**NG-LE29790R1.**

## Supplementary online material

Genome-wide association study in people of South Asian ancestry identifies six novel susceptibility loci for Type 2 Diabetes.

Kooner et al

### *Supplementary note*

*GWA cohort descriptions*

London Life Sciences Population (LOLIPOP) study

The LOLIPOP study is a population-based cohort of South Asian and European men and women aged 35-75 years living in West London.[1] 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, 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,[2] 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 at the 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.

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.[3] 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.

*Replication cohort descriptions*

The COBRA study

COBRA is a population based sample of adults in Karachi, Pakistan recruited in a cluster randomized trial of strategies to control hypertension (‘Population Based Strategies for Effective Control of High Blood Pressure in Pakistan’, Trial registration number NCT00327574).[4] A multi-stage cluster random sampling design was used to randomly select 12 geographical clusters in Karachi, the largest metropolitan city in Pakistan. A census was done, and a listing of all individuals from all households in the selected areas was made. All subjects aged 40 years or above, and able to consent were invited to participate by trained community health workers. This included blood pressure measurement with a calibrated automated device (“Omron HEM-737 TM Blood Pressure Monitor”) in the sitting position after 5 minutes of rest, anthropometry (height, weight, waist and hip circumferences), laboratory tests for fasting plasma glucose (Synchron Cx-7/Delta, Beckman, US) and DNA extraction. T2D was defined as physician diagnosis on antidiabetic medications, or fasting blood glucose >= 7 mmol/L. Controls had no history of T2D, and had fasting glucose <7mmol/L. Ethical approval was obtained from the Ethics Review Committee at the Aga Khan University, Pakistan.

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.[5] 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.[6] Subjects with type 2 diabetes (physician diagnosed on treatment, N=840) were recruited either from hospitals within Mirpur District or from specifically organised Diabetes Awareness camps. Control subjects (N=1225) 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.

Mauritius cohort

Mauritius is a subtropical island located in the south western Indian Ocean with a population of about 1.2 million. An estimated 70% of the population are of South Asian origin (54% Hindu and 16% Muslim), 2% are of Chinese origin and 28% are of the ‘general’ population, which mainly comprises people with mixed African and Malagasy ancestry with some European and Indian admixture (Creoles). A population based survey was undertaken in 1998 that included participants who were 20 years and older, with a total of 6,291 participants examined.[7,8] Participants of self-reported South Asian ancestry were included in the present study.

All subjects not taking diabetes medication had a 2-h 75-g oral glucose (glucose monohydrate) tolerance test (OGTT). Venous blood samples were drawn at baseline fasting and at 2 hours post ingestion of glucose and were centrifuged and separated immediately. Plasma glucose was measured using the YSI glucose analyzer (Yellow Springs Instruments, OH, USA). Glucose tolerance status was determined according to 1999 WHO criteria. Diabetes was diagnosed if subjects reported a history of diabetes and were taking hypoglycaemic medication, or the fasting plasma glucose level was >=7.0 mmol/L and/or the 2-h value was >=11.1 mmol/L. Normal glucose tolerance was assigned if the fasting plasma glucose level was < 6.1 mmol/L and the 2-h value was <7.8 mmol/L.

## Ragama Health Study (RHS)

The Ragama Health Study (RHS) is a population-based study of South Asian men and women aged 35-64yrs living in the Ragama Medical Officer of Health (MOH) administrative area, near Colombo, Sri Lanka.[9] Consenting adults attended after a 12-h fast with their available health records, and were interviewed by trained personnel to obtain information on medical, sociodemographic, and lifestyle variables. Blood pressure and anthropometric measurements were made. A 10-mL sample of venous blood was obtained from each subject, for measurement of fasting glucose and HbA1c; T2D was defined as physician diagnosis on treatment or fasting glucose >7mmol/L or HbA1c level more than 6.5%. Controls had no history of T2D, fasting glucose <6.1 mmol/l, and HbA1c <6.0. The concurrent study is being performed in two tea plantation estates in the Talawakele MOH area, near Nuwara Eliya (180 km from Colombo), to investigate the gene-environment interaction in a community with differing lifestyles (e.g., physical activity and diet). Ethical approval for the study was obtained from the Ethics Committees of the Faculty of Medicine, University of Kelaniya and the National Center for Global Health and Medicine.

## Sikh Diabetes Study (SDS)

Participants of SDS were recruited from Sikhs living in the Northern states of India, including Punjab, Haryana, Himachal Pradesh, Delhi, and Jammu and Kashmir.[10] Type 2 diabetes mellitus was defined as physician diagnosis on treatment, a fasting plasma glucose level of ≥7.0mmol/L, or 2-hour post glucose load level of ≥11.1mmol/L, on more than one occasion with symptoms of diabetes. Controls had no prior history of diabetes and normal glucose tolerance (fasting glucose <6mmol/L, post glucose <7.8mmol/L). Subjects with impaired fasting glucose and/or impaired glucose tolerance were excluded from analysis. All participants provided a written informed consent for investigations. All SDS protocols and consent documents were reviewed and approved by the University of Oklahoma and the University of Pittsburgh Institutional Review Boards as well as the Human Subject Protection Committees at the participating hospitals and institutes in India.

## Singapore Consortium of Cohort Studies (SCCS)

SCCS includes cases with T2D and controls recruited in Singapore. T2D cases are recruited from hospitals and polyclinics, namely Alexandra and Changi General Hospital and Ang Mo Kio, Jurong, Choa Chu Kang, Yishun and Pasir Ris Polyclinics . Controls are recruited from the general population. All participants complete a structured questionnaire, providing information on demographics, socio-economic status and medical history (including history of diabetes) and have measurement of anthropometric measures and blood pressure. Fasting blood samples are collected for blood glucose and lipid measurements. Participants gave broad consent for i) future biomedical research, ii) access to their medical records and iii) linkages to various registries. For the purpose of this study, only participants of self reported South Asian ancestry are included. Type 2 diabetes mellitus was defined as physician diagnosis on treatment; controls had no prior history of diabetes and fasting glucose <6.1mmol/L.

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 4388 subjects (40% male).[11] Among recruited subjects, 3372 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 to 1576.

T2D cases were mostly derived from the Sri Lankan Young Diabetes Study (SLYDS). A total of 992 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), 890 were considered to have clinical type 2 diabetes. The mean (SD) age at diagnosis for this group was 32.4 (5.4) years and the mean BMI was 24.9 (3.9) $kgm^{-2}$. The SLYDS case sample was augmented with 176 diabetes cases from SLDCS. Additional exclusion criteria were applied to the combined cases set (GADA ≥ 14units/ml, age ≥80 years, and missing sex information) to generate a total of 1066 cases available for genotyping.

Genotyping was carried out at the Diabetes Research Laboratory, Oxford. Analyses of genotyping data excluded 330 samples based on a per-sample genotype call rate ≤90%. After these exclusions a total of 841 cases and 1471 controls were taken forward for association testing. PLINK was used to carry out the data analysis.

United Kingdom Asian Diabetes Study (UKADS)

UK-resident South Asians subjects with type 2 diabetes (physician diagnosed, on treatment, n=892) were recruited to UKADS from Birmingham and Coventry, UK.[12] All subjects were of Punjabi ancestry, confirmed over three generations, and originated predominantly from Mirpur region of Azad Kashmir, Pakistan. Ethnically-matched control subjects (n=449) 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.

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The COBRA study

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### Diabetes Genetics in Pakistan and United Kingdom Asian Diabetes studies

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### London Life Sciences Population study

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### Sikh Diabetes Study

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### Singapore Consortium of Cohort Studies

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### Singapore Indian Eye Study

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### DIAGRAM+ study[13]

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MuTHER study (www.muther.org)[14]
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**Supplementary Table 1**. Characteristics of participants in the genome-wide association cohorts.

| | **LOLIPOP 610** | | | **LOLIPOP 317** | | | **SINDI** | | | **PROMIS** | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | T2D | Controls | P | T2D | Controls | P | T2D | Controls | P | T2D | Controls | P |
| N | 1783 | 4773 | - | 440 | 1699 | - | 977 | 1169 | -- | 2361 | 6817 | - |
| Age | 59.4 (9.2) | 53.9 (10.7) | <0.001 | 54.1 (10.1) | 46.8 (10.1) | <0.001 | 60.7 (9.9) | 55.7 (9.7) | <0.001 | 55.0 (9.4) | 52.9 (10.5) | <0.001 |
| Gender (% male) | 82.9 | 84.8 | 0.058 | 100.0 | 100.0 | - | 54.4 | 48.4 | 0.007 | 76.5 | 83 | <0.001 |
| CHD (%) | 63.0 | 35.1 | <0.001 | 3.4 | 0.5 | <0.001 | 22.7 | 9.3 | <0.001 | 60.8 | 46.6 | <0.001 |
| Ever smoked (%) | 27.4 | 21.1 | <0.001 | 28.0 | 28.5 | 0.806 | 28.3 | 26.4 | 0.364 | 49.4 | 55.7 | <0.001 |
| Hypertension (%) | 80.1 | 56.1 | <0.001 | 70.7 | 40.6 | <0.001 | 74.2 | 46.2 | <0.001 | 36.5 | 25 | <0.001 |
| SBP (mmHg) | 140. 6 (20.4) | 133.5 (18.9) | <0.001 | 139.8 (20.6) | 132.0 (20.2) | <0.001 | 140.0 (19.7) | 131.7 (19.2) | <0.001 | 129.9 (21.5) | 127.1 (20.5) | <0.001 |
| DBP (mmHg) | 80.7 (10.9) | 82.4 (10.7) | <0.001 | 84.0 (11.7) | 82.5 (12.1) | 0.020 | 77.1 (10.1) | 77.2 (9.9) | 0.801 | 81.6 (11.9) | 80.8 (11.6) | 0.005 |
| Weight (kg) | 78.1 (14.0) | 75.6 (13.0) | <0.001 | 80.0 (15.9) | 78.4 (13.9) | 0.035 | 70.9 (14.0) | 66.7 (12.5) | <0.001 | 71.0 (12.5) | 69.1 (13.2) | <0.001 |
| BMI (kg/m$^2$) | 28.1 (4.6) | 26.8 (4.2) | <0.001 | 27.6 (4.7) | 26.6 (4.2) | <0.001 | 27.1 (5.1) | 25.3 (4.4) | <0.001 | 26.0 (4.0) | 25.3 (3.9) | <0.001 |
| Waist | 100.8 (11.5) | 96.6 (10.9) | <0.001 | 100.0 (12.2) | 96.3 (11.4) | <0.001 | -- | -- | -- | 92.0 (12.0) | 90.1 (11.7) | <0.001 |
| WHR | 0.99 (0.07) | 0.95 (0.07) | <0.001 | 0.99 (0.07) | 0.95 (0.07) | <0.001 | - | - | - | 0.95 (0.06) | 0.94 (0.07) | <0.001 |
| Cholesterol (mmol/L) | 4.65 (1.20) | 5.21 (1.12) | <0.001 | 4.94 (1.09) | 5.46 (1.04) | <0.001 | 4.86 (1.11) | 5.36 (0.98) | <0.001 | 4.81 (1.39) | 4.74 (1.29) | 0.03 |
| HDL chol (mmol/L) | 1.16 (0.30) | 1.22 (0.30) | <0.001 | 1.17 (0.29) | 1.247 (0.31) | <0.001 | 1.02 (0.30) | 1.10 (0.31) | <0.001 | 0.88 (0.25) | 0.89 (0.25) | 0.09 |
| Triglycerides (mmol/L) | 1.94 (1.55) | 1.77 (1.12) | <0.001 | 1.82 (0.86) | 1.65 (0.82) | <0.001 | 2.09 (1.22) | 1.85 (1.13) | <0.001 | 2.51 (1.58) | 2.20 (1.36) | <0.001 |
| Glucose (mmol/L) | 8.6 (3.1) | 5.2 (0.6) | <0.001 | 8.9 (2.9) | 5.1 (0.6) | <0.001 | 9.71 (4.44) | 5.38 (1.06) | <0.001 | 13.31 (5.47) | 6.89 (2.91) | <0.001 |
| HbA1c (%) | 7.9 (1.7) | 5.63 (0.549) | <0.001 | 8.0 (1.8) | 5.5 (0.5) | <0.001 | 7.6 (1.5) | 5.5 (0.28) | <0.001 | 8.9 (1.93) | 5.8 (0.45) | <0.001 |
| Genotyping array | Illumina 610Quad | | | Illumina Hap317 | | | Illumina 610Quad | | | Illumina 660Quad | | |
| Calling algorithm | GenCall | | | GenCall | | | GenCall | | | Illuminus | | |

**Supplementary Table 2.** Genomic control inflation factors in the individual samples, and in meta-analysis.

| | **Lambda** |
|---|---|
| **Individual samples** | |
| LOLIPOP Illumina 610 array - Male | 1.030 |
| LOLIPOP Illumina 610 array - Female | 1.013 |
| LOLIPOP Illumina 317 array - Male | 1.014 |
| PROMIS – Male | 1.017 |
| PROMIS – Female | 1.002 |
| SINDHI – Male | 1.023 |
| SINDHI – Female | 1.029 |
| | |
| **Meta-analysis** | |
| Primary - Gender stratified | 1.023 |
| Secondary - Male only | 1.008 |
| Secondary - Female only | 1.005 |

**Supplementary Table 3**. Sentinel SNP for loci associated with T2D at $P<10^{-4}$ in the primary GWA analysis. RAF: Risk allele frequency: SA = South Asians, EW = Europeans. Dir: 1=concordant SAT2D and DIAGRAM+, -1=discordant SAT2D and DIAGRAM+. $R_S$ = rank in SAT2D GWA data. $R_N$ = rank amongst novel SAT2D loci. $R_M$ = rank in meta-analysis of SAT2D and DIAGRAM GWA data. ** = Locus previously reported in Europeans.

