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Supporting Online Material for

A Genome-Wide Association Study of Type 2 Diabetes in Finns Detects Multiple Susceptibility Variants

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This PDF file includes:

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Methods

Sample description

Stage 1: In the results reported here, we analyzed 1,161 T2D cases and 1,174 NGT controls from the Finland-United States Investigation of NIDDM Genetics (FUSION) (*1, 2*) and Finrisk 2002 (*3*) studies as our stage 1 sample (Tables S1, S2A). T2D was defined according to 1999 World Health Organization (WHO) criteria (*4*) of fasting plasma glucose concentration ≥ 7.0 mmol/l or 2-h plasma glucose concentration ≥ 11.1 mmol/l, by report of diabetes medication use, or based on medical record review. FUSION cases with known or probable type 1 diabetes among their first degree relatives were excluded. Normal glucose tolerance (NGT) was defined as having fasting glucose < 6.1 mmol/l and 2-h glucose < 7.8 mmol/l (*4*). The 789 FUSION cases each reported at least one T2D sibling; the 372 Finrisk 2002 T2D cases came from a Finnish population-based risk factor survey. Controls included 219 subjects from Vantaa, Finland who were NGT at ages 65 and 70 years, 304 NGT spouses of FUSION subjects, and 651 Finrisk 2002 NGT subjects. The stage 1 controls were approximately frequency-matched to the stage 1 cases by five-year age category, sex, and birth province. We refer to these FUSION and Finrisk 2002 cases and controls in the text as the FUSION stage 1 sample. For quantitative trait and quality control analyses, we genotyped 122 FUSION offspring, yielding 119 mother-father-offspring trios, 1 mother-father-two-offspring quartet, and one parent-offspring pair. For quality control, we successfully genotyped 79 duplicate samples and five CEU HapMap parent-child trios.

Stage 2: 1,215 Finnish T2D cases and 1,258 Finnish NGT controls were selected for stage 2 from the Dehko 2D (D2D) (*5*), Health 2000 (*6*), Finrisk 1987 (*7*), Finrisk 2002 (*3*), Savitaipale

Diabetes (*8*), and Action LADA (*9*) studies (Tables S1, S2B) and classified according to WHO 1999 criteria (*4*). The D2D, Health 2000, Finrisk 1987, and Savitaipale Diabetes studies are population-based surveys; Action LADA is a study of latent autoimmune diabetes in adults (LADA) in recently-diagnosed diabetes patients. We chose T2D cases from Action LADA who were GAD antibody negative and therefore unlikely to have LADA. For all studies except Action LADA, NGT controls were approximately frequency-matched within each study to the T2D cases by five-year age category, sex, and birth province. Action LADA cases were approximately frequency-matched in the same way with additional controls from the other studies. Our stage 2 sample consists of 327 cases and 399 controls from D2D, 127 cases and 224 controls from Health 2000, 266 cases and 397 controls from Finrisk 1987, 52 controls from Finrisk 2002, 122 cases and 186 controls from Savitaipale, and 373 cases from Action LADA (Table S2B). For quality control in stage 2, we successfully genotyped 56 duplicate samples.

Informed consent: Informed consent was obtained from each study participant, and the study protocol was approved by the ethics committee or institutional review board in each of the participating centers.

Genotyping

GWA genotyping: Stage 1 and quality control samples were genotyped on Illumina Infinium™ II HumanHap300 BeadChips v.1.0 in the Johns Hopkins University Genetic Resources Core Facility (GRCF) SNP Center at the Center for Inherited Disease Research (CIDR) using the Illumina Infinium II assay protocol (*10*). An in-house LIMS was used for sample and reagent

tracking and lab workflow control (*11*). ~1 μg of genomic DNA (15 μL at 70 ng/μl) was used as input for the Infinium II assay.

Intensity data for each sample were normalized using BeadStudio v.2.3.25 and, for quality control within CIDR, genotypes were determined using the Illumina-provided standard definition cluster-file for the HumanHap300 v.1.0 product. These cluster boundaries were determined by Illumina using 111 unique HapMap samples: 47 CEU, 36 YRI, and 28 CHB/JPT. BeadStudio sample sheets were generated from our in-house LIMS. Sample and batch level quality control was done by monitoring sample call rates, sex, heterozygote frequencies, and lab workflow related variables using data generated from BeadStudio and our LIMS. 35 genotyped samples fell below our sample call rate threshold of < 97.5% and were repeated; 28 of the repeated samples gave call rates > 97.5%. The remaining 7 samples were excluded from analyses.

To obtain genotypes for analysis, we re-clustered the genotype data using cluster boundaries determined with our own data. We removed samples for 15 people identified as likely first or second degree relatives of other sampled individuals based on their genotype data (*12*). We checked for consistency in genotyping within each of 79 duplicate sample pairs, with Mendelian inheritance among the 122 parent-offspring sets, and with Hardy-Weinberg Equilibrium (HWE) using the unrelated individuals (*13*). After initial analyses, we manually reviewed in BeadStudio the clustering of the genotype data for our most strongly associated SNPs.

SNPs were dropped from all analyses if the HWE p-value was < 10^{-6}, the total number of Mendelian inconsistencies and duplicate pair discrepancies was > 3, or the SNP call rate was <

90%; and flagged for further attention if the HWE p-value was < 10^{-4}, the total number of Mendelian inconsistencies and duplicate pair discrepancies was > 1, or the SNP call rate < 95%. All genotypes were oriented to the forward strand. There is little risk of strand ambiguities as there are no C/G or A/T polymorphisms included in the Illumina 300K HumanHap panel.

For the 315,635 SNPs that passed our quality control criteria, the genotype consistency rate among 79 duplicate sample pairs was 99.996%, the Mendelian consistency rate in 122 parent-child sets was 99.967%, and the concordance rate for 15 samples genotyped both in our study and by the HapMap consortium was 99.82%. 80.8% of SNPs had call frequency of 100%, and 99.68% of SNPs had call frequencies > 95%.

Confirmation and replication genotyping: We carried out focused, lower-throughput genotyping with the Sequenom Homogeneous MassEXTEND or iPLEX Gold SBE assays at the National Human Genome Research Institute (NHGRI). For 26 GWA SNPs re-genotyped in the stage 1 samples on a different genotyping platform (Sequenom), we observed a genotype consistency rate of 99.92%; these included the SNPs with the strongest evidence of T2D association. We also genotyped SNPs in the FUSION stage 2 samples or in the combined FUSION stage 1+2 samples to follow up interesting results based on (a) FUSION genotyped and imputed SNPs; (b) the FUSION-DGI-WTCCC GWA results comparison; and (c) prior T2D association results in our own or other studies. 80 of the 82 attempted SNPs had genotype call frequency > 94% and HWE p-value > .001. The genotype consistency rate among duplicate samples was 99.9% and the average call frequency was 97.1%.

Statistical analysis

T2D association: We tested for T2D-SNP association using logistic regression under the additive genetic model that is multiplicative on the OR scale with adjustment for five-year age category, sex, and birthplace. This test is the logistic regression equivalent to the Cochran-Armitage test for trend (*14*) and is hence robust to departures from Hardy-Weinberg equilibrium. We repeated some analyses including BMI, waist, systolic blood pressure, or diastolic blood pressure as an additional covariate to assess the impact of these variables on evidence for SNP-T2D association. For X-chromosome markers, we treated hemizygous males as homozygotes, consistent with X inactivation for most of the chromosome. We presented and followed up on results based on this additive model for ease of comparison between groups. We also analyzed SNPs using recessive and dominant models; no SNP reached genome-wide significance in FUSION stage 1 data, although additional T2D-prediposing variants may be among the SNPs identified by these models.

To evaluate empirically the distribution of p-values observed in our GWA stage 1 study, we permuted case/control status and re-ran the entire GWA analysis 100 times. We counted the number of p-values $< 10^{-5}$ or $< 10^{-4}$ within each permuted dataset and found our study to fall within the permuted distribution.

Statistical significance: Following the recommendation of the International HapMap Consortium based on analysis of the ENCODE data, we declared a T2D-SNP association "genome-wide significant" if the nominal p-value for the SNP was $< 5 \times 10^{-8}$ (*15*). In so doing,

we dealt with the multiple comparisons problem suggested by carrying out the equivalent of ~1 million tests.

Sample size calculation: For each SNP in Table 1, we calculated the sample size necessary to detect T2D-SNP association at significance level .05 and power 80% under an additive model. We converted the FUSION-DGI-WTCCC/UKT2D all-data OR to a risk ratio assuming T2D prevalence 10%, and used this risk ratio and FUSION stage 1+2 control risk allele frequency as the population allele frequency in the sample size calculation (*16*).

Imputation: We applied a computationally efficient hidden Markov model based algorithm (*17, 18*) to impute genotypes in FUSION samples for 2.25 million autosomal SNPs genotyped by the International HapMap Consortium (*15*), but not present on the Illumina HumanHap300 BeadChip. The method combines our FUSION Illumina GWA genotype data with phased chromosomes for the HapMap CEU samples and then infers the unknown FUSION genotypes probabilistically by searching for similar stretches of flanking haplotype in the HapMap CEU reference sample. In this process, we used the genotype data from the 290,690 FUSION Illumina GWA autosomal SNPs which passed our quality control criteria and had minor allele frequency > 5%. For each individual at each imputed SNP, we calculated an average allele dosage score based on 90 iterations of the imputation algorithm. We assessed the quality of the results for each SNP by calculating (a) the proportion of iterations that agreed with the most likely genotype (imputation consistency) and (b) the ratio of the observed variance of dosage scores across samples to the expected variance given the imputed allele frequency of the SNP

(estimated r^2). 2.15 million of the HapMap autosomal SNPs had minor allele frequency > 1% in the CEU sample; of these, 2.09 million met our quality control criterion of an estimated $r^2 > .30$.

We evaluated the accuracy of our imputation procedure by comparing imputed genotypes to actual genotypes for 510 SNPs not present on the Illumina GWA panel but that we had previously genotyped in 1,190 individuals in our stage 1 samples (*19*). The average concordance rate between imputed and actual alleles (genotypes) was 98.5% (97.1%), suggesting that the HapMap CEU sample provides an appropriate basis for SNP genotype imputation in Finns, consistent with our previous findings that allele frequencies, haplotype frequencies, and linkage disequilibrium (LD) measures are remarkably similar between the CEU samples and a set of the Finnish individuals that overlaps with those included in this study (*19*). We also genotyped 23 SNPs imputed in our stage 1 data; 16 of these SNPs had stage 1 imputation-based p-values $< 10^{-5}$. For most of these SNPs, the p-values for the actual genotypes were very similar to those for the imputed genotypes, although often slightly less significant (Table S6); large differences occurred most often for estimated r^2 values nearer the quality control threshold. Differences reflect variability in the imputation-based p-value estimates and our choice to follow up strong imputation-based association results, an example of the "winner's curse." This variability in p-value estimates for imputed SNPs did not lead to an increased overall false positive rate for the study since we have chosen to genotype each such SNP in stage 1 as well as stage 2.

To test for disease-SNP association for imputed SNPs allowing for the effects of covariates, we used logistic regression models in which the SNP effect was represented by its mean imputed

allele dosage score, an approach that takes into account the degree of uncertainty of genotype imputation (*18*).

Combined analysis: We used a fixed effects model to estimate the combined ORs, 95% confidence intervals (CIs), and p-values for the GWA genotype or imputed data for FUSION and the GWA genotype data from DGI and WTCCC studies (*20*). We used the same approach to combine all available data from the FUSION, DGI, and WTCCC/UKT2D studies. All results are based on genotypes predicted from the forward strand of the genome sequence. When we describe results across studies for non-identical SNPs, we report LD estimates based on FUSION genotype data when available and on imputed data when not.

SNP selection for stage 2 genotyping: We selected SNPs for genotyping in the FUSION stage 2 samples based on the results of the FUSION GWA and the comparison of the FUSION, DGI, and WTCCC GWA results. To enrich for SNPs with interesting biological functions from the FUSION GWA, we weighted the association p-value according to our interest in the SNP based on genome annotation, using an algorithm similar to the one described by Roeder et al. (*21*), with weights as described in Table S7. Our algorithm advantaged genotyped SNPs that tagged any HapMap SNP annotated as non-synonymous, frameshift, or critical splice site variants, or located in or around interesting T2D candidate genes using an LD threshold of $r^2 \geq .8$ in the CEU HapMap sample. It did so by dividing the p-value by the product of the maximal relevant weighting factor and the relevant bonus factors. For imputed SNPs, we assigned the weight based only on the imputed SNP itself. From SNPs with weighted p-values $\leq 10^{-4}$, we formed sets of SNPs within 100 kb of each other and ranked these sets based on the smallest weighted p-

value. From each of these sets, we selected a strongly associated SNP for stage 2 genotyping, giving some preference to genotyped over imputed SNPs to reduce stage 1 genotyping requirements and to focus on SNPs for which we had more accurate genotype information. If an imputed SNP was chosen, we genotyped stage 1 and 2 samples.

Risk prediction: We predicted T2D risk in the FUSION sample based on the ten identified T2D susceptibility variants listed in Table 1. T2D cases and NGT controls with complete genotype data were included in the analysis. To obtain a sample with ~10% T2D prevalence, the 2,176 NGT controls were included nine times each and the 2,102 T2D cases once each in a logistic regression analysis. Figure 2 displays the proportion of T2D individuals for twenty equal intervals of predicted T2D risk. 95% CIs for the proportion of T2D cases were constructed using the original, not the expanded, sample.

Linkage and association: To assess the possible predictive value of T2D linkage for T2D association, we counted the number of our ten T2D-associated loci (Table 1) for which the T2D linkage LOD score was > 0.2 in our FUSION affected sibling pair families (*2*). We then divided the genome into 5 cM bins and noted that 22% of such bins had T2D LOD score > 0.2 in our T2D linkage scan. The observed count of six of the ten loci with T2D LOD > 0.2 is ~3-times greater than expected by chance, and has exact binomial p-value of .01, consistent with the hypothesis that very modest linkage evidence is somewhat predictive of the presence of a locus detectable by association methods.

