SUPPLEMENTARY DATA

Online-only Supplemental Materials

Data collection

Genotype study data was collected from publicly available repositories, with exception of the CHOP-McGill CaCo and CHOPTDT studies (provided by C.P.[1])(**Table S1**). Publicly available genotype data was obtained from the following sources: dbGaP for cohorts GoKinD (https://www.ncbi.nlm.nih.gov/projects/gap/cgi-bin/study.cgi?study_id=phs000088.v1.p1), EDIC-DCCT (https://www.ncbi.nlm.nih.gov/projects/gap/cgi-bin/study.cgi?study_id=phs000086.v2.p1), and T1DGC (http://www.ncbi.nlm.nih.gov/projects/gap/cgi-bin/study.cgi?study_id=phs000180.v1.p1); WTCCC for cohorts Type 1 Diabetes, Hypertension, Type 2 Diabetes, and Bipolar Disorder, 1958 Birth Cohort, and UK Blood Service[2]; the TwinsUK Resource for the TwinsUK cohort (http://www.twinsuk.ac.uk/data-access/). In total we collected genotype data for 9,684 cases and 17,153 controls. Specifically, in the 3,173 type 1 diabetes cases genotyped on the Affymetrix platform, we included 1,173 subjects from the Genetics of Kidneys in Diabetes Study (GoKinD) and 2,000 from the Wellcome Trust Cases Control Consortium (WTCCC). These were then compared with 5,998 similarly genotyped controls from WTCCC, and specifically 1,999 subjects from the type 2 diabetes (T2D) study, 2001 subjects from the hypertension (HT) study and 1,998 individuals from the bipolar disorder (BD) study. Among the 6,511 type 1 diabetes cases genotyped on Illumina arrays, 514 individuals were from McGill University, 483 from The Children's Hospital of Philadelphia (CHOP), 1,385 from The Diabetes Control and Complications Trial – Epidemiology of Diabetes Interventions and Complications (DCCT-EDIC) cohort, and 4,129 from the Type 1 Diabetes Genetics Consortium (T1DGC). These were compared with 11,155 similarly genotyped controls recruited from Twins UK (n=3,461), and two WTCCC studies (2,930 individuals from the 1958 British Cohort (58BC) and 2,737 individuals from the UK Blood Service sample (NBS) respectively). Genotyping was performed using Affymetrix or Illumina arrays for 3,173 or 6,511 cases and 5,998 or 11,155 controls, respectively.

Genotype quality control

Genotype quality assessment was performed according to published guidelines[3]. Quality control was conducted in the following manner: (1) convert position of array markers to human genome build version hg19/GRCh37, (2) remove individuals with problematic sex assignment, (3) remove individuals with genotype missingness > 0.05 and heterozygosity > 3 s.d., (4) remove individuals with proportion identity-by-descent > 0.1875, and (5) removed array makers with minor allele frequency of < 0.01, missingness > 0.05, and Hardy-Weinberg equilibrium p-value < 0.00001. In addition, the CHOPTDT cohort from CHOP-McGill consists of case-parent trios, thus we retained the single type 1 diabetes case per trio for association analysis as the model used does not adjust for familial relatedness. Count of remaining individuals per cohort is listed in **Table S1.** Following the aforementioned quality control, all individuals from cohorts genotyped by the same array manufacturer where merged into a single data set, retaining only the array markers that were in common between all cohorts being merged (337,727 and 456,168 markers for Affymetrix- and Illumina-based arrays, respectively).

Assessment of population stratification

Population stratification was assessed using EIGENSTRAT version 6.0.1[4]. This assessment was performed for the merged cohorts genotyped by the same array manufacturer and that passed quality control and removal of related individuals (CHOP-McGill only) (**Table S1**, N(total)=25,063). SNPs used as input into EIGENSTRAT included those that pass the aforementioned genotype quality control, followed by further filtering in the following manner: (1) remove markers with genotype missingness >

0.05 and Hardy-Weinberg p-value < 0.00001, (2) remove markers with p-value < 0.00001 of Fisher's exact test of association between missingness and case/control status, and (3) remove markers with > 0.2 difference in minor allele frequency between cases and controls and (4) prune for markers in approximate linkage equilibrium (r^2 < 0.1), resulting in a set of 52,598 and 99,742 markers for the Affymetrix- and Illumina-based data sets. Analysis using EIGENSTRAT was performed using the default parameters and identified 268 and 545 individuals as outliers from the Affymetrix- and Illumina-based arrays, respectively; that is those individuals that have a standard deviation of > 6 sd from one or more of the top 10 principal components. The top 10 principal components from this analysis were used in the GWAS to adjust for population stratification.

The total count of samples remaining is 24,250, with 2,903/5,678 cases/controls and 6,093/9,576 cases/control for the Affymetrix- and Illumina-based data sets, respectively.
To assess the outlier removal of EIGENSTRAT we performed an additional principal component analysis by combining the type 1 diabetes genotype data with data from 1000 Genomes phase 3 (N=2,504). For each genotype platform, we merged the marker data used in the EIGENSTRAT analysis to a matched set of markers from all 1000 Genomes phase 3 individuals. Analysis using the PLINK 2 "--pca approx." command was performed to obtain the top 20 principal components. Results of this analysis for the entire Affymetrix or Illumina cohorts, separately in cases and controls, or by individual cohort are depicted in **Figure S2**, and demonstrate that the outliers removed by EIGENSTRAT lie outside the 1000 Genomes European super-population, whereas the inliers largely overlap or are in close proximity to the European super-population.

Genotype Imputation

Genotype imputation was performed using the Sanger Imputation Service[5]. Imputation was performed for all individuals from cohorts genotyped using the same manufacturer, that passed quality control, removal of related individuals (CHOP-McGill only) and assessment for population stratification. Genotype data was prepared for imputation using the HRC-checking tool (http://www.well.ox.ac.uk/~wrayner/tools/), and resulted in 276,940 and 454,944 SNPs being used as input for imputation from the Affymetrix- and Illumina-based cohorts, respectively. Genotype data was pre-phased by the Sanger Imputation Service using EAGLE[6], following by imputation using PBWT [7] to the Haplotype Reference Consortium (r1.1). The imputation process resulted in 39,131,578 autosomal SNPs.

GWAS of type 1 diabetes by genotyping platform

Genome-wide association analysis was performed using SNPTEST version 2.5.2, where we tested the additive effect of each imputed probability allele (GP field in VCF format) on type 1 diabetes status using the 'newml' method. The GWAS was performed for all individuals from cohorts genotyped using the same manufacturer, that passed quality control, removal of related individuals (CHOP-McGill only) and assessment for population stratification (N(total) = 24,250). The GWAS was performed separately for all individuals from the Affymetrix (N(cases) = 2,903 and N(controls) = 5,678) and Illumina (N(cases) = 6,093 and N(controls) = 9,576) genotyped cohorts using type 1 diabetes case/control status as the phenotype, as well as the top 10 principal components from the assessment of population stratification. For computational efficiency the genome-wide genotype data was split into 7,212 chunks of 400kb and run in parallel on a compute cluster consisting of nodes with 20-cores and 128GB of memory.

SUPPLEMENTARY DATA

Meta-analysis of the GWAS

Meta-analysis of the effect estimates from the Affymetrix and Illumina GWAS analyses was performed using METAL version 2011-03-25[8]. We used as input all computed GWAS summary statistics derived from the analysis of the Affymetrix and Illumina genotyped cohorts. Meta-analytic results where then filtered in the following manner: (1) comprised of summary statistics from both the Affymetrix- and Illumina-based GWAS, (2) had a minor allele frequency in controls > 0.005, and (3) had an INFO imputation quality > 0.3. This resulted in a total of 9,061,522 SNPs used for further analyses.

Determining independent loci

Conditionally independent loci from the meta-analytic summary statistics were identified using GCTA-COJO version 1.91.1[8]. Because meta-analysis consisted of both Affymetrix and Illumina genotyped cohorts, we merged the imputed genotype data derived from both genotype platforms using bcftools and used the resulting dataset as the reference panel for selecting independently associated SNPs with GCTA-COJO, using the following parameters: --cojo-wind 20000 --cojo-slct --cojo-collinear 0.9 --cojo-p 1.2e-8 . Analysis using GCTA-COJO resulted in 107 conditionally independent loci (**Table S2**) at p-value < 1.2×10^{-8}. We further excluded independent SNPs according to the following exclusion criteria: (1) overlapping the major histocompatibility complex locus (chr6:27,477,797-34,448,354, hg19/GRCh37), (2) meta-analytic or conditional p-value > 1.2×10^{-8}, and (3) supported by fewer that 3 SNPs within 40 kb with discovery p-value < 0.0001. This resulted in a total of 27 independent loci used for further analysis.

Replication of Discovery Association Signals

Data sources

Replication of discovery association signals was performed by combining *de novo* genotyping of type 1 diabetes cases from a sib-pair cohort (N=5,501) with 10,000 randomly selected controls from UK Biobank. DNA samples for type 1 diabetes cases were provided by C.P., and 4,542 of 5,501 individuals were genotyped using a Affymetrix CIDR 6K array (5,651 SNPs) as part of a past study[1], which will be used to account for population stratification to UK Biobank controls (described below). We removed individuals with > 10% genotype missingness on the Affymetrix CIDR 6K array, resulting in 4,466 type 1 diabetes cases used for population stratification analysis with UK Biobank controls.