| | | | | | RAF | | SAT2D | | | DIAGRAM+ | | | COMBINED | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **SNP** | **Chr** | **Position** | **Nearest Gene** | **(A/R)** | **SA** | **EW** | **N** | **OR** | **P** | **N** | **OR** | **P** | **OR** | **P** | **Dir** | **$R_{SA}$** | **$R_N$** | **$R_M$** |
| rs12730665 | 1 | 96456230 | *PTBP2* | A / G | 0.19 | 0.33 | 15486 | 1.13 (1.06-1.20) | $7.7x10^{-5}$ | 22570 | 1.01 (0.96-1.05) | 0.74 | 1.05 (1.01-1.09) | $8.6x10^{-3}$ | 1 | 49 | 42 | 30 |
| rs10495334 | 1 | 230879034 | *KIAA1383* | G / A | 0.03 | 0.09 | 18194 | 1.27 (1.13-1.43) | $8.7x10^{-5}$ | 13971 | 0.98 (0.89-1.08) | 0.70 | 1.08 (1.01-1.17) | $3.3x10^{-2}$ | -1 | 53 | 45 | 40 |
| rs4803 | 2 | 27520801 | *IFT172* | A / G | 0.41 | 0.39 | 18177 | 1.10 (1.05-1.15) | $9.3x10^{-5}$ | 22570 | 1.00 (0.96-1.04) | 0.91 | 1.04 (1.01-1.08) | $6.8x10^{-3}$ | 1 | 58 | ** | ** |
| rs17031236 | 2 | 105538433 | *FHL2* | C / A | 0.68 | 0.73 | 18173 | 1.11 (1.05-1.16) | $4.7x10^{-5}$ | 22570 | 1.02 (0.98-1.07) | 0.38 | 1.06 (1.03-1.10) | $5.3x10^{-4}$ | 1 | 35 | 28 | 14 |
| rs10206685 | 2 | 107921321 | *RGPD4* | G / A | 0.86 | 0.95 | 15503 | 1.16 (1.08-1.25) | $3.1x10^{-5}$ | 22570 | 0.93 (0.86-1.01) | 0.09 | 1.06 (1.00-1.12) | $3.5x10^{-2}$ | -1 | 25 | 18 | 41 |
| rs6749633 | 2 | 111704487 | *BCL2L11* | A / G | 0.86 | 0.70 | 15503 | 1.16 (1.08-1.24) | $5.4x10^{-5}$ | 22570 | 1.00 (0.95-1.04) | 0.87 | 1.04 (1.00-1.08) | $4.2x10^{-2}$ | -1 | 39 | 32 | 42 |
| rs7588481 | 2 | 137365673 | *THSD7B* | C / A | 0.75 | 0.87 | 15499 | 1.12 (1.06-1.19) | $4.0x10^{-5}$ | 22570 | 1.00 (0.94-1.06) | 0.98 | 1.07 (1.02-1.11) | $2.1x10^{-3}$ | -1 | 30 | 23 | 21 |
| rs3923113 | 2 | 165210095 | *GRB14* | C / A | 0.74 | 0.64 | 18174 | 1.15 (1.09-1.21) | $3.7x10^{-7}$ | 22570 | 1.05 (1.01-1.10) | 0.02 | 1.09 (1.05-1.13) | $4.9x10^{-7}$ | 1 | 2 | 1 | 3 |
| rs2577583 | 2 | 197313645 | *FLJ39660* | G / A | 0.70 | 0.73 | 8688 | 1.17 (1.09-1.26) | $4.3x10^{-5}$ | NA | - | - | - | - | - | 33 | 26 | |
| rs3731918 | 2 | 220123961 | *OBSL1* | G / A | 0.73 | 0.53 | 18184 | 1.11 (1.06-1.17) | $5.9x10^{-5}$ | 22570 | 0.98 (0.94-1.02) | 0.26 | 1.03 (0.99-1.06) | $1.0x10^{-1}$ | -1 | 42 | 35 | 46 |
| rs4672997 | 2 | 221864514 | *EPHA4* | G / A | 0.69 | 0.66 | 15487 | 1.11 (1.05-1.17) | $9.1x10^{-5}$ | 22570 | 0.98 (0.93-1.02) | 0.30 | 1.03 (1.00-1.07) | $6.9x10^{-2}$ | -1 | 55 | 47 | 45 |
| rs11711167 | 3 | 126521709 | *ZNF148* | A / G | 0.32 | 0.23 | 18190 | 1.10 (1.05-1.16) | $7.8x10^{-5}$ | 22570 | 1.02 (0.98-1.07) | 0.35 | 1.06 (1.03-1.10) | $5.7x10^{-4}$ | 1 | 50 | 43 | 15 |
| rs4298067 | 3 | 140437463 | *MRPS22* | A / G | 0.77 | 0.75 | 15500 | 1.13 (1.07-1.20) | $3.1x10^{-5}$ | 22570 | 1.00 (0.95-1.06) | 0.94 | 1.06 (1.02-1.10) | $2.8x10^{-3}$ | 1 | 26 | 19 | 24 |
| rs13322501 | 3 | 179075818 | *KCNMB2* | A / G | 0.83 | 0.93 | 15500 | 1.15 (1.08-1.23) | $2.6x10^{-5}$ | 22570 | 0.94 (0.86-1.02) | 0.12 | 1.07 (1.01-1.12) | $1.6x10^{-2}$ | -1 | 21 | 14 | 35 |
| rs1470579 | 3 | 187011774 | *IGF2BP2* | A / C | 0.41 | 0.31 | 18185 | 1.12 (1.07-1.17) | $3.1x10^{-6}$ | 22570 | 1.14 (1.09-1.19) | $2.2x10^{-9}$ | 1.13 (1.09-1.16) | $1.8x10^{-14}$ | 1 | 6 | ** | ** |
| rs16861329 | 3 | 188149155 | *ST6GAL1* | A / G | 0.76 | 0.86 | 18186 | 1.12 (1.07-1.19) | $2.3x10^{-5}$ | 13971 | 1.02 (0.95-1.09) | 0.62 | 1.09 (1.04-1.13) | $2.0x10^{-4}$ | 1 | 19 | 12 | 10 |
| rs709087 | 3 | 192938993 | *POP2* | A / G | 0.70 | 0.72 | 18170 | 1.10 (1.05-1.16) | $9.8x10^{-5}$ | 22570 | 1.01 (0.97-1.06) | 0.62 | 1.05 (1.02-1.09) | $2.7x10^{-3}$ | 1 | 60 | 50 | 23 |
| rs6835176 | 4 | 40199309 | *RBM47* | G / A | 0.04 | 0.03 | 18196 | 1.27 (1.14-1.42) | $3.4x10^{-5}$ | 22570 | 1.03 (0.93-1.15) | 0.57 | 1.14 (1.05-1.23) | $9.6x10^{-4}$ | 1 | 28 | 21 | 18 |
| rs2882659 | 4 | 113466153 | *ALPK1* | A / G | 0.64 | 0.72 | 18185 | 1.10 (1.05-1.15) | $9.0x10^{-5}$ | 13971 | 0.99 (0.94-1.05) | 0.83 | 1.05 (1.02-1.09) | $4.5x10^{-3}$ | -1 | 54 | 46 | 28 |
| rs9496773 | 6 | 144183238 | *PHACTR2* | G / A | 0.65 | 0.75 | 15490 | 1.11 (1.06-1.17) | $2.9x10^{-5}$ | 20049 | 1.04 (0.98-1.09) | 0.22 | 1.08 (1.04-1.12) | $7.0x10^{-5}$ | 1 | 23 | 16 | 9 |
| rs6462276 | 7 | 31430557 | *NEUROD6* | G / A | 0.91 | 1.00 | 15430 | 1.19 (1.09-1.30) | $9.1x10^{-5}$ | 22570 | 0.96 (0.89-1.04) | 0.31 | 1.06 (1.00-1.12) | $5.9x10^{-2}$ | -1 | 56 | 48 | 43 |
| rs17146516 | 7 | 123384357 | *SPAM1* | G / A | 0.80 | 0.84 | 15505 | 1.13 (1.07-1.20) | $5.3x10^{-5}$ | 22570 | 0.98 (0.92-1.04) | 0.46 | 1.05 (1.01-1.09) | $2.2x10^{-2}$ | -1 | 38 | 31 | 37 |
| rs2111815 | 7 | 132349786 | *CHCHD3* | G / A | 0.41 | 0.33 | 18191 | 1.10 (1.05-1.15) | $4.2x10^{-5}$ | 22570 | 1.05 (1.00-1.09) | 0.04 | 1.07 (1.04-1.10) | $1.3x10^{-5}$ | 1 | 32 | 25 | 5 |
| rs16923500 | 8 | 59551647 | *CYP7A1* | G / A | 0.24 | 0.20 | 15493 | 1.12 (1.06-1.18) | $4.5x10^{-5}$ | 22570 | 1.05 (1.00-1.10) | 0.05 | 1.08 (1.04-1.12) | $2.8x10^{-5}$ | 1 | 34 | 27 | 7 |
| rs12056692 | 8 | 87699905 | *CNGB3* | C / A | 0.25 | 0.17 | 15501 | 1.12 (1.06-1.18) | $4.1x10^{-5}$ | 22570 | 0.95 (0.90-1.01) | 0.10 | 1.04 (1.00-1.08) | $6.6x10^{-2}$ | -1 | 31 | 24 | 44 |
| rs13266634 | 8 | 118253964 | *SLC30A8* | A / G | 0.76 | 0.70 | 18192 | 1.13 (1.07-1.19) | $1.6x10^{-5}$ | 21198 | 1.15 (1.10-1.21) | $1.5x10^{-8}$ | 1.14 (1.10-1.18) | $9.0x10^{-13}$ | 1 | 14 | ** | ** |
| rs13255292 | 8 | 129145755 | *PVT1* | G / A | 0.22 | 0.33 | 15496 | 1.13 (1.07-1.19) | $3.3x10^{-5}$ | 22570 | 1.00 (0.96-1.04) | 0.96 | 1.04 (1.01-1.08) | $1.2x10^{-2}$ | -1 | 27 | 20 | 33 |
| rs16904391 | 8 | 132063575 | *ADCY8* | A / G | 0.14 | 0.06 | 15505 | 1.14 (1.07-1.22) | $8.2x10^{-5}$ | 22570 | 1.00 (0.92-1.09) | 0.97 | 1.09 (1.03-1.15) | $1.5x10^{-3}$ | 1 | 52 | 44 | 20 |
| rs2570961 | 9 | 8835429 | *PTPRD* | G / A | 0.15 | 0.19 | 18190 | 1.15 (1.08-1.22) | $1.4x10^{-5}$ | 22570 | 1.00 (0.95-1.06) | 0.97 | 1.06 (1.02-1.10) | $3.9x10^{-3}$ | 1 | 13 | 8 | 27 |
| rs2383208 | 9 | 22122076 | *ANRIL* | G / A | 0.86 | 0.83 | 18185 | 1.19 (1.11-1.28) | $5.7x10^{-7}$ | 22570 | 1.19 (1.13-1.25) | $1.8x10^{-10}$ | 1.19 (1.14-1.24) | $6.9x10^{-16}$ | 1 | 4 | ** | ** |
| rs4295736 | 9 | 81072159 | *CHCHD9* | A / G | 0.88 | 0.94 | 15485 | 1.19 (1.10-1.28) | $1.6x10^{-5}$ | 22570 | 1.22 (1.12-1.32) | $3.1x10^{-6}$ | 1.20 (1.13-1.27) | $1.7x10^{-10}$ | 1 | 15 | ** | ** |
| rs10512225 | 9 | 95266921 | *FAM120A* | G / A | 0.61 | 0.45 | 18189 | 1.11 (1.06-1.16) | $2.3x10^{-5}$ | 22570 | 0.99 (0.96-1.04) | 0.79 | 1.04 (1.01-1.07) | $9.8x10^{-3}$ | -1 | 18 | 11 | 31 |
| rs1562042 | 9 | 105747435 | *SMC2* | A / G | 0.77 | 0.90 | 15492 | 1.12 (1.06-1.19) | $7.2x10^{-5}$ | 22570 | 1.04 (0.97-1.11) | 0.31 | 1.09 (1.04-1.13) | $2.1x10^{-4}$ | 1 | 46 | 39 | 11 |

| | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| rs10983119 | 9 | 118177001 | *PAPPA* | A / G | 0.01 | 0.03 | 13369 | 1.62 (1.28-2.04) | 6.3x10$^{-5}$ | NA | - | - | - | - | - | 44 | 37 | |
| rs10903814 | 10 | 2611182 | *PFKP* | C / A | 0.15 | 0.09 | 18183 | 1.14 (1.07-1.21) | 5.9x10$^{-5}$ | 22570 | 1.00 (0.93-1.07) | 0.99 | 1.08 (1.03-1.13) | 2.1x10$^{-3}$ | 1 | 43 | 36 | 22 |
| rs11257622 | 10 | 12335345 | *CDC123* | A / G | 0.12 | 0.18 | 18166 | 1.17 (1.10-1.26) | 5.8x10$^{-6}$ | 22570 | 1.04 (0.99-1.10) | 0.11 | 1.09 (1.04-1.13) | 5.6x10$^{-5}$ | 1 | 9 | ** | ** |
| rs1802295 | 10 | 70601480 | *VPS26A* | G / A | 0.27 | 0.31 | 15506 | 1.14 (1.08-1.20) | 1.9x10$^{-6}$ | 22570 | 1.04 (1.00-1.09) | 0.06 | 1.08 (1.04-1.11) | 7.2x10$^{-6}$ | 1 | 5 | 3 | 4 |
| rs2616646 | 10 | 78559423 | *KCNMA1* | A / G | 0.15 | 0.17 | 18185 | 1.16 (1.09-1.23) | 4.8x10$^{-6}$ | 22570 | 1.02 (0.96-1.08) | 0.50 | 1.08 (1.03-1.12) | 4.0x10$^{-4}$ | 1 | 8 | 5 | 13 |
| rs2497304 | 10 | 94482696 | *HHEX* | G / A | 0.28 | 0.47 | 18166 | 1.11 (1.05-1.16) | 8.1x10$^{-5}$ | 22570 | 1.13 (1.08-1.18) | 5.2x10$^{-9}$ | 1.12 (1.08-1.16) | 2.7x10$^{-12}$ | 1 | 51 | ** | ** |
| rs7903146 | 10 | 114748339 | *TCF7L2* | G / A | 0.30 | 0.30 | 18193 | 1.25 (1.19-1.31) | 2.8x10$^{-19}$ | 22570 | 1.40 (1.34-1.46) | 2.2x10$^{-51}$ | 1.33 (1.29-1.37) | 5.1x10$^{-68}$ | 1 | 1 | ** | ** |
| rs234857 | 11 | 2809105 | *KCNQ1* | G / A | 0.75 | 0.69 | 18193 | 1.13 (1.07-1.19) | 6.5x10$^{-6}$ | 22570 | 1.07 (1.02-1.12) | 0.01 | 1.09 (1.06-1.13) | 4.0x10$^{-7}$ | 1 | 10 | ** | ** |
| rs4287347 | 11 | 132191217 | *OPCML* | A / G | 0.48 | 0.51 | 18187 | 1.10 (1.05-1.15) | 7.7x10$^{-5}$ | 22570 | 1.02 (0.98-1.07) | 0.24 | 1.06 (1.02-1.09) | 3.9x10$^{-4}$ | 1 | 48 | 41 | 12 |
| rs10082842 | 12 | 24192169 | *SOX5* | A / G | 0.45 | 0.62 | 18180 | 1.10 (1.05-1.15) | 6.7x10$^{-5}$ | NA | - | - | - | - | | 45 | 38 | |
| rs3748265 | 12 | 122982416 | *DNAH10* | G / A | 0.01 | 0.04 | 8952 | 2.86 (1.72-4.73) | 5.7x10$^{-5}$ | 22570 | 1.09 (0.98-1.21) | 0.11 | 1.14 (1.02-1.26) | 1.6x10$^{-2}$ | 1 | 40 | 33 | 36 |
| rs17084821 | 13 | 26340325 | *GPR12* | A / G | 0.14 | 0.10 | 15502 | 1.15 (1.08-1.23) | 4.0x10$^{-5}$ | 22570 | 0.99 (0.91-1.07) | 0.72 | 1.08 (1.03-1.13) | 3.5x10$^{-3}$ | -1 | 29 | 22 | 26 |
| rs7996689 | 13 | 49291645 | *KPNA3* | G / A | 0.23 | 0.28 | 15508 | 1.13 (1.07-1.19) | 2.9x10$^{-5}$ | 22570 | 1.00 (0.95-1.05) | 0.93 | 1.05 (1.01-1.09) | 7.6x10$^{-3}$ | -1 | 22 | 15 | 29 |
| rs4981720 | 14 | 19609145 | *OR4L1* | A / G | 0.87 | 0.91 | 18185 | 1.15 (1.08-1.24) | 5.3x10$^{-5}$ | 22570 | 0.99 (0.91-1.07) | 0.81 | 1.08 (1.03-1.14) | 3.0x10$^{-3}$ | -1 | 37 | 30 | 25 |
| rs10873073 | 14 | 53159106 | *BMP4* | A / G | 0.70 | 0.60 | 18171 | 1.11 (1.05-1.17) | 7.4x10$^{-5}$ | 22570 | 1.00 (0.96-1.04) | 0.93 | 1.04 (1.01-1.08) | 1.1x10$^{-2}$ | -1 | 47 | 40 | 32 |
| rs6576426 | 15 | 23254656 | *UBE3A* | A / G | 0.17 | 0.10 | 15498 | 1.15 (1.08-1.23) | 7.5x10$^{-6}$ | 22570 | 1.03 (0.97-1.10) | 0.29 | 1.09 (1.05-1.14) | 6.4x10$^{-5}$ | 1 | 11 | 6 | 8 |
| rs17560758 | 15 | 24387495 | *GABRB3* | A / G | 0.62 | 0.57 | 15496 | 1.11 (1.06-1.17) | 2.9x10$^{-5}$ | 22570 | 0.99 (0.95-1.03) | 0.71 | 1.04 (1.01-1.08) | 1.3x10$^{-2}$ | -1 | 24 | 17 | 34 |
| rs620739 | 15 | 47852704 | *ATP8B4* | A / G | 0.36 | 0.43 | 18173 | 1.11 (1.06-1.16) | 2.2x10$^{-5}$ | 22570 | 1.02 (0.98-1.06) | 0.41 | 1.05 (1.02-1.09) | 6.0x10$^{-4}$ | 1 | 17 | 10 | 16 |
| rs7178572 | 15 | 75534245 | *HMG20A* | A / G | 0.52 | 0.71 | 18193 | 1.10 (1.05-1.15) | 2.4x10$^{-5}$ | 22570 | 1.07 (1.02-1.12) | 2.6x10$^{-3}$ | 1.08 (1.05-1.12) | 2.8x10$^{-7}$ | 1 | 20 | 13 | 2 |
| rs2028299 | 15 | 88175261 | *AP3S2* | A / C | 0.31 | 0.28 | 18076 | 1.11 (1.05-1.16) | 4.8x10$^{-5}$ | 22570 | 1.05 (1.00-1.09) | 0.04 | 1.07 (1.04-1.11) | 1.8x10$^{-5}$ | 1 | 36 | 29 | 6 |
| rs4392054 | 16 | 20630271 | *ACSM1* | G / A | 0.12 | 0.09 | 15511 | 1.17 (1.09-1.26) | 1.0x10$^{-5}$ | 22570 | 0.99 (0.92-1.07) | 0.87 | 1.09 (1.03-1.15) | 1.3x10$^{-3}$ | -1 | 12 | 7 | 19 |
| rs1560916 | 17 | 28973892 | *ACCN1* | G / A | 0.46 | 0.51 | 18177 | 1.11 (1.06-1.16) | 1.6x10$^{-5}$ | 21198 | 0.98 (0.94-1.02) | 0.31 | 1.03 (1.00-1.07) | 2.7x10$^{-2}$ | -1 | 16 | 9 | 38 |
| rs3744763 | 17 | 33164998 | *HNF1B* | A / G | 0.41 | 0.41 | 18191 | 1.10 (1.05-1.15) | 9.2x10$^{-5}$ | 13971 | 1.08 (1.03-1.14) | 2.1x10$^{-3}$ | 1.09 (1.05-1.13) | 6.0x10$^{-7}$ | 1 | 57 | ** | ** |
| rs2280146 | 17 | 76490264 | *KIAA1303* | A / G | 0.39 | 0.24 | 15505 | 1.10 (1.05-1.16) | 5.7x10$^{-5}$ | 22570 | 0.97 (0.92-1.02) | 0.19 | 1.04 (1.00-1.08) | 3.2x10$^{-2}$ | -1 | 41 | 34 | 39 |
| rs1912379 | 18 | 66460710 | *RPS2P6* | A / G | 0.25 | 0.16 | 15492 | 1.14 (1.08-1.20) | 3.8x10$^{-6}$ | 22570 | 1.00 (0.94-1.06) | 0.87 | 1.07 (1.03-1.11) | 8.5x10$^{-4}$ | -1 | 7 | 4 | 17 |
| rs4812829 | 20 | 42422681 | *HNF4A* | G / A | 0.29 | 0.16 | 18186 | 1.14 (1.08-1.19) | 4.5x10$^{-7}$ | 22570 | 1.08 (1.02-1.14) | 0.01 | 1.11 (1.07-1.15) | 2.4x10$^{-8}$ | 1 | 3 | 2 | 1 |
| rs6005312 | 22 | 25878374 | *MIAT* | A / G | 0.05 | 0.21 | 18178 | 1.21 (1.10-1.34) | 9.4x10$^{-5}$ | 22570 | 0.95 (0.91-1.01) | 0.08 | 1.01 (0.96-1.06) | 7.3x10$^{-1}$ | -1 | 59 | 49 | 47 |