Gene expression analysis

RNAs from human tissues were purchased from Clontech and represented pooled samples from several individuals. Purified human pancreatic islets were obtained from Islet Cell Resource Centers (IRB Exemption number 3072) and the National Disease Research Interchange (IRB Exemption number 3269) with approval by the National Institutes of Health Office of Human Subjects Research. Anonymous human blood donor samples from the NIH Clinical Center Division of Transfusion Medicine were provided as buffy coat isolations from whole blood centrifugation. Human adipocytes were purchased from Cambrex as differentiated cultures, and cell cultures -- 293T (human embryonic kidney), HeLa (human cervical carcinoma), and HepG2 (human hepatocellular carcinoma) -- were purchased from ATCC (the American Type Culture Collection). Lymphoblastoid cell lines from CEPH individuals were purchased from the Coriell Cell Repositories. RNA from cell cultures, islets, blood, and adipocytes was prepared with Trizol Reagent (Invitrogen) followed by RNeasy Kit (Qiagen). RNA from four individual samples was used to prepare pooled cDNA for islets, adipocytes, blood, and lymphoblasts. cDNA was prepared from 1 ug of total RNA, using SuperScript III reverse transcriptase and random hexamers (Invitrogen). cDNA equivalent to 25-50 ng of total RNA was used for each quantitative PCR. All PCRs were performed in 10 ul volume in replicates of 3 or 4 using the 7900 Real-Time PCR System (ABI) in 384 well plates; average values were used for calculations. The PCR with 2xSYBR Green PCR mix (Qiagen) and specific primers was designed over exon boundaries to amplify only from cDNA:

CDKAL1_f: GAAGAATCTTTTGATTCCAAGTTTT

CDKAL1_r: GCAGCACCATTCTGGAACTC

CDKN2A_f: ATCTATGCGGGCATGGTTACT

CDKN2A_r: CAACGCACCGAATAGTTACG

CDKN2B_f: CGGGGACTAGTGGAGAAGGT

CDKN2B_r: ACCAGCGTGTCCAGGAAG

PCRs were carried out for 15 min at 95 C, followed by 40 cycles of 15 sec at 95 C, 15 sec at 59 C, and 45 sec at 72 C. Post-PCR melting curve analysis was used after each run. Gel-purified PCR fragments were also sequenced to ensure the specificity of amplification and splicing. An expression assay for human beta-2 microglobulin (*B2M*) Hs00187842_m1 was purchased from ABI and used according to the instructions. Ct values (cycle at threshold) were determined from real-time PCR. The expression of target genes was normalized to expression of B2M according to the equation $dCt = Ct_{B2M} - Ct_{target}$, compared to expression in pancreas by equation $ddCt = dCt_{tissue} - dCt_{pancreas}$, then converted to fold difference as fold difference $= 2^{ddCt}$ (ABI, User Bulletin #2 on relative quantification). We were unable to assess confidently the tissue distribution of *IGF2BP2* mRNA because of very high similarity (> 95%) to three processed pseudogenes on chromosomes 1, 8, and 12.

Supplementary Figure Legends

Figure S1. Quantile-quantile plot for T2D association -$\log_{10}$ p-values for FUSION stage 1 samples and p-values expected under the null distribution for FUSION GWA SNPs.

Figure S2. Plot of T2D association and LD in FUSION stage 1 sample for region surrounding *SLC30A8*. The top panel contains RefSeq genes. The second panel shows the T2D association -$\log_{10}$ p-values in FUSION stage 1 samples for SNPs genotyped in the GWA panel (•) or imputed (o). The third panel shows T2D association -$\log_{10}$ p-values for each SNP in a logistic regression model correcting for the reference SNP rs13266634 (•, red dot). A decrease in the -$\log_{10}$ p-value from the second to the third panel indicates that the association signal of the tested SNPs can be explained, at least in part, by the reference SNP. The reference SNP is a non-synonymous coding SNP, and was chosen because of its potential of being the actual functional variant responsible for the association signal; choice of another strongly associated SNP nearby would have resulted in a similar picture. The fourth panel shows recombination rate in cM per Mb for the HapMap CEU sample (*15*). The fifth and sixth panels show linkage disequilibrium r^2 and D' based on FUSION stage 1 genotyped and imputed data.

Figure S3. Expression of *CDKAL1* (first panel), *CDKN2A* (second panel), and *CDKN2B* (third panel) in human tissues and cells. The level of expression of each gene was determined by quantitative RT-PCR, and normalized to the beta-2-microglobulin (*B2M*) housekeeping gene. The data are presented as fold difference relative to expression in pancreas, which is set at 1.0.

293T cells are human embryonic kidney, HeLa are human cervical carcinoma, and HepG2 are human hepatocellular carcinoma.

Figure S1

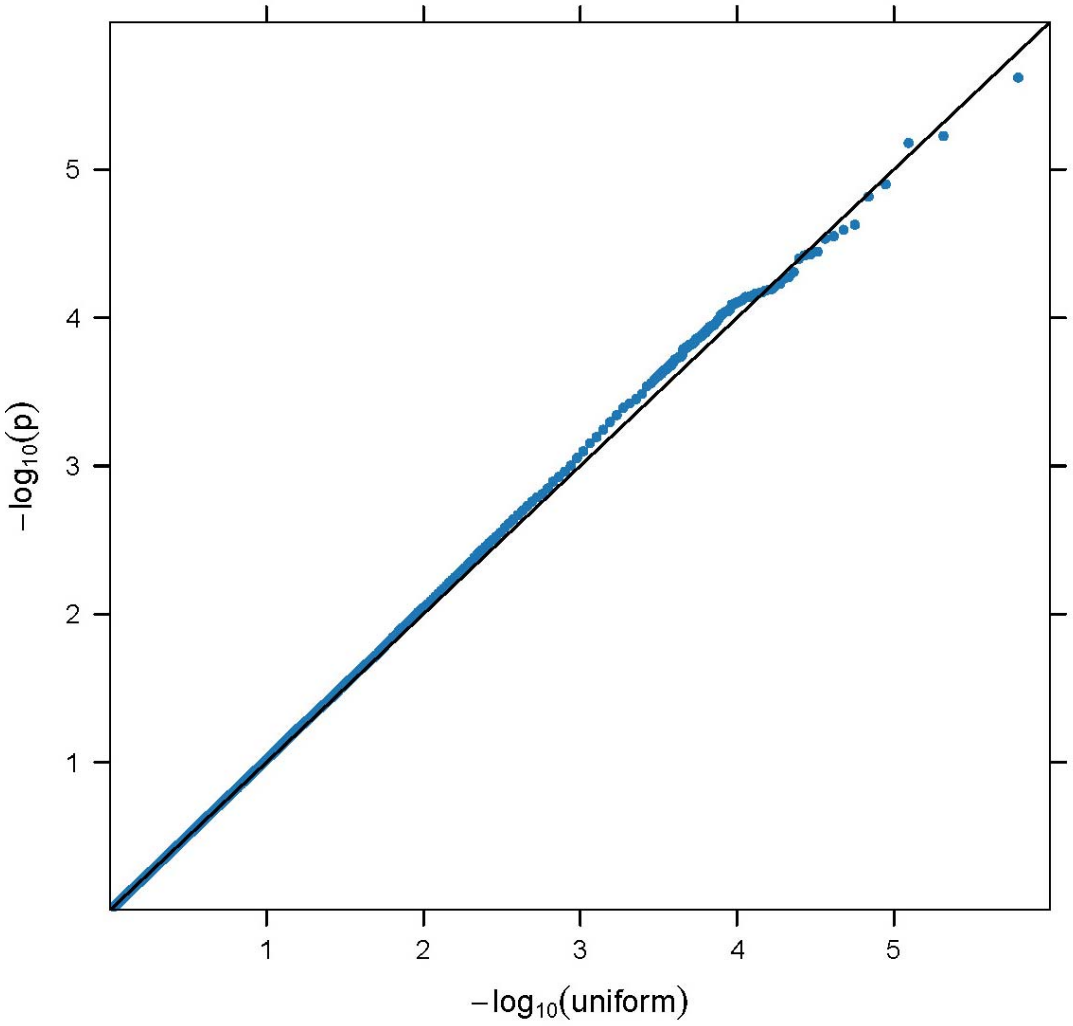
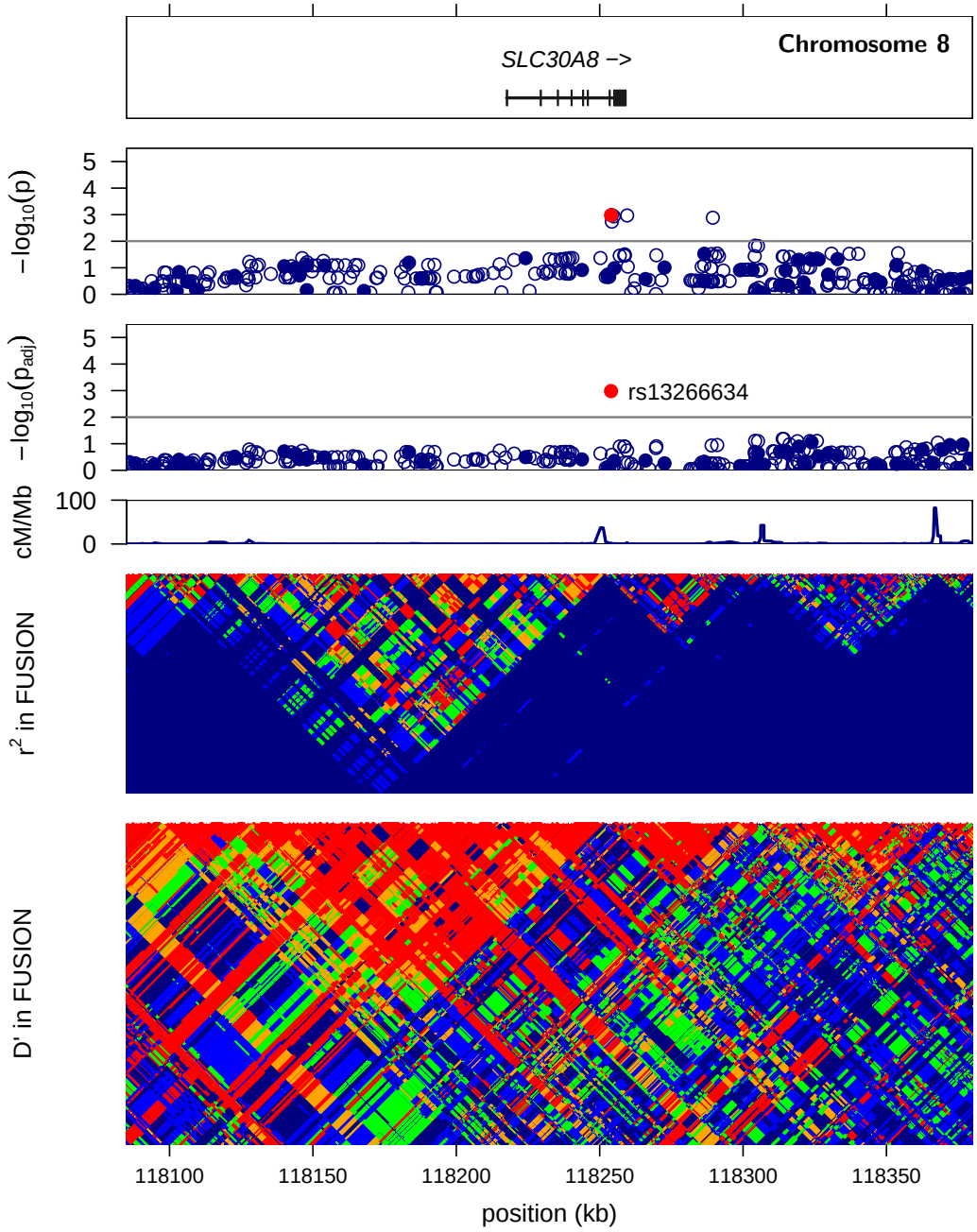


