SUPPLEMENTARY DATA

South Asian Studies

Asian Indian Diabetic Heart Study/Sikh Diabetes Study (Discovery)

Our primary Punjabi Sikh cohort (discovery and replication) used in this study is comprised of 4,510 individuals (2,553 cases 1,957 controls) and is part of the Asian Indian Diabetic Heart Study or Sikh Diabetes Study (AIDHS/SDS) [1, 2]. The Punjabi Sikh population has unique characteristics that are ideal for genetic studies. Sikhs are strictly a non-smoking population and about 50% of participants are life-long vegetarians. All individuals of Stage 1 (discovery) cohort (N=1,616) for GWAS were recruited from one geographical location. Diagnosis of type 2 diabetes (T2D) was confirmed in all the participants by scrutinizing medical records for symptoms, use of medication, and measuring fasting glucose levels following the guidelines of the American Diabetes Association [3]**.** Impaired fasting glucose (IFG) is defined as a fasting blood glucose level ≥100 mg/dL (5.6 mmol/L) but ≤126 mg/dL (7.0 mmol/L). Impaired glucose tolerance (IGT) is defined as a 2h OGTT >140 mg/dL (7.8 mmol/L) but <200 mg/dL (11.1 mmol/L). Participants with IFG or IGT were considered pre-diabetics and were excluded. The selection of controls was based on a fasting glycemia < 100.8 mg/dL (<5.6 mmol/L) or a 2h glucose <141.0 mg/dL (<7.8 mmol/L) and were clinically free of T2D, IGT or IFG. Lipid, insulin and glucose and anthropometric measurements (height, weight, waist and hip circumference), education, socio-economic status, job grade, dietary and physical activity are available on >95% of the AIDHS/SDS individuals selected for this study. Dietary questions involving alcohol consumption were scored using a scale from 0-5, details are described elsewhere[1]. Participants with type I diabetes, or those having a family member with type I diabetes, or rare forms of T2D sub-types (maturity onset diabetes of young or MODY, or secondary diabetes (from e.g. hemochromatosis, pancreatitis) were excluded from the study. All participants signed a written informed consent for the investigations. The study was reviewed and approved by the University of Oklahoma Health Sciences Center's Institutional Review Board, as well as the Human Subject Protection Committees at the participating hospitals and institutes in India.

AIDHS/SDS (Replication)

Our in-house replication cohort was part of AIDHS/SDS comprising a total of 2,894 individuals (1,711 T2D cases and 1,183 controls). The vast majorities (87%) of these participants belongs to the State of Punjab and were originally from the same geographic location as the discovery (GWAS) cohort. The details of diagnosis of T2D and other recruitment details are explained above under AIDHS/SDS GWA cohort details and as described elsewhere [1].

London Life Sciences Population study (LOLIPOP)

The LOLIPOP study is a population-based cohort of South Asian and European men and women aged 35-75 years living in West London [4]. Participants were recruited from the lists of 58 GPs between 2002 and 2008. South Asians were of self-reported South Asian ancestry, and were recruited to the study if all 4 grandparents were born in the Indian Subcontinent (countries of India, Pakistan, Sri Lanka or Bangladesh). Data on medical history, family history, current prescribed medication, cardiovascular risk factors, and alcohol intake and leisure-time physical activity were obtained by a trained research nurse using an interviewer-administered questionnaire. Country of birth of participants, parents, and grandparents were recorded together with language and religion, for assignment of ethnic subgroups. Physical measurements included blood pressure (mean of 3 readings, taken with an Omron 705CP), height, weight, waist and hip circumference, and 12 lead ECG. Blood was collected after an 8 hour fast for plasma glucose, total and HDL cholesterol, triglycerides, insulin and high sensitivity C-reactive protein. T2D was defined as physician diagnosis on treatment or fasting glucose ≥7.0mmol/L. Controls had no history of T2D, and had fasting glucose <7mmol/L. All participants gave written informed consent, and the study was approved by the Local Research Ethics Committee.

Pakistan Risk of Myocardial Infarction Study (PROMIS)

PROMIS is an ongoing case-control study of acute myocardial infarction (MI) and other cardiometabolic traits in urban Pakistan [5], which, as of October 2010, included ~7,500 MI cases and ~7,500 controls. MI cases have typical ECG changes, a positive troponin test, and MI symptoms within the previous 24 hours. Controls are frequency-matched to cases by sex and age (in 5 year bands) and are visitors of patients attending the out-patient department, patients attending the out-patient department for routine non-cardiac complaints, or non-blood related visitors of index MI cases. Non-fasting blood samples were collected from each participant; for MI cases this was within 24 hours of symptom onset.T2D was diagnosed based on physician diagnosis, prior use of oral hypoglycemics, and/or HbA1c >6.5%. Controls had no history of T2D, and had HbA1c <6.0%. All laboratory analyses were conducted centrally at the Center for Non-Communicable Diseases (CNCD), Pakistan. PROMIS has been approved by the research ethics committee of the CNCD, Pakistan, and research ethics committee of each of the institutions involved in participant recruitment.

Risk Assessment of Cerebrovascular Events Study (RACE)

RACE is a retrospective case-control study designed to identify and evaluate genetic, lifestyle and biomarker determinants of stroke and its subtypes in Pakistan. Samples were recruited from six hospital centres in Pakistan. Cases were eligible for inclusion in the study if they: (1) were aged at least 18 years; (2) presented with a sudden onset of neurological deficit affecting a vascular territory with sustained deficit at 24 hours verified by medical attention within 72 hours after onset (onset is defined by when the patient was last seen normal and not when found with deficit); (3) the diagnosis was supported by CT/MRI; and (4) presented with a Modified Rankin Score of <2 prior to the stroke. TOAST and Oxfordshire classification systems were used to sub-phenotype all stroke cases. T2D was diagnosed based on physician diagnosis, prior use of oral hypoglycemics, and/or HbA1c >6.5%. Controls for T2D in RACE had no history of T2D, and had HbA1c <6.0%.

Singapore Indian Eye Study (SINDI)

SINDI is a population-based, cross-sectional study of 3,400 men and women of South Asian ancestry (self reported), living in the South-Western part of Singapore, recruited as part of the Singapore Indian Chinese Cohort Eye Study. Age stratified random sampling was used to select 6,350 eligible participants, of which 3,400 participated in the study (75.6% response rate). Detailed methodology has been published [6]. T2D cases and controls were selected from the population based cross sectional study where T2D was defined as either a history of diabetes or HbA1c level more than 6.5%. Controls had no history of diabetes and HbA1c level <6.0%. This yielded 977 Indian T2D cases and 1,169 controls.

Chennai Urban Rural Epidemiology Study (CURES)

CURES is an ongoing epidemiology study of a representative sample of 26,001 South Asians in Chennai, the fourth largest city in India (population ~5 million), recruited using a random sampling technique[7]. T2D was defined as self-reported diabetes on drug treatment, fasting glucose ≥7.8 or post-load glucose ≥11.1. Controls were selected as people with no history of T2D, fasting glucose <6.1 mmol/L and 2-hour glucose <7.8 mmol/L. Written informed consent was obtained from all study subjects, and the protocol was approved by the Institutional Ethics Committee of the Madras Diabetes Research Foundation.

Diabetes Genetics in Pakistan (DGP) study

Indigenous Pakistani subjects were recruited in collaboration with Baqai Institute of Diabetology and Endocrinology (BIDE), Karachi, Pakistan [8]. Subjects with T2D (physician diagnosed, on treatment) were recruited either from hospitals within Mirpur District or from specifically organized Diabetes Awareness camps. Control subjects were recruited from community screening camps set up throughout Mirpur District. Normal glucose tolerance was defined as fasting whole blood glucose ≤5.6mmol/L. Genomic DNA was extracted from saliva using the Oragene® DNA sample collection kit and extraction protocol (DNA Genotek Inc., Ontario, Canada). Informed consent was obtained from all study participants and the study was approved by the BIDE Institutional Review Board.

United Kingdom Asian Diabetes Study (UKADS)

UK-resident South Asian subjects with T2D (physician diagnosed, on treatment) were recruited to UKADS from Birmingham and Coventry, UK [9]. All subjects were of Punjabi ancestry, confirmed over three generations, and originated predominantly from the Mirpur region of Azad Kashmir, Pakistan. Ethnically-matched control subjects were recruited from the same geographical areas through community screening. Normal glucose tolerance was defined as either fasting plasma glucose <6.1mmol/L and 2hr plasma glucose <7.8mmol/L on a 75g OGTT (where possible) or random blood glucose <7mmol/L. Genomic DNA was extracted from venous blood using the Nucleon® protocol (Nucleon Biosciences, Coatbridge, UK). Informed consent was obtained from all study participants and the study was approved by the Birmingham East, North and Solihull Research Ethics Committee.

Sri Lankan Diabetes Studies

Control subjects were participants in the Sri Lankan Diabetes Cardiovascular Study (SLDCS), a cross-sectional nationally–representative epidemiological investigation which recruited 4,388 subjects (40% male) [10]. Among recruited subjects, 3,372 had normal glucose tolerance based on the results of a 75g oral glucose tolerance test (OGTT), interpreted using ADA and WHO criteria. DNA collection was only initiated midway through the SLDCS collection, limiting the number of control samples available for genotyping in the present study to 1,613. The mean (SD) age at diagnosis for this group was 44.8 years (14.5) years and the mean BMI was 21.3 (4.0) kgm^{-2} [11]. T2D cases were derived from the Sri Lankan Young Diabetes Study (SLYDS). A total of 1,001 patients with early onset diabetes (42.1% male) were recruited from the three largest hospitals in Sri Lanka in 2005-2006. All patients had been diagnosed with diabetes between the ages of 16 and 40 and were ≤45 years when they first joined the study. On the basis of clinical history (independence from insulin for at least 6 months after diagnosis), biochemistry and immunological testing (absence of anti-GAD antibodies) and exclusion for mitochondrial diabetes (mt3243 A>G) [11], 879 were considered to have clinical T2D and available for inclusion in this study. The mean (SD) age at diagnosis for this group was 37.3 (5.2) years and the mean BMI was 24.9 (3.9) kgm^{-2}. Genotyping was performed using Applied Biosystems TaqMan® SNP genotyping assays on an Applied Biosystems 7900HT system.

East Asian Replication Studies

Bio Bank Japan

The BioBank Japan Project aims to gather basic information for personalized medicine. GWAS data are available on 4,878 individuals with T2D and 3,345 controls using Illumina HumanHap610-Quad and 550K BeadChip, respectively. We then selected 7,541 subjects belonging to the Hondo cluster (4,470 cases and 3,071 controls) for an association study with T2D. We performed genome-wide imputation by using IMPUTE (https://mathgen.stats.ox.ac.uk/impute/impute.html) with data from 89 HapMap samples (44 JPT and 45 CHB in HapMap phase 2)[12]. T2D cases were selected from individuals registered as having T2D. Control groups were individuals registered as not having T2D but affected by other illnesses, or healthy volunteers.

RIKEN T2D study

We selected another 5,339 T2D cases from the BioBank Japan or from subjects with T2D who visited outpatient clinics at one of 4 different institutions: St. Marianna University School of Medicine, Kawasaki Medical School, Toyama University Hospital; or the Shiga University of Medical Science. We also examined 2,141 controls enrolled during an annual health check-up at Keio University, St. Marianna University School of Medicine; or Toyama University Hospital. Diabetes was diagnosed according to World Health Organization (WHO) criteria. We excluded individuals who were positive for antibody to glutamic acid decarboxylase (GAD) or those with diabetes due to (1) liver dysfunction, (2) steroids and other drugs that might raise glucose levels, (3) malignancy, or (4) a monogenic disorder known to cause diabetes [13].

AGEN Consortium

Korea Association Resource Study (KARE)

The KARE study was initiated in 2007 to undertake a large scale GWA analysis for T2D and numerous complex quantitative traits amongst the 10,038 participants (aged between 40 and 69) of the Ansung (N=5,018) and Ansan (N=5,020) population-based cohorts. About 10,000 subjects from KARE study cohorts were genotyped with Affymetrix Genome-Wide Human SNP array 5.0. Two KARE study cohorts were established as part of the Korean Genome Epidemiology Study (KoGES) in 2001. The sampling base for both cohorts is in KyungGi-Do province, close to Seoul, the capital of the Republic of Korea. Both cohorts were designed to allow longitudinal prospective study and adopted the same investigational strategy. Participants have been examined every two years since baseline (2001). More than 260 traits have been extensively examined through epidemiological surveys, physical examinations, and laboratory tests applied to Ansung and Ansan cohort members. Among a total of 10,038 KARE study participants, 1,042 subjects were included as T2D cases according to the following criteria: (1) treatment of T2D, (2) fasting plasma glucose ≥7 mmol/L or plasma glucose 2-h after ingestion of 75g oral glucose load ≥11.1 mmol/L and (3) age of disease onset ≥40 years. About 10,000 (1,042 T2D cases and 8,958 controls) participants from KARE study cohorts were genotyped with Affymetrix Genome-Wide Human SNP array 5.0.

Singapore Diabetes Cohort Study (SDCS)/Singapore Prospective Study Program (SP2)

T2D cases were selected from The Singapore Diabetes Cohort Study (SDCS). SDCS is a research initiative to identify genetic and environmental risk factors for diabetic complications. Since 2004, all T2D patients seen at participating polyclinics and hospitals were invited to be part of the cohort. Questionnaire data as well as clinical data of consenting patients were obtained together with bio-specimens such as blood and urine archived at -80°C. For the purpose of this study, 2,202 Chinese subjects were available for genome-wide analysis [14]. T2D controls were selected from The Singapore Prospective Study Program (SP2). From 2003–2007, participants were invited to participate by linking their unique national identification numbers with national registries, where 7,742 attended the interview and of these 7,742 participants, 5,163 attended the clinical examination. A total of 5,499 Chinese, 1,405 Malays and 1,138 Asian-Indians were available at the time of the study and only the Chinese were used for this study. Detailed population selection and methodology have been previously reported [14, 15]. Controls were individuals with no prior history of diabetes and had a fasting glucose level of not more than 6.0 mmol/L**.**

Singapore Malay Eye Study (SiMES)

The Singapore Malay Eye Study (SiMES) is a population-based, cross-sectional study of Malay adults, aged 40 – 80 years living in Singapore (N=3,280). Of the 4,168 eligible participants invited, 3,280 participated in the study with a 78.7% response rate. Briefly, age-stratified random sampling of all Malay adults aged from 40–80 years residing in 15 residential districts in the southwestern part of Singapore was performed. Details of the study participants and methods have been published previously [14, 16]. For the SiMES study, 3,072 samples from the population based study were genotyped on the Illumina HumanHap 610Quad. Diabetic cases were defined as having either a history of diabetes or had HbA1c level ≥6.5%. Controls had no history of diabetes and HbA1c level <6%. This yielded 794 Malay diabetic cases with 1,240 controls.

Cardiometabolic Genome Epidemiology (CAGE) Network

In the case-control panel of the CAGE Network, T2D cases (N=1,110) were enrolled according to the 1999 WHO criteria, while unaffected controls (N=1,014) were enrolled according to the following criteria: (1) no past history of urinary glucose or glucose intolerance; (2) HbA1c, <5.6% or a normal glucose (75g) tolerance test; and (3) age at examination, ≥55 years. In addition, population-based subjects (740 cases and 4,889 controls from the CAGE-Fukuoka Study) and the Biobank Japan (http://biobankjp.org/) cases (N=3,403, BBJ samples independent of those used for the stage-2 analysis) were included in this case-control study. In the CAGE-Fukuoka Study (12,569 participants in total), diabetes was defined as HbA1c ≥7.0% or under treatment of diabetes; the controls were chosen as nondiabetic subjects who met the following conditions: age, ≥55 years; HbA1c, ≤5.0%; no previous and/or current treatment for diabetes; and absence of renal failure (serum creatinine, <3.0 mg/dL), as previously described [17].

Shanghai Diabetes Genetic Study (SDGS)

The SDGS includes genome wide scan data of 1,019 diabetes case and 1,710 controls. Details of the study design have been described elsewhere [18]. Briefly, diabetes cases in the SDGS included 886 incident T2D cases identified in the Shanghai Women's Health Study (SWHS)[19], a population-based cohort study of 75,000 women, and 133 prevalent T2D cases identified from female controls of the Shanghai Breast Cancer Study (SBCS), a population-based case control study [20]. The 886 diabetes cases identified from the SWHS all met the following criteria: (1) age ≤65 with a self-reported diabetes diagnosed after study enrollment; (2) used diabetes medication; (3) had fasting glucose level >7 mmol/L at least twice, and (4) donated a blood sample. The 133 diabetes cases identified from the controls of SBCS were women who were diagnosed with T2D and were on diabetes medication or had a blood glucose level >7 mmol/L (measured by study). The 1,710 controls used in this GWAS were shared with a GWAS of breast cancer that was recently completed and was based primarily on the Shanghai Breast Cancer Study (SBCS). Excluded from the control group are women who (1) had a self-reported history of diabetes; or (2) had a blood glucose level between 5.5 and 7mmol/L and had HbA1c >6.1% or had no HbA1C data.