**Supplementary Table 4.** Characteristics of participants in the replication cohorts.

| | Location | Genotyping method | Group | Number | Male (%) | Age (yrs) | BMI (kg/m$^2$) | Glucose (mmol/L) | HbA1c (%) |
|---|---|---|---|---|---|---|---|---|---|
| **COBRA** | Pakistan | Kaspar | **Cases** | 465 | 40.9 | 53.3 (10.5) | 26.9 (5.6) | 10.5 (3.9) | NA |
| | | | **Controls** | 1580 | 47.1 | 51.0 (10.5) | 25.3 (5.3) | 5.4 (0.6) | NA |
| **Chennai Urban Rural Epidemiology Study** | India | Sequenom | **Cases** | 1316 | 47.3 | 52.9 (10.8) | 25.3 (4.6) | 9.6 (3.9) | 8.9 (2.2) |
| | | | **Controls** | 1265 | 43.1 | 47.0 (12.0) | 24.4 (4.5) | 4.9 (0.5) | 5.6 (0.4) |
| **Diabetes Genetics in Pakistan study** | Pakistan | Kaspar | **Cases** | 840 | 47.0 | 54.7 (11.7) | 26.1 (4.7) | NA | 9.7 (3.2) |
| | | | **Controls** | 1225 | 47.4 | 56.5 (10.8) | 24.3 (5.0) | 4.8 (0.5) | NA |
| **London Life Sciences Population study** | UK | Kaspar | **Cases** | 1132 | 40.0 | 54.0 (10.6) | 29.2 (5.1) | 8.5 (10.6) | 8.0 (1.7) |
| | | | **Controls** | 7652 | 38.2 | 46.6 (10.4) | 27.3 (4.7) | 5.0 (0.5) | 5.6 (0.5) |
| **Mauritius study** | Mauritius | Kaspar | **Cases** | 780 | 47.2 | 54.9 (11.5) | 26.2 (4.4) | 9.7(3.5) | NA |
| | | | **Controls** | 1536 | 43.8 | 46.3 (11.4) | 24.3 (4.2) | 5.2 (0.4) | NA |
| **Pakistan Risk of Myocardial Infarction Study** | Pakistan | Kaspar | **Cases** | 3128 | 64.3 | 56.7 (10.5) | 26.6 (4.3) | NA | 8.7 (2.1) |
| | | | **Controls** | 5277 | 74.3 | 53.9 (12.3) | 25.7 (4.4) | NA | 5.8 (0.4) |
| **Ragama Health study** | Sri Lanka | TaqMan | **Cases** | 776 | 44.6 | 54.7 (6.9) | 24.6 (4.0) | 9.2 (3.1) | 7.8 (2.0) |
| | | | **Controls** | 1981 | 44.1 | 50.8 (8.3) | 23.2 (4.3) | 5.4 (0.4) | 5.3 (0.4) |
| **Sikh Diabetes Study** | India | Sequenom | **Cases** | 1387 | 56.5 | 54.7 (10.5) | 27.1 (4.9) | 9.2 (3.6) | NA |
| | | | **Controls** | 1732 | 54.0 | 49.2 (14.4) | 26.0 (4.7) | 5.3 (0.7) | NA |
| **Singapore Consortium of Cohort Studies** | Singapore | Sequenom | **Cases** | 1613 | 38.8 | 55.4 (9.5) | 27.7 (5.0) | NA | NA |
| | | | **Controls** | 1230 | 50.1 | 41.8 (12.0) | 25.8 (5.1) | 4.9 (0.4) | 5.7 (0.4) |
| **Sri Lankan Diabetes Studies** | Sri Lanka | TaqMan | **Cases** | 841 | 40.2 | 39.0 (8.1) | 24.7 (4.0) | 8.9 (3.8) | NA |
| | | | **Controls** | 1471 | 43.3 | 44.7 (14.4) | 21.2 (4.2) | 4.8 (1.2) | NA |
| **United Kingdom Asian Diabetes Study** | UK | Kaspar | **Cases** | 892 | 54.9 | 57.1 (12.0) | 28.5 (4.6) | NA | 8.3 (1.9) |
| | | | **Controls** | 449 | 48.3 | 55.0 (11.8) | 28.0 (4.7) | 5.4 (0.9) | NA |

NA: not available

**Supplementary Table 5.** Association with T2D for the 14 SNPs which failed to replicate in further testing. Results presented as odds ratio (OR) with 95%CI per copy of risk allele in the genome-wide association stage, in replication testing amongst South Asians, and in combined analysis of South Asian data.

| | | | | **Alleles** | | **Genome-wide association** | | **Replication testing** | | **Combined analysis** | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| **SNP** | **Chr** | **Position** | **Nearest gene** | **Alt** | **Risk** | **OR** | **P** | **OR** | **P** | **OR** | **P** |
| rs17031236 | 2 | 105538433 | *FHL2* | C | A | 1.11 (1.05-1.16) | 4.7x10$^{-5}$ | 1.03 (0.99-1.06) | 0.15 | 1.05 (1.02-1.09) | 3.1x10$^{-4}$ |
| rs11711167 | 3 | 126521709 | *ZNF148* | A | G | 1.10 (1.05-1.16) | 7.8x10$^{-5}$ | 1.02 (0.99-1.06) | 0.20 | 1.05 (1.02-1.08) | 6.0x10$^{-4}$ |
| rs6835176 | 4 | 40199309 | *RBM47* | G | A | 1.27 (1.14-1.42) | 3.4x10$^{-5}$ | 1.01 (0.92-1.11) | 0.81 | 1.09 (1.02-1.17) | 1.5x10$^{-2}$ |
| rs9496773 | 6 | 144183238 | *PHACTR2* | G | A | 1.11 (1.06-1.17) | 2.9x10$^{-5}$ | 1.00 (0.97-1.04) | 0.95 | 1.04 (1.01-1.07) | 1.7x10$^{-2}$ |
| rs2111815 | 7 | 132349786 | *CHCHD3* | G | A | 1.10 (1.05-1.15) | 4.2x10$^{-5}$ | 1.02 (0.98-1.05) | 0.35 | 1.05 (1.02-1.08) | 9.0x10$^{-4}$ |
| rs16923500 | 8 | 59551647 | *CYP7A1* | G | A | 1.12 (1.06-1.18) | 4.5x10$^{-5}$ | 1.01 (0.97-1.05) | 0.54 | 1.05 (1.02-1.08) | 3.5x10$^{-3}$ |
| rs1562042 | 9 | 105747435 | *SMC2* | A | G | 1.12 (1.06-1.19) | 7.2x10$^{-5}$ | 1.01 (0.97-1.05) | 0.65 | 1.03 (1.00-1.07) | 4.9x10$^{-2}$ |
| rs2616646 | 10 | 78559423 | *KCNMA1* | A | G | 1.16 (1.09-1.23) | 4.8x10$^{-6}$ | 1.01 (0.96-1.06) | 0.77 | 1.05 (1.01-1.09) | 9.4x10$^{-3}$ |
| rs4287347 | 11 | 132191217 | *OPCML* | A | G | 1.10 (1.05-1.15) | 7.7x10$^{-5}$ | 1.01 (0.97-1.04) | 0.74 | 1.03 (1.00-1.06) | 2.6x10$^{-2}$ |
| rs6576426 | 15 | 23254656 | *UBE3A* | A | G | 1.15 (1.08-1.23) | 7.5x10$^{-6}$ | 1.04 (0.99-1.09) | 0.10 | 1.02 (0.99-1.06) | 1.9x10$^{-1}$ |
| rs620739 | 15 | 47852704 | *ATP8B4* | A | G | 1.11 (1.06-1.16) | 2.2x10$^{-5}$ | 1.03 (0.99-1.06) | 0.17 | 1.06 (1.03-1.09) | 2.1x10$^{-4}$ |
| rs4392054 | 16 | 20630271 | *ACSM1* | G | A | 1.17 (1.09-1.26) | 1.0x10$^{-5}$ | 1.04 (0.99-1.10) | 0.12 | 1.03 (0.99-1.07) | 1.6x10$^{-1}$ |
| rs17052370* | 17 | 21660480 | *UBBP4* | G | A | 1.37 (1.23-1.52) | 8.9x10$^{-9}$ | 1.02 (0.97-1.08) | 0.38 | 1.09 (1.04-1.14) | 6.9x10$^{-4}$ |
| rs1912379 | 18 | 66460710 | *RPS2P6* | A | G | 1.14 (1.08-1.20) | 3.8x10$^{-6}$ | 1.01 (0.97-1.05) | 0.60 | 1.05 (1.02-1.09) | 1.6x10$^{-3}$ |

*SNP rs17052370 identified through female specific GWA analysis, and retested in women only.

**Supplementary Table 6.** Association of sentinel SNPs with secondary quantitative anthropometric and metabolic traits in the LOLIPOP and PROMIS cohorts. Association results are given as change in phenotype per copy of risk allele, and are adjusted for age and gender. Associations were calculated in LOLIPOP and PROMIS separately, and results combined by inverse variance meta-analysis. Associations nominally significant at P<0.05 are shaded in grey. P values are not corrected for multiple testing.

| | **rs3923113** | | **rs16861329** | | **rs1802295** | | **rs2028299** | | **rs7178572** | | **rs4812829** | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Phenotype** | **Beta** | **P** | **Beta** | **P** | **Beta** | **P** | **Beta** | **P** | **Beta** | **P** | **Beta** | **P** |
| **Weight (kg)** | -0.30 | 2.8E-02 | 0.15 | 2.9E-01 | 0.18 | 1.8E-01 | 0.16 | 2.1E-01 | -0.24 | 4.9E-02 | -0.03 | 8.3E-01 |
| **BMI (kg/m$^2$)** | -0.09 | 6.9E-02 | 0.08 | 1.3E-01 | 0.07 | 1.7E-01 | -0.02 | 7.0E-01 | -0.07 | 1.5E-01 | -0.02 | 7.0E-01 |
| **WHR** | -0.001 | 2.4E-01 | 0.001 | 3.9E-01 | 0.000 | 8.8E-01 | 0.000 | 6.0E-01 | -0.001 | 3.0E-01 | 0.000 | 6.0E-01 |
| **Systolic BP (mmHg)** | 0.33 | 1.5E-01 | 0.04 | 8.8E-01 | 0.11 | 6.2E-01 | 0.19 | 3.8E-01 | -0.22 | 2.8E-01 | -0.01 | 9.7E-01 |
| **Diastolic BP (mmHg)** | 0.07 | 6.3E-01 | 0.16 | 2.8E-01 | 0.11 | 4.1E-01 | 0.00 | 9.8E-01 | -0.05 | 6.8E-01 | -0.08 | 5.6E-01 |
| **Insulin (% change)** | 4.71 | 1.0E-03 | 1.62 | 2.0E-01 | 1.16 | 3.7E-01 | 0.69 | 6.1E-01 | -0.69 | 4.6E-01 | 0.46 | 7.7E-01 |
| **Glucose (% change)** | 1.62 | 3.1E-04 | -1.37 | 3.0E-03 | 1.16 | 8.0E-03 | -0.46 | 2.7E-01 | -0.92 | 4.4E-02 | 2.33 | 1.0E-06 |
| **HOMA-S (% change)** | -4.50 | 5.0E-04 | -0.23 | 8.8E-01 | 41.25 | 6.6E-01 | -0.46 | 7.1E-01 | 1.62 | 1.9E-01 | -2.28 | 8.0E-02 |
| **HOMA-B (% change)** | 0.93 | 4.8E-01 | 3.28 | 2.0E-02 | -1.83 | 1.7E-01 | 1.86 | 1.4E-01 | 1.39 | 2.2E-01 | -4.50 | 1.0E-03 |
| **Cholesterol (mmol/L)** | 0.01 | 5.6E-01 | 0.00 | 7.8E-01 | 0.01 | 6.4E-01 | 0.00 | 7.8E-01 | -0.01 | 5.7E-01 | 0.00 | 8.6E-01 |
| **HDL cholesterol (% change)** | -0.56 | 3.8E-01 | 0.91 | 1.6E-01 | 1.09 | 8.5E-02 | -0.94 | 1.2E-01 | -0.80 | 1.7E-01 | -0.32 | 6.0E-01 |
| **Triglycerides (% change)** | 1.86 | 4.5E-02 | 2.09 | 2.0E-02 | 0.46 | 6.1E-01 | -0.92 | 2.9E-01 | -1.37 | 1.0E-01 | 0.69 | 3.6E-01 |

**Supplementary Table 7.** Association of sentinel SNPs with T2D in the replication samples, with no adjustment amongst for adiposity, with adjustment for BMI or with adjustment for waist-hip ratio. Results are presented as odds ratio [OR] (95% confidence interval) for T2D per copy of risk allele, with P value. All analyses are adjusted for age and gender. Associations were calculated in each replication sample separately, then combined by inverse variance meta-analysis.

| | | | | | **Unadjusted** | | **BMI adjusted** | | **WHR adjusted** | |
|---|---|---|---|---|---|---|---|---|---|---|
| **SNP** | **Chr** | **Position** | **Nearest gene** | **Risk allele** | **OR** | **P** | **OR** | **P** | **OR** | **P** |
| rs3923113 | 2 | 165210095 | *GRB14* | A | 1.07 (1.03-1.11) | 6.7E-04 | 1.09 (1.04-1.14) | 1.0E-04 | 1.05 (1.01-1.10) | 2.6E-02 |
| rs16861329 | 3 | 188149155 | *ST6GAL1* | G | 1.07 (1.03-1.11) | 1.6E-04 | 1.07 (1.02-1.11) | 3.4E-03 | 1.07 (1.03-1.12) | 1.7E-03 |
| rs1802295 | 10 | 70601480 | *VPS26A* | A | 1.06 (1.03-1.10) | 6.6E-04 | 1.07 (1.02-1.11) | 1.9E-03 | 1.06 (1.02-1.11) | 3.7E-03 |
| rs7178572 | 15 | 75534245 | *HMG20A* | G | 1.08 (1.05-1.12) | 7.0E-07 | 1.07 (1.02-1.11) | 1.4E-03 | 1.07 (1.03-1.11) | 1.1E-03 |
| rs2028299 | 15 | 88175261 | *AP3S2* | C | 1.09 (1.06-1.13) | 1.1E-07 | 1.09 (1.05-1.13) | 6.1E-06 | 1.09 (1.05-1.13) | 2.7E-05 |
| rs4812829 | 20 | 42422681 | *HNF4A* | A | 1.07 (1.04-1.11) | 2.8E-05 | 1.08 (1.03-1.12) | 2.1E-04 | 1.08 (1.04-1.12) | 2.0E-04 |

**Supplementary Table 8.** Results of sequencing 1MB either side of the sentinel SNPs at the 6 loci associated with T2D, in 109 South Asians. Results given as total number of SNPs, with number not already annotated in 1000G or HapMap3 datasets in parentheses.

| Sentinel SNP | Chr | Position | SNPs in region | nsSNPs in region | nsSNPs in LD ($r^2$>0.5) with sentinel SNP |
|---|---|---|---|---|---|
| rs3923113 | 2 | 165210095 | 6026 (2683) | 24 (15) | 0 |
| rs16861329 | 3 | 188149155 | 8614 (4131) | 81 (37) | 0 |
| rs1802295 | 10 | 70601480 | 9731 (4755) | 83 (34) | 0 |
| rs7178572 | 15 | 75534245 | 7760 (4235) | 31 (14) | 0 |
| rs2028299 | 15 | 88175261 | 9030 (4965) | 130 (66) | 0 |
| rs4812829 | 20 | 42422681 | 7984 (4133) | 105 (59) | 0 |

**Supplementary Table 9.** Expression Quantitative Trait Loci (eQTLs) for SNPs associated with type-2 diabetes amongst South Asians. Results are for all eQTLS associated with the GWA SNP, or a close proxy, at P<10-5 in available public and proprietary datasets (see methods). Results are also provided for the SNP most closely associated with eQTL in the experiment, to assess whether the GWA SNP is coincident with the peak eQTL SNP. LCL = lymphoblastoid cell lines

| | | | | | | | **GWA SNP** | | **Peak eQTL SNP** | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| **GWA SNP** | **Chr** | **Position** | **Nearest Gene** | **Source** | **Tissue** | **eQTL** | **Beta** | ***P*** | **ID** | **$r^2$ between SNPs** | ***P*** |
| rs3923113 | 2 | 165210095 | *GRB14* | Heid et al | Subcutaneous fat | *GRB14* | n/a | n/a | rs10195252 | 0.83 | $4.4x10^{-11}$ |
| rs3923113 | 2 | 165210095 | *GRB14* | Heid et al | Subcutaneous fat | *GRB14* | n/a | n/a | rs10184004 | 0.83 | $5.5x10^{-6}$ |
| rs3923113 | 2 | 165210095 | *GRB14* | Heid et al | Omental fat | *GRB14* | n/a | n/a | rs10195252 | 0.83 | $1.0x10^{-13}$ |
| rs7178572 | 15 | 75534245 | *HMG20A* | MuTHER | LCL | *PSTPIP1* | 0.060 | $8.8x10^{-6}$ | rs12908255 | <0.3 | $3.3x10^{-14}$ |
| rs2028299 | 15 | 88175261 | *AP3S2* | MuTHER | Fat | *C15orf38* | -0.143 | $9.0x10^{-27}$ | rs3803534 | 0.88 | $1.9x10^{-28}$ |
| rs2028299 | 15 | 88175261 | *AP3S2* | MuTHER | Skin | *C15orf38* | -0.135 | $8.0x10^{-17}$ | rs3803534 | 0.88 | $2.9x10^{-19}$ |

**Supplementary Table 10.** Tests for heterogeneity of effect ($P_{hetero}$) between the SAT2D GWA cohorts at the previously reported T2D loci, and at the loci identified in the present study. Statistical significance for heterogeneity was inferred at P<0.001 (allowing correction for multiple testing).