Figure S2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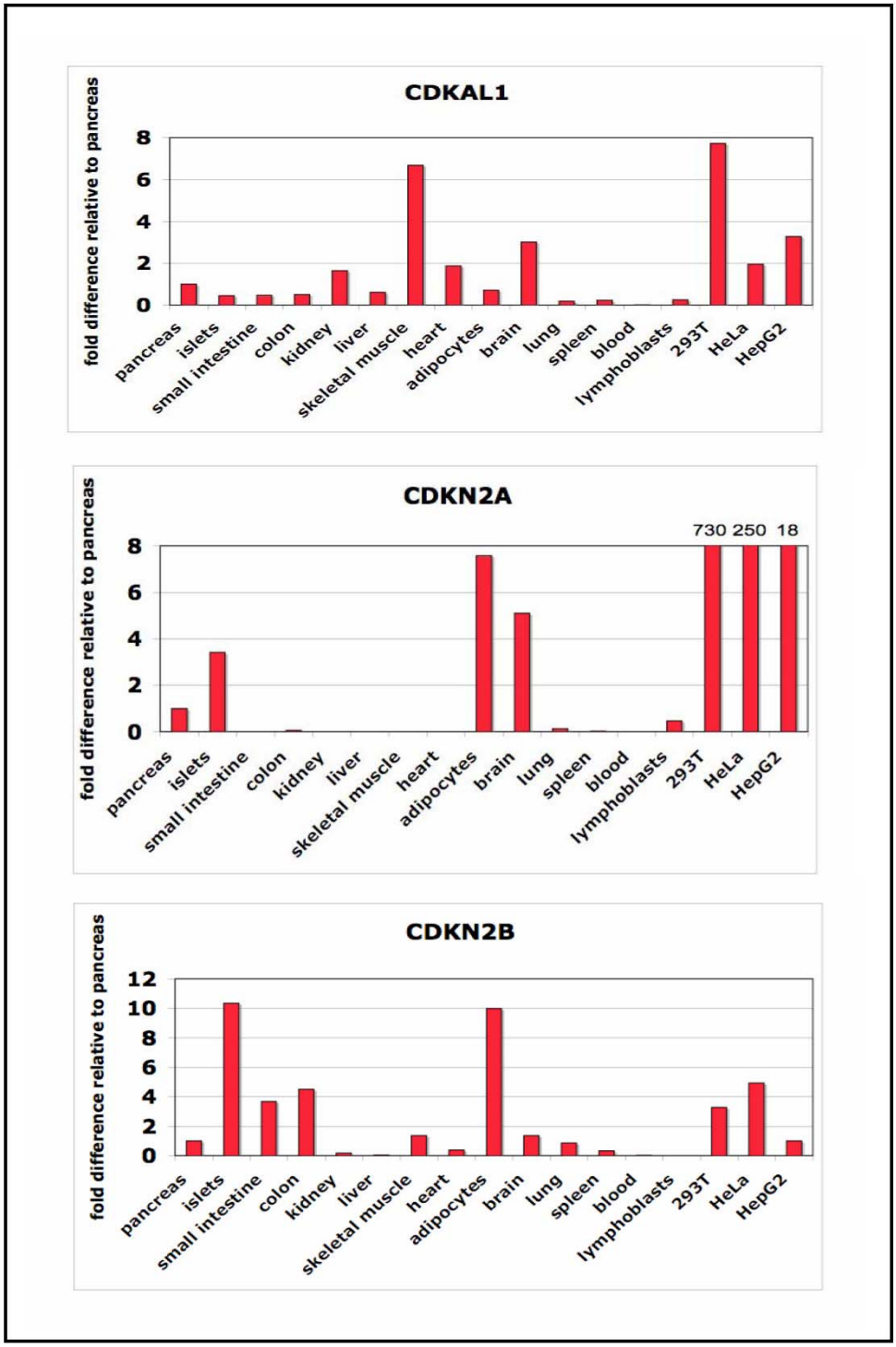
SLC30A8 ->
−log10(p)
−log10(padj)
rs13266634
cM/Mb
r2 in FUSION
D' in FUSION
118100
118150
118200
118250
118300
118350
position (kb)

Figure S3


CDKAL1
fold difference relative to pancreas
0
2
4
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8
pancreas
islets
small intestine
colon
kidney
liver
skeletal muscle
heart
adipocytes
brain
lung
spleen
blood
lymphoblasts
293T
HeLa
HepG2
CDKN2A
fold difference relative to pancreas
730 250 18
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6
8
pancreas
islets
small intestine
colon
kidney
liver
skeletal muscle
heart
adipocytes
brain
lung
spleen
blood
lymphoblasts
293T
HeLa
HepG2
CDKN2B
fold difference relative to pancreas
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12
pancreas
islets
small intestine
colon
kidney
liver
skeletal muscle
heart
adipocytes
brain
lung
spleen
blood
lymphoblasts
293T
HeLa
HepG2

Table S1. Characteristics of stage 1 and stage 2 case and control samples

	Stage 1				Stage 2			
	Cases		Controls		Cases		Controls	
	Median	IQR	Median	IQR	Median	IQR	Median	IQR
N	1161		1174		1215		1258	
Male	653		574		724		768	
Female	508		600		491		490	
Age of Diagnosis (years)	53.0	12.0	---	---	56.0	12.0	---	---
Study Age (years)	63.4	11.2	64.0	11.7	60.0	11.5	59.0	10.6
BMI (kg/m^2)	29.8	6.1	26.8	5.0	30.1	6.7	26.4	4.9
Fasting Plasma Glucose (mmol/l)	8.4	3.9	5.4	0.7	7.2[a]	2.1[a]	5.4[b]	0.6[b]

[a]n=204 and [b]n=583 values converted from whole blood to plasma glucose equivalent using prediction equation from the European Diabetes Epidemiology Group (*22*), of which [b]n=262 fasted < 8 hours

Table S2A. Detailed characteristics of stage 1 case and control samples

	FUSION						Finrisk 2002			
	Cases		Controls		Controls from Finrisk 2002		Cases		Controls	
	Median	IQR	Median	IQR	Median	IQR	Median	IQR	Median	IQR
N	789		523[a]		276		372		375	
Male	429		194		163		224		217	
Female	360		329		113		148		158	
Age of Diagnosis (years)	51.0	11.0	---	---	---	---	59.0	12.0	---	---
Study Age (years)	64.2	10.1	69.6	7.7	62.0	9.0	61.0	12.0	61.0	12.0
BMI (kg/m^2)	29.3	6.2	27.3	5.5	26.5	4.5	30.7	6.0	26.6	4.4
Fasting Plasma Glucose (mmol/l)	9.6	4.7	5.1	0.6	5.6	0.5	7.3	1.3	5.6	0.5

[a]Comprised of 219 FUSION controls from Vantaa who were NGT at ages 65 and 70 years, and 304 NGT spouses of FUSION T2D subjects

Table S2B. Detailed characteristics of stage 2 case and control samples

	D2D				Health 2000				Action LADA				Finrisk 1987				Savitaipale Diabetes Study			
	Cases		Controls		Cases		Controls		Cases		Controls		Cases		Controls		Cases		Controls	
	Median	IQR	Median	IQR	Median	IQR	Median	IQR	Median	IQR	Median	IQR	Median	IQR	Median	IQR	Median	IQR	Median	IQR
N	327		314		127		124		373		402[a]		266		300		122		118	
Male	184		176		67		66		235		259		171		202		67		65	
Female	143		138		60		58		138		143		95		98		55		53	
Age of Diagnosis (years)	60.0	13.0	---	---	55.0	13.0	---	---	55.0	10.0	---	---	55.0	13.0	---	---	55.1	11.7	---	---
Study Age (years)	64.0	11.4	64.3	12.0	61.0	15.0	59.0	12.0	60.2	10.8	58.0	9.0	58.0	11.0	57.0	12.0	57.9	13.4	57.0	13.0
BMI (kg/m^2)	29.9	7.1	26.4	4.9	30.3	5.4	26.5	5.6	30.3	6.9	26.3	4.7	30.5	6.1	26.7	4.8	28.3	7.1	25.4	4.5
Fasting Plasma Glucose (mmol/l)	7.2	2.0	5.4	0.5	7.3	2.0	5.4	0.5	7.3	2.4	5.5[b]	0.6[b]	6.9[c]	3.0[c]	5.1[cd]	0.6[cd]	7.2[c]	0.9[c]	5.6[c]	0.4[c]

[a]85 D2D, 100 Health 2000, 52 Finrisk 2002, 97 Finrisk 1987, and 68 Savitaipale Diabetes Study controls
[b]n=165 values converted from whole blood to plasma glucose equivalent using prediction equation from the European Diabetes Epidemiology Group (*22*) , of which n=52 fasted < 8 hours
[c]all values converted from whole blood to plasma glucose equivalent using prediction equation from the European Diabetes Epidemiology Group (*22*)
[d]n=210 fasted < 8 hours

Table S3. FUSION stage 1 T2D association: **genotyped** (**bold**) and imputed (non-bold) SNPs with p-value < .0001. Sets of SNPs, where each SNP is within 100kb of the preceding SNP, are delimited by lines.

SNP	Genes	Chr	Position (bp)	FUSION risk allele/ non-risk allele	Control risk frequency	Case risk frequency	OR	95% CI	p-value	Genotyped p-value for imputed SNP	Genotyped in Stage 2?
rs527912	*CDA*	1	20,679,589	G/A	.670	.723	1.304	1.141-1.49	9.4×10^{-5}		
rs3820321	*PINK1*	1	20,708,133	G/A	.602	.663	1.291	1.142-1.459	4.0×10^{-5}		
rs607254	*DDOST, KIF17, PINK1*	1	20,726,186	G/A	.601	.663	1.294	1.145-1.463	3.4×10^{-5}		
rs589709	*DDOST, KIF17, PINK1*	1	20,729,293	G/A	.601	.663	1.297	1.147-1.465	2.9×10^{-5}		
rs640742	***DDOST, KIF17, PINK1***	**1**	**20,729,860**	**A/C**	**.601**	**.663**	**1.297**	**1.147-1.465**	**2.9×10^{-5}**		Yes
rs623817	*DDOST, KIF17, PINK1*	1	20,731,384	G/A	.601	.663	1.297	1.147-1.467	3.1×10^{-5}		
rs674114	*DDOST, KIF17*	1	20,734,978	G/A	.615	.668	1.321	1.151-1.516	6.8×10^{-5}		
rs630484	*DDOST, KIF17*	1	20,737,912	G/T	.616	.670	1.332	1.159-1.530	4.8×10^{-5}		
rs12118760	*DDOST, KIF17*	1	20,745,110	T/C	.736	.767	1.708	1.331-2.191	2.2×10^{-5}		
rs1932397		**1**	**`29,732,290**	**T/C**	**.168**	**.215**	**1.351**	**1.164-1.569**	**7.1×10^{-5}**		
rs6603926		1	29,735,248	A/G	.168	.215	1.352	1.164-1.57	7.0×10^{-5}		
rs9662524		1	29,739,496	G/C	.168	.215	1.351	1.164-1.569	7.3×10^{-5}		
rs915409		1	29,740,363	T/C	.168	.215	1.351	1.164-1.569	7.3×10^{-5}		
rs9286938		**1**	**29,746,194**	**T/C**	**.168**	**.214**	**1.345**	**1.159-1.562**	**9.1×10^{-5}**		
rs9659523		1	29,746,693	A/C	.169	.215	1.344	1.157-1.56	1.0×10^{-4}		
rs271306		1	29,751,757	G/C	.168	.214	1.344	1.157-1.561	1.0×10^{-4}		
rs17356414		1	59,031,529	C/T	.548	.607	1.311	1.158-1.485	1.7×10^{-5}	8.0×10^{-4}	Yes
rs6676059		1	59,041,777	G/A	.548	.606	1.312	1.159-1.485	1.7×10^{-5}		
rs12133457		1	59,042,784	G/A	.548	.606	1.312	1.159-1.485	1.7×10^{-5}		
rs17025978	***KCNA10***	**1**	**110,781,653**	**G/A**	**.914**	**.947**	**1.705**	**1.347-2.158**	**6.6×10^{-6}**		Yes
rs17025982	*KCNA10*	1	110,782,336	T/C	.910	.943	1.699	1.342-2.151	7.8×10^{-6}		
rs2790372		1	110,799,166	C/A	.937	.962	1.750	1.320-2.319	7.5×10^{-5}		
rs2799765		1	110,800,193	T/C	.937	.962	1.748	1.317-2.319	8.5×10^{-5}		
rs1626078		1	110,801,281	C/T	.937	.962	1.748	1.316-2.322	8.9×10^{-5}		
rs1622675		1	110,801,684	A/T	.937	.962	1.758	1.321-2.338	8.3×10^{-5}		
rs1627572		1	110,801,712	G/A	.938	.962	1.756	1.319-2.338	8.9×10^{-5}		
rs2501354	***SLAMF8, VSIG8***	**1**	**156,628,715**	**G/A**	**.355**	**.415**	**1.274**	**1.129-.437**	**8.1×10^{-5}**		
rs2501350	*SLAMF8, VSIG8*	1	156,630,077	G/C	.379	.437	1.288	1.136-.459	7.0×10^{-5}		
rs357973		2	3,292,094	G/A	.942	.961	1.975	1.394-2.798	9.3×10^{-5}		
rs357971		2	3,292,963	G/C	.942	.961	1.977	1.395-2.802	9.1×10^{-5}		
rs2338545	***PLB1***	**2**	**28,711,426**	**G/A**	**.202**	**.252**	**1.332**	**1.157-.534**	**6.3×10^{-5}**		
rs2249434	*SCLY*	2	238,757,753	C/G	.076	.110	1.497	1.221-.835	9.1×10^{-5}		
rs1391136		3	21,136,392	C/T	.838	.874	1.425	1.195-1.700	7.5×10^{-5}		
rs11926889		3	30,253,294	G/A	.880	.911	1.537	1.243-1.900	6.1×10^{-5}		
rs1434006		3	30,268,508	C/T	.904	.934	1.586	1.268-1.984	4.4×10^{-5}		
rs13075234		3	30,269,434	C/T	.922	.946	1.707	1.311-2.223	5.8×10^{-5}		
rs10440137		3	30,270,978	G/T	.904	.934	1.581	1.266-1.974	4.4×10^{-5}		
rs9870410		**3**	**30,283,763**	**C/T**	**.904**	**.935**	**1.579**	**1.267-1.967**	**3.8×10^{-5}**		
rs13092602		3	30,284,949	G/A	.906	.939	1.660	1.324-2.081	8.2×10^{-6}		
rs1495586		3	30,302,792	G/A	.907	.940	1.666	1.327-2.091	8.2×10^{-6}		
rs17081352		3	30,307,851	C/A	.910	.942	1.698	1.342-2.148	7.6×10^{-6}	5.5×10^{-6}	Yes
rs9843153		3	30,308,252	G/T	.913	.944	1.722	1.351-2.195	8.4×10^{-6}		
rs11714343		**3**	**34,437,873**	**T/C**	**.084**	**.118**	**1.472**	**1.210-1.791**	**9.6×10^{-5}**		

Table S3. FUSION stage 1 T2D association: **genotyped** (**bold**) and imputed (non-bold) SNPs with p-value < .0001 (continued)