Taiwan T2D study (TDS)

A total of 2,798 unrelated individuals with T2D, age >20 years, were recruited from China Medical University Hospital (CMUH), Taichung, Taiwan; Chia-Yi Christian Hospital (CYCH), Chia-Yi, Taiwan; and National Taiwan University Hospital (NTUH), Taipei, Taiwan. All of the T2D cases were diagnosed according to medical records and fasting plasma glucose levels using American Diabetic Association criteria. Subjects with type 1 diabetes, gestational diabetes, and maturity-onset diabetes of the young (MODY) were excluded from this study. The controls were randomly selected from the Taiwan Han Chinese Cell and Genome Bank. The criteria for controls in the association study were (1) no past diagnostic history of T2D, (2) HbA1c ranging from 3.4% to 6%, and (3) BMI ≤32 kg/m^2. The two control groups were comparable with respect to BMI, gender, age at study, and level of HbA1c. All of the participating T2D cases and controls were of Han Chinese origin, which is the origin of 98% of the Taiwan population [21].

Cebu Longitudinal Health and Nutrition Survey (CLHNS)

The CLHNS is a community-based birth cohort study that originally enrolled 3,327 pregnant women from the Metropolitan Cebu, Philippines area in 1983-4 (3,080 singleton live births), and has since followed them and their offspring. For this study of CLHNS mothers, glucose levels were collected in the year 2005, and the study sample consists of 159 T2D cases and 1624 controls. T2D was defined as overnight fasting plasma glucose level ≥7.0 mmol/L or current use of anti-diabetic medication. Controls were defined as overnight fasting plasma glucose level <7.0 mmol/L and treatment naive. Whole blood glucose levels were converted to plasma glucose level by subtracting 0.97 mmol/L[22].

SUPPLEMENTARY DATA

European Replication Studies

DIAbetes Genetics Replication And Meta-analysis (DIAGRAM)

The DIAGRAM consortium is focused on performing large-scale studies to characterize the genetic basis of T2D, with a principal focus on samples of European descent. An incremental meta-analysis (DIAGRAM)+ is comprised of a total of 8,130 cases and 38,987 controls available with GWAS genotyping. T2D case-control status was defined using study-specific criteria. SNP associations were tested using an additive genetic model, and combined across studies by inverse variance meta-analysis using a fixed effects model [23].

Acknowledgements

Collaborators

DIAGRAM+ study [23]

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London Life Sciences Population study (LOLIPOP)

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United Kingdom Asian Diabetes Study

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Diabetes Genetics in Pakistan study

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The Singapore Indian Eye Study (SINDI)

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SUPPLEMENTARY DATA

Supplementary Table 1 . Stage 1 Discovery and Stage 2 Replication Cohorts (N=33,592)

Study	Ethnic Group	Replication Stage	Replication	Cases (N)	Controls (N)	Total
AIDHS/SDS GWAS	**Punjabi Sikh**	**Discovery Stage 1**	**--**	**842**	**774**	**1616**
LOLIPOP	**Punjabi Sikh**	**Stage 2a**	**Look-up**	**801**	**2018**	**2819**
LOLIPOP	**South Asian**	**Stage 2b**	**Look-up**	**982**	**1742**	**2724**
PROMIS	**South Asian**	**Stage 2b**	**Look-up**	**1765**	**5267**	**7032**
PROMIS GWAS1[a]	**South Asian**	**Stage 2b**	**Look-up**	**2110**	**5236**	**7346**
PROMIS GWAS2[b]	**South Asian**	**Stage 2b**	**Look-up**	**2995**	**2711**	**5706**
PROMIS GWAS3[c]	**South Asian**	**Stage 2b**	**Look-up**	**1533**	**1194**	**2727**
RACE GWAS 1[d]	**South Asian**	**Stage 2b**	**Look-up**	**503**	**510**	**1013**
RACE GWAS 2[e]	**South Asian**	**Stage 2b**	**Look-up**	**1083**	**1526**	**2609**

PROMIS/RACE sub-components of Punjabi origin: [a] 641 cases/1466 controls; [b] 1259 cases/1074 controls; [c] 669 cases/484 controls; [d] 164 cases/129 controls; [e] 523 cases/775 controls

Supplementary Table 2. Stage 3 Replication Cohorts (N= 85,638)

Study	Ethnic Group	Replication Stage	Replication	Cases (N)	Controls (N)	Total
AIDHS/SDS Replication cohort	**Punjabi Sikhs**	**Stage 3a**	**Genotyped**	**1711**	**1183**	**2894**
CURES	**South Indians**	**Stage 3b**	**Genotyped**	**1164**	**1163**	**2327**
SINDI	**South Indians**	**Stage 3b**	**Look-up**	**974**	**1165**	**2139**
UKADS	**UK Pakistani**	**Stage 3b**	**Genotyped**	**827**	**438**	**1265**
DGP	**Pakistani**	**Stage 3b**	**Genotyped**	**1313**	**1281**	**2594**
SLDS	**Sri Lankan**	**Stage 3b**	**Genotyped**	**879**	**1613**	**2492**
RIKEN/Bio Bank	**Japanese**	**Stage 3c**	**Look-up**	**4455**	**2955**	**7410**
RIKEN/Bio Bank	**Japanese**	**Stage 3c**	**Genotyped**	**5339**	**2141**	**7480**
AGEN	**East Asians**	**Stage 3c**	**Look-up**	**6952**	**11865**	**18817**
DIAGRAM[+]	**European Caucasians**	**Stage 3d**	**Look-up**	**8130**	**38987**	**47117**

Supplementary Table 3. Clinical Characteristics of Stage 1 discovery and Stage 2 replication samples

	SDS Sikh		LOLIPOP Sikh		LOLIPOP other South Asian		PROMIS South Asian	
	NG Controls	T2D	NG Controls	T2D	NG Controls	T2D	NG Controls	T2D
Age	51.6 (14.0)	54.0 (10.4)	52.4 (10.9)	59.5 (9.3)	54.3 (10.6)	59.2 (9.2)	52.9 (10.5)	55.0 (9.3)
Gender (%males)	51.0	53.0	82.7	83	85.5	82.8	83.0	76.0
SYBP (mmHg)	135.4 (22.9)	145.3 (23.1)	133.0 (19.5)	142.5 (20.4)	131.5 (18.1)	139.0 (20.2)	126.0 (19.9)	128.1 (20.3)
DYSBP (mmHg)	81.7 (12.8)	85.4 (12.3)	82.9 (11.0)	81.8 (11.2)	81.0 (10.3)	79.8 (10.6)	80.3 (11.2)	80.7 (11.3)
Weight (kg)	69.3 (14.5)	70.3 (13.9)	75.9 (12.9)	79.4 (13.8)	73.3 (12.5)	77.0 (14.2)	NA	NA
BMI (kg/m^2)	26.3 (5.0)	27.3 (5.0)	26.6 (4.0)	28.3 (4.4)	26.3 (4.1)	27.9 (4.8)	25.3 (4.4)	26.0 (4.4)
Waist (cm)	91.9 (12.7)	94.8 (11.7)	96.4 (10.8)	101.6 (11.4)	95.0 (10.7)	100.2 (11.5)	90.1 (11.8)	92.3 (12.0)
WHR	0.94 (0.07)	0.96 (0.07)	0.95 (0.07)	0.99 (0.07)	0.95 (0.07)	0.99 (0.07)	0.94 (0.06)	0.95 (0.06)
FBG (mmol/L)	5.3 (0.7)	9.6 (3.8)	4.9 (0.5)	8.1 (3.2)	5.0 (0.4)	8.2 (3.2)	NA	NA
Cholesterol (mmol/L)	4.8 (1.4)	4.7 (1.3)	5.3 (1.1)	4.7 (1.1)	5.1 (1.1)	4.6 (1.2)	4.8 (1.3)	4.8 (1.4)
HDL (mmol/L)	1.1 (0.4)	1.0 (0.3)	1.2 (0.3)	1.1 (0.3)	1.2 (0.3)	1.1 (0.3)	0.9 (0.3)	0.9 (0.3)
LDL (mmol/L)	2.9 (1.1)	2.8 (1.0)	3.2 (0.9)	2.7 (0.9)	3.2 (0.9)	2.6 (1.0)	3.0 (1.1)	3.0 (1.2)
TG (mmol/L)	1.9 (1.2)	2.1 (1.4)	1.5 (1.0)	1.6 (1.2)	1.4 (1.0)	1.6 (1.2)	0.6 (0.6)	0.8 (0.6)

SYBP- systolic blood pressure, DYSBP-diastolic blood pressure, BMI-body mass index, WHR-waist to hip ratio, FBG-fasting blood glucose, HDL-high density lipoprotein cholesterol, LDL-low density lipoprotein cholesterol, TG-triglyceride

Supplementary Table 4. Clinical Characteristics of Stage 3 replication samples

	Location	Replication	Group	n	Male	Age	BMI	Age of	FBG	CAD	HTN	SBP	DBP	Waist	Hip	Weight	Height	Total Chol	HDL	LDL	TG
					(%)	(yrs)	(kg/m2)	onset (yrs)	mmol/L	(%)	(%)	(mmHg)	(mmHg)	(cm)	(cm)	(kg)	(cm)	mmol/L	mmol/L	mmol/L	mmol/L
South Asian																					
AIDHS/SDS	India	*genotype*	**Cases**	1711	56	55.3±11.9	27.2±4.7	46.9±12.4	9.5±4.0	23.9	27.1	142.9±24.5	84.1±12.3	94.1±13.9	98.2±12.5	72.8±16.8	162.3±9.8	4.8±1.2	1.1±0.4	2.8±1.1	2.0±1.3
			Controls	1183	58	46.0±14.2	26.0±5.1	NA	5.3±0.6	20.9	14.4	129.8±35.5	80.3±11.5	86.5±17.3	95.5±16.5	72.5±20.5	163.9±9.6	4.9±2.1	1.1±0.4	3.1±1.0	1.7±1.1
SINDI South Asian	Singapore	*in silico*	**Cases**	974	54	60.7±9.8	27.1±5.1	51.4±10.6	NA	10.0	57.0	139.9±19.7	77.1±10.1	NA	NA	73.4±4.2	180.1±35.6	4.9±1.2	1.0±0.3	3.0±0.96	2.1±1.2
			Controls	1165	48	55.7±9.7	25.3±4.4	NA	NA	3.0	25.0	131.7±19.2	77.2±9.9	NA	NA	73.6±4.2	169.4±31.8	5.4±0.9	1.1±0.3	3.5±0.87	1.8±1.1
CURES	India	*genotype*	**Cases**	1164	46	52.4±10.8	25.5±4.2	NA	9.5±3.9	NA	NA	130.7±20.5	78.1±11.2	NA	NA	NA	NA	5.1±1.1	1.1±0.2	3.1±0.9	1.9±1.1
			Controls	1163	42	46.9±12.2	24.4±4.4	NA	4.8±0.5	NA	NA	114.2±18.5	83.9±22.3	NA	NA	NA	NA	4.8±0.9	1.1±0.3	3.0±0.8	1.4±0.7
UKADS	UK	*genotype*	**Cases**	827	54	57.0±11.9	28.6±4.6	49.7±11.8	NA	18.7	23.0	140.5±20.6	83.9±11.0	102.5±10.4	NA	77.1±13.0	NA	4.8±1.2	1.3±0.5	2.4±1.0	2.6±2.1
			Controls	438	48	54.9±11.8	28.0±4.8*	NA	NA	NA	22.3	134.9±20.1*	84.4±11.9*	99.7±11.4*	NA	74.9±13.7*	NA	NA	NA	NA	NA
DGP	Pakistan	*genotype*	**Cases**	1313	45	54.7±11.7	25.8±4.5	48.5±11.5	NA	NA	33.8	134.8±21.0	85.4±11.9	97.4±11.7	NA	68.3±13.4	NA	4.9±1.2	1.0±0.3	2.8±1.1	2.4±1.5
			Controls	1281	47	56.5±10.9	24.3±5.0	NA	4.8±0.5	NA	25.0	128.4±20.5	81.5±12.3	91.9±13.2	NA	64.5±14.4	NA	4.7±1.1	1.2±0.3	2.9±1.1	1.7±1.0
SLDS	Sri Lanka	*genotype*	**Cases**	879	41	37.3±5.2	24.9±3.9	32.4±5.2	9.1±3.5	NA	33.3	120.0±25.0	75.0±16.0	88.1±9.3	95.8±8.0	62.8±12.2	NA	5.0±1.2	1.1±0.3	3.2±1.0	1.7±0.9
			Controls	1613	43	44.8±14.5	21.3±4.0	NA	4.8±0.9	NA	14.1	125.0±19.0	74.0±11.0	74.8±10.9	87.7±8.7	52.1±10.8	NA	5.2±1.1	1.2±0.3	3.4±0.9	1.3±0.7
East Asian																					
SINDI Malays	Singapore	*in silico*	**Cases**	782	49	62.3±9.9	27.8±4.9	54.4±11.2	NA	5.0	59.0	153.9±23.5	80.3±11.4	NA	NA	71.6±4.2	176.3±35.3	5.6±1.3	1.3±0.3	3.5±1.1	1.9±1.5
			Controls	1235	48	56.9±11.4	25.1±4.8	NA	NA	3.0	26.0	143.7±23.5	79.5±11.3	NA	NA	71.8±4.2	160.3±33.0	5.6±1.1	1.4±0.3	3.5±1.0	1.4±1.2
SINDI Chinese	Singapore	*in silico*	**Cases**	1992	50	64.3±10.2	25.3±3.9	53.9±13.2	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
			Controls	1942	42	47.2±10.7	22.6±3.6	NA	4.7±0.5	1.0	15.0	127.4±18.9	76.1±10.7	80.1±10.8	95.8±9.5	60.4±11.8	163.3±8.5	5.2±0.9	1.5±0.4	3.1±0.8	1.3±0.8
KARE+	Korea	*in silico*	**Cases**	1042	51	56.4±8.6	25.5±3.3	NA	7.0±2.6	NA	NA	122.3±17.8	76.9±11.1	86.5±8.2	94.3±6.3	65.1±10.5	NA	5.2±1.1	1.1±0.3	3.1±0.9	2.4±1.7
			Controls	2943	46	51.1±8.6	24.1±2.9	NA	4.5±0.4	NA	NA	113.4±15.9	73.2±10.9	81.4±8.6	92.8±9.0	51.0±9.9	NA	4.8±0.8	1.2±0.3	2.9±0.8	1.6±0.9
RIKEN/Bio Bank	Japan	*genotype*	**Cases**	5339	61	62.9±11.5	24.3±4.1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
			Controls	2141	47	49.5±17.0	22.4±3.2	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
RIKEN/Bio Bank	Japan	*in silico*	**Cases**	4455	68	65.8±10.0	24.1±3.8	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
			Controls	2955	54	51.9±15.2	22.4±3.7	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA

Abbreviations: AIDHS/SDS-Asian Indian Diabetes Heart Study/Sikh Diabetes Study; UKADS-United Kingdom Asian Diabetes Study; DGP-Diabetes Genetics in Pakistan; KARE-Korean Association Resource; CURES-Madras Diabetes Foundation; SLDS- Sri Lanka Diabetes Study
FBG, Fasting Blood Glucose; CAD, Coronary Artery Disease; HTN, Hypertension (>140/90mmHg); SBP, Systolic Blood Pressure; DBP, Diastolic Blood Pressure; HDL, High-Density Lipoprotein; LDL, Low-Density Lipoprotein; TG, Triglyceride
*Data were available for a maximum of 265 samples

Supplementary Table 5. Stage 1, 2a and 3a meta-analysis results of 66 SNPs with a new T2D locus in Punjabi Sikhs