We selected a total of 8 conditionally independent SNPs for replication analysis (**Table S4):** 2 SNPs at known loci; the INS locus and a variant of low allele frequency at TYK2, 2 novel SNPs with MAF > 0.05, and all 4 novel low-frequency SNPs (MAF < 0.05). *De novo* genotyping of these SNPs on the replication type 1 diabetes cases was performed using SNP assays custom designed by LGC Genomics using the KASP genotyping. KASP genotyping assays are based on competitive allele-specific PCR and enable bi-allelic scoring of single nucleotide polymorphisms (SNPs) and insertions and deletions (Indels) at specific loci). Assays were deemed to be working successfully if clusters were distinct and call rates were consistently high. The data is automatically quality control checked on a per SNP basis. No Template Controls (NTCs) are included on each plate to enable the detection of contamination or non-specific amplification. For further information, see https://biosearch-cdn.azureedge.net/assetsv6/kasp-explanation-fact-sheet.pdf and https://www.biosearchtech.com/support/resources/starting-a-genotyping-project/genotyping-laboratory-workflow

SUPPLEMENTARY DATA

Assessment for population stratification

Population stratification analysis was conducted using 4,466 type 1 diabetes cases and 10,000 randomly selected controls from UK Biobank. SNPs used were those genotyped for the type 1 diabetes cases on the Affymetrix CIDR 6k array (N=5,651). Prior to analysis of population stratification, we performed the following SNP quality filtering: For type 1 diabetes cases, we retained array genotyped SNPs with missingness > 0.1, MAF < 0.05, and discovery association p-value < 0.1, resulting in a total of 3,997 SNPs. This was followed by extraction of these 3,997 variants from UK Biobank imputed genotype data where we retained SNPs with INFO > 0.9, Hardy-Weinberg equilibrium p-value > 0.000001, and had < 10% difference in MAF to the type 1 diabetes cases. This resulted in a total of 3,759 SNPs used for population stratification analysis. The top 20 principal components from population stratification analysis was obtained from PLINK 2.0 using the method developed by Galinsky et al.[9]. K-means clustering of the top 4 principal components was used to obtain the largest subset of ancestrally homogeneous individuals (Ncases=4,329 and Ncontrols=9,543**).** The plots of the first two principal components of the entire replication cohort, and separately of replication cases and of replication controls were then projected and compared to that of a set of 2,504 individuals from 1000 Genomes phase 3 (**Figure S3**). Association analysis on the subset of ancestrally homogeneous individuals (N=13,872) was performed by adjusting for familial relatedness in the type 1 diabetes case sib-pairs by generating a standardized relatedness matrix using GEMMA 0.96 followed by using this kinship matrix when performing association analysis using the binomial method in GMMAT[10].

Fine-mapping

Putatively causal SNPs were identified using FINEMAP version 1.3[11] for a 500 kb region spanning each of the 27 independent loci. Prior to analysis with FINEMAP, correlation matrices for each genomic region was generated using (n=24,250) LDSTORE[12]. FINEMAP was run with default parameters except for the following: --n-causal-snps 20, --prior-std 0.0242, --group-snps, --corr-config 0.9, and --corr-group 0.9. We post-processed the FINEMAP results to obtain a list of putatively causal SNPs that are LD-independent at the FINEMAP specified parameters (--corr-config 0.9, and --corr-group 0.9) and have a log10 Bayes factor > 2. These putatively causal SNPs are provided in **Table S6. Figure 3 and Figure S4** depict the FINEMAP results for the 6 replicated loci.

In-silico functional annotation of GWAS loci

In-silico annotation of genomic loci was conducted using the following publicly available resources in reference to human genome build hg19/GRCh37. From the UCSC Genome Browser (genome.ucsc.edu) used the following annotation tracks: “UCSC Genes”, “H3K27Ac Mark on 7 cell lines from ENCODE”, “DNaseI hypersensitivity clusters in 125 cell types from ENCODE (v3)”, “chromHMM tracks from Roadmap”,“Transcription Factor ChIP-seq (161 factors) from ENCODE with Factorbook Motifs”, and “Simple nucleotide polymorphisms (dbSNP 150) Found in >1% of Samples”. For the topological associating domain (TAD) analysis, we used the Juicebox tool from the Aiden lab (aidenlab.org/juicebox/) to obtain Hi-C interaction plots using the “4DN Dekker Lab H1 hESC combined” map at 5kb resolution and balanced normalization.

In vitro experiments

Murine T-cell experiments

Mice

C57BL/6.Foxp3GFP reporter mice were bred and housed at the RI-MUHC under specific pathogen free conditions and used in accordance with the institution’s animal research practices. Both female and male

mice were used, and all mice were used between 8-12 weeks of age. The CD4+ T cells were isolated from lymph nodes and spleens from C57BL/6.Foxp3GFP reporter mice[13].

T Cell Purification

Lymph nodes and spleens from C57BL/6.Foxp3GFP reporter mice were dissociated using glass slides and treated ACK lysis buffer to remove red blood cells. Cells were then filtered through 70 μm nylon mesh filters and resuspended in complete cRPMI-1640 containing 10% FBS (Wisent). CD4+ T cells were isolated by staining cells with Miltenyi CD4-positive selection beads and separated using a Miltenyi AutoMACS. The CD4-negative fraction was kept for use as antigen presenting cells. The CD4-positive fraction was further stained for CD4 (clone: RM4-5, eBioscience) and cells were sorted on a BD FACSAria to obtain CD4+GFP- (Foxp3-) TEFF cells.

In Vitro Assays

Cytokine secretion assays were preformed using total CD4+ T cells activated using soluble α-CD3 (BD Biosciences) and co-cultured with irradiated antigen presenting cells in the presence or absence of Closantel (Abcam) at titrated doses (10uM and 20uM). Cytokine secretion was assessed 72 hours post-activation with PMA and Ionomycin (SigmaAldrich), and Monensin (BD Golgi Stop) for 3 hours prior to intracellular staining cells for flow cytometry.

Flow Cytometry

Cells were stained with Fixable Viability Dye (eBioscience) for 15 min at 4C prior to extracellular staining. Cells were then stained for CD4 (clone: GK1.5) and CD25 (clone: PC61.5) for 30 min at 4C. As for the antibodies, they were all used at a concentration of 1 uL/ 100uL and all staining carried out in 50 uL in a 96 v-well plate. Cells were fixed using Foxp3 fixation buffer (eBioscience) for 30 min, prior to being intracellularly stained in permeabilization buffer (eBioscience) containing antibodies for IFNγ (clone: XMG1.2) or IL-2 (clone: JES6-1A12). All antibodies were purchased from eBioscience. Cells were acquired using a BD Fortessa X-20 flow cytometer and results were analysed using Treestar FlowJo (v10).

References

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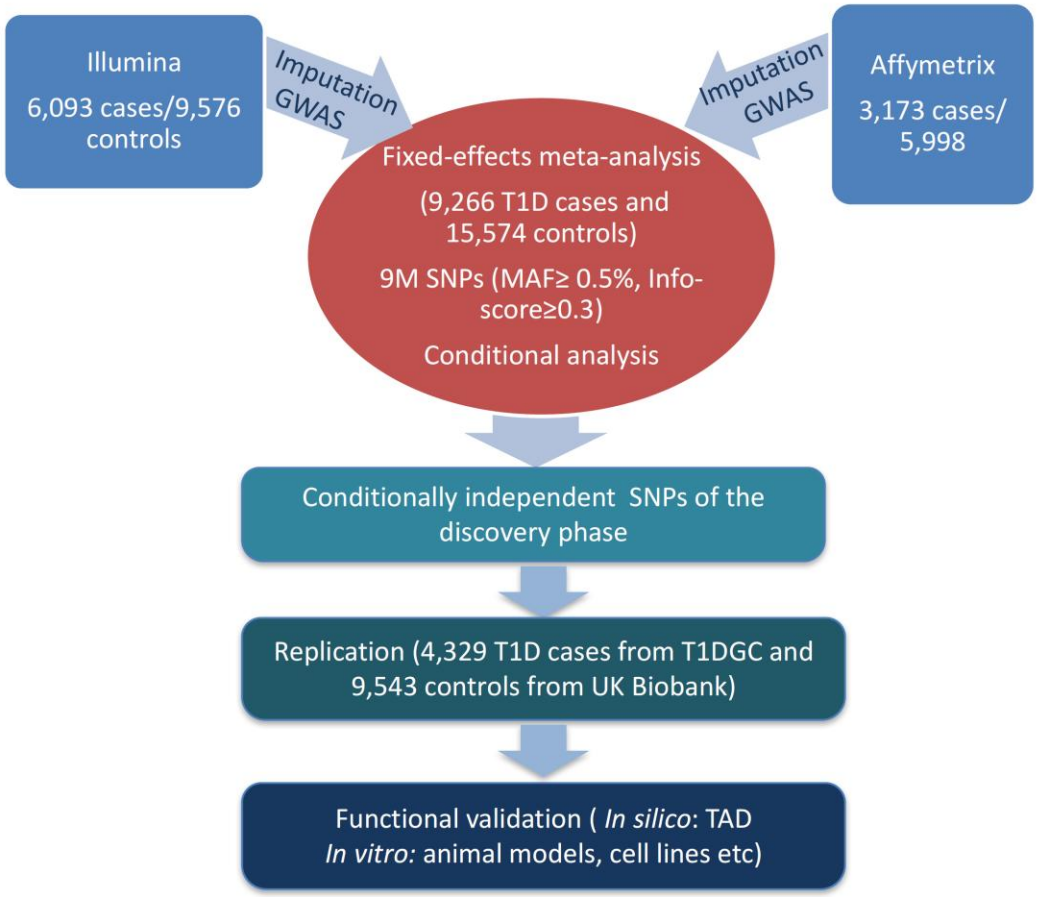
SUPPLEMENTARY DATA