| | | | | | | **LOLIPOP 610** | | **LOLIPOP 317** | | **PROMIS** | | **SINDI** | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **SNP** | **Chr** | **Pos** | **Nearest gene** | **Ref** | **Alleles (A/R)** | **OR** | **P** | **OR** | **P** | **OR** | **P** | **OR** | **P** | **$P_{hetero}$** |
| **Reported loci** | | | | | | | | | | | | | | |
| rs10923931 | 1 | 120230001 | *NOTCH2* | DIAG | G/T | 0.97 (0.87-1.08) | 0.59 | 0.95 (0.78-1.15) | 0.58 | 1.03 (0.95-1.13) | 0.48 | 1.05 (0.91-1.22) | 0.51 | 0.78 |
| rs340874 | 1 | 210547651 | *PROX1* | Pub | T/C | 1.02 (0.94-1.10) | 0.67 | 1.12 (0.96-1.30) | 0.16 | 1.05 (0.98-1.12) | 0.17 | 0.91 (0.81-1.03) | 0.13 | 0.33 |
| rs780094 | 2 | 27652888 | *GCKR* | Pub | T/C | 1.15 (1.04-1.26) | 4E-03 | 1.48 (1.23-1.79) | 2.0E-05 | 1.02 (0.95-1.11) | 0.53 | 1.13 (0.98-1.32) | 0.10 | 6.0E-03 |
| rs11899863 | 2 | 43530470 | *THADA* | DIAG | T/C | NA | NA | NA | NA | 0.96 (0.80-1.15) | 0.66 | NA | NA | NA |
| rs243021 | 2 | 60496470 | *BCL11A* | DIAG | G/A | 1.09 (1.00-1.18) | 0.04 | 1.03 (0.88-1.19) | 0.74 | 1.00 (0.94-1.07) | 0.89 | 1.14 (1.01-1.29) | 0.04 | 0.41 |
| rs7593730 | 2 | 160996961 | *RBMS1* | Pub | T/C | 1.02 (0.92-1.13) | 0.69 | 1.15 (0.95-1.40) | 0.15 | 1.01 (0.93-1.09) | 0.85 | 0.93 (0.81-1.07) | 0.33 | 0.50 |
| rs7578326 | 2 | 226846158 | *IRS1* | DIAG | G/A | 1.11 (1.01-1.22) | 0.02 | 1.09 (0.91-1.29) | 0.36 | 1.07 (0.99-1.16) | 0.09 | 1.05 (0.89-1.22) | 0.57 | 0.93 |
| rs13081389 | 3 | 12264800 | *PPARG* | DIAG | G/A | 1.10 (0.94-1.29) | 0.23 | NA | NA | 1.06 (0.93-1.20) | 0.39 | NA | NA | 0.69 |
| rs6780569 | 3 | 23173488 | *UBE2E2* | Pub | A/G | 1.08 (0.99-1.19) | 0.10 | 1.09 (0.92-1.31) | 0.31 | 1.06 (0.99-1.15) | 0.11 | 1.05 (0.92-1.20) | 0.45 | 0.99 |
| rs6795735 | 3 | 64680405 | *ADAMTS9* | DIAG | T/C | 1.01 (0.92-1.10) | 0.89 | 1.10 (0.93-1.30) | 0.28 | 1.07 (0.99-1.15) | 0.09 | 1.16 (1.00-1.35) | 0.04 | 0.53 |
| rs11708067 | 3 | 124548468 | *ADCY5* | Pub | G/A | 1.13 (1.02-1.25) | 0.02 | 1.28 (1.05-1.56) | 0.01 | 1.07 (0.98-1.16) | 0.11 | 1.04 (0.88-1.22) | 0.67 | 0.40 |
| rs1470579 | 3 | 187011782 | *IGF2BP2* | DIAG | A/C | 1.13 (1.04-1.23) | 3E-03 | 1.09 (0.93-1.27) | 0.28 | 1.13 (1.06-1.21) | 3.1E-04 | 1.08 (0.95-1.22) | 0.23 | 0.93 |
| rs1801214 | 4 | 6421094 | *WFS1* | DIAG | C/T | 1.11 (1.02-1.22) | 0.02 | 0.94 (0.79-1.12) | 0.49 | 1.09 (1.01-1.17) | 0.03 | 1.05 (0.91-1.22) | 0.49 | 0.47 |
| rs4457053 | 5 | 76460705 | *ZBED3* | DIAG | A/G | 0.98 (0.88-1.08) | 0.63 | NA | NA | NA | NA | NA | NA | NA |
| rs10440833 | 6 | 20796100 | *CDKAL1* | DIAG | T/A | 1.02 (0.93-1.11) | 0.74 | 0.96 (0.81-1.15) | 0.69 | 1.13 (1.05-1.22) | 1.6E-03 | 1.14 (0.99-1.32) | 0.07 | 0.25 |
| rs2191349 | 7 | 14837549 | *DGKB* | Pub | G/T | 1.10 (1.01-1.19) | 0.03 | 1.08 (0.93-1.27) | 0.31 | 1.01 (0.95-1.09) | 0.70 | 1.08 (0.95-1.22) | 0.26 | 0.64 |
| rs849134 | 7 | 27969462 | *JAZF1* | DIAG | G/A | 1.11 (1.01-1.21) | 0.02 | 1.15 (0.97-1.36) | 0.12 | 1.02 (0.94-1.09) | 0.68 | 1.09 (0.94-1.25) | 0.26 | 0.48 |
| rs4607517 | 7 | 44008908 | *GCK* | Pub | G/A | 1.14 (1.01-1.29) | 0.04 | 0.98 (0.77-1.24) | 0.84 | 0.95 (0.86-1.05) | 0.29 | 1.01 (0.84-1.21) | 0.95 | 0.25 |
| rs972283 | 7 | 129924109 | *KLF14* | DIAG | A/G | 1.04 (0.95-1.13) | 0.38 | 0.96 (0.81-1.12) | 0.58 | 0.94 (0.88-1.01) | 0.09 | 1.01 (0.89-1.15) | 0.84 | 0.47 |
| rs896854 | 8 | 96029687 | *TP53INP1* | DIAG | C/T | 1.08 (0.99-1.17) | 0.07 | 1.08 (0.93-1.25) | 0.33 | 1.09 (1.02-1.17) | 0.01 | 1.02 (0.90-1.16) | 0.75 | 0.91 |
| rs3802177 | 8 | 118254206 | *SLC30A8* | DIAG | A/G | 1.11 (1.01-1.22) | 0.03 | 1.13 (0.95-1.35) | 0.17 | 1.15 (1.06-1.24) | 7.4E-04 | 1.07 (0.93-1.24) | 0.35 | 0.92 |
| rs17584499 | 9 | 8869118 | *PTPRD* | Pub | C/T | 1.01 (0.92-1.11) | 0.86 | 1.19 (0.85-1.67) | 0.31 | 0.97 (0.90-1.05) | 0.43 | 0.95 (0.83-1.09) | 0.48 | 0.37 |
| rs10965250 | 9 | 22123284 | *CDKN2A/B* | DIAG | A/G | 1.11 (0.98-1.26) | 0.09 | NA | NA | 1.26 (1.14-1.40) | 1.7E-05 | NA | NA | 0.13 |
| rs13292136 | 9 | 79181682 | *CHCD9* | DIAG | T/C | 1.08 (0.96-1.22) | 0.19 | 1.09 (0.88-1.36) | 0.43 | 1.13 (1.03-1.25) | 0.01 | 1.04 (0.87-1.24) | 0.68 | 0.90 |
| rs12779790 | 10 | 12368016 | *CDC123* | DIAG | A/G | 1.12 (1.00-1.25) | 0.04 | 1.23 (0.99-1.52) | 0.07 | 1.10 (1.00-1.21) | 0.06 | 1.14 (0.96-1.35) | 0.14 | 0.87 |
| rs5015480 | 10 | 94455539 | *HHEX* | DIAG | T/C | 1.11 (1.03-1.21) | 0.01 | 0.97 (0.83-1.13) | 0.68 | 1.04 (0.97-1.11) | 0.27 | 1.20 (1.06-1.35) | 4.6E-03 | 0.20 |
| rs7903146 | 10 | 114748339 | *TCF7L2* | DIAG | C/T | 1.22 (1.12-1.33) | 1E-05 | 1.51 (1.29-1.76) | 2.9E-07 | 1.25 (1.16-1.34) | 1.5E-09 | 1.21 (1.06-1.39) | 3.9E-03 | 0.17 |
| rs2334499 | 11 | 1653425 | *DUSP8* | Pub | C/T | 1.03 (0.94-1.13) | 0.54 | 1.04 (0.89-1.23) | 0.60 | 1.06 (0.98-1.14) | 0.12 | 0.87 (0.76-0.99) | 0.04 | 0.27 |
| rs231362 | 11 | 2648047 | *KCNQ1* | DIAG | A/G | 1.10 (1.00-1.20) | 0.06 | 1.23 (0.97-1.56) | 0.09 | 1.08 (1.00-1.17) | 0.05 | 1.04 (0.90-1.19) | 0.62 | 0.66 |
| rs163184 | 11 | 2803645 | *KCNQ1* | DIAG | T/G | 1.11 (1.02-1.20) | 0.01 | 1.03 (0.89-1.20) | 0.70 | 1.06 (1.00-1.14) | 0.07 | 1.11 (0.98-1.25) | 0.09 | 0.81 |
| rs5215 | 11 | 17365206 | *KCNJ11* | DIAG | T/C | 1.11 (1.02-1.21) | 0.01 | 0.98 (0.84-1.15) | 0.83 | 1.00 (0.93-1.07) | 0.97 | 1.02 (0.90-1.16) | 0.73 | 0.35 |
| rs1552224 | 11 | 72110746 | *CENTD2* | DIAG | C/A | 1.14 (1.02-1.26) | 0.02 | 1.09 (0.89-1.33) | 0.40 | 0.99 (0.91-1.08) | 0.80 | 0.97 (0.83-1.14) | 0.71 | 0.32 |
| rs1387153 | 11 | 92313476 | *MTNR1B* | DIAG | C/T | 1.09 (1.00-1.18) | 0.05 | 1.08 (0.92-1.26) | 0.35 | 1.07 (1.00-1.14) | 0.07 | 1.01 (0.89-1.14) | 0.93 | 0.88 |
| rs1531343 | 12 | 64461161 | *HMGA2* | DIAG | G/C | 1.03 (0.93-1.14) | 0.60 | 1.22 (1.00-1.48) | 0.05 | 1.08 (0.99-1.17) | 0.10 | 1.05 (0.89-1.22) | 0.58 | 0.57 |

| | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| rs4760790 | 12 | 69921061 | *TSPAN8* | DIAG | G/A | 1.04 (0.96-1.13) | 0.36 | 0.92 (0.78-1.08) | 0.32 | 1.13 (1.06-1.22) | 5.2E-04 | 0.98 (0.87-1.11) | 0.76 | 0.10 |
| rs7957197 | 12 | 119923406 | *HNF1A* | DIAG | A/T | NA | NA | NA | NA | 1.14 (0.98-1.34) | 0.10 | NA | NA | NA |
| rs7172432 | 15 | 60183681 | *C2CD4A/B* | Pub | G/A | 1.08 (1.00-1.18) | 0.06 | 1.00 (0.86-1.16) | 0.98 | 1.06 (0.99-1.13) | 0.10 | 1.01 (0.89-1.14) | 0.89 | 0.79 |
| rs11634397 | 15 | 78219277 | *ZFAND6* | DIAG | A/G | 1.07 (0.98-1.17) | 0.12 | NA | NA | 1.04 (0.97-1.12) | 0.27 | NA | NA | 0.64 |
| rs8042680 | 15 | 89322341 | *PRC1* | DIAG | C/A | 1.05 (0.97-1.14) | 0.21 | 1.04 (0.89-1.21) | 0.65 | 1.08 (1.00-1.15) | 0.04 | 1.00 (0.87-1.16) | 0.99 | 0.89 |
| rs11642841 | 16 | 52402988 | *FTO* | DIAG | C/A | 0.95 (0.86-1.05) | 0.31 | 1.07 (0.88-1.30) | 0.49 | 1.17 (1.08-1.27) | 8.1E-05 | 1.05 (0.91-1.22) | 0.49 | 0.04 |
| rs391300 | 17 | 2163008 | *SRR* | Pub | T/C | 0.93 (0.86-1.01) | 0.09 | 1.01 (0.86-1.17) | 0.94 | 1.02 (0.95-1.09) | 0.57 | 1.00 (0.89-1.13) | 0.97 | 0.54 |
| rs4430796 | 17 | 33172153 | *HNF1B* | DIAG | A/G | 1.14 (1.05-1.24) | 2E-03 | 1.15 (0.95-1.37) | 0.14 | 1.07 (1.00-1.15) | 0.05 | 0.93 (0.81-1.06) | 0.26 | 0.20 |
| **SAT2D loci** | | | | | | | | | | | | | | |
| rs17031236 | 2 | 105538433 | *FHL2* | *SAT2D* | C/A | 1.10 (1.01-1.20) | 0.03 | 1.21 (1.03-1.43) | 0.02 | 1.09 (1.02-1.17) | 0.02 | 1.06 (0.93-1.20) | 0.40 | 0.68 |
| rs3923113 | 2 | 165210095 | *GRB14* | *SAT2D* | C/A | 1.18 (1.07-1.29) | 5E-04 | 1.24 (1.02-1.50) | 0.03 | 1.11 (1.03-1.20) | 0.01 | 1.16 (1.00-1.35) | 0.06 | 0.72 |
| rs11711167 | 3 | 126521709 | *ZNF148* | *SAT2D* | A/G | 1.11 (1.02-1.21) | 0.02 | 1.20 (1.03-1.41) | 0.02 | 1.10 (1.02-1.18) | 0.01 | 1.01 (0.89-1.15) | 0.84 | 0.58 |
| rs16861329 | 3 | 188149155 | *ST6GAL1* | *SAT2D* | A/G | 1.15 (1.05-1.27) | 4E-03 | 1.24 (1.03-1.49) | 0.02 | 1.11 (1.03-1.20) | 0.01 | 1.06 (0.92-1.22) | 0.44 | 0.65 |
| rs6835176 | 4 | 40199309 | *RBM47* | *SAT2D* | G/A | 1.44 (1.17-1.76) | 6E-04 | 1.44 (0.99-2.09) | 0.07 | 1.14 (0.97-1.35) | 0.12 | 1.25 (0.92-1.68) | 0.15 | 0.46 |
| rs9496773 | 6 | 144183238 | *PHACTR2* | *SAT2D* | G/A | 1.12 (1.03-1.22) | 0.01 | 0.95 (0.80-1.13) | 0.56 | 1.09 (1.02-1.17) | 0.01 | 1.19 (1.05-1.34) | 0.01 | 0.29 |
| rs2111815 | 7 | 132349786 | *CHCHD3* | *SAT2D* | G/A | 1.15 (1.06-1.24) | 9E-04 | 1.06 (0.91-1.24) | 0.45 | 1.07 (1.00-1.15) | 0.05 | 1.08 (0.95-1.22) | 0.23 | 0.70 |
| rs16923500 | 8 | 59551647 | *CYP7A1* | *SAT2D* | G/A | 1.15 (1.05-1.26) | 4E-03 | 1.02 (0.84-1.24) | 0.85 | 1.12 (1.04-1.21) | 3.0E-03 | 1.05 (0.91-1.21) | 0.53 | 0.66 |
| rs1562042 | 9 | 105747435 | *SMC2* | *SAT2D* | A/G | 1.13 (1.02-1.25) | 0.01 | 0.99 (0.82-1.20) | 0.92 | 1.15 (1.06-1.25) | 5.9E-04 | 1.04 (0.90-1.19) | 0.62 | 0.48 |
| rs1802295 | 10 | 70601480 | *VPS26A* | *SAT2D* | G/A | 1.17 (1.07-1.28) | 6E-04 | NA | NA | 1.09 (1.01-1.17) | 0.03 | 1.20 (1.04-1.39) | 0.01 | 0.50 |
| rs2616646 | 10 | 78559423 | *KCNMA1* | *SAT2D* | A/G | 1.13 (1.01-1.26) | 0.03 | 1.17 (0.95-1.43) | 0.14 | 1.16 (1.06-1.28) | 2.1E-03 | 1.18 (0.99-1.40) | 0.07 | 0.98 |
| rs4287347 | 11 | 132191217 | *OPCML* | *SAT2D* | A/G | 1.10 (1.01-1.19) | 0.02 | 1.06 (0.91-1.23) | 0.47 | 1.13 (1.06-1.21) | 4.0E-04 | 1.00 (0.89-1.13) | 0.94 | 0.59 |
| rs6576426 | 15 | 23254656 | *UBE3A* | *SAT2D* | A/G | 1.15 (1.03-1.28) | 0.01 | 1.14 (0.93-1.41) | 0.21 | 1.18 (1.08-1.29) | 1.7E-04 | 1.11 (0.95-1.31) | 0.19 | 0.95 |
| rs620739 | 15 | 47852704 | *ATP8B4* | *SAT2D* | A/G | 1.13 (1.04-1.23) | 2E-03 | 1.03 (0.88-1.20) | 0.76 | 1.10 (1.03-1.18) | 4.8E-03 | 1.15 (1.00-1.31) | 0.04 | 0.74 |
| rs7178572 | 15 | 75534245 | *HMG20A* | *SAT2D* | A/G | 1.06 (0.98-1.15) | 0.15 | 1.17 (1.00-1.36) | 0.05 | 1.10 (1.03-1.18) | 0.01 | 1.17 (1.03-1.32) | 0.01 | 0.64 |
| rs2028299 | 15 | 88175261 | *AP3S2* | *SAT2D* | A/C | 1.11 (1.01-1.20) | 0.02 | 0.96 (0.82-1.13) | 0.63 | 1.10 (1.02-1.18) | 0.01 | 1.24 (1.09-1.41) | 1.0E-03 | 0.24 |
| rs4392054 | 16 | 20630271 | *ACSM1* | *SAT2D* | G/A | 1.17 (1.04-1.32) | 0.01 | NA | NA | 1.18 (1.06-1.31) | 1.8E-03 | 1.17 (0.98-1.40) | 0.09 | 1.00 |
| rs17052370 | 17 | 21660480 | *UBBP4* | *SAT2D* | G/A | 1.07 (0.98-1.17) | 0.13 | 1.10 (0.91-1.33) | 0.33 | 1.08 (1.01-1.17) | 0.03 | 1.13 (0.99-1.29) | 0.07 | 0.95 |
| rs1912379 | 18 | 66460710 | *RPS2P6* | *SAT2D* | A/G | 1.15 (1.04-1.26) | 4E-03 | 0.97 (0.82-1.16) | 0.75 | 1.15 (1.06-1.24) | 5.3E-04 | 1.11 (0.96-1.28) | 0.16 | 0.44 |
| rs4812829 | 20 | 42422681 | *HNF4A* | *SAT2D* | G/A | 1.21 (1.11-1.32) | 3E-05 | 1.19 (1.01-1.40) | 0.04 | 1.04 (0.96-1.12) | 0.33 | 1.28 (1.12-1.46) | 1.9E-04 | 0.05 |

**Supplementary Table 11.** Tests for heterogeneity of effect ($P_{hetero}$) between male and female participants in the SAT2D GWA cohorts at the previously reported T2D loci, and at the loci identified in the present study. Statistical significance for heterogeneity was inferred at P<0.001 (allowing correction for multiple testing).