SNP	Chr	BP	Gene	Effect allele	Non-effect allele	Effect Allele Freq(Sikh)	Effect Allele Freq(CEU)	OR(95%CI)	*P*	Direction	$P_{\text{heterogeneity}}$
rs7903146	10	114748339	*TCF7L2*	t	c	0.31	0.5	1.44 (1.33 - 1.56)	**3.32E-19**	+++	6.78E-03
rs9552911	**13**	**22762657**	***SGCG***	**a**	**g**	**0.07**	**0**	**0.67 (0.58 - 0.77)**	**1.82E-08**	---	5.58E-01
rs17053082	**5**	**155326808**	**-**	**t**	**c**	**0.1**	**0.06**	**1.49 (1.28 - 1.73)**	**4.17E-07**	**+?+**	**6.36E-01**
rs6426514	**1**	**226946738**	***RHOU***	**a**	**g**	**0.06**	**0.09**	**1.51 (1.27 - 1.78)**	**1.91E-06**	**+-+**	**7.81E-05**
rs4527850	**8**	**134266031**	***WISP1***	**t**	**c**	**0.75**	**0.73**	**1.23 (1.13 - 1.34)**	**2.34E-06**	**+++**	**1.07E-01**
rs623323	**17**	**646770**	***NXN***	**t**	**c**	**0.15**	**0.19**	**1.28 (1.15 - 1.42)**	**3.73E-06**	**+++**	**2.43E-01**
rs1470579	**3**	**187011774**	***IGF2BP2***	**a**	**c**	**0.59**	**0.5**	**0.84 (0.78 - 0.9)**	**5.02E-06**	**---**	**2.47E-01**
rs6461477	**7**	**20086589**	**-**	**a**	**g**	**0.73**	**0.68**	**0.83 (0.77 - 0.91)**	**1.87E-05**	**---**	**1.45E-01**
rs1595665	**4**	**161630317**	**-**	**t**	**c**	**0.09**	**0.08**	**1.33 (1.17 - 1.51)**	**1.90E-05**	**+-+**	**8.86E-04**
rs6443876	**3**	**184553100**	***MCF2L2***	**t**	**c**	**0.89**	**0.95**	**1.3 (1.15 - 1.46)**	**2.16E-05**	**+++**	**3.41E-01**
rs11683782	**2**	**30384693**	**-**	**a**	**c**	**0.71**	**0.64**	**0.84 (0.77 - 0.91)**	**2.71E-05**	**---**	**1.77E-01**
rs4340250	**14**	**23285337**	**-**	**t**	**c**	**0.09**	**0.09**	**1.39 (1.19 - 1.62)**	**3.71E-05**	**+?+**	**8.84E-05**
rs912697	**13**	**95846724**	***HS6ST3***	**a**	**g**	**0.57**	**0.42**	**1.17 (1.09 - 1.27)**	**5.17E-05**	**+++**	**9.77E-02**
rs12070355	**1**	**182947237**	***EDEM3***	**t**	**c**	**0.02**	**0.01**	**1.82 (1.36 - 2.43)**	**5.41E-05**	**+++**	**7.18E-02**
rs817575	**17**	**64911849**	**-**	**t**	**c**	**0.07**	**0.01**	**1.44 (1.2 - 1.73)**	**7.18E-05**	**+?-**	**7.43E-06**
rs11862438	**16**	**82879154**	***WFDC1***	**c**	**g**	**0.83**	**0.9**	**0.82 (0.74 - 0.9)**	**8.81E-05**	**---**	**1.84E-02**
rs1273153	**14**	**59016212**	***C14orf149***	**t**	**c**	**0.97**	**0.96**	**0.62 (0.49 - 0.79)**	**9.38E-05**	**-+-**	**7.34E-05**
rs9494335	**6**	**136053557**	***C6orf217***	**a**	**g**	**0.61**	**0.67**	**0.86 (0.79 - 0.93)**	**9.56E-05**	**---**	**3.74E-02**
rs16910638	9	26616729	-	a	g	0.92	0.94	0.77 (0.67 - 0.88)	0.000111	--+	6.26E-06
rs17767562	13	96073933	*HS6ST3*	t	c	0.62	0.56	1.16 (1.08 - 1.25)	0.000117	+++	5.90E-02
rs6854968	4	94452990	*GRID2*	t	c	0.51	0.31	0.86 (0.8 - 0.93)	0.000132	---	4.33E-02
rs1541318	1	4534838	-	a	g	0.58	0.59	0.86 (0.8 - 0.93)	0.000143	---	6.89E-03
rs6904271	6	109822899	*PPIL6*	c	g	0.94	0.99	0.72 (0.6 - 0.85)	0.000153	-+-	4.34E-08
rs7149193	14	96574852	-	t	c	0.06	0.07	1.35 (1.15 - 1.58)	0.000165	+-+	1.91E-04
rs2264692	2	57585448	-	a	g	0.79	0.89	1.22 (1.1 - 1.35)	0.000208	+++	1.26E-01
rs11680070	2	236209220	*AGAP1*	a	g	0.47	0.3	0.87 (0.8 - 0.94)	0.000354	---	2.19E-02
rs12595602	15	57257509	*MIR2116*	t	c	0.96	0.99	0.68 (0.55 - 0.84)	0.000382	-+-	2.28E-04

rs6872716	5	86441204	-	a	g	0.02	0.01	1.53 (1.21 - 1.94)	0.000423	+++	4.83E-03
rs16900672	5	31136814	-	a	g	0.12	0.15	1.22 (1.09 - 1.37)	0.000446	+++	5.15E-02
rs13066950	3	37428116	*C3orf35*	t	g	0.37	0.31	1.15 (1.06 - 1.24)	0.000498	+++	4.35E-02
rs17650811	18	32303423	*FHOD3*	t	c	0.59	0.5	0.88 (0.81 - 0.94)	0.000543	---	8.06E-02
rs7848936	9	120352453	-	a	g	0.16	0.06	0.84 (0.76 - 0.93)	0.000838	---	3.01E-03
rs1967678	20	2312386	*TGM6*	t	c	0.04	0.04	1.33 (1.12 - 1.59)	0.00149	+++	8.59E-02
rs8025697	15	58070503	-	a	c	0.45	0.47	0.89 (0.83 - 0.96)	0.002585	--+	7.63E-04
rs12146944	13	52224438	-	a	g	0.11	0.07	1.21 (1.07 - 1.36)	0.002645	+-+	1.70E-05
rs173483	5	73408092	-	a	c	0.53	0.64	0.9 (0.83 - 0.96)	0.003321	--+	3.16E-03
rs6506395	18	6464590	-	a	g	0.82	0.74	0.86 (0.78 - 0.95)	0.003401	--+	6.47E-05
rs2367278	3	194244411	-	a	g	0.74	0.77	0.89 (0.81 - 0.96)	0.003899	--+	8.98E-03
rs10068422	5	120150593	-	a	c	0.46	0.46	0.89 (0.83 - 0.96)	0.004022	--+	5.28E-04
rs1257906	14	97748922	-	a	g	0.18	0.23	1.14 (1.04 - 1.25)	0.006499	+++	6.34E-02
rs7613969	3	23308027	*UBE2E2*	a	g	0.63	0.6	1.11 (1.03 - 1.19)	0.009247	+++	5.50E-02
rs878578	14	95016748	*C14orf49*	a	c	0.15	0.15	1.14 (1.03 - 1.27)	0.009433	++-	7.47E-03
rs12267292	10	120591273	-	a	g	0.07	0.11	1.2 (1.04 - 1.39)	0.01152	++-	4.11E-03
rs1078439	17	69055901	*SDK2*	t	c	0.72	0.81	0.9 (0.83 - 0.98)	0.01315	---	1.90E-02
rs11035260	11	39395904	-	a	c	0.95	0.96	0.81 (0.69 - 0.96)	0.01541	---	3.16E-02
rs737337	19	11208493	*DOCK6*	t	c	0.88	0.93	0.88 (0.79 - 0.98)	0.0186	--+	1.23E-03
rs26642	5	61820146	*IPO11*	a	g	0.52	0.49	1.09 (1.01 - 1.18)	0.02124	+-+	2.43E-04
rs11968879	6	150202935	*LRP11*	a	g	0.09	0	1.16 (1.01 - 1.32)	0.03308	+--	1.47E-07
rs242387	14	55661157	*PELI2*	a	g	0.35	0.45	0.92 (0.86 - 1)	0.04235	--+	1.34E-02
rs12028808	1	185745432	-	t	g	0.95	0.98	0.83 (0.7 - 0.99)	0.04286	--+	7.04E-05
rs9803782	1	218590144	-	t	g	0.68	0.7	1.08 (1 - 1.17)	0.05934	+-+	6.77E-04
rs1320322	15	79126926	-	a	g	0.12	0.09	1.11 (0.99 - 1.25)	0.06482	++-	4.46E-05
rs8091187	18	10086503	-	t	c	0.19	0.3	0.91 (0.81 - 1.01)	0.06703	--+	1.83E-03
rs334527	7	47533752	*TNS3*	t	c	0.72	0.64	1.07 (0.98 - 1.16)	0.1099	++-	3.54E-04
rs7743464	6	3906287	-	t	c	0.47	0.55	1.06 (0.98 - 1.14)	0.1448	+-+	8.91E-05
rs13283425	9	89513040	*DAPK1*	a	g	0.98	0.98	1.23 (0.89 - 1.71)	0.2122	+-+	3.00E-05
rs3890384	19	19136735	*MEF2B*	t	c	0.27	0.16	1.05 (0.96 - 1.14)	0.2942	+--	1.36E-06
rs3806185	1	158015510	*DUSP23*	t	c	0.29	0.18	1.04 (0.96 - 1.13)	0.3088	++-	4.83E-07

rs12162546	21	14898510	-	a	t	0.53	0.5	1.04 (0.96 - 1.12)	0.3116	+--	6.59E-06
rs10991125	9	105957591	-	a	g	0.62	0.64	0.97 (0.9 - 1.05)	0.4336	-++	3.25E-04
rs7617587	3	149857801	-	t	c	0.04	0.01	0.92 (0.72 - 1.18)	0.513	+--	9.97E-15
rs9934375	16	6656877	*A2BP1*	c	g	0.88	0.94	0.97 (0.86 - 1.09)	0.5923	+--	2.22E-05
rs4968967	17	64389259	*ABCA8*	c	g	0.17	0.29	0.98 (0.89 - 1.08)	0.682	-++	1.14E-05
rs2470983	7	122561839	*SLC13A1*	a	c	0.19	0.15	0.99 (0.89 - 1.09)	0.7661	--+	6.64E-06
rs700952	2	5428205	-	t	c	0.9	0.83	1.02 (0.89 - 1.16)	0.7822	+--	4.77E-06

Supplementary Table 6. T2D results for lead SNPs unadjusted for BMI and after inclusion of 10 principal components (PCs)

SNP	Effect Allele		Age, sex, BMI, 5 PCs	Age, sex, 5 PCs	Age, sex, BMI, 10 PCs
rs9552911	A	OR (95% CI)	0.61 (0.47-0.80)	0.62 (0.47-0.80)	0.60 (0.46-0.79)
		P	3.08E-04	3.40E-04	2.45E-04
rs1470579	A	OR (95% CI)	0.76 (0.66-0.88)	0.77 (0.67-0.85)	0.75 (0.65-0.87)
		P	2.53E-04	3.35E-04	
rs7903146	T	OR (95% CI)	1.32 (1.13-1.52)	1.29 (1.12- 1.50)	1.33 (1.15-1.54)
		P	3.23E-04	6.31E-04	1.16E-04

Principal components were constructed only from the Sikh population

Supplementary Table 7. Stage 1, 2a, 2b and 3a meta-analysis results in Punjabis (including non Sikh Punjabis from PROMIS) with P<0.01

CHR	SNP	BP	*Gene*	Effect/other allele	Effect Allele Frequency	OR(95%CI)	P	Direction	$P_{\text{heterogeneity}}$
10	rs7903146	114748339	*TCF7L2*	t/c	0.31	1.3 (1.23 - 1.37)	5.50E-22	++++++++	2.34E-03
5	**rs17053082**	**155326808**	***N/A***	**t/c**	**0.10**	**1.49 (1.28 - 1.73)**	**4.17E-07**	**+?+?????**	**6.36E-01**
3	rs1470579	187011774	*IGF2BP2*	a/c	0.59	0.88 (0.83 - 0.92)	4.21E-07	--------	4.63E-01
18	**rs1893835**	**43971662**	***ZBTB7C***	**a/g**	**0.54**	**0.89 (0.84 - 0.94)**	**2.10E-05**	**-+?-----**	**4.31E-02**
13	**rs17767562**	**96073933**	***HS6ST3***	**t/c**	**0.64**	**1.12 (1.06 - 1.18)**	**3.17E-05**	**++++++++**	**2.73E-01**
20	**rs328506**	**55463010**	***HMG1L1***	**t/c**	**0.21**	**0.87 (0.81 - 0.93)**	**3.22E-05**	**-+?-----**	**6.54E-02**
2	rs12471062	221613429	.	t/c	0.14	0.83 (0.76 - 0.91)	0.0001024	-??---?-	1.02E-01
1	rs767015	95169520	*N/A*	t/c	0.35	1.12 (1.06 - 1.19)	0.0001271	++?+++?+	8.60E-02
8	rs13261832	1123422	.	a/g	0.48	1.12 (1.05 - 1.18)	0.0001421	++?+++++	1.07E-01
7	rs10081175	146291857	*N/A*	a/g	0.12	0.85 (0.78 - 0.93)	0.0001691	--?-----	2.44E-01
7	rs4281065	120189033	*N/A*	a/t	0.91	1.21 (1.09 - 1.33)	0.0001941	++?+++?+	4.34E-02
18	rs12455915	51995450	*ENSG00000206129*	t/c	0.81	0.88 (0.82 - 0.94)	0.0002031	--?--+--	9.75E-02
2	rs6733255	127378856	*N/A*	t/c	0.88	1.17 (1.08 - 1.28)	0.0002954	++?++-++	2.80E-01
15	rs12594126	95916500	.	a/g	0.40	0.9 (0.85 - 0.95)	0.0003178	--?---+-	8.69E-02
3	rs1688334	55152926	*N/A*	t/c	0.58	0.9 (0.85 - 0.95)	0.0003219	--?---+-	2.64E-01
11	rs2005833	2819863	*KCNQ1*	a/g	0.55	0.9 (0.85 - 0.95)	0.0003243	--?---++	6.88E-02
10	rs867221	10895303	*CUGBP2*	t/g	0.39	1.11 (1.05 - 1.17)	0.0003542	++?++-++	3.72E-02
5	rs9293474	86003890	*COX7C*	a/g	0.92	1.2 (1.09 - 1.33)	0.0004149	++?-++++	1.67E-01
7	rs4719818	25670890	.	t/g	0.40	0.9 (0.85 - 0.96)	0.0004819	--?----+	1.29E-01
1	rs9726220	219748197	*DUSP10*	a/c	0.63	1.11 (1.05 - 1.17)	0.0004987	++?+++++	3.56E-01
17	rs623323	646770	*NXN*	t/c	0.14	1.13 (1.06 - 1.22)	0.0005597	++++--+-	5.19E-02
4	rs6854968	94452990	*GRID2*	t/c	0.50	0.92 (0.87 - 0.96)	0.0005727	-----++-	2.68E-02
14	rs4340250	23285337	*N/A*	t/c	0.09	1.31 (1.12 - 1.54)	0.0006024	+?+?????	1.27E-03
16	rs17831104	24538439	*RBBP6*	t/c	0.91	0.85 (0.77 - 0.93)	0.0007228	--?-----	2.94E-01
8	rs7823751	29383843	*N/A*	a/g	0.94	0.81 (0.72 - 0.92)	0.0007258	--?--++-	1.01E-01
13	rs9556576	95811689	*HS6ST3*	a/g	0.58	0.85 (0.77 - 0.93)	0.0007335	-?-?????	7.03E-02
7	rs6978494	120194821	*KCND2*	t/c	0.89	1.17 (1.07 - 1.28)	0.0008088	++?++++-	1.34E-01

13	rs912697	95846724	*HS6ST3*	a/g	0.57	1.09 (1.04 - 1.15)	0.0008979	++++++?+	3.33E-02
8	rs4527850	134266031	*WISP1*	t/c	0.73	1.1 (1.04 - 1.17)	0.0009449	++++-++-	1.07E-02
2	rs1032838	49253850	*N/A*	a/g	0.34	0.91 (0.86 - 0.96)	0.0009948	--?-----	1.87E-01
2	rs11677281	70683359	*TGFA*	t/c	0.78	1.12 (1.05 - 1.2)	0.001087	+-?+++++	1.31E-01
2	rs11680070	236209220	*CENTG2*	a/g	0.48	0.92 (0.87 - 0.97)	0.001159	-----+?+	1.07E-02
1	rs1983967	101379491	*N/A*	t/c	0.95	0.81 (0.71 - 0.92)	0.00122	-+?-----	1.98E-02
22	rs4345013	25711837	*N/A*	t/c	0.68	0.91 (0.86 - 0.96)	0.00127	--?---++	7.46E-03
6	rs9494335	136053557	*C6orf217*	a/g	0.60	0.92 (0.87 - 0.97)	0.001328	---+-+?-	9.29E-03
2	rs2264692	57585448	-	a/g	0.83	1.13 (1.05 - 1.22)	0.001401	++++--?-	3.73E-02
3	rs2531747	45803590	*N/A*	t/c	0.39	0.91 (0.86 - 0.97)	0.001553	--?+----	2.71E-02
2	rs1435172	221609128	.	t/g	0.84	1.13 (1.05 - 1.22)	0.001585	+-?+++++	1.58E-02
22	rs140572	43830391	*N/A*	a/c	0.23	0.9 (0.84 - 0.96)	0.001605	--?--+-+	1.66E-01
3	rs12490338	126682734	*SNX4*	c/g	0.94	0.82 (0.73 - 0.93)	0.001858	--?---?-	4.34E-02
14	rs7154126	46696235	*MDGA2*	t/c	0.86	1.14 (1.05 - 1.23)	0.002021	++?-++--	1.24E-01
7	rs10235225	25872124	.	a/g	0.72	1.11 (1.04 - 1.18)	0.002104	++?+++?+	4.54E-02
9	rs16910638	26616729	.	a/g	0.93	0.86 (0.78 - 0.95)	0.002145	--+---?-	3.06E-03
13	rs9552911	22762657	*SGCG*	a/g	0.08	0.86 (0.79 - 0.95)	0.002167	---+-+++	3.40E-04
13	rs7337905	112376526	*ENSG00000197595*	a/g	0.69	0.91 (0.86 - 0.97)	0.002265	--?+---+	4.71E-02
12	rs10437877	92682154	*CRADD*	a/g	0.58	1.09 (1.03 - 1.16)	0.002368	++?++-?+	4.63E-03
2	rs12693236	180876095	*N/A*	t/c	0.47	1.16 (1.05 - 1.28)	0.002431	+?+?????	5.56E-02
8	rs16937619	72455638	*N/A*	a/c	0.81	1.11 (1.04 - 1.2)	0.002593	++?+++-+	3.33E-02
14	rs4523859	80328831	*C14orf145*	a/g	0.34	1.1 (1.03 - 1.16)	0.003053	++?+++?+	1.07E-02
22	rs877161	48143787	*N/A*	a/g	0.65	1.09 (1.03 - 1.16)	0.00323	++?+++++	2.78E-01
6	rs9401003	117824996	*ROS1*	a/g	0.77	0.91 (0.85 - 0.97)	0.003409	--?--++-	1.10E-01
3	rs6804610	2844944	*CNTN4*	t/g	0.28	1.1 (1.03 - 1.17)	0.003827	++?+-+++	1.55E-01
6	rs1475345	11338388	*NEDD9*	a/g	0.66	1.09 (1.03 - 1.16)	0.004185	++?-+-++	1.74E-03
11	rs12271603	104617228	*N/A*	a/g	0.35	0.92 (0.87 - 0.97)	0.004211	--?+-++-	1.15E-03
14	rs7149193	96574852	*VRK1*	t/c	0.06	1.18 (1.05 - 1.31)	0.004276	+-++++?+	1.16E-01
11	rs10501118	29851786	*N/A*	a/g	0.80	1.11 (1.03 - 1.18)	0.00438	++?+++++	8.28E-02
3	rs4855496	68735025	*FAM19A1*	a/g	0.19	0.89 (0.82 - 0.97)	0.004715	-??--+?-	1.56E-03
14	rs1950670	58593561	*DAAM1*	a/g	0.31	0.92 (0.86 - 0.97)	0.004925	--?-----	3.10E-01