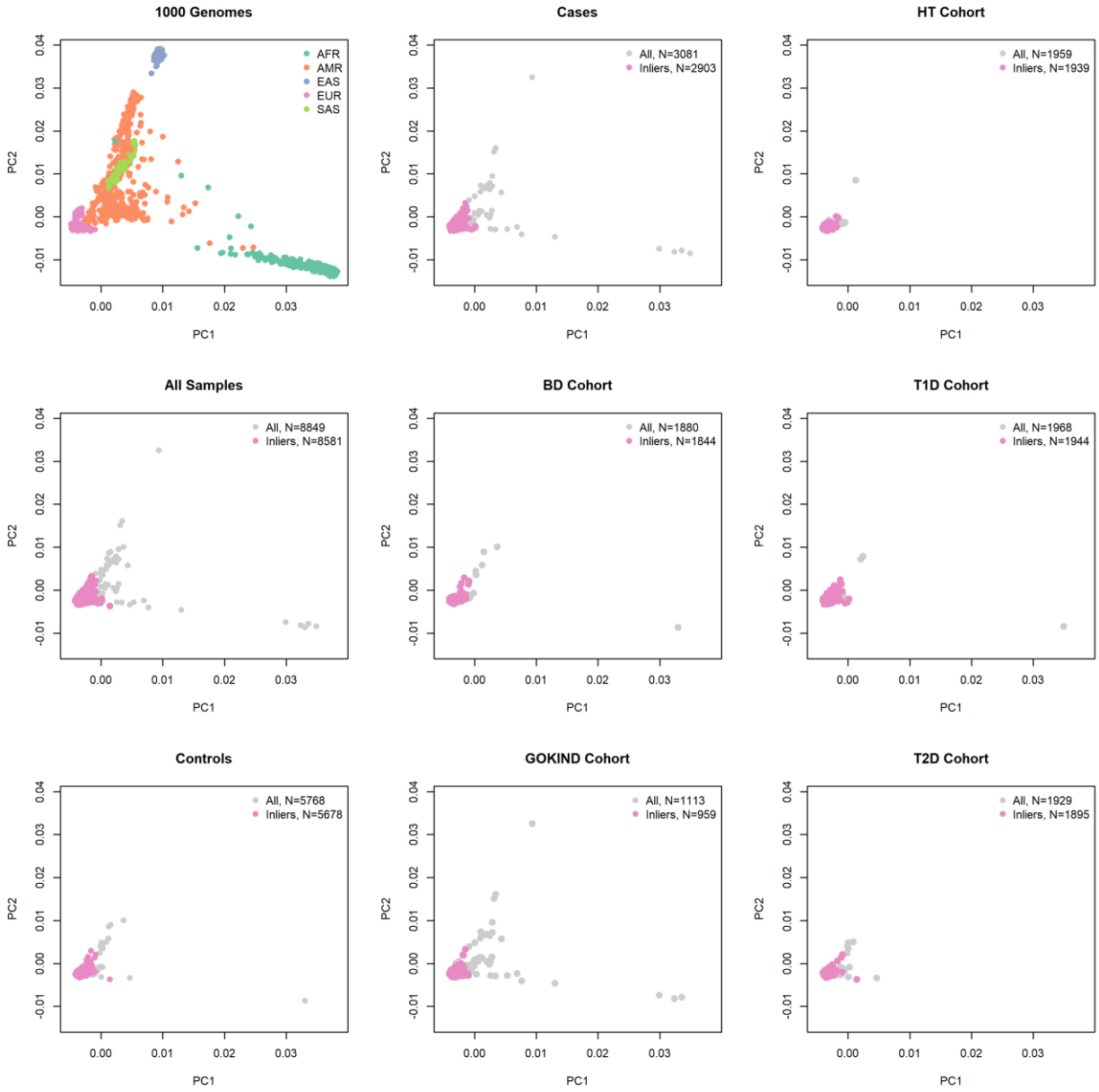
Supplementary Figure S1. Study flow-chart



SUPPLEMENTARY DATA

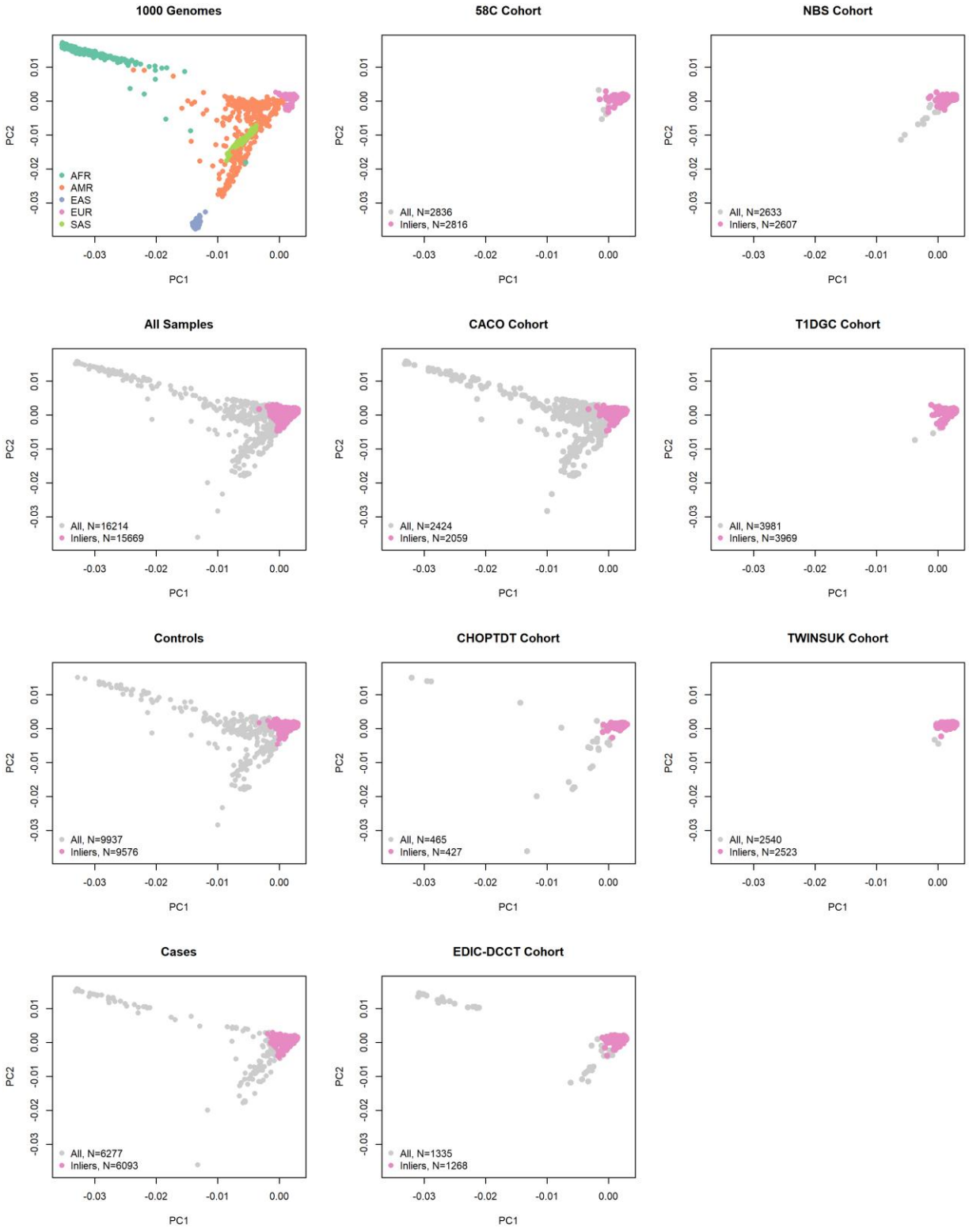
Supplementary Figure S2. Principal component analysis in Affymetrix-platform genotyped individuals (a) and in Illumina-platform genotyped individuals (b). The first panel represents comparison of PC1 vs PC2 in 2,504 individuals from the 1000 Genomes phase 3, and serves as a reference. The subsequent panels depict comparisons of PC1 vs PC2 in the entire Affymetrix or Illumina datasets, separately in cases and controls, and in the respective individual cohorts. Grey points are individuals from the type 1 diabetes datasets that were removed due to being outliers in EIGENSTRAT. Pink points are individuals that where retained for GWAS analysis.