| | | | | | | Male | | Female | | |
|---|---|---|---|---|---|---|---|---|---|---|
| **SNP** | **Chr** | **Pos** | **Nearest gene** | **Reference** | **Alleles (A/R)** | **OR** | **P** | **OR** | **P** | **$P_{hetero}$** |
| Reported loci | | | | | | | | | | |
| rs10923931 | 1 | 120230001 | *NOTCH2* | DIAGRAM | G/T | 0.99 (0.93-1.06) | 0.79 | 1.06 (0.94-1.21) | 0.33 | 0.32 |
| rs340874 | 1 | 210547651 | *PROX1* | Published | T/C | 1.03 (0.98-1.09) | 0.21 | 0.99 (0.90-1.09) | 0.87 | 0.46 |
| rs780094 | 2 | 27652888 | *GCKR* | Published | T/C | 1.18 (1.08-1.28) | 1.5E-04 | 1.25 (1.07-1.47) | 0.01 | 0.49 |
| rs11899863 | 2 | 43530470 | *THADA* | DIAGRAM | T/C | 0.98 (0.80-1.21) | 0.86 | 0.87 (0.59-1.28) | 0.49 | 0.59 |
| rs243021 | 2 | 60496470 | *BCL11A* | DIAGRAM | G/A | 1.06 (1.01-1.12) | 0.02 | 1.00 (0.91-1.11) | 0.93 | 0.30 |
| rs7593730 | 2 | 160996961 | *RBMS1* | Published | T/C | 1.01 (0.95-1.08) | 0.70 | 0.99 (0.88-1.12) | 0.92 | 0.78 |
| rs7578326 | 2 | 226846158 | *IRS1* | DIAGRAM | G/A | 1.08 (1.02-1.15) | 0.01 | 1.10 (0.97-1.23) | 0.14 | 0.84 |
| rs13081389 | 3 | 12264800 | *PPARG* | DIAGRAM | G/A | 1.04 (0.93-1.16) | 0.49 | 1.24 (0.98-1.57) | 0.07 | 0.19 |
| rs6780569 | 3 | 23173488 | *UBE2E2* | Published | A/G | 1.10 (1.04-1.17) | 1.6E-03 | 0.98 (0.88-1.10) | 0.76 | 0.08 |
| rs6795735 | 3 | 64680405 | *ADAMTS9* | DIAGRAM | T/C | 1.05 (0.99-1.11) | 0.12 | 1.12 (1.00-1.25) | 0.05 | 0.32 |
| rs11708067 | 3 | 124548468 | *ADCY5* | Published | G/A | 1.11 (1.04-1.19) | 1.5E-03 | 1.06 (0.94-1.20) | 0.36 | 0.52 |
| rs1470579 | 3 | 187011782 | *IGF2BP2* | DIAGRAM | A/C | 1.16 (1.10-1.22) | 5.1E-08 | 0.99 (0.90-1.10) | 0.87 | 7.1E-03 |
| rs1801214 | 4 | 6421094 | *WFS1* | DIAGRAM | C/T | 1.11 (1.04-1.17) | 8.9E-04 | 0.97 (0.87-1.09) | 0.60 | 0.05 |
| rs4457053 | 5 | 76460705 | *ZBED3* | DIAGRAM | A/G | 1.00 (0.90-1.12) | 0.96 | 0.83 (0.64-1.08) | 0.16 | 0.19 |
| rs10440833 | 6 | 20796100 | *CDKAL1* | DIAGRAM | T/A | 1.07 (1.01-1.14) | 0.03 | 1.12 (1.00-1.25) | 0.05 | 0.50 |
| rs2191349 | 7 | 14837549 | *DGKB* | Published | G/T | 1.06 (1.00-1.12) | 0.05 | 1.04 (0.94-1.16) | 0.43 | 0.82 |
| rs849134 | 7 | 27969462 | *JAZF1* | DIAGRAM | G/A | 1.07 (1.01-1.14) | 0.02 | 1.02 (0.91-1.14) | 0.74 | 0.42 |
| rs4607517 | 7 | 44008908 | *GCK* | Published | G/A | 0.98 (0.91-1.06) | 0.59 | 1.14 (0.99-1.32) | 0.07 | 0.07 |
| rs972283 | 7 | 129924109 | *KLF14* | DIAGRAM | A/G | 0.97 (0.92-1.03) | 0.36 | 1.01 (0.91-1.12) | 0.89 | 0.58 |
| rs896854 | 8 | 96029687 | *TP53INP1* | DIAGRAM | C/T | 1.09 (1.03-1.15) | 1.4E-03 | 1.04 (0.94-1.14) | 0.49 | 0.38 |
| rs3802177 | 8 | 118254206 | *SLC30A8* | DIAGRAM | A/G | 1.13 (1.06-1.20) | 8.9E-05 | 1.11 (0.99-1.25) | 0.09 | 0.78 |
| rs17584499 | 9 | 8869118 | *PTPRD* | Published | C/T | 1.00 (0.94-1.07) | 0.93 | 0.92 (0.83-1.03) | 0.15 | 0.20 |
| rs10965250 | 9 | 22123284 | *CDKN2A/B* | DIAGRAM | A/G | 1.19 (1.08-1.30) | 2.6E-04 | 1.24 (1.03-1.51) | 0.03 | 0.65 |
| rs13292136 | 9 | 79181682 | *CHCD9* | DIAGRAM | T/C | 1.09 (1.02-1.18) | 0.02 | 1.11 (0.96-1.28) | 0.17 | 0.88 |
| rs12779790 | 10 | 12368016 | *CDC123* | DIAGRAM | A/G | 1.16 (1.08-1.25) | 1.1E-04 | 1.01 (0.87-1.16) | 0.93 | 0.08 |
| rs5015480 | 10 | 94455539 | *HHEX* | DIAGRAM | T/C | 1.05 (0.99-1.10) | 0.09 | 1.19 (1.08-1.31) | 6.4E-04 | 0.03 |
| rs7903146 | 10 | 114748339 | *TCF7L2* | DIAGRAM | C/T | 1.30 (1.23-1.38) | 1.2E-20 | 1.09 (0.98-1.22) | 0.10 | 4.5E-03 |
| rs2334499 | 11 | 1653425 | *DUSP8* | Published | C/T | 1.04 (0.98-1.10) | 0.22 | 0.97 (0.87-1.08) | 0.57 | 0.28 |
| rs231362 | 11 | 2648047 | *KCNQ1* | DIAGRAM | A/G | 1.08 (1.01-1.15) | 0.02 | 1.12 (1.00-1.26) | 0.06 | 0.58 |
| rs163184 | 11 | 2803645 | *KCNQ1* | DIAGRAM | T/G | 1.06 (1.00-1.11) | 0.04 | 1.17 (1.06-1.29) | 2.1E-03 | 0.08 |
| rs5215 | 11 | 17365206 | *KCNJ11* | DIAGRAM | T/C | 1.05 (1.00-1.11) | 0.07 | 1.00 (0.90-1.10) | 0.97 | 0.37 |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| rs1552224 | 11 | 72110746 | *CENTD2* | DIAGRAM | C/A | 1.03 (0.96-1.11) | 0.35 | 1.06 (0.93-1.21) | 0.37 | 0.73 |
| rs1387153 | 11 | 92313476 | *MTNR1B* | DIAGRAM | C/T | 1.08 (1.02-1.14) | 4.6E-03 | 1.02 (0.92-1.12) | 0.76 | 0.29 |
| rs1531343 | 12 | 64461161 | *HMGA2* | DIAGRAM | G/C | 1.07 (1.00-1.14) | 0.05 | 1.06 (0.94-1.21) | 0.35 | 0.97 |
| rs4760790 | 12 | 69921061 | *TSPAN8* | DIAGRAM | G/A | 1.05 (0.99-1.11) | 0.08 | 1.10 (0.99-1.22) | 0.07 | 0.45 |
| rs7957197 | 12 | 119923406 | *HNF1A* | DIAGRAM | A/T | 1.11 (0.93-1.33) | 0.26 | 1.24 (0.88-1.76) | 0.22 | 0.57 |
| rs7172432 | 15 | 60183681 | *C2CD4A/B* | Published | G/A | 1.06 (1.01-1.12) | 0.03 | 1.03 (0.94-1.14) | 0.51 | 0.66 |
| rs11634397 | 15 | 78219277 | *ZFAND6* | DIAGRAM | A/G | 1.04 (0.98-1.11) | 0.22 | 1.11 (0.98-1.27) | 0.11 | 0.37 |
| rs8042680 | 15 | 89322341 | *PRC1* | DIAGRAM | C/A | 1.06 (1.00-1.11) | 0.05 | 1.06 (0.95-1.17) | 0.31 | 1.00 |
| rs11642841 | 16 | 52402988 | *FTO* | DIAGRAM | C/A | 1.05 (0.99-1.12) | 0.09 | 1.15 (1.02-1.29) | 0.02 | 0.22 |
| rs391300 | 17 | 2163008 | *SRR* | Published | T/C | 0.99 (0.94-1.04) | 0.68 | 0.98 (0.89-1.08) | 0.73 | 0.91 |
| rs4430796 | 17 | 33172153 | *HNF1B* | DIAGRAM | A/G | 1.09 (1.03-1.15) | 2.8E-03 | 1.03 (0.93-1.14) | 0.60 | 0.35 |
| | | | | | | | | | | |
| **SAT2D loci** | | | | | | | | | | |
| rs17031236 | 2 | 105538433 | *FHL2* | *SAT2D* | C/A | 1.11 (1.05-1.18) | 1.4E-04 | 1.04 (0.94-1.16) | 0.43 | 0.27 |
| rs3923113 | 2 | 165210095 | *GRB14* | *SAT2D* | C/A | 1.17 (1.10-1.24) | 9.3E-07 | 1.08 (0.96-1.22) | 0.19 | 0.27 |
| rs11711167 | 3 | 126521709 | *ZNF148* | *SAT2D* | A/G | 1.11 (1.05-1.17) | 2.0E-04 | 1.05 (0.95-1.17) | 0.34 | 0.37 |
| rs16861329 | 3 | 188149155 | *ST6GAL1* | *SAT2D* | A/G | 1.14 (1.07-1.21) | 5.1E-05 | 1.10 (0.97-1.23) | 0.13 | 0.59 |
| rs6835176 | 4 | 40199309 | *RBM47* | *SAT2D* | G/A | 1.29 (1.13-1.47) | 1.4E-04 | 1.21 (0.94-1.56) | 0.15 | 0.65 |
| rs9496773 | 6 | 144183238 | *PHACTR2* | *SAT2D* | G/A | 1.09 (1.03-1.15) | 2.9E-03 | 1.15 (1.04-1.28) | 0.01 | 0.32 |
| rs2111815 | 7 | 132349786 | *CHCHD3* | *SAT2D* | G/A | 1.08 (1.02-1.13) | 0.01 | 1.17 (1.06-1.29) | 1.8E-03 | 0.14 |
| rs16923500 | 8 | 59551647 | *CYP7A1* | *SAT2D* | G/A | 1.12 (1.05-1.18) | 3.8E-04 | 1.10 (0.98-1.23) | 0.10 | 0.83 |
| rs1562042 | 9 | 105747435 | *SMC2* | *SAT2D* | A/G | 1.12 (1.05-1.19) | 5.3E-04 | 1.09 (0.97-1.23) | 0.13 | 0.75 |
| rs1802295 | 10 | 70601480 | *VPS26A* | *SAT2D* | G/A | 1.14 (1.07-1.21) | 3.3E-05 | 1.11 (0.99-1.24) | 0.07 | 0.69 |
| rs2616646 | 10 | 78559423 | *KCNMA1* | *SAT2D* | A/G | 1.18 (1.10-1.27) | 6.5E-06 | 1.05 (0.91-1.21) | 0.49 | 0.15 |
| rs4287347 | 11 | 132191217 | *OPCML* | *SAT2D* | A/G | 1.09 (1.04-1.15) | 8.7E-04 | 1.10 (1.00-1.21) | 0.06 | 0.93 |
| rs6576426 | 15 | 23254656 | *UBE3A* | *SAT2D* | A/G | 1.17 (1.09-1.25) | 9.4E-06 | 1.13 (0.99-1.29) | 0.07 | 0.66 |
| rs620739 | 15 | 47852704 | *ATP8B4* | *SAT2D* | A/G | 1.13 (1.07-1.19) | 8.0E-06 | 1.05 (0.94-1.16) | 0.40 | 0.18 |
| rs7178572 | 15 | 75534245 | *HMG20A* | *SAT2D* | A/G | 1.08 (1.03-1.14) | 3.1E-03 | 1.18 (1.07-1.30) | 1.0E-03 | 0.13 |
| rs2028299 | 15 | 88175261 | *AP3S2* | *SAT2D* | A/C | 1.11 (1.05-1.17) | 3.2E-04 | 1.11 (1.00-1.24) | 0.05 | 0.92 |
| rs4392054 | 16 | 20630271 | *ACSM1* | *SAT2D* | G/A | 1.16 (1.07-1.26) | 5.2E-04 | 1.23 (1.06-1.42) | 0.01 | 0.53 |
| rs17052370 | 17 | 21660480 | *UBBP4* | *SAT2D* | G/A | 1.02 (0.97-1.08) | 0.43 | 1.36 (1.22-1.52) | 3.2E-08 | 6.1E-06 |
| rs1912379 | 18 | 66460710 | *RPS2P6* | *SAT2D* | A/G | 1.13 (1.06-1.20) | 8.7E-05 | 1.11 (0.99-1.25) | 0.07 | 0.85 |
| rs4812829 | 20 | 42422681 | *HNF4A* | *SAT2D* | G/A | 1.12 (1.06-1.19) | 7.3E-05 | 1.17 (1.05-1.31) | 3.5E-03 | 0.46 |

**Supplementary Table 12**. Association of SNPs reported to be associated with T2D in other populations, with T2D amongst South Asians in the GWA phase of the present study, and Europeans from the GWA phase of DIAGRAM+. N: effective sample size. RAF: risk allele frequency: SA = South Asians, EW = Europeans. Dir: +=concordant SAT2D and DIAGRAM+, -1=discordant SAT2D and DIAGRAM+. $P_{hetero}$ is for comparison of effect size between SA and EW.