5	rs1707082	22829091	*CDH12*	t/g	0.91	0.87 (0.79 - 0.96)	0.005269	-+?-----	1.90E-01
11	rs680465	118006173	*PHLDB1*	a/g	0.13	1.12 (1.04 - 1.22)	0.005513	+-?+++--	4.17E-02
8	rs4840341	8279075	*PRAGMIN*	a/g	0.49	1.09 (1.02 - 1.15)	0.005516	++?+++?+	7.66E-02
22	rs1860945	15774989	*N/A*	t/c	0.76	1.1 (1.03 - 1.17)	0.005612	++?++---	5.73E-02
13	rs9549880	111910189	*SOX1*	a/g	0.35	1.09 (1.02 - 1.15)	0.005658	+-?++-++	1.38E-02
7	rs12700664	25841676	*.*	t/c	0.41	0.92 (0.87 - 0.98)	0.006104	--?+----	1.60E-01
16	rs10492807	31687619	*ZNF267*	c/g	0.94	0.83 (0.72 - 0.95)	0.006182	-??--+?+	6.18E-03
11	rs7121134	15119762	*INSC*	t/g	0.06	1.21 (1.06 - 1.39)	0.006313	++?-++?+	9.90E-03
4	rs10024068	186300335	*SLC25A4*	a/g	0.70	0.92 (0.87 - 0.98)	0.006398	--?---+-	9.81E-03
8	rs2843835	37197978	*.*	t/c	0.17	1.11 (1.03 - 1.19)	0.006691	+-?++++-	8.36E-03
9	rs1215177	15197485	*TTC39B*	t/c	0.19	1.1 (1.03 - 1.18)	0.00714	++?-++++	1.07E-01
2	rs17356557	5429867	*N/A*	t/c	0.95	1.35 (1.08 - 1.68)	0.007265	+?-?????	1.38E-06
7	rs4632970	140919185	*N/A*	a/g	0.33	1.08 (1.02 - 1.15)	0.007312	++?++++-	2.10E-01
11	rs217727	1973484	*H19*	a/g	0.19	1.1 (1.03 - 1.18)	0.007335	++?++---	1.03E-01
4	rs2435530	38692470	*N/A*	t/c	0.18	0.91 (0.84 - 0.97)	0.007449	--?---++	2.02E-01
20	rs764673	41987407	*TOX2*	t/c	0.37	0.92 (0.87 - 0.98)	0.007557	--?---++	1.61E-01
13	rs2181502	98781320	*UBAC2*	a/g	0.47	0.93 (0.88 - 0.98)	0.007752	--?+-+--	2.12E-02
15	rs1672460	39975327	*N/A*	a/g	0.17	0.9 (0.84 - 0.97)	0.00839	--?-+++-	9.66E-02
3	rs6793237	2844449	*CNTN4*	a/g	0.70	1.08 (1.02 - 1.15)	0.008465	+-?-++++	3.14E-03
8	rs2741200	134141015	*TG,SLA*	t/c	0.71	0.92 (0.87 - 0.98)	0.008687	-+?--+--	3.75E-02
18	rs1708693	32264996	*FHOD3*	a/c	0.22	1.1 (1.03 - 1.19)	0.008843	++?+++-+	1.14E-01
13	rs912130	98830403	*UBAC2*	t/g	0.47	0.93 (0.88 - 0.98)	0.008959	--?+-+?-	1.60E-03
11	rs626466	119342322	*N/A*	t/c	0.27	0.92 (0.86 - 0.98)	0.009407	--?+--+-	1.00E-01
3	rs4688128	62369308	*CADPS*	t/c	0.59	1.08 (1.02 - 1.14)	0.009989	++?+-+-+	6.80E-02

SUPPLEMENTARY DATA

Supplementary Table 8. Meta-analysis results in South Asians with P<0.01

CHR	SNP	BP	*Gene*	Effect/other allele	Effect Allele Frequency	OR(95%CI)	*P*	Direction	$P_{\text{heterogeneity}}$
10	rs7903146	114748339	*TCF7L2*	t/c	0.30	1.15 (1.13 - 1.18)	2.71E-35	+++++++++++++++++++?	1.22E-12
3	rs1470579	187011774	*IGF2BP2*	a/c	0.55	0.94 (0.92 - 0.96)	4.19E-09	---------------???-?	2.97E-02
20	**rs328506**	**55463010**	***HMG1L1***	**t/c**	**0.20**	**0.9 (0.87 - 0.94)**	**1.55E-06**	**-+--?-------+--?????**	**1.74E-01**
7	**rs1593304**	**131270387**	***PLXNA4***	**a/g**	**0.29**	**1.08 (1.04 - 1.12)**	**6.67E-05**	**+-++?-++--+++-+?????**	**1.34E-01**
3	**rs4858889**	**47455361**	***SCAP***	**a/g**	**0.95**	**0.84 (0.77 - 0.91)**	**7.41E-05**	**-??-?++-?+---?-?????**	**4.16E-02**
5	**rs13155082**	**46190994**	**.**	**a/g**	**0.50**	**0.93 (0.9 - 0.96)**	**7.74E-05**	**-??-?-+-?+---?-?????**	**1.27E-01**
11	rs2005833	2819863	*KCNQ1*	a/g	0.51	0.96 (0.94 - 0.98)	1.22E-04	----?---++---+---?-?	1.53E-02
7	rs4719818	25670890	.	t/g	0.40	0.94 (0.91 - 0.97)	2.19E-04	----?----+-+-+-?????	1.58E-01
7	rs10235225	25872124	.	a/g	0.72	1.07 (1.03 - 1.12)	3.20E-04	++-+?+++?++++?-?????	8.17E-02
13	rs9549880	111910189	*SOX1*	a/g	0.35	1.06 (1.03 - 1.1)	3.25E-04	+-++?++-++++-+-?????	5.91E-03
13	rs912130	98830403	*UBAC2*	t/g	0.47	0.94 (0.91 - 0.97)	4.11E-04	--+-?+-+?----?-?????	6.52E-03
14	rs7149193	96574852	*VRK1*	t/c	0.06	1.13 (1.06 - 1.21)	4.29E-04	+-++++++?++++?+?????	3.50E-01
7	rs4722537	25893353	.	t/g	0.23	0.93 (0.9 - 0.97)	4.48E-04	----?+---+---+-?????	4.48E-02
13	rs2181502	98781320	*UBAC2*	a/g	0.47	0.94 (0.91 - 0.98)	6.78E-04	--+-?+-+---+---?????	5.62E-02
7	rs12700664	25841676	.	t/c	0.41	0.94 (0.91 - 0.98)	6.88E-04	--+-?+-------++?????	3.98E-01
18	rs1893835	43971662	*ZBTB7C*	a/g	0.54	0.95 (0.92 - 0.98)	1.07E-03	-++-?--------+-?????	1.64E-02
17	rs1078439	69055901	*SDK2*	t/c	0.71	0.96 (0.94 - 0.99)	1.19E-03	-------++----+-+-+-?	2.43E-01
8	rs4840341	8279075	*PRAGMIN*	a/g	0.50	1.06 (1.02 - 1.1)	1.46E-03	++++?+++?++++?+?????	3.44E-01
14	rs12880791	23268791	*DHRS2*	t/c	0.47	0.95 (0.92 - 0.98)	1.71E-03	----?-++?++--?-?????	1.15E-02
8	rs16895122	122411127	.	t/c	0.95	0.89 (0.83 - 0.96)	1.93E-03	-+--?--++-----+?????	6.23E-02
7	rs13234192	7762204	*RPA3*	a/g	0.42	0.95 (0.92 - 0.98)	2.20E-03	----?-+----+-++?????	2.72E-01
2	rs12693236	180876095	*N/A*	t/c	0.47	1.16 (1.05 - 1.28)	2.43E-03	+???+???????????????	5.56E-02
16	rs17831104	24538439	*RBBP6*	t/c	0.91	0.91 (0.86 - 0.97)	2.44E-03	--+-?-------+--?????	2.25E-01
7	rs10081175	146291857	*N/A*	a/g	0.12	0.93 (0.88 - 0.97)	2.50E-03	--+-?-----+----?????	2.89E-01
3	rs11129155	2494956	*CNTN4*	t/c	0.27	0.94 (0.91 - 0.98)	2.57E-03	-++-?-+-+---+-+?????	5.67E-02
2	rs1032838	49253850	*N/A*	a/g	0.34	0.95 (0.92 - 0.98)	2.71E-03	--+-?---------+?????	1.22E-01
3	rs4855496	68735025	*FAM19A1*	a/g	0.19	0.93 (0.89 - 0.98)	4.54E-03	-??-?--+?---+?-?????	6.77E-03

5	rs11956899	20938564	.	t/c	0.13	0.92 (0.86 - 0.97)	4.55E-03	-+--?++-?+---?+?????	1.70E-02
5	rs10068422	120150593	*PRR16*	a/c	0.46	0.95 (0.92 - 0.99)	4.55E-03	--+-+-+-?+---?+?????	1.25E-02
4	rs6854968	94452990	*GRID2*	t/c	0.50	0.96 (0.93 - 0.99)	4.59E-03	---+---++-++---?????	3.41E-03
2	rs12471062	221613429	.	t/c	0.14	0.93 (0.88 - 0.98)	4.62E-03	-??-?---?--++?-?????	1.87E-03
14	rs2144057	87837408	*KCNK10*	a/g	0.46	1.05 (1.01 - 1.08)	4.98E-03	+--+?+++-++--++?????	1.81E-02
18	rs7504544	69085647	.	t/c	0.91	0.92 (0.87 - 0.98)	5.22E-03	-+--?------+---?????	6.42E-02
22	rs140572	43830391	*N/A*	a/c	0.23	0.94 (0.91 - 0.98)	5.51E-03	--+-?--+-+----+?????	2.96E-01
3	rs12632150	151432992	*N/A*	t/g	0.85	0.94 (0.89 - 0.98)	5.61E-03	-+--?---++---++?????	1.11E-01
3	rs2531747	45803590	*N/A*	t/c	0.38	0.95 (0.92 - 0.99)	5.90E-03	---+?+------++-?????	5.15E-03
7	rs6965643	129194800	*NRF1*	a/g	0.61	0.95 (0.92 - 0.99)	5.91E-03	-+--?-++-----++?????	1.92E-02
7	rs17158049	110288215	*IMMP2L*	t/c	0.87	1.07 (1.02 - 1.12)	6.41E-03	+-++?+--+-++--+?????	1.19E-01
2	rs17356557	5429867	*N/A*	t/c	0.95	1.35 (1.08 - 1.68)	7.27E-03	+???-???????????????	1.38E-06
11	rs680465	118006173	*PHLDB1*	a/g	0.13	1.07 (1.02 - 1.12)	7.27E-03	+--+?+++--+-++-?????	9.01E-02
5	rs9654488	147221889	*N/A*	a/g	0.59	0.96 (0.92 - 0.99)	7.55E-03	-++-?+--++---++?????	9.71E-02
21	rs2833800	32704523	*C21orf63*	t/c	0.45	1.05 (1.01 - 1.08)	7.62E-03	++++?+---++++++?????	1.11E-01
2	rs7592134	132889535	*GPR39*	a/g	0.62	1.05 (1.01 - 1.09)	7.85E-03	+--+?+-+?-++-?+?????	3.37E-03
6	rs9494335	136053557	*C6orf217*	a/g	0.59	0.97 (0.95 - 0.99)	7.96E-03	---+-+-+?----?+???-?	1.13E-02
20	rs6097573	51827864	*N/A*	a/c	0.27	1.05 (1.01 - 1.09)	8.00E-03	+--+?++++-++-++?????	9.14E-02
15	rs7166244	58073942	*N/A*	a/g	0.28	1.05 (1.01 - 1.09)	8.26E-03	+++-?-+--++++++?????	1.27E-01
3	rs12490338	126682734	*SNX4*	c/g	0.94	0.91 (0.84 - 0.98)	9.28E-03	----?---?----?+?????	1.46E-01
2	rs3769845	230863948	*SP140*	t/c	0.27	1.05 (1.01 - 1.09)	9.78E-03	+--+?+-++++-+-+?????	1.76E-03
13	rs9552911	22762657	*SGCG*	a/g	0.13	1.01 (0.98 - 1.05)	4.66E-01	---+-+-++++++-+???+?	2.07E-04

SUPPLEMENTARY DATA

Supplementary Table 9. Meta-analysis results in all Asians (including South and East Asians)