SNP	Genes	Chr	Position (bp)	FUSION risk allele/ non-risk allele	Control risk frequency	Case risk frequency	OR	95% CI	p-value	Genotyped p-value for imputed SNP	Genotyped in Stage 2?
rs739984	***PTPRG***	**3**	**61,975,357**	**G/A**	**.729**	**.777**	**1.320**	**1.150-1.515**	**7.2×10^{-5}**		
rs12490128	*TMEM108*	3	134,391,491	A/C	.118	.162	1.465	1.234-1.739	1.1×10^{-5}		
rs13072106	***TMEM108***	**3**	**134,425,451**	**T/C**	**.118**	**.155**	**1.414**	**1.188-1.682**	**8.7×10^{-5}**		Yes
rs10512891	*TMEM108*	3	134,431,557	A/T	.118	.156	1.415	1.189-1.684	8.3×10^{-5}		
rs7650741	*TMEM108*	3	134,432,277	T/C	.118	.156	1.416	1.189-1.684	8.2×10^{-5}		
rs7612595	*TMEM108*	3	134,439,991	T/C	.118	.156	1.418	1.192-1.688	7.5×10^{-5}		
rs16840161	*TMEM108*	3	134,478,424	A/G	.117	.158	1.444	1.213-1.718	3.1×10^{-5}		
rs17297332	*TMEM108*	3	134,480,782	G/C	.121	.162	1.447	1.216-1.723	2.9×10^{-5}		
rs7625110	*TMEM108*	3	134,494,477	T/G	.117	.158	1.446	1.215-1.722	2.9×10^{-5}		
rs10512896	*TMEM108*	3	134,499,457	G/C	.117	.158	1.450	1.218-1.726	2.7×10^{-5}		
rs1708373	*TMEM108*	3	134,502,025	G/A	.117	.158	1.451	1.219-1.728	2.5×10^{-5}		
rs1197316	*TMEM108*	3	134,522,283	G/A	.117	.158	1.455	1.222-1.734	2.3×10^{-5}		
rs1920021	*TMEM108*	3	134,554,123	T/C	.118	.158	1.450	1.216-1.729	3.1×10^{-5}		
rs823968		**3**	**136,542,755**	**C/T**	**.382**	**.436**	**1.274**	**1.131-1.436**	**6.7×10^{-5}**		
rs4687296	*MAP3K13*	3	186,595,002	T/C	.225	.276	1.325	1.158-1.516	3.9×10^{-5}		
rs4687299	***MAP3K13***	**3**	**186,595,361**	**A/G**	**.225**	**.276**	**1.325**	**1.158-1.515**	**4.0×10^{-5}**		Yes
rs886374	***SORCS2***	**4**	**7,856,440**	**T/C**	**.211**	**.270**	**1.385**	**1.209-1.587**	**2.4×10^{-6}**		Yes
rs6815292	*ATP8A1*	4	42,251,192	A/G	.244	.291	1.308	1.144-1.496	7.9×10^{-5}		
rs7665824	*ATP8A1*	4	42,252,481	T/G	.244	.291	1.309	1.145-1.496	7.8×10^{-5}		
rs11726581	*ATP8A1*	4	42,257,935	C/T	.244	.291	1.309	1.145-1.497	7.7×10^{-5}		
rs11722556	*ATP8A1*	4	42,258,828	T/C	.244	.291	1.309	1.145-1.497	7.5×10^{-5}		
rs17630357	*ATP8A1*	4	42,266,042	A/T	.774	.821	1.346	1.160-1.562	8.2×10^{-5}		
rs4317238	*ATP8A1*	4	42,267,105	A/G	.774	.821	1.346	1.160-1.562	8.1×10^{-5}		
rs16854359	*ATP8A1*	4	42,269,100	C/G	.241	.290	1.313	1.149-1.501	5.7×10^{-5}		
rs9994372	*ATP8A1*	4	42,269,138	T/C	.251	.301	1.335	1.166-1.527	2.5×10^{-5}		
rs10034439	*ATP8A1*	4	42,287,090	C/T	.776	.826	1.374	1.182-1.598	3.1×10^{-5}		
rs13139219	***ATP8A1***	**4**	**42,294,231**	**C/A**	**.779**	**.827**	**1.346**	**1.160-1.561**	**7.8×10^{-5}**		Yes
rs6812080	*ATP8A1*	4	42,319,554	G/A	.779	.828	1.349	1.163-1.565	7.0×10^{-5}		
rs13116032	*ATP8A1*	4	42,320,518	G/T	.779	.828	1.349	1.163-1.565	7.0×10^{-5}		
rs5022521	*ELOVL6*	4	111,486,191	T/C	.858	.884	1.785	1.349-2.361	4.1×10^{-5}		
rs1030231		**5**	**66,353,021**	**G/A**	**.198**	**.245**	**1.330**	**1.152-1.536**	**9.3×10^{-5}**		
rs10476844		5	142,096,902	T/C	.014	.023	4.666	2.212-9.841	3.5×10^{-5}		
rs961730	*ARHGAP26*	5	142,114,126	C/T	.014	.024	4.696	2.254-9.784	2.4×10^{-5}		
rs1347133	*ARHGAP26*	5	142,114,290	C/T	.014	.024	4.745	2.275-9.899	2.1×10^{-5}		
rs968076	*ARHGAP26*	5	142,116,491	G/A	.014	.024	4.787	2.293-9.993	2.0×10^{-5}		
rs7714907	*ARHGAP26*	5	142,125,570	G/A	.014	.023	5.319	2.473-11.441	1.2×10^{-5}		
rs7732207	*ARHGAP26*	5	142,125,613	A/G	.014	.023	5.317	2.472-11.439	1.2×10^{-5}		
rs764387	*ARHGAP26*	5	142,125,869	T/C	.014	.023	5.326	2.472-11.474	1.2×10^{-5}		
rs7737018	*ARHGAP26*	5	142,126,283	C/G	.014	.023	5.317	2.462-11.483	1.3×10^{-5}		
rs6898675	*ARHGAP26*	5	142,131,843	T/C	.014	.023	5.320	2.456-11.526	1.4×10^{-5}		
rs6894433	*ARHGAP26*	5	142,133,535	C/T	.014	.023	5.315	2.452-11.523	1.4×10^{-5}		
rs707177	*ARHGAP26*	5	142,232,076	A/G	.372	.424	1.308	1.146-1.493	6.4×10^{-5}		
rs447923	*ARHGAP26*	5	142,232,441	T/C	.325	.373	1.321	1.148-1.519	9.2×10^{-5}		
rs26707	*ARHGAP26*	5	142,233,857	G/C	.250	.303	1.325	1.160-1.513	3.0×10^{-5}		

Table S3. FUSION stage 1 T2D association: **genotyped** (**bold**) and imputed (non-bold) SNPs with p-value < .0001 (continued)

SNP	Genes	Chr	Position (bp)	FUSION risk allele/ non-risk allele	Control risk frequency	Case risk frequency	OR	95% CI	p-value	Genotyped p-value for imputed SNP	Genotyped in Stage 2?
rs26706	*ARHGAP26*	5	142,237,044	C/G	.253	.306	1.324	1.159-1.513	3.2×10^{-5}		
rs27779	***ARHGAP26***	**5**	**142,239,267**	**A/C**	**.250**	**.304**	**1.326**	**1.162-1.513**	**2.5×10^{-5}**		Yes
rs27546	*ARHGAP26*	5	142,245,929	T/A	.250	.302	1.321	1.157-1.508	3.5×10^{-5}		
rs11970389	*TUBB2B, LOC389362*	6	3,195,655	T/C	.041	.063	1.845	1.351-2.518	9.2×10^{-5}		
rs4713992		6	36,720,183	A/G	.730	.764	1.525	1.240-1.875	5.7×10^{-5}		
rs7750445	*ZFAND3*	6	37,872,955	G/C	.114	.158	1.483	1.244-1.769	9.4×10^{-6}	4.1×10^{-5}	Yes
rs17235125		6	79,437,555	A/G	.871	.906	1.459	1.207-1.762	8.0×10^{-5}		
rs17235167		6	79,437,614	C/G	.871	.906	1.459	1.208-1.763	7.8×10^{-5}		
rs17235209		6	79,437,636	C/T	.871	.906	1.461	1.209-1.765	7.6×10^{-5}		
rs17826801		6	79,437,741	A/G	.871	.906	1.460	1.208-1.764	7.8×10^{-5}		
rs2021966	*ENPP1*	6	132,192,132	A/G	.585	.634	1.320	1.150-1.516	7.2×10^{-5}	2.6×10^{-4}	Yes
rs2813539	*SYNE1*	6	152,613,828	G/A	.382	.435	1.312	1.150-1.496	4.8×10^{-5}		
rs1408460	*SYNE1*	6	152,614,232	C/G	.460	.518	1.267	1.126-1.426	8.3×10^{-5}		
rs719764	*SYNE1*	6	152,614,487	C/G	.483	.538	1.293	1.141-1.466	5.4×10^{-5}		
rs2673776	***SYNE1***	**6**	**152,614,926**	**G/T**	**.458**	**.516**	**1.265**	**1.125-1.422**	**8.0×10^{-5}**		
rs2635441	*SYNE1*	6	152,615,257	A/G	.460	.517	1.264	1.123-1.422	9.4×10^{-5}		
rs13212052		6	166,264,601	T/C	.979	.992	2.979	1.668-5.323	8.2×10^{-5}		
rs2791300		7	18,102,317	C/G	.704	.752	1.319	1.149-1.514	7.7×10^{-5}		
rs4721708		7	18,143,542	C/T	.702	.760	1.373	1.199-1.572	3.8×10^{-6}		
rs615545		**7**	**18,165,111**	**C/T**	**.694**	**.751**	**1.361**	**1.190-1.556**	**5.9×10^{-6}**		Yes
rs2470984	***SLC13A1***	**7**	**122,368,680**	**A/C**	**.297**	**.348**	**1.279**	**1.130-1.448**	**9.0×10^{-5}**		Yes
rs6466855	*SLC13A1*	7	122,371,141	A/G	.294	.346	1.289	1.137-1.462	7.0×10^{-5}		
rs6964272	*SLC13A1*	7	122,373,978	T/C	.265	.317	1.333	1.168-1.52	1.7×10^{-5}		
rs13444183	*SLC13A1*	7	122,377,232	G/T	.265	.317	1.333	1.168-1.521	1.8×10^{-5}		
rs6963735	*SLC13A1*	7	122,394,634	C/T	.256	.306	1.350	1.176-1.549	1.8×10^{-5}		
rs10280430	*SLC13A1*	7	122,399,306	C/T	.255	.305	1.350	1.176-1.549	1.9×10^{-5}		
rs1880178	*SLC13A1*	7	122,403,062	T/C	.255	.305	1.350	1.176-1.55	1.9×10^{-5}		
rs10954654		**7**	**138,816,342**	**C/T**	**.725**	**.776**	**1.337**	**1.166-1.533**	**2.8×10^{-5}**		Yes
rs10277603		7	138,816,687	C/T	.592	.645	1.354	1.179-1.554	1.5×10^{-5}		
rs10261979		7	138,816,832	G/C	.601	.653	1.367	1.187-1.574	1.3×10^{-5}		
rs10262338		7	138,816,913	A/G	.592	.645	1.355	1.180-1.555	1.5×10^{-5}		
rs9692401		7	138,817,247	C/T	.584	.637	1.364	1.187-1.567	1.1×10^{-5}		
rs9691662		7	138,817,453	A/G	.592	.645	1.353	1.179-1.554	1.6×10^{-5}		
rs9690418		7	138,817,495	G/A	.592	.645	1.353	1.179-1.553	1.6×10^{-5}		
rs12707449		7	138,817,983	A/T	.592	.645	1.353	1.179-1.553	1.6×10^{-5}		
rs10271287		7	138,819,517	T/C	.592	.645	1.353	1.179-1.554	1.6×10^{-5}		
rs38732	*MRPS33*	7	140,158,346	T/A	.069	.096	1.680	1.296-2.178	6.9×10^{-5}		
rs9274	*MRPS33*	7	140,159,215	A/G	.048	.076	1.639	1.279-2.101	7.5×10^{-5}		
rs544081		7	140,209,733	G/A	.048	.076	1.643	1.282-2.106	6.7×10^{-5}		
rs488795		7	140,211,070	T/G	.048	.076	1.643	1.282-2.105	6.8×10^{-5}		
rs512509		7	140,211,331	T/C	.048	.076	1.643	1.282-2.105	6.7×10^{-5}		
rs548245		7	140,212,951	T/C	.047	.075	1.635	1.274-2.099	8.9×10^{-5}		
rs471817		7	140,214,431	A/C	.048	.076	1.643	1.282-2.105	6.8×10^{-5}		
rs801155		7	140,221,134	A/G	.048	.076	1.642	1.282-2.105	6.8×10^{-5}		

Table S3. FUSION stage 1 T2D association: **genotyped** (**bold**) and imputed (non-bold) SNPs with p-value < .0001 (continued)

