

Genome-wide trans-ethnic meta-analysis reveals novel insights into the genetic architecture of type 2 diabetes susceptibility

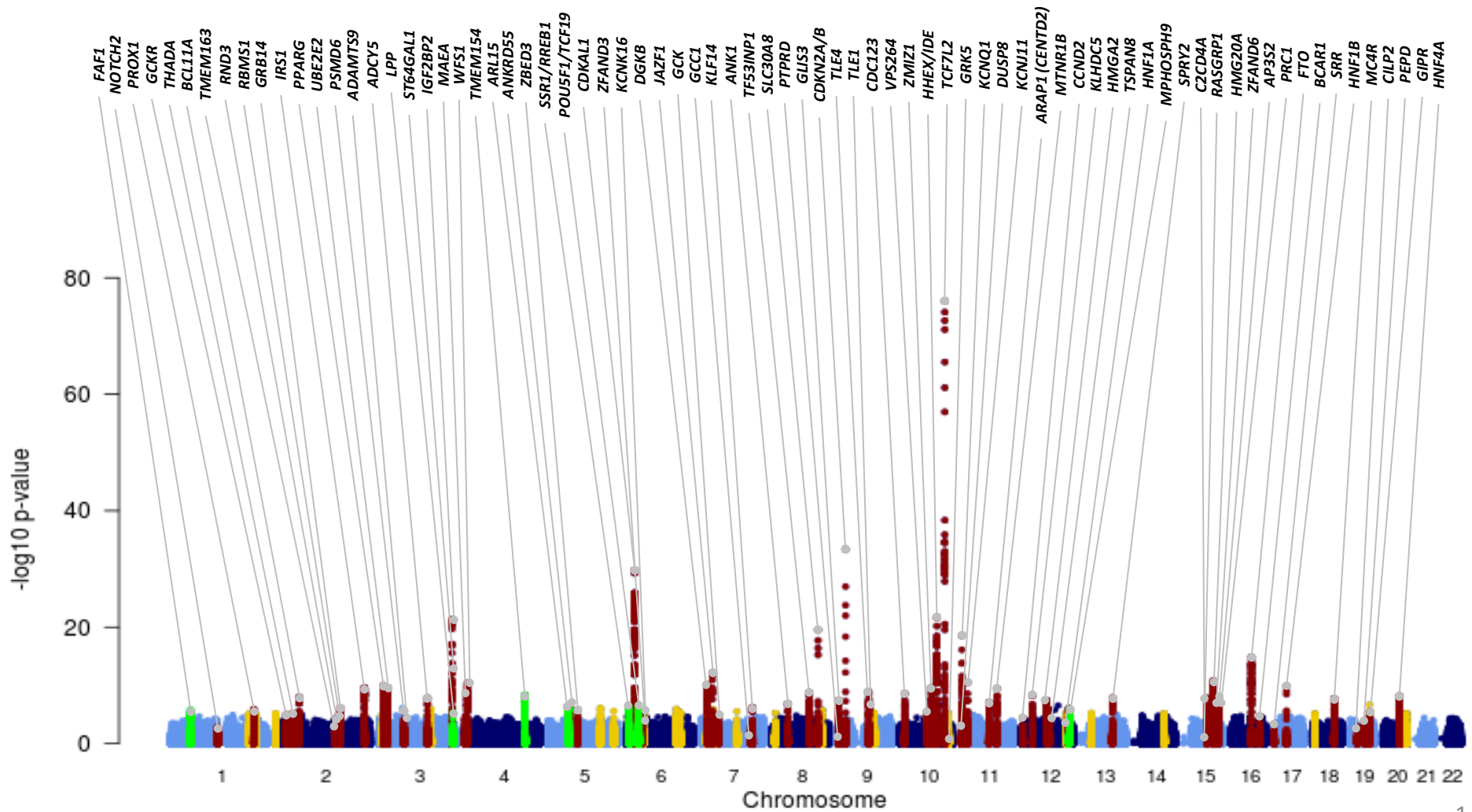
DIAbetes Genetics Replication And Meta-analysis (DIAGRAM) Consortium, Asian Genetic Epidemiology Network Type 2 Diabetes (AGEN-T2D) Consortium, South Asian Type 2 Diabetes (SAT2D) Consortium, Mexican American Type 2 Diabetes (MAT2D) Consortium and Type 2 Diabetes Genetic Exploration by Next-generation sequencing in multi-Ethnic Samples (T2D-GENES) Consortium

SUPPLEMENTARY INFORMATION

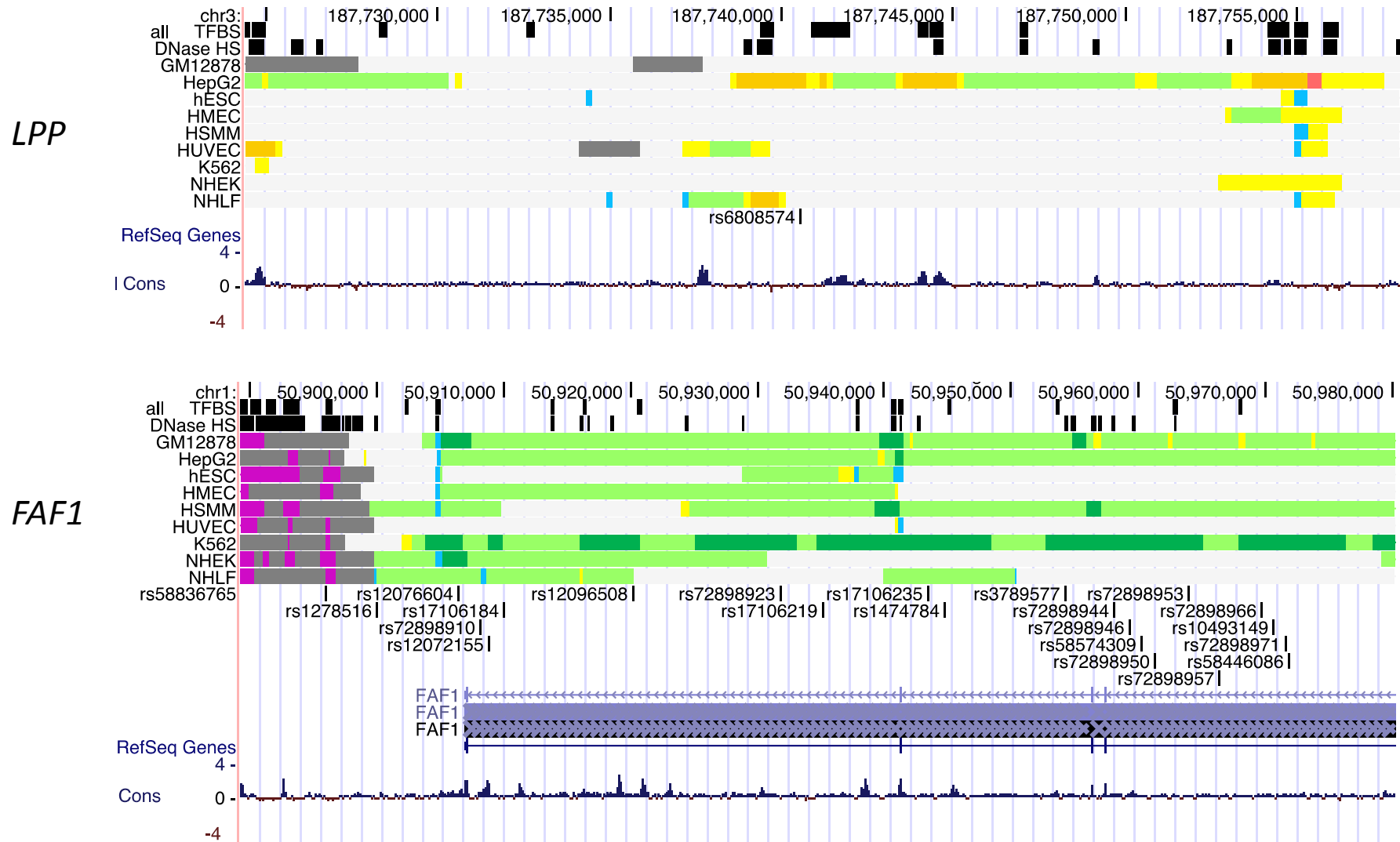
Contents

| | |
|-----------------------|----|
| Supplementary Figures | 1 |
| Supplementary Tables | 5 |
| Supplementary Note | 25 |

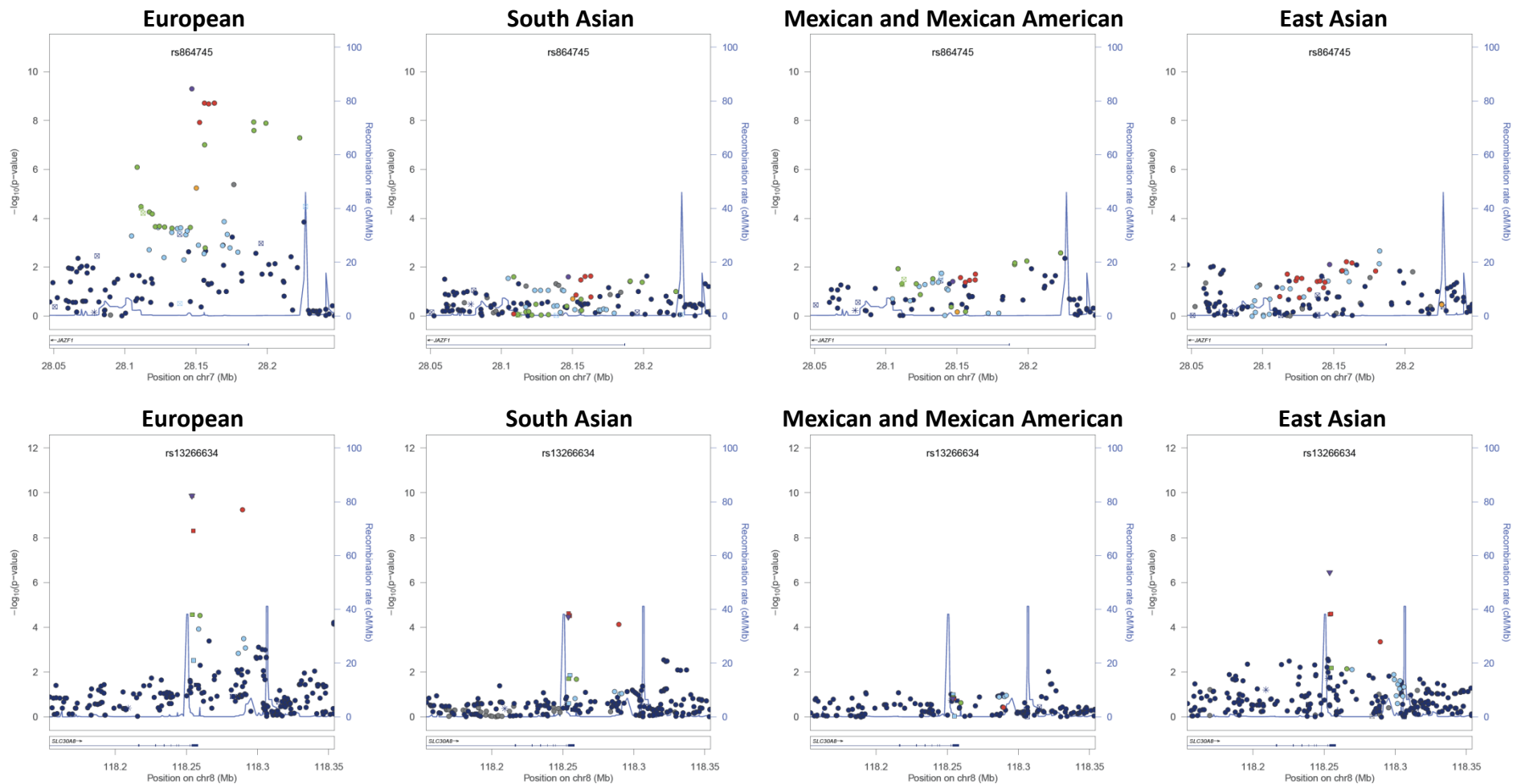
Supplementary Figure 1. Manhattan plot of trans-ethnic “discovery” GWAS meta-analysis. The trans-ethnic meta-analysis comprises 26,488 T2D cases and 83,964 controls from populations of European, East Asian, South Asian, and Mexican and Mexican American ancestry, imputed up to 2.5 million Phase II/III HapMap autosomal SNPs. Previously established T2D susceptibility loci are highlighted in red. Novel loci achieving nominal significance ($p < 10^{-5}$) in the stage 1 meta-analysis, and genome-wide significance ($p < 5 \times 10^{-8}$) after the addition of the “validation” meta-analysis of 21,491 cases and 55,647 controls of European ancestry, are highlighted in green. Loci achieving nominal significance in the discovery meta-analysis, but not achieving genome-wide significance after the addition of the validation meta-analysis are highlighted in yellow.



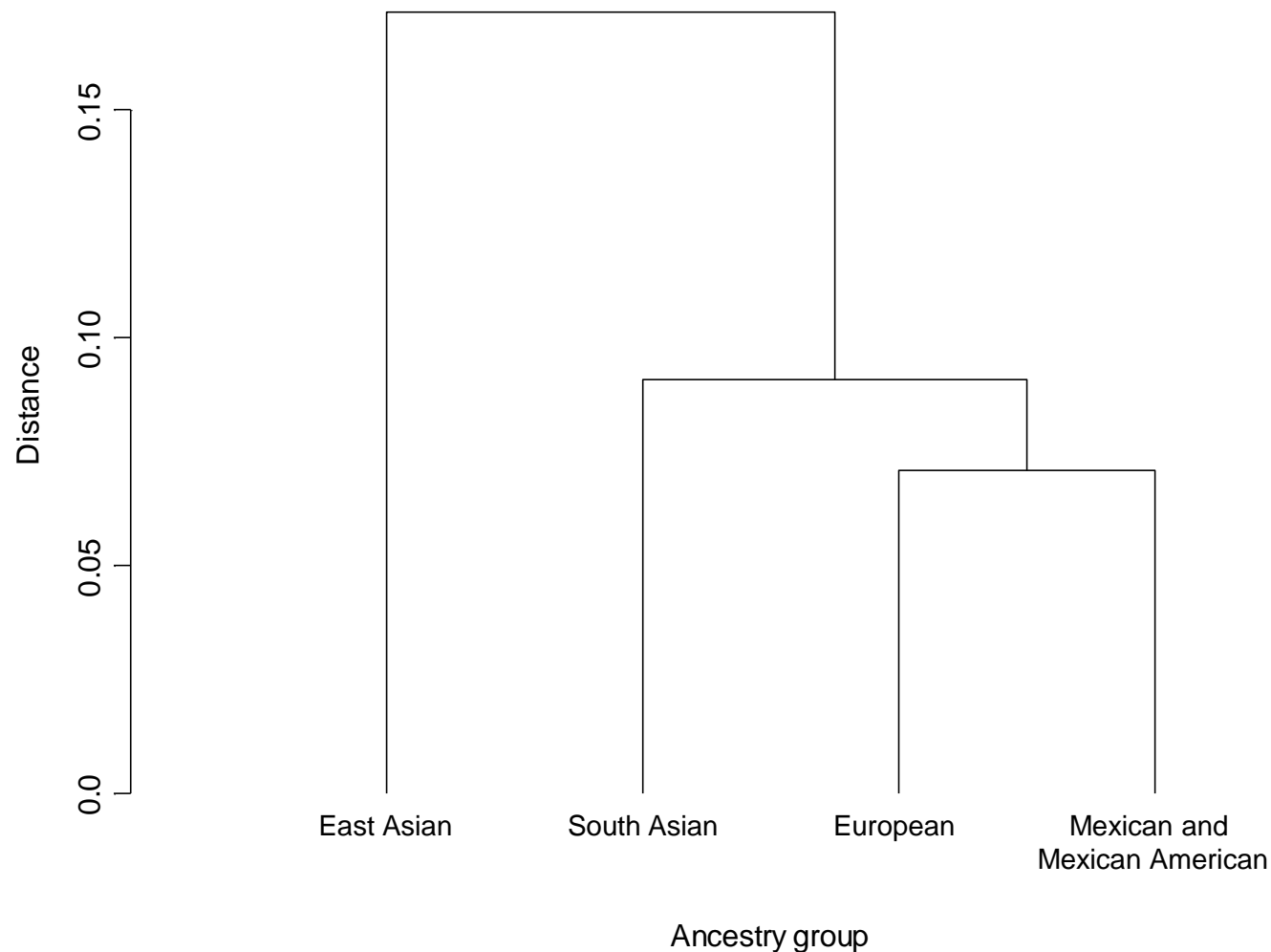
Supplementary Figure 2. ENCODE annotation of *LPP* and *FAF1* loci. Transcription factor binding sites (TFBS) and DNase I hypersensitivity sites (DNase HS) are highlighted in black. Chromatin states in 9 ENCODE cell lines (GM12878, HepG2, hESC, HMEC, HSMM, HUVEC, K562, NHEK, and NHLF) are highlighted as follows: strong enhancer (orange), weak enhancer (yellow), active promoter (red), poised promoter (pink), insulator (blue), transcribed (pale green), transcription transition (dark green), repressed (dark grey) and heterochromatin (pale grey).



Supplementary Figure 3. Signal plots constructed on the basis of ancestry-specific meta-analyses at two loci showing greatest improvements in fine-mapping resolution after trans-ethnic meta-analysis: *JAZF1* (top) and *SLC30A8* (bottom). The ancestry-specific meta-analyses were imputed at up to 2.5 million Phase II/III HapMap autosomal SNPs. Each point represents a SNP passing quality control in the ancestry-specific meta-analysis, plotted with their p -value (on a $-\log_{10}$ scale) as a function of genomic position (NCBI Build 36). In each plot, the lead SNP from the trans-ethnic meta-analysis across ancestry groups is represented by the purple symbol. The colour coding of all other SNPs indicates LD with the lead SNP (estimated by r^2 from the most closely related reference panel from Phase II HapMap, i.e. CEU for the European, South Asian, and Mexican and Mexican American ancestry groups, and CHB+JPT for the East Asian ancestry group): red $r^2 \geq 0.8$; gold $0.6 \leq r^2 < 0.8$; green $0.4 \leq r^2 < 0.6$; cyan $0.2 \leq r^2 < 0.4$; blue $r^2 < 0.2$; grey r^2 unknown. The shape of the plotting symbol corresponds to the annotation of the SNP: upward triangle for frameshift or splice; downward triangle for non-synonymous; square for synonymous or UTR; and circle for intronic or non-coding. Recombination rates are estimated from Phase II HapMap and gene annotations are taken from the University of California Santa Cruz genome browser.



Supplementary Figure 4. Dendrogram representing relatedness between ancestry groups included in the trans-ethnic meta-analysis. The distance between each ethnic group is estimated by the genome-wide autosomal mean effect allele frequency difference from the ancestry-specific meta-analysis. The dendrogram represents our prior beliefs about the heterogeneity in allelic effects on T2D susceptibility between ancestry groups in the MANTRA analysis.



Supplementary Table 1. Study sample characteristics and genotyping.

(a) Trans-ethnic meta-analysis.

| Study | Ethnic group (country of origin) | Case-control status | Sample characteristics | | | | | Genotyping array |
|-------------|----------------------------------|---------------------|-----------------------------|-----------------------|--------------------------------|------------------------------------|------------------------------------|-------------------------------------|
| | | | Sample size (males/females) | Age (years) mean (SD) | Age at onset (years) mean (SD) | Fasting glucose (mmol/l) mean (SD) | BMI (kg/m ²) mean (SD) | |
| ARIC | European (USA) | Cases | 775 (416/359) | 56.1 (5.6) | 50.9 (10.4) | 9.3 (3.6) | 30.4 (5.4) | Affymetrix Human SNP Array 6.0 |
| | | Controls | 7,159 (3,167/3,992) | 54.0 (5.7) | | 5.4 (0.4) | 26.4 (4.5) | |
| deCODE | European (Iceland) | Cases | 1,465 (868/597) | 68.4 (10.1) | 55.1 (12.7) | 8.5 (2.7) | 30.1 (5.4) | Illumina Human 300K/370K |
| | | Controls | 23,194 (7,316/15,878) | 59.7 (18.1) | | 5.3 (0.7) | 26.8 (5.0) | |
| DGDG | European (France) | Cases | 679 (413/266) | 59.5 (10.1) | 45.1 (8.4) | 9.2 (3.1) | 25.9 (2.8) | Illumina Human 300K |
| | | Controls | 697 (281/416) | 53.9 (5.6) | | 5.1 (0.4) | 23.2 (1.8) | |
| DGI | European (Sweden/Finland) | Cases | 1,022 (529/493) | 65.9 (10.0) | 58.0 (10.0) | 9.5 (3.1) | 28.1 (4.1) | Affymetrix GeneChip 500K |
| | | Controls | 1,075 (540/535) | 58.0 (10.0) | | 5.3 (0.5) | 27.6 (3.7) | |
| EUROSPAN | European (various isolates) | Cases | 269 (127/142) | 62.9 (N/A) | N/A | 8.0 (N/A) | 29.8 (N/A) | Illumina Human 300K/370K |
| | | Controls | 3,710 (1,557/2,153) | 49.9 (N/A) | | 4.8 (N/A) | 26.5 (N/A) | |
| FHS | European (USA) | Cases | 674 (386/288) | 63.7 (12.4) | N/A | 8.6 (2.8) | 31.4 (6.5) | Affymetrix GeneChip 500K & MIPS 50K |
| | | Controls | 7,664 (3,443/4,221) | 52.3 (16.0) | | 5.3 (0.5) | 27.0 (5.1) | |
| FUSION | European (Finland) | Cases | 1,161 (653/508) | 62.9 (7.6) | 53.7 (9.1) | 9.4 (3.1) | 30.2 (4.7) | Illumina Human 300K |
| | | Controls | 1,174 (574/600) | 63.6 (7.4) | | 5.3 (0.5) | 27.1 (3.9) | |
| HPFS | European (USA) | Cases | 1,124 (1,124/0) | 55.0 (8.6) | 64.0 (8.4) | N/A | 27.8 (4.0) | Affymetrix Human SNP Array 6.0 |
| | | Controls | 1,298 (1,298/0) | 55.0 (8.4) | | N/A | 25.0 (2.9) | |
| KORAGen | European (Germany) | Cases | 433 (255/178) | 65.2 (8.3) | 58.2 (10.3) | N/A | 30.9 (5.0) | Affymetrix GeneChip 500K |
| | | Controls | 1,438 (693/745) | 61.9 (7.4) | | N/A | 27.7 (4.3) | |
| NHS | European (USA) | Cases | 1,467 (0/1,467) | 43.5 (6.7) | 58.7 (10.6) | N/A | 27.4 (0.1) | Affymetrix Human SNP Array 6.0 |
| | | Controls | 1,754 (0/1,754) | 43.1 (6.8) | | N/A | 23.5 (0.1) | |
| RS1 | European (Netherlands) | Cases | 1,178 (488/690) | 71.7 (8.9) | 71.5 (8.9) | N/A | 27.4 (4.0) | Illumina Human 550K |
| | | Controls | 4,761 (1,928/2,833) | 69.0 (9.1) | | N/A | 26.0 (3.6) | |
| WTCCC | European (UK) | Cases | 1,924 (1,118/806) | 58.6 (9.2) | 50.3 (9.2) | N/A | 30.7 (6.1) | Affymetrix GeneChip 500K |
| | | Controls | 2,938 (1,446/1,492) | N/A | | N/A | N/A | |
| CAGE | East Asian (Japan) | Cases | 931 (623/308) | 66.1 (9.5) | N/A | N/A | 24.4 (3.4) | Illumina Human 550K/610K |
| | | Controls | 1,404 (844/560) | 65.9 (7.4) | | N/A | 23.1 (3.0) | |
| CLHNS | East Asian (Philippines) | Cases | 159 (0/159) | 49.6 (6.1) | N/A | 10.7 (3.5) | 25.9 (4.3) | Affymetrix GeneChip 500K |
| | | Controls | 1,624 (0/1,624) | 48.3 (6.1) | | 5.0 (0.6) | 24.4 (4.3) | |
| KARE | East Asian (Korea) | Cases | 1,042 (539/503) | 56.4 (8.6) | N/A | 7.0 (2.6) | 25.5 (3.3) | Affymetrix Human SNP Array 5.0 |
| | | Controls | 2,943 (1,355/1,588) | 51.5 (8.6) | | 4.5 (0.4) | 24.1 (3.0) | |
| SDCS/SP2(1) | East Asian (Singapore) | Cases | 1,082 (402/680) | 65.1 (9.7) | 55.7 (12.0) | N/A | 25.3 (3.9) | Illumina Human 610K |
| | | Controls | 1,006 (217/789) | 47.7 (11.1) | | 4.7 (0.5) | 22.3 (3.7) | |
| SDCS/SP(2) | East Asian (Singapore) | Cases | 928 (602/326) | 63.7 (10.8) | 52.2 (14.4) | N/A | 25.4 (3.8) | Illumina Human 1M |
| | | Controls | 939 (599/340) | 46.7 (10.2) | | 4.7 (0.5) | 22.8 (3.4) | |
| SDGS | East Asian | Cases | 1,019 (0/1,019) | 51.7 (6.7) | 51.7 (6.7) | N/A | 26.5 (3.7) | Affymetrix Human SNP Array 6.0 |