a



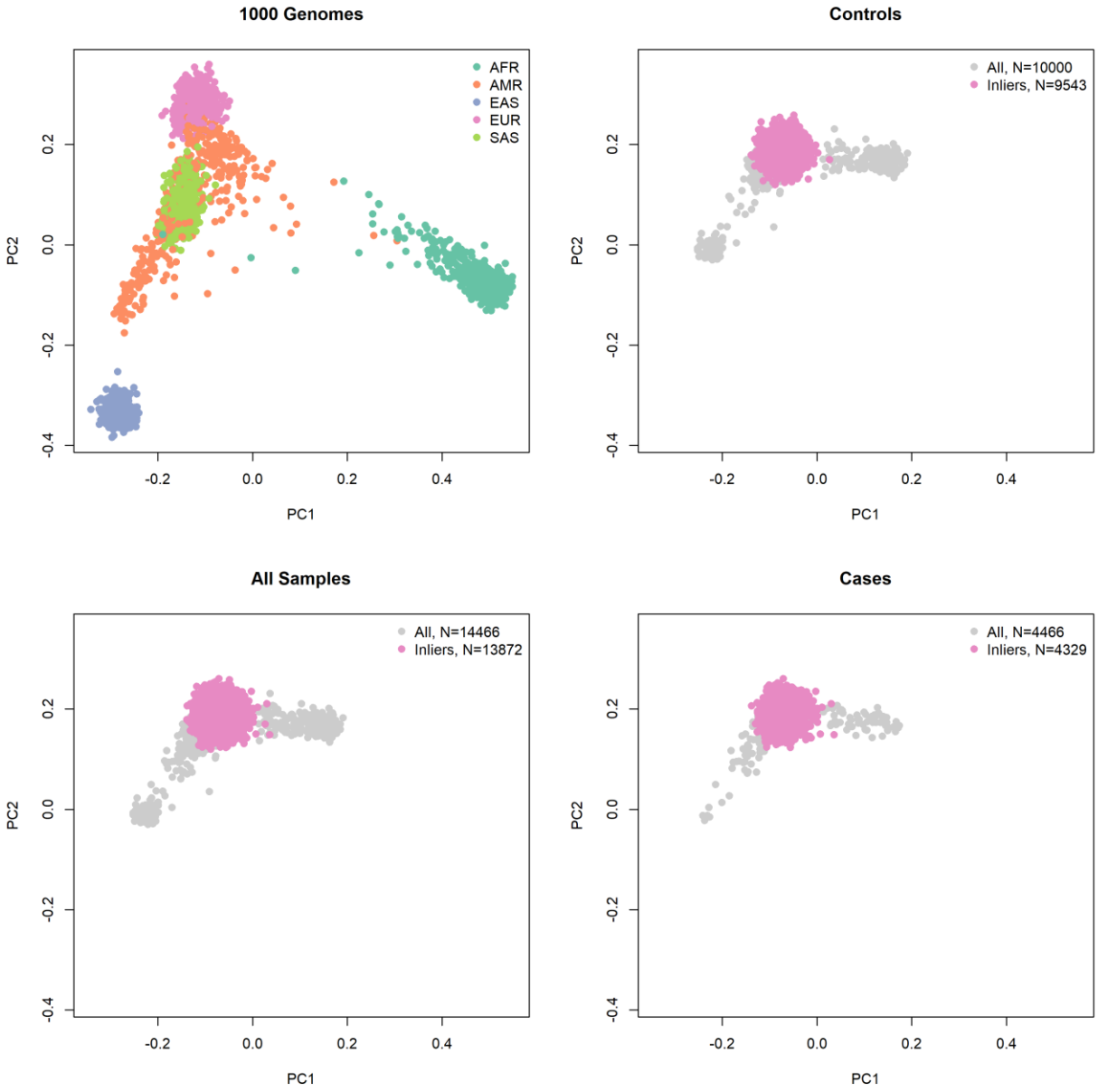
SUPPLEMENTARY DATA

b



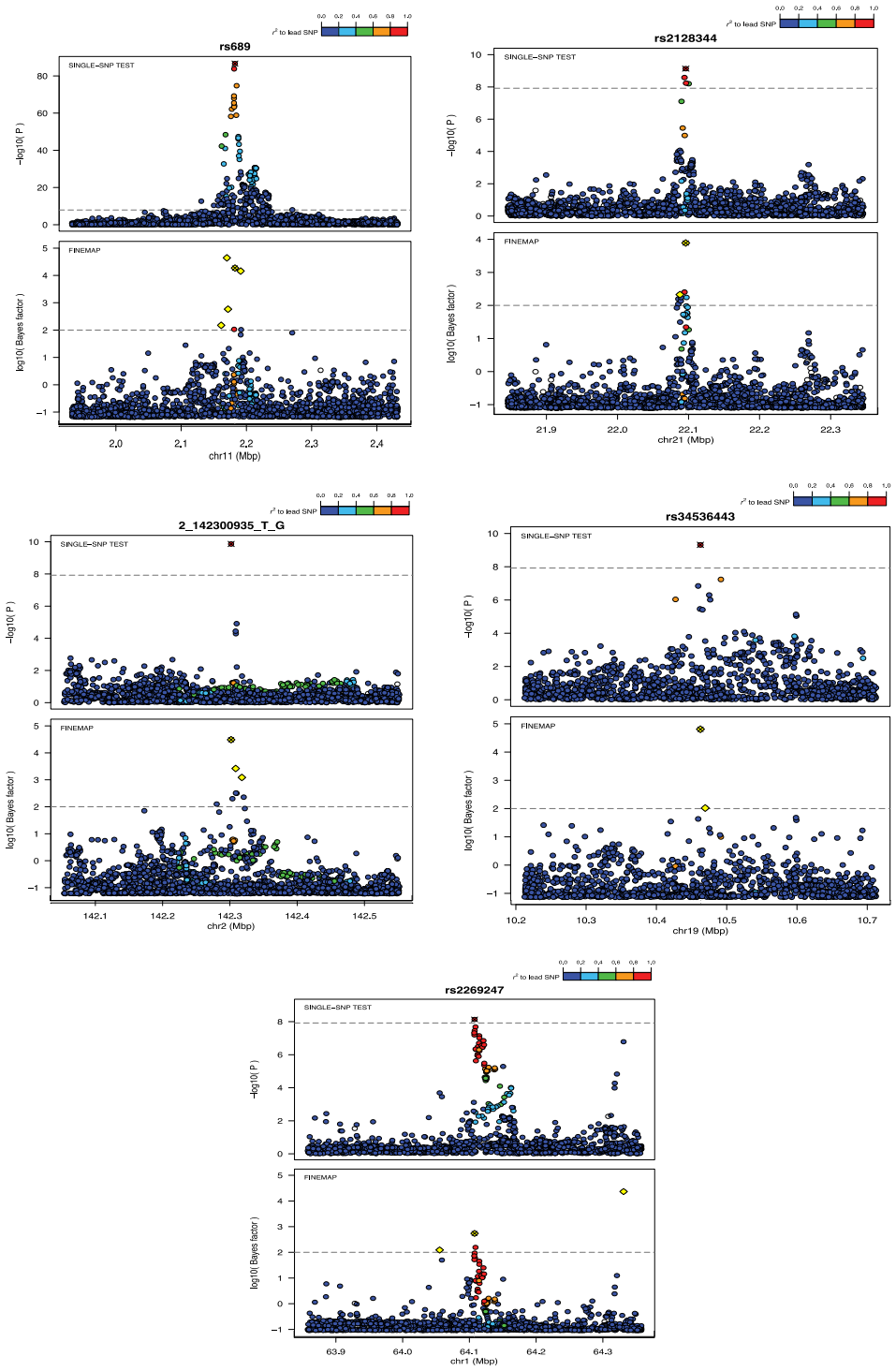
SUPPLEMENTARY DATA

Supplementary Figure S3. Principal component analysis in the replication cohort. The first panel depicts comparison of PC1 vs PC2 in 2,504 individuals from the 1000 Genomes phase 3, and serves as a reference. The subsequent panels depict comparisons of the PC1 vs PC2 in the entire replication cohort, and separately in cases (from T1DGC4) and in controls (from random sub-sample of UK Biobank). The set of individuals retained for replication association analyses are depicted in pink, and removed outliers appear in grey.



SUPPLEMENTARY DATA

Supplementary Figure S4. Regional Manhattan and fine-mapping plots for the 5 top variants from replication from Table 1 other than the *STK39* variant. Top panels depict the results from the discovery meta-analysis of regions centered on the variants. These genetic variants are the lead signals, and are supported by multiple genome-wide suggestive genetic variants. In the bottom panel, statistical fine-mapping of these further loci supports the respective variants as the lead putatively causal genetic variants (yellow ×), accompanied by highly correlated genetic variants with of lower log10 Bayes factor (yellow diamonds).