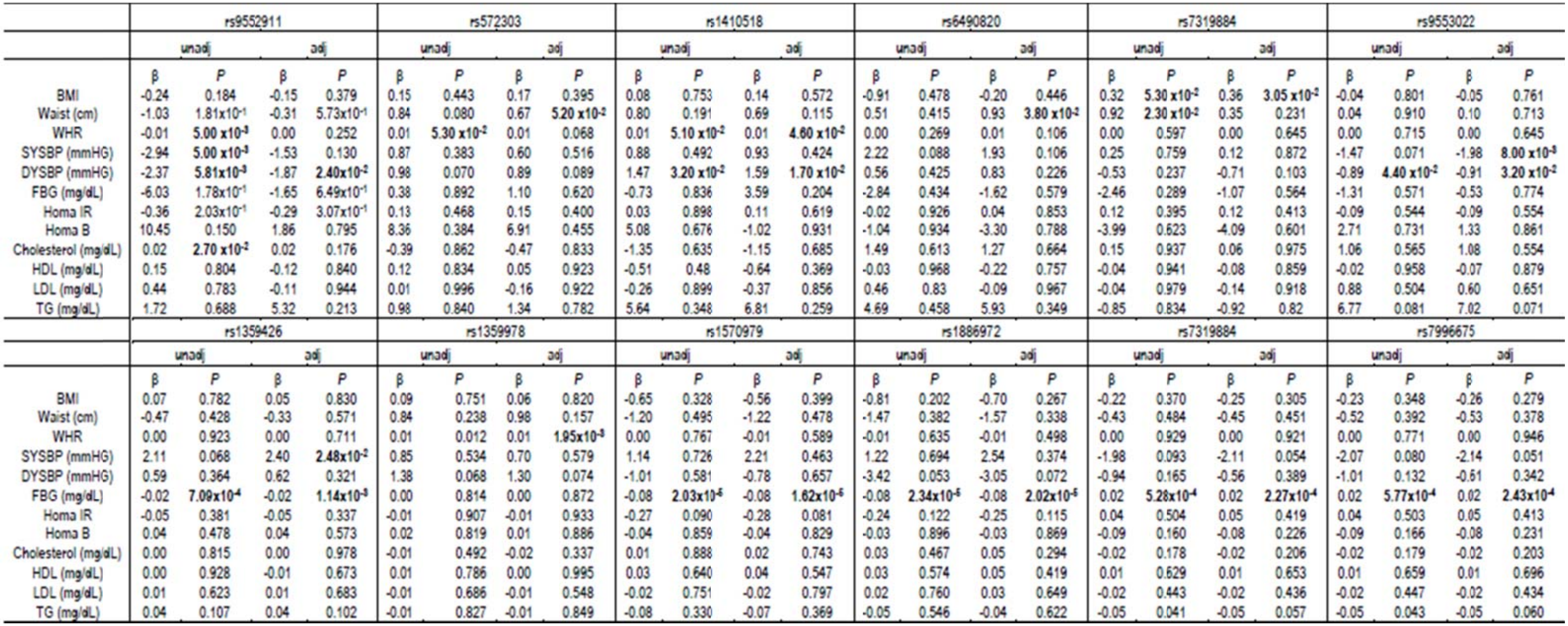
CHR	SNP	BP	*Gene*	Effect/other allele	OR(95%CI)	*P*	Direction	$P_{heterogeneity}$
10	rs7903146	114748339	*TCF7L2*	t/c	1.15 (1.12 - 1.17)	1.93E-38	+++++++++++++++++++?++++-	4.45E-14
3	rs1470579	187011774	*IGF2BP2*	a/c	0.94 (0.93 - 0.96)	1.54E-13	---------------???-?---+-	7.45E-08
11	rs2005833	2819863	*KCNQ1*	a/g	0.97 (0.95 - 0.99)	0.00041	----?---++---+---?-?---+?	1.53E-02
3	rs7613969	23308027	*UBE2E2*	a/g	1.03 (1.01 - 1.04)	0.0010	++++++--++---+-++++?+++++	4.68E-02
11	rs11035260	39395904	-	a/c	0.94 (0.91 - 0.98)	0.0053	------++-+-+-+++-?+?----?	1.66E-02
2	rs2264692	57585448	-	a/g	1.04 (1.01 - 1.07)	0.011	++++++--?-+-+?+???-?+?+-+	1.00E-02
3	rs7617587	149857801	-	t/c	0.96 (0.92 - 0.99)	0.025	+------+?----?-??--?++---	7.85E-10
17	rs1078439	69055901	*SDK2*	t/c	0.98 (0.96 - 1.00)	0.026	-------++----+-+-+-?++--?	1.68E-01
14	rs1273153	59016212	*C14orf149*	t/c	0.94 (0.89 - 0.99)	0.027	-++--++-?+---?+-0?-?+-+-+	3.47E-03
1	rs12070355	182947237	*EDEM3*	t/c	1.12 (1.01 - 1.24)	0.037	+++-+---?-+-+?-???????+?+	1.01E-02
13	rs912697	95846724	*HS6ST3*	a/g	1.01 (1.00 - 1.03)	0.094	++--++++?+---?+???+?-?+++	1.93E-02
17	rs623323	646770	*NXN*	t/c	1.02 (0.99 - 1.04)	0.14	++++++--+---++-++?-?++--+	9.09E-04
3	rs13066950	37428116	*C3orf35*	t/g	1.01 (0.99 - 1.03)	0.19	++++++--+-++-+-+-+-?+++-?	7.74E-02
1	rs6426514	226946738	*RHOU*	a/g	1.03 (0.98 - 1.08)	0.23	+-++++-+?-++-?-???+?+?+--	7.82E-05
2	rs11683782	30384693	-	a/c	0.99 (0.97 - 1.01)	0.29	---+-+-++-++--+???-?-?-++	1.83E-03
6	rs11968879	150202935	*LRP11*	a/g	1.02 (0.98 - 1.05)	0.29	+--+-+--?-+++?+---++-+-+-	1.54E-05
20	rs1967678	2312386	*TGM6*	t/c	1.03 (0.98 - 1.08)	0.31	+++++++-+-+++-+--+-????-?	1.78E-02
6	rs9494335	136053557	*C6orf217*	a/g	0.99 (0.98 - 1.01)	0.32	---+-+-+?----?+???-?+?+++	3.46E-03
14	rs1257906	97748922	-	a/g	1.01 (0.99 - 1.03)	0.39	++++++++-++-++-+-?+?+----	2.30E-01
4	rs1595665	161630317	-	t/c	1.01 (0.98 - 1.05)	0.41	+-+-+--+?----?+???-?-?+++	2.11E-02
5	rs17053082	155326808	*N/A*	t/c	1.02 (0.98 - 1.06)	0.43	+???+?????????????-?-?+-+	6.79E-06
2	rs700952	5428205	-	t/c	0.99 (0.96 - 1.02)	0.48	+-------?---+?+------+-+?	8.57E-06
13	rs9552911	22762657	*SGCG*	a/g	1.01 (0.99 - 1.03)	0.49	---+-+-++++++-+???+?-?-++	1.05E-03
16	rs11862438	82879154	*WFDC1*	c/g	1.01 (0.98 - 1.03)	0.53	-----+-+?---+?+???+?+?-++	2.86E-02
14	rs242387	55661157	*PELI2*	a/g	1.00 (0.99 - 1.02)	0.66	----+-+-+++++-+++-+?--++-	3.52E-03
3	rs6443876	184553100	*MCF2L2*	t/c	1.00 (0.98 - 1.03)	0.68	++--+--++---+++???-?-?+-+	2.26E-02
7	rs6461477	20086589	-	a/g	1.00 (0.97 - 1.02)	0.68	--++-+++++++-++???-?-?+--	6.78E-04
6	rs6904271	109822899	*PPIL6*	c/g	1.01 (0.97 - 1.04)	0.77	-+-+-+--?++--?+++--?--++-	1.98E-05
15	rs12595602	57257509	*MIR2116*	t/c	1.00 (0.95 - 1.04)	0.86	-+++-+--?-+++?++++-?+---+	2.11E-03
8	rs4527850	134266031	*WISP1*	t/c	1.00 (0.98 - 1.02)	0.93	++++++-++-+--+-++?-+-+--+	1.21E-02

Supplementary Table 10. Multi-ethnic Meta-analysis results

CHR	SNP	BP	*Gene*	Effect/other allele	OR(95%CI)	*P*	Direction	$P_{\text{heterogeneity}}$
10	rs7903146	114748339	*TCF7L2*	t/c	1.19 (1.17 - 1.21)	8.53E-75	++++++++++++++?+++++++++-+	8.08E-26
3	rs1470579	187011774	*IGF2BP2*	a/c	0.93 (0.92 - 0.95)	1.81E-19	----------???-?--------+--	5.34E-09
3	rs7613969	23308027	*UBE2E2*	a/g	1.03 (1.01 - 1.04)	1.69E-04	++++++--++++++?---+-++++++	5.66E-02
11	rs2005833	2819863	*KCNQ1*	a/g	0.97 (0.96 - 0.99)	5.13E-04	----?---++--?-?---+----+?-	1.88E-02
11	rs11035260	39395904	-	a/c	0.95 (0.91 - 0.98)	4.25E-03	------++-++-?+?-+-++----?-	2.23E-02
3	rs7617587	149857801	-	t/c	0.96 (0.92 - 0.99)	0.025	+------+?-??--?---?-++---?	7.85E-10
2	rs2264692	57585448	-	a/g	1.03 (1.00 - 1.06)	0.028	++++++--?-???-?+-+?++?+-+-	8.58E-03
14	rs1273153	59016212	*C14orf149*	t/c	0.95 (0.91 - 0.99)	0.029	-++--++-?+-0?-?---?++-+-+-	4.55E-03
1	rs12070355	182947237	*EDEM3*	t/c	1.12 (1.01 - 1.24)	0.037	+++-+---?-?????+-+?-??+?+?	1.01E-02
1	rs6426514	226946738	*RHOU*	a/g	1.04 (1.00 - 1.08)	0.037	+-++++-+?-???+?++-?-+?+--+	9.75E-05
13	rs912697	95846724	*HS6ST3*	a/g	1.02 (1.00 - 1.03)	0.044	++--++++?+???+?---?+-?++++	2.59E-02
17	rs1078439	69055901	*SDK2*	t/c	0.98 (0.97 - 1.00)	0.044	-------++-+-+-?---+-++--?+	1.70E-01
17	rs623323	646770	*NXN*	t/c	1.02 (1.00 - 1.04)	0.084	++++++--+-++?-?--++-++--++	1.37E-03
2	rs700952	5428205	-	t/c	0.98 (0.96 - 1.01)	0.21	+-------?--------+?+-+-+?-	1.08E-05
4	rs1595665	161630317	-	t/c	1.02 (0.99 - 1.05)	0.24	+-+-+--+?-???-?---?+-?++++	2.74E-02
5	rs17053082	155326808	*N/A*	t/c	1.02 (0.98 - 1.06)	0.26	+???+????????-??????-?+-++	1.57E-05
6	rs11968879	150202935	*LRP11*	a/g	1.02 (0.98 - 1.05)	0.29	+--+-+--?----+++++?+-+-+-?	1.54E-05
3	rs13066950	37428116	*C3orf35*	t/g	1.01 (0.99 - 1.02)	0.30	++++++--+-+-+-?++-+-+++-?-	8.34E-02
20	rs1967678	2312386	*TGM6*	t/c	1.03 (0.98 - 1.08)	0.31	+++++++-+---+-?+++-+???-??	1.78E-02
14	rs1257906	97748922	-	a/g	1.01 (0.99 - 1.03)	0.39	++++++++-++-?+?+-++-+----+	2.76E-01
13	rs9552911	22762657	*SGCG*	a/g	1.01 (0.99 - 1.03)	0.49	---+-+-+++???+?+++-+-?-++?	1.05E-03
3	rs6443876	184553100	*MCF2L2*	t/c	1.01 (0.99 - 1.03)	0.50	++--+--++-???-?--+++-?+-++	2.16E-02
6	rs9494335	136053557	*C6orf217*	a/g	1.00 (0.98 - 1.01)	0.53	---+-+-+?-???-?---?++?++++	3.62E-03
2	rs11683782	30384693	-	a/c	1.00 (0.98 - 1.01)	0.56	---+-+-++-???-?++--+-?-+++	1.65E-03
16	rs11862438	82879154	*WFDC1*	c/g	1.00 (0.98 - 1.03)	0.71	-----+-+?-???+?--+?++?-++-	3.17E-02
6	rs6904271	109822899	*PPIL6*	c/g	1.00 (0.97 - 1.04)	0.79	-+-+-+--?+++--?+--?+--++--	3.40E-05
14	rs242387	55661157	*PELI2*	a/g	1.00 (0.98 - 1.01)	0.84	----+-+-++++-+?+++-+--++--	2.09E-03

15	rs12595602	57257509	*MIR2116*	t/c	1.00 (0.95 - 1.04)	0.86	-+++-+--?-+++-?+++?++---+?	2.11E-03
8	rs4527850	134266031	*WISP1*	t/c	1.00 (0.99 - 1.02)	0.90	++++++-++-++?-++--+--+--++	1.70E-02
7	rs6461477	20086589	-	a/g	1.00 (0.98 - 1.02)	0.92	--++-+++++???-?++-++-?+--+	7.39E-04

Supplementary Table 11. Association of SNPs near *SGCG* locus (chr 13q12) with T2D-related quantitative traits



	rs9552911				rs572303				rs1410518				rs6490820				rs7319884				rs9553022			
	unadj		adj		unadj		adj		unadj		adj		unadj		adj		unadj		adj		unadj		adj	
	β	P	β	P	β	P	β	P	β	P	β	P	β	P	β	P	β	P	β	P	β	P	β	P
BMI	-0.24	0.184	-0.15	0.379	0.15	0.443	0.17	0.395	0.08	0.753	0.14	0.572	-0.91	0.478	-0.20	0.446	0.32	**5.30×10^{-2}**	0.36	**3.05×10^{-2}**	-0.04	0.801	-0.05	0.761
Waist (cm)	-1.03	1.81×10^{-1}	-0.31	5.73×10^{-1}	0.84	0.080	0.67	**5.20×10^{-2}**	0.80	0.191	0.69	0.115	0.51	0.415	0.93	**3.80×10^{-2}**	0.92	**2.30×10^{-2}**	0.35	0.231	0.04	0.910	0.10	0.713
WHR	-0.01	**5.00×10^{-3}**	0.00	0.252	0.01	**5.30×10^{-2}**	0.01	0.068	0.01	**5.10×10^{-2}**	0.01	**4.60×10^{-2}**	0.00	0.269	0.01	0.106	0.00	0.597	0.00	0.645	0.00	0.715	0.00	0.645
SYSBP (mmHG)	-2.94	**5.00×10^{-3}**	-1.53	0.130	0.87	0.383	0.60	0.516	0.88	0.492	0.93	0.424	2.22	0.088	1.93	0.106	0.25	0.759	0.12	0.872	-1.47	0.071	-1.98	**8.00×10^{-3}**
DYSBP (mmHG)	-2.37	**5.81×10^{-3}**	-1.87	**2.40×10^{-2}**	0.98	0.070	0.89	0.089	1.47	**3.20×10^{-2}**	1.59	**1.70×10^{-2}**	0.56	0.425	0.83	0.226	-0.53	0.237	-0.71	0.103	-0.89	**4.40×10^{-2}**	-0.91	**3.20×10^{-2}**
FBG (mg/dL)	-6.03	1.78×10^{-1}	-1.65	6.49×10^{-1}	0.38	0.892	1.10	0.620	-0.73	0.836	3.59	0.204	-2.84	0.434	-1.62	0.579	-2.46	0.289	-1.07	0.564	-1.31	0.571	-0.53	0.774
Homa IR	-0.36	2.03×10^{-1}	-0.29	3.07×10^{-1}	0.13	0.468	0.15	0.400	0.03	0.898	0.11	0.619	-0.02	0.926	0.04	0.853	0.12	0.395	0.12	0.413	-0.09	0.544	-0.09	0.554
Homa B	10.45	0.150	1.86	0.795	8.36	0.384	6.91	0.455	5.08	0.676	-1.02	0.931	-1.04	0.934	-3.30	0.788	-3.99	0.623	-4.09	0.601	2.71	0.731	1.33	0.861
Cholesterol (mg/dL)	0.02	**2.70×10^{-2}**	0.02	0.176	-0.39	0.862	-0.47	0.833	-1.35	0.635	-1.15	0.685	1.49	0.613	1.27	0.664	0.15	0.937	0.06	0.975	1.06	0.565	1.08	0.554
HDL (mg/dL)	0.15	0.804	-0.12	0.840	0.12	0.834	0.05	0.923	-0.51	0.48	-0.64	0.369	-0.03	0.968	-0.22	0.757	-0.04	0.941	-0.08	0.859	-0.02	0.958	-0.07	0.879
LDL (mg/dL)	0.44	0.783	-0.11	0.944	0.01	0.996	-0.16	0.922	-0.26	0.899	-0.37	0.856	0.46	0.83	-0.09	0.967	-0.04	0.979	-0.14	0.918	0.88	0.504	0.60	0.651
TG (mg/dL)	1.72	0.688	5.32	0.213	0.98	0.840	1.34	0.782	5.64	0.348	6.81	0.259	4.69	0.458	5.93	0.349	-0.85	0.834	-0.92	0.82	6.77	0.081	7.02	0.071

	rs1359426				rs1359978				rs1570979				rs1886972				rs7319884				rs7996675			
	unadj		adj		unadj		adj		unadj		adj		unadj		adj		unadj		adj		unadj		adj	
	β	P	β	P	β	P	β	P	β	P	β	P	β	P	β	P	β	P	β	P	β	P	β	P
BMI	0.07	0.782	0.05	0.830	0.09	0.751	0.06	0.820	-0.65	0.328	-0.56	0.399	-0.81	0.202	-0.70	0.267	-0.22	0.370	-0.25	0.305	-0.23	0.348	-0.26	0.279
Waist (cm)	-0.47	0.428	-0.33	0.571	0.84	0.238	0.98	0.157	-1.20	0.495	-1.22	0.478	-1.47	0.382	-1.57	0.338	-0.43	0.484	-0.45	0.451	-0.52	0.392	-0.53	0.378
WHR	0.00	0.923	0.00	0.711	0.01	0.012	0.01	**1.95×10^{-3}**	0.00	0.767	-0.01	0.589	-0.01	0.635	-0.01	0.498	0.00	0.929	0.00	0.921	0.00	0.771	0.00	0.946
SYSBP (mmHG)	2.11	0.068	2.40	**2.48×10^{-2}**	0.85	0.534	0.70	0.579	1.14	0.726	2.21	0.463	1.22	0.694	2.54	0.374	-1.98	0.093	-2.11	0.054	-2.07	0.080	-2.14	0.051
DYSBP (mmHG)	0.59	0.364	0.62	0.321	1.38	0.068	1.30	0.074	-1.01	0.581	-0.78	0.657	-3.42	0.053	-3.05	0.072	-0.94	0.165	-0.56	0.389	-1.01	0.132	-0.61	0.342
FBG (mg/dL)	-0.02	**7.09×10^{-4}**	-0.02	**1.14×10^{-3}**	0.00	0.814	0.00	0.872	-0.08	**2.03×10^{-5}**	-0.08	**1.62×10^{-5}**	-0.08	**2.34×10^{-5}**	-0.08	**2.02×10^{-5}**	0.02	**5.28×10^{-4}**	0.02	**2.27×10^{-4}**	0.02	**5.77×10^{-4}**	0.02	**2.43×10^{-4}**
Homa IR	-0.05	0.381	-0.05	0.337	-0.01	0.907	-0.01	0.933	-0.27	0.090	-0.28	0.081	-0.24	0.122	-0.25	0.115	0.04	0.504	0.05	0.419	0.04	0.503	0.05	0.413
Homa B	0.04	0.478	0.04	0.573	0.02	0.819	0.01	0.886	-0.04	0.859	-0.04	0.829	-0.03	0.896	-0.03	0.869	-0.09	0.160	-0.08	0.226	-0.09	0.166	-0.08	0.231
Cholesterol (mg/dL)	0.00	0.815	0.00	0.978	-0.01	0.492	-0.02	0.337	0.01	0.888	0.02	0.743	0.03	0.467	0.05	0.294	-0.02	0.178	-0.02	0.206	-0.02	0.179	-0.02	0.203
HDL (mg/dL)	0.00	0.928	-0.01	0.673	0.01	0.786	0.00	0.995	0.03	0.640	0.04	0.547	0.03	0.574	0.05	0.419	0.01	0.629	0.01	0.653	0.01	0.659	0.01	0.696
LDL (mg/dL)	0.01	0.623	0.01	0.683	-0.01	0.686	-0.01	0.548	-0.02	0.751	-0.02	0.797	0.02	0.760	0.03	0.649	-0.02	0.443	-0.02	0.436	-0.02	0.447	-0.02	0.434
TG (mg/dL)	0.04	0.107	0.04	0.102	-0.01	0.827	-0.01	0.849	-0.08	0.330	-0.07	0.369	-0.05	0.546	-0.04	0.622	-0.05	0.041	-0.05	0.057	-0.05	0.043	-0.05	0.060

rs9552911, rs572303, rs1410518 SGCG; rs9553022 TNFRSF19; rs6490820, rs7319884 MIPEP. Analysis for fasting blood glucose was performed in controls.