| SNP | Chr | Pos | Nearest gene | Source | Alleles | | N | | RAF | | Europeans | | SAT2D | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | Alt | Risk | EW | SA | EW | SA | OR | P | OR | P | Dir | $P_{hetero}$ |
| rs10923931 | 1 | 120230001 | *NOTCH2* | DIAGRAM | G | T | 22570 | 19796 | 0.12 | 0.18 | 1.14 (1.07-1.21) | 6.5E-05 | 1.01 (0.95-1.07) | 8.3E-01 | + | 5.5E-03 |
| rs340874 | 1 | 210547651 | *PROX1* | Published | T | C | 22570 | 19802 | 0.51 | 0.55 | 1.07 (1.02-1.11) | 2.0E-03 | 1.02 (0.98-1.07) | 3.1E-01 | + | 2.0E-01 |
| rs780094 | 2 | 27652888 | *GCKR* | Published | T | C | 22570 | 10816 | 0.62 | 0.74 | 1.01 (0.97-1.05) | 6.0E-01 | 1.19 (1.11-1.29) | 4.1E-06 | + | 1.2E-04 |
| rs11899863 | 2 | 43530470 | *THADA* | DIAGRAM | T | C | 22570 | 8987 | 0.93 | 0.96 | 1.17 (1.09-1.25) | 1.0E-05 | 0.96 (0.80-1.15) | 6.3E-01 | - | 4.4E-02 |
| rs243021 | 2 | 60496470 | *BCL11A* | DIAGRAM | G | A | 22570 | 19803 | 0.46 | 0.51 | 1.09 (1.05-1.14) | 8.1E-06 | 1.05 (1.00-1.10) | 3.6E-02 | + | 1.9E-01 |
| rs7593730 | 2 | 160996961 | *RBMS1* | Published | T | C | 22570 | 19799 | 0.80 | 0.80 | 1.07 (1.02-1.13) | 6.5E-03 | 1.01 (0.95-1.07) | 7.8E-01 | + | 1.1E-01 |
| rs7578326 | 2 | 226846158 | *IRS1* | DIAGRAM | G | A | 22570 | 19803 | 0.64 | 0.77 | 1.12 (1.07-1.17) | 8.7E-07 | 1.08 (1.03-1.14) | 4.4E-03 | + | 4.2E-01 |
| rs13081389 | 3 | 12264800 | *PPARG* | DIAGRAM | G | A | 22570 | 15543 | 0.96 | 0.93 | 1.24 (1.14-1.35) | 2.0E-07 | 1.07 (0.97-1.19) | 1.7E-01 | + | 2.8E-02 |
| rs6780569 | 3 | 23173488 | *UBE2E2* | Published | A | G | 22570 | 19796 | 0.95 | 0.74 | 1.11 (1.04-1.18) | 1.5E-03 | 1.07 (1.02-1.13) | 8.9E-03 | + | 4.4E-01 |
| rs6795735 | 3 | 64680405 | *ADAMTS9* | DIAGRAM | T | C | 22570 | 19798 | 0.54 | 0.28 | 1.09 (1.04-1.13) | 8.4E-05 | 1.06 (1.01-1.12) | 2.4E-02 | + | 5.1E-01 |
| rs11708067 | 3 | 124548468 | *ADCY5* | Published | G | A | 22570 | 19668 | 0.78 | 0.78 | 1.10 (1.05-1.16) | 1.7E-04 | 1.10 (1.04-1.17) | 1.4E-03 | + | 9.8E-01 |
| rs1470579 | 3 | 187011782 | *IGF2BP2* | DIAGRAM | A | C | 22570 | 19802 | 0.29 | 0.42 | 1.14 (1.09-1.19) | 2.2E-09 | 1.12 (1.07-1.17) | 2.5E-06 | + | 5.8E-01 |
| rs1801214 | 4 | 6421094 | *WFS1* | DIAGRAM | C | T | 22570 | 19639 | 0.73 | 0.68 | 1.13 (1.08-1.18) | 3.2E-08 | 1.08 (1.02-1.13) | 7.2E-03 | + | 1.6E-01 |
| rs4457053 | 5 | 76460705 | *ZBED3* | DIAGRAM | A | G | 20049 | 6556 | 0.26 | 0.22 | 1.16 (1.10-1.23) | 4.2E-08 | 0.97 (0.88-1.08) | 6.3E-01 | - | 3.0E-03 |
| rs10440833 | 6 | 20796100 | *CDKAL1* | DIAGRAM | T | A | 22570 | 19748 | 0.25 | 0.26 | 1.25 (1.20-1.31) | 1.8E-22 | 1.08 (1.02-1.14) | 4.9E-03 | + | 2.8E-05 |
| rs2191349 | 7 | 14837549 | *DGKB* | Published | G | T | 22570 | 19719 | 0.47 | 0.62 | 1.07 (1.03-1.11) | 1.2E-03 | 1.05 (1.00-1.11) | 3.5E-02 | + | 6.7E-01 |
| rs849134 | 7 | 27969462 | *JAZF1* | DIAGRAM | G | A | 22570 | 19729 | 0.53 | 0.69 | 1.13 (1.08-1.17) | 2.8E-09 | 1.06 (1.01-1.12) | 2.3E-02 | + | 6.5E-02 |
| rs4607517 | 7 | 44008908 | *GCK* | Published | G | A | 22570 | 19803 | 0.20 | 0.13 | 1.03 (0.97-1.09) | 3.1E-01 | 1.01 (0.95-1.08) | 7.1E-01 | + | 7.3E-01 |
| rs972283 | 7 | 129924109 | *KLF14* | DIAGRAM | A | G | 22570 | 19629 | 0.55 | 0.61 | 1.10 (1.06-1.15) | 1.8E-06 | 0.98 (0.94-1.03) | 4.6E-01 | - | 2.7E-04 |
| rs896854 | 8 | 96029687 | *TP53INP1* | DIAGRAM | C | T | 22570 | 19801 | 0.48 | 0.41 | 1.10 (1.06-1.15) | 1.2E-06 | 1.08 (1.03-1.13) | 1.8E-03 | + | 4.5E-01 |
| rs3802177 | 8 | 118254206 | *SLC30A8* | DIAGRAM | A | G | 21198 | 19785 | 0.75 | 0.76 | 1.15 (1.10-1.21) | 1.5E-08 | 1.13 (1.07-1.19) | 2.4E-05 | + | 5.7E-01 |
| rs17584499 | 9 | 8869118 | *PTPRD* | Published | C | T | 18352 | 19800 | 0.25 | 0.25 | 1.03 (0.96-1.10) | 3.8E-01 | 0.98 (0.93-1.04) | 5.5E-01 | - | 2.8E-01 |
| rs10965250 | 9 | 22123284 | *CDKN2A/B* | DIAGRAM | A | G | 22570 | 15543 | 0.81 | 0.87 | 1.20 (1.13-1.27) | 1.2E-10 | 1.20 (1.10-1.30) | 2.6E-05 | + | 9.6E-01 |
| rs13292136 | 9 | 79181682 | *CHCD9* | DIAGRAM | T | C | 22570 | 19796 | 0.93 | 0.86 | 1.20 (1.11-1.29) | 1.5E-06 | 1.10 (1.03-1.17) | 7.5E-03 | + | 8.0E-02 |
| rs12779790 | 10 | 12368016 | *CDC123* | DIAGRAM | A | G | 22570 | 19536 | 0.23 | 0.17 | 1.09 (1.04-1.15) | 6.8E-04 | 1.12 (1.05-1.20) | 5.9E-04 | + | 4.9E-01 |
| rs5015480 | 10 | 94455539 | *HHEX* | DIAGRAM | T | C | 22570 | 19801 | 0.57 | 0.45 | 1.18 (1.13-1.23) | 1.3E-15 | 1.08 (1.03-1.13) | 2.1E-03 | + | 3.3E-03 |
| rs7903146 | 10 | 114748339 | *TCF7L2* | DIAGRAM | C | T | 22570 | 19803 | 0.25 | 0.31 | 1.40 (1.34-1.46) | 2.2E-51 | 1.25 (1.19-1.32) | 3.4E-19 | + | 1.1E-03 |
| rs2334499 | 11 | 1653425 | *DUSP8* | Published | C | T | 22570 | 19801 | 0.44 | 0.28 | 1.08 (1.04-1.13) | 1.2E-04 | 1.02 (0.97-1.07) | 4.2E-01 | + | 7.8E-02 |
| rs231362 | 11 | 2648047 | *KCNQ1* | DIAGRAM | A | G | 22570 | 19625 | 0.52 | 0.73 | 1.11 (1.06-1.16) | 6.4E-06 | 1.09 (1.03-1.15) | 3.0E-03 | + | 5.9E-01 |
| rs163184 | 11 | 2803645 | *KCNQ1* | DIAGRAM | T | G | 22570 | 19796 | 0.44 | 0.53 | 1.09 (1.04-1.13) | 6.8E-05 | 1.08 (1.03-1.13) | 1.2E-03 | + | 8.4E-01 |
| rs5215 | 11 | 17365206 | *KCNJ11* | DIAGRAM | T | C | 22570 | 19793 | 0.41 | 0.37 | 1.09 (1.05-1.14) | 1.6E-05 | 1.04 (0.99-1.09) | 1.1E-01 | + | 1.1E-01 |
| rs1552224 | 11 | 72110746 | *CENTD2* | DIAGRAM | C | A | 22570 | 19800 | 0.88 | 0.83 | 1.13 (1.07-1.19) | 7.0E-06 | 1.04 (0.98-1.10) | 2.2E-01 | + | 4.2E-02 |
| rs1387153 | 11 | 92313476 | *MTNR1B* | DIAGRAM | C | T | 22570 | 19803 | 0.28 | 0.39 | 1.12 (1.07-1.17) | 1.0E-06 | 1.07 (1.02-1.12) | 8.7E-03 | + | 1.3E-01 |
| rs1531343 | 12 | 64461161 | *HMGA2* | DIAGRAM | G | C | 22570 | 19785 | 0.10 | 0.18 | 1.20 (1.12-1.29) | 1.7E-07 | 1.07 (1.01-1.13) | 3.4E-02 | + | 1.0E-02 |
| rs4760790 | 12 | 69921061 | *TSPAN8* | DIAGRAM | G | A | 22570 | 19671 | 0.23 | 0.34 | 1.11 (1.06-1.16) | 3.6E-06 | 1.06 (1.01-1.11) | 1.8E-02 | + | 1.6E-01 |
| rs7957197 | 12 | 119923406 | *HNF1A* | DIAGRAM | A | T | 22570 | 8987 | 0.85 | 0.95 | 1.14 (1.08-1.19) | 4.6E-07 | 1.14 (0.97-1.34) | 1.2E-01 | + | 9.9E-01 |
| rs7172432 | 15 | 60183681 | *C2CD4A/B* | Published | G | A | 22570 | 19801 | 0.52 | 0.61 | 1.07 (1.03-1.12) | 1.1E-03 | 1.05 (1.01-1.11) | 2.6E-02 | + | 6.4E-01 |
| rs11634397 | 15 | 78219277 | *ZFAND6* | DIAGRAM | A | G | 22570 | 15543 | 0.60 | 0.53 | 1.11 (1.06-1.16) | 5.1E-06 | 1.05 (1.00-1.12) | 7.5E-02 | + | 1.8E-01 |
| rs8042680 | 15 | 89322341 | *PRC1* | DIAGRAM | C | A | 22570 | 19799 | 0.22 | 0.63 | 1.10 (1.06-1.15) | 8.2E-06 | 1.06 (1.01-1.11) | 2.8E-02 | + | 2.0E-01 |
| rs11642841 | 16 | 52402988 | *FTO* | DIAGRAM | C | A | 22570 | 19033 | 0.45 | 0.32 | 1.13 (1.08-1.18) | 3.4E-08 | 1.07 (1.02-1.14) | 1.2E-02 | + | 1.7E-01 |
| rs391300 | 17 | 2163008 | *SRR* | Published | T | C | 22570 | 19799 | 0.64 | 0.51 | 1.00 (0.96-1.04) | 9.5E-01 | 0.99 (0.94-1.03) | 6.1E-01 | - | 6.7E-01 |
| rs4430796 | 17 | 33172153 | *HNF1B* | DIAGRAM | A | G | 13971 | 19803 | 0.53 | 0.37 | 1.14 (1.08-1.20) | 1.5E-06 | 1.07 (1.02-1.13) | 4.1E-03 | + | 1.1E-01 |

**Supplementary Table 13.** Comparison of LD structure between South Asians (LOLIPOP, SINDI) and CEU (HapMap2). Results are given as P value for comparison of pairwise LD between SNPs at the loci by VarLD.

| Region | Sentinel SNP | Nearest Gene | CEU – LOLIPOP | CEU – SINDI | LOLIPOP – SINDI |
|---|---|---|---|---|---|
| **Chr2 (165.06 – 165.36)** | rs3923113 | *GRB14* | 0.40 | 0.16 | 0.56 |
| **Chr3 (188.01 – 188.30)** | rs16861329 | *ST6GAL1* | 0.08 | 0.05 | 0.69 |
| **Chr10 (70.46 – 70.75)** | rs1802295 | *VPS26A* | 0.006 | 0.002 | 0.18 |
| **Chr15 (75.38 – 75.67)** | rs7178572 | *HMG20A* | 0.62 | 0.33 | 0.90 |
| **Chr15 (88.03 – 88.32)** | rs2028299 | *AP3S2* | 0.84 | 0.11 | 0.38 |
| **Chr20 (42.28 – 42.57)** | rs4812829 | *HNF4A* | 0.06 | 0.13 | 0.58 |

**Supplementary Table 14.** The 10 top ranking SNPs associated with T2D at each of the six genetic loci identified in the present study. Results are presented as odds ratio [OR] (95% confidence interval) for T2D per copy of risk allele. Genotyped: 1 = directly genotyped; 0 = imputed. Sentinel SNPs from the primary analysis of directly genotyped SNPs are highlighted (yellow); pairwise LD with sentinel SNP at each locus is given as $r^2$ based on data from CEU in HapMap.

| SNP | Chr | Position | Nearest gene | Alt | Risk | Genotyped | OR | P | Sentinel SNP | $r^2$ with sentinel SNP |
|---|---|---|---|---|---|---|---|---|---|---|
| rs3923113 | 2 | 165210095 | *GRB14* | C | A | 1 | 1.15 (1.09-1.21) | 3.6E-07 | Yes | NA |
| rs6713419 | 2 | 165216546 | *GRB14* | C | T | 0 | 1.15 (1.09-1.21) | 1.1E-06 | No | 1.00 |
| rs7592412 | 2 | 165234584 | *GRB14* | C | T | 0 | 1.15 (1.09-1.21) | 1.1E-06 | No | 1.00 |
| rs12692735 | 2 | 165212811 | *GRB14* | T | G | 0 | 1.14 (1.09-1.21) | 1.1E-06 | No | 1.00 |
| rs10930133 | 2 | 165214970 | *GRB14* | A | T | 0 | 1.14 (1.09-1.21) | 1.2E-06 | No | 1.00 |
| rs10179126 | 2 | 165220040 | *GRB14* | G | C | 0 | 1.14 (1.08-1.21) | 1.5E-06 | No | 0.96 |
| rs10195252 | 2 | 165221337 | *GRB14* | C | T | 1 | 1.13 (1.07-1.19) | 2.6E-06 | No | 0.78 |
| rs13432797 | 2 | 165234833 | *GRB14* | C | G | 0 | 1.15 (1.08-1.21) | 3.0E-06 | No | 1.00 |
| rs10184004 | 2 | 165216635 | *GRB14* | T | C | 0 | 1.14 (1.08-1.20) | 3.5E-06 | No | 0.78 |
| rs13389219 | 2 | 165237122 | *GRB14* | T | C | 0 | 1.14 (1.08-1.20) | 3.6E-06 | No | 0.81 |
| rs3852060 | 3 | 188148233 | *ST6GAL1* | G | C | 0 | 1.14 (1.08-1.20) | 7.9E-06 | No | 1.00 |
| rs6444187 | 3 | 188156832 | *ST6GAL1* | C | G | 0 | 1.12 (1.06-1.17) | 1.1E-05 | No | 0.178 |
| rs12632862 | 3 | 188151908 | *ST6GAL1* | A | G | 0 | 1.11 (1.06-1.17) | 1.1E-05 | No | 0.176 |
| rs16861317 | 3 | 188147422 | *ST6GAL1* | A | G | 0 | 1.13 (1.07-1.20) | 1.9E-05 | No | 1.00 |
| rs16861329 | 3 | 188149155 | *ST6GAL1* | T | C | 1 | 1.13 (1.07-1.19) | 2.3E-05 | Yes | NA |
| rs3887925 | 3 | 188148339 | *ST6GAL1* | C | T | 1 | 1.11 (1.06-1.16) | 2.9E-05 | No | 0.215 |
| rs6444188 | 3 | 188160630 | *ST6GAL1* | G | T | 1 | 1.10 (1.05-1.16) | 2.3E-04 | No | 0.299 |
| rs698103 | 3 | 188476335 | *ST6GAL1* | T | C | 0 | 1.19 (1.08-1.32) | 4.4E-04 | No | |
| rs4686819 | 3 | 188163901 | *ST6GAL1* | G | C | 0 | 1.14 (1.06-1.23) | 5.9E-04 | No | 0.006 |
| rs4686814 | 3 | 188125559 | *ST6GAL1* | T | C | 0 | 1.12 (1.05-1.19) | 7.4E-04 | No | 0.006 |
| rs1802295 | 10 | 70601480 | *VPS26A* | C | T | 1 | 1.13 (1.07-1.20) | 1.9E-06 | Yes | NA |
| rs4746821 | 10 | 70638205 | *VPS26A* | G | T | 1 | 1.12 (1.06-1.18) | 9.6E-06 | No | 1.00 |
| rs3847345 | 10 | 71118906 | *VPS26A* | A | G | 0 | 1.14 (1.07-1.21) | 8.5E-05 | No | 0.00 |
| rs2394597 | 10 | 71210030 | *VPS26A* | G | A | 0 | 1.11 (1.05-1.17) | 2.8E-04 | No | 0.00 |
| rs12774027 | 10 | 71115324 | *VPS26A* | A | C | 0 | 1.12 (1.05-1.20) | 5.7E-04 | No | 0.002 |
| rs731016 | 10 | 71206453 | *VPS26A* | G | A | 1 | 1.11 (1.05-1.17) | 6.1E-04 | No | 0.01 |
| rs12780021 | 10 | 71098693 | *VPS26A* | G | T | 0 | 1.25 (1.10-1.43) | 7.8E-04 | No | 0.007 |
| rs2394656 | 10 | 71546388 | *VPS26A* | T | C | 0 | 1.09 (1.04-1.15) | 9.4E-04 | No | 0.00 |
| rs12761954 | 10 | 71107985 | *VPS26A* | C | T | 1 | 1.12 (1.05-1.20) | 1.1E-03 | No | 0.003 |
| rs7093577 | 10 | 71156557 | *VPS26A* | C | T | 0 | 1.09 (1.03-1.14) | 1.2E-03 | No | 0.004 |
| rs7178572 | 15 | 75534245 | *HMG20A* | A | G | 1 | 1.10 (1.05-1.15) | 2.4E-05 | Yes | NA |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| rs2175941 | 15 | 75371553 | *HMG20A* | T | C | 0 | 1.11 (1.06-1.16) | 2.4E-05 | No | 0.56 |
| rs1446312 | 15 | 75199244 | *HMG20A* | G | C | 0 | 1.11 (1.06-1.16) | 2.6E-05 | No | 0.54 |
| rs1191196 | 15 | 75433559 | *HMG20A* | T | C | 1 | 1.10 (1.05-1.15) | 2.7E-05 | No | 0.56 |
| rs4243045 | 15 | 75242969 | *HMG20A* | A | C | 0 | 1.11 (1.06-1.16) | 2.8E-05 | No | 0.63 |
| rs11857294 | 15 | 75383780 | *HMG20A* | C | T | 0 | 1.10 (1.05-1.16) | 2.9E-05 | No | 0.56 |
| rs11858641 | 15 | 75372875 | *HMG20A* | C | T | 0 | 1.10 (1.05-1.16) | 2.9E-05 | No | 0.55 |
| rs7163503 | 15 | 75280560 | *HMG20A* | C | A | 0 | 1.10 (1.05-1.16) | 3.1E-05 | No | 0.54 |
| rs11857450 | 15 | 75589846 | *HMG20A* | G | C | 0 | 1.10 (1.06-1.16) | 3.1E-05 | No | 0.92 |
| rs4886850 | 15 | 75191215 | *HMG20A* | G | C | 0 | 1.10 (1.05-1.16) | 3.1E-05 | No | 0.54 |
| | | | | | | | | | | |
| rs4932143 | 15 | 88173071 | *AP3S2* | C | G | 0 | 1.11 (1.06-1.17) | 2.1E-05 | No | 1.00 |
| rs2028299 | 15 | 88175261 | *AP3S2* | A | C | 1 | 1.11 (1.06-1.16) | 4.7E-05 | Yes | NA |
| rs9920775 | 15 | 88169277 | *AP3S2* | C | T | 0 | 1.11 (1.06-1.17) | 5.1E-05 | No | 0.96 |
| rs9920421 | 15 | 88169071 | *AP3S2* | A | G | 0 | 1.11 (1.06-1.17) | 5.2E-05 | No | 0.96 |
| rs4932148 | 15 | 88195360 | *AP3S2* | T | C | 0 | 1.11 (1.05-1.16) | 6.6E-05 | No | 1.00 |
| rs2351706 | 15 | 88185119 | *AP3S2* | G | A | 0 | 1.10 (1.05-1.16) | 8.8E-05 | No | 1.00 |
| rs893617 | 15 | 88182282 | *AP3S2* | T | C | 0 | 1.10 (1.05-1.16) | 9.1E-05 | No | 1.00 |
| rs12912009 | 15 | 88230152 | *AP3S2* | A | G | 0 | 1.10 (1.05-1.16) | 1.0E-04 | No | 0.85 |
| rs11634658 | 15 | 88170152 | *AP3S2* | G | T | 0 | 1.11 (1.05-1.16) | 1.1E-04 | No | 0.92 |
| rs2043880 | 15 | 88233530 | *AP3S2* | A | G | 0 | 1.11 (1.05-1.16) | 1.1E-04 | No | 0.85 |
| | | | | | | | | | | |
| rs4812831 | 20 | 42451674 | *HNF4A* | G | A | 0 | 1.21 (1.13-1.30) | 5.5E-08 | No | 0.42 |
| rs12625067 | 20 | 42377438 | *HNF4A* | C | T | 0 | 1.18 (1.11-1.26) | 1.3E-07 | No | 0.16 |
| rs1884609 | 20 | 42355542 | *HNF4A* | C | T | 0 | 1.17 (1.11-1.25) | 1.6E-07 | No | 0.07 |
| rs4366964 | 20 | 42329320 | *HNF4A* | C | A | 0 | 1.17 (1.11-1.24) | 1.9E-07 | No | 0.07 |
| rs12481568 | 20 | 42334669 | *HNF4A* | A | T | 0 | 1.17 (1.10-1.24) | 2.2E-07 | No | 0.05 |
| rs2143641 | 20 | 42323433 | *HNF4A* | G | A | 0 | 1.17 (1.10-1.24) | 2.6E-07 | No | 0.07 |
| rs3843762 | 20 | 42273404 | *HNF4A* | T | C | 0 | 1.19 (1.11-1.26) | 3.3E-07 | No | 0.07 |
| rs16988852 | 20 | 42275043 | *HNF4A* | G | A | 0 | 1.17 (1.10-1.24) | 4.2E-07 | No | 0.07 |
| rs12624924 | 20 | 42278683 | *HNF4A* | T | C | 0 | 1.17 (1.10-1.24) | 4.2E-07 | No | 0.07 |
| rs4812829 | 20 | 42422681 | *HNF4A* | G | A | 1 | 1.13 (1.08-1.19) | 4.4E-07 | Yes | NA |