SUPPLEMENTARY DATA

Table S1. Summary of GWAS discovery cohorts

			Pre-QC		Post-QC				
Repository	Study	Array	Cases	Controls	Cases	Controls	%males in Cases	%males in Controls	study description link
NIDDK (dbGaP)	GOKIND	Affymetrix 500K	1173	0	1113	0	49%		https://www.ncbi.nlm.nih.gov/projects/gap/cgi-bin/study.cgi?study_id=phs000088.v1.p1
WTCCC (EGA)	T1D	Affymetrix 500K	2000	0	1968	0	51%		http://scholar.google.com/scholar?q=Genome-wide+association+study+of+14%2C000+cases+of+seven+common+diseases+and+3%2C000+shared+controls.++2007
WTCCC (EGA)	T2D	Affymetrix 500K	0	1999	0	1929		58%	http://scholar.google.com/scholar?q=Genome-wide+association+study+of+14%2C000+cases+of+seven+common+diseases+and+3%2C000+shared+controls.++2007
WTCCC (EGA)	HT	Affymetrix 500K	0	2001	0	1959		40%	http://scholar.google.com/scholar?q=Genome-wide+association+study+of+14%2C000+cases+of+seven+common+diseases+and+3%2C000+shared+controls.++2007
WTCCC (EGA)	BD	Affymetrix 500K	0	1998	0	1880		37%	http://scholar.google.com/scholar?q=Genome-wide+association+study+of+14%2C000+cases+of+seven+common+diseases+and+3%2C000+shared+controls.++2007
NIDDK (dbGaP)	EDIC-DCCT	Illumina HumanHap550	1385	0	1335	0	53%		https://www.ncbi.nlm.nih.gov/projects/gap/cgi-bin/study.cgi?study_id=phs000086.v2.p1
NIDDK (dbGaP)	T1DGC	Illumina HumanHap550	4129	0	3981	0	53%		https://www.ncbi.nlm.nih.gov/projects/gap/cgi-bin/study.cgi?study_id=phs000180.v1.p1
CHOP-McGill	CACO	Illumina HumanHap550	514	2027	496	1928	55%	51%	https://scholar.google.com/scholar?q=A+genome-wide+association+study+identifies+KIAA0350+as+a+type+1+diabetes+gene.+Hakonarson+2007
CHOP-McGill	CHOPTDT*	Illumina HumanHap550	483	0	465	0	46%		https://scholar.google.com/scholar?q=A+genome-wide+association+study+identifies+KIAA0350+as+a+type+1+diabetes+gene.+Hakonarson+2007
TwinsUK Resource	TwinsUK	Illumina HumanHap610	0	3461	0	2540		13%	https://scholar.google.com/scholar?hl=en&as_sdt=0%2C5&q=TwinsUK%3A+The+UK+Adult+Twin+Registry+Update.&btnG=
WTCCC (EGA)	1958C	Human1-2M-DuoCustom_v1_A	0	2930	0	2836		51%	http://scholar.google.com/scholar?q=Genome-wide+association+study+of+14%2C000+cases+of+seven+common+diseases+and+3%2C000+shared+controls.++2007
WTCCC (EGA)	NBS	Human1-2M-DuoCustom_v1_A	0	2737	0	2633		50%	http://scholar.google.com/scholar?q=Genome-wide+association+study+of+14%2C000+cases+of+seven+common+diseases+and+3%2C000+shared+controls.++2007
Affymetrix Total			3173	5998	3081	5768	50%	45%	
Illumina Total			6511	11155	6277	9937	53%	41%	
Grand Total			9684	17153	9358	15705	52%	43%	

*children only, excludes 1449 parents

SUPPLEMENTARY DATA

Table S2. All conditionally independent GWAS SNPs. Columns are chromosome; SNP; physical position; effect allele;frequency of the effect allele in the original data; effect size, standard error and p-value from the discovery GWAS; estimated effective sample size; frequency of the effect allele in the reference sample; effect size, standard error and p-value from a joint analysis of all the selected SNPs; LD correlation between the SNP i and SNP i + 1 for the SNPs on the list; being within 1Mb of the MHC; having more than 3 satellite SNPs