| | | | | | | | | |
|--------------|-------------------------|----------|---------------------|-------------|-------------|------------|------------|--------------------------------|
| | (China) | Controls | 1,710 (1,710/0) | 48.7 (8.5) | | N/A | 23.1 (3.3) | |
| SIMES | East Asian (Singapore) | Cases | 794 (388/406) | 62.3 (9.9) | 54.4 (11.2) | N/A | 27.8 (4.9) | Illumina Human 610K |
| | | Controls | 1,240 (595/645) | 56.9 (11.4) | | N/A | 25.1 (4.8) | |
| TDS | East Asian (China) | Cases | 999 (504/495) | 59.2 (NA) | 50.0 (N/A) | N/A | 23.8 (N/A) | Illumina Human 550K |
| | | Controls | 1,000 (502/498) | 51.2 (NA) | | N/A | 23.8 (N/A) | |
| LOLIPOP610 | South Asian (UK) | Cases | 1,783 (1,478/305) | 59.4 (9.2) | N/A | 8.6 (3.1) | 28.1 (4.6) | Illumina Human 610K |
| | | Controls | 4,773 (4,048/725) | 53.9 (10.7) | | 5.2 (0.6) | 26.8 (4.2) | |
| LOLIPOP317 | South Asian (UK) | Cases | 440 (440/0) | 54.1 (10.1) | N/A | 8.9 (2.9) | 27.6 (4.7) | Illumina Human 300K |
| | | Controls | 1,699 (1,699/0) | 46.8 (10.1) | | 5.1 (0.6) | 26.6 (4.2) | |
| PROMIS | South Asian (Pakistan) | Cases | 2,361 (1,806/555) | 55.0 (9.4) | N/A | 13.3 (5.5) | 26.0 (4.0) | Illumina Human 650K |
| | | Controls | 6,817 (5,658/1,159) | 52.9 (10.5) | | 6.9 (2.9) | 25.3 (3.9) | |
| SINDI | South Asian (Singapore) | Cases | 977 (531/446) | 60.7 (9.9) | N/A | 9.7 (4.4) | 27.1 (5.1) | Illumina Human 610K |
| | | Controls | 1,169 (566/603) | 55.7 (9.7) | | 5.4 (1.1) | 25.3 (4.4) | |
| Mexico City | Mexican (Mexico) | Cases | 967 (303/664) | 50.5 (9.2) | 43.7 (7.1) | 10.2 (4.3) | 29.6 (4.8) | Affymetrix Human SNP Array 5.0 |
| | | Controls | 343 (169/174) | 50.7 (5.0) | | 4.8 (0.4) | 27.4 (3.6) | |
| Starr County | Mexican American (USA) | Cases | 837 (333/504) | 56.5 (11.8) | 46.7 (10.9) | 10.0 (4.1) | 31.8 (6.4) | Affymetrix Human SNP Array 6.0 |
| | | Controls | 436 (137/299) | 37.6 (9.0) | | 4.7 (0.5) | 29.5 (6.5) | |

(b) European ancestry “validation” meta-analysis.

| Study | Ethnic group (country of origin) | Case-control status | Sample characteristics | | | | | Genotyping array |
|----------------|----------------------------------|---------------------|-----------------------------|-----------------------|--------------------------------|------------------------------------|------------------------------------|------------------|
| | | | Sample size (males/females) | Age (years) mean (SD) | Age at onset (years) mean (SD) | Fasting glucose (mmol/l) mean (SD) | BMI (kg/m ²) mean (SD) | |
| AMC-PAS | European (Netherlands) | Cases | 48 (35/13) | 44.0 (4.7) | N/A | 8.6 (3.2) | 29.3 (4.4) | Metabochip |
| | | Controls | 442 (333/109) | 43.2 (5.3) | | 5.3 (0.6) | 26.6 (4.1) | |
| BHS | European (Australia) | Cases | 51 (38/13) | 72.3 (7.8) | N/A | 7.8 (4.0) | 27.2 (3.9) | Metabochip |
| | | Controls | 359 (224/135) | 70.0 (9.6) | | 5.1 (0.9) | 26.6 (3.9) | |
| deCODE Stage 2 | European (Iceland) | Cases | 722 (433/289) | 67.3 (13.6) | N/A | N/A | 31.2 (6.3) | Metabochip |
| | | Controls | 10,153 (6,604/3,549) | 44.3 (26.5) | | N/A | N/A | |
| DILGOM | European (Finland) | Cases | 541 (298/243) | 60.5 (10.3) | N/A | N/A | 30.1 (5.6) | Metabochip |
| | | Controls | 3,357 (1,480/1,877) | 50.9 (13.5) | | N/A | 26.5 (4.5) | |
| DUNDEE | European (UK) | Cases | 3,298 (1,940/1,358) | 63.5 (9.6) | 55.9 (8.9) | N/A | 31.9 (6.3) | Metabochip |
| | | Controls | 3,708 (1,918/1,790) | 59.1 (11.3) | | 4.9 (0.5) | 27.0 (4.5) | |
| EAS | European (UK) | Cases | 110 (64/46) | 64.0 (5.6) | N/A | N/A | 25.9 (3.3) | Metabochip |
| | | Controls | 641 (301/340) | 64.5 (5.6) | | N/A | 25.5 (3.9) | |
| EGCUT | European (Estonia) | Cases | 938 (342/596) | 64.1 (10.5) | N/A | N/A | 33.4 (5.4) | Metabochip |
| | | Controls | 915 (326/589) | 51.7 (10.7) | | N/A | 22.3 (2.5) | |
| EMIL-ULM | European (Germany) | Cases | 755 (510/245) | 48.7 (12.0) | 45.5 (10.8) | N/A | 28.6 (7.1) | Metabochip |
| | | Controls | 1,632 (765/867) | 45.1 (10.9) | | N/A | 26.7 (5.0) | |
| EPIC | European (UK) | Cases | 727 (432/295) | 61.8 (8.2) | N/A | N/A | 29.5 (4.4) | Metabochip |
| | | Controls | 927 (393/534) | 58.8 (9.4) | | N/A | 26.1 (3.7) | |
| FUSION Stage 2 | European (Finland) | Cases | 1,037 (584/453) | 59.7 (8.4) | N/A | 7.7 (2.3) | 30.8 (5.4) | Metabochip |
| | | Controls | 1,157 (691/466) | 59.0 (7.6) | | 5.4 (0.4) | 26.9 (3.9) | |

| | | | | | | | | |
|-----------------|---------------------------|----------|---------------------|-------------|-------------|-----------|------------|------------|
| D2D2007 | European (Finland) | Cases | 454 (269/185) | 63.4 (7.6) | N/A | 7.7 (1.8) | 30.6 (5.6) | MetaboChip |
| | | Controls | 1,229 (455/774) | 58.1 (8.2) | | 5.6 (0.3) | 26.2 (4.3) | |
| Dr's Extra | European (Finland) | Cases | 110 (53/57) | 68.4 (5.8) | N/A | 6.6 (0.8) | 30.9 (5.6) | MetaboChip |
| | | Controls | 785 (341/444) | 66.0 (5.3) | | 5.4 (0.3) | 26.7 (4.0) | |
| HUNT | European (Norway) | Cases | 1,239 (628/611) | 64.0 (12.9) | 61.9 (11.9) | N/A | 29.2 (4.8) | MetaboChip |
| | | Controls | 1,375 (691/684) | 63.5 (13.9) | | N/A | 26.5 (4.0) | |
| METSIM | European (Finland) | Cases | 1,169 (1,169/0) | 60.5 (6.6) | 57.0 (8.0) | 7.5 (2.0) | 30.2 (5.2) | MetaboChip |
| | | Controls | 651 (651/0) | 53.8 (5.0) | | 5.5 (0.3) | 25.9 (3.1) | |
| GMetS | European (France) | Cases | 507 (334/173) | 55.9 (9.9) | N/A | N/A | 28.5 (3.9) | MetaboChip |
| | | Controls | 2,553 (1,134/1,419) | 47.3 (11.1) | | N/A | 24.8 (3.8) | |
| HNR | European (Germany) | Cases | 520 (315/205) | 62.6 (7.2) | N/A | N/A | 30.4 (5.2) | MetaboChip |
| | | Controls | 3,932 (1,911/2,021) | 59.2 (7.8) | | N/A | 27.5 (4.4) | |
| IMPROVE | European (Sweden) | Cases | 898 (513/385) | 64.3 (5.6) | N/A | 7.7 (2.2) | 29.2 (4.6) | MetaboChip |
| | | Controls | 2,521 (1,134/1,387) | 64.2 (5.3) | | 5.3 (0.7) | 26.5 (3.9) | |
| KORAGen Stage 2 | European (Germany) | Cases | 940 (504/436) | 61.6 (10.0) | N/A | N/A | 30.8 (5.4) | MetaboChip |
| | | Controls | 4,209 (2,000/2,209) | 53.8 (13.2) | | N/A | 27.2 (4.6) | |
| PIVUS | European (Sweden) | Cases | 113 (70/43) | 70.2 (0.2) | N/A | N/A | 29.5 (5.1) | MetaboChip |
| | | Controls | 864 (419/445) | 70.2 (0.2) | | N/A | 26.8 (4.2) | |
| PMB | European (Sweden/Finland) | Cases | 4,976 (2,911/2,065) | 58.8 (12.5) | N/A | N/A | 28.2 (8.7) | MetaboChip |
| | | Controls | 3,500 (1,700/1,800) | 58.3 (8.4) | | N/A | 26.4 (4.4) | |
| SCARFSHEEP | European (Sweden) | Cases | 341 (246/95) | 59.6 (7.0) | N/A | 8.12(5.4) | 27.4 (8.4) | MetaboChip |
| | | Controls | 3,073 (2,211/862) | 57.9 (7.3) | | 4.0 (3.8) | 25.4 (6.1) | |
| STR | European (Sweden) | Cases | 320 (141/179) | 71.5 (9.3) | N/A | N/A | 27.0 (4.1) | MetaboChip |
| | | Controls | 1,318 (612/706) | 74.3 (10.5) | | N/A | 24.9 (3.8) | |
| THISEAS | European (Greece) | Cases | 327 (229/98) | 63.6 (10.6) | N/A | 8.0 (2.6) | 29.4 (4.8) | MetaboChip |
| | | Controls | 1,180 (643/537) | 58.2 (13.6) | | 5.3 (0.6) | 28.3 (5.0) | |
| ULSAM | European (Sweden) | Cases | 233 (233/0) | 71.0 (0.6) | N/A | N/A | 27.7 (3.8) | MetaboChip |
| | | Controls | 942 (942/0) | 71.0 (0.6) | | N/A | 25.9 (3.2) | |
| WARREN2 | European (UK) | Cases | 1,117 (647/470) | N/A | 45.5 (11.0) | N/A | 32.2 (6.6) | MetaboChip |
| | | Controls | 4,224 (2,394/1,830) | N/A | | N/A | N/A | |

Supplementary Table 2. Summary of study-specific quality control, imputation and analysis.

(a) Trans-ethnic meta-analysis.

| Study | Ethnic group (Country of origin) | Sample quality control | | SNP quality control | | | | | Imputation | | Analysis | | |
|-------------|-------------------------------------|------------------------|--|----------------------------|--------------------|-------|---------------------|-------------|------------|-------------------------|------------------------------------|---------------------------------|----------------|
| | | Call rate | Exclusions | Call rate | HWE | MAF | Imputation | Passed SNPs | Software | Reference panel | Software | Covariates | λ_{GC} |
| ARIC | European (USA) | ≥0.95 | Relatedness and duplicates | ≥0.90 | p>10 ⁻⁶ | ≥0.01 | r ² >0.3 | 2,443,161 | MACH | HapMap2 CEU | ProbABEL | Age, sex, and study centre | 1.01 |
| deCODE | European (Iceland) | ≥0.98 | Duplicates | ≥0.96 | p>10 ⁻⁶ | ≥0.01 | proper-info>0.5 | 2,338,113 | IMPUTE | HapMap2 CEU | SNPTEST | None | 1.31 |
| DGDG | European (France) | ≥0.95 | Duplicates | ≥0.95 | p>10 ⁻⁴ | ≥0.01 | proper-info>0.5 | 2,051,387 | IMPUTE | HapMap2 CEU | SNPTEST | None | 1.10 |
| DGI | European (Sweden/Finland) | ≥0.95 | Duplicates | ≥0.95 | p>10 ⁻⁶ | ≥0.01 | proper-info>0.5 | 2,230,032 | IMPUTE | HapMap2 CEU | PLINK and SNPTEST | Age, sex, BMI, and study centre | 1.06 |
| EUROSPAN | European (various isolates) | ≥0.98 | Duplicates | ≥0.98 | p>10 ⁻⁶ | ≥0.01 | r ² >0.5 | 2,359,525 | MACH | HapMap2 CEU | GenABEL and SNPTEST | Age and sex | 0.98 |
| FHS | European (USA) | ≥0.95 | Duplicates | ≥0.95 | p>10 ⁻⁶ | ≥0.01 | r ² >0.3 | 2,389,929 | MACH | HapMap2 CEU | R (GEE correction for relatedness) | Age, sex, and cohort | 1.02 |
| FUSION | European (Finland) | ≥0.975 | Duplicates | ≥0.90 | p>10 ⁻⁶ | ≥0.01 | r ² >0.3 | 2,413,085 | MACH | HapMap2 CEU | MACH2DAT | Age, sex, and birth province | 1.04 |
| HPFS | European (USA) | ≥0.95 | Relatedness and duplicates | ≥0.95 | p>10 ⁻⁶ | ≥0.01 | N/A | 622,575 | N/A | N/A | PLINK | Age and BMI | 1.03 |
| KORAGen | European (Germany) | ≥0.93 | Duplicates | ≥0.95 | p>10 ⁻⁶ | ≥0.01 | proper-info>0.5 | 2,325,232 | IMPUTE | HapMap2 CEU | SNPTEST | Age and sex | 1.04 |
| NHS | European (USA) | ≥0.98 | Relatedness and duplicates | ≥0.98 | p>10 ⁻⁶ | ≥0.02 | N/A | 615,391 | N/A | N/A | PLINK | Age and BMI | 0.98 |
| RS1 | European (Netherlands) | ≥0.975 | Duplicates | ≥0.98 | p>10 ⁻⁶ | ≥0.01 | r ² >0.5 | 2,439,672 | MACH | HapMap2 CEU | GenABEL and SNPTEST | None | 1.01 |
| WTCCC | European (UK) | ≥0.97 | Duplicates | ≥0.95 (≥0.99 for MAF<0.05) | p>10 ⁻³ | ≥0.01 | proper-info>0.5 | 2,308,535 | IMPUTE | HapMap2 CEU | PLINK and SNPTEST | None | 1.08 |
| CAGE | East Asian (Japan) | ≥0.90 | Relatedness, duplicates and ethnic outliers | ≥0.95 | p>10 ⁻⁶ | ≥0.01 | r ² >0.3 | 1,988,685 | IMPUTE | HapMap2 CHB+JPT | PLINK | Sex and BMI | 1.06 |
| CLHNS | East Asian (Philippines) | ≥0.97 | Duplicates | ≥0.90 | p>10 ⁻⁶ | ≥0.01 | r ² >0.3 | 2,049,920 | MACH | HapMap2 CHB+JPT+CEU | MACH2DAT | BMI and PCs | 1.01 |
| KARE | East Asian (Korea) | ≥0.98 | Relatedness, duplicates and ethnic outliers | ≥0.95 | p>10 ⁻⁶ | ≥0.01 | proper-info>0.5 | 1,419,177 | IMPUTE | HapMap2 CHB+JPT | PLINK | Sex, BMI and study centre | 1.01 |
| SDCS/SP2(1) | East Asian (Singapore) | ≥0.95 | Relatedness, duplicates and ethnic outliers | ≥0.95 | p>10 ⁻⁶ | N/A | proper-info>0.5 | 1,965,414 | IMPUTE | HapMap2 CHB+JPT | SNPTEST | Sex and BMI | 1.05 |
| SDCS/SP2(2) | East Asian (Singapore) | ≥0.95 | Relatedness, duplicates and ethnic outliers | ≥0.95 | p>10 ⁻⁶ | N/A | proper-info>0.5 | 2,248,003 | IMPUTE | HapMap2 CHB+JPT | SNPTEST | Sex and BMI | 1.06 |
| SDGS | East Asian (China) | ≥0.95 | Relatedness and duplicates | ≥0.95 | p>10 ⁻⁵ | ≥0.05 | r ² >0.3 | 2,241,970 | MACH | HapMap2 CHB+JPT | MACH2DAT, PLINK | BMI | 1.04 |
| SiMES | East Asian (Singapore) | ≥0.95 | Relatedness, duplicates and ethnic outliers | ≥0.95 | p>10 ⁻⁶ | N/A | proper-info>0.5 | 1,625,733 | IMPUTE | HapMap2 CHB+JPT+CEU+YRI | SNPTEST | Sex, BMI and PCs | 1.04 |
| TDS | East Asian (China) | N/A | N/A | ≥0.95 | p>10 ⁻⁶ | ≥0.05 | r ² >0.3 | 1,890,143 | MACH | HapMap2 CHB+JPT | SAS | Sex and BMI | 1.04 |
| LOLIPOP610 | South Asian (UK) | ≥0.95 | Relatedness, duplicates, and ethnic outliers | ≥0.95 | p>10 ⁻⁶ | ≥0.01 | r ² >0.3 | 2,220,688 | MACH | HapMap2 CHB+JPT+CEU+YRI | MACH2DAT, PLINK | Study centre, CHD, and PCs | 1.02 |
| LOLIPOP317 | South Asian | ≥0.95 | Relatedness, duplicates, | ≥0.95 | p>10 ⁻⁶ | ≥0.01 | r ² >0.3 | 1,950,903 | MACH | HapMap2 | MACH2DAT, PLINK | PCs | 1.01 |

| | | | | | | | | | | | | | |
|--------------|-------------------------|-------|--|-------|-------------------|-------|---------------------|-----------|--------|-------------------------------|------------|-------------------|------|
| | (UK) | | and ethnic outliers | | | | | | | CHB+JPT+CEU+YRI | | | |
| PROMIS | South Asian (Pakistan) | ≥0.95 | Relatedness | ≥0.97 | p>10-6 | ≥0.01 | proper-info>0.4 | 2,527,357 | IMPUTE | HapMap2&3 CEU+GIH | SNPTEST v2 | PCs | 1.01 |
| SINDI | South Asian (Singapore) | ≥0.95 | Relatedness, duplicates, and ethnic outliers | ≥0.95 | p>10-6 | ≥0.01 | proper-info>0.3 | 2,035,725 | IMPUTE | HapMap2 CHB+JPT+CEU+YRI | SNPTEST | PCs | 1.03 |
| Mexico City | Mexican (Mexico) | ≥0.95 | Relatedness and duplicates | ≥0.95 | p>10-4 (controls) | ≥0.05 | proper-info>0.5 | 1,829,070 | IMPUTE | HapMap2&3 CHB+JPT+CEU+YRI+MXL | SNPTEST | Age, sex, and PCs | 1.03 |
| Starr County | Mexican American (USA) | ≥0.90 | Relatedness and duplicates | ≥0.90 | None | ≥0.05 | r ² >0.7 | 1,782,420 | MACH | HapMap2 CHB+JPT+CEU+YRI | SNPTEST | Age and sex | 1.03 |

(b) European ancestry “validation” meta-analysis.