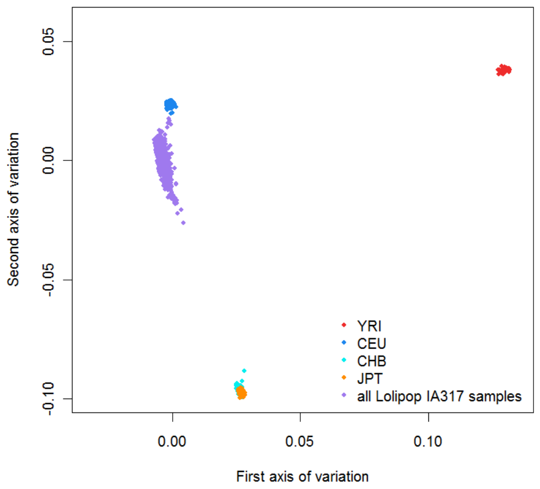
**Supplementary Table 15.** Conditional analysis of the four genotyped SNPs at the *HNF4A* locus that were associated with T2D at $P<10^{-5}$ in the genome-wide association study. Results are presented as odds ratio (OR) for T2D per allele copy of risk allele of the "Lead SNP": i. in single marker tests; ii. in two marker SNP tests with additional adjustment for the second SNP; and iii. in a four-marker SNP test containing all four genotyped SNPs in the regression model. A/R = Alternate / Risk allele of SNP. $r^2$ = pairwise LD beteen the SNPs named in the two-marker tests.

| | | **Single SNP tests** | | **Two-SNP tests, with additional adjustment for** | | | | | | | | | | | | **Four-SNP test** | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | **rs4812829** | | | **rs6103716** | | | **rs16988857** | | | **rs6017291** | | | | |
| **Lead SNP** | **A/R** | **OR** | **P** | **OR** | **P** | $r^2$ | **OR** | **P** | $r^2$ | **OR** | **P** | $r^2$ | **OR** | **P** | $r^2$ | **OR** | **P** |
| rs4812829 | G / A | 1.14 (1.08-1.19) | $4x10^{-7}$ | NA | NA | NA | 1.08 (1.02-1.15) | $1.3x10^{-2}$ | 0.26 | 1.08 (1.02-1.15) | $7.2x10^{-3}$ | 0.20 | 1.09 (1.02-1.15) | $5.8x10^{-3}$ | 0.22 | 1.05 (0.99-1.12) | $1.2x10^{-1}$ |
| rs6103716 | A / C | 1.13 (1.08-1.19) | $8x10^{-7}$ | 1.08 (1.02-1.15) | $7.5x10^{-3}$ | 0.26 | NA | NA | NA | 1.08 (1.03-1.14) | $2.7x10^{-3}$ | 0.17 | 1.09 (1.03-1.15) | $1.5x10^{-3}$ | 0.16 | 1.06 (1.00-1.13) | $3.7x10^{-2}$ |
| rs16988857 | G / A | 1.16 (1.10-1.24) | $1x10^{-6}$ | 1.12 (1.04-1.20) | $1.3x10^{-3}$ | 0.20 | 1.12 (1.05-1.20) | $6.9x10^{-4}$ | 0.17 | NA | NA | NA | 1.14 (1.01-1.30) | $3.9x10^{-2}$ | 0.79 | 1.12 (0.98-1.27) | $9.3x10^{-2}$ |
| rs6017291 | A / G | 1.14 (1.08-1.21) | $5x10^{-6}$ | 1.10 (1.02-1.17) | $9.8x10^{-3}$ | 0.22 | 1.10 (1.03-1.18) | $5.0x10^{-3}$ | 0.16 | 1.02 (0.90-1.16) | $7.4x10^{-1}$ | 0.79 | NA | NA | NA | 0.99 (0.87-1.12) | $8.3x10^{-1}$ |

**Supplementary Figure 1.** Principal component maps of the individual studies with Hapmap II panels of YRI, CEU, CHB and JPT. For comparison, results are also shown for Indians from a survey of genetic variation in India by Reich and colleagues.[15]

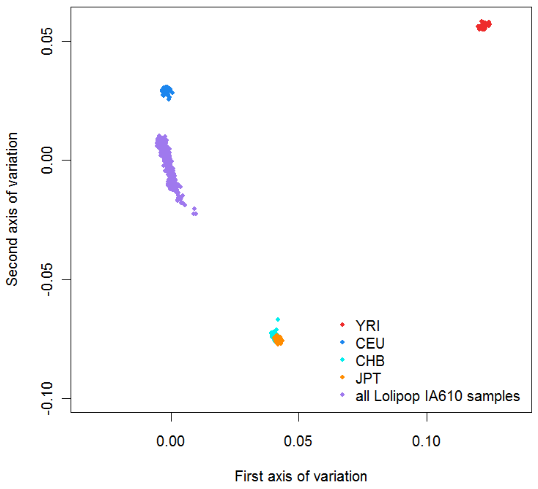
## LOLIPOP study

Illumina 317 array

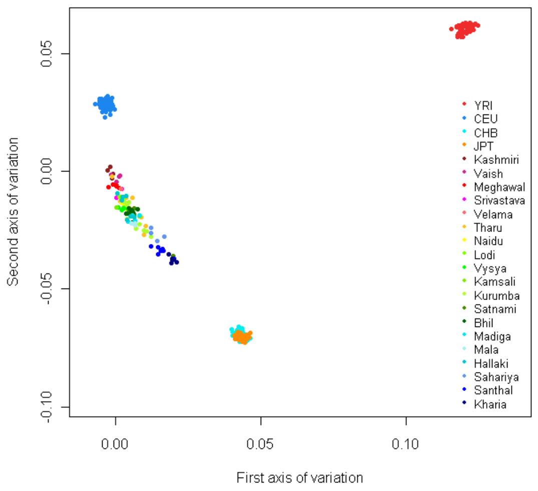


## LOLIPOP study

Illumina 610 array

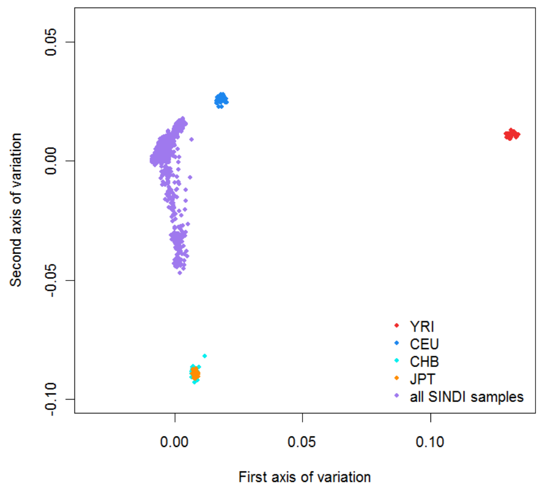


## Reich samples



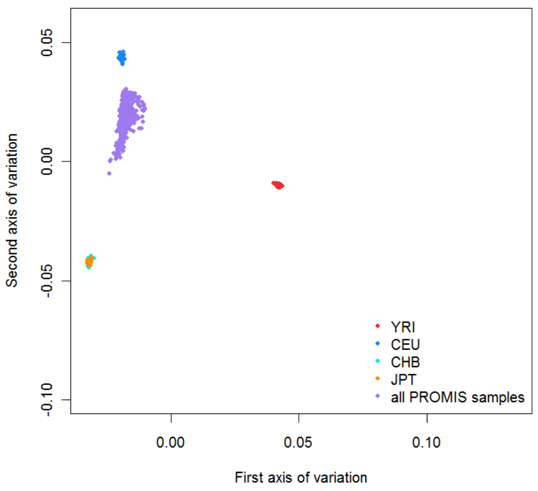
## SINDI study

Illumina 610 array

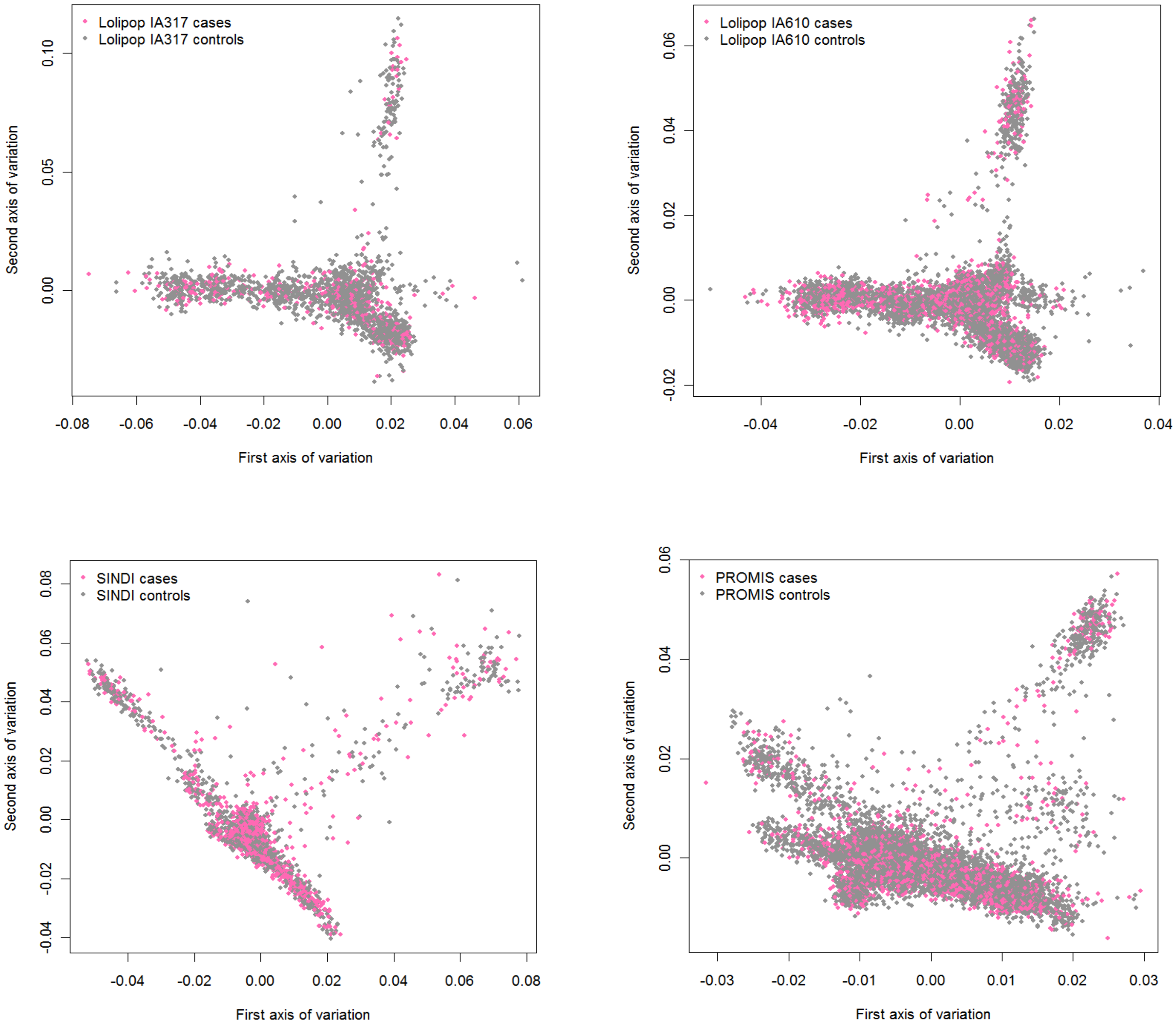


## PROMIS study

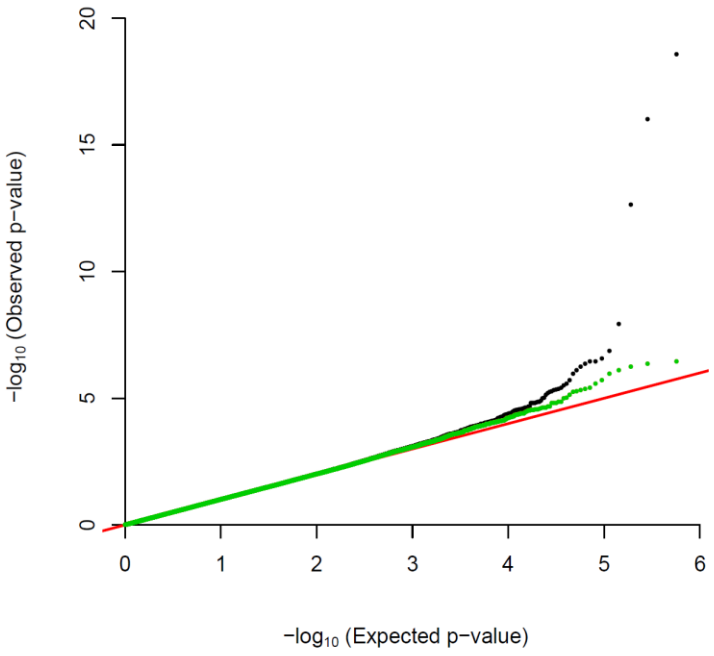
Illumina 660 array



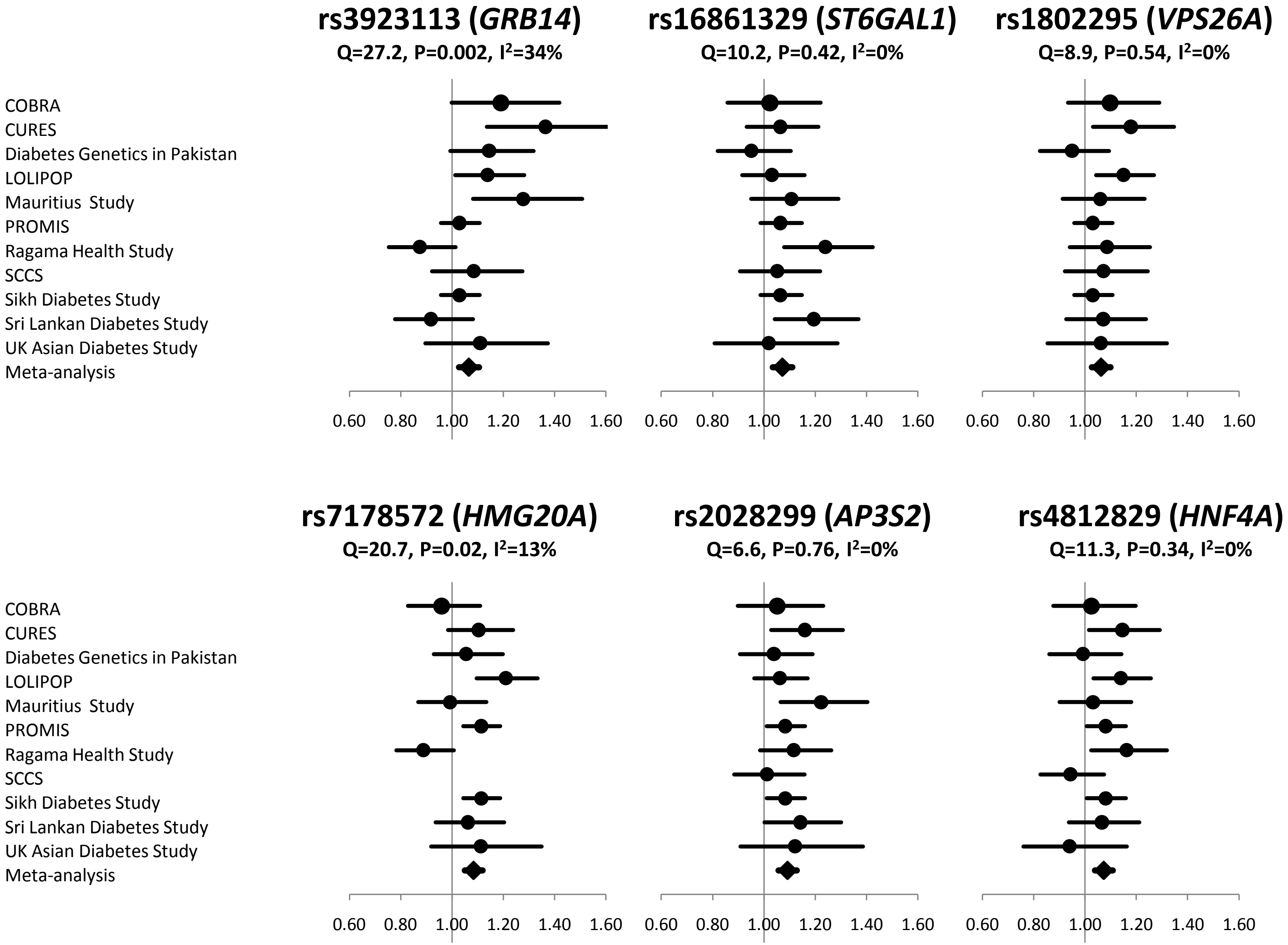
**Supplementary Figure 2.** Principal component maps of the individual studies without HapMap scaling. T2D cases and controls are coloured pink and grey respectively.



**Supplementary Figure 3.** QQ plot for SNPs in the genome-wide association. Black symbols - all genotyped SNPs included; green symbols – known T2D loci removed. Red line expected distribution under the null hypothesis.

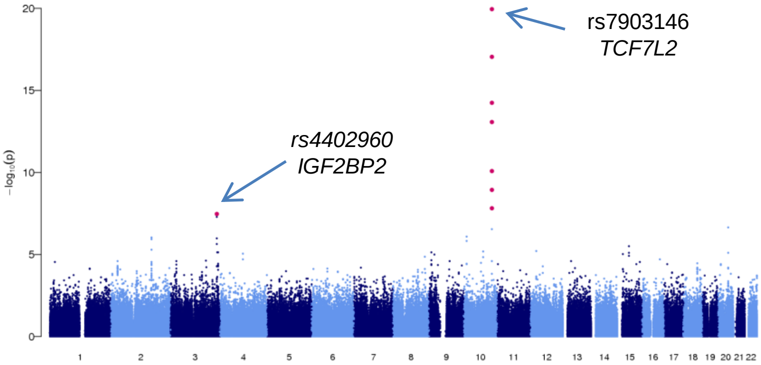


**Supplementary Figure 4.** Forest plots showing the association with T2D in the replication cohorts (individually and in meta-analysis), for the six SNPs associated with T2D in the present study. Genotyping for rs7178572 was unsuccessful in SCCS.