SNP	Genes	Chr	Position (bp)	FUSION risk allele/ non-risk allele	Control risk frequency	Case risk frequency	OR	95% CI	p-value	Genotyped p-value for imputed SNP	Genotyped in Stage 2?
rs528957	***LOC642421***	**7**	**140,222,643**	**T/C**	**.048**	**.076**	**1.634**	**1.276-2.094**	**7.8×10^{-5}**		
rs557962		**7**	**140,232,924**	**T/C**	**.047**	**.076**	**1.650**	**1.287-2.115**	**5.9×10^{-5}**		Yes
rs7842241	*C8orf68*	8	1,056,317	G/A	.634	.688	1.285	1.134-1.456	8.1×10^{-5}		
rs979728	*DLC1*	8	13,435,309	T/C	.371	.405	1.464	1.209-1.772	8.6×10^{-5}		
rs1852027	***CNBD1***	**8**	**88,076,230**	**G/A**	**.552**	**.611**	**1.269**	**1.127-1.428**	**7.6×10^{-5}**		
rs17707746	*PTDSS1*	8	97,384,821	C/A	.041	.065	1.750	1.317-2.326	8.7×10^{-5}		
rs883655	*PTDSS1*	8	97,386,357	C/T	.041	.065	1.751	1.317-2.328	8.9×10^{-5}		
rs13439240	*PTDSS1*	8	97,387,836	T/C	.041	.065	1.752	1.317-2.330	8.9×10^{-5}		
rs7830293	*GPR20*	8	142,442,691	C/T	.066	.099	1.597	1.276-1.999	3.6×10^{-5}		
rs6578167	*GPR20*	8	142,450,474	C/A	.065	.098	1.578	1.264-1.970	4.7×10^{-5}		
rs7839244	***GPR20***	**8**	**142,457,437**	**A/G**	**.066**	**.098**	**1.553**	**1.248-1.932**	**6.8×10^{-5}**		Yes
rs4961268	*GPR20*	8	142,464,393	G/A	.064	.097	1.586	1.271-1.980	3.7×10^{-5}		
rs4961755	*BNC2*	9	16,759,812	C/G	.121	.158	1.467	1.213-1.774	7.0×10^{-5}		
rs12683158	*NFIL3*	9	91,266,820	C/T	.927	.954	1.736	1.333-2.261	3.2×10^{-5}		
rs13297268	*NFIL3*	9	91,267,696	G/A	.927	.954	1.745	1.338-2.277	3.0×10^{-5}	9.0×10^{-5}	Yes
rs13289738	*NFIL3*	9	91,271,701	G/T	.926	.951	1.793	1.354-2.372	3.3×10^{-5}		
rs7856348	*CYLC2*	9	102,835,550	C/A	.541	.591	1.308	1.144-1.495	7.9×10^{-5}		
rs1330146		9	107,631,794	G/A	.545	.603	1.289	1.142-1.455	3.7×10^{-5}		
rs10816576		9	107,633,222	G/A	.545	.603	1.289	1.142-1.455	3.7×10^{-5}		
rs10121193		9	107,660,601	A/G	.382	.426	1.348	1.161-1.565	8.4×10^{-5}		
rs4543877		10	65,172,027	C/G	.439	.497	1.330	1.173-1.507	7.7×10^{-6}		
rs3864799		10	65,172,388	G/C	.439	.497	1.330	1.173-1.508	7.5×10^{-6}		
rs3912165		10	65,187,697	A/G	.427	.485	1.349	1.186-1.534	4.5×10^{-6}		
rs10740140		10	65,189,760	A/G	.428	.485	1.290	1.145-1.452	2.5×10^{-5}		
rs4746396		10	65,194,129	C/G	.436	.494	1.274	1.136-1.429	3.1×10^{-5}		
rs16918864		10	65,228,767	G/C	.430	.487	1.275	1.136-1.431	3.4×10^{-5}		
rs3104056		10	71,180,045	G/A	.974	.986	3.162	1.736-5.758	6.3×10^{-5}		
rs17747324	*TCF7L2*	10	114,742,493	C/T	.141	.181	1.445	1.214-1.719	3.0×10^{-5}		
rs7903146	***TCF7L2***	**10**	**114,748,339**	**T/C**	**.179**	**.229**	**1.388**	**1.197-1.610**	**1.2×10^{-5}**		Yes
rs12243326	*TCF7L2*	10	114,778,805	C/T	.163	.213	1.429	1.224-1.667	5.0×10^{-6}		
rs12255372	***TCF7L2***	**10**	**114,798,892**	**T/G**	**.156**	**.203**	**1.400**	**1.201-1.632**	**1.5×10^{-5}**		Yes
rs12288214		11	41,772,225	G/A	.915	.946	1.681	1.316-2.147	2.5×10^{-5}		
rs12284861		11	41,787,876	A/G	.915	.946	1.685	1.320-2.150	2.1×10^{-5}		
rs11036577		11	41,792,460	C/T	.914	.946	1.684	1.320-2.148	2.1×10^{-5}		
rs12797436		11	41,798,917	A/C	.913	.944	1.624	1.279-2.062	5.4×10^{-5}		
rs12274732		11	41,805,501	C/T	.914	.946	1.682	1.319-2.145	2.1×10^{-5}		
rs12275923		11	41,818,526	A/C	.914	.946	1.685	1.321-2.150	2.0×10^{-5}		
rs12294552		11	41,821,081	G/C	.913	.944	1.629	1.282-2.069	5.2×10^{-5}		
rs11036600		11	41,823,651	A/G	.914	.946	1.685	1.321-2.150	2.0×10^{-5}		
rs11600495		11	41,828,609	C/A	.914	.944	1.622	1.273-2.065	7.3×10^{-5}		
rs10160442		11	41,833,678	T/C	.914	.946	1.683	1.318-2.148	2.2×10^{-5}		
rs3763827		11	41,834,454	G/C	.913	.943	1.625	1.278-2.066	5.9×10^{-5}		
rs6485288		11	41,837,914	A/G	.906	.939	1.616	1.285-2.032	3.2×10^{-5}		
rs12280294		11	41,838,323	G/T	.914	.945	1.683	1.318-2.150	2.3×10^{-5}		

Table S3. FUSION stage 1 T2D association: **genotyped** (**bold**) and imputed (non-bold) SNPs with p-value < .0001 (continued)

SNP	Genes	Chr	Position (bp)	FUSION risk allele/ non-risk allele	Control risk frequency	Case risk frequency	OR	95% CI	p-value	Genotyped p-value for imputed SNP	Genotyped in Stage 2?
rs12281155		11	41,843,640	C/G	.914	.945	1.684	1.318-2.151	2.3×10^{-5}		
rs12786634		11	41,845,196	C/T	.914	.945	1.683	1.318-2.150	2.3×10^{-5}		
rs12277557		11	41,849,152	A/T	.912	.943	1.686	1.320-2.155	2.2×10^{-5}		
rs12793795		11	41,854,702	G/A	.906	.936	1.588	1.258-2.005	8.4×10^{-5}		
rs12271525		11	41,858,437	G/A	.891	.925	1.512	1.228-1.860	8.1×10^{-5}		
rs7928200		11	41,859,109	A/G	.891	.925	1.512	1.229-1.861	8.0×10^{-5}		
rs12273344		**11**	**41,859,353**	**G/T**	**.890**	**.925**	**1.516**	**1.233-1.863**	$\mathbf{6.5 \times 10^{-5}}$		
rs12788548		11	41,862,957	C/T	.891	.925	1.513	1.229-1.862	7.9×10^{-5}		
rs12288738		11	41,868,875	T/C	.890	.924	1.511	1.229-1.858	7.5×10^{-5}		
rs1588439		11	41,871,182	G/A	.890	.924	1.511	1.229-1.858	7.5×10^{-5}		
rs16936067		11	41,871,820	G/T	.906	.936	1.580	1.252-1.993	9.5×10^{-5}		
rs9300039		**11**	**41,871,942**	**C/A**	**.890**	**.925**	**1.520**	**1.236-1.869**	$\mathbf{6.0 \times 10^{-5}}$		Yes
rs11036622		11	41,872,742	C/T	.890	.924	1.516	1.232-1.864	6.9×10^{-5}		
rs11036624		11	41,878,246	T/C	.891	.925	1.525	1.236-1.881	6.8×10^{-5}		
rs12797038		11	41,880,453	C/T	.907	.937	1.598	1.260-2.026	9.0×10^{-5}		
rs12804210		11	41,880,999	T/C	.891	.925	1.549	1.251-1.919	5.1×10^{-5}		
rs11036627		11	41,881,290	C/A	.904	.937	1.662	1.314-2.103	1.8×10^{-5}	1.9×10^{-5}	Yes
rs11036628		11	41,881,352	G/A	.904	.937	1.662	1.313-2.103	1.8×10^{-5}		
rs7114241		11	41,882,103	T/C	.891	.925	1.552	1.251-1.924	5.2×10^{-5}		
rs7128743		11	41,882,275	C/A	.891	.925	1.552	1.252-1.925	5.2×10^{-5}		
rs12288361		11	41,883,303	C/T	.891	.925	1.553	1.252-1.927	5.1×10^{-5}		
rs12802634		11	41,886,138	T/C	.891	.925	1.554	1.252-1.928	5.2×10^{-5}		
rs12802862		11	41,886,267	T/C	.891	.925	1.554	1.252-1.928	5.2×10^{-5}		
rs11608189		11	41,887,387	G/T	.907	.937	1.609	1.267-2.045	7.9×10^{-5}		
rs11602004		11	41,900,843	G/T	.907	.938	1.616	1.271-2.053	7.0×10^{-5}		
rs11602127		11	41,901,557	G/A	.907	.938	1.628	1.280-2.070	5.6×10^{-5}		
rs10501281		**11**	**41,922,935**	**C/T**	**.915**	**.947**	**1.617**	**1.276-2.048**	$\mathbf{5.3 \times 10^{-5}}$		
rs11823992		11	41,926,856	A/T	.918	.949	1.651	1.294-2.105	4.0×10^{-5}		
rs7101809		11	41,933,715	T/C	.918	.949	1.653	1.295-2.109	4.1×10^{-5}		
rs12287052		11	41,935,144	A/G	.918	.949	1.651	1.289-2.114	5.6×10^{-5}		
rs11036642		11	41,940,997	T/A	.921	.951	1.699	1.318-2.191	3.3×10^{-5}		
rs17553408		11	41,951,928	T/G	.918	.949	1.650	1.288-2.115	5.8×10^{-5}		
rs12293408		11	41,956,332	C/T	.921	.951	1.695	1.315-2.186	3.5×10^{-5}		
rs16936200		11	41,963,315	A/C	.906	.939	1.635	1.294-2.067	3.0×10^{-5}		
rs11036649		11	41,965,524	A/G	.906	.939	1.634	1.293-2.066	3.1×10^{-5}		
rs12576408		11	41,971,203	G/T	.906	.939	1.633	1.292-2.064	3.2×10^{-5}		
rs11036652		11	41,971,269	T/C	.907	.939	1.629	1.288-2.058	3.5×10^{-5}		
rs7107246		11	41,972,428	C/A	.883	.915	1.630	1.287-2.064	4.0×10^{-5}		
rs11604966		11	41,972,736	T/C	.907	.940	1.623	1.285-2.051	3.8×10^{-5}		
rs10837766		11	41,984,377	T/C	.840	.882	1.472	1.232-1.759	1.8×10^{-5}	8.6×10^{-5}	Yes
rs17554005		11	41,989,148	A/C	.916	.947	1.686	1.312-2.166	3.4×10^{-5}		
rs17554054		11	41,990,218	T/C	.916	.947	1.682	1.310-2.161	3.6×10^{-5}		
rs17554081		11	41,990,280	A/G	.916	.946	1.677	1.306-2.154	3.9×10^{-5}		
rs2862456		11	41,990,769	C/T	.916	.946	1.668	1.300-2.140	4.5×10^{-5}		
rs17462952		11	41,991,795	A/G	.916	.946	1.666	1.299-2.137	4.6×10^{-5}		

Table S3. FUSION stage 1 T2D association: **genotyped** (**bold**) and imputed (non-bold) SNPs with p-value < .0001 (continued)

SNP	Genes	Chr	Position (bp)	FUSION risk allele/ non-risk allele	Control risk frequency	Case risk frequency	OR	95% CI	p-value	Genotyped p-value for imputed SNP	Genotyped in Stage 2?
rs17462994		11	41,991,889	T/C	.916	.946	1.666	1.299-2.137	4.6×10^{-5}		
rs12792932		11	127,226,772	G/A	.967	.984	2.303	1.515-3.500	5.2×10^{-5}		
rs12806859		11	127,234,379	T/G	.967	.984	2.299	1.514-3.492	5.2×10^{-5}		
rs12799032		11	127,328,409	G/A	.963	.980	2.197	1.469-3.287	8.3×10^{-5}		
rs12792749		11	127,336,192	G/A	.963	.980	2.191	1.465-3.275	8.6×10^{-5}		
rs12797631		11	127,341,608	T/G	.963	.980	2.191	1.465-3.278	8.7×10^{-5}		
rs12796900		11	127,341,924	C/A	.963	.980	2.191	1.465-3.276	8.8×10^{-5}		
rs12793901		11	127,345,185	G/A	.963	.980	2.198	1.468-3.290	8.6×10^{-5}		
rs11616188	*LTBR, SCNN1A*	12	6,373,003	A/G	.474	.522	1.400	1.201-1.633	1.6×10^{-5}	4.8×10^{-5}	Yes
rs7313533		12	6,386,116	A/G	.702	.742	1.394	1.179-1.649	9.8×10^{-5}		
rs12581386	*CORO1C*	12	107,585,465	C/A	.962	.977	2.546	1.571-4.126	7.6×10^{-5}		
rs3825253	***CORO1C***	**12**	**107,611,747**	**A/G**	**.973**	**.989**	**2.575**	**1.604-4.134**	**3.6×10^{-5}**		Yes
rs7957463	*FLJ20674, WSB2*	12	116,981,026	T/C	.577	.633	1.274	1.134-1.432	4.2×10^{-5}		
rs7958110	*FLJ20674, WSB2*	12	116,981,479	T/C	.577	.633	1.273	1.133-1.430	4.4×10^{-5}		
rs4767658	***FLJ20674, WSB2***	**12**	**116,982,161**	**T/C**	**.577**	**.633**	**1.274**	**1.134-1.430**	**4.1×10^{-5}**		Yes
rs7488309	*FLJ20674, WSB2*	12	116,982,890	G/A	.577	.633	1.273	1.133-1.430	4.3×10^{-5}		
rs2711747	*CCDC60*	12	118,360,953	T/G	.014	.025	3.401	1.842-6.280	4.9×10^{-5}		
rs1918416		**12**	**118,463,133**	**C/T**	**.808**	**.853**	**1.383**	**1.181-1.618**	**4.9×10^{-5}**		
rs804628		12	118,468,458	G/C	.816	.856	1.432	1.204-1.702	4.4×10^{-5}		
rs2669161		12	120,663,139	C/G	.846	.884	1.457	1.210-1.755	6.3×10^{-5}		
rs2707069		12	120,666,804	C/T	.846	.884	1.462	1.212-1.764	6.4×10^{-5}		
rs1287527		13	80,731,274	T/C	.085	.120	1.493	1.226-1.819	6.1×10^{-5}		
rs1287526		**13**	**80,734,028**	**G/A**	**.088**	**.123**	**1.480**	**1.219-1.796**	**6.4×10^{-5}**		
rs982864		13	80,735,627	C/T	.075	.109	1.512	1.229-1.859	7.7×10^{-5}		
rs2801597		13	80,736,045	G/A	.075	.109	1.512	1.229-1.859	7.8×10^{-5}		
rs1287533		13	80,740,650	A/T	.083	.117	1.490	1.220-1.820	8.2×10^{-5}		
rs9545851		13	81,234,888	T/C	.525	.583	1.279	1.135-1.441	5.1×10^{-5}		
rs9545852		13	81,237,495	C/T	.525	.583	1.278	1.134-1.440	5.2×10^{-5}		
rs9531246		13	81,239,573	C/A	.525	.583	1.278	1.134-1.439	5.3×10^{-5}		
rs9545853		13	81,242,579	T/C	.526	.583	1.277	1.134-1.438	5.4×10^{-5}		
rs11149214		13	81,283,609	C/A	.526	.583	1.276	1.133-1.438	5.5×10^{-5}		
rs9545870		13	81,286,274	A/G	.526	.583	1.276	1.133-1.438	5.5×10^{-5}		
rs3891591		13	81,291,969	C/T	.517	.573	1.276	1.131-1.440	6.9×10^{-5}		
rs9545903		**13**	**81,344,914**	**T/C**	**.459**	**.514**	**1.270**	**1.128-1.430**	**7.2×10^{-5}**		
rs10135197		14	38,123,411	T/C	.598	.654	1.288	1.138-1.458	6.1×10^{-5}		
rs8014198		14	38,132,529	G/A	.616	.670	1.291	1.137-1.464	7.0×10^{-5}		
rs9788490		14	38,132,689	C/G	.603	.659	1.287	1.138-1.455	5.5×10^{-5}		
rs11849174		**14**	**38,147,149**	**G/A**	**.603**	**.660**	**1.287**	**1.138-1.455**	**5.4×10^{-5}**		
rs10145493		14	38,151,139	G/A	.603	.659	1.287	1.138-1.455	5.6×10^{-5}		
rs12435438		14	38,154,195	T/C	.553	.612	1.318	1.161-1.495	1.7×10^{-5}		
rs1349241		14	38,155,189	T/C	.553	.612	1.318	1.161-1.495	1.8×10^{-5}		
rs10141957		14	38,157,020	G/A	.549	.610	1.323	1.167-1.500	1.1×10^{-5}		
rs2122331		14	38,163,358	G/C	.514	.575	1.275	1.133-1.435	5.2×10^{-5}		
rs8010489		14	38,163,618	G/A	.523	.584	1.281	1.137-1.444	4.5×10^{-5}		