| Study | Ethnic group (Country of origin) | Sample quality control | | SNP quality control | | | | Imputation | | | Analysis | | |
|-----------------|----------------------------------|------------------------|---------------------------------|----------------------------|------------|-------|------------|-------------|----------|-----------------|----------|------------------------------|-----------------|
| | | Call rate | Exclusions | Call rate | HWE | MAF | Imputation | Passed SNPs | Software | Reference panel | Software | Covariates | λ _{QT} |
| AMC-PAS | European (Netherlands) | ≥0.95 | Duplicates and ethnic outliers | ≥0.98 | p>10-4 | ≥0.01 | N/A | 109,525 | N/A | N/A | PLINK | Age and sex | 1.00 |
| BHS | European (Australia) | ≥0.95 | Relatedness | ≥0.95 | p>10-6 | ≥0.01 | N/A | 119,893 | N/A | N/A | PLINK | Age and sex | 0.96 |
| deCODE Stage 2 | European (Iceland) | N/A | N/A | N/A | N/A | ≥0.01 | N/A | 125,236 | N/A | N/A | SNPTEST | Sex | 0.95 |
| DILGOM | European (Finland) | ≥0.95 | Relatedness | ≥0.95 | p>10-6 | ≥0.01 | N/A | 116,634 | N/A | N/A | PLINK | Age, sex, and PCs | 0.93 |
| DUNDEE | European (UK) | ≥0.95 | Duplicates and ethnic outliers | ≥0.95 (≥0.99 for MAF<0.05) | p>5.7x10-7 | ≥0.01 | N/A | 121,365 | N/A | N/A | PLINK | PCs | 1.07 |
| EAS | European (UK) | ≥0.95 | | ≥0.95 | p>10-6 | ≥0.01 | N/A | 119,523 | N/A | N/A | PLINK | Age and sex | 1.00 |
| EGCUT | European (Estonia) | ≥0.95 | Relatedness and ethnic outliers | ≥0.95 | p>10-6 | ≥0.01 | N/A | 120,720 | N/A | N/A | SNPTEST | Age, sex, and PCs | 1.00 |
| EMIL-ULM | European (Germany) | ≥0.95 | Relatedness | ≥0.95 | p>10-6 | ≥0.01 | N/A | 121,684 | N/A | N/A | PLINK | Age and sex | 1.14 |
| EPIC | European (UK) | ≥0.95 | Duplicates | ≥0.90 | p>10-6 | ≥0.01 | N/A | 120,527 | N/A | N/A | PLINK | Age and sex | 0.97 |
| FUSION Stage 2 | European (Finland) | ≥0.98 | Relatedness | ≥0.98 | p>10-5 | ≥0.01 | N/A | 123,853 | N/A | N/A | PLINK | Age and sex | 0.97 |
| D2D2007 | European (Finland) | ≥0.98 | Relatedness | ≥0.98 | p>10-5 | ≥0.01 | N/A | 123,461 | N/A | N/A | PLINK | Age and sex | 0.96 |
| Dr’s Extra | European (Finland) | ≥0.98 | Relatedness | ≥0.98 | p>10-5 | ≥0.01 | N/A | 120,746 | N/A | N/A | PLINK | Age and sex | 0.94 |
| HUNT | European (Norway) | ≥0.98 | Relatedness | ≥0.98 | p>10-5 | ≥0.01 | N/A | 125,644 | N/A | N/A | PLINK | Age, sex and collection site | 1.10 |
| METSIM | European (Finland) | ≥0.98 | Relatedness | ≥0.98 | p>10-5 | ≥0.01 | N/A | 122,600 | N/A | N/A | PLINK | Age | 1.01 |
| GMetS | European (France) | ≥0.95 | Duplicates | ≥0.95 | p>10-4 | ≥0.01 | N/A | 123,359 | N/A | N/A | PLINK | Age, sex, and BMI | 1.11 |
| HNR | European (Germany) | ≥0.97 | Relatedness and ethnic outliers | ≥0.95 | p>10-6 | ≥0.01 | N/A | 126,675 | N/A | N/A | PLINK | Age and sex | 1.00 |
| IMPROVE | European (Sweden) | ≥0.95 | Relatedness and ethnic outliers | ≥0.95 | p>10-6 | ≥0.01 | N/A | 122,320 | N/A | N/A | PLINK | Age, sex, and PCs | 1.13 |
| KORAGen Stage 2 | European | ≥0.95 | Relatedness | ≥0.95 | p>10-6 | ≥0.01 | N/A | 120,547 | N/A | N/A | PLINK | Age and sex | 1.02 |

| | | | | | | | | | | | | | |
|------------|---------------------------|-------|---------------------------------|-------|--------------------|-------|-----|---------|-----|-----|-------|-----------------------|------|
| | (Germany) | | | | | | | | | | | | |
| PIVUS | European (Sweden) | ≥0.95 | Relatedness | ≥0.95 | p>10 ⁻⁶ | ≥0.01 | N/A | 120,892 | N/A | N/A | PLINK | Age and sex | 0.97 |
| PMB | European (Sweden/Finland) | ≥0.95 | Relatedness and ethnic outliers | ≥0.95 | p>10 ⁻⁶ | ≥0.01 | N/A | 119,674 | N/A | N/A | PLINK | PCs | 1.05 |
| SCARFSHEEP | European (Sweden) | ≥0.95 | Relatedness | ≥0.95 | p>10 ⁻⁶ | ≥0.01 | N/A | 121,792 | N/A | N/A | PLINK | Age, sex, PCs, and MI | 1.00 |
| STR | European (Sweden) | ≥0.95 | Relatedness | ≥0.95 | p>10 ⁻⁶ | ≥0.01 | N/A | 119,375 | N/A | N/A | PLINK | Age, sex, PCs and CAD | 0.98 |
| THISEAS | European (Greece) | ≥0.95 | N/A | ≥0.95 | p>10 ⁻⁶ | ≥0.01 | N/A | 120,509 | N/A | N/A | PLINK | Age and sex | 0.99 |
| ULSAM | European (Sweden) | ≥0.95 | Duplicates and ethnic outliers | ≥0.98 | p>10 ⁻⁴ | ≥0.01 | N/A | 108,868 | N/A | N/A | PLINK | Age | 1.00 |
| WARREN2 | European (UK) | ≥0.95 | Relatedness | ≥0.95 | p>10 ⁻⁶ | ≥0.01 | N/A | 119,018 | N/A | N/A | PLINK | Age and sex | 0.95 |

Supplementary Table 3. Association summary statistics in each ancestry group (European, East Asian, South Asian, and Mexican and Mexican American) for previously reported lead SNPs at established autosomal T2D susceptibility loci and assessment of heterogeneity in allelic effects after fixed-effects trans-ethnic GWAS meta-analysis of 26,488 cases and 83,964 controls.

| Locus | Lead SNP | Chr | Build 36 position (bp) | Alleles | | European 12,171 cases and 56,862 controls | | | East Asian 6,952 cases and 11,865 controls | | | South Asian 5,561 cases and 14,458 controls | | | Mexican and Mexican American 1,804 cases and 779 controls | | | Trans-ethnic meta-analysis | |
|-----------------------|------------|-----|------------------------|---------|-------|--|------------------|---------|---|------------------|---------|--|------------------|---------|--|------------------|---------|-------------------------------|-------------|
| | | | | Risk | Other | RAF | OR (95% CI) | p-value | RAF | OR (95% CI) | p-value | RAF | OR (95% CI) | p-value | RAF | OR (95% CI) | p-value | p-value | Cochran's Q |
| <i>TCF7L2</i> | rs7903146 | 10 | 114,748,339 | T | C | 0.30 | 1.40 (1.35-1.46) | 1.9E-59 | 0.05 | 1.18 (1.03-1.35) | 1.6E-02 | 0.31 | 1.25 (1.19-1.32) | 3.6E-19 | 0.23 | 1.16 (0.97-1.38) | 1.1E-01 | 7.8E-75 | 5.5E-04 |
| <i>PEPD</i> | rs3786897 | 19 | 38,584,848 | A | G | 0.57 | 1.02 (0.98-1.06) | 3.3E-01 | 0.40 | 1.17 (1.10-1.24) | 3.5E-07 | 0.72 | 1.04 (0.99-1.10) | 1.5E-01 | 0.74 | 0.90 (0.76-1.07) | 2.3E-01 | 3.3E-04 | 5.5E-04 |
| <i>KLF14</i> | rs13233731 | 7 | 130,088,229 | G | A | 0.49 | 1.10 (1.06-1.13) | 1.7E-07 | 0.68 | 0.99 (0.94-1.04) | 6.5E-01 | 0.61 | 0.99 (0.94-1.04) | 6.1E-01 | 0.61 | 1.07 (0.93-1.23) | 3.4E-01 | 7.0E-04 | 6.4E-04 |
| <i>CDKAL1</i> | rs7756992 | 6 | 20,787,688 | G | A | 0.26 | 1.20 (1.16-1.25) | 1.1E-21 | 0.60 | 1.14 (1.09-1.20) | 4.8E-08 | 0.27 | 1.06 (1.01-1.12) | 2.0E-02 | 0.34 | 1.09 (0.94-1.27) | 2.4E-01 | 1.6E-26 | 2.6E-03 |
| <i>VPS26A</i> | rs1802295 | 10 | 70,601,480 | T | C | 0.33 | 1.02 (0.98-1.06) | 3.0E-01 | 0.22 | 1.01 (0.94-1.09) | 8.0E-01 | 0.27 | 1.13 (1.07-1.20) | 7.7E-06 | N/A | N/A | N/A | 1.4E-03 | 4.4E-03 |
| <i>GCC1</i> | rs6467136 | 7 | 126,952,194 | G | A | 0.55 | 0.99 (0.95-1.03) | 5.5E-01 | 0.68 | 1.11 (1.05-1.18) | 2.4E-04 | 0.56 | 1.01 (0.96-1.06) | 7.6E-01 | 0.49 | 0.96 (0.84-1.10) | 5.8E-01 | 2.0E-01 | 5.6E-03 |
| <i>TSPAN8</i> | rs7955901 | 12 | 69,719,560 | C | T | 0.47 | 1.09 (1.05-1.13) | 9.0E-06 | 0.49 | 0.97 (0.92-1.02) | 2.7E-01 | 0.42 | 1.03 (0.98-1.08) | 2.3E-01 | 0.54 | 1.00 (0.87-1.14) | 9.9E-01 | 1.6E-03 | 6.1E-03 |
| <i>GCKR</i> | rs780094 | 2 | 27,594,741 | C | T | 0.62 | 1.04 (1.00-1.08) | 3.2E-02 | 0.38 | 1.06 (1.01-1.11) | 2.1E-02 | 0.75 | 1.19 (1.11-1.29) | 4.2E-06 | 0.65 | 0.99 (0.85-1.14) | 8.5E-01 | 1.0E-05 | 8.7E-03 |
| <i>GRB14</i> | rs3923113 | 2 | 165,210,095 | A | C | 0.61 | 1.04 (1.00-1.09) | 4.0E-02 | 0.77 | 1.03 (0.95-1.12) | 4.8E-01 | 0.75 | 1.15 (1.09-1.21) | 8.9E-07 | 0.76 | 1.22 (1.03-1.45) | 2.3E-02 | 1.5E-06 | 1.3E-02 |
| <i>BCAR1</i> | rs7202877 | 16 | 73,804,746 | T | G | 0.90 | 1.15 (1.07-1.23) | 5.0E-05 | 0.64 | 1.00 (0.93-1.07) | 1.0E+00 | 0.93 | 1.06 (0.97-1.16) | 1.9E-01 | 0.93 | 1.38 (1.02-1.87) | 3.5E-02 | 5.7E-04 | 1.3E-02 |
| <i>ZFAND3</i> | rs9470794 | 6 | 38,214,822 | C | T | 0.19 | 0.99 (0.93-1.06) | 8.1E-01 | 0.32 | 1.11 (1.05-1.18) | 2.4E-04 | 0.12 | 1.07 (0.99-1.15) | 7.3E-02 | 0.08 | 0.82 (0.63-1.06) | 1.2E-01 | 3.6E-03 | 1.4E-02 |
| <i>PSMD6</i> | rs831571 | 3 | 64,023,337 | C | T | 0.81 | 1.03 (0.99-1.08) | 1.8E-01 | 0.45 | 1.11 (1.05-1.16) | 4.5E-05 | 0.79 | 1.03 (0.98-1.09) | 2.6E-01 | 0.91 | 0.80 (0.63-1.01) | 6.3E-02 | 3.7E-04 | 1.5E-02 |
| <i>CILP2</i> | rs10401969 | 19 | 19,268,718 | C | T | 0.07 | 1.13 (1.05-1.21) | 9.3E-04 | 0.42 | 1.01 (0.90-1.12) | 8.9E-01 | 0.10 | 1.00 (0.92-1.09) | 9.7E-01 | 0.04 | 1.59 (1.08-2.35) | 1.8E-02 | 9.7E-03 | 2.0E-02 |
| <i>RASGRP1</i> | rs7403531 | 15 | 36,610,197 | T | C | 0.22 | 1.02 (0.98-1.06) | 3.8E-01 | 0.55 | 1.08 (1.02-1.13) | 3.8E-03 | 0.25 | 0.97 (0.92-1.03) | 3.5E-01 | 0.39 | 0.90 (0.77-1.05) | 1.8E-01 | 1.5E-01 | 2.1E-02 |
| <i>RBMS1</i> | rs7593730 | 2 | 160,879,700 | C | T | 0.79 | 1.11 (1.06-1.16) | 4.3E-06 | 0.72 | 1.00 (0.94-1.07) | 9.2E-01 | 0.79 | 1.01 (0.95-1.07) | 7.7E-01 | 0.86 | 1.05 (0.86-1.28) | 6.2E-01 | 4.7E-04 | 2.7E-02 |
| <i>TLE4</i> | rs17791513 | 9 | 81,095,410 | A | G | 0.93 | 1.21 (1.13-1.31) | 4.3E-07 | 0.90 | 1.00 (0.89-1.11) | 9.4E-01 | 0.87 | 1.12 (1.05-1.21) | 1.1E-03 | 0.85 | 1.21 (0.99-1.47) | 6.6E-02 | 3.2E-08 | 3.0E-02 |
| <i>ZBED3</i> | rs6878122 | 5 | 76,463,067 | G | A | 0.25 | 1.13 (1.07-1.18) | 3.2E-06 | 0.09 | 1.08 (0.94-1.24) | 3.0E-01 | 0.20 | 1.01 (0.96-1.08) | 6.4E-01 | N/A | N/A | N/A | 6.3E-05 | 3.1E-02 |
| <i>HHEX/IDE</i> | rs1111875 | 10 | 94,452,862 | C | T | 0.58 | 1.15 (1.11-1.19) | 1.2E-14 | 0.34 | 1.15 (1.09-1.22) | 2.3E-06 | 0.44 | 1.07 (1.02-1.12) | 6.9E-03 | 0.64 | 1.00 (0.87-1.16) | 9.6E-01 | 3.2E-19 | 3.4E-02 |
| <i>CDC123</i> | rs11257655 | 10 | 12,347,900 | T | C | 0.23 | 1.06 (1.01-1.11) | 1.7E-02 | 0.61 | 1.15 (1.09-1.23) | 3.4E-06 | 0.23 | 1.12 (1.06-1.18) | 5.9E-05 | 0.30 | 0.96 (0.81-1.13) | 6.2E-01 | 2.6E-09 | 4.3E-02 |
| <i>ARAP1 (CENTD2)</i> | rs1552224 | 11 | 72,110,746 | A | C | 0.83 | 1.13 (1.08-1.19) | 1.5E-06 | 0.89 | 1.16 (1.05-1.28) | 2.5E-03 | 0.83 | 1.04 (0.98-1.11) | 2.2E-01 | N/A | N/A | N/A | 1.2E-07 | 5.5E-02 |
| <i>KCNQ1</i> | rs163184 | 11 | 2,803,645 | G | T | 0.50 | 1.09 (1.04-1.13) | 4.3E-05 | 0.39 | 1.16 (1.10-1.23) | 1.6E-08 | 0.53 | 1.08 (1.03-1.13) | 1.2E-03 | 0.48 | 1.23 (1.06-1.43) | 6.6E-03 | 1.7E-14 | 5.8E-02 |
| <i>NOTCH2</i> | rs10923931 | 1 | 120,319,482 | T | G | 0.11 | 1.10 (1.04-1.17) | 5.8E-04 | 0.05 | 1.00 (0.86-1.16) | 9.9E-01 | 0.18 | 1.01 (0.95-1.07) | 8.3E-01 | 0.10 | 0.89 (0.70-1.13) | 3.3E-01 | 1.7E-02 | 6.8E-02 |
| <i>JAZF1</i> | rs849135 | 7 | 28,162,938 | G | A | 0.52 | 1.12 (1.08-1.17) | 1.9E-09 | 0.51 | 1.01 (0.76-1.33) | 9.5E-01 | 0.73 | 1.04 (0.98-1.10) | 1.6E-01 | 0.67 | 1.19 (1.03-1.38) | 1.9E-02 | 1.7E-09 | 6.9E-02 |
| <i>KCNJ11</i> | rs5215 | 11 | 17,365,206 | C | T | 0.38 | 1.08 (1.04-1.12) | 1.1E-05 | 0.35 | 1.14 (1.09-1.20) | 1.6E-07 | 0.37 | 1.04 (0.99-1.09) | 1.1E-01 | 0.39 | 1.11 (0.96-1.28) | 1.8E-01 | 3.2E-11 | 7.2E-02 |
| <i>DGKB</i> | rs17168486 | 7 | 14,864,807 | T | C | 0.19 | 1.13 (1.07-1.19) | 2.1E-06 | 0.58 | 1.08 (1.02-1.14) | 5.5E-03 | 0.30 | 1.04 (0.99-1.10) | 1.1E-01 | 0.45 | 0.96 (0.82-1.13) | 6.5E-01 | 3.4E-07 | 7.6E-02 |
| <i>THADA</i> | rs10203174 | 2 | 43,543,534 | C | T | 0.90 | 1.15 (1.08-1.21) | 4.7E-06 | 0.99 | 1.57 (0.46-5.34) | 4.7E-01 | 0.85 | 1.01 (0.92-1.11) | 8.3E-01 | N/A | N/A | N/A | 4.8E-05 | 8.3E-02 |
| <i>KCNK16</i> | rs1535500 | 6 | 39,392,028 | T | G | N/A | N/A | N/A | 0.59 | 1.13 (1.08-1.19) | 1.8E-06 | 0.50 | 1.04 (0.98-1.10) | 2.3E-01 | 0.48 | 1.06 (0.92-1.22) | 4.2E-01 | 7.5E-06 | 9.2E-02 |
| <i>ST6GAL1</i> | rs16861329 | 3 | 188,149,155 | C | T | 0.85 | 1.03 (0.96-1.10) | 4.1E-01 | 0.60 | 0.92 (0.86-0.99) | 1.8E-02 | 0.77 | 1.13 (1.07-1.19) | 2.2E-05 | N/A | N/A | N/A | 8.5E-06 | 1.1E-01 |
| <i>MTNR1B</i> | rs10830963 | 11 | 92,348,358 | G | C | 0.27 | 1.11 (1.06-1.16) | 2.5E-06 | 0.59 | 1.00 (0.93-1.08) | 9.5E-01 | 0.37 | 1.10 (1.03-1.16) | 2.3E-03 | 0.22 | 1.12 (0.94-1.33) | 2.2E-01 | 2.0E-07 | 1.2E-01 |
| <i>PTPRD</i> | rs17584499 | 9 | 8,869,118 | T | C | 0.18 | 1.00 (0.94-1.07) | 9.4E-01 | 0.22 | 1.09 (1.00-1.19) | 4.0E-02 | 0.26 | 0.98 (0.93-1.04) | 5.5E-01 | N/A | N/A | N/A | 6.0E-01 | 1.2E-01 |
| <i>PROX1</i> | rs2075423 | 1 | 212,221,342 | G | T | 0.66 | 1.08 (1.04-1.12) | 1.6E-04 | 0.73 | 1.10 (1.02-1.18) | 1.3E-02 | 0.75 | 1.03 (0.98-1.09) | 2.9E-01 | 0.72 | 1.23 (1.05-1.46) | 1.2E-02 | 2.2E-06 | 1.4E-01 |
| <i>HNF4A</i> | rs4812829 | 20 | 42,422,681 | A | G | 0.16 | 1.07 (1.01-1.12) | 1.3E-02 | 0.33 | 1.07 (1.01-1.13) | 1.6E-02 | 0.29 | 1.13 (1.08-1.19) | 1.6E-06 | 0.51 | 0.98 (0.84-1.14) | 7.8E-01 | 4.6E-08 | 1.5E-01 |
| <i>GIPR</i> | rs8108269 | 19 | 50,850,353 | G | T | 0.30 | 1.06 (1.02-1.11) | 5.0E-03 | 0.40 | 1.12 (1.05-1.19) | 3.5E-04 | 0.32 | 1.06 (1.01-1.11) | 2.8E-02 | 0.44 | 0.93 (0.80-1.09) | 3.8E-01 | 4.9E-06 | 1.5E-01 |
| <i>HMG2</i> | rs2261181 | 12 | 64,498,585 | T | C | 0.09 | 1.16 (1.10-1.23) | 3.9E-07 | 0.19 | 1.09 (1.01-1.18) | 2.3E-02 | 0.18 | 1.07 (1.00-1.13) | 3.6E-02 | 0.08 | 0.99 (0.78-1.28) | 9.6E-01 | 3.6E-08 | 1.8E-01 |
| <i>SPRY2</i> | rs1359790 | 13 | 79,615,157 | G | A | 0.73 | 1.10 (1.05-1.14) | 3.2E-06 | 0.68 | 1.05 (0.99-1.11) | 1.0E-01 | 0.83 | 1.02 (0.96-1.09) | 4.7E-01 | 0.60 | 1.02 (0.89-1.18) | 7.6E-01 | 5.8E-06 | 2.2E-01 |
| <i>AP352</i> | rs2028299 | 15 | 88,175,261 | C | A | 0.29 | 1.04 (1.00-1.09) | 4.4E-02 | 0.26 | 1.08 (1.02-1.14) | 1.3E-02 | 0.32 | 1.11 (1.05-1.16) | 4.5E-05 | 0.16 | 1.17 (0.97-1.42) | 1.0E-01 | 5.2E-07 | 2.4E-01 |
| <i>ADAMTS9</i> | rs6795735 | 3 | 64,680,405 | C | T | 0.59 | 1.07 (1.03-1.10) | 4.4E-04 | 0.35 | 1.00 (0.94-1.05) | 9.1E-01 | 0.28 | 1.06 (1.01-1.12) | 2.5E-02 | 0.25 | 1.06 (0.91-1.24) | 4.6E-01 | 2.1E-04 | 2.5E-01 |
| <i>GCK</i> | rs10278336 | 7 | 44,211,888 | A | G | 0.54 | 1.05 (1.01-1.09) | 2.7E-02 | 0.51 | 1.01 (0.93-1.08) | 9.0E-01 | 0.55 | 1.00 (0.95-1.04) | 8.6E-01 | N/A | N/A | N/A | 1.3E-01 | 2.6E-01 |
| <i>ZFAND6</i> | rs11634397 | 15 | 78,219,277 | G | A | 0.64 | 1.09 (1.05-1.13) | 1.8E-05 | 0.13 | 1.00 (0.90-1.11) | 9.9E-01 | 0.53 | 1.05 (0.99-1.12) | 7.6E-02 | N/A | N/A | N/A | 1.4E-05 | 2.8E-01 |

