0.35
	Finland/Helsinki (59/147)	0.093	0.044	2.22 (0.94,5.27)	0.070
	Finland/Kuusamo (123/49)	0.085	0.051	1.74 (0.64,4.71)	0.28
	Germany/Bonn (483/366)	0.072	0.048	1.56 (1.02,2.37)	0.040
	Germany/Munich (574/604)	0.074	0.067	1.11 (0.81,1.54)	0.52
	Iceland (589/11475)	0.065	0.050	1.30 (0.99,1.70)	0.059
	Italy (84/88)	0.042	0.091	0.43 (0.18,1.07)	0.069
	Scotland (658/661)	0.059	0.042	1.40 (0.97,2.03)	0.069
	All (2663/13478)	-	-	1.30 (1.11,1.51)	0.0011
	Follow-up				
	Set 1				
	Netherlands (714/3625)	0.077	0.062	1.27 (1.01,1.59)	0.044
	Set 2				
	Denmark/Aarhus (327/633)	0.064	0.055	1.19 (0.80,1.77)	0.39
	Denmark/Copenhagen (499/1328)	0.050	0.050	1.00 (0.73,1.38)	1.0

SNP[allele]	Study group (*N* cases / *N* controls)	Frequency		OR (95% CI)	*P* value
		Cases	Controls		
	Germany/Bonn (611/1532)	0.066	0.055	1.21 (0.92,1.59)	0.18
	Germany/Munich (301/1606)	0.070	0.051	1.40 (0.98,2.01)	0.066
	Hungary (262/225)	0.069	0.047	1.51 (0.87,2.60)	0.14
	Netherlands (91/87)	0.066	0.069	0.95 (0.42,2.18)	0.91
	Norway (114/164)	0.066	0.049	1.37 (0.66,2.84)	0.39
	Russia (482/488)	0.045	0.050	0.88 (0.58,1.34)	0.56
	Sweden (254/291)	0.077	0.043	1.85 (1.11,3.09)	0.018
	Set 3				
	Finland (286/3979)	0.086	0.060	1.46 (1.06,2.01)	0.021
	Set 4				
	Spain/Santiago (295/618)	0.098	0.096	1.02 (0.74,1.42)	0.89
	Spain/Valencia (360/410)	0.092	0.094	0.97 (0.69,1.37)	0.88
	All follow-up (4596/14986)	-	-	1.20 (1.08,1.33)	0.00044

Allelic frequencies and OR are shown along with *P* values based on the multiplicative model. *P* values for the SGENE-plus study groups and follow-up set 1 are adjusted using genomic control. Combined results are based on the Mantel-Haenszel model.

Supplementary Table 5. Linkage Disequilibrium (LD) between the five genome-wide significant markers in the MHC region

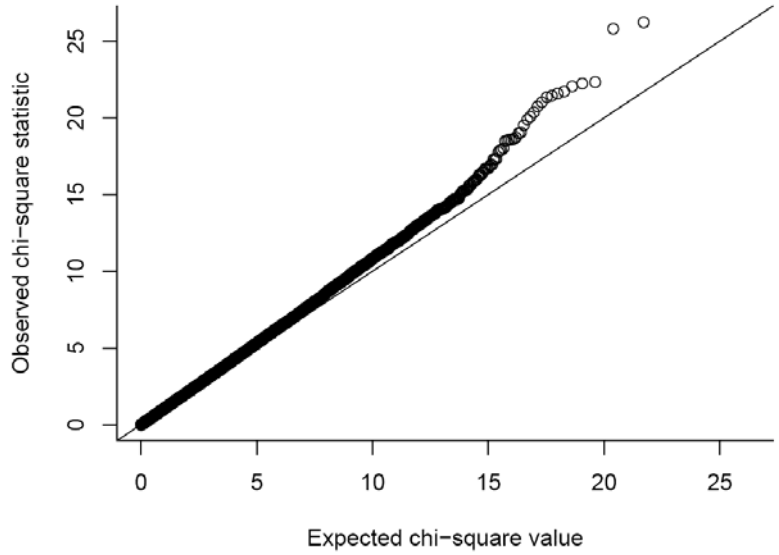
	rs6913660	rs13219354	rs6932590	rs13211507	rs3131296
rs6913660	1.0/1.0	0.99/0.70	0.98/0.67	0.90/0.43	0.41/0.12
rs13219354		1.0/1.0	1.0/0.50	0.91/0.62	0.43/0.18
rs6932590			1.0/1.0	0.93/0.32	0.43/0.090
rs13211507				1.0/1.0	0.60/0.27
rs3131296					1.0/1.0

Shown is D'/r^2 in 11,492 Icelandic controls.

Supplementary Table 6. Conditional association results for the five genome-wide significant markers in the MHC region

SNP	Chr	Mb	*P* value	*P* value[2]	*P* value[3]
rs6913660	6	27.2	4.7×10^{-6}	0.38	0.82
rs13219354[1]	6	27.3	4.4×10^{-7}	0.035	0.036
rs6932590	6	27.4	4.4×10^{-9}	1.0	1.0
rs13211507	6	28.4	3.1×10^{-8}	0.0012	0.11
rs3131296	6	32.3	2.1×10^{-8}	3.4×10^{-6}	1.0

[1]does not include follow-up set 4 (marker not typed in this set) [2]adjusted for the effect of rs6932590 [3]adjusted for the effect of rs6932590 and rs3131296



Supplementary Figure 1. Quantile-Quantile (QQ) plot of the 314,868 chi-square statistics from the genome-wide association analysis of SGENE-plus (2,663 cases/13,498 controls). Following application of genomic control to each study group, some over-dispersion remained (λ=1.05).

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