Chr	SNP	bp	refA	freq	b	se	p	n	freq_geno	bJ	bJ_se	pJ	LD_r	MHC	>=3 satellites
10	rs12722495	6097283	C	0.1122	-0.3145	0.0408	1.27E-14	20536.7	0.0985	-0.3119	0.0409	2.30E-14	0.0113	NO	YES
10	rs201580745	25340868	T	0.093	-0.472	0.0601	4.23E-15	11148	0.0446	-0.4682	0.0603	7.94E-15	0	NO	NO
10	rs77523242	62395516	C	0.0623	-0.3705	0.0635	5.42E-09	14464.5	0.0420	-0.3683	0.0636	6.91E-09	0.0059	NO	YES
10	rs201844300	63379883	C	0.0812	-0.4198	0.0631	2.88E-11	11453	0.0370	-0.4179	0.0632	3.85E-11	0	NO	NO
10	rs199548940	94052740	C	0.0548	-0.5045	0.0812	5.08E-10	9961.86	0.0215	-0.5045	0.0814	5.60E-10	0	NO	NO
11	rs689	2182224	T	0.7109	0.7004	0.0354	2.30E-87	12872.1	0.7695	0.7004	0.0359	1.29E-84	0	NO	YES
11	rs10830227	88890822	A	0.5741	0.1582	0.0233	1.02E-11	25687.4	0.6165	0.1570	0.0233	1.66E-11	-0.0118	NO	YES
11	rs79075295	108114749	A	0.0921	-0.4192	0.0621	1.46E-11	10548.2	0.0405	-0.4160	0.0622	2.31E-11	0	NO	NO
12	rs2071647	9914005	A	0.2755	0.1526	0.0258	3.30E-09	25732.6	0.2822	0.1526	0.0258	3.40E-09	0	NO	YES
12	rs201980362	46530157	A	0.0443	-0.6077	0.0892	9.61E-12	10117.1	0.0199	-0.6085	0.0894	1.00E-11	0.0017	NO	NO
12	rs11131017	56435929	G	0.5803	-0.2461	0.0238	4.24E-25	24708.8	0.5592	-0.2429	0.0239	2.37E-24	-0.0152	NO	YES
12	rs74094155	60969507	T	0.0065	0.8633	0.112	1.29E-14	42202.5	0.0148	0.8491	0.1121	3.59E-14	-0.0093	NO	YES
12	rs201909803	71287755	T	0.0471	-0.4916	0.0842	5.18E-09	10725.7	0.0202	-0.4827	0.0843	1.04E-08	0	NO	NO
12	rs10774624	111833788	A	0.5037	-0.2556	0.0244	1.34E-25	22893	0.4847	-0.2532	0.0245	4.07E-25	-0.0145	NO	YES
12	rs61944716	118915240	A	0.1912	0.2126	0.0308	5.35E-12	23289.3	0.1916	0.2080	0.0308	1.52E-11	0	NO	YES
13	rs202019816	45973877	T	0.0717	-0.4056	0.0675	1.84E-09	11207	0.0325	-0.4056	0.0676	1.98E-09	0	NO	NO
13	rs201630594	91897739	C	0.0675	-0.4422	0.0723	9.73E-10	10325.4	0.0278	-0.4422	0.0724	1.03E-09	0	NO	NO
14	rs139140717	37424426	C	0.0055	1	0.1404	1.04E-12	31862.6	0.0097	1.0000	0.1405	1.10E-12	0	NO	NO
14	rs194739	69301874	T	0.2655	-0.161	0.0276	5.68E-09	23129.5	0.2483	-0.1610	0.0276	5.57E-09	0	NO	YES
14	rs200639691	89616782	G	0.0718	-0.4653	0.0697	2.44E-11	10583.9	0.0314	-0.4365	0.0700	4.44E-10	-0.0146	NO	YES
14	rs17125653	89771348	A	0.077	0.2355	0.0402	4.75E-09	29924.8	0.1022	0.2330	0.0402	6.96E-09	-0.0027	NO	NO
14	rs74085189	100671003	A	0.0732	-0.4555	0.0736	6.15E-10	9325.52	0.0266	-0.4260	0.0739	8.16E-09	0	NO	NO
15	rs200494724	49049214	A	0.0749	-0.4582	0.0701	6.43E-11	10139.6	0.0300	-0.4573	0.0702	7.53E-11	-0.0031	NO	NO
15	rs4566101	49219631	C	0.2697	0.1755	0.0255	6.23E-12	27021.1	0.3291	0.1752	0.0255	6.70E-12	0	NO	YES
15	rs78852152	81650586	C	0.0326	-0.6509	0.1085	1.96E-09	9302.43	0.0127	-0.6509	0.1087	2.13E-09	0	NO	NO
16	rs741172	11200798	T	0.3205	-0.2034	0.0258	3.11E-15	24299.5	0.3062	-0.2046	0.0258	2.37E-15	0.0077	NO	YES
16	16_28536519_A_G	28536519	G	0.1026	0.2411	0.0399	1.55E-09	24056.1	0.0894	0.2435	0.0399	1.07E-09	0	NO	YES
16	rs8056814	75252327	A	0.0793	0.2641	0.0415	1.99E-10	28044.5	0.0874	0.2639	0.0415	2.08E-10	-0.0011	NO	YES
16	rs199807703	79926755	C	0.0733	-0.4236	0.0691	8.60E-10	10851.4	0.0295	-0.4233	0.0692	9.62E-10	0	NO	NO
17	rs140339358	47362736	C	0.1209	-0.4061	0.0555	2.41E-13	10913.1	0.0524	-0.4061	0.0556	2.89E-13	0	NO	NO
18	rs200941228	24900339	T	0.0602	-0.4977	0.0761	6.26E-11	10488.2	0.0260	-0.4601	0.0765	1.80E-09	0.0850	NO	NO
18	rs372063934	29523372	G	0.1326	-0.3341	0.0498	2.04E-11	12051	0.0668	-0.3102	0.0500	5.69E-10	0	NO	NO
18	rs145224611	69778474	C	0.0126	1.1337	0.1623	2.82E-12	10479.8	0.0034	1.1337	0.1627	3.18E-12	0	NO	NO
19	rs34536443	10463118	C	0.0515	-0.4139	0.0665	4.84E-10	17478.3	0.0360	-0.4139	0.0666	5.06E-10	0	NO	YES
1	rs72661618	36380971	C	0.0959	-0.4369	0.0663	4.50E-11	8996.05	0.0340	-0.4369	0.0665	4.89E-11	0	NO	NO
1	rs2269247	64107284	T	0.1804	0.1709	0.0295	7.28E-09	26739.1	0.1879	0.1709	0.0295	7.05E-09	0	NO	YES
1	rs6679677	114303808	A	0.0993	0.6527	0.0346	3.42E-79	31817	0.1237	0.6527	0.0348	1.61E-78	0	NO	YES
1	rs201886798	164935903	A	0.064	-0.4224	0.0733	8.32E-09	10670.5	0.0269	-0.4238	0.0734	7.81E-09	-0.0043	NO	NO
1	rs10911399	183646903	G	0.0455	-0.3707	0.064	6.75E-09	19332.1	0.0377	-0.3719	0.0641	6.40E-09	0	NO	NO
20	rs202525	1673775	A	0.7226	-0.1574	0.0256	8.02E-10	26447	0.7110	-0.1565	0.0256	1.01E-09	0.0088	NO	YES
20	rs200152879	17433315	G	0.0414	-0.6024	0.091	3.55E-11	10543.5	0.0186	-0.5993	0.0912	4.95E-11	0	NO	NO
21	rs2128344	22096544	A	0.0055	0.7827	0.1271	7.36E-10	39278.3	0.0317	0.7827	0.1272	7.50E-10	0	NO	YES
22	rs201423380	22161282	G	0.0415	-0.5695	0.0977	5.58E-09	9420.46	0.0141	-0.5695	0.0979	5.92E-09	0	NO	NO
2	rs200920407	12723911	G	0.0362	-0.587	0.1017	7.70E-09	9455.95	0.0137	-0.5870	0.1019	8.31E-09	0	NO	NO
2	rs1869449	33613232	A	0.2967	0.1769	0.0269	4.55E-11	22633.5	0.3258	0.1769	0.0269	5.03E-11	0	NO	YES
2	rs10183097	74914779	C	0.1362	0.2053	0.0322	1.82E-10	28029	0.1472	0.2056	0.0322	1.75E-10	0.0019	NO	YES
2	rs10865468	84040260	C	0.2527	-0.1624	0.0277	4.66E-09	23596.7	0.2215	-0.1627	0.0277	4.36E-09	0	NO	YES
2	2_142300935_T_G	142300935	G	0.0131	0.562	0.0875	1.37E-10	34550.8	0.0199	0.5620	0.0876	1.37E-10	0	NO	YES
2	rs2111485	163110536	G	0.6033	0.1577	0.0248	1.89E-10	23221.4	0.6157	0.1596	0.0248	1.28E-10	-0.0146	NO	YES
2	rs60587303	169046632	C	0.0051	0.7948	0.1355	4.43E-09	36719.9	0.0119	0.7987	0.1356	3.84E-09	-0.0145	NO	YES
2	rs201270504	171809973	G	0.028	-0.739	0.1157	1.68E-10	9358.15	0.0112	-0.7350	0.1159	2.32E-10	0	NO	NO
2	rs11571297	204745003	C	0.4844	-0.1964	0.0237	1.11E-16	24339.1	0.4688	-0.1962	0.0237	1.36E-16	0.0018	NO	YES
2	rs200743609	221229333	A	0.1005	-0.3873	0.0619	4.00E-10	9846.83	0.0389	-0.3848	0.0620	5.50E-10	-0.0083	NO	NO
2	rs17863786	234607863	G	0.0293	0.4144	0.0628	4.26E-11	30482.2	0.0405	0.4126	0.0628	5.21E-11	0	NO	NO
3	rs201495159	69522710	C	0.1002	-0.363	0.0566	1.43E-10	11814.4	0.0478	-0.3630	0.0567	1.53E-10	0	NO	NO
3	rs201539385	135731473	A	0.1198	-0.3387	0.0537	2.77E-10	11221.3	0.0557	-0.3387	0.0538	3.05E-10	0	NO	NO
3	rs80224989	179301170	G	0.0608	-0.4791	0.0743	1.17E-10	10820.9	0.0251	-0.4791	0.0744	1.23E-10	0	NO	NO
4	rs62410259	41713671	A	0.077	-0.3796	0.0533	1.02E-12	16920.2	0.0579	-0.3770	0.0534	1.63E-12	-0.0117	NO	NO
4	rs150445692	58384375	T	0.0052	0.8205	0.1417	7.04E-09	32954.9	0.0064	0.8121	0.1418	1.01E-08	0	NO	NO
5	rs199552154	57982406	T	0.0653	-0.4164	0.0701	2.78E-09	11366.7	0.0296	-0.4164	0.0702	3.01E-09	0	NO	NO
5	rs202091821	135727349	G	0.0652	-0.4344	0.073	2.69E-09	10493.8	0.0278	-0.4344	0.0731	2.83E-09	0	NO	NO
5	rs184405565	157776381	A	0.0591	-0.4946	0.0751	4.58E-11	10860.8	0.0265	-0.4946	0.0752	4.93E-11	0	NO	NO
6	rs1770129	28095146	T	0.0171	0.8145	0.0966	3.35E-17	21793.9	0.0129	0.5724	0.0973	4.03E-09	-0.0393	YES	NO
6	6_29819325_C_T	29819325	T	0.2658	0.0296	0.0299	0.3219	19655.3	0.2305	-0.2084	0.0322	1.04E-10	0.0044	YES	NO
6	6_31247135_T_C	31247135	C	0.1099	-0.608	0.0525	5.37E-31	12585.4	0.0808	-0.3486	0.0547	1.82E-10	0.0319	YES	NO
6	6_31745284_C_T	31745284	T	0.5365	0.5662	0.0301	4.50E-79	14868	0.5806	0.2714	0.0335	5.40E-16	-0.0962	YES	NO
6	6_32199239_C_T	32199239	T	0.2486	-0.6982	0.0373	2.40E-78	12845.3	0.1913	-0.3813	0.0410	1.34E-20	-0.1257	YES	NO
6	6_32373378_A_T	32373378	T	0.0368	1.4324	0.0596	1.22E-127	26658.8	0.0487	0.6135	0.0670	5.66E-20	-0.0323	YES	NO
6	6_32390751_T_C	32390751	C	0.0282	1.189	0.0699	6.18E-65	25321.7	0.0303	0.5144	0.0735	2.52E-12	-0.0064	YES	NO
6	6_32395942_C_T	32395942	T	0.0236	1.4118	0.0691	9.09E-93	30750.5	0.0312	0.6295	0.0744	2.57E-17	0.0963	YES	NO
6	6_32397309_A_G	32397309	G	0.815	1.7582	0.0633	1.21E-169	4905.66	0.8800	0.7451	0.0814	5.38E-20	0.3163	YES	NO
6	rs67216854	32512766	T	0.5556	0.3745	0.0357	8.64E-26	10788.2	0.6086	0.2599	0.0390	2.62E-11	0.0358	YES	NO
6	6_32560107_G_T	32560107	T	0.3307	0.24	0.0331	4.25E-13	14089.4	0.2942	0.5880	0.0409	9.40E-47	-0.1332	YES	NO
6	6_32560385_A_T	32560385	T	0.1145	0.9761	0.0462	5.61E-99	15400.3	0.0757	0.4174	0.0514	4.84E-16	0.1567	YES	NO
6	6_32583742_G_A	32583742	A	0.6793	1.2547	0.0414	3.59E-202	8266.44	0.7894	0.5777	0.0561	7.05E-25	0.0473	YES	NO
6	6_32589101_T_G	32589101	G	0.0299	-2.0182	0.1745	5.95E-31	3749.74	0.0164	-1.3839	0.1796	1.33E-14	-0.0648	YES	NO
6	6_32596908_G_C	32596908	C	0.1967	0.4037	0.0368	5.07E-28	15906.2	0.1797	-0.7610	0.0637	6.38E-33	-0.0442	YES	NO
6	6_32600057_A_G	32600057	G	0.14	-0.8881	0.0533	2.12E-62	9748.94	0.0735	-0.5677	0.0605	6.13E-21	0.3702	YES	NO
6	6_32600803_T_C	32600803	C	0.3748	0.0407	0.0303	0.1792	15939.1	0.3727	1.8939	0.0811	1.64E-120	0.9234	YES	NO
6	6_32602334_C_A	32602334	A	0.4154	-0.2271	0.0302	5.94E-14	15427.3	0.3888	-1.9349	0.0779	3.23E-136	-0.5715	YES	NO
6	6_32603825_C_T	32603825	T	0.5037	0.612	0.0288	2.87E-100	16087.7	0.5530	0.7349	0.0463	1.21E-56	0.0948	YES	NO
6	6_32603973_T_C	32603973	C	0.0344	0.5525	0.0783	1.66E-12	16790	0.0195	0.5219	0.0840	5.26E-10	0.0341	YES	NO
6	6_32606970_G_A	32606970	A	0.066	0.9188	0.0612	6.82E-51	14628	0.0425	0.5694	0.0692	1.81E-16	0.4500	YES	NO
6	6_32611641_A_G	32611641	G	0.1983	0.6818	0.0351	4.49E-84	17131.9	0.1643	0.8071	0.0611	6.75E-40	0.3516	YES	NO
6	rs9273326	32623219	C	0.5412	0.656	0.0301	2.65E-105	14769.2	0.6211	-0.9435	0.0521	3.14E-73	0.3270	YES	NO
6	rs756940976	32625082	C	0.1859	0.781	0.0426	4.46E-75	12150.6	0.1398	0.3193	0.0467	8.35E-12	0.1126	YES	NO
6	rs115749644	32627818	A	0.0439	1.4278	0.0692	1.68E-94	16636.5	0.0253	0.4504	0.0743	1.38E-09	0.0848	YES	NO
6	6_32628084_C_T	32628084	T	0.0611	1.2312	0.0583	4.15E-99	17142	0.0392	0.5158	0.0645	1.22E-15	0.0319	YES	NO
6	rs36203457	32628548	G	0.1971	0.6227	0.0409	2.22E-52	12722.9	0.1565	0.3450	0.0456	3.86E-14	0.1703	YES	NO
6	6_32634137_A_C	32634137	C	0.129	0.8818	0.0469	5.31E-79	13522.6	0.0809	0.3285	0.0506	8.40E-11	0.0396	YES	NO
6	6_32646998_T_C	32646998	C	0.0907	-0.6001	0.0649	2.46E-20	9787.07	0.0532	-0.4506	0.0682	3.81E-11	-0.0869	YES	NO
6	6_32667937_A_T	32667937	T	0.1212	1.4728	0.0402	1.78E-294	18581.3	0.1374	0.5753	0.0574	1.21E-23	-0.0619	YES	NO
6	6_32673893_C_A	32673893	A	0.1578	1.0151	0.0332	4.29E-205	22475.6	0.1780	0.7261	0.0459	2.34E-56	-0.1550	YES	NO
6	6_32681355_T_C	32681355	C	0.2298	0.8732	0.0315	1.10E-168	18758.7	0.2524	0.5353	0.0442	1.07E-33	0.1189	YES	NO
6	6_32796521_C_T	32796521	T	0.2455	-0.6999	0.0375	1.34E-77	12817.5	0.1898	-0.2628	0.0418	3.12E-10	0.1069	YES	NO
6	6_33034815_G_A	33034815	A	0.1221	-0.5866	0.0474	3.30E-35	14086.6	0.0836	-0.4505	0.0483	1.07E-20	-0.0563	YES	NO
6	rs78238190	33650433	A	0.0311	0.871	0.0604	3.87E-47	30987.5	0.0359	0.4004	0.0628	1.86E-10	0	YES	NO
7	rs201092169	10476666	G	0.0249	-0.8778	0.1278	6.57E-12	8653.31	0.0098	-0.8778	0.1281	7.37E-12	0	NO	NO
7	rs189650556	41068348	A	0.0052	0.9283	0.1567	3.13E-09	27125.7	0.0084	0.9283	0.1568	3.21E-09	0	NO	NO
7	7_67673753_C_T	67673753	T	0.0594	-0.5591	0.0777	6.31E-13	10176.7	0.0254	-0.5591	0.0779	7.09E-13	0	NO	NO
7	rs200794640	89482016	T	0.0825	-0.5202	0.0666	5.49E-15	10215.3	0.0364	-0.4915	0.0670	2.15E-13	0.0754	NO	NO
7	rs200236873	106836335	C	0.0765	-0.4477	0.0704	1.98E-10	9813.38	0.0296	-0.4093	0.0707	7.18E-09	0	NO	NO
7	7_142637502_T_G	142637502	G	0.0551	-0.4943	0.0851	6.25E-09	9116.98	0.0194	-0.4943	0.0853	6.71E-09	0	NO	NO
8	rs202140639	92226109	G	0.0594	-0.484	0.0765	2.48E-10	10411.3	0.0245	-0.4840	0.0766	2.70E-10	0	NO	NO
8	rs200494646	131690564	G	0.0249	-0.6912	0.1195	7.22E-09	9822.65	0.0099	-0.6912	0.1197	7.72E-09	0	NO	NO
9	rs200391977	18285778	T	0.064	-0.4967	0.074	1.91E-11	10442.2	0.0275	-0.4967	0.0742	2.11E-11	0	NO	NO
9	rs201708268	93323749	G	0.0528	-0.4921	0.081	1.26E-09	10447.3	0.0223	-0.4921	0.0811	1.32E-09	0	NO	NO