| | | | | | | | | | | | | | | | | | | | |
|-----------------|------------|----|-------------|---|---|------|------------------|---------|------|------------------|---------|------|------------------|---------|------|------------------|---------|---------|---------|
| <i>FTO</i> | rs9936385 | 16 | 52,376,670 | C | T | 0.39 | 1.13 (1.09-1.18) | 3.2E-10 | 0.42 | 1.09 (1.01-1.17) | 3.4E-02 | 0.32 | 1.07 (1.02-1.13) | 1.0E-02 | 0.27 | 1.17 (1.00-1.37) | 5.7E-02 | 1.2E-12 | 3.0E-01 |
| <i>GLIS3</i> | rs7041847 | 9 | 4,277,466 | A | G | 0.50 | 1.05 (1.01-1.09) | 1.4E-02 | 0.43 | 1.10 (1.05-1.15) | 9.3E-05 | 0.56 | 1.04 (0.99-1.08) | 1.5E-01 | 0.63 | 1.07 (0.93-1.24) | 3.5E-01 | 5.4E-06 | 3.1E-01 |
| <i>CCND2</i> | rs11063069 | 12 | 4,244,634 | G | A | 0.21 | 1.10 (1.04-1.15) | 3.2E-04 | 0.05 | 0.97 (0.84-1.13) | 7.0E-01 | 0.12 | 1.02 (0.92-1.14) | 6.8E-01 | 0.11 | 1.15 (0.92-1.43) | 2.1E-01 | 7.5E-04 | 3.2E-01 |
| <i>IGF2BP2</i> | rs4402960 | 3 | 186,994,381 | T | G | 0.31 | 1.13 (1.09-1.17) | 1.8E-10 | 0.42 | 1.08 (1.02-1.13) | 5.9E-03 | 0.42 | 1.12 (1.07-1.18) | 1.9E-06 | 0.25 | 1.22 (1.04-1.43) | 1.3E-02 | 9.5E-18 | 3.3E-01 |
| <i>TMEM163</i> | rs6723108 | 2 | 135,196,450 | T | G | 0.48 | 1.01 (0.97-1.05) | 7.2E-01 | 0.50 | 1.90 (0.65-5.56) | 2.4E-01 | 0.85 | 1.05 (0.97-1.15) | 2.4E-01 | N/A | N/A | N/A | 4.0E-01 | 3.3E-01 |
| <i>PPARG</i> | rs1801282 | 3 | 12,368,125 | C | G | 0.88 | 1.16 (1.10-1.23) | 1.7E-08 | 0.93 | 1.15 (1.01-1.30) | 3.2E-02 | 0.87 | 1.09 (1.00-1.18) | 4.1E-02 | N/A | N/A | N/A | 5.7E-10 | 3.5E-01 |
| <i>HNF1B</i> | rs4430796 | 17 | 33,172,153 | G | A | 0.53 | 1.13 (1.07-1.09) | 6.6E-06 | 0.42 | 1.12 (1.05-1.19) | 8.3E-04 | 0.37 | 1.07 (1.02-1.13) | 4.2E-03 | N/A | N/A | N/A | 8.9E-10 | 3.6E-01 |
| <i>PRC1</i> | rs12899811 | 15 | 89,345,080 | G | A | 0.30 | 1.09 (1.04-1.13) | 7.1E-05 | 0.52 | 1.16 (1.00-1.35) | 5.1E-02 | 0.55 | 1.05 (1.00-1.10) | 3.6E-02 | 0.66 | 1.17 (1.01-1.36) | 1.4E-02 | 5.7E-07 | 3.9E-01 |
| <i>CDKN2A/B</i> | rs10811661 | 9 | 22,124,094 | T | C | 0.82 | 1.18 (1.13-1.24) | 1.2E-12 | 0.67 | 1.25 (1.17-1.32) | 6.3E-13 | 0.87 | 1.20 (1.11-1.31) | 1.4E-05 | N/A | N/A | N/A | 1.1E-27 | 3.9E-01 |
| <i>HNF1A</i> | rs12427353 | 12 | 119,911,284 | G | C | 0.77 | 1.12 (1.07-1.18) | 2.8E-06 | N/A | N/A | N/A | 0.95 | 1.04 (0.87-1.23) | 6.9E-01 | N/A | N/A | N/A | 3.9E-06 | 3.9E-01 |
| <i>GRK5</i> | rs10886471 | 10 | 121,139,393 | C | T | 0.49 | 0.99 (0.95-1.03) | 6.1E-01 | 0.64 | 1.06 (0.99-1.13) | 1.0E-01 | 0.60 | 1.01 (0.96-1.05) | 8.3E-01 | 0.50 | 1.03 (0.88-1.20) | 7.4E-01 | 6.1E-01 | 4.3E-01 |
| <i>ANK1</i> | rs1516946 | 8 | 41,638,405 | C | T | 0.77 | 1.10 (1.06-1.15) | 2.1E-06 | 0.72 | 1.04 (0.97-1.12) | 2.7E-01 | 0.80 | 1.08 (1.02-1.14) | 1.0E-02 | 0.81 | 1.01 (0.85-1.20) | 9.4E-01 | 1.5E-07 | 4.4E-01 |
| <i>SRR</i> | rs391300 | 17 | 2,163,008 | C | T | 0.62 | 1.00 (0.96-1.04) | 9.5E-01 | 0.63 | 1.03 (0.97-1.09) | 2.7E-01 | 0.51 | 0.99 (0.94-1.03) | 6.1E-01 | 0.66 | 1.09 (0.92-1.28) | 3.2E-01 | 6.8E-01 | 5.1E-01 |
| <i>KLHDC5</i> | rs10842994 | 12 | 27,856,417 | C | T | 0.80 | 1.09 (1.04-1.13) | 3.0E-04 | 0.65 | 1.03 (0.95-1.12) | 5.2E-01 | 0.88 | 1.11 (1.03-1.20) | 9.1E-03 | 0.85 | 1.14 (0.95-1.37) | 1.7E-01 | 7.9E-06 | 5.3E-01 |
| <i>TP53INP1</i> | rs7845219 | 8 | 96,006,678 | T | C | 0.53 | 1.08 (1.04-1.12) | 3.2E-05 | 0.37 | 1.07 (1.01-1.13) | 1.4E-02 | 0.42 | 1.07 (1.02-1.12) | 4.9E-03 | 0.37 | 0.97 (0.84-1.12) | 6.8E-01 | 6.4E-08 | 5.4E-01 |
| <i>C2CD4A</i> | rs7163757 | 15 | 60,178,900 | C | T | 0.56 | 1.06 (1.02-1.11) | 2.2E-03 | 0.46 | 1.12 (1.04-1.20) | 2.0E-03 | 0.62 | 1.05 (1.00-1.11) | 4.1E-02 | 0.52 | 1.05 (0.91-1.21) | 5.1E-01 | 3.6E-06 | 5.5E-01 |
| <i>BCL11A</i> | rs243088 | 2 | 60,422,249 | T | A | 0.46 | 1.09 (1.04-1.13) | 2.6E-05 | 0.57 | 1.06 (1.00-1.13) | 6.4E-02 | 0.53 | 1.04 (0.99-1.09) | 1.1E-01 | 0.57 | 1.03 (0.89-1.20) | 7.0E-01 | 3.2E-06 | 5.5E-01 |
| <i>DUSP8</i> | rs2334499 | 11 | 1,653,425 | T | C | 0.40 | 1.07 (1.03-1.11) | 1.3E-03 | 0.63 | 1.04 (0.98-1.10) | 1.7E-01 | 0.28 | 1.02 (0.97-1.08) | 4.2E-01 | 0.49 | 1.00 (0.87-1.15) | 9.6E-01 | 1.0E-03 | 5.6E-01 |
| <i>SLC30A8</i> | rs3802177 | 8 | 118,254,206 | G | A | 0.70 | 1.16 (1.11-1.22) | 1.3E-10 | 0.64 | 1.11 (1.06-1.17) | 2.6E-05 | 0.76 | 1.13 (1.07-1.19) | 2.5E-05 | 0.75 | 1.14 (0.95-1.36) | 1.5E-01 | 1.8E-18 | 6.2E-01 |
| <i>WFS1</i> | rs4458523 | 4 | 6,340,887 | G | T | 0.59 | 1.09 (1.06-1.13) | 5.8E-07 | 0.95 | 1.07 (0.96-1.20) | 1.9E-01 | 0.68 | 1.07 (1.02-1.12) | 1.0E-02 | 0.76 | 1.19 (1.01-1.39) | 3.6E-02 | 2.1E-09 | 6.2E-01 |
| <i>ANKRD55</i> | rs459193 | 5 | 55,842,508 | G | A | 0.74 | 1.05 (1.01-1.10) | 2.7E-02 | 0.66 | 1.05 (1.00-1.11) | 4.3E-02 | 0.64 | 1.03 (0.98-1.08) | 2.7E-01 | 0.76 | 1.14 (0.97-1.34) | 1.2E-01 | 8.9E-04 | 6.7E-01 |
| <i>TLE1</i> | rs2796441 | 9 | 83,498,768 | G | A | 0.63 | 1.07 (1.03-1.12) | 4.9E-04 | 0.51 | 1.10 (1.03-1.17) | 6.1E-03 | 0.52 | 1.05 (1.00-1.10) | 5.6E-02 | 0.51 | 1.07 (0.92-1.25) | 3.6E-01 | 1.6E-06 | 7.7E-01 |
| <i>IRS1</i> | rs2943640 | 2 | 226,801,829 | C | A | 0.63 | 1.09 (1.05-1.13) | 4.8E-06 | 0.57 | 1.13 (1.02-1.25) | 1.8E-02 | 0.76 | 1.09 (1.03-1.16) | 6.3E-03 | N/A | N/A | N/A | 7.2E-09 | 7.9E-01 |
| <i>UBE2E2</i> | rs7612463 | 3 | 23,311,454 | C | A | 0.87 | 1.10 (1.04-1.16) | 1.6E-03 | 0.64 | 1.13 (1.06-1.20) | 9.4E-05 | 0.78 | 1.09 (1.03-1.15) | 3.7E-03 | 0.94 | 1.16 (0.86-1.56) | 3.3E-01 | 6.7E-09 | 8.3E-01 |
| <i>HMG20A</i> | rs7178572 | 15 | 75,534,245 | G | A | 0.70 | 1.08 (1.04-1.13) | 1.9E-04 | 0.59 | 1.09 (1.04-1.14) | 4.4E-04 | 0.52 | 1.10 (1.05-1.15) | 4.2E-05 | 0.66 | 1.15 (0.99-1.33) | 6.7E-02 | 1.5E-11 | 8.4E-01 |
| <i>ZMIZ1</i> | rs12571751 | 10 | 80,612,637 | A | G | 0.51 | 1.09 (1.06-1.13) | 7.1E-07 | 0.47 | 1.07 (1.00-1.13) | 3.7E-02 | 0.57 | 1.08 (1.03-1.14) | 1.4E-03 | 0.50 | 1.09 (0.95-1.25) | 2.3E-01 | 2.4E-10 | 9.3E-01 |
| <i>ADCY5</i> | rs11717195 | 3 | 124,565,088 | T | C | 0.78 | 1.09 (1.05-1.14) | 2.6E-05 | 0.50 | 1.18 (0.67-2.05) | 5.7E-01 | 0.78 | 1.10 (1.04-1.17) | 9.9E-04 | 0.73 | 1.15 (0.98-1.36) | 8.9E-02 | 2.2E-08 | 9.4E-01 |
| <i>MC4R</i> | rs12970134 | 18 | 56,035,730 | A | G | 0.27 | 1.08 (1.03-1.12) | 2.3E-04 | 0.37 | 1.07 (1.01-1.14) | 3.0E-02 | 0.37 | 1.09 (1.04-1.15) | 3.6E-04 | 0.15 | 1.06 (0.87-1.28) | 5.6E-01 | 2.6E-08 | 9.5E-01 |
| <i>RND3</i> | rs7560163 | 2 | 151,346,182 | C | G | N/A | N/A | N/A | 0.74 | 1.05 (0.90-1.22) | 5.5E-01 | 0.97 | 1.05 (0.84-1.30) | 6.9E-01 | N/A | N/A | N/A | 4.7E-01 | 9.9E-01 |
| <i>MAEA</i> | rs6815464 | 4 | 1,299,901 | C | G | N/A | N/A | N/A | 0.47 | 1.10 (1.04-1.16) | 4.3E-04 | N/A | N/A | N/A | N/A | N/A | N/A | 4.4E-04 | N/A |

Supplementary Table 4. Concordance in the direction of effect of T2D risk alleles identified in meta-analyses of GWAS of European (12,171 cases and 56,862 controls), East Asian (6,952 cases and 11,865 controls), South Asian (5,561 cases and 14,458 controls), and Mexican and Mexican American (1,804 cases and 779 controls) ancestry, after exclusion of the 69 established autosomal susceptibility loci, defined as mapping within 500kb of the previously reported lead SNP.

| p-value threshold | Trans-ethnic concordance | | | | | | | | |
|---|---|----------|------------------------------|---|----------|------------------------------|--|----------|------------------------------|
| | Concordant SNPs / Total SNPs | % | Binomial test p-value | Concordant SNPs / Total SNPs | % | Binomial test p-value | Concordant SNPs / Total SNPs | % | Binomial test p-value |
| European meta-analysis | European into East Asian | | | European into South Asian | | | European into Mexican and Mexican American | | |
| $p \leq 0.001$ | 180/316 | 57.0 | 0.0077 | 175/316 | 55.4 | 0.032 | 179/316 | 56.6 | 0.010 |
| $0.001 < p \leq 0.01$ | 877/1624 | 54.0 | 0.00068 | 861/1624 | 53.0 | 0.0080 | 886/1624 | 54.6 | 0.00013 |
| $0.01 < p \leq 0.5$ | 2556/5053 | 50.6 | 0.21 | 2604/5053 | 51.5 | 0.015 | 2588/5053 | 51.2 | 0.043 |
| $0.5 < p \leq 1$ | 2535/5039 | 50.3 | 0.34 | 2532/5039 | 50.2 | 0.37 | 2519/5039 | 50.0 | 0.51 |
| East Asian meta-analysis | East Asian into European | | | East Asian into South Asian | | | East Asian into Mexican and Mexican American | | |
| $p \leq 0.001$ | 233/416 | 56.0 | 0.0081 | 220/416 | 52.9 | 0.13 | 214/416 | 51.4 | 0.29 |
| $0.001 < p \leq 0.01$ | 1117/2120 | 52.7 | 0.0071 | 1090/2120 | 51.4 | 0.10 | 1047/2120 | 49.4 | 0.72 |
| $0.01 < p \leq 0.5$ | 2549/5075 | 50.2 | 0.38 | 2661/5075 | 52.4 | 0.00028 | 2539/5075 | 50.0 | 0.49 |
| $0.5 < p \leq 1$ | 2561/5069 | 50.5 | 0.23 | 2555/5069 | 50.4 | 0.29 | 2563/5069 | 50.6 | 0.22 |
| South Asian meta-analysis | South Asian into European | | | South Asian into East Asian | | | South Asian into Mexican and Mexican American | | |
| $p \leq 0.001$ | 176/281 | 62.6 | 1.4×10^{-5} | 153/281 | 54.4 | 0.076 | 150/281 | 53.4 | 0.14 |
| $0.001 < p \leq 0.01$ | 837/1552 | 53.9 | 0.0011 | 793/1552 | 51.1 | 0.20 | 788/1552 | 50.8 | 0.28 |
| $0.01 < p \leq 0.5$ | 2625/5045 | 52.0 | 0.0020 | 2558/5045 | 50.7 | 0.16 | 2575/5045 | 51.0 | 0.071 |
| $0.5 < p \leq 1$ | 2521/5037 | 50.0 | 0.48 | 2524/5037 | 50.1 | 0.44 | 2530/5037 | 50.2 | 0.38 |
| Mexican and Mexican American meta-analysis | Mexican and Mexican American into European | | | Mexican and Mexican American into East Asian | | | Mexican and Mexican American into South Asian | | |
| $p \leq 0.001$ | 155/282 | 55.0 | 0.054 | 143/282 | 50.7 | 0.43 | 151/282 | 53.5 | 0.13 |
| $0.001 < p \leq 0.01$ | 796/1501 | 53.0 | 0.010 | 763/1501 | 50.8 | 0.27 | 745/1501 | 49.6 | 0.62 |
| $0.01 < p \leq 0.5$ | 2542/5026 | 50.6 | 0.21 | 2518/5026 | 50.1 | 0.45 | 2542/5026 | 50.6 | 0.21 |
| $0.5 < p \leq 1$ | 2539/5025 | 50.5 | 0.23 | 2521/5025 | 50.2 | 0.41 | 2531/5025 | 50.4 | 0.31 |

Supplementary Table 5. T2D susceptibility loci attaining strong evidence of association ($p < 10^{-5}$), not previously reported at genome-wide significance in any ancestry group, identified through trans-ethnic “discovery” GWAS meta-analysis of 26,488 cases and 83,964 controls of European, East Asian, South Asian, and Mexican and Mexican American ancestry, and follow-up in a “validation” meta-analysis of an additional 21,491 cases and 55,647 controls of European ancestry, genotyped with the MetaboChip.

| Locus | Lead SNP | MetaboChip proxy SNP | HapMap r^2 | | Chr | Build 36 position (bp) | Alleles | | Trans-ethnic “discovery” meta-analysis | | | European ancestry “validation” meta-analysis | | | Combined meta-analysis | | | |
|---------------------|------------|----------------------|--------------|---------|-----|------------------------|---------|-------|--|------------------|------------|--|------------------|------------|------------------------|------------------|----------------|------------------------|
| | | | CEU | CHB JPT | | | Risk | Other | Sample size | OR (95% CI) | p -value | Sample size | OR (95% CI) | p -value | Sample size | OR (95% CI) | p -value | Cochran’s Q p -value |
| <i>TMEM154</i> | rs6813195 | | | | 4 | 153,739,925 | C | T | 110,214 | 1.08 (1.05-1.11) | 4.2E-09 | 51,425 | 1.08 (1.05-1.11) | 2.0E-06 | 161,639 | 1.08 (1.06-1.10) | 4.1E-14 | 9.6E-01 |
| <i>SSR1/RREB1</i> | rs9502570 | rs9505118 | 0.256 | 0.264 | 6 | 7,235,436 | A | G | 106,952 | 1.06 (1.04-1.09) | 1.9E-06 | 51,396 | 1.06 (1.03-1.09) | 1.7E-04 | 158,348 | 1.06 (1.04-1.08) | 1.4E-09 | 7.7E-01 |
| <i>FAF1</i> | rs17106184 | | | | 1 | 50,682,573 | G | A | 110,157 | 1.11 (1.07-1.16) | 1.9E-06 | 51,428 | 1.09 (1.04-1.15) | 4.8E-04 | 161,585 | 1.10 (1.07-1.14) | 4.1E-09 | 6.1E-01 |
| <i>POU5F1/TCF19</i> | rs3132524 | rs3130501 | 0.961 | 1.000 | 6 | 31,244,432 | G | A | 106,231 | 1.07 (1.04-1.10) | 1.5E-06 | 49,584 | 1.06 (1.03-1.10) | 7.0E-04 | 155,815 | 1.07 (1.04-1.09) | 4.2E-09 | 7.9E-01 |
| <i>LPP</i> | rs6808574 | | | | 3 | 189,223,217 | C | T | 94,079 | 1.08 (1.04-1.11) | 4.3E-06 | 46,008 | 1.06 (1.03-1.09) | 2.6E-04 | 140,087 | 1.07 (1.04-1.09) | 5.8E-09 | 4.8E-01 |
| <i>ARL15</i> | rs702634 | | | | 5 | 53,307,177 | A | G | 103,376 | 1.08 (1.05-1.11) | 3.4E-07 | 51,421 | 1.05 (1.02-1.08) | 2.1E-03 | 154,797 | 1.06 (1.04-1.09) | 6.9E-09 | 1.7E-01 |
| <i>MPHOSPH9</i> | rs1727313 | rs4275659 | 0.476 | 0.039 | 12 | 122,013,881 | C | T | 110,015 | 1.06 (1.03-1.09) | 5.5E-06 | 51,444 | 1.06 (1.02-1.09) | 4.4E-04 | 161,459 | 1.06 (1.04-1.08) | 9.5E-09 | 8.5E-01 |
| <i>PLEKHA1</i> | rs10510110 | rs2421016 | 1.000 | 1.000 | 10 | 124,157,502 | C | T | 107,847 | 1.05 (1.03-1.08) | 1.9E-05 | 50,197 | 1.05 (1.02-1.08) | 1.6E-03 | 158,044 | 1.05 (1.03-1.07) | 1.1E-07 | 7.0E-01 |
| <i>TMEM75</i> | rs1561927 | | | | 8 | 129,637,260 | C | T | 104,569 | 1.08 (1.05-1.11) | 1.9E-06 | 51,435 | 1.04 (1.01-1.08) | 6.6E-03 | 156,004 | 1.06 (1.04-1.09) | 1.2E-07 | 1.5E-01 |
| <i>TMEM18</i> | rs10190052 | | | | 2 | 636,674 | C | T | 104,516 | 1.09 (1.05-1.13) | 7.5E-06 | 51,447 | 1.06 (1.02-1.10) | 3.4E-03 | 155,963 | 1.07 (1.04-1.10) | 1.5E-07 | 3.2E-01 |
| <i>RNF6</i> | rs10507349 | | | | 13 | 25,679,528 | G | A | 110,032 | 1.07 (1.04-1.09) | 5.0E-06 | 51,447 | 1.05 (1.01-1.08) | 6.7E-03 | 161,479 | 1.06 (1.04-1.08) | 1.5E-07 | 4.6E-01 |
| <i>VEGFA</i> | rs9472138 | | | | 6 | 43,919,740 | T | C | 106,235 | 1.07 (1.04-1.10) | 3.0E-06 | 51,450 | 1.04 (1.01-1.07) | 8.8E-03 | 157,685 | 1.06 (1.04-1.08) | 2.0E-07 | 2.0E-01 |
| <i>ETV1</i> | rs7795991 | | | | 7 | 13,867,256 | G | A | 99,500 | 1.07 (1.04-1.10) | 1.7E-06 | 51,446 | 1.03 (1.00-1.06) | 3.1E-02 | 150,946 | 1.05 (1.03-1.07) | 7.1E-07 | 8.4E-02 |
| <i>PCBD2</i> | rs319598 | | | | 5 | 134,268,134 | C | T | 104,492 | 1.06 (1.04-1.09) | 7.7E-07 | 51,425 | 1.02 (0.99-1.05) | 1.3E-01 | 155,917 | 1.05 (1.03-1.07) | 2.2E-06 | 3.6E-02 |
| <i>LYPLAL1</i> | rs2820446 | | | | 1 | 217,815,441 | C | G | 110,143 | 1.06 (1.04-1.09) | 6.9E-06 | 51,390 | 1.03 (1.00-1.06) | 4.3E-02 | 161,533 | 1.05 (1.03-1.07) | 2.3E-06 | 1.6E-01 |
| <i>C6orf173</i> | rs4273712 | | | | 6 | 127,006,203 | G | A | 100,585 | 1.07 (1.04-1.10) | 1.2E-06 | 51,447 | 1.02 (0.99-1.06) | 1.3E-01 | 152,032 | 1.05 (1.03-1.07) | 3.0E-06 | 4.3E-02 |
| <i>C10orf35</i> | rs2812533 | rs17578395 | 0.671 | 0.373 | 10 | 71,085,247 | C | A | 107,876 | 1.08 (1.05-1.12) | 3.9E-06 | 26,019 | 1.03 (0.99-1.08) | 1.8E-01 | 133,895 | 1.07 (1.04-1.09) | 5.0E-06 | 1.3E-01 |
| <i>IL20RA</i> | rs6937795 | rs4407733 | 1.000 | 1.000 | 6 | 137,340,845 | A | G | 102,178 | 1.06 (1.03-1.09) | 8.9E-06 | 49,574 | 1.03 (1.00-1.06) | 7.5E-02 | 151,752 | 1.04 (1.02-1.06) | 6.6E-06 | 1.1E-01 |
| <i>CRHR2</i> | rs2284219 | rs2284218 | 1.000 | 0.888 | 7 | 30,680,858 | T | C | 94,286 | 1.07 (1.04-1.10) | 2.5E-06 | 26,033 | 1.02 (0.98-1.06) | 3.0E-01 | 120,319 | 1.05 (1.03-1.08) | 7.7E-06 | 7.3E-02 |
| <i>PTEN</i> | rs10788575 | | | | 10 | 89,758,564 | A | G | 110,091 | 1.08 (1.04-1.11) | 2.3E-06 | 51,440 | 1.02 (0.98-1.07) | 2.7E-01 | 161,531 | 1.06 (1.03-1.08) | 8.7E-06 | 5.3E-02 |
| <i>CPNE4</i> | rs6792706 | rs9840453 | 1.000 | 0.955 | 3 | 133,260,155 | T | G | 98,256 | 1.08 (1.05-1.12) | 3.1E-06 | 51,395 | 1.03 (0.99-1.06) | 1.3E-01 | 149,651 | 1.05 (1.03-1.08) | 1.2E-05 | 2.7E-02 |
| <i>THRAP2</i> | rs7133159 | rs10774811 | 0.799 | 0.602 | 12 | 114,349,025 | T | C | 103,559 | 1.06 (1.03-1.09) | 4.2E-05 | 51,447 | 1.03 (1.00-1.06) | 7.3E-02 | 155,006 | 1.04 (1.02-1.06) | 2.4E-05 | 1.5E-01 |
| <i>MSRA</i> | rs17150816 | | | | 8 | 9,828,147 | C | A | 61,864 | 1.27 (1.15-1.41) | 5.5E-06 | 51,450 | 1.06 (0.99-1.13) | 8.1E-02 | 113,314 | 1.12 (1.06-1.18) | 9.3E-05 | 3.7E-03 |
| <i>PFTK1</i> | rs17163563 | | | | 7 | 90,546,497 | A | G | 78,195 | 1.19 (1.11-1.28) | 2.9E-06 | 51,439 | 1.03 (0.98-1.08) | 2.8E-01 | 129,634 | 1.08 (1.03-1.12) | 3.9E-04 | 1.2E-03 |
| <i>SLIT3</i> | rs11739950 | | | | 5 | 168,346,952 | A | G | 70,709 | 1.29 (1.16-1.43) | 2.5E-06 | 50,417 | 1.03 (0.94-1.12) | 5.5E-01 | 121,126 | 1.12 (1.05-1.20) | 6.4E-04 | 9.7E-04 |
| <i>WNK2</i> | rs10761209 | rs10821106 | 1.000 | 0.935 | 9 | 95,100,580 | T | C | 104,496 | 1.06 (1.03-1.09) | 1.5E-05 | 50,409 | 1.02 (0.99-1.05) | 2.4E-01 | 154,905 | 1.03 (1.01-1.05) | 9.7E-03 | 2.4E-04 |
| <i>PKP1</i> | rs6427896 | N/A | | | | | | | | | | | | | | | | |
| <i>ATP2B2</i> | rs13071035 | N/A | | | | | | | | | | | | | | | | |
| <i>PLAC9</i> | rs7088994 | N/A | | | | | | | | | | | | | | | | |
| <i>C14orf174</i> | rs11844594 | N/A | | | | | | | | | | | | | | | | |
| <i>LAMA1</i> | rs9948462 | N/A | | | | | | | | | | | | | | | | |
| <i>APOC1</i> | rs4420638 | N/A | | | | | | | | | | | | | | | | |
| <i>C20orf166</i> | rs6062238 | N/A | | | | | | | | | | | | | | | | |