Table S3. FUSION stage 1 T2D association: **genotyped** (**bold**) and imputed (non-bold) SNPs with p-value < .0001 (continued)

SNP	Genes	Chr	Position (bp)	FUSION risk allele/ non-risk allele	Control risk frequency	Case risk frequency	OR	95% CI	p-value	Genotyped p-value for imputed SNP	Genotyped in Stage 2?
rs1449720		**14**	**38,165,318**	**A/G**	**.512**	**.573**	**1.269**	**1.128-1.428**	**6.8×10^{-5}**		
rs12164874		14	38,172,603	C/T	.515	.577	1.278	1.136-1.439	4.5×10^{-5}		
rs10138342		14	38,186,108	A/C	.526	.587	1.284	1.139-1.448	4.0×10^{-5}		
rs7153699		14	38,188,807	C/T	.518	.579	1.279	1.136-1.440	4.4×10^{-5}		
rs6571865		14	38,191,421	T/C	.518	.580	1.281	1.137-1.442	4.1×10^{-5}		
rs7141696		14	38,192,126	T/C	.518	.580	1.281	1.138-1.443	4.0×10^{-5}		
rs8006474		14	38,196,248	G/C	.527	.589	1.290	1.144-1.454	3.1×10^{-5}		
rs2122333		14	38,233,119	C/T	.542	.610	1.321	1.171-1.491	5.3×10^{-6}		
rs1449725		14	38,246,572	C/T	.543	.610	1.322	1.172-1.492	4.9×10^{-6}	1.1×10^{-5}	Yes
rs2899883		14	38,255,604	G/T	.539	.604	1.320	1.169-1.491	7.0×10^{-6}		
rs2319392	*GPHN*	14	66,136,844	T/A	.014	.023	4.396	2.050-9.426	5.0×10^{-5}		
rs3825569	***LOC388015***	**14**	**100,420,051**	**C/T**	**.583**	**.640**	**1.292**	**1.143-1.46**	**3.7×10^{-5}**		
rs12910827		15	56,417,311	T/G	.024	.047	2.592	1.738-3.866	1.3×10^{-6}	6.3×10^{-6}	Yes
rs11634708	*LOC56964, PEX11A, PLIN*	15	88,037,214	C/T	.433	.485	1.315	1.153-1.500	4.1×10^{-5}		
rs10521095		**16**	**13,528,936**	**A/G**	**.206**	**.256**	**1.351**	**1.174-1.554**	**2.3×10^{-5}**		Yes
rs6498423		16	13,531,381	A/G	.206	.256	1.351	1.174-1.555	2.4×10^{-5}		
rs12162088		16	13,547,393	G/A	.130	.169	1.407	1.185-1.671	8.8×10^{-5}		
rs16962270		16	13,547,426	T/A	.130	.169	1.409	1.186-1.673	8.7×10^{-5}		
rs2033254	*CETP*	16	55,567,486	T/C	.646	.693	1.367	1.177-1.587	4.0×10^{-5}		
rs12708980	*CETP*	16	55,569,880	T/G	.633	.677	1.385	1.184-1.621	4.4×10^{-5}		
rs1800774	*CETP*	16	55,573,046	C/T	.640	.686	1.399	1.195-1.639	2.8×10^{-5}	7.3×10^{-6}	Yes
rs11646114	*FOXC2, MTHFSD*	16	85,141,275	T/A	.868	.894	1.658	1.285-2.140	8.9×10^{-5}	0.002	Yes
rs9911259	*PRKCA*	17	62,085,377	C/A	.435	.493	1.274	1.134-1.432	4.4×10^{-5}		
rs16959880	*PRKCA*	17	62,085,528	A/G	.435	.493	1.274	1.134-1.432	4.3×10^{-5}		
rs8077110	*PRKCA*	17	62,087,049	A/G	.435	.493	1.274	1.134-1.432	4.3×10^{-5}		
rs1024740	*PRKCA*	17	62,088,152	C/G	.435	.493	1.275	1.134-1.432	4.3×10^{-5}		
rs7207345	***PRKCA***	**17**	**62,093,747**	**T/C**	**.707**	**.755**	**1.307**	**1.144-1.492**	**7.5×10^{-5}**		
rs17384005		18	1,565,020	A/G	.810	.839	1.864	1.409-2.467	1.1×10^{-5}	.10	Yes
rs1785710		18	21,612,825	G/C	.648	.702	1.295	1.142-1.468	5.1×10^{-5}		
rs7229654		18	35,549,984	A/G	.959	.978	2.024	1.412-2.902	8.0×10^{-5}		
rs1596583		18	35,550,893	G/A	.959	.979	2.033	1.418-2.916	7.3×10^{-5}		
rs9675995		18	35,574,907	G/A	.959	.978	2.020	1.410-2.895	8.3×10^{-5}		
rs10853467		18	35,582,328	A/G	.959	.978	2.021	1.410-2.896	8.2×10^{-5}		
rs616444	***SETBP1***	**18**	**40,739,522**	**A/C**	**.882**	**.917**	**1.465**	**1.208-1.778**	**9.0×10^{-5}**		
rs175200		22	18,543,063	A/G	.494	.555	1.282	1.138-1.445	4.1×10^{-5}	5.5×10^{-5}	Yes
rs438798		22	18,544,053	G/A	.494	.555	1.282	1.138-1.444	4.2×10^{-5}		
rs520698	*LOC150207*	22	19,349,434	G/A	.702	.757	1.377	1.199-1.582	5.4×10^{-6}		
rs565979		**22**	**19,353,500**	**C/T**	**.679**	**.730**	**1.295**	**1.139-1.472**	**7.0×10^{-5}**		Yes
rs479275		22	19,353,777	T/A	.656	.708	1.283	1.131-1.455	9.5×10^{-5}		
rs491228	*DKFZp434N035*	22	19,357,925	G/A	.679	.730	1.294	1.138-1.471	7.5×10^{-5}		
rs591446	*DKFZp434N035*	22	19,359,204	A/G	.656	.708	1.283	1.131-1.454	9.7×10^{-5}		
rs2267339	*CACNG2*	22	35,290,742	G/T	.610	.666	1.333	1.169-1.521	1.6×10^{-5}	4.5×10^{-6}	Yes

Table S4. Confirmed T2D susceptibility loci: expanded FUSION results

SNP	Gene	Stage	Risk allele R/ Non-risk allele N	Controls (n)			Cases (n)			Risk allele frequency		Additive			Dominant			Recessive		
				RR	RN	NN	RR	RN	NN	control	case	OR	95% CI	p-value	OR	95% CI	p-value	OR	95% CI	p-value
rs1801282	*PPARG*	1	C/G	778	336	45	834	298	19	.816	.854	1.303	1.111-1.529	.0011	2.399	1.387-4.151	.0011	1.270	1.059-1.523	.0097
		2	C/G	840	337	38	838	293	37	.830	.843	1.077	0.924-1.256	0.34	0.975	0.612-1.555	.92	1.110	0.929-1.327	.25
		1+2	C/G	1618	673	83	1672	591	56	.823	.848	1.195	1.071-1.333	.0014	1.494	1.056-2.114	.022	1.200	1.058-1.362	.0046
rs4402960	*IGF2BP2*	1	T/G	102	471	585	148	495	498	.291	.347	1.276	1.126-1.446	1.2×10^{-4}	1.316	1.115-1.555	.0012	1.520	1.160-1.992	.0022
		2	T/G	142	498	595	122	553	515	.317	.335	1.073	0.951-1.211	.25	1.197	1.018-1.408	.029	0.872	0.672-1.131	.30
		1+2	T/G	244	969	1180	270	1048	1013	.304	.341	1.175	1.078-1.281	2.4×10^{-4}	1.263	1.125-1.418	7.3×10^{-5}	1.155	0.960-1.390	.13
rs7754840	*CDKAL1*	1	C/G	154	522	439	190	531	400	.372	.406	1.155	1.022-1.304	.021	1.165	0.979-1.387	.084	1.288	1.019-1.628	.034
		2	C/G	141	574	509	153	565	466	.350	.368	1.083	0.959-1.223	.20	1.093	0.926-1.290	.29	1.141	0.890-1.463	.30
		1+2	C/G	295	1096	948	343	1096	866	.360	.387	1.120	1.028-1.220	.0095	1.129	1.002-1.271	.046	1.220	1.030-1.444	.021
rs13266634	*SLC30A8*	1	C/T	421	577	176	506	500	155	.604	.651	1.222	1.084-1.379	.0010	1.157	0.913-1.466	.23	1.380	1.166-1.634	1.8×10^{-4}
		2	C/T	470	561	192	505	516	160	.614	.646	1.143	1.016-1.286	.026	1.199	0.952-1.511	.12	1.190	1.008-1.406	.040
		1+2	C/T	891	1138	368	1011	1016	315	.609	.649	1.184	1.089-1.287	6.8×10^{-5}	1.175	0.997-1.385	.053	1.289	1.146-1.449	2.3×10^{-5}
rs10811661	*CDKN2A/B*	1	T/C	809	308	13	850	256	18	.852	.870	1.168	0.980-1.392	.082	0.763	0.369-1.576	.46	1.223	1.011-1.480	.038
		2	T/C	893	309	33	911	256	23	.848	.873	1.223	1.039-1.441	.015	1.345	0.779-2.322	.28	1.254	1.042-1.510	.017
		1+2	T/C	1702	617	46	1761	512	41	.850	.872	1.204	1.069-1.356	.0022	1.112	0.724-1.708	.63	1.245	1.091-1.421	.001
rs1111875	*HHEX*	1	C/T	333	568	273	372	549	240	.526	.557	1.128	1.006-1.266	.039	1.164	0.954-1.420	.13	1.187	0.992-1.420	.061
		2	C/T	332	596	285	333	581	250	.519	.536	1.058	0.943-1.187	.34	1.126	0.926-1.369	.23	1.039	0.866-1.246	.68
		1+2	C/T	665	1164	558	705	1130	490	.522	.546	1.097	1.012-1.189	.025	1.148	0.999-1.318	.051	1.120	0.986-1.271	.081
rs7903146	*TCF7L2*	1	T/C	32	356	786	55	422	684	.179	.229	1.388	1.197-1.610	1.3×10^{-5}	1.422	1.198-1.688	5.3×10^{-5}	1.819	1.161-2.850	.0079
		2	T/C	33	383	810	68	393	711	.183	.226	1.295	1.122-1.495	3.9×10^{-4}	1.266	1.069-1.498	.0061	2.123	1.382-3.262	4.1×10^{-4}
		1+2	T/C	65	739	1596	123	815	1395	.181	.227	1.343	1.213-1.488	1.4×10^{-8}	1.344	1.192-1.514	1.2×10^{-6}	1.993	1.464-2.712	7.1×10^{-6}
rs5219	*KCNJ11*	1	T/C	221	562	346	271	538	296	.445	.489	1.204	1.069-1.357	.0022	1.214	1.007-1.463	.042	1.366	1.114-1.675	.0027
		2	T/C	284	622	328	271	624	295	.482	.490	1.035	0.922-1.162	.56	1.112	0.925-1.338	.26	0.979	0.807-1.186	.83
		1+2	T/C	505	1184	674	542	1162	591	.464	.489	1.109	1.021-1.204	.014	1.152	1.011-1.312	.034	1.142	0.994-1.312	.060
rs9300039		1	C/A	929	232	13	992	161	7	.890	.925	1.520	1.236-1.869	6.0×10^{-5}	1.797	0.702-4.600	.21	1.563	1.254-1.948	6.2×10^{-5}
		2	C/A	988	227	17	1007	170	5	.894	.924	1.442	1.179-1.764	3.2×10^{-4}	3.445	1.247-9.520	.0094	1.427	1.150-1.771	.0012
		1+2	C/A	1917	459	30	1999	331	12	.892	.924	1.478	1.280-1.705	6.8×10^{-8}	2.470	1.252-4.874	.0062	1.490	1.279-1.737	2.7×10^{-7}
rs8050136	*FTO*	1	A/C	192	562	420	213	538	410	.403	.415	1.034	0.920-1.162	.58	0.999	0.841-1.186	.99	1.124	0.904-1.397	.29
		2	A/C	150	585	492	185	566	427	.361	.397	1.179	1.046-1.329	.0070	1.179	0.998-1.394	.053	1.363	1.077-1.725	.0098
		1+2	A/C	342	1147	912	398	1104	837	.381	.406	1.107	1.019-1.203	.017	1.091	0.969-1.229	.15	1.240	1.058-1.453	.0078

Table S5. FUSION stage 1, stage2, and stage 1 + 2 T2D association results for 80 SNPs. SNPs were selected for stage 1 or stage 2 genotyping based on results in the FUSION GWA, combined evidence from FUSION, DGI, and WTCCC GWAs, or previous reports.