SUPPLEMENTARY DATA

Supplementary Table 12. eQTL analysis showing significant cis-association ($P \leq 10^{-4}$) between SNPs 1 Mb around lead SNP in *SGCG*

								Adipose			**Skin**			**LCL**		
Gene	**SNP**	**TSS**	**TSE**	**INFO**	**SNP_Coor**	**A1**	**Freq1**	**β**	**SE**	**P eQTL**	**β**	**SE**	**P eQTL**	**β**	**SE**	**P eQTL**
SGCG	rs2225833	22653059	22797304	0.969	22647741	C	0.633	0.092	0.0155	**2.86E-09**	0.0421	0.0122	5.73E-04	-0.0004	0.005	9.36E-01
SGCG	rs1753096	22653059	22797304	0.993	22776547	G	0.193	-0.1144	0.0193	**3.18E-09**	-0.0011	0.0147	9.40E-01	0.0005	0.0061	9.37E-01
SGCG	rs1753097	22653059	22797304	0.999	22776686	G	0.193	-0.1141	0.0193	**3.20E-09**	-0.0009	0.0147	9.50E-01	0.0004	0.0061	9.49E-01
SGCG	rs497691	22653059	22797304	0.987	22775923	G	0.807	0.1143	0.0193	**3.38E-09**	0.0014	0.0147	9.24E-01	-0.0005	0.0061	9.31E-01
SGCG	rs17078394	22653059	22797304	0.961	22651669	T	0.192	-0.1068	0.0181	**3.87E-09**	-0.0494	0.0141	4.61E-04	0.0034	0.0058	5.59E-01
SGCG	rs529005	22653059	22797304	0.892	22643070	T	0.638	0.0917	0.0157	**5.55E-09**	0.0439	0.0124	3.93E-04	-0.0002	0.0051	9.64E-01
SGCG	rs577379	22653059	22797304	0.997	22653788	G	0.532	0.0862	0.0153	**1.78E-08**	0.028	0.0122	2.14E-02	-0.0024	0.005	6.33E-01
SGCG	rs4770402	22653059	22797304	0.987	22652744	T	0.536	0.085	0.0154	**3.46E-08**	0.0274	0.0123	2.53E-02	-0.0021	0.005	6.70E-01
SGCG	rs9550961	22653059	22797304	0.846	22848277	G	0.47	-0.0871	0.0162	**7.35E-08**	-0.0148	0.0128	2.47E-01	0.0052	0.0052	3.22E-01
SGCG	rs4770437	22653059	22797304	0.836	22849626	T	0.465	-0.0855	0.0162	**1.32E-07**	-0.0148	0.0128	2.45E-01	0.0052	0.0053	3.21E-01
SGCG	rs1800353	22653059	22797304	0.882	22796509	T	0.319	-0.0871	0.0171	**3.36E-07**	-0.0185	0.0133	1.64E-01	0.0015	0.0055	7.91E-01
SGCG	rs3794370	22653059	22797304	0.999	22654627	T	0.51	-0.0767	0.0151	**3.52E-07**	-0.0141	0.0119	2.38E-01	0.0036	0.0049	4.56E-01
SGCG	rs3764064	22653059	22797304	0.953	22651104	T	0.269	-0.0823	0.0165	**6.42E-07**	-0.0477	0.0131	2.67E-04	0.003	0.0053	5.69E-01
SGCG	rs9317535	22653059	22797304	0.992	22653892	G	0.733	0.0796	0.0163	**1.00E-06**	0.0473	0.0129	2.45E-04	-0.0033	0.0052	5.31E-01
SGCG	rs2182497	22653059	22797304	0.866	22855488	T	0.105	-0.124	0.0259	**1.73E-06**	-0.0052	0.0204	7.99E-01	-0.004	0.0084	6.33E-01
SGCG	rs11619233	22653059	22797304	0.898	22857999	G	0.893	0.1218	0.026	**2.70E-06**	0.0039	0.0204	8.49E-01	0.0068	0.0084	4.20E-01
SGCG	rs2709235	22653059	22797304	0.888	22854140	T	0.889	0.1185	0.0254	**2.99E-06**	0.0013	0.02	9.49E-01	0.0042	0.0082	6.10E-01
SGCG	rs12871934	22653059	22797304	0.996	22749568	G	0.116	-0.1047	0.0226	**3.63E-06**	-0.0152	0.0175	3.85E-01	-0.0079	0.0072	2.69E-01
SGCG	rs17315411	22653059	22797304	0.995	22749106	G	0.116	-0.1047	0.0226	**3.63E-06**	-0.0152	0.0175	3.85E-01	-0.0079	0.0072	2.69E-01

SGCG	rs17315474	22653059	22797304	0.996	22749430	T	0.116	-0.1047	0.0226	**3.63E-06**	-0.0152	0.0175	3.85E-01	-0.0079	0.0072	2.69E-01
SGCG	rs17315901	22653059	22797304	0.996	22758285	T	0.884	0.1047	0.0226	**3.63E-06**	0.0153	0.0175	3.84E-01	0.0079	0.0072	2.69E-01
SGCG	rs12872214	22653059	22797304	0.996	22749716	G	0.116	-0.1047	0.0226	**3.64E-06**	-0.0152	0.0175	3.85E-01	-0.0079	0.0072	2.69E-01
SGCG	rs12875241	22653059	22797304	0.996	22750526	G	0.884	0.1047	0.0226	**3.64E-06**	0.0152	0.0175	3.85E-01	0.0079	0.0072	2.69E-01
SGCG	rs17374896	22653059	22797304	0.996	22751700	T	0.116	-0.1047	0.0226	**3.64E-06**	-0.0152	0.0175	3.85E-01	-0.0079	0.0072	2.69E-01
SGCG	rs12864851	22653059	22797304	0.999	22760901	T	0.116	-0.1046	0.0226	**3.68E-06**	-0.0154	0.0175	3.78E-01	-0.0083	0.0072	2.48E-01
SGCG	rs17316242	22653059	22797304	0.994	22761137	T	0.116	-0.1047	0.0226	**3.70E-06**	-0.0154	0.0175	3.80E-01	-0.0081	0.0072	2.62E-01
SGCG	rs1536365	22653059	22797304	0.931	22827095	T	0.884	0.1146	0.025	**4.42E-06**	0.0008	0.0193	9.68E-01	0.0076	0.008	3.46E-01
SGCG	rs2031640	22653059	22797304	0.93	22828055	T	0.116	-0.1145	0.025	**4.56E-06**	-0.0007	0.0193	9.69E-01	-0.0076	0.008	3.42E-01
SGCG	rs9552923	22653059	22797304	0.963	22790786	G	0.464	0.069	0.0152	**5.23E-06**	0.0061	0.0119	6.11E-01	-0.0056	0.0049	2.53E-01
SGCG	rs2050578	22653059	22797304	0.968	22649626	G	0.667	0.0694	0.0154	**6.28E-06**	0.029	0.0122	1.75E-02	-0.0028	0.005	5.66E-01
SGCG	rs1409497	22653059	22797304	1	22815281	G	0.093	-0.1192	0.0267	**8.22E-06**	-0.0152	0.0206	4.60E-01	-0.0027	0.0086	7.54E-01
SGCG	rs4770434	22653059	22797304	0.994	22816177	T	0.907	0.1193	0.0268	**8.32E-06**	0.0151	0.0206	4.65E-01	0.0024	0.0086	7.77E-01
SGCG	rs9552932	22653059	22797304	0.982	22821893	G	0.46	0.0657	0.0149	**1.10E-05**	0.0038	0.0118	7.46E-01	-0.0054	0.0048	2.60E-01
SGCG	rs2737700	22653059	22797304	0.988	22806034	G	0.461	0.0653	0.0149	**1.17E-05**	0.0041	0.0117	7.26E-01	-0.0055	0.0048	2.53E-01
SGCG	rs4770433	22653059	22797304	0.996	22801791	G	0.464	0.065	0.0148	**1.20E-05**	0.0042	0.0117	7.18E-01	-0.0053	0.0048	2.65E-01
SGCG	rs518727	22653059	22797304	0.898	22784236	T	0.487	-0.0684	0.0156	**1.22E-05**	-0.0045	0.0124	7.14E-01	0.007	0.005	1.65E-01
SGCG	rs4770431	22653059	22797304	0.973	22793151	T	0.092	-0.1184	0.0273	**1.40E-05**	-0.0151	0.021	4.72E-01	-0.0007	0.0088	9.39E-01
SGCG	rs2031641	22653059	22797304	0.97	22828245	G	0.908	0.1179	0.0272	**1.49E-05**	0.0151	0.021	4.73E-01	0.0009	0.0088	9.16E-01
SGCG	rs10507329	22653059	22797304	0.968	22830133	T	0.092	-0.118	0.0273	**1.50E-05**	-0.0151	0.021	4.74E-01	-0.0009	0.0088	9.18E-01
SGCG	rs1415130	22653059	22797304	0.926	22651879	T	0.269	-0.0704	0.0167	**2.63E-05**	-0.0501	0.0132	1.52E-04	0.003	0.0054	5.80E-01
SGCG	rs7333173	22653059	22797304	0.881	22648385	G	0.761	-0.0744	0.0177	**2.75E-05**	-0.002	0.0141	8.85E-01	0.0064	0.0057	2.65E-01
SGCG	rs9580556	22653059	22797304	0.881	22645255	T	0.238	0.0744	0.0178	**2.90E-05**	0.0022	0.0141	8.75E-01	-0.0065	0.0058	2.62E-01

SGCG	rs510407	22653059	22797304	0.931	22688992	G	0.241	0.0702	0.0172	**4.37E-05**	0.0003	0.0139	9.85E-01	0	0.0056	9.97E-01
SGCG	**rs572303**	**22653059**	**22797304**	**0.999**	**22684773**	**T**	**0.293**	**-0.0565**	**0.0163**	**5.47E-04**	**-0.0193**	**0.013**	**1.37E-01**	**0.0029**	**0.0053**	**5.81E-01**
TNFRSF19	rs9507129	23051638	23141412	0.965	23117423	G	0.285	-0.0131	0.0062	3.35E-02	-0.0288	0.0067	**1.51E-05**	0.0001	0.0063	9.89E-01
TNFRSF19	rs3794348	23051638	23141412	0.987	23110954	T	0.714	0.0128	0.006	3.40E-02	0.028	0.0065	**1.81E-05**	-0.0012	0.0061	8.48E-01
TNFRSF19	rs3794347	23051638	23141412	0.988	23113236	T	0.714	0.0128	0.006	3.40E-02	0.028	0.0065	**1.83E-05**	-0.0012	0.0061	8.49E-01
TNFRSF19	rs9507128	23051638	23141412	0.99	23115092	T	0.298	-0.0103	0.0059	8.20E-02	-0.0272	0.0064	**2.14E-05**	0.0016	0.006	7.96E-01
TNFRSF19	rs9507127	23051638	23141412	0.991	23114955	T	0.702	0.0103	0.0059	8.22E-02	0.0272	0.0064	**2.16E-05**	-0.0016	0.006	7.93E-01
TNFRSF19	rs7992255	23051638	23141412	0.957	23112813	G	0.31	-0.0102	0.0059	8.52E-02	-0.0273	0.0064	**2.17E-05**	0.0022	0.006	7.21E-01
TNFRSF19	rs12429914	23051638	23141412	0.992	23110486	G	0.701	0.0102	0.0059	8.34E-02	0.0271	0.0064	**2.20E-05**	-0.0017	0.006	7.73E-01
TNFRSF19	rs1983958	23051638	23141412	0.93	23096460	T	0.25	-0.0091	0.0065	1.65E-01	-0.0297	0.007	**2.24E-05**	-0.0034	0.0066	6.09E-01
TNFRSF19	rs12429900	23051638	23141412	0.992	23110353	G	0.702	0.0102	0.0059	8.29E-02	0.0271	0.0064	**2.26E-05**	-0.0017	0.006	7.73E-01
TNFRSF19	rs9507126	23051638	23141412	0.993	23114033	C	0.702	0.0102	0.0059	8.28E-02	0.0271	0.0064	**2.27E-05**	-0.0017	0.006	7.79E-01
TNFRSF19	rs9510793	23051638	23141412	0.993	23111120	T	0.702	0.0102	0.0059	8.31E-02	0.027	0.0064	**2.31E-05**	-0.0017	0.006	7.71E-01
TNFRSF19	rs7991222	23051638	23141412	0.995	23112657	C	0.702	0.0102	0.0059	8.33E-02	0.027	0.0064	**2.37E-05**	-0.0018	0.006	7.68E-01
TNFRSF19	rs9510788	23051638	23141412	0.979	23105224	T	0.258	-0.0093	0.0063	1.40E-01	-0.0283	0.0068	**2.86E-05**	-0.0032	0.0064	6.13E-01
TNFRSF19	rs9510787	23051638	23141412	0.991	23103195	G	0.26	-0.0092	0.0063	1.45E-01	-0.0281	0.0067	**3.07E-05**	-0.0033	0.0064	6.03E-01
TNFRSF19	rs7989882	23051638	23141412	0.999	23112603	G	0.7	0.0103	0.0059	7.81E-02	0.0264	0.0064	**3.19E-05**	-0.002	0.006	7.39E-01
TNFRSF19	rs4400900	23051638	23141412	0.929	23089203	G	0.747	0.0096	0.0065	1.40E-01	0.029	0.007	**3.39E-05**	0.0032	0.0066	6.28E-01
TNFRSF19	rs12584129	23051638	23141412	0.977	23101273	T	0.258	-0.0089	0.0063	1.58E-01	-0.0281	0.0068	**3.44E-05**	-0.0034	0.0064	5.96E-01
TNFRSF19	rs1983957	23051638	23141412	0.964	23098532	T	0.743	0.0092	0.0064	1.47E-01	0.0283	0.0068	**3.62E-05**	0.0034	0.0065	5.96E-01
SGCG	rs4769245	22653059	22797304	0.998	22703627	G	0.772	-0.0126	0.0177	4.75E-01	-0.0566	0.0138	**4.16E-05**	-0.0086	0.0058	1.38E-01
TNFRSF19	rs9510790	23051638	23141412	0.962	23107302	T	0.254	-0.0091	0.0064	1.57E-01	-	0.0069	**4.77E-05**	-	0.0065	5.64E-01

											0.0279			0.0038		
SGCG	rs9580573	22653059	22797304	0.92	22682242	C	0.229	0.0061	0.0179	7.32E-01	0.0564	0.014	**5.78E-05**	0.0089	0.0058	1.26E-01
SGCG	rs4770411	22653059	22797304	0.92	22681140	T	0.771	-0.0061	0.0179	7.32E-01	-0.0564	0.014	**5.78E-05**	-0.0089	0.0058	1.26E-01
SGCG	rs1887757	22653059	22797304	0.922	22686362	T	0.229	0.0063	0.0179	7.24E-01	0.0562	0.014	**6.05E-05**	0.009	0.0058	1.25E-01
TNFRSF19	rs1575666	23051638	23141412	0.934	23120688	C	0.707	0.0129	0.0062	3.70E-02	0.0265	0.0067	**7.54E-05**	0	0.0063	1.00E+00
TNFRSF19	rs12585977	23051638	23141412	0.962	23138151	T	0.684	0.0101	0.006	8.94E-02	0.0254	0.0064	**8.15E-05**	0.0019	0.0061	7.50E-01
TNFRSF19	rs3794344	23051638	23141412	0.964	23130708	G	0.304	-0.0125	0.006	3.80E-02	-0.0256	0.0065	**8.66E-05**	-0.0014	0.0062	8.17E-01
TNFRSF19	rs1034068	23051638	23141412	0.96	23128811	G	0.685	0.0102	0.006	8.81E-02	0.0253	0.0064	**8.69E-05**	0.0009	0.0061	8.84E-01
TNFRSF19	rs9507136	23051638	23141412	0.958	23127353	G	0.686	0.0102	0.006	8.66E-02	0.0252	0.0065	**9.37E-05**	0.0005	0.0061	9.34E-01
TNFRSF19	rs9510800	23051638	23141412	0.972	23138285	G	0.304	-0.0124	0.006	3.93E-02	-0.0253	0.0065	**9.81E-05**	-0.0021	0.0061	7.30E-01
TNFRSF19	rs679482	23051638	23141412	0.88	22663635	C	0.865	0.0005	0.0076	9.46E-01	0.015	0.0081	6.40E-02	-0.0302	0.0076	**8.05E-05**