Supplementary Table 6. Association summary statistics in each ancestry group (European, East Asian, South Asian, and Mexican and Mexican American) for lead SNPs at novel T2D susceptibility loci identified through fixed-effects trans-ethnic GWAS meta-analysis of 26,488 cases and 83,964 controls.

| Locus | Lead SNP | Chr | Build 36 position (bp) | Alleles | | European 12,171 cases and 56,862 controls | | | East Asian 6,952 cases and 11,865 controls | | | South Asian 5,561 cases and 14,458 controls | | | Mexican and Mexican American 1,804 cases and 779 controls | | | Stage 1 trans-ethnic meta-analysis | |
|---------------------|------------|-----|------------------------|---------|-------|--|------------------|---------|---|------------------|---------|--|------------------|---------|--|------------------|---------|---------------------------------------|-------------|
| | | | | Risk | Other | RAF | OR (95% CI) | p-value | RAF | OR (95% CI) | p-value | RAF | OR (95% CI) | p-value | RAF | OR (95% CI) | p-value | p-value | Cochran's Q |
| <i>TMEM154</i> | rs6813195 | 4 | 153,739,925 | C | T | 0.71 | 1.08 (1.04-1.12) | 1.4E-04 | 0.39 | 1.10 (1.05-1.15) | 1.1E-04 | 0.62 | 1.05 (1.00-1.11) | 3.4E-02 | 0.63 | 1.11 (0.96-1.28) | 1.6E-01 | 4.2E-09 | 6.8E-01 |
| <i>POU5F1/TCF19</i> | rs3132524 | 6 | 31,244,693 | C | T | 0.73 | 1.08 (1.04-1.12) | 1.1E-04 | 0.43 | 1.03 (0.98-1.09) | 2.0E-01 | 0.70 | 1.08 (1.03-1.14) | 2.5E-03 | 0.76 | 1.19 (1.01-1.40) | 3.7E-02 | 2.5E-07 | 3.2E-01 |
| <i>ARL15</i> | rs702634 | 5 | 53,307,177 | A | G | 0.67 | 1.08 (1.04-1.12) | 4.3E-05 | 0.75 | 1.10 (1.00-1.20) | 4.2E-02 | 0.77 | 1.07 (1.01-1.13) | 2.4E-02 | 0.86 | 1.06 (0.87-1.29) | 5.5E-01 | 3.4E-07 | 9.7E-01 |
| <i>SSR1/RREB1</i> | rs9502570 | 6 | 7,203,616 | C | T | 0.73 | 1.08 (1.03-1.12) | 1.1E-03 | 0.35 | 1.05 (1.00-1.11) | 7.0E-02 | 0.61 | 1.09 (1.04-1.14) | 5.1E-04 | 0.75 | 1.03 (0.85-1.21) | 7.5E-01 | 5.7E-07 | 7.7E-01 |
| <i>MPHOSPH9</i> | rs1727313 | 12 | 122,206,806 | G | C | 0.78 | 1.07 (1.03-1.12) | 9.4E-04 | 0.53 | 1.20 (1.03-1.41) | 2.1E-02 | 0.74 | 1.08 (1.02-1.14) | 4.6E-03 | 0.77 | 1.10 (0.93-1.30) | 2.5E-01 | 1.2E-06 | 5.9E-01 |
| <i>FAF1</i> | rs17106184 | 1 | 50,682,573 | G | A | 0.91 | 1.10 (1.04-1.16) | 1.8E-03 | 0.58 | 1.14 (1.05-1.22) | 2.7E-03 | 0.94 | 1.08 (0.98-1.19) | 1.3E-01 | 0.95 | 1.36 (1.06-1.66) | 4.7E-02 | 1.9E-06 | 5.2E-01 |
| <i>LPP</i> | rs6808574 | 3 | 189,223,217 | C | T | 0.60 | 1.08 (1.03-1.12) | 2.6E-04 | 0.98 | 1.13 (0.85-1.51) | 4.1E-01 | 0.76 | 1.05 (0.99-1.10) | 1.1E-01 | 0.82 | 1.49 (1.23-1.80) | 3.4E-05 | 4.3E-06 | 5.5E-03 |

Supplementary Table 7. Association summary statistics from the European ancestry validation meta-analysis, stratified according to covariate adjustment: (i) studies that account only for age, sex (unless male- or female-specific), and population structure where necessary (11,327 cases and 31,342 controls); and (ii) all other studies (10,164 cases and 24,305 controls).

| Locus | Lead SNP | Chr | Build 36 position (bp) | Alleles ^a | | Studies adjusting for age, sex and population structure | | Other studies | | Cochran's Q statistic p-value |
|---------------------|------------|-----|------------------------|----------------------|-------|---|---------|------------------|---------|-------------------------------|
| | | | | Risk | Other | OR (95% CI) | p-value | OR (95% CI) | p-value | |
| <i>TMEM154</i> | rs6813195 | 4 | 153,739,925 | C | T | 1.08 (1.04-1.12) | 1.4E-04 | 1.08 (1.03-1.12) | 1.1E-03 | 8.6E-01 |
| <i>SSR1/RREB1</i> | rs9505118 | 6 | 7,235,436 | A | G | 1.07 (1.03-1.10) | 6.2E-04 | 1.04 (1.01-1.08) | 3.6E-02 | 4.0E-01 |
| <i>FAF1</i> | rs17106184 | 1 | 50,682,573 | G | A | 1.06 (0.99-1.12) | 1.2E-01 | 1.14 (1.07-1.20) | 1.5E-04 | 7.9E-02 |
| <i>POU5F1/TCF19</i> | rs3130501 | 6 | 31,244,432 | G | A | 1.06 (1.02-1.10) | 7.0E-03 | 1.06 (1.01-1.11) | 1.8E-02 | 9.6E-01 |
| <i>LPP</i> | rs6808574 | 3 | 189,223,217 | C | T | 1.06 (1.02-1.10) | 8.6E-03 | 1.06 (1.02-1.10) | 4.2E-03 | 8.9E-01 |
| <i>ARL15</i> | rs702634 | 5 | 53,307,177 | A | G | 1.03 (0.99-1.07) | 1.7E-01 | 1.08 (1.04-1.12) | 5.1E-04 | 7.5E-02 |
| <i>MPHOSPH9</i> | rs4275659 | 12 | 122,013,881 | C | T | 1.07 (1.03-1.11) | 5.7E-04 | 1.04 (1.00-1.08) | 9.8E-02 | 2.3E-01 |

Supplementary Table 8. T2D association summary statistics for lead SNPs at T1D susceptibility loci identified through fixed-effects trans-ethnic GWAS meta-analysis of 26,488 cases and 83,964 controls.

| Locus | T1D lead SNP | Chr | Build 36 position (bp) | Alleles | | T2D association | |
|----------------|--------------|-----|------------------------|----------|-------|------------------|---------|
| | | | | T1D risk | Other | OR (95% CI) | p-value |
| <i>GLIS3</i> | rs10758593 | 9 | 4,282,083 | A | G | 1.07 (1.04-1.10) | 5.1E-07 |
| 6q22.32 | rs9388489 | 6 | 126,740,412 | G | A | 1.06 (1.03-1.08) | 9.8E-05 |
| 16q23.1 | rs7202877 | 16 | 73,804,746 | G | T | 0.93 (0.89-0.97) | 5.7E-04 |
| 7p12.1 | rs4948088 | 7 | 50,994,688 | | | | 1.5E-02 |
| <i>LMO7</i> | rs539514 | 13 | 75,224,283 | T | A | 0.97 (0.95-1.00) | 8.8E-02 |
| 10q23.31 | rs10509540 | 10 | 90,013,013 | T | C | 0.98 (0.95-1.00) | 9.3E-02 |
| 14q24.1 | rs1465788 | 14 | 68,333,352 | C | T | 1.02 (1.00-1.05) | 9.4E-02 |
| <i>IL2RA</i> | rs12251307 | 10 | 6,163,501 | C | T | 1.02 (0.99-1.06) | 1.3E-01 |
| <i>IL2</i> | rs4505848 | 4 | 123,351,942 | G | A | 1.02 (0.99-1.05) | 1.8E-01 |
| <i>PRKCQ</i> | rs11258747 | 10 | 6,512,897 | T | G | 0.98 (0.95-1.01) | 2.0E-01 |
| <i>AFF3</i> | rs9653442 | 2 | 100,191,799 | C | T | 1.01 (0.99-1.04) | 2.6E-01 |
| <i>IL27</i> | rs4788084 | 16 | 28,447,349 | C | T | 0.98 (0.96-1.01) | 2.6E-01 |
| <i>CYP27B1</i> | rs10877012 | 12 | 56,448,352 | | | | 3.0E-01 |
| <i>INS</i> | rs3741208 | 11 | 2,126,350 | A | G | 0.98 (0.95-1.02) | 3.1E-01 |
| <i>STAT4</i> | rs7574865 | 2 | 191,672,878 | T | G | 1.01 (0.99-1.04) | 3.1E-01 |
| <i>BACH2</i> | rs3757247 | 6 | 91,014,184 | T | C | 0.99 (0.96-1.01) | 3.3E-01 |
| <i>ORMDL3</i> | rs2290400 | 17 | 35,319,766 | C | T | 0.99 (0.96-1.02) | 3.3E-01 |
| <i>HLA</i> | rs9268645 | 6 | 32,516,505 | G | C | 1.01 (0.99-1.04) | 3.3E-01 |
| 19q13.32 | rs425105 | 19 | 51,900,321 | T | C | 0.98 (0.95-1.02) | 3.8E-01 |
| 12q13.2 | rs1701704 | 12 | 54,698,754 | G | T | 0.99 (0.96-1.02) | 3.8E-01 |
| 14q32.2 | rs4900384 | 14 | 97,568,704 | G | A | 1.01 (0.99-1.04) | 4.1E-01 |
| <i>RGS1</i> | rs2816316 | 1 | 190,803,436 | A | C | 1.01 (0.98-1.05) | 4.1E-01 |
| <i>PTPN22</i> | rs2476601 | 1 | 114,179,091 | A | G | 1.02 (0.97-1.08) | 4.2E-01 |
| <i>RASGRP1</i> | rs17574546 | 15 | 36,689,768 | C | A | 1.01 (0.98-1.05) | 4.2E-01 |
| <i>CTLA4</i> | rs3087243 | 2 | 204,447,164 | G | A | 0.99 (0.97-1.02) | 4.6E-01 |
| <i>GPR183</i> | rs9585056 | 13 | 98,879,767 | C | T | 0.99 (0.96-1.02) | 4.7E-01 |
| <i>DLK1</i> | rs941576 | 14 | 100,375,798 | A | G | 1.01 (0.98-1.04) | 4.8E-01 |
| 4p15.2 | rs10517086 | 4 | 25,694,609 | A | G | 1.01 (0.98-1.05) | 4.8E-01 |
| <i>SKAP2</i> | rs7804356 | 7 | 26,858,190 | T | C | 1.01 (0.98-1.04) | 5.2E-01 |
| <i>CD226</i> | rs763361 | 18 | 65,682,622 | T | C | 1.01 (0.98-1.03) | 5.7E-01 |
| <i>IFIH1</i> | rs1990760 | 2 | 162,832,297 | T | C | 0.99 (0.97-1.02) | 5.9E-01 |
| <i>IL10</i> | rs3024505 | 1 | 205,006,527 | G | A | 0.99 (0.95-1.03) | 6.1E-01 |
| 22q12.2 | rs5753037 | 22 | 28,911,722 | T | C | 1.01 (0.98-1.03) | 6.4E-01 |
| <i>PTPN2</i> | rs478582 | 18 | 12,825,976 | T | C | 0.99 (0.97-1.02) | 6.5E-01 |
| <i>TNFAIP3</i> | rs10499194 | 6 | 138,044,330 | C | T | 0.99 (0.96-1.02) | 6.6E-01 |
| 15q25.1 | rs3825932 | 15 | 77,022,501 | C | T | 0.99 (0.97-1.02) | 6.7E-01 |
| <i>SH2B3</i> | rs3184504 | 12 | 110,368,991 | T | C | 1.01 (0.97-1.04) | 7.0E-01 |
| <i>EFR3B</i> | rs478222 | 2 | 25,155,259 | A | T | 1.00 (0.98-1.03) | 7.1E-01 |
| 20p13 | rs2281808 | 20 | 1,558,551 | C | T | 0.99 (0.97-1.02) | 7.2E-01 |
| 12p13.31 | rs4763879 | 12 | 9,801,431 | A | G | 1.00 (0.98-1.03) | 7.5E-01 |
| 6q27 | rs924043 | 6 | 170,220,950 | C | T | 1.00 (0.96-1.03) | 7.6E-01 |
| <i>TAGAP</i> | rs1738074 | 6 | 159,385,965 | C | T | 1.00 (0.97-1.02) | 8.2E-01 |
| 17q21.2 | rs7221109 | 17 | 36,023,812 | C | T | 1.00 (0.98-1.03) | 8.5E-01 |
| <i>UBASH3A</i> | rs9976767 | 21 | 42,709,459 | G | A | 1.00 (0.98-1.03) | 8.5E-01 |
| <i>TYK2</i> | rs2304256 | 19 | 10,336,652 | | | | 9.7E-01 |
| <i>IL2RB</i> | rs229541 | 22 | 35,921,264 | A | G | 1.00 (0.98-1.02) | 9.7E-01 |
| <i>CCRS</i> | rs11711054 | 3 | 46,320,615 | G | A | 1.00 (0.97-1.03) | 9.7E-01 |
| 16p13.13 | rs2903692 | 16 | 11,146,284 | G | A | 1.00 (0.97-1.03) | 9.7E-01 |

Supplementary Table 9. Association summary statistics for lead SNPs at novel T2D susceptibility loci in a meta-analysis of glycaemic traits in non-diabetic individuals of European descent from the MAGIC Investigators.

(a) Fasting glucose (FG) and fasting glucose adjusted for body-mass index (FGadjBMI) in up to 133,010 individuals.

| Locus | Lead SNP | Chr | Build 36 position (bp) | Alleles | | FG | | | | FGadjBMI | | | |
|---------------------|------------|-----|------------------------|---------|-------|---------|---------|--------|---------|----------|---------|--------|---------|
| | | | | Risk | Other | N | β | SE | p-value | N | β | SE | p-value |
| <i>TMEM154</i> | rs6813195 | 4 | 153,739,925 | C | T | 131,758 | -0.0015 | 0.0023 | 5.3E-01 | 123,101 | -0.0045 | 0.0024 | 6.1E-02 |
| <i>SSR1/RREB1</i> | rs9505118 | 6 | 7,235,436 | A | G | 132,932 | 0.0091 | 0.0021 | 1.0E-05 | 123,203 | 0.0084 | 0.0022 | 1.2E-04 |
| <i>FAF1</i> | rs17106184 | 1 | 50,682,573 | G | A | 133,005 | 0.0089 | 0.0036 | 1.4E-02 | 123,259 | 0.0072 | 0.0038 | 6.0E-02 |
| <i>POU5F1/TCF19</i> | rs3130501 | 6 | 31,244,432 | G | A | 131,862 | 0.0001 | 0.0024 | 9.7E-01 | 123,243 | 0.0005 | 0.0025 | 8.3E-01 |
| <i>LPP</i> | rs6808574 | 3 | 189,223,217 | C | T | 115,536 | 0.0113 | 0.0023 | 8.6E-07 | 107,010 | 0.0114 | 0.0024 | 2.5E-06 |
| <i>ARL15</i> | rs702634 | 5 | 53,307,177 | A | G | 127,759 | 0.0041 | 0.0022 | 6.4E-02 | 117,917 | 0.0049 | 0.0023 | 3.7E-02 |
| <i>MPHOSPH9</i> | rs4275659 | 12 | 122,013,881 | C | T | 132,968 | -0.0030 | 0.0022 | 1.8E-01 | 123,216 | -0.0022 | 0.0023 | 3.5E-01 |

(b) Fasting insulin (FI) and fasting insulin adjusted for body-mass index (FIadjBMI) in up to 108,557 individuals.

| Locus | Lead SNP | Chr | Build 36 position (bp) | Alleles | | FI | | | | FIadjBMI | | | |
|---------------------|------------|-----|------------------------|---------|-------|---------|---------|--------|---------|----------|---------|--------|---------|
| | | | | Risk | Other | N | β | SE | p-value | N | β | SE | p-value |
| <i>TMEM154</i> | rs6813195 | 4 | 153,739,925 | C | T | 107,414 | -0.0048 | 0.0027 | 7.4E-02 | 103,342 | -0.0036 | 0.0023 | 1.1E-01 |
| <i>SSR1/RREB1</i> | rs9505118 | 6 | 7,235,436 | A | G | 108,480 | -0.0022 | 0.0024 | 3.6E-01 | 103,434 | -0.0007 | 0.0021 | 7.4E-01 |
| <i>FAF1</i> | rs17106184 | 1 | 50,682,573 | G | A | 108,555 | 0.0031 | 0.0042 | 4.7E-01 | 103,492 | 0.0008 | 0.0037 | 8.3E-01 |
| <i>POU5F1/TCF19</i> | rs3130501 | 6 | 31,244,432 | G | A | 107,507 | 0.0021 | 0.0027 | 4.4E-01 | 103,473 | 0.0050 | 0.0024 | 3.2E-02 |
| <i>LPP</i> | rs6808574 | 3 | 189,223,217 | C | T | 93,485 | -0.0023 | 0.0027 | 3.9E-01 | 89,488 | 0.0000 | 0.0023 | 1.0E+00 |
| <i>ARL15</i> | rs702634 | 5 | 53,307,177 | A | G | 103,440 | 0.0140 | 0.0026 | 4.5E-08 | 98,281 | 0.0151 | 0.0022 | 5.0E-12 |
| <i>MPHOSPH9</i> | rs4275659 | 12 | 122,013,881 | C | T | 108,549 | 0.0039 | 0.0026 | 1.3E-01 | 103,480 | 0.0040 | 0.0022 | 7.2E-02 |

(c) Homeostatic model of assessment indices of beta-cell function (HOMA-B) and insulin resistance (HOMA-IR) in up to 37,037 individuals.