SUPPLEMENTARY DATA

Table S3. Filtered conditionally independent GWAS SNPs. Columns are chromosome; SNP; physical position;effect allele; frequency of the effect allele in the original data; effect size, standard error and p-value from the discovery GWAS; estimated effective sample size; frequency of the effect allele in the reference sample; effect size, standard error and p-value from a joint analysis of all the selected SNPs; LD correlation between the SNP i and SNP i + 1 for the SNPs on the list.

Chr	SNP	bp	refA	freq	b	se	p	n	freq_geno	bJ	bJ_se	pJ	LD_r
1	rs2269247	64107284	T	0.1804	0.1709	0.0295	7.28E-09	26739.1	0.1879	0.1709	0.0295	7.05E-09	0.0000
1	rs6679677	114303808	A	0.0993	0.6527	0.0346	3.42E-79	31817	0.1237	0.6527	0.0348	1.61E-78	0.0000
2	rs1869449	33613232	A	0.2967	0.1769	0.0269	4.55E-11	22633.5	0.3258	0.1769	0.0269	5.03E-11	0.0000
2	rs10183097	74914779	C	0.1362	0.2053	0.0322	1.82E-10	28029	0.1472	0.2056	0.0322	1.75E-10	0.0019
2	rs10865468	84040260	C	0.2527	-0.1624	0.0277	4.66E-09	23596.7	0.2215	-0.1627	0.0277	4.36E-09	0.0000
2	142300935_T_	142300935	G	0.0131	0.562	0.0875	1.37E-10	34550.8	0.0199	0.5620	0.0876	1.37E-10	0.0000
2	rs2111485	163110536	G	0.6033	0.1577	0.0248	1.89E-10	23221.4	0.6157	0.1596	0.0248	1.28E-10	-0.0146
2	rs60587303	169046632	C	0.0051	0.7948	0.1355	4.43E-09	36719.9	0.0119	0.7987	0.1356	3.84E-09	-0.0145
2	rs11571297	204745003	C	0.4844	-0.1964	0.0237	1.11E-16	24339.1	0.4688	-0.1962	0.0237	1.36E-16	0.0018
10	rs12722495	6097283	C	0.1122	-0.3145	0.0408	1.27E-14	20536.7	0.0985	-0.3119	0.0409	2.30E-14	0.0113
10	rs77523242	62395516	C	0.0623	-0.3705	0.0635	5.42E-09	14464.5	0.0420	-0.3683	0.0636	6.91E-09	0.0059
11	rs689	2182224	T	0.7109	0.7004	0.0354	2.30E-87	12872.1	0.7695	0.7004	0.0359	1.29E-84	0.0000
11	rs10830227	88890822	A	0.5741	0.1582	0.0233	1.02E-11	25687.4	0.6165	0.1570	0.0233	1.66E-11	-0.0118
12	rs2071647	9914005	A	0.2755	0.1526	0.0258	3.30E-09	25732.6	0.2822	0.1526	0.0258	3.40E-09	0.0000
12	rs1131017	56435929	G	0.5803	-0.2461	0.0238	4.24E-25	24708.8	0.5592	-0.2429	0.0239	2.37E-24	-0.0152
12	rs74094155	60969507	T	0.0065	0.8633	0.112	1.29E-14	42202.5	0.0148	0.8491	0.1121	3.59E-14	-0.0093
12	rs10774624	111833788	A	0.5037	-0.2556	0.0244	1.34E-25	22893	0.4847	-0.2532	0.0245	4.07E-25	-0.0145
12	rs61944716	118915240	A	0.1912	0.2126	0.0308	5.35E-12	23289.3	0.1916	0.2080	0.0308	1.52E-11	0.0000
14	rs194739	69301874	T	0.2655	-0.161	0.0276	5.68E-09	23129.5	0.2483	-0.1610	0.0276	5.57E-09	0.0000
14	rs17125653	89771348	A	0.077	0.2355	0.0402	4.75E-09	29924.8	0.1022	0.2330	0.0402	6.96E-09	-0.0027
15	rs4566101	49219631	C	0.2697	0.1755	0.0255	6.23E-12	27021.1	0.3291	0.1752	0.0255	6.70E-12	0.0000
16	rs741172	11200798	T	0.3205	-0.2034	0.0258	3.11E-15	24299.5	0.3062	-0.2046	0.0258	2.37E-15	0.0077
16	_28536519_A_	28536519	G	0.1026	0.2411	0.0399	1.55E-09	24056.1	0.0894	0.2435	0.0399	1.07E-09	0.0000
16	rs8056814	75252327	A	0.0793	0.2641	0.0415	1.99E-10	28044.5	0.0874	0.2639	0.0415	2.08E-10	-0.0011
19	rs34536443	10463118	C	0.0515	-0.4139	0.0665	4.84E-10	17478.3	0.0360	-0.4139	0.0666	5.06E-10	0.0000
20	rs202525	1673775	A	0.7226	-0.1574	0.0256	8.02E-10	26447	0.7110	-0.1565	0.0256	1.01E-09	0.0088
21	rs2128344	22096544	A	0.0055	0.7827	0.1271	7.36E-10	39278.3	0.0317	0.7827	0.1272	7.50E-10	0.0000

SUPPLEMENTARY DATA

Table S4. Conditionally independent SNPs chosen for replication. Columns are candidate gene; chromosome; SNP; physical position; effect allele;frequency of the effect allele in the original data; effect size; standard error and p-value from the discovery GWAS; estimated effective sample size; frequency of the effect allele in the reference sample; effect size, standard error and p-value from a joint analys of all the selected SNPs; LD correlation between the SNP i and SNP i + 1 for the SNPs on the list.