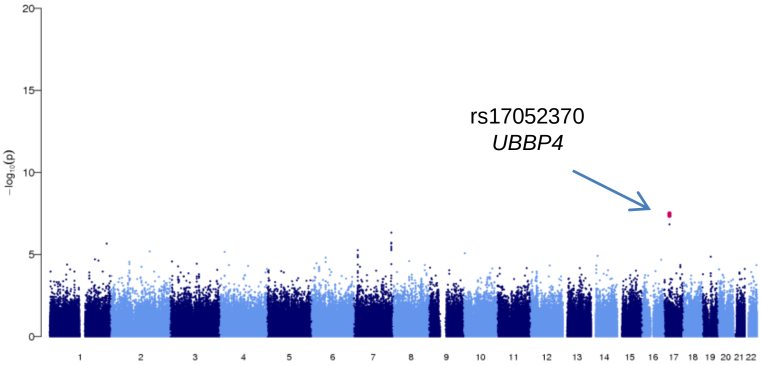


**Supplementary Figure 5.** Manhattan plots for secondary GWA analyses.

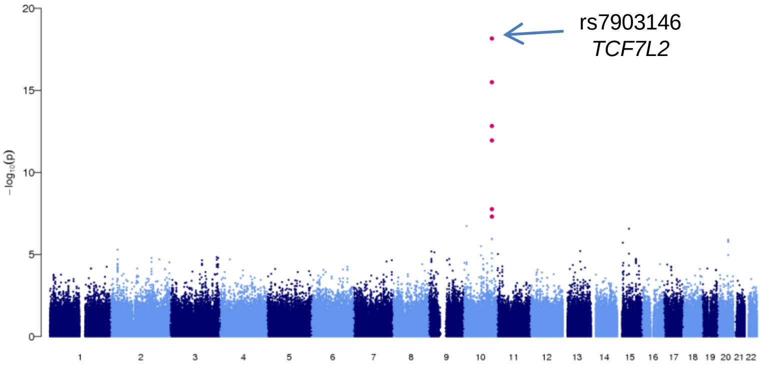
**5a. Male specific**



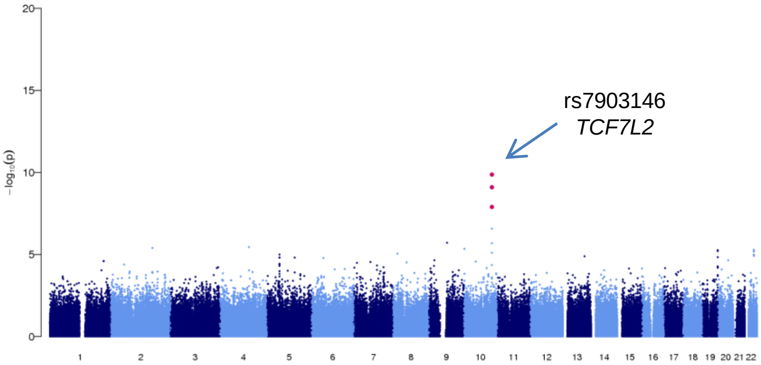
**5b. Female specific**



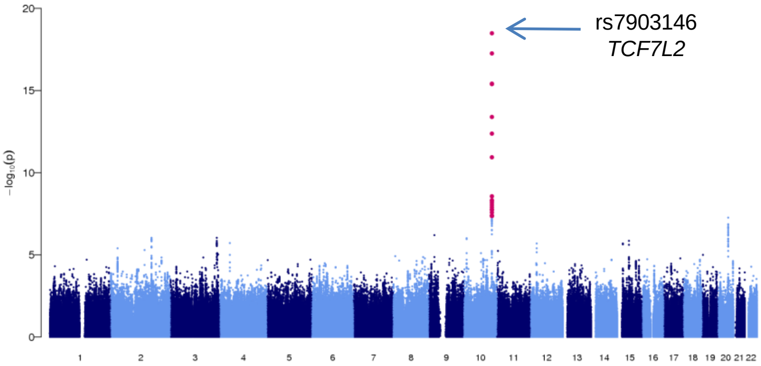
**5c. BMI adjusted**



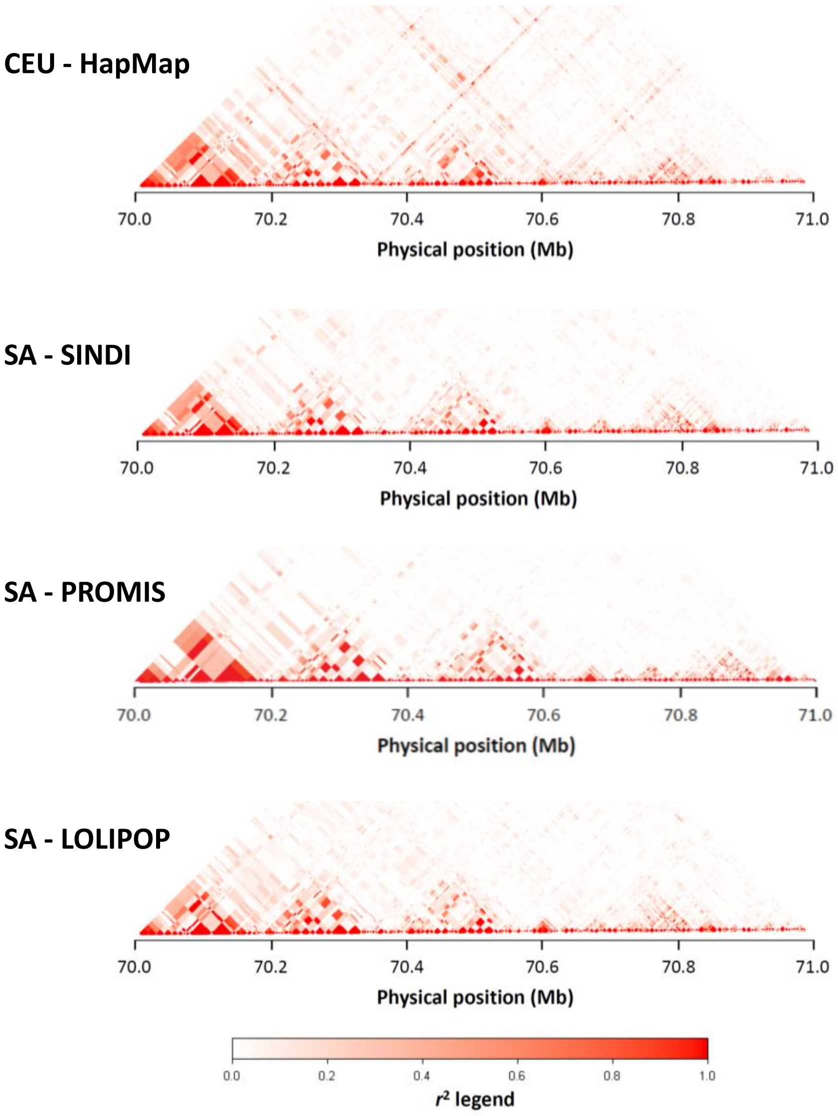
**5d. BMI extremes**



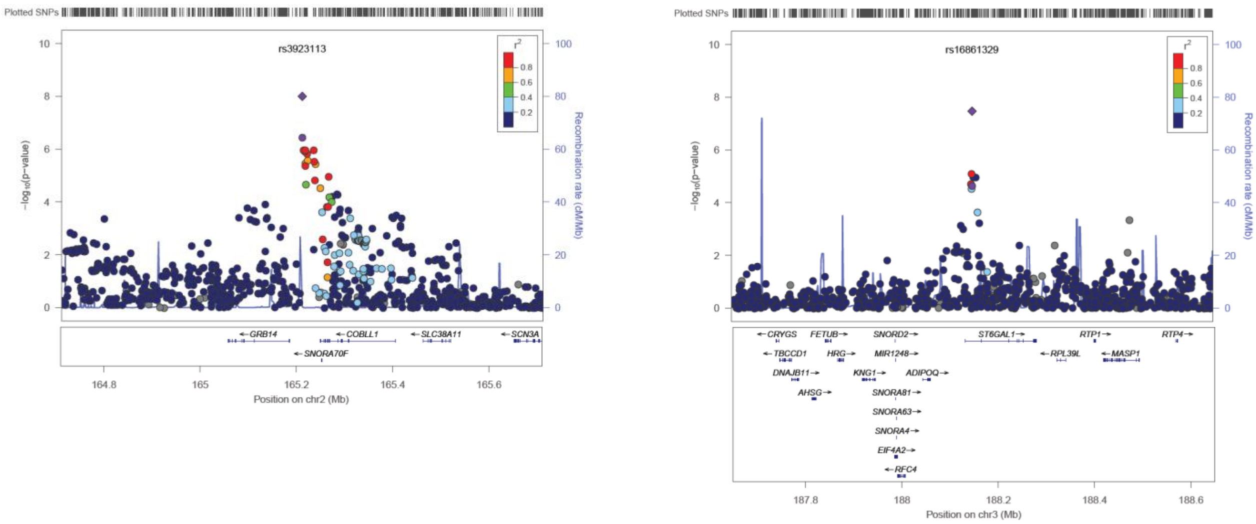
**5e. Imputed data**



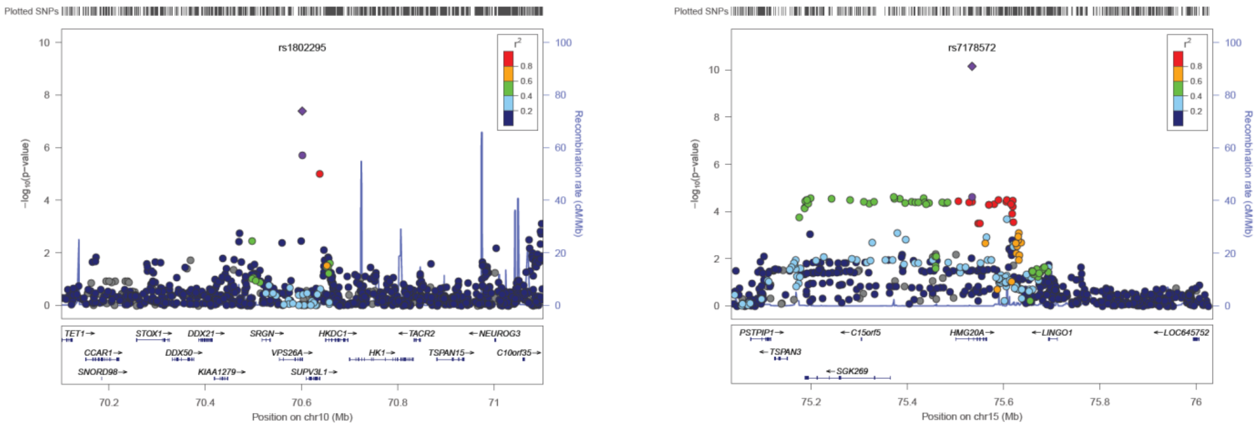
**Supplementary Figure 6.** Heatmap showing pairwise LD between SNPs at the *VPS26A* locus on chromosome 10, amongst South Asians (SA, present study) and Europeans (CEU, HapMap).



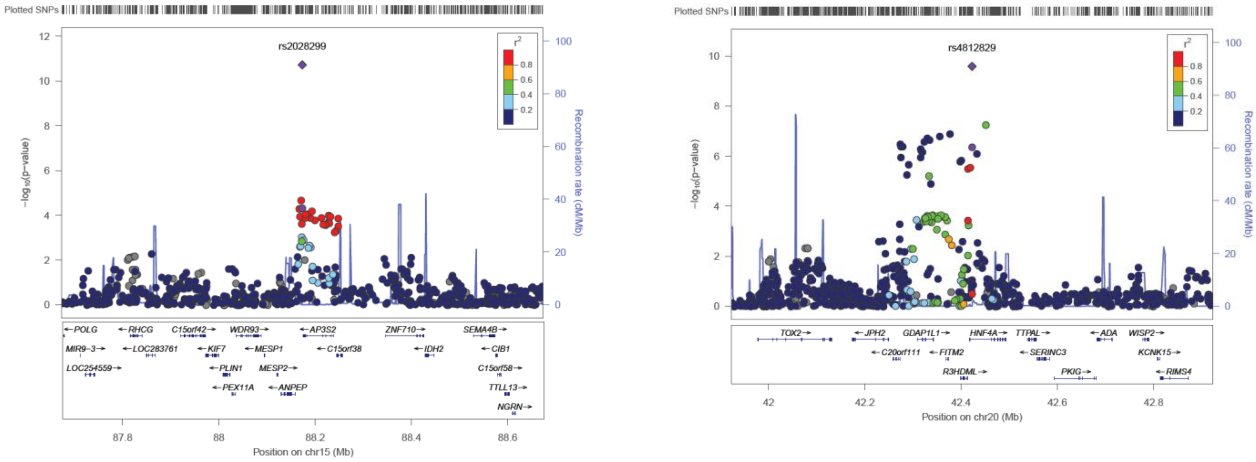
**Supplementary Figure 7.** Regional plots for the six novel loci including results for both genotyped and imputed (HapMap2) SNPs.SNPs are colour coded accoridng to LD wth sentinel SNP.


(A) *GRB14* region on chromosome 2

(B) *ST6GAL1* region on chromosome 3

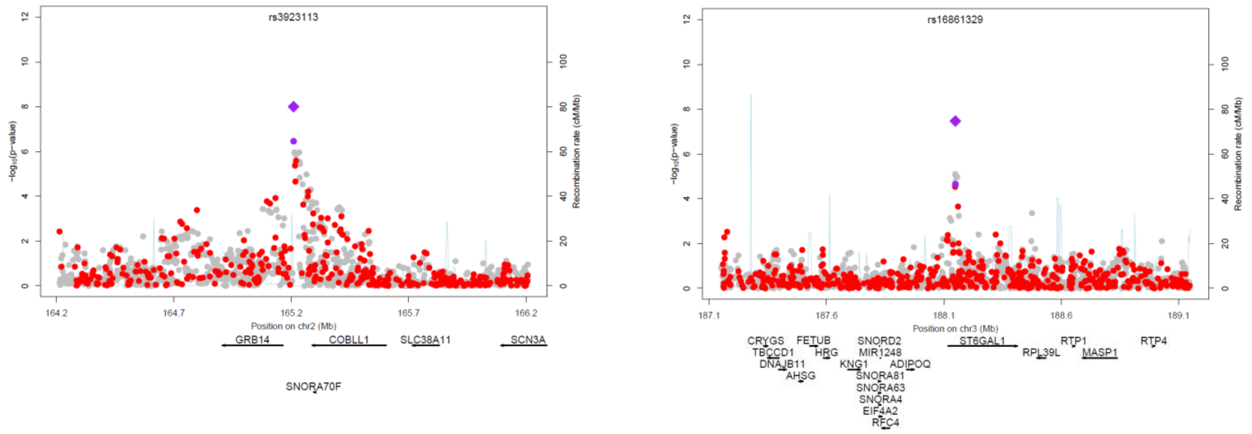

(C) *VPS26A* region on chromosome 10

(D) *HMG20A* region on chromosome 15


(E) *AP3S2* region on chromosome 15

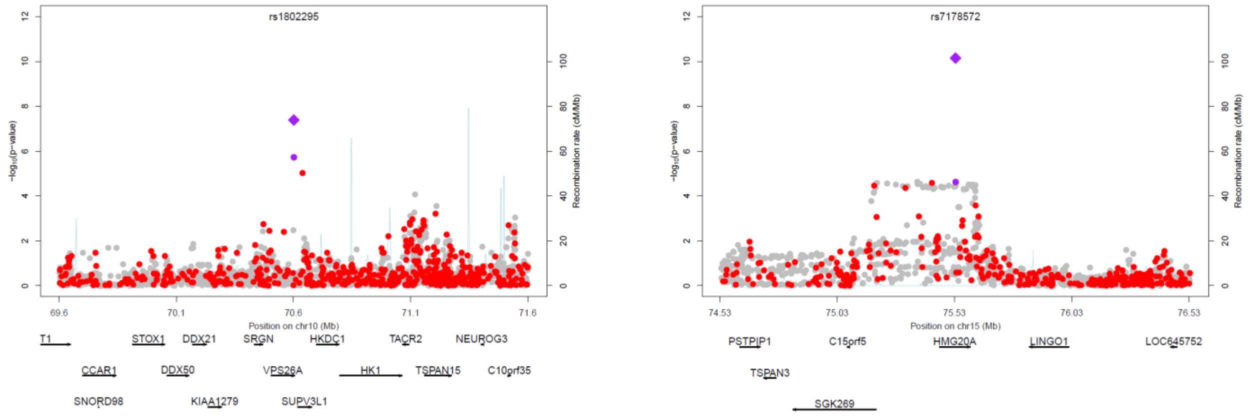
(F) *HNF4A* region on chromosome 20

**Supplementary Figure 8.** Regional plots for the six novel loci identifying SNPs that were genotyped (red dots) compared with those that were imputed (grey dots).



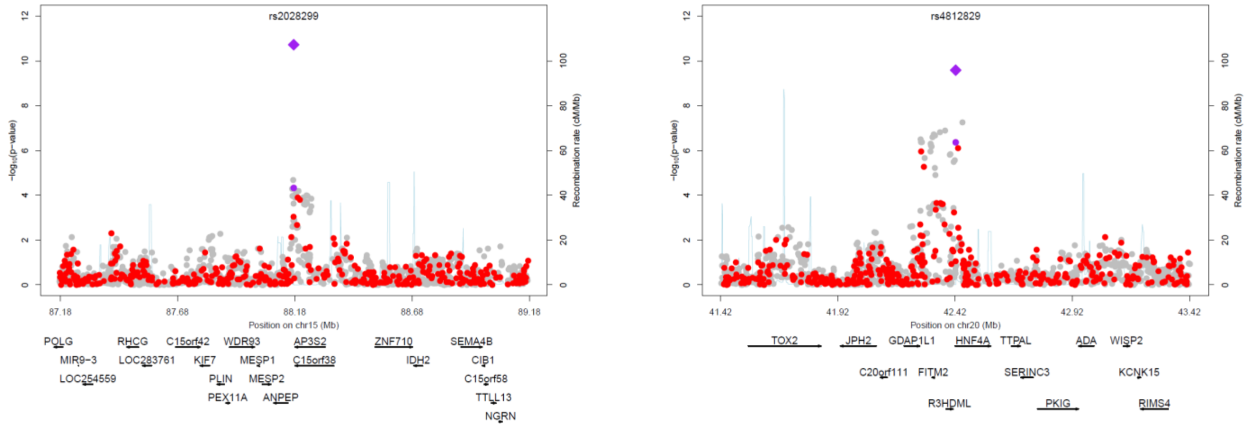
(A) *GRB14* region on chromosome 2

(B) *ST6GAL1* region on chromosome 3



(C) *VPS26A* region on chromosome 10

(D) *HMG20A* region on chromosome 15



(E) *AP3S2* region on chromosome 15

(F) *HNF4A* region on chromosome 20