| Locus | Lead SNP | Chr | Build 36 position (bp) | Alleles | | HOMA-B | | | | HOMA-IR | | | |
|---------------------|------------|-----|------------------------|---------|-------|----------|---------|--------|-----------------|----------|---------|--------|-----------------|
| | | | | Risk | Other | <i>N</i> | β | SE | <i>p</i> -value | <i>N</i> | β | SE | <i>p</i> -value |
| <i>TMEM154</i> | rs6813195 | 4 | 153,739,925 | C | T | 35,361 | -0.0024 | 0.0038 | 5.4E-01 | 35,827 | -0.0052 | 0.0047 | 2.6E-01 |
| <i>SSR1/RREB1</i> | rs9505118 | 6 | 7,235,436 | A | G | 36,439 | -0.0052 | 0.0033 | 1.1E-01 | 37,010 | -0.0020 | 0.0040 | 6.2E-01 |
| <i>FAF1</i> | rs17106184 | 1 | 50,682,573 | G | A | 36,466 | -0.0082 | 0.0060 | 1.7E-01 | 37,037 | -0.0042 | 0.0070 | 5.5E-01 |
| <i>POU5F1/TCF19</i> | rs3130501 | 6 | 31,244,432 | G | A | 35,437 | -0.0017 | 0.0038 | 6.5E-01 | 35,903 | -0.0012 | 0.0046 | 7.9E-01 |
| <i>LPP</i> | rs6808574 | 3 | 189,223,217 | C | T | 35,428 | -0.0086 | 0.0034 | 1.1E-02 | 35,894 | -0.0021 | 0.0041 | 6.1E-01 |
| <i>ARL15</i> | rs702634 | 5 | 53,307,177 | A | G | 36,449 | 0.0060 | 0.0035 | 8.7E-02 | 37,020 | 0.0099 | 0.0043 | 2.1E-02 |
| <i>MPHOSPH9</i> | rs4275659 | 12 | 122,013,881 | C | T | 36,459 | 0.0038 | 0.0036 | 2.9E-01 | 37,030 | -0.0024 | 0.0044 | 5.9E-01 |

Supplementary Table 10. Association summary statistics for lead SNPs at novel T2D susceptibility loci in a meta-analysis of body-mass index (BMI) and waist-hip ratio adjusted for body-mass index (WHRadjBMI) in up to 123,865 and 77,167 individuals, respectively, of European ancestry from the GIANT Consortium.

| Locus | Lead SNP | Chr | Build 36 position (bp) | Alleles | | BMI | | | | WHRadjBMI | | | |
|---------------------|------------|-----|------------------------|---------|-------|---------|---------|--------|---------|-----------|---------|--------|---------|
| | | | | Risk | Other | N | β | SE | p-value | N | β | SE | p-value |
| <i>TMEM154</i> | rs6813195 | 4 | 153,739,925 | C | T | 123,768 | -0.0057 | 0.0054 | 2.9E-01 | 77,077 | 0.0048 | 0.0052 | 3.9E-01 |
| <i>SSR1/RREB1</i> | rs9505118 | 6 | 7,235,436 | A | G | 123,744 | -0.0017 | 0.0047 | 7.2E-01 | 77,048 | -0.0111 | 0.0046 | 2.1E-02 |
| <i>FAF1</i> | rs17106184 | 1 | 50,682,573 | G | A | 123,778 | -0.0171 | 0.0080 | 3.4E-02 | 77,159 | 0.0136 | 0.0078 | 9.7E-02 |
| <i>POU5F1/TCF19</i> | rs3130501 | 6 | 31,244,432 | G | A | 123,830 | -0.0133 | 0.0053 | 1.3E-02 | 77,152 | 0.0065 | 0.0052 | 2.3E-01 |
| <i>LPP</i> | rs6808574 | 3 | 189,223,217 | C | T | 123,829 | 0.0095 | 0.0048 | 4.9E-02 | 77,162 | 0.0120 | 0.0047 | 1.4E-02 |
| <i>ARL15</i> | rs702634 | 5 | 53,307,177 | A | G | 123,791 | -0.0205 | 0.0051 | 5.6E-05 | 77,100 | -0.0041 | 0.0049 | 4.2E-01 |
| <i>MPHOSPH9</i> | rs4275659 | 12 | 122,013,881 | C | T | 123,839 | -0.0129 | 0.0052 | 1.3E-02 | 77,149 | 0.0012 | 0.0050 | 8.1E-01 |

Supplementary Table 11. Association summary statistics for lead SNPs at novel T2D susceptibility loci in a meta-analysis of lipid traits in up to 100,184 individuals of European ancestry from the Global Lipids Genetics Consortium.

| Locus | Lead SNP | Chr | Build 36 position (bp) | Alleles | | Total cholesterol | | | High-density lipoprotein | | | Low-density lipoprotein | | | Triglycerides | | |
|---------------------|------------|-----|------------------------|---------|-------|-------------------|---------|---------|--------------------------|---------|---------|-------------------------|---------|---------|---------------|---------|---------|
| | | | | Risk | Other | N | Z-score | p-value | N | Z-score | p-value | N | Z-score | p-value | N | Z-score | p-value |
| <i>TMEM154</i> | rs6813195 | 4 | 153,739,925 | C | T | 100,065 | -0.114 | 9.1E-01 | 99,787 | -1.271 | 2.0E-01 | 95,341 | -0.159 | 8.7E-01 | 96,479 | 0.033 | 9.7E-01 |
| <i>SSR1/RREB1</i> | rs9505118 | 6 | 7,235,436 | A | G | 100,117 | -0.147 | 8.8E-01 | 99,832 | 0.147 | 8.8E-01 | 95,389 | -0.427 | 6.7E-01 | 96,530 | 0.450 | 6.5E-01 |
| <i>FAF1</i> | rs17106184 | 1 | 50,682,573 | G | A | 100,183 | 1.399 | 1.6E-01 | 99,899 | 0.087 | 9.3E-01 | 95,454 | 0.306 | 7.6E-01 | 96,597 | 2.007 | 4.5E-02 |
| <i>POU5F1/TCF19</i> | rs3130501 | 6 | 31,244,432 | G | A | 97,134 | 4.160 | 3.2E-05 | 96,895 | 0.857 | 3.9E-01 | 92,490 | 2.592 | 9.5E-03 | 93,548 | 3.140 | 1.7E-03 |
| <i>LPP</i> | rs6808574 | 3 | 189,223,217 | C | T | 100,184 | -0.008 | 9.9E-01 | 99,900 | -0.788 | 4.3E-01 | 95,454 | 0.273 | 7.9E-01 | 96,598 | -0.076 | 9.4E-01 |
| <i>ARL15</i> | rs702634 | 5 | 53,307,177 | A | G | 100,115 | 1.299 | 1.9E-01 | 99,837 | -2.287 | 2.2E-02 | 95,391 | 0.762 | 4.5E-01 | 96,529 | 2.563 | 1.0E-02 |
| <i>MPHOSPH9</i> | rs4275659 | 12 | 122,013,881 | C | T | 100,159 | -1.756 | 7.9E-02 | 99,877 | -1.820 | 6.9E-02 | 95,431 | -1.167 | 2.4E-01 | 96,573 | 0.995 | 3.2E-01 |

Supplementary Table 12. Evidence for *cis*-eQTL expression with lead T2D SNPs at novel T2D susceptibility loci in multiple tissues from public databases and unpublished resources.

| Locus | Lead SNP | Chr | Build 36 position (bp) | Transcript | Tissue | <i>p</i> -value | Lead <i>cis</i> -eQTL SNP | | | | | |
|---------------------|-----------|-----|------------------------|-------------------|-----------------|-----------------|---------------------------|-----|------------------------|-----------|---------------|-----------------|
| | | | | | | | SNP | Chr | Build 36 position (bp) | CEU r^2 | CHB+JPT r^2 | <i>p</i> -value |
| <i>SSR1/RREB1</i> | rs9505118 | 6 | 7,235,436 | <i>SSR1</i> | B cells (CD19+) | 2.2E-06 | rs1050226 | 6 | 7,226,653 | 0.965 | 1.000 | 2.1E-06 |
| <i>POU5F1/TCF19</i> | rs3130501 | 6 | 31,244,432 | <i>HCG27</i> | Blood | 8.8E-20 | rs9263871 | 6 | 31,278,507 | 0.028 | 0.545 | 5.2E-62 |
| | | | | <i>HCG22</i> | LCL | 1.9E-16 | rs2517552 | 6 | 31,115,569 | 0.426 | 0.000 | 2.9E-34 |
| | | | | <i>AL662833.4</i> | Lymph | 2.6E-06 | rs1265112 | 6 | 31,225,998 | 0.207 | 0.042 | 5.3E-29 |
| | | | | <i>HCG27</i> | Monocytes | 1.3E-69 | Same SNP | | | | | |
| | | | | <i>HLA-DRB5</i> | Monocytes | 1.7E-33 | rs3129868 | 6 | 32,278,507 | N/A | N/A | 1.0E-320 |
| | | | | <i>HLA-C</i> | Monocytes | 7.5E-15 | rs4394274 | 6 | 31,426,143 | N/A | N/A | 2.6E-158 |
| | | | | <i>HLA-DRB1</i> | Monocytes | 8.3E-15 | rs2395166 | 6 | 32,496,253 | N/A | N/A | 4.0E-192 |
| <i>MPHOSPH9</i> | rs4275659 | 12 | 122,013,881 | <i>ABCB9</i> | Liver | 7.4E-12 | Same SNP | | | | | |
| | | | | <i>SETD8</i> | Lung | 2.0E-16 | Same SNP | | | | | |

Supplementary Table 13. Potential functional variants in pilot data from the 1000 Genomes Project that are in strong LD (CEU and CHB+JPT $r^2 > 0.8$) with the lead SNPs in the novel susceptibility loci.

| Locus | Lead SNP | Chr | Build 36 position (bp) | Functional proxy SNP | | | | | | |
|---------------------|-----------|-----|------------------------|----------------------|-----|------------------------|-----------|---------------|----------------|------------|
| | | | | SNP | Chr | Build 36 position (bp) | CEU r^2 | CHB+JPT r^2 | Gene | Annotation |
| <i>SSR1/RREB1</i> | rs9505118 | 6 | 7,235,436 | rs1050226 | 6 | 7,226,653 | 0.97 | 0.93 | <i>SSR1</i> | 3'-UTR |
| | | | | rs8955 | 6 | 7,233,296 | 1.00 | 1.00 | <i>SSR1</i> | 3'-UTR |
| | | | | rs11071 | 6 | 7,233,543 | 1.00 | 0.94 | <i>SSR1</i> | 3'-UTR |
| | | | | rs3087986 | 6 | 7,234,165 | 1.00 | 1.00 | <i>SSR1</i> | 3'-UTR |
| <i>POU5F1/TCF19</i> | rs3130501 | 6 | 31,244,432 | rs113581344 | 6 | 31,237,595 | 0.96 | 0.80 | <i>TCF19</i> | Missense |
| <i>MPHOSPH9</i> | rs4275659 | 12 | 122,013,881 | rs61955196 | 12 | 122,016,971 | 0.92 | 1.00 | <i>ABCB9</i> | 5'-UTR |
| | | | | rs3759115 | 12 | 122,030,232 | 0.92 | 0.97 | <i>OGFOD2</i> | 3'-UTR |
| | | | | rs3741530 | 12 | 122,035,600 | 0.92 | 0.81 | <i>PITPNM2</i> | 3'-UTR |

Supplementary Table 14. Properties of the 99% credible set at ten established T2D susceptibility loci as a function of SNP quality on the basis of association summary statistics from the trans-ethnic meta-analysis of European, East Asian, South Asian and Mexican American ancestry GWAS (26,488 cases and 83,964 controls) for three subsets of variants: (i) all SNPs; (ii) SNPs reported in at least 80% ($N=88,361$) individuals; and (iii) SNPs reported in at least 90% ($N=99,406$) individuals.

| Locus | Chr | 99% credible set: all SNPs | | | 99% credible set: SNPs reported for $\geq 80\%$ of individuals | | | 99% credible set: SNPs reported for $\geq 90\%$ of individuals | | |
|-----------------|-----|-------------------------------|---------------|-------------------------|---|---------------|-------------------------|---|---------------|-------------------------|
| | | SNPs | Interval (bp) | Build 36 location (bp) | SNPs | Interval (bp) | Build 36 location (bp) | SNPs | Interval (bp) | Build 36 location (bp) |
| <i>JAZF1</i> | 7 | 4 | 15,667 | 28,147,081-28,162,747 | 4 | 15,667 | 28,147,081-28,162,747 | 4 | 15,667 | 28,147,081-28,162,747 |
| <i>SLC30A8</i> | 8 | 2 | 243 | 118,253,964-118,254,206 | 2 | 243 | 118,253,964-118,254,206 | 2 | 243 | 118,253,964-118,254,206 |
| <i>CDKAL1</i> | 6 | 2 | 1,549 | 20,794,552-20,796,100 | 2 | 1,549 | 20,794,552-20,796,100 | 2 | 1,549 | 20,794,552-20,796,100 |
| <i>HHEX/IDE</i> | 10 | 2 | 937 | 94,455,539-94,456,475 | 2 | 937 | 94,455,539-94,456,475 | 2 | 937 | 94,455,539-94,456,475 |
| <i>TCF7L2</i> | 10 | 2 | 2,309 | 114,746,031-114,748,339 | 2 | 2,309 | 114,746,031-114,748,339 | 2 | 2,309 | 114,746,031-114,748,339 |
| <i>IGF2BP2</i> | 3 | 12 | 24,504 | 186,988,481-187,012,984 | 12 | 24,504 | 186,988,481-187,012,984 | 12 | 24,504 | 186,988,481-187,012,984 |
| <i>FTO</i> | 16 | 10 | 39,335 | 52,361,075-52,400,409 | 10 | 39,335 | 52,361,075-52,400,409 | 10 | 39,335 | 52,361,075-52,400,409 |
| <i>CDKN2A/B</i> | 9 | 1 | 1 | 22,122,076-22,122,076 | 1 | 1 | 22,122,076-22,122,076 | 1 | 1 | 22,122,076-22,122,076 |
| <i>PPARG</i> | 3 | 21 | 265,269 | 12,106,687-12,371,955 | 21 | 265,269 | 12,106,687-12,371,955 | 17 | 265,269 | 12,106,687-12,371,955 |
| <i>MTNR1B</i> | 11 | 15 | 55,032 | 92,307,378-92,362,409 | 13 | 55,032 | 92,307,378-92,362,409 | 7 | 55,032 | 92,307,378-92,362,409 |

Genome-wide trans-ethnic meta-analysis reveals novel insights into the genetic architecture of type 2 diabetes susceptibility

DIAbetes Genetics Replication And Meta-analysis (DIAGRAM) Consortium, Asian Genetic Epidemiology Network Type 2 Diabetes (AGEN-T2D) Consortium, South Asian Type 2 Diabetes (SAT2D) Consortium, Mexican American Type 2 Diabetes (MAT2D) Consortium and Type 2 Diabetes Genetic Exploration by Next-generation sequencing in multi-Ethnic Samples (T2D-GENES) Consortium

SUPPLEMENTARY NOTE

Membership of the DIAbetes Genetics Replication And Meta-analysis (DIAGRAM) Consortium

As at publication of the European ancestry meta-analysis, August 2012

Andrew P Morris¹, Benjamin F Voight^{2,3}, Tanya M Teslovich⁴, Teresa Ferreira¹, Ayellet V Segre^{2,5,6}, Valgerdur Steinthorsdottir⁷, Rona J Strawbridge^{8,9}, Hassan Khan¹⁰, Harald Grallert¹¹, Anubha Mahajan¹, Inga Prokopenko^{1,12}, Hyun Min Kang⁴, Christian Dina^{13–15}, Tonu Esko^{16,17}, Ross M Fraser¹⁸, Stavroula Kanoni¹⁹, Ashish Kumar¹, Vasiliki Lagou¹, Claudia Langenberg²⁰, Jian'an Luan²⁰, Cecilia M Lindgren¹, Martina Müller-Nurasyid^{21–23}, Sonali Pechlivanis²⁴, N William Rayner^{1,12}, Laura J Scott⁴, Steven Wiltshire¹, Loic Yengo^{25,26}, Leena Kinnunen²⁷, Elizabeth J Rossin^{2,5,28,29}, Soumya Raychaudhuri^{2,30,31}, Andrew D Johnson³², Antigone S Dimas^{1,33,34}, Ruth J F Loos^{20,35–37}, Sailaja Vedantam^{38,39}, Han Chen⁴⁰, Jose C Florez^{5,6,38,41}, Caroline Fox^{32,42}, Ching-Ti Liu⁴⁰, Denis Rybin⁴³, David J Couper⁴⁴, Wen Hong L Kao⁴⁵, Man Li⁴⁵, Marilyn C Cornelis⁴⁶, Peter Kraft^{46,47}, Qi Sun^{46,48}, Rob M van Dam^{46,49}, Heather M Stringham⁴, Peter S Chines⁵⁰, Krista Fischer¹⁶, Pierre Fontanillas², Oddgeir L Holmen⁵¹, Sarah E Hunt¹⁹, Anne U Jackson⁴, Augustine Kong⁷, Robert Lawrence⁵², Julia Meyer²², John R B Perry^{1,53}, Carl G P Platou^{51,54}, Simon Potter¹⁹, Emil Rehnberg⁵⁵, Neil Robertson^{1,12}, Suthesh Sivapalaratnam⁵⁶, Alena Stančáková⁵⁷, Kathleen Stirrups¹⁹, Gudmar Thorleifsson⁷, Emmi Tikkanen^{58,59}, Andrew R Wood⁵³, Peter Almgren⁶⁰, Mustafa Atalay⁶¹, Rafn Benediktsson^{62,63}, Lori L Bonnycastle⁵⁰, Noël Burtt², Jason Carey², Guillaume Charpentier⁶⁴, Andrew T Crenshaw², Alex S F Doney^{65,66}, Mozhgan Dorkhan⁶⁰, Sarah Ekins¹⁹, Valur Emilsson⁶⁷, Elodie Eury²⁵, Tom Forsen^{68,69}, Karl Gertow^{8,9}, Bruna Gigante⁷⁰, George B Grant², Christopher J Groves¹², Candace Guiducci², Christian Herder⁷¹, Astradur B Hreidarsson⁶³, Jennie Hui^{72–75}, Alan James^{72,76,77}, Anna Jonsson⁶⁰, Wolfgang Rathmann⁷⁸, Norman Klopp¹¹, Jasmina Kravic⁶⁰, Kaarel Krjutškov¹⁶, Cordelia Langford¹⁹, Karin Leander⁷⁰, Eero Lindholm⁶⁰, Stéphane Lobbens²⁵, Satu Männistö⁵⁹, Ghazala Mirza¹, Thomas W Mühleisen^{79,80}, Bill Musk^{72,75,77,81}, Melissa Parkin², Loukianos Rallidis⁸², Jouko Saramies⁸³, Bengt Sennblad^{8,9}, Sonia Shah⁸⁴, Gunnar Sigurðsson^{63,67}, Angela Silveira^{8,9}, Gerald Steinbach⁸⁵, Barbara Thorand⁸⁶, Joseph Trakalo¹, Fabrizio Veglia⁸⁷, Roman Wennauer⁸⁵, Wendy Winckler², Delilah Zabaneh⁸⁴, Harry Campbell^{18,88}, Cornelia van Duijn^{89,90}, Andre G Uitterlinden^{89–91}, Albert Hofman⁸⁹, Eric Sijbrands⁹¹, Goncalo R Abecasis⁴, Katharine R Owen^{12,92}, Eleftheria Zeggini¹⁹, Mieke D Trip⁵⁶, Nita G Forouhi²⁰, Ann-Christine Syvänen⁹³, Johan G Eriksson^{59,68,94,95}, Leena Peltonen¹³⁸, Markus M Nöthen^{79,80}, Beverley Balkau^{96,97}, Colin N A Palmer^{65,66}, Valeriya Lyssenko⁶⁰, Tiinamaija Tuomi^{95,98}, Bo Isomaa^{95,99}, David J Hunter^{46–48}, Lu Qi^{46,48}, Alan R Shuldiner^{100–102}, Michael Roden^{71,103}, Ines Barroso^{19,104,105}, Tom Wilsgaard¹⁰⁶, John Beilby^{72–74}, Kees Hovingh⁵⁶, Jackie F Price¹⁸, James F Wilson^{18,88}, Rainer Rauramaa^{107,108}, Timo A Lakka^{61,107}, Lars Lind¹⁰⁹, George Dedoussis¹¹⁰, Inger Njølstad¹⁰⁶, Nancy L Pedersen⁵⁵, Kay-Tee Khaw¹⁰, Nicholas J Wareham²⁰, Sirkka M Keinänen-Kiukaanniemi^{111,112}, Timo E Saaristo^{113,114}, Eeva Korpi-Hyövälti¹¹⁵, Juha Saltevo¹¹⁶, Markku Laakso⁵⁷, Johanna Kuusisto⁵⁷, Andres Metspalu^{16,17}, Francis S Collins⁵⁰, Karen L Mohlke¹¹⁷, Richard N Bergman¹¹⁸, Jaakko Tuomilehto^{27,115,119,120}, Bernhard O Boehm¹²¹, Christian Gieger²², Kristian Hveem⁵¹, Stephane Cauchi²⁵, Philippe Froguel^{25,122}, Damiano Baldassarre^{87,123}, Elena Tremoli^{87,123}, Steve E Humphries¹²⁴, Danish Saleheen^{10,125}, John Danesh¹⁰, Erik Ingelsson⁵⁵, Samuli Ripatti^{19,58,59}, Veikko Salomaa⁵⁹, Raimund Erbel¹²⁶, Karl-Heinz Jöckel²⁴, Susanne Moebus²⁴, Annette Peters⁸⁶, Thomas Illig^{11,127}, Ulf de Faire⁷⁰, Anders Hamsten^{8,9}, Andrew D Morris^{65,66}, Peter J Donnelly^{1,128}, Timothy M Frayling⁵³, Andrew T

Hattersley¹²⁹, Eric Boerwinkle^{130,131}, Olle Melander⁶⁰, Sekar Kathiresan^{2,5,132}, Peter M Nilsson⁶⁰, Panos Deloukas¹⁹, Unnur Thorsteinsdottir^{7,62}, Leif C Groop⁶⁰, Kari Stefansson^{7,62}, Frank Hu^{46,48}, James S Pankow¹³³, Josée Dupuis^{32,40}, James B Meigs^{6,134}, David Altshuler^{2,5,6,135–137}, Michael Boehnke⁴, and Mark I McCarthy^{1,12,92}