Supplementary Table 13. Details of the participating studies, samples, quality control, minor allele frequency of the *SGCG* variant (rs9552911), ORs and *P* values

			N cases	N controls	Genotype call rate	Controls HWE P value	MAF cases	MAF controls	OR	95% CI L	95% CI U	P value	Imputed
Ethnic Group		**STUDIES**											
Punjabi Sikhs	SDS/AIDHS	Discovery GWAS	842	774	1.00	0.390	0.06	0.09	0.61	0.47	0.80	0.0003	
Punjabi Sikhs		LOLIPOP Sikh GWAS	801	2017	1.00	0.876	0.07	0.08	0.75	0.58	0.96	0.021	
Punjabi Sikhs		*De novo* Sikh Replication	977	1493	0.97	0.049	0.06	0.09	0.66	0.53	0.82	0.0001	
		LOLIPOP non-Sikh South Asians	982	1741	99.95	0.380	0.11	0.11	0.95	0.78	1.16	0.621	
Pakistani South Asians	PROMIS	Others_GWAS1	1468	3769	1.00	0.035	0.11	0.10	0.96	0.84	1.10	0.606	
		Punjabi_GWAS1	641	1465	1.00	1.000	0.09	0.08	0.92	0.73	1.16	0.532	
		Others_GWAS2	1736	1637	0.94	0.017	0.10	0.10	1.01	0.86	1.19	0.744	yes
		Punjabi_GWAS2	1259	1074	0.94	0.580	0.08	0.09	0.92	0.75	1.13	0.432	yes
		Other_GWAS3	864	710	0.94	0.241	0.12	0.11	1.12	0.90	1.40	0.379	yes
		Punjabi_GWAS3	669	484	0.90	1.000	0.09	0.08	1.16	0.85	1.57	0.223	yes
Pakistani South Asians	RACE	RACE1_Other	339	381	0.99	0.733	0.07	0.08	1.23	0.83	1.82	0.219	
		RACE1_Punjabi	164	129	1.00	1.000	0.12	0.10	0.83	0.49	1.40	0.506	
		RACE2_Others	561	752	0.94	1.000	0.11	0.11	1.02	0.79	1.30	0.735	yes
		RACE2_Punjabi	523	775	0.92	0.070	0.10	0.09	1.17	0.90	1.53	0.299	yes
South Asians (Singapore)	SINDI	Singapore Indian	973	1164	1.00	0.807	0.17	0.14	0.96	0.92	1.00	0.060	
East Asians	RIKEN	Japanese	4455	2955	1.00	0.391	0.26	0.26	1.00	0.93	1.08	0.832	
		Singapore Chinese	1992	1941	0.99	0.931	0.23	0.24	0.94	0.84	1.06	0.323	
		Singapore Malay	781	1234	1.00	0.333	0.26	0.26	0.99	0.96	1.02	0.544	
	AGEN	Koreans, Chinese, Japanese	6952	11865	NA	NA	NA	NA	1.00	0.95	1.06	0.915	NA
Caucasians	DIAGRAM	Europeans, US whites	8130	38987	NA	NA	NA	NA	NA	NA	NA	NA	

Supplementary Table 14. Association results in the AIDHS/SDS discovery cohort for previously reported T2D loci

SNP	Chr	Pos	*Gene*	Alt	Risk	SDS RAF	SDS OR	SDS P	CEU RAF	CEU OR	CEU P
rs10923931	1	120230001	*NOTCH2*	G	T	0.22	1.21 (1.00-1.47)	5.30E-02	0.12	1.13 (1.08-1.17)	4.00E-08
rs243021	2	60496470	*BCL11A*	G	A	0.53	1.10 (0.96-1.25)	1.70E-01	0.46	1.08 (1.06-1.10)	3.00E-15
rs3923113	2	165210095	*GRB14*	C	A	0.73	1.06 (0.91-1.24)	4.58E-01	0.74[‡]	1.09 (1.06-1.13)	1.00E-08
rs2943641	2	226801989	*IRS1*	T	C	0.72	1.20 (1.03-1.39)	1.83E-02	0.65	1.19 (1.13–1.25)	9.28E-12
rs7578326	2	226846158	*IRS1*	G	A	0.76	1.09 (0.93-1.27)	2.68E-01	0.64	1.11 (1.08-1.13)	5.00E-20
rs7578597	2	43586327	*THADA*	C	T	0.85	1.21 (0.58-2.51)	6.05E-01	0.90	1.15 (1.10–1.20)	1.10E-09
rs4607103	3	64686944	*ADAMTS9*	T	C	-	-	-	0.76	1.09 (1.06-1.12)	1.00E-08
rs6795735	3	64680405	*ADAMTS9*	T	C	0.31	1.04 (0.90-1.21)	5.84E-01	0.54	1.09 (1.04-1.13)	8.40E-05
rs4402960	3	186994381	*IGF2BP2*	G	T	0.45	1.21 (1.06-1.38)	**4.32E-03**	0.30	1.14 (1.11-1.18)	8.90E-16
rs1470579	3	187011782	*IGF2BP2*	A	C	0.39	1.29 (1.12-1.47)	**2.48E-04**	0.29	1.14 (1.09-1.19)	2.20E-09
rs1801282	3	12333125	*PPARG*	G	C	0.87	0.12 (0.03-0.52)	**5.00E-03**	0.82	1.14 (1.08–1.20)	1.70E-06
rs13081389	3	12264800	*PPARG*	G	A	-	-	-	0.96	1.24 (1.14-1.35)	2.00E-07
rs831571	3	64023337	*PSMD6*	T	C	0.76	1.04 (0.89-1.21)	6.57E-01	0.57[ϕ]	1.09 (1.06–1.12)	8.41E-11
rs16861329	3	188149155	*ST6GAL1*	A	G	0.76	1.04 (0.89-1.21)	6.63E-01	0.75[‡]	1.09 (1.06-1.12)	3.40E-08
rs257108	3	188228830	*ST6GAL1*	G	A	0.38	1.23 (1.06-1.42)	4.99E-03	-	-	-
rs9812056	3	23179028	*UBE2E2*	G	A	0.78	1.27 (1.08-1.51)	**4.95E-03**	0.84*	1.17 (1.11-1.24)*	1.83E-08

rs7612463	3	23311454	*UBE2E2*	A	C	0.77	1.28 (1.10-1.49)	**1.59E-03**	0.84*	1.19 (1.12-1.26)*	2.27E-09
rs6780569	3	23173488	*UBE2E2*	A	G	0.78	1.22 (1.04-1.43)	1.36E-02	0.95*	1.21 (1.14-1.30)*	6.76E-09
rs10012946	4	6344251	*WFS1*	A	G	0.70	1.31 (1.12-1.53)	**5.55E-04**	-	-	-
rs1801214	4	6421094	*WFS1*	C	T	-	-	-	0.73	1.13 (1.08-1.18)	3.20E-08
rs1001960	5	76406875	*ZBED3*	G	A	0.29	1.06 (0.92-1.22)	4.35E-01	-	-	-
rs4457053	5	76460705	*ZBED3*	A	G	-	-	-	0.26	1.16 (1.10-1.23)	4.20E-08
rs7754840	6	20769229	*CDKAL1*	G	C	0.27	1.09 (0.93-1.27)	2.77E-01	0.36	1.12 (1.08–1.16)	4.10E-11
rs10440833	6	20796100	*CDKAL1*	T	A	-	-	-	0.25	1.25 (1.20-1.31)	1.80E-22
rs9470794	6	38214822	*ZFAND3*	T	C	0.12	1.08 (0.88-1.34)	4.67E-01	0.33[ϕ]	1.12 (1.08–1.16)	2.06E-10
rs6467136	7	126952194	*GCC1-PAX4*	A	G	0.59	1.04 (0.91-1.19)	5.68E-01	0.78[ϕ]	1.11 (1.07–1.14)	4.96E-11
rs864745	7	28147081	*JAZF1*	C	T	0.68	1.07 (0.90-1.26)	4.70E-01	0.50	1.10 (1.07–1.13)	5.00E-14
rs290794	7	130066934	*KLF14*	G	A	0.22	1.03 (0.89-1.21)	6.76E-01	-	-	-
rs972283	7	129924109	*KLF14*	A	G	-	-	-	0.55	1.07 (1.05-1.10)	2.00E-10
rs13266634	8	118253964	*SLC30A8*	T	C	0.73	1.03 (0.89-1.20)	6.66E-01	0.61	1.12 (1.07–1.16)	5.30E-08
rs2047962	8	118109252	*SLC30A8*	A	G	0.57	0.87 (0.75-1.00)	4.00E-02	-	-	-
rs896854	8	96029687	*TP53INP1*	C	T	0.44	1.07 (0.93-1.23)	3.32E-01	0.48	1.06 (1.04-1.09)	1.00E-09
rs10965250	9	22123284	*CDKN2A/B*	A	G	-	-	-	0.81	1.20 (1.13-1.27)	1.20E-10
rs1333049	9	22115503	*CDKN2A/B*	C	G	0.50	1.14 (1.01-1.30)	**4.20E-03**	-	-	-
rs7041847	9	4277466	*GLIS3*	G	A	0.57	1.04 (0.91-1.20)	5.41E-01	0.59[ϕ]	1.10 (1.07–1.13)	1.99E-14

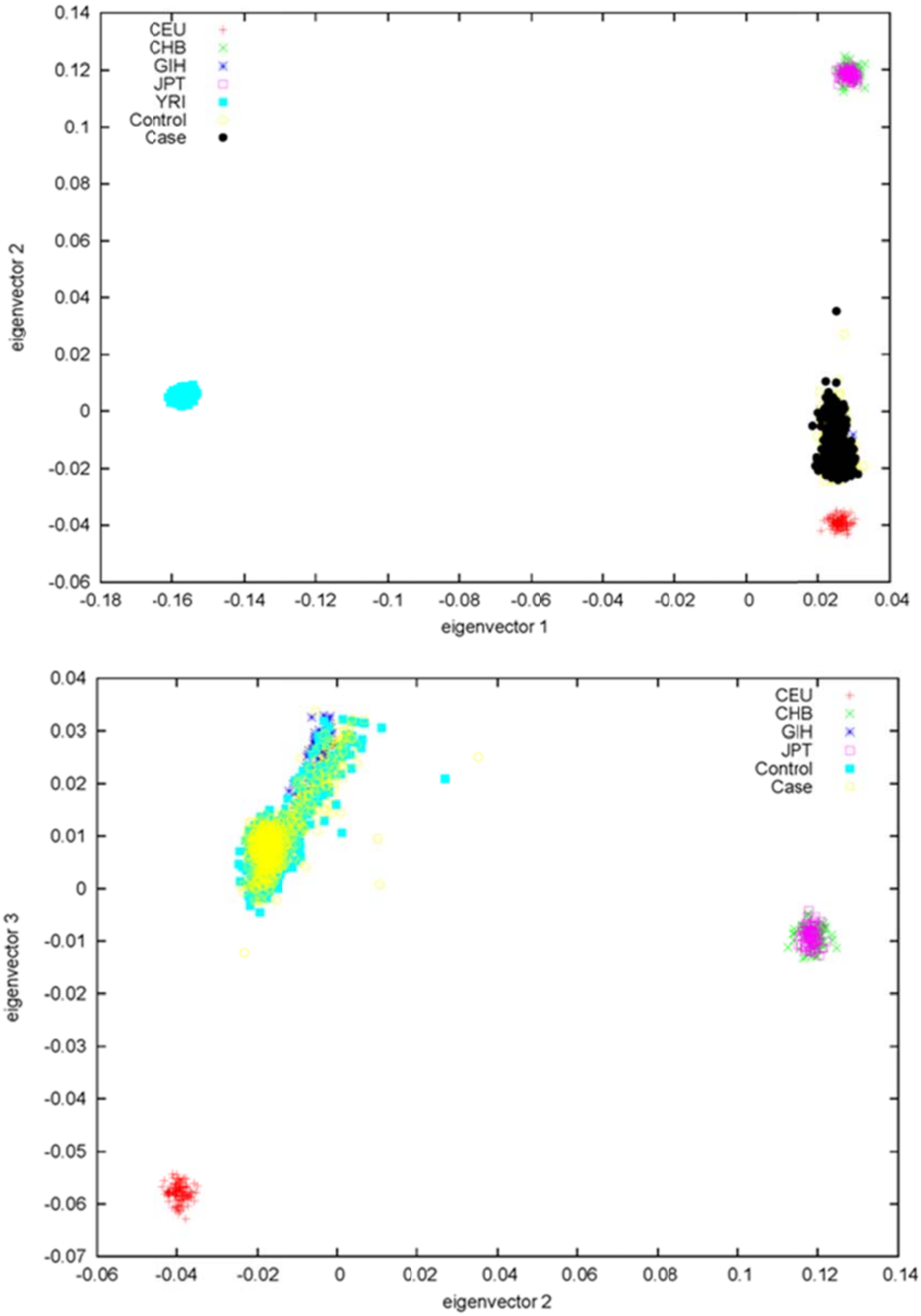
rs17584499	9	8869118	*PTPRD*	C	T	0.28	1.09 (0.94-1.26)	2.72E-01	0.25[Ψ]	1.57 (1.36-1.82)	9.00E-10
rs12779790	10	12368016	*CDC123*	A	G	0.13	1.27 (1.02-1.57)	3.10E-02	0.23	1.11 (1.07-1.14)	1.00E-10
rs5015480	10	94455539	*HHEX*	T	C	0.45	1.12 (0.98-1.28)	8.82E-02	0.57	1.18 (1.13-1.23)	1.30E-15
rs7903146	10	114748339	*TCF7L2*	C	T	0.36	1.37 (1.20-1.57)	**5.36E-06**[¥]	0.25	1.40 (1.34-1.46)	2.20E-51
rs1802295	10	70601480	*VPS26A*	G	A	0.34	1.09 (0.95-1.24)	2.13E-01	0.26[‡]	1.08 (1.05-1.12)	4.10E-08
rs5215	11	17365206	*KCNJ11*	T	C	0.37	1.00 (0.87-1.15)	9.74E-01	0.41	1.14 (1.10-1.19)	5.00E-11
rs163182	11	2844216	*KCNQ1*	G	C	-	-	-	0.40[Ψ]	1.28 (NR)	2.00E-17
rs163184	11	2803645	*KCNQ1*	T	G	0.54	1.11 (0.97-1.27)	1.26E-01	0.44	1.09 (1.04-1.13)	6.80E-05
rs231362	11	2648047	*KCNQ1*	A	G	0.77	1.21 (1.06-1.37)	**4.00E-03**	0.52	1.08 (1.06-1.10)	3.00E-13
rs1387153	11	92313476	*MTNR1B*	C	T	0.36	1.07 (0.93-1.23)	3.63E-01	0.28	1.12 (1.07-1.17)	1.00E-06
rs7957197	12	119923406	*HNF1A*	A	T	-	-	-	0.85	1.07 (1.05-1.10)	2.00E-08
rs2245407	12	119908381	*HNF1A*	A	C	0.87	1.05 (0.86-1.28)	6.50E-01	-	-	-
rs7961581	12	69949369	*TSPAN8/ LGR5*	T	C	0.35	1.29 (0.98-1.70)	6.70E-02	0.27	1.09 (1.06–1.12)	1.10E-09
rs2028299	15	88175261	*AP3S2*	A	C	0.28	1.05 (0.91-1.22)	4.92E-01	0.31[‡]	1.10 (1.07-1.13)	1.90E-11
rs7172432	15	62396389	*C2CD4A/B*	G	A	-	-	-	0.58*	1.14 (1.09-1.20)	7.48E-08
rs7172432	15	60183681	*C2CD4A/B*	G	A	0.62	1.06 (0.92-1.22)	4.15E-01	0.52	1.07 (1.03-1.12)	1.10E-03
rs7178572	15	75534245	*HMG20A*	A	G	0.54	1.06 (0.93-1.21)	3.90E-01	0.52[‡]	1.09 (1.06-1.12)	7.10E-11
rs8042680	15	89322341	*PRC1*	C	A	0.61	1.10 (0.96-1.26)	1.59E-01	0.22	1.07 (1.05-1.09)	2.00E-10
rs8050136	16	52373776	*FTO*	C	A	0.35	1.19 (1.04-1.37)	1.26E-02	0.38	1.17 (1.12-1.22)	1.30E-12

rs11642841	16	52402988	*FTO*	C	A	-	-	-	0.45	1.13 (1.08-1.18)	3.40E-08
rs9939609	16	52378028	*FTO*	T	A	0.31	1.31 (1.09-1.59)	5.00E-03	0.17[Ŧ]	1.15 (1.09-1.21)	5.50E-08
rs17797882	16	77964419	*WWOX*	C	T	-	-	-	0.20[ϕ]	1.08 (1.05–1.12)	9.49E-07
rs2287972	16	76701108	*WWOX*	A	G	0.44	1.13 (0.99-1.29)	6.44E-02	-	-	-
rs391300	17	2163008	*SRR*	T	C	0.54	1.02 (0.90-1.17)	7.33E-01	0.64[Ψ]	1.28 (1.18-1.39)	3.00E-09
rs6017317	20	42380380	*FITM2-R3HDML-HNF4A*	T	G	-	-	-	0.45[ϕ]	1.09 (1.07–1.12)	1.12E-11
rs4812829	20	42422681	*HNF4A*	G	A	0.25	1.18 (1.01-1.37)	3.67E-02	0.19[‡]	1.09 (1.06-1.12)	2.60E-10
rs5945326	X	152553116	*DUSP9*	G	A	0.65	1.10 (0.98-1.23)	1.22E-01	0.79	1.27 (1.18–1.37)	3.00E-10