					Stage 1		Stage 2		Stage 1 + 2										
SNP	Chr	Position (bp)	Genes	Risk allele/ non-risk allele	Control risk allele freq	Case risk allele freq	Control risk allele freq	Case risk allele freq	Control risk allele freq	Case risk allele freq	Stage 1 OR	Stage 1 95% CI	Stage 1 p-value	Stage 2 OR	Stage 2 95% CI	Stage 2 p-value	Stage 1 + 2 OR	Stage 1 + 2 95% CI	Stage 1 + 2 p-value	Reason for follow-up
rs640742	1	20,729,860	*CDA, DDOST, KIF17, PINK1*	A/C	.601	.663	.616	.613	.609	.638	1.297	1.147-1.465	2.9×10^{-5}	0.992	0.884-1.112	.89	1.127	1.037-1.225	.0047	FUSION GWA
rs17356414	1	59,031,529	-	C/T	.694	.736	.719	.708	.707	.722	1.248	1.096-1.422	8.0×10^{-4}	0.953	0.841-1.081	.46	1.084	0.991-1.186	.077	FUSION Imputed
rs17025978	1	110,781,653	*KCNA10*	G/A	.914	.947	.934	.930	.924	.939	1.705	1.347-2.158	6.6×10^{-6}	0.941	0.752-1.178	.60	1.270	1.082-1.491	.0033	FUSION GWA
rs10494217	1	119,181,230	*TBX15*	G/T	.708	.735	.740	.725	.724	.730	1.142	1.004-1.298	.044	0.929	0.816-1.058	.27	1.026	0.937-1.124	.58	Combined GWA
rs7599781	2	43,590,377	*PLEKHH2, THADA*	T/C	.942	.958	.954	.950	.948	.954	1.478	1.119-1.953	.0056	0.895	0.683-1.172	.42	1.147	0.947-1.390	.16	Combined GWA
rs6704803	2	158,175,059	*ACVR1C, PSCDBP*	C/T	.928	.946	.938	.942	.933	.944	1.316	1.033-1.675	.025	1.084	0.851-1.380	.52	1.198	1.011-1.419	.036	Combined GWA
rs1801282	3	12,368,125	*PPARG, LOC643925*	C/G	.816	.854	.830	.843	.823	.848	1.303	1.111-1.529	.0011	1.077	0.924-1.256	.34	1.195	1.071-1.333	.0014	Combined GWA
rs17081352	3	30,307,851	-	C/A	.905	.940	.928	.927	.917	.933	1.680	1.339-2.109	5.5×10^{-6}	0.978	0.780-1.224	.84	1.276	1.090-1.494	.0023	FUSION Imputed
rs13072106	3	134,425,451	*BFSP2, TMEM108*	T/C	.118	.155	.143	.142	.130	.149	1.414	1.188-1.682	8.7×10^{-5}	1.000	0.852-1.174	.10	1.166	1.038-1.311	.0098	FUSION GWA
rs4687299	3	186,595,361	*MAP3K13*	A/G	.225	.276	.268	.260	.247	.268	1.325	1.158-1.515	3.9×10^{-5}	0.959	0.841-1.092	.53	1.116	1.017-1.225	.020	FUSION GWA
rs17289925	3	186,917,362	*C3orf65, IGF2BP2, LOC646600*	C/T	.018	.022	.020	.020	.019	.021	1.181	0.775-1.801	.44	1.077	0.719-1.613	.72	1.117	0.836-1.492	.46	Follow-up
rs4402960	3	186,994,389	*IGF2BP2*	T/G	.291	.347	.317	.335	.304	.341	1.276	1.126-1.446	1.2×10^{-4}	1.073	0.951-1.211	.25	1.175	1.078-1.281	2.4×10^{-4}	Combined GWA
rs734312	4	6,421,426	*WFS1*	A/G	.478	.506	.482	.485	.480	.496	1.101	0.980-1.236	.11	1.010	0.899-1.134	.87	1.056	0.973-1.145	.19	Combined GWA
rs886374	4	7,856,440	*SORCS2*	T/C	.211	.270	.233	.221	.222	.245	1.385	1.209-1.587	2.4×10^{-6}	0.943	0.824-1.081	.40	1.140	1.036-1.253	.007	FUSION GWA
rs13139219	4	42,294,231	*ATP8A1*	C/A	.779	.827	.796	.805	.788	.816	1.346	1.160-1.561	7.9×10^{-5}	1.052	0.911-1.214	.50	1.186	1.070-1.314	.0011	FUSION GWA
rs6834248	4	95,447,456	*LOC644429, PGDS, SMARCAD1*	T/C	.772	.786	.779	.765	.775	.776	1.108	0.963-1.275	.15	0.919	0.800-1.056	.23	1.001	0.907-1.104	.99	Combined GWA
rs2720460	4	104,412,290	*BDH2, CENPE, DHRS6, LOC133308*	A/G	.571	.607	.574	.579	.573	.593	1.154	1.025-1.299	.018	1.012	0.899-1.140	.84	1.084	0.998-1.179	.057	Combined GWA
rs27779	5	142,239,267	*ARHGAP26*	A/C	.250	.304	.259	.269	.255	.286	1.326	1.162-1.513	2.5×10^{-5}	1.044	0.917-1.190	.52	1.171	1.068-1.283	7.5×10^{-4}	FUSION GWA
rs3733876	5	176,315,601	*RAP80*	G/A	.765	.805	.791	.798	.778	.801	1.277	1.109-1.471	6.6×10^{-4}	1.051	0.909-1.215	.50	1.156	1.046-1.278	.0046	FUSION GWA
rs4712523	6	20,765,543	*CDKAL1*	G/A	.372	.407	.349	.366	.360	.387	1.164	1.032-1.312	.013	1.084	0.959-1.224	.20	1.123	1.032-1.222	.0073	Follow-up
rs10946398	6	20,769,013	*CDKAL1*	C/A	.368	.404	.347	.364	.357	.384	1.163	1.029-1.315	.016	1.081	0.956-1.222	.22	1.122	1.029-1.223	.0087	Combined Imputed
rs7754840	6	20,769,229	*CDKAL1*	C/G	.372	.406	.350	.368	.360	.387	1.155	1.022-1.304	.021	1.083	0.959-1.223	.20	1.120	1.028-1.220	.0095	Follow-up
rs2206734	6	20,802,863	*CDKAL1*	T/C	.174	.200	.168	.174	.171	.187	1.182	1.016-1.375	.030	1.060	0.911-1.234	.45	1.116	1.003-1.241	.043	Combined GWA
rs4496780	6	21,187,627	*CDKAL1*	G/T	.104	.093	.092	.106	.098	.100	0.890	0.730-1.086	.25	1.209	0.994-1.471	.057	1.046	0.911-1.200	.53	Follow-up
rs9271366	6	32,694,832	*HLADQA1, HLADRA, HLADRB1*	A/G	.858	.862	.857	.867	.858	.864	1.044	0.878-1.241	.63	1.104	0.936-1.303	.24	1.067	0.948-1.202	.28	Combined GWA
rs11751469	6	33,912,525	-	C/T	.563	.609	.574	.585	.568	.597	1.209	1.073-1.362	.0018	1.050	0.933-1.182	.41	1.122	1.032-1.219	.007	Combined GWA
rs7750445	6	37,872,955	*ZFAND3*	G/C	.136	.180	.163	.135	.150	.157	1.407	1.194-1.659	4.2×10^{-5}	0.814	0.694-0.956	.012	1.053	0.941-1.179	.37	FUSION Imputed
rs9472138	6	43,919,740	-	T/C	.310	.314	.305	.321	.308	.318	1.031	0.911-1.166	.63	1.071	0.946-1.212	.28	1.050	0.963-1.145	.27	New Assoc
rs7450789	6	111,923,668	*LOC643749, REV3L, TRAF3IP2*	T/G	.903	.919	.908	.912	.906	.916	1.228	1.001-1.506	.048	1.069	0.877-1.304	.51	1.141	0.990-1.314	.068	Combined GWA
rs2021966	6	132,192,132	*ENPP1*	A/G	.576	.630	.606	.621	.592	.626	1.246	1.107-1.403	2.6×10^{-4}	1.057	0.939-1.190	.36	1.148	1.056-1.247	.0012	FUSION Imputed
rs615545	7	18,165,111	-	C/T	.694	.751	.708	.733	.701	.742	1.361	1.190-1.556	5.9×10^{-6}	1.134	0.998-1.289	.053	1.236	1.127-1.355	6.1×10^{-6}	FUSION GWA
rs10281305	7	54,664,618	-	G/T	.735	.772	.738	.757	.737	.765	1.224	1.069-1.401	.0033	1.101	0.961-1.261	.16	1.153	1.048-1.268	0.0033	Combined GWA
rs17158686	7	83,439,407	*SEMA3A*	T/G	.951	.957	.959	.958	.955	.958	1.156	0.874-1.528	.31	1.007	0.751-1.351	.96	1.077	0.881-1.316	.47	Combined GWA
rs2470984	7	122,368,680	*SLC13A1*	A/C	.297	.348	.316	.298	.307	.323	1.279	1.130-1.448	9.0×10^{-5}	0.930	0.822-1.054	.26	1.083	0.993-1.181	.073	FUSION GWA
rs10954654	7	138,816,342	-	C/T	.725	.776	.735	.749	.730	.762	1.337	1.166-1.533	2.8×10^{-5}	1.089	0.952-1.245	.21	1.201	1.092-1.321	1.6×10^{-4}	FUSION GWA
rs557962	7	140,232,924	*LOC642421, MRPS33*	T/C	.047	.076	.059	.058	.053	.067	1.650	1.287-2.115	5.9×10^{-5}	0.982	0.770-1.253	.89	1.275	1.075-1.514	.0052	FUSION GWA
rs13266634	8	118,253,964	*SLC30A8*	C/T	.604	.651	.614	.646	.609	.649	1.222	1.084-1.379	.001	1.143	1.016-1.286	.026	1.184	1.089-1.287	6.8×10^{-5}	FUSION GWA
rs7839244	8	142,457,437	*GPR20*	A/G	.066	.098	.082	.080	.074	.089	1.553	1.248-1.932	6.8×10^{-5}	0.967	0.784-1.192	.75	1.212	1.044-1.407	.012	FUSION GWA
rs1063192	9	21,993,367	*CDKN2A, CDKN2B*	A/G	.556	.582	.587	.584	.572	.583	1.094	0.975-1.228	.13	0.989	0.879-1.114	.85	1.045	0.963-1.134	.29	Follow-up
rs564398	9	22,019,547	*CDKN2A, CDKN2B*	T/C	.566	.596	.596	.590	.582	.593	1.118	0.994-1.258	.064	0.970	0.863-1.091	.61	1.045	0.962-1.135	.30	Follow-up
rs2383208	9	22,122,076	-	A/G	.842	.862	.836	.864	.839	.863	1.184	1.002-1.400	.047	1.240	1.057-1.456	.0082	1.219	1.086-1.367	7.2×10^{-4}	Combined GWA
rs10811661	9	22,124,094	-	T/C	.852	.870	.848	.873	.850	.872	1.168	0.980-1.392	.082	1.223	1.039-1.441	.015	1.204	1.069-1.356	.0022	Follow-up
rs13297268	9	91,267,696	*NFIL3*	G/A	.924	.952	.945	.949	.935	.950	1.650	1.280-2.128	9.0×10^{-5}	1.094	0.848-1.413	.49	1.353	1.132-1.618	8.3×10^{-4}	FUSION Imputed
rs2185935	9	114,581,796	-	C/T	.667	.675	.661	.662	.664	.669	1.024	0.904-1.160	.71	1.008	0.895-1.136	.89	1.018	0.935-1.110	.68	Combined GWA
rs1416904	9	131,363,871	*KIAA0515, POMT1, UCK1*	T/C	.931	.952	.925	.935	.928	.943	1.479	1.150-1.902	.0021	1.116	0.892-1.397	.34	1.269	1.074-1.498	.0049	Combined GWA
rs1270874	10	29,879,870	*SVIL*	C/A	.753	.799	.780	.777	.767	.788	1.297	1.123-1.498	3.9×10^{-4}	0.976	0.849-1.120	.72	1.118	1.012-1.234	.028	FUSION Imputed
rs9422546	10	43,391,505	*ZNF239, ZNF485*	G/T	.628	.631	.640	.651	.634	.641	1.009	0.894-1.138	.89	1.066	0.945-1.203	.30	1.036	0.951-1.127	.42	Combined GWA
rs13088	10	49,985,899	*C10orf72*	G/A	.369	.398	.363	.384	.366	.391	1.132	1.003-1.277	.044	1.073	0.953-1.207	.24	1.102	1.013-1.198	.024	Combined GWA
rs1359624	10	91,385,408	*FLJ37201, MPHOSPH1, PANK1*	C/T	.247	.290	.268	.265	.258	.277	1.222	1.072-1.394	.0027	0.973	0.853-1.110	.68	1.108	1.010-1.215	.030	FUSION GWA