¹Wellcome Trust Centre for Human Genetics, University of Oxford, Oxford, UK. ²Broad Institute of Harvard and Massachusetts Institute of Technology (MIT), Cambridge, Massachusetts, USA. ³Department of Pharmacology, University of Pennsylvania–Perelman School of Medicine, Philadelphia, Pennsylvania, USA. ⁴Department of Biostatistics, University of Michigan, Ann Arbor, Michigan, USA. ⁵Center for Human Genetic Research, Massachusetts General Hospital, Boston, Massachusetts, USA. ⁶Department of Medicine, Harvard Medical School, Boston, Massachusetts, USA. ⁷deCODE Genetics, Reykjavik, Iceland. ⁸Atherosclerosis Research Unit, Department of Medicine Solna, Karolinska Institutet, Stockholm, Sweden. ⁹Center for Molecular Medicine, Karolinska University Hospital Solna, Stockholm, Sweden. ¹⁰Department of Public Health and Primary Care, University of Cambridge, Cambridge, UK. ¹¹Research Unit of Molecular Epidemiology, Helmholtz Zentrum Muenchen, Neuherberg, Germany. ¹²Oxford Centre for Diabetes, Endocrinology and Metabolism, University of Oxford, Oxford, UK. ¹³Institut National de la Santé et de la Recherche Médicale (INSERM) Unité Mixte de Recherche (UMR) 1087, Nantes, France. ¹⁴Centre National de la Recherche Scientifique (CNRS) UMR 6291, Nantes, France. ¹⁵Department of Biology, Medicine and Health, Nantes University, Nantes, France. ¹⁶Estonian Genome Center, University of Tartu, Tartu, Estonia. ¹⁷Institute of Molecular and Cell Biology, University of Tartu, Tartu, Estonia. ¹⁸Centre for Population Health Sciences, University of Edinburgh, Edinburgh, UK. ¹⁹Wellcome Trust Sanger Institute, Hinxton, Cambridge, UK. ²⁰Medical Research Council (MRC) Epidemiology Unit, Institute of Metabolic Science, Addenbrooke’s Hospital, Cambridge, UK. ²¹Institute of Medical Informatics, Biometry and Epidemiology, Ludwig-Maximilians-Universität, Munich, Germany. ²²Institute of Genetic Epidemiology, Helmholtz Zentrum Muenchen, Neuherberg, Germany. ²³Department of Medicine I, University Hospital Grosshadern, Ludwig-Maximilians-Universität, Munich, Germany. ²⁴Institute for Medical Informatics, Biometry and Epidemiology, University Hospital of Essen, University Duisburg-Essen, Essen, Germany. ²⁵CNRS UMR 8199, Institute of Biology and Lille 2 University, Pasteur Institute, Lille, France. ²⁶Laboratory of Mathematics, CNRS UMR 8524, University Lille 1, Model for Data Analysis and Learning (MODAL) Team, Institut National de Recherche en Informatique et en Automatique (INRIA) Lille Nord-Europe, Lille, France. ²⁷Diabetes Prevention Unit, National Institute for Health and Welfare, Helsinki, Finland. ²⁸Health Science and Technology MD Program, Harvard University and Massachusetts Institute of Technology, Boston, Massachusetts, USA. ²⁹Harvard Biological and Biomedical Sciences Program, Harvard University, Boston, Massachusetts, USA. ³⁰Division of Rheumatology, Immunology and Allergy, Brigham and Women’s Hospital, Harvard Medical School, Boston, Massachusetts, USA. ³¹Partners Center for Personalized Genomic Medicine, Boston, Massachusetts, USA. ³²National Heart, Lung, and Blood Institute’s Framingham Heart Study, Framingham, Massachusetts, USA. ³³Department of Genetic Medicine and Development, University of Geneva Medical School, Geneva, Switzerland. ³⁴Biomedical Sciences Research Center Al Fleming, Vari, Greece. ³⁵Charles R Bronfman Institute for Personalized Medicine, Mount Sinai School of Medicine, New York, New York, USA. ³⁶Child Health and Development Institute, Mount Sinai School of Medicine, New York, New York, USA. ³⁷Department of Preventive Medicine, Mount Sinai School of Medicine, New York, New York, USA. ³⁸Program in Medical and Population Genetics, Broad Institute of Harvard and MIT, Cambridge, Massachusetts, USA. ³⁹Division of Genetics and Endocrinology, Children’s Hospital, Boston, Massachusetts, USA. ⁴⁰Department of Biostatistics, Boston University School of Public Health, Boston, Massachusetts, USA. ⁴¹Diabetes Research Center, Diabetes Unit, Massachusetts General Hospital, Boston, Massachusetts, USA. ⁴²Division of Endocrinology and Metabolism, Brigham and Women’s Hospital and Harvard Medical School, Boston, Massachusetts, USA. ⁴³Boston University Data Coordinating Center, Boston, Massachusetts, USA. ⁴⁴Collaborative Studies Coordinating Center, Department of Biostatistics, University of North Carolina at Chapel Hill, Chapel Hill, North Carolina, USA. ⁴⁵Department of Epidemiology, Johns Hopkins Bloomberg School of Public Health, Baltimore, Maryland, USA. ⁴⁶Department of Nutrition and Epidemiology, Harvard School of Public Health, Boston, Massachusetts, USA. ⁴⁷Program in Molecular and Genetic Epidemiology, Harvard School of Public Health, Boston, Massachusetts, USA. ⁴⁸Channing Laboratory, Department of Medicine, Brigham and Women’s Hospital and Harvard Medical School, Boston, Massachusetts, USA. ⁴⁹Saw Swee Hock School of Public Health, National University of Singapore, Singapore. ⁵⁰National Human Genome Research Institute, US National Institutes of Health, Bethesda, Maryland, USA. ⁵¹Nord-Trondelag Health Study (HUNT) Research Centre, Department of Public Health and General Practice, Norwegian University of Science and Technology, Levanger, Norway. ⁵²Centre for Genetic Epidemiology and Biostatistics, The University of Western Australia,

Nedlands, Western Australia, Australia. ⁵³Genetics of Complex Traits, Institute of Biomedical and Clinical Science, Peninsula Medical School, University of Exeter, Exeter, UK. ⁵⁴Department of Internal Medicine, Levanger Hospital, Nord-Trøndelag Health Trust, Levanger, Norway. ⁵⁵Department of Medical Epidemiology and Biostatistics, Karolinska Institutet, Stockholm, Sweden. ⁵⁶Department of Vascular Medicine, Academic Medical Center, University of Amsterdam, Amsterdam, The Netherlands. ⁵⁷Department of Medicine, University of Eastern Finland and Kuopio University Hospital, Kuopio, Finland. ⁵⁸Institute for Molecular Medicine Finland (FIMM), Helsinki, Finland. ⁵⁹Department of Chronic Disease Prevention, National Institute for Health and Welfare, Helsinki, Finland. ⁶⁰Department of Clinical Science Malmö, Lund University Diabetes Centre, Scania University Hospital, Lund University, Malmö, Sweden. ⁶¹Institute of Biomedicine, Physiology, University of Eastern Finland, Kuopio, Finland. ⁶²Faculty of Medicine, University of Iceland, Reykjavík, Iceland. ⁶³Department of Endocrinology and Metabolism, Landspítali University Hospital, Reykjavík, Iceland. ⁶⁴Endocrinology-Diabetology Unit, Corbeil-Essonnes Hospital, Corbeil-Essonnes, France. ⁶⁵Diabetes Research Centre, Biomedical Research Institute, University of Dundee, Ninewells Hospital, Dundee, UK. ⁶⁶Pharmacogenomics Centre, Biomedical Research Institute, University of Dundee, Ninewells Hospital, Dundee, UK. ⁶⁷Icelandic Heart Association, Kopavogur, Iceland. ⁶⁸Department of General Practice and Primary Health Care, University of Helsinki, Helsinki, Finland. ⁶⁹Vaasa Health Care Centre, Vaasa, Finland. ⁷⁰Division of Cardiovascular Epidemiology, Institute of Environmental Medicine, Karolinska Institutet, Stockholm, Sweden. ⁷¹Institute for Clinical Diabetology, German Diabetes Center, Leibniz Center for Diabetes Research at Heinrich Heine University Düsseldorf, Düsseldorf, Germany. ⁷²Busselton Population Medical Research Institute, Sir Charles Gairdner Hospital, Nedlands, Western Australia, Australia. ⁷³PathWest Laboratory Medicine of Western Australia, Queen Elizabeth II Medical Centre, Nedlands, Western Australia, Australia. ⁷⁴School of Pathology and Laboratory Medicine, The University of Western Australia, Nedlands, Western Australia, Australia. ⁷⁵School of Population Health, The University of Western Australia, Nedlands, Western Australia, Australia. ⁷⁶Department of Pulmonary Physiology and Sleep Medicine, West Australian Sleep Disorders Research Institute, Queen Elizabeth II Medical Centre, Nedlands, Western Australia, Australia. ⁷⁷School of Medicine and Pharmacology, University of Western Australia, Nedlands, Western Australia, Australia. ⁷⁸Institute of Biometrics and Epidemiology, German Diabetes Center, Leibniz Center for Diabetes Research at Heinrich Heine University Düsseldorf, Düsseldorf, Germany. ⁷⁹Institute of Human Genetics, University of Bonn, Bonn, Germany. ⁸⁰Department of Genomics, Life & Brain Center, University of Bonn, Bonn, Germany. ⁸¹Respiratory Medicine, Sir Charles Gairdner Hospital, Nedlands, Western Australia, Australia. ⁸²Department of Cardiology, University General Hospital Attikon, Athens, Greece. ⁸³South Karelia Central Hospital, Lappeenranta, Finland. ⁸⁴Department of Genetics, Evolution and Environment, University College London (UCL) Genetics Institute, University College London, London, UK. ⁸⁵Department of Clinical Chemistry and Central Laboratory, University of Ulm, Ulm, Germany. ⁸⁶Institute of Epidemiology II, Helmholtz Zentrum Muenchen, Neuherberg, Germany. ⁸⁷Centro Cardiologico Monzino, IRCCS, Milan, Italy. ⁸⁸MRC Institute of Genetics and Molecular Medicine at the University of Edinburgh, Western General Hospital, Edinburgh, UK. ⁸⁹Department of Epidemiology, Erasmus University Medical Center, Rotterdam, The Netherlands. ⁹⁰Netherlands Genomics Initiative, Netherlands Consortium for Healthy Ageing and Centre for Medical Systems Biology, Rotterdam, The Netherlands. ⁹¹Department of Internal Medicine, Erasmus University Medical Center, Rotterdam, The Netherlands. ⁹²Oxford National Institute for Health Research Biomedical Research Centre, Churchill Hospital, Oxford, UK. ⁹³Molecular Medicine, Department of Medical Sciences, Uppsala University, Uppsala, Sweden. ⁹⁴Unit of General Practice, Helsinki University General Hospital, Helsinki, Finland. ⁹⁵Folkhälsan Research Center, Helsinki, Finland. ⁹⁶INSERM CESP U1018, Villejuif, France. ⁹⁷University Paris Sud 11, UMRS 1018, Villejuif, France. ⁹⁸Department of Medicine, Helsinki University Hospital, University of Helsinki, Helsinki, Finland. ⁹⁹Department of Social Services and Health Care, Jakobstad, Finland. ¹⁰⁰Division of Endocrinology, Diabetes and Nutrition, University of Maryland School of Medicine, Baltimore, Maryland, USA. ¹⁰¹Geriatric Research Education and Clinical Center, Baltimore Veterans Administration Medical Center, Baltimore, Maryland, USA. ¹⁰²Program in Personalized and Genomic Medicine, University of Maryland School of Medicine, Baltimore, Maryland, USA. ¹⁰³Department of Medicine/Metabolic Diseases, Heinrich Heine University Düsseldorf, Düsseldorf, Germany. ¹⁰⁴University of Cambridge Metabolic Research Laboratories, Institute of Metabolic Science, Addenbrooke's Hospital, Cambridge, UK. ¹⁰⁵National Institute for Health Research (NIHR) Cambridge Biomedical Research Centre, Institute of Metabolic Science, Addenbrooke's Hospital, Cambridge, UK. ¹⁰⁶Department of Community Medicine, Faculty of Health Sciences, University of Tromsø, Tromsø, Norway. ¹⁰⁷Kuopio Research Institute of Exercise Medicine, Kuopio, Finland. ¹⁰⁸Department of Clinical Physiology and Nuclear Medicine, Kuopio University Hospital, Kuopio, Finland. ¹⁰⁹Department of Medical Sciences, Uppsala University, Akademiska Sjukhuset, Uppsala, Sweden. ¹¹⁰Department of Dietetics-Nutrition, Harokopio University, Athens, Greece. ¹¹¹Faculty of Medicine, Institute of Health Sciences, University of Oulu, Oulu, Finland. ¹¹²Unit of General

Practice, Oulu University Hospital, Oulu, Finland. ¹¹³Finnish Diabetes Association, Tampere, Finland. ¹¹⁴Pirkanmaa Hospital District, Tampere, Finland. ¹¹⁵Department of Internal Medicine, South Ostrobothnia Central Hospital, Seinäjoki, Finland. ¹¹⁶Department of Medicine, Central Finland Central Hospital, Jyväskylä, Finland. ¹¹⁷Department of Genetics, University of North Carolina at Chapel Hill, Chapel Hill, North Carolina, USA. ¹¹⁸Diabetes and Obesity Research Institute, Cedars-Sinai Medical Center, Los Angeles, California, USA. ¹¹⁹Red RECAVA Grupo RD06/0014/0015, Hospital Universitario La Paz, Madrid, Spain. ¹²⁰Centre for Vascular Prevention, Danube-University Krems, Krems, Austria. ¹²¹Division of Endocrinology and Diabetes, Department of Internal Medicine, University Medical Centre Ulm, Ulm, Germany. ¹²²Genomic Medicine, Imperial College London, Hammersmith Hospital, London, UK. ¹²³Department of Pharmacological Sciences, University of Milan, Milan, Italy. ¹²⁴Institute of Cardiovascular Science, University College London, London, UK. ¹²⁵Center for Non Communicable Diseases Pakistan, Karachi, Pakistan. ¹²⁶Clinic of Cardiology, West German Heart Centre, University Hospital of Essen, University Duisburg-Essen, Essen, Germany. ¹²⁷Hannover Unified Biobank, Hannover Medical School, Hannover, Germany. ¹²⁸Department of Statistics, University of Oxford, Oxford, UK. ¹²⁹Diabetes Genetics, Institute of Biomedical and Clinical Science, Peninsula Medical School, University of Exeter, Exeter, UK. ¹³⁰Human Genetics Center, University of Texas Health Science Center at Houston, Houston, Texas, USA. ¹³¹Human Genome Sequencing Center at Baylor College of Medicine, Houston, Texas, USA. ¹³²Cardiovascular Research Center, Massachusetts General Hospital, Boston, Massachusetts, USA. ¹³³Division of Epidemiology and Community Health, University of Minnesota, Minneapolis, Minnesota, USA. ¹³⁴General Medicine Division, Massachusetts General Hospital, Boston, Massachusetts, USA. ¹³⁵Department of Genetics, Harvard Medical School, Boston, Massachusetts, USA. ¹³⁶Department of Molecular Biology, Harvard Medical School, Boston, Massachusetts, USA. ¹³⁷Diabetes Unit, Massachusetts General Hospital, Boston, Massachusetts, USA. ¹³⁸Deceased.

Membership of the Asian Genetic Epidemiology Network Type 2 Diabetes (AGEN-T2D) Consortium

As at publication of the East Asian ancestry meta-analysis, December 2011

Yoon Shin Cho¹, Chien-Hsiun Chen^{2,3}, Cheng Hu⁴, Jirong Long⁵, Rick Twee Hee Ong⁶, Xueling Sim⁷, Fumihiko Takeuchi⁸, Ying Wu⁹, Min Jin Go¹, Toshimasa Yamauchi¹⁰, Yi-Cheng Chang¹¹, Soo Heon Kwak¹², Ronald C W Ma¹³, Ken Yamamoto¹⁴, Linda S Adair¹⁵, Tin Aung^{16,17}, Qiuyin Cai⁵, Li-Ching Chang², Yuan-Tsong Chen², Yutang Gao¹⁸, Frank B Hu¹⁹, Hyung-Lae Kim^{1,20}, Sangsoo Kim²¹, Young Jin Kim¹, Jeannette Jen-Mai Lee²², Nanette R Lee²³, Yun Li^{9,24}, Jian Jun Liu²⁵, Wei Lu²⁶, Jiro Nakamura²⁷, Eitaro Nakashima^{27,28}, Daniel Peng-Keat Ng²², Wan Ting Tay¹⁶, Fuu-Jen Tsai³, Tien Yin Wong^{16,17,29}, Mitsuhiro Yokota³⁰, Wei Zheng⁵, Rong Zhang⁴, Congrong Wang⁴, Wing Yee So¹³, Keizo Ohnaka³¹, Hiroshi Ikegami³², Kazuo Hara¹⁰, Young Min Cho¹², Nam H Cho³³, Tien-Jyun Chang¹¹, Yuqian Bao⁴, Åsa K Hedman³⁴, Andrew P Morris³⁴, Mark I McCarthy^{34,35}, Ryoichi Takayanagi³⁶, Kyong Soo Park^{12,37}, Weiping Jia⁴, Lee-Ming Chuang^{11,38}, Juliana C N Chan¹³, Shiro Maeda³⁹, Takashi Kadowaki¹⁰, Jong-Young Lee¹, Jer-Yuarn Wu^{2,3}, Yik Ying Teo^{6,7,22,25,40}, E Shyong Tai^{22,41,42}, Xiao Ou Shu⁵, Karen L Mohlke⁹, Norihiro Kato⁸, Bok-Ghee Han¹, and Mark Seielstad^{25,43,44}

¹Center for Genome Science, National Institute of Health, Osong Health Technology Administration Complex, Chungcheongbuk-do, Cheongwon-gun, Gangoe-myeon, Yeonje-ri, Korea. ²Institute of Biomedical Sciences, Academia Sinica, Nankang, Taipei, Taiwan. ³School of Chinese Medicine, China Medical University, Taichung, Taiwan. ⁴Shanghai Diabetes Institute, Shanghai Key Laboratory of Diabetes Mellitus, Department of Endocrinology and Metabolism, Shanghai Jiao Tong University Affiliated Sixth People's Hospital, Shanghai, China. ⁵Department of Medicine, Vanderbilt Epidemiology Center, Vanderbilt-Ingram Cancer Center, Vanderbilt University School of Medicine, Nashville, Tennessee, USA. ⁶Graduate School for Integrative Science and Engineering, National University of Singapore, Singapore, Singapore. ⁷Centre for Molecular Epidemiology, National University of Singapore, Singapore, Singapore. ⁸Research Institute, National Center for Global Health and Medicine, Shinjuku-ku, Tokyo, Japan. ⁹Department of Genetics, University of North Carolina, Chapel Hill, North Carolina, USA. ¹⁰Department of Diabetes and Metabolic Diseases, Graduate School of Medicine, The University of Tokyo, Tokyo, Japan. ¹¹Department of Internal Medicine, National Taiwan University Hospital, Taipei, Taiwan. ¹²Department of Internal Medicine, Seoul National University College of Medicine, Seoul, Korea. ¹³Department of Medicine and Therapeutics, Chinese University of Hong Kong, Prince of Wales Hospital, Hong Kong, China. ¹⁴Division of Genome Analysis, Research Center for Genetic Information, Medical Institute of Bioregulation, Kyushu University, Higashi-ku, Fukuoka, Japan. ¹⁵Department of Nutrition, University of North Carolina, Chapel Hill, North Carolina, USA. ¹⁶Singapore Eye Research Institute, Singapore National Eye Centre, Singapore, Singapore. ¹⁷Department of Ophthalmology, National University of Singapore, Singapore, Singapore. ¹⁸Department of Epidemiology, Shanghai Cancer Institute, Shanghai, China. ¹⁹Department of Nutrition and Epidemiology, Harvard School of Public Health, Boston, Massachusetts, USA. ²⁰Department of Biochemistry, School of Medicine, Ewha Womans University, Seoul, Korea. ²¹School of Systems Biomedical Science, Soongsil University, Dongjak-gu, Seoul, Korea. ²²Department of Epidemiology and Public Health, National University of Singapore, Singapore, Singapore. ²³Office of Population Studies Foundation Inc., University of San Carlos, Cebu City, Philippines. ²⁴Department of Biostatistics, University of North Carolina, Chapel Hill, North Carolina, USA. ²⁵Genome Institute of Singapore, Agency for Science, Technology and Research, Singapore, Singapore. ²⁶Shanghai Institute of Preventive Medicine, Shanghai, China. ²⁷Division of Endocrinology and Diabetes, Department of Internal Medicine, Nagoya University Graduate School of Medicine, Nagoya, Japan. ²⁸Department of Diabetes and Endocrinology, Chubu Rosai Hospital, Nagoya, Japan. ²⁹Centre for Eye Research Australia, University of Melbourne, East Melbourne, Victoria, Australia. ³⁰Department of Genome Science, Aichi-Gakuin University, School of Dentistry, Nagoya, Japan. ³¹Department of Geriatric Medicine, Graduate School of Medical Sciences, Kyushu University, Higashi-ku, Fukuoka, Japan. ³²Department of Endocrinology, Metabolism and Diabetes, Kinki University School of Medicine, Osaka-sayama, Osaka, Japan. ³³Department of Preventive Medicine, Ajou University School of Medicine, Suwon, Korea. ³⁴Wellcome Trust Centre for Human Genetics, University of Oxford, Oxford, UK. ³⁵Oxford Centre for Diabetes,

Endocrinology and Metabolism, University of Oxford, Churchill Hospital, Oxford, UK. ³⁶Department of Internal Medicine and Bioregulatory Science, Graduate School of Medical Sciences, Kyushu University, Higashi-ku, Fukuoka, Japan. ³⁷World Class University program, Department of Molecular Medicine and Biopharmaceutical Sciences, Graduate School of Convergence Science and Technology and College of Medicine, Seoul National University, Seoul, Korea. ³⁸Graduate Institute of Clinical Medicine, National Taiwan University School of Medicine, Taipei, Taiwan. ³⁹Laboratory for Endocrinology and Metabolism, RIKEN Center for Genomic Medicine, Yokohama, Japan. ⁴⁰Department of Statistics and Applied Probability, National University of Singapore, Singapore, Singapore. ⁴¹Department of Medicine, National University of Singapore, Singapore, Singapore. ⁴²Duke-National University of Singapore Graduate Medical School, Singapore, Singapore. ⁴³Institute for Human Genetics, University of California, San Francisco, California, USA. ⁴⁴Blood Systems Research Institute, San Francisco, California, USA.

Membership of the South Asian Type 2 Diabetes (SAT2D) Consortium

As at publication of the South Asian ancestry meta-analysis, August 2011

Jaspal S Kooner¹⁻³, Danish Saleheen^{4,5}, Xueling Sim⁶, Joban Sehmi^{1,2}, Weihua Zhang⁷, Philippe Frossard⁴, Latonya F Been⁸, Kee-Seng Chia^{6,9}, Antigone S Dimas^{10,11}, Neelam Hassanali¹², Tazeen Jafar^{13,14}, Jeremy B M Jowett¹⁵, Xinzhong Li¹, Venkatesan Radha¹⁶, Simon D Rees^{17,18}, Fumihiko Takeuchi¹⁹, Robin Young⁵, Tin Aung^{20,21}, Abdul Basit²², Manickam Chidambaram¹⁶, Debashish Das², Elin Grundberg²³, Åsa K Hedman¹¹, Zafar I Hydrie²², Muhammed Islam¹³, Chiea-Chuen Khor^{6,21,24}, Sudhir Kowlessur²⁵, Malene M Kristensen¹⁵, Samuel Liju¹⁶, Wei-Yen Lim⁶, David R Matthews¹², Jianjun Liu²⁴, Andrew P Morris¹¹, Alexandra C Nica¹⁰, Janani M Pinidiyapathirage²⁶, Inga Prokopenko¹¹, Asif Rasheed⁴, Maria Samuel⁴, Nabi Shah⁴, A Samad Shera²⁷, Kerrin S Small^{23,28}, Chen Suo⁶, Ananda R Wickremasinghe²⁶, Tien Yin Wong^{20,21,29}, Mingyu Yang³⁰, Fan Zhang³⁰, Goncalo R Abecasis³¹, Anthony H Barnett^{17,18}, Mark Caulfield³², Panos Deloukas³³, Timothy M Frayling³⁴, Philippe Froguel³⁵, Norihiro Kato¹⁹, Prasad Katulanda^{12,36}, M Ann Kelly^{17,18}, Junbin Liang³⁰, Viswanathan Mohan^{16,37}, Dharambir K Sanghera⁸, James Scott¹, Mark Seielstad³⁸, Paul Z Zimmet¹⁵, Paul Elliott^{7,39}, Yik Ying Teo^{6,9,24,40,41}, Mark I McCarthy^{11,12,42}, John Danesh⁵, E Shyong Tai^{9,43,44}, and John C Chambers^{2,3,7}

¹National Heart and Lung Institute (NHLI), Imperial College London, Hammersmith Hospital, London, UK.