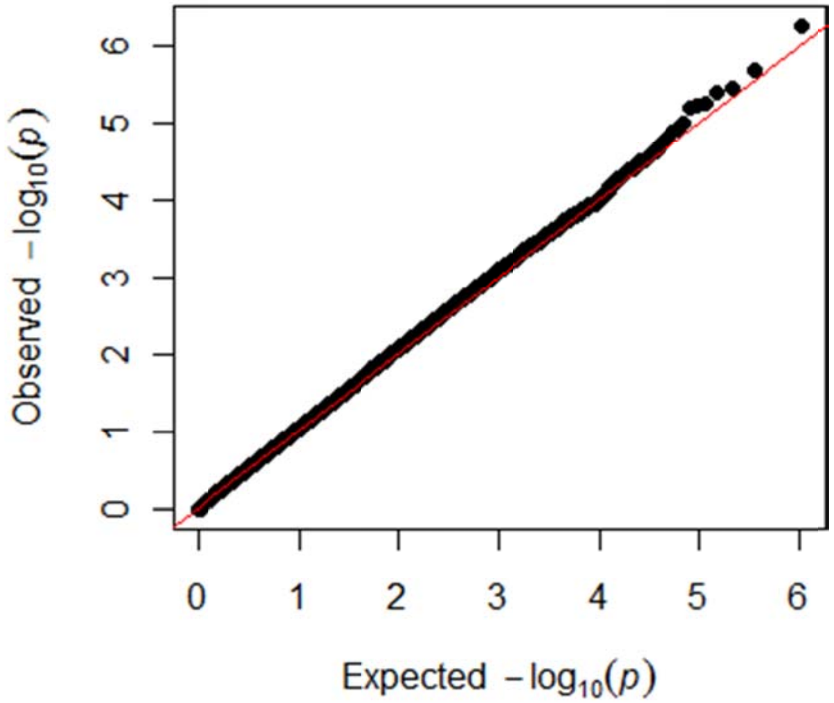
*Japanese Cohort, [‡] South Asian, [ϕ] Asian, [Ψ] Han Chinese, [Ŧ] South/East Asian, [¥] p values are based on discovery and stage 3a, Chr- chromosome, Pos- position

Supplementary Figure 1. Principal components analysis of the Sikh GWAS population and HapMap3 founder populations GIH, CEU, CHB, JPT and YRI.

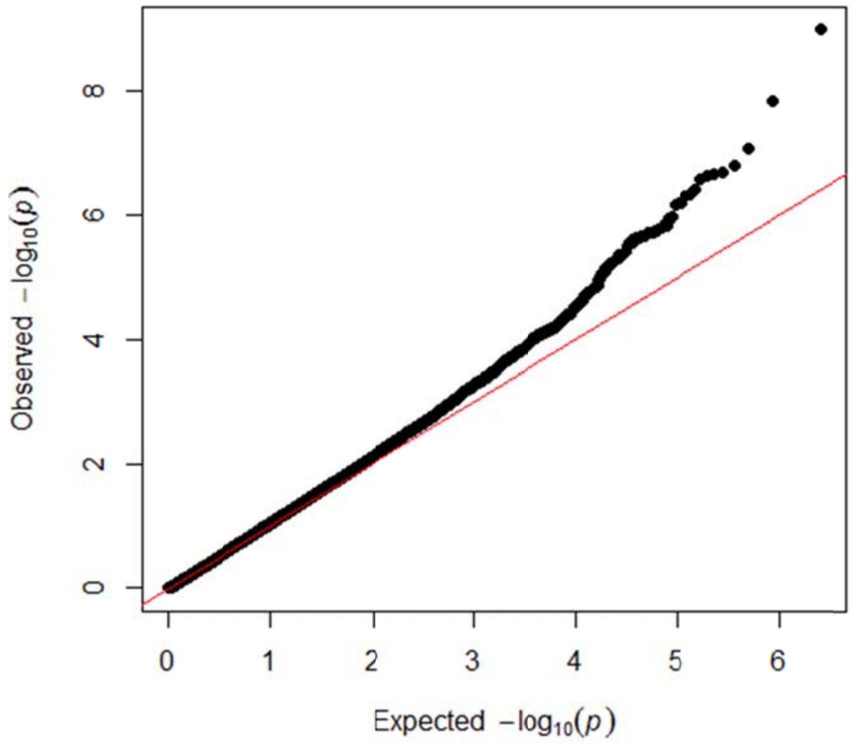
Eigenvectors demonstrate the close proximity of the Sikh GWAS population to the GIH and CEU populations, and the close matching of cases and controls



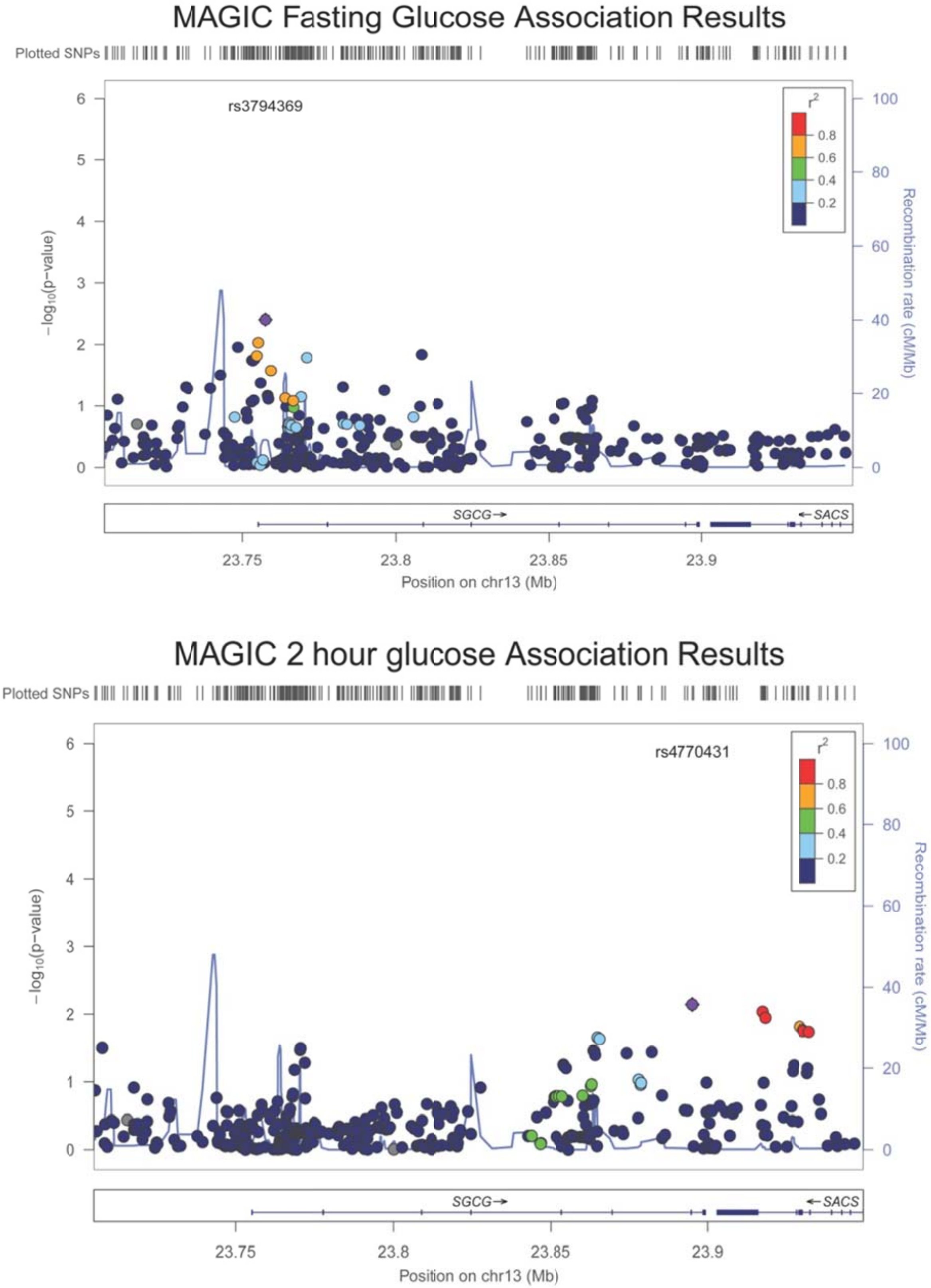
Supplementary Figure 2a. QQ Plot of GWAS discovery results (524,216 genotyped SNPs; l =1.0)



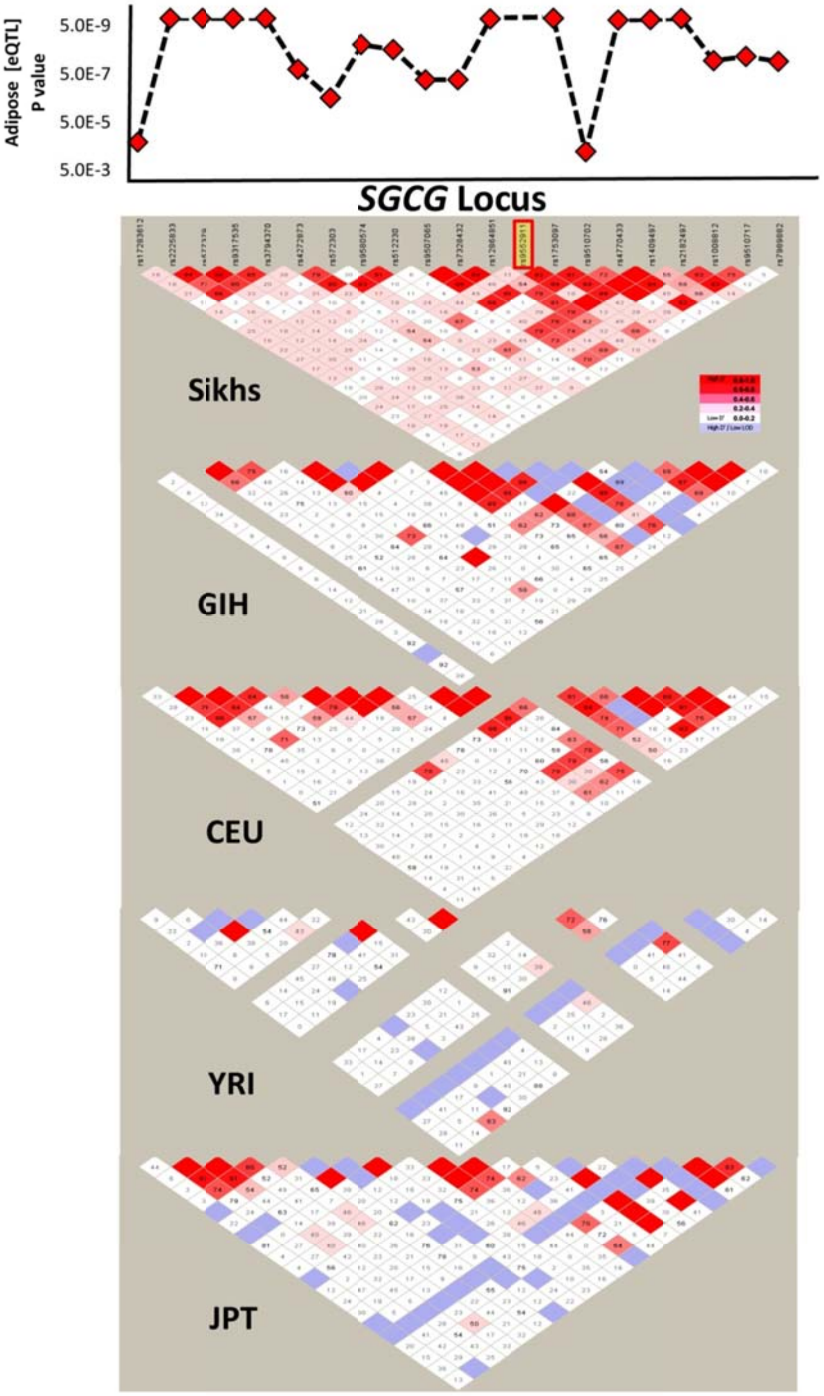
Supplementary Figure 2b. QQ Plot of HM3-imputed GWAS discovery results (1,232,008 SNPs; l =1.02)



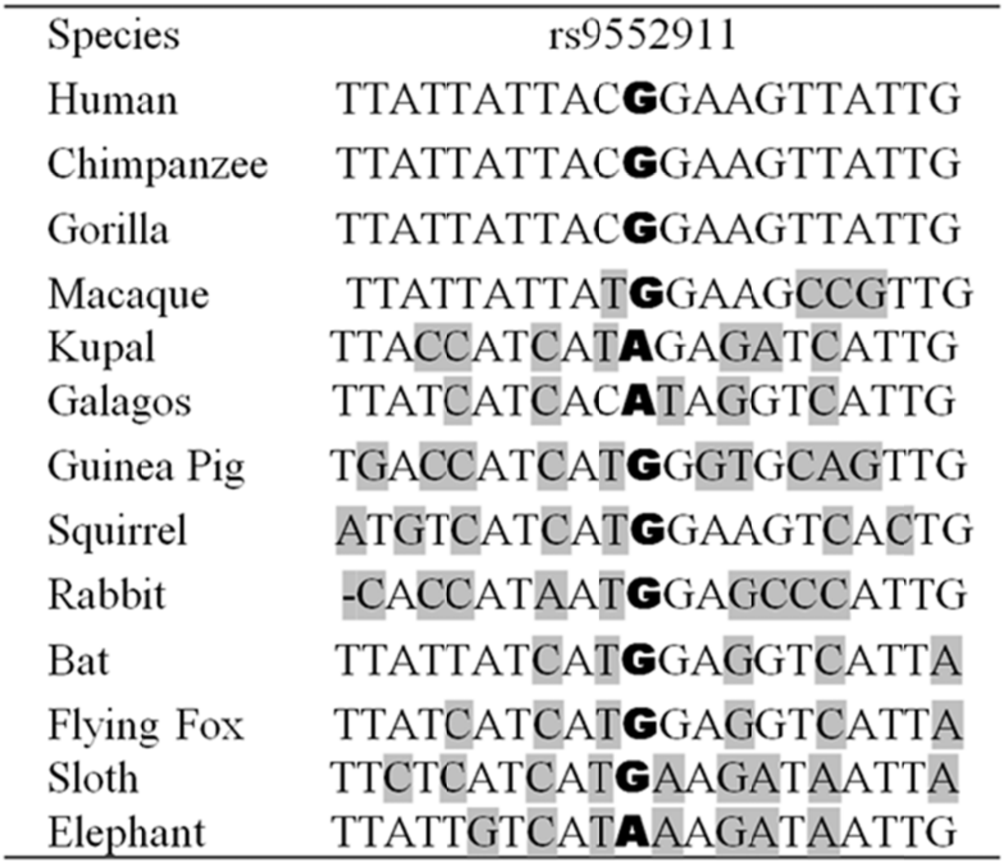
Supplementary Figure 3. Summary of MAGIC GWAS results for glycemic traits for the *SGCG* locus and 50 kb upstream/downstream of the gene.



Supplementary Figure 4. Figure 4A shows several SNPs in the *SGCG* region (~638Kb) at chromosome 13q12 to be associated with significantly elevated expression of SGCG mRNA ($P_{eQTL}<10^{-4}$) in adipose tissues from the data from MuTHER Consortium. Log *P* values of cis-expression adipose eQTL are shown on Y axis and SNPs in the *SGCG* on X axis. Note that the lead variant (rs9552911) was absent in both MuTHER data and in Caucasian HapMap. Figure 4B shows linkage disequilibrium (LD) maps of the *SGCG* SNPs from the MuTHER study showing patterns of variation in pair-wise LD between Punjabi Sikhs , Gujarati Indians (GIH), Caucasians (CEU), Africans (YRI), and Japanese (JPT) taken from Hap Map. The strongest LD (r2=0.26) with rs9552911 was observed in two (rs12864851 and rs7328432) in Japanese HapMap.



Supplementary Figure 5. Comparative Genomic Analysis showing evolution of Index SNP(rs9552911) in the SGCG.



Species	rs9552911
Human	TTATTATTAC**G**GAAGTTATTG
Chimpanzee	TTATTATTAC**G**GAAGTTATTG
Gorilla	TTATTATTAC**G**GAAGTTATTG
Macaque	TTATTATTAT**G**GAAGCCGTTG
Kupal	TTACCATCAT**A**GAGATCATTG
Galagos	TTATCATCAC**A**TAGGTCATTG
Guinea Pig	TGACCATCAT**G**GGTGCAGTTG
Squirrel	ATGTCATCAT**G**GAAGTCACTG
Rabbit	-CACCATAAT**G**GAGCCCATTG
Bat	TTATTATCAT**G**GAGGTCATTA
Flying Fox	TTATCATCAT**G**GAGGTCATTA
Sloth	TTCTCATCAT**G**AAGATAATTA
Elephant	TTATTGTCAT**A**AAGATAATTG

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