Table S5. FUSION stage 1, stage2, and stage 1 + 2 T2D association results for 80 SNPs (continued)

SNP	Chr	Position (bp)	Genes	Risk allele/ non-risk allele	Stage 1 Control risk allele freq	Stage 1 Case risk allele freq	Stage 2 Control risk allele freq	Stage 2 Case risk allele freq	Stage 1 + 2 Control risk allele freq	Stage 1 + 2 Case risk allele freq	Stage 1 OR	Stage 1 95% CI	Stage 1 p-value	Stage 2 OR	Stage 2 95% CI	Stage 2 p-value	Stage 1 + 2 OR	Stage 1 + 2 95% CI	Stage 1 + 2 p-value	Reason for follow-up
rs1111875	10	94,452,862	*HHEX*	C/T	.526	.557	.519	.536	.522	.546	1.128	1.006-1.266	.039	1.058	0.943-1.187	.35	1.097	1.012-1.189	.025	New Assoc
rs7923837	10	94,471,897	-	G/A	.603	.631	.591	.613	.597	.622	1.122	0.997-1.263	.057	1.090	0.970-1.226	.15	1.107	1.019-1.203	.016	Combined GWA/ New Assoc
rs4506565	10	114,746,031	*TCF7L2*	T/A	.214	.250	.217	.248	.216	.249	1.257	1.089-1.450	.0017	1.187	1.037-1.360	.013	1.221	1.107-1.346	6.4×10^{-5}	FUSION Imputed/ Prev Assoc
rs7903146	10	114,748,339	*TCF7L2*	T/C	.179	.229	.183	.226	.181	.227	1.388	1.197-1.610	1.3×10^{-5}	1.295	1.122-1.495	3.9×10^{-4}	1.343	1.213-1.488	1.4×10^{-8}	FUSION GWA/ Prev Assoc
rs12255372	10	114,798,892	*TCF7L2*	T/G	.156	.203	.165	.199	.161	.201	1.400	1.201-1.632	1.5×10^{-5}	1.244	1.070-1.447	.0044	1.318	1.184-1.467	3.6×10^{-7}	FUSION GWA/ Prev Assoc
rs5219	11	17,366,148	*ABCC8, KCNJ11*	T/C	.445	.489	.482	.490	.464	.489	1.204	1.069-1.357	.0022	1.035	0.922-1.162	.56	1.109	1.021-1.204	.014	Combined Imputed/ Prev Assoc
rs9300039	11	41,871,942	-	C/A	.890	.925	.894	.924	.892	.924	1.520	1.236-1.869	6.0×10^{-5}	1.442	1.179-1.764	3.2×10^{-4}	1.478	1.280-1.705	6.8×10^{-8}	FUSION GWA
rs11036627	11	41,881,290	-	C/A	.912	.946	.924	.946	.918	.946	1.665	1.313-2.110	1.9×10^{-5}	1.466	1.159-1.856	.0013	1.563	1.324-1.846	9.2×10^{-8}	FUSION Imputed
rs10837766	11	41,984,377	-	T/C	.827	.869	.846	.870	.836	.870	1.397	1.181-1.652	8.6×10^{-5}	1.252	1.058-1.482	.0088	1.313	1.166-1.477	5.8×10^{-6}	FUSION Imputed
rs7480010	11	42,203,294	*LOC387761*	G/A	.174	.174	.162	.171	.168	.172	1.004	0.863-1.169	.96	1.078	0.925-1.257	.333	1.034	0.929-1.151	.54	New Assoc
rs4379834	11	44,115,014	*ALX4, EXT2, PHACS*	G/A	.316	.316	.295	.306	.305	.311	0.980	0.865-1.111	.76	1.063	0.936-1.207	.35	1.027	0.940-1.123	.55	New Assoc
rs11616188	12	6,373,003	*LTBR, SCNN1A*	A/G	.426	.484	.445	.455	.436	.470	1.270	1.131-1.426	4.8×10^{-5}	1.040	0.927-1.167	.50	1.148	1.059-1.244	8.3×10^{-4}	FUSION Imputed
rs3751262	12	12,509,957	*DUSP16, LOH12CR1*	G/A	.914	.932	.917	.904	.916	.918	1.298	1.038-1.623	.022	0.853	0.698-1.043	.12	1.039	0.896-1.205	.61	Combined GWA
rs1153188	12	53,385,263	-	A/T	.699	.721	.682	.702	.690	.711	1.100	0.966-1.251	.15	1.118	0.989-1.266	.075	1.109	1.015-1.212	.022	Combined Imputed
rs7132840	12	69,697,828	-	T/G	.425	.442	.426	.438	.425	.440	1.070	0.949-1.205	.27	1.065	0.951-1.193	.27	1.063	0.979-1.153	.14	Combined Imputed
rs3825253	12	107,611,747	*CORO1C, DAO, SSH1*	A/G	.973	.989	.987	.986	.908	.988	2.575	1.604-4.134	3.6×10^{-5}	0.991	0.602-1.631	.97	1.678	1.204-2.337	.0019	FUSION GWA
rs2300455	12	108,086,236	*ACACB*	G/A	.815	.839	.821	.820	.818	.829	1.166	0.999-1.361	.051	0.997	0.857-1.161	.97	1.075	0.965-1.197	.19	Combined GWA
rs4767658	12	116,982,161	*FLJ20674, WSB2*	T/C	.577	.633	.609	.613	.593	.623	1.274	1.134-1.430	4.1×10^{-5}	1.025	0.912-1.151	.68	1.134	1.045-1.230	.0025	FUSION GWA
rs1033594	14	36,281,317	*SLC25A21*	C/T	.479	.502	.496	.507	.487	.505	1.069	0.951-1.202	.26	1.049	0.933-1.178	.42	1.067	0.982-1.158	.13	Combined GWA
rs1449725	14	38,246,572	-	C/T	.540	.607	.584	.595	.562	.600	1.315	1.163-1.486	1.1×10^{-5}	1.063	0.943-1.197	.32	1.180	1.084-1.284	1.3×10^{-4}	FUSION Imputed
rs2268974	14	68,492,917	*ACTN1*	G/A	.231	.242	.221	.221	.226	.231	1.058	0.920-1.216	.43	0.990	0.863-1.136	.89	1.020	0.926-1.124	.69	Combined Imputed
rs12910827	15	56,417,311	-	T/G	.021	.045	.029	.032	.025	.039	2.195	1.541-3.127	6.3×10^{-6}	1.109	0.800-1.539	.53	1.559	1.232-1.972	1.8×10^{-4}	FUSION Imputed
rs10521095	16	13,528,936	-	A/G	.206	.256	.228	.229	.217	.243	1.351	1.174-1.554	2.3×10^{-5}	1.008	0.882-1.153	.90	1.157	1.051-1.274	.0028	FUSION GWA
rs8050136	16	52,373,776	*FTO*	A/C	.403	.415	.361	.397	.381	.406	1.034	0.920-1.162	.58	1.179	1.046-1.329	.0070	1.107	1.019-1.203	.017	Combined GWA
rs1800774	16	55,573,046	*CETP*	C/T	.667	.726	.705	.699	.687	.712	1.348	1.182-1.537	7.3×10^{-6}	0.967	0.851-1.098	.60	1.138	1.040-1.246	.005	FUSION Imputed
rs11646114	16	85,141,275	*FLJ12998, FOXC2, MTHFSD*	T/A	.895	.921	.915	.905	.905	.913	1.382	1.124-1.698	.002	0.892	0.728-1.092	.27	1.110	0.962-1.281	.15	FUSION Imputed
rs7222308	17	25,301,167	*CCDC55, EFCAB5, FLJ46247, SLC6A4, SSH2*	T/C	.532	.553	.535	.552	.533	.553	1.094	0.973-1.229	.13	1.075	0.958-1.206	.22	1.086	1.001-1.179	.047	Combined GWA
rs17384005	18	1,565,020	-	A/G	.842	.859	.858	.859	.851	.859	1.147	0.974-1.351	.10	1.004	0.850-1.186	.96	1.074	0.956-1.206	.23	FUSION Imputed
rs175200	22	18,543,063	-	A/G	.490	.552	.538	.553	.515	.553	1.285	1.137-1.452	5.5×10^{-5}	1.069	0.954-1.198	.25	1.165	1.072-1.265	2.9×10^{-4}	FUSION Imputed
rs565979	22	19,353,500	*DKFZp434N035, LOC150207, LOC645289, PIK4CA, SERPIND1*	C/T	.679	.730	.727	.709	.703	.720	1.295	1.139-1.472	7.0×10^{-5}	0.929	0.816-1.056	.26	1.090	0.996-1.193	.060	FUSION GWA
rs2267339	22	35,290,742	*CACNG2*	G/T	.611	.674	.630	.618	.621	.646	1.341	1.182-1.521	4.5×10^{-6}	0.939	0.832-1.060	.31	1.112	1.020-1.213	.016	FUSION Imputed

Table S6: Comparison of T2D association results for SNPs that were imputed with a p-value < .001 and then genotyped in the FUSION stage 1 sample

		Risk allele frequency in controls		FUSION Stage 1 Imputed[a]		FUSION Stage 1 Genotyped		Imputation quality measures		Observed allelic concordance	Maximum r^2 with SNPs used for imputation
SNP	Genes	Imputed	Genotyped	p-value[a]	OR[a]	p-value	OR	Imputation consistency[c]	Estimated r^2 [d]		
rs12910827		.024	.021	2.5×10^{-6}	2.57	6.3×10^{-6}	2.20	.977	.720	.994	.39
rs1449725		.544	.540	5.3×10^{-6}	1.33	1.1×10^{-5}	1.31	.989	.977	.990	.90
rs17081352		.909	.905	7.3×10^{-6}	1.70	5.5×10^{-6}	1.68	.994	.954	1.000	.87
rs11616188	*SCNN1A/LTBR*	.474	.426	1.5×10^{-5}	1.40	4.8×10^{-5}	1.27	.760	.585	.919	.27
rs10837766		.840	.827	1.5×10^{-5}	1.49	8.6×10^{-5}	1.40	.975	.930	.975	.46
rs11036627		.903	.912	1.7×10^{-5}	1.67	1.9×10^{-5}	1.66	.976	.901	.987	.75
rs17384005		.811	.842	1.9×10^{-5}	1.84	.10	1.15	.743	.309	.874	.11
rs7750445		.116	.136	2.0×10^{-5}	1.47	4.1×10^{-5}	1.41	.986	.965	.977	.50
rs2267339	*CACNG2*	.613	.611	2.8×10^{-5}	1.33	4.5×10^{-6}	1.34	.939	.873	.990	.72
rs17356414		.551	.694	3.0×10^{-5}	1.30	8.0×10^{-4}	1.25	.944	.920	.878	.34
rs1800774	*CETP*	.642	.667	3.9×10^{-5}	1.39	7.3×10^{-6}	1.35	.810	.617	.972	.29
rs175200		.493	.490	6.6×10^{-5}	1.28	5.5×10^{-5}	1.28	.993	.976	.997	.85
rs6103716		.342	.342	7.3×10^{-5}	1.28	4.8×10^{-5}	1.29	.993	.978	.999	.33
rs13297268	*NFIL3*	.928	.924	7.5×10^{-5}	1.72	9.0×10^{-5}	1.65	.988	.916	.998	.28
rs11646114	*FOXC2/FLJ12998*	.868	.895	9.1×10^{-5}	1.66	.0020	1.38	.860	.512	.956	.13
rs2021966	*ENPP1*	.584	.576	9.1×10^{-5}	1.32	2.6×10^{-4}	1.25	.846	.769	.937	.46
rs1270874	*SVIL*	.745	.753	1.4×10^{-4}	1.33	3.9×10^{-4}	1.30	.983	.954	.988	.24
rs4812831		.150	.116	1.6×10^{-4}	1.53	.0055	1.28	.831	.516	.944	.45
rs4402960	*IGF2BP2*	.290	.291	1.7×10^{-4}	1.27	1.2×10^{-4}	1.28	.997	1.026	.998	1.00
rs2466291	*SLC30A8*	.399	.361	6.3×10^{-4}	1.26	.0016	1.22	.874	.830	.935	.47
rs1801282	*PPARG*	.816	.816	9.5×10^{-4}	1.31	.0011	1.30	.999	1.002	1.000	1.00
rs3802177	*SLC30A8*	.604	.605	9.9×10^{-4}	1.23	.0012	1.22	.999	1.015	.999	1.00
rs4506565	*TCF7L2*	.213	.214	.0015[b]	1.26	.0017	1.26	.999	.965	1.000	.92

[a]Imputation-based analysis restricted to individuals with successful genotypes for the same SNP; these results may differ from the imputed results in Table S2 which are based on all stage 1 individuals

[b]Imputed p-value = 7.0×10^{-4} in stage 1 sample

[c]Imputation consistency is the proportion of imputation iterations that agreed with the most likely genotype

[d]The estimated r^2 is the ratio of observed variance of dosage scores across samples to the expected variance given the imputed SNP allele frequency

Table S7. SNP annotation weights used in SNP picking for stage 2 genotyping

Annotation	Weight
Maximum of:	
Frameshift	50
Stop codon	50
Critical splice site	50
Poly A signal	30
Any change to initial ATG signal	30
Non-synonymous coding:	
Identical amino acid seen in more than 75% of mammals	20
Similar amino acid seen in more than 75% of mammals	20
Non-conservative amino acid change	6 to 9[a]
Other non-synonymous	5
SNP in exon, includes 5′ and 3′ UTRs	2
Bonus:	
FUSION linkage LOD>1	1 to 3[b]
SNP near candidate gene	1.5
SNP near gene over-expressed in tissue of interest	1.5
Conserved	1.2
Near any gene	1.2

[a] For non-conservative amino acid changes, the weight is 5 - x, where -4 < x < -1 is the BLOSUM62 score for the amino acid substitution (*23*)

[b] For linkage, the weight is the T2D LOD score in the FUSION 1+2 families (*2*) if that LOD score is >1

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