²Ealing Hospital National Health Service (NHS) Trust, Middlesex, UK. ³Imperial College Healthcare NHS Trust, London, UK. ⁴Center for Non-Communicable Diseases Pakistan, Karachi, Pakistan. ⁵Department of Public Health and Primary Care, University of Cambridge, Cambridge, UK. ⁶Centre for Molecular Epidemiology, National University of Singapore, Singapore. ⁷Epidemiology and Biostatistics, Imperial College London, London, UK. ⁸Department of Pediatrics, Section of Genetics, College of Medicine, University of Oklahoma Health Sciences Center, Oklahoma City, Oklahoma, USA. ⁹Department of Epidemiology and Public Health, National University of Singapore, Singapore. ¹⁰Department of Genetic Medicine and Development, University of Geneva Medical School, Geneva, Switzerland. ¹¹Wellcome Trust Centre for Human Genetics, University of Oxford, Oxford, UK. ¹²Oxford Centre for Diabetes, Endocrinology & Metabolism, University of Oxford, Churchill Hospital, Oxford, UK. ¹³Department of Community Health Sciences, Aga Khan University, Karachi, Pakistan. ¹⁴Department of Medicine, Aga Khan University, Karachi, Pakistan. ¹⁵Baker IDI Heart and Diabetes Institute, Melbourne, Victoria, Australia. ¹⁶Department of Molecular Genetics, Madras Diabetes Research Foundation–Indian Council of Medical Research (ICMR) Advanced Centre for Genomics of Diabetes, Chennai, India. ¹⁷College of Medical and Dental Sciences, University of Birmingham, Birmingham, UK. ¹⁸BioMedical Research Centre, Heart of England NHS Foundation Trust, Birmingham, UK. ¹⁹Department of Gene Diagnostics and Therapeutics, Research Institute, National Center for Global Health and Medicine, Tokyo, Japan. ²⁰Department of Ophthalmology, National University of Singapore, Singapore. ²¹Singapore Eye Research Institute, Singapore National Eye Centre, Singapore. ²²Baqai Institute of Diabetology and Endocrinology, Karachi, Pakistan. ²³Department of Twin Research and Genetic Epidemiology, King's College London, London, UK. ²⁴Genome Institute of Singapore, Agency for Science, Technology and Research, Singapore. ²⁵Ministry of Health, Port Louis, Mauritius. ²⁶Department of Public Health, Faculty of Medicine, University of Kelaniya, Ragama, Sri Lanka. ²⁷Diabetic Association Pakistan, Karachi, Pakistan. ²⁸Wellcome Trust Sanger Institute, Wellcome Trust Genome Campus, Hinxton, UK. ²⁹Center for Eye Research Australia, University of Melbourne, Melbourne, Victoria, Australia. ³⁰Beijing Genomics Institute, Shenzhen, China. ³¹Center for Statistical Genetics, Department of Biostatistics, University of Michigan School of Public Health, Ann Arbor, Michigan, USA. ³²Clinical Pharmacology and Barts and the London Genome Centre, William Harvey Research Institute, Barts and the London School of Medicine, Queen Mary University of London, London, UK. ³³Human Genetics, Wellcome Trust Sanger Institute, Wellcome Trust Genome Campus, Hinxton, UK. ³⁴Genetics of Complex Traits, Institute of Biomedical and Clinical Science, Peninsula Medical School, University of Exeter, Exeter, UK. ³⁵Genomics of Common Diseases, School of Public Health, Imperial College London, Hammersmith Hospital, London, UK. ³⁶Diabetes Research Unit, Department of Clinical Medicine, University of Colombo, Colombo, Sri Lanka. ³⁷Dr Mohan's Diabetes Specialties Centre, Chennai, India. ³⁸Institute of Human Genetics, University of California, San Francisco,

California, USA. ³⁹Medical Research Council (MRC)-Health Protection Agency (HPA) Centre for Environment and Health, Imperial College London, London, UK. ⁴⁰Department of Statistics and Applied Probability, National University of Singapore, Singapore. ⁴¹National University of Singapore Graduate School for Integrative Science and Engineering, National University of Singapore, Singapore. ⁴²Oxford National Institute for Health Research (NIHR) Biomedical Research Centre, Churchill Hospital, Oxford, UK. ⁴³Department of Medicine, National University of Singapore, Singapore. ⁴⁴Duke-National University of Singapore Graduate Medical School, Singapore.

Membership of the Mexican American Type 2 Diabetes (MAT2D) Consortium

As at publication of the Mexican and Mexican American ancestry meta-analysis, May 2011

Jennifer E Below¹, Graeme I Bell^{2,3}, Jorge Escobedo⁴, S Krithika⁵, Jesus Kumate⁶, Adan Valladares-Salgado⁷, Nancy J Cox^{2,3}, Miguel Cruz⁷, Craig L Hanis⁸, and Esteban J Parra⁵

¹Department of Genome Sciences, University of Washington, Seattle, WA 98195, USA. ²Department of Medicine, University of Chicago, Chicago, IL, 60637, USA. ³Department of Human Genetics, University of Chicago, Chicago, IL, 60637, USA. ⁴Unidad de Investigacion en Epidemiologia Clinica, Hospital General Regional I, Dr. Carlos MacGregor, IMSS, Mexico City, Mexico. ⁵Department of Anthropology, University of Toronto at Mississauga, 3359 Mississauga Road North, Mississauga, ON L5L 1C6, Canada. ⁶Fundacion IMSS, Av. Paseo de la Reforma 476, Mz. Poniente, Col. Juarez, Deleg. Cuauhtemoc, C.P. 06600, Mexico City, Mexico. ⁷Unidad de Investigacion Medica en Bioquimica, Hospital de Especialidades, Centro Medico Nacional Siglo XXI, IMSS, Av. Cuauhtemoc 330, Col. Doctores, C.P. 06720, Mexico City, Mexico. ⁸Human Genetics Center, University of Texas Health Science Center at Houston, P.O. Box 20186, Houston, TX 77225, USA.

Membership of the Type 2 Diabetes Genetic Exploration by Next-generation sequencing in multi-Ethnic Samples (T2D-GENES) Consortium

As at June 2013

Gonçalo Abecasis¹, Marcio Almeida², David Altshuler^{3,4,5,6,7,8,9}, Jennifer L Asimit¹⁰, Gil Atzmon¹¹, Mathew Barber¹², Nicola L Beer¹³, Graeme I Bell^{12,14}, Jennifer Below¹⁵, Tom Blackwell¹, John Blangero², Michael Boehnke¹, Donald W Bowden^{16,17,18,19}, Noël Burt³, John Chambers^{20,21,22}, Han Chen²³, Peng Chen²⁴, Peter S Chines²⁵, Yoon Shin Cho²⁶, Sungkyoung Choi²⁷, Claire Churchhouse³, Pablo Cingolani²⁸, Belinda K Cornes²⁹, Nancy Cox^{12,14}, Aaron G Day-Williams¹⁰, Ravindranath Duggirala², Josée Dupuis²³, Thomas Dyer², Shuang Feng¹, Juan Fernandez-Tajes³⁰, Teresa Ferreira³⁰, Tasha E Fingerlin³¹, Jason Flannick^{3,5}, Jose Florez^{3,5,6}, Pierre Fontanillas³, Timothy M Frayling³², Christian Fuchsberger¹, Eric R Gamazon¹⁴, Kyle Gaulton³⁰, Saurabh Ghosh³³, Anna Gloyn¹³, Robert L Grossman^{14,34}, Jason Grundstad³⁴, Craig Hanis¹⁵, Allison Heath³⁴, Heather Highland¹⁵, Momoko Horikoshi³⁰, Ik-Soo Huh²⁷, Jeroen R Huyghe¹, Kamran Ikram^{29,35,36,37}, Kathleen A Jablonski³⁸, Goo Jun¹, Norihiro Kato³⁹, Jayoun Kim²⁷, Young Jin Kim⁴⁰, C Ryan King⁴¹, Jaspal Kooner^{21,22,42}, Min-Seok Kwon²⁷, Hae Kyung Im⁴¹, Markku Laakso⁴³, Kevin Koi-Yau Lam²⁴, Jaehoon Lee²⁷, Jong Young Lee⁴⁴, Selyeong Lee²⁷, Sungyoung Lee²⁷, Donna M Lehman⁴⁵, Heng Li³, Cecilia M Lindgren³⁰, Xuanyao Liu^{24,46}, Oren E Livne¹², Adam E Locke¹, Anubha Mahajan³⁰, Julian B Maller^{30,47}, Alisa K Manning³, Taylor J Maxwell¹⁵, Alexander Mazouze⁴⁸, Mark I McCarthy^{13,30,49}, James B Meigs^{6,50}, Byungju Min²⁷, Karen L Mohlke⁵¹, Andrew P Morris³⁰, Solomon Musani⁵², Yoshihiko Nagai⁴⁸, Maggie C Y Ng^{16,17}, Dan Nicolae^{12,14,53}, Sohee Oh²⁷, Nicholette Palmer^{16,17,18}, Taesung Park²⁷, Toni I Pollin⁵⁴, Inga Prokopenko^{30,55}, David Reich^{3,4}, Manuel A Rivas³⁰, Laura J Scott¹, Mark Seielstad⁵⁶, Xueling Sim¹, Robert Sladek^{48,57}, Philip Smith⁵⁸, Ioanna Tachmazidou¹⁰, E Shyong Tai^{24,35,59}, Yik Ying Teo^{60,61,62,63,64}, Tanya M Teslovich¹, Jason Torres^{12,14}, Vasily Trubetsky^{12,14}, Sara M Willems⁶⁵, Amy L Williams^{3,4}, James G Wilson⁶⁶, Steven Wiltshire^{30,69}, Sungho Won⁶⁷, Andrew R Wood³², Wang Xu⁵⁹, Joon Yoon²⁷, Matthew Zawistowski¹, Eleftheria Zeggini¹⁰, Weihua Zhang²⁰, and Sebastian Zöllner^{1,68}

¹Department of Biostatistics, Center for Statistical Genetics, University of Michigan, Ann Arbor, Michigan 48109, USA. ²Department of Genetics, Texas Biomedical Research Institute, San Antonio, Texas 78227, USA. ³Program in Medical and Population Genetics, Broad Institute of Harvard and MIT, Cambridge, Massachusetts 02142, USA. ⁴Department of Genetics, Harvard Medical School, Boston, Massachusetts 02115, USA. ⁵Center for Human Genetic Research and Diabetes Research Center (Diabetes Unit), Massachusetts General Hospital, Boston 02114, Massachusetts, USA. ⁶Department of Medicine, Harvard Medical School, Boston, Massachusetts 02115, USA. ⁷Center for Human Genetic Research, Massachusetts General Hospital, Boston, Massachusetts 02114, USA. ⁸Department of Molecular Biology, Harvard Medical School, Boston, Massachusetts 02114, USA. ⁹Department of Biology, Massachusetts Institute of Technology, Cambridge, Massachusetts 02139, USA. ¹⁰Wellcome Trust Sanger Institute, Hinxton, Cambridge, CB10 1HH, UK. ¹¹Department of Medicine, Department of Genetics, Albert Einstein College of Medicine, Bronx, New York 10461, USA. ¹²Department of Human Genetics, University of Chicago, Chicago, Illinois 60637, USA. ¹³Oxford Centre for Diabetes, Endocrinology and Metabolism, University of Oxford, Oxford, OX3 7LJ, UK. ¹⁴Department of Medicine, University of Chicago, Chicago, Illinois 60637, USA. ¹⁵Human Genetics Center, University of Texas Health Science Center at Houston, Houston, Texas 77030, USA. ¹⁶Center for Genomics and Personalized Medicine Research, Wake Forest School of Medicine, Winston-Salem, North Carolina 27157, USA. ¹⁷Center for Diabetes Research, Wake Forest School of Medicine, Winston-Salem, North Carolina 27157, USA. ¹⁸Department of Biochemistry, Wake Forest School of Medicine, Winston-Salem, North Carolina 27157, USA. ¹⁹Internal Medicine-Endocrinology, Wake Forest School of Medicine, Winston-Salem, North Carolina 27157, USA. ²⁰Department of Epidemiology and Biostatistics, Imperial College London, London SW7 2AZ, UK. ²¹Imperial College Healthcare NHS Trust, London W2 1NY, UK. ²²Ealing Hospital National Health Service (NHS) Trust, Middlesex UB1 3HW, UK. ²³Department of Biostatistics,

Boston University School of Public Health, Boston, Massachusetts 02115, USA. ²⁴Saw Swee Hock School of Public Health, National University of Singapore, Singapore 117597, Singapore. ²⁵National Human Genome Research Institute, National Institutes of Health, Bethesda, MD 20892, USA. ²⁶Department of Biomedical Science, Hallym University, Chuncheon, Gangwon-do, 200-702 South Korea. ²⁷Seoul National University, Seoul 110-799, South Korea. ²⁸McGill Centre for Bioinformatics, McGill University, Montréal, Quebec, H3G 0B1, Canada. ²⁹Singapore Eye Research Institute, Singapore National Eye Centre, Singapore 168751, Singapore. ³⁰Wellcome Trust Centre for Human Genetics, University of Oxford, Oxford, OX3 7BN, UK. ³¹Department of Epidemiology, Colorado School of Public Health, Aurora, Colorado 80045, USA. ³²Genetics of Complex Traits, University of Exeter Medical School, Exeter, EX4 4SB, UK. ³³Human Genetics Unit, Indian Statistical Institute, 203 B.T. Road, Kolkata 700018, India ³⁴Institute for Genomics and Systems Biology, University of Chicago, Chicago, Illinois 60637, USA. ³⁵Duke National University of Singapore Graduate Medical School, Singapore 169857, Singapore. ³⁶Department of Ophthalmology, National University of Singapore and National University Health System, Singapore 119228, Singapore. ³⁷Department of Ophthalmology, Erasmus Medical Center, Rotterdam 3000 CA, the Netherlands. ³⁸The Biostatistics Center, George Washington University, Rockville, Maryland 20852, USA. ³⁹Department of Gene Diagnostics and Therapeutics, Research Institute, National Center for Global Health and Medicine, Tokyo 162-8655, Japan. ⁴⁰Department of Neurology, Konkuk University School of Medicine, Seoul 143-701, South Korea. ⁴¹Department of Health Studies, University of Chicago, Chicago, Illinois 60637, USA. ⁴²National Heart and Lung Institute (NHLI), Imperial College London, Hammersmith Hospital, London W12 0HS, UK. ⁴³Department of Medicine, University of Eastern Finland, Kuopio Campus and Kuopio University Hospital, FI-70211 Kuopio, Finland. ⁴⁴Center for Genome Science, Korea National Institute of Health, Osong Health Technology Administration Complex, Chungcheongbuk-do, 363-951, South Korea. ⁴⁵Division of Clinical Epidemiology, Department of Medicine, University of Texas Health Science Center at San Antonio, San Antonio, Texas 78229, USA. ⁴⁶Graduate School for Integrative Science and Engineering, National University of Singapore, Singapore 117456, Singapore. ⁴⁷Department of Statistics, University of Oxford, Oxford, OX1 3TG, UK. ⁴⁸McGill University, Montréal, Québec H3A 0G4, Canada. ⁴⁹Oxford NIHR Biomedical Research Centre, Churchill Hospital, Headington, OX3 7LE, UK. ⁵⁰General Medicine Division, Massachusetts General Hospital, Boston, Massachusetts 02114, USA. ⁵¹Department of Genetics, University of North Carolina-Chapel Hill, Chapel Hill, North Carolina 27599, USA. ⁵²Department of Medicine, University of Mississippi Medical Center, Jackson, Mississippi 39126, USA. ⁵³Department of Statistics, University of Chicago, Chicago, Illinois 60637, USA. ⁵⁴Department of Medicine, Program for Personalized and Genomic Medicine, University of Maryland School of Medicine, Baltimore, Maryland 21201, USA. ⁵⁵Genomics of Common Disease, Imperial College London, Hammersmith Hospital, London, W12 0NN, UK. ⁵⁶University of California San Francisco, San Francisco, California 94143, USA. ⁵⁷Department of Medicine, Royal Victoria Hospital, Montréal, Québec H3A 1A1, Canada. ⁵⁸National Institute of Diabetes and Digestive and Kidney Disease, National Institutes of Health, Bethesda, MD 20817, USA. ⁵⁹Department of Medicine, Yong Loo Lin School of Medicine, National University of Singapore, Singapore 117597, Singapore. ⁶⁰Department of Epidemiology and Public Health, National University of Singapore, Singapore 117597, Singapore. ⁶¹Centre for Molecular Epidemiology, National University of Singapore, Singapore 117456, Singapore. ⁶²Genome Institute of Singapore, Agency for Science, Technology and Research, Singapore 138672, Singapore. ⁶³Graduate School for Integrative Science and Engineering, National University of Singapore, Singapore 117456, Singapore. ⁶⁴Department of Statistics and Applied Probability, National University of Singapore, Singapore 117546, Singapore. ⁶⁵Department of Genetic Epidemiology, Erasmus Medical Center, Rotterdam 3000 CA, the Netherlands. ⁶⁶Department of Physiology and Biophysics, University of Mississippi Medical Center, Jackson, Mississippi 39216, USA. ⁶⁷Chung-Ang University, Seoul 156-756, South Korea. ⁶⁸Department of Psychiatry, University of Michigan, Ann Arbor, Michigan 48109, USA. ⁶⁹Deceased.

Resources interrogated for expression analyses

We interrogated public databases and unpublished resources for *cis*-eQTL expression with lead Ps in the novel susceptibility loci in multiple tissues: fresh lymphocytes¹, fresh leukocytes², leukocyte samples in individuals with Celiac disease³, lymphoblastoid cell lines (LCL) derived from asthmatic children⁴, HapMap LCL from 3 populations⁵, a separate study on HapMap CEU LCL⁶, CD19+ B cells⁷, peripheral blood monocytes⁷⁻⁹, dendritic cells before and after *Mycobacterium tuberculosis* infection¹⁰, omental and subcutaneous adipose^{11,12}, stomach¹² and whole blood samples^{11,13,14}, endometrial carcinomas¹⁵, brain cortex^{7,16,17}, 3 large studies of brain regions including prefrontal cortex, visual cortex and cerebellum, (Emilsson, personal communication), liver^{12,18,19}, osteoblasts²⁰, lung²¹, skin²² and additional fibroblast, T cell and LCL samples^{23,24}.

1. Goring HH, *et al.* (2007). Discovery of expression QTLs using large-scale transcriptional profiling in human lymphocytes. *Nat Genet* 39: 1208-16.
2. Idaghdour Y, *et al.* (2010). Geographical genomics of human leukocyte gene expression variation in southern Morocco. *Nat Genet* 42: 62-7.
3. Heap GA, *et al.* (2009). Complex nature of SNP genotype effects on gene expression in primary human leucocytes. *BMC Med Genomics* 2: 1.
4. Dixon AL, *et al.* (2007). A genome-wide association study of global gene expression. *Nat Genet* 39: 1202-7.
5. Stranger BE, *et al.* (2007). Population genomics of human gene expression. *Nat Genet* 39: 1217-24.
6. Kwan T, *et al.* (2008). Genome-wide analysis of transcript isoform variation in humans. *Nat Genet* 40: 225-31.
7. Fairfax BP, *et al.* (2012). Genetics of gene expression in primary immune cells identifies cell type-specific master regulators and roles of HLA alleles. *Nat Genet* 44: 502-10.
8. Heinzen EL, *et al.* (2008). Tissue-specific genetic control of splicing: implications for the study of complex traits. *PLoS Biol* 6: e1.
9. Zeller T, *et al.* (2010). Genetics and beyond - the transcriptome of human monocytes and disease susceptibility. *PLoS One* 5: e10693.
10. Barreiro LB, *et al.* (2012). Deciphering the genetic architecture of variation in the immune response to *Mycobacterium tuberculosis* infection. *Proc Natl Acad Sci USA* 109: 1204-9.
11. Emilsson V, *et al.* (2008). Genetics of gene expression and its effect on disease. *Nature* 452: 423-8.
12. Greenawalt DM, *et al.* (2011). A survey of the genetics of stomach, liver and adipose gene expression from a morbidly obese cohort. *Genome Res* 21: 1008-16.
13. Fehrmann RS, *et al.* (2011). Trans-eQTLs reveal that independent genetic variants associated with a complex phenotype converge on intermediate genes with a major role for the HLA. *PLoS Genet* 7: e1002197.
14. Mehta D, *et al.* (2013). Impact of common regulatory single-nucleotide variants on gene expression profiles in whole blood. *Eur J Hum Genet* 21: 48- 54.
15. Kompass KS, Witte JS (2011). Co-regulatory expression quantitative trait loci mapping: method and application to endometrial cancer. *BMC Med Genomics* 4: 6.

16. Webster JA, *et al.* (2009). Genetic control of human brain transcript expression in Alzheimer disease. *Am J Hum Genet* 84: 445-58.
17. Zou F, *et al.* (2012). Brain expression genome-wide association study (eGWAS) identifies human disease-associated variants. *PLoS Genet* 8: e1002707.
18. Schadt EE, *et al.* (2008). Mapping the genetic architecture of gene expression in human liver. *PLoS Biol* 6: e107.
19. Innocenti F, *et al.* (2011). Identification, replication, and functional fine-mapping of expression quantitative trait loci in primary human liver tissue. *PLoS Genet* 7: e1002078.
20. Grundberg E, *et al.* (2009). Population genomics in a disease targeted primary cell model. *Genome Res* 19: 1942-52.
21. Hao K, *et al.* (2012). Lung eQTLs to help reveal the molecular underpinnings of asthma. *PLoS Genet* 8: e1003029.
22. Ding J, *et al.* (2010). Gene expression in skin and lymphoblastoid cells: refined statistical method reveals extensive overlap in *cis*-eQTL signals. *Am J Hum Genet* 87: 779-89.
23. Dimas AS, *et al.* (2009). Common regulatory variation impacts gene expression in a cell type-dependent manner. *Science* 325: 1246-50.
24. Cusanovich DA, *et al.* (2012). The combination of a genome-wide association study of lymphocyte count and analysis of gene expression data reveals novel asthma candidate genes. *Hum Mol Genet* 21: 2111-23