Candidate gene	Chr	SNP	bp	refA	freq	b	se	p	n	freq_geno	bJ	bJ_se	pJ	LD_r
PGM1	1	rs2269247	64107284	T	0.1804	0.1709	0.0295	7.28E-09	26739.1	0.1879	0.1709	0.0295	7.05E-09	0
LRP1B	2	2_142300935_T_G	142300935	G	0.0131	0.562	0.0875	1.37E-10	34550.8	0.0199	0.5620	0.0876	1.37E-10	0
STK39	2	rs60587303	169046632	C	0.0051	0.7948	0.1355	4.43E-09	36719.9	0.0119	0.7987	0.1356	3.84E-09	-0.0145
INS	11	rs689	2182224	T	0.7109	0.7004	0.0354	2.30E-87	12872.1	0.7695	0.7004	0.0359	1.29E-84	0
intergenic	12	rs74094155	60969507	T	0.0065	0.8633	0.112	1.29E-14	42202.5	0.0148	0.8491	0.1121	3.59E-14	-0.0093
intergenic	12	rs61944716	118915240	A	0.1912	0.2126	0.0308	5.35E-12	23289.3	0.1916	0.2080	0.0308	1.52E-11	0
TYK2	19	rs34536443	10463118	C	0.0515	-0.4139	0.0665	4.84E-10	17478.3	0.0360	-0.4139	0.0666	5.06E-10	0
intergenic	21	rs2128344	22096544	A	0.0055	0.7827	0.1271	7.36E-10	39278.3	0.0317	0.7827	0.1272	7.50E-10	0

SUPPLEMENTARY DATA

Table S5. Results of the replication. Columns are chromosome; SNP; physical position; the effect allele; the non-effect allele; replication sample size; effect allele frequency in the replication cohort; effect size, standard error and p-value from the replication GWAS

Chr	SNP	bp	A1	A2	n	AF	b	se	p
1	rs2269247	64107284	T	C	13848	0.182	0.133	0.042	1.66E-03
2	rs192324744*	142300935	G	T	13849	0.016	0.344	0.124	5.56E-03
2	rs60587303	169046632	C	T	13857	0.006	0.448	0.198	2.37E-02
11	rs689	2182224	T	A	13676	0.759	0.897	0.043	2.28E-96
12	rs74094155	60969507	T	G	13858	0.006	-0.405	0.229	7.73E-02
19	rs34536443	10463118	C	G	13668	0.037	-0.310	0.092	6.97E-04
21	rs2128344	22096544	A	T	13836	0.005	0.658	0.217	2.46E-03

*discovery GWAS SNP identifier: 2_142300935_T_G

SUPPLEMENTARY DATA

Table S6: Results of the FINEMAP for all 27 independent loci of the discovery GWAS. maf: minor allele frequency of allele1; prob: marginal Posterior Inclusion Probabilities;log10bf:log10 Bayes factors;mean: marginalized shrinkage estimates of the posterior effect size mean;sd: marginalized shrinkage estimates of the posterior effect size standard deviation; mean incl:conditional estimates of the posterior effect size mean;sd_incl: conditional estimates of the posterior effect size standard deviation

Locus	SNP	Chr	position	allele1	allele2	maf	beta	se	z	prob	log10bf	group	corr_group	prob_group	log10bf_group	mean	sd	mean_incl	sd_incl
L1	rs527839674	1	64330523	T	A	0.0054	-1.043	0.1992	-5.2359	0.9581	4.3653	1510	1	0.9581	4.3653	-0.2846	0.0836	-0.2971	0.0599
L1	rs2269247	1	64107284	C	T	0.1804	-0.1709	0.0295	-5.7932	0.3501	2.7372	700	1	0.9742	4.5821	-0.0220	0.0307	-0.0628	0.0115
L1	rs151163995	1	64054976	G	A	0.0052	-0.6241	0.1681	-3.7127	0.1085	2.0913	521	1	0.1085	2.0913	-0.0243	0.0724	-0.2235	0.0610
L2	rs77425734	1	114174506	A	G	0.0638	0.3475	0.0714	4.8670	0.9978	5.5083	312	1	0.9978	5.5083	0.0956	0.0184	0.0958	0.0178
L2	rs6679677	1	114303808	C	A	0.0993	-0.6527	0.0346	-18.8642	0.9795	4.5239	574	1	1.0000	12.8444	-0.2582	0.0427	-0.2636	0.0210
L3	rs1869449	2	33613232	G	A	0.2967	-0.1769	0.0269	-6.5762	1.0000	13.1289	1085	1	1.0000	13.1289	-0.1541	0.0179	-0.1541	0.0179
L3	rs17012922	2	33610073	G	A	0.2842	-0.0426	0.0274	-1.5547	0.5642	3.2411	1073	1	0.5971	3.2998	0.0615	0.0561	0.1090	0.0201
L3	rs76108377	2	33587496	A	T	0.0402	-0.1072	0.0617	-1.7374	0.4126	2.9756	985	1	0.4126	2.9756	-0.0562	0.0692	-0.1363	0.0264
L3	rs13009128	2	33605568	A	G	0.3605	-0.0275	0.026	-1.0577	0.3057	2.7726	1054	1	0.4397	3.0236	0.0331	0.0512	0.1083	0.0208
L4	rs10183097	2	74914779	T	C	0.1362	-0.2053	0.0322	-6.3758	0.9992	5.9308	343	1	1.0000	12.8456	-0.3125	0.0373	-0.3128	0.0362
L4	rs191289495	2	74920495	C	G	0.0183	0.1386	0.0927	1.4952	0.5408	2.9167	200	0.9322	0.9644	4.2778	0.1488	0.1415	0.2751	0.0478
L4	rs11126435	2	74789700	A	T	0.1198	-0.0875	0.0351	-2.4929	0.4866	2.8223	224	0.9761	0.9883	4.7738	0.1011	0.1071	0.2079	0.0373
L4	rs6748041	2	74893041	T	G	0.1513	-0.0501	0.0331	-1.5136	0.4775	2.8065	310	1	0.4775	2.8065	0.0457	0.0508	0.0957	0.0250
L5	rs60482136	2	84039267	T	C	0.2172	0.1662	0.0294	5.6531	0.4884	3.0074	827	0.9120	1.0000	13.0275	0.0734	0.0764	0.1503	0.0196
L5	rs7577133	2	84030966	A	G	0.2109	0.0429	0.029	1.4793	0.1125	2.1306	839	0.9208	0.9577	4.3828	-0.0126	0.0359	-0.1116	0.0199
L6	2_142300935_T_G	2	142300935	T	G	0.0131	-0.562	0.0875	-6.4229	0.9541	4.4870	1291	1	0.9541	4.4870	-0.1929	0.0642	-0.2022	0.0494
L6	rs12476844	2	142307636	C	T	0.2779	0.1092	0.0264	4.1364	0.6409	3.4210	1329	0.9443	0.9966	5.6425	0.0798	0.0617	0.1245	0.0194
L6	rs16846467	2	142316877	T	A	0.2658	-0.0123	0.0265	-0.4642	0.4528	3.0872	1296	0.9523	0.9454	4.4077	-0.0502	0.0566	-0.1108	0.0192
L7	rs2111485	2	163110536	A	G	0.3967	-0.1577	0.0248	-6.3589	0.6606	3.1074	643	1	0.7807	3.3696	-0.0325	0.0247	-0.0491	0.0101
L7	rs141102226	2	162992004	A	T	0.0231	0.5348	0.1016	5.2638	0.6520	3.0907	384	1	0.6520	3.0907	0.0833	0.0655	0.1278	0.0299
L7	rs79077660	2	163250620	C	T	0.0196	0.4453	0.1049	4.2450	0.1819	2.1653	898	1	0.2363	2.3087	0.0221	0.0488	0.1213	0.0323
L8	rs60587303	2	169046632	T	C	0.0051	-0.7948	0.1355	-5.8657	0.9882	4.9948	940	1	0.9882	4.9948	-0.4346	0.0815	-0.4398	0.0667
L8	rs114348754	2	169046585	A	G	0.0142	-0.4155	0.0849	-4.8940	0.4928	3.0585	937	1	1.0000	8.7269	-0.1629	0.1685	-0.3305	0.0473
L8	rs3769381	2	169022315	A	G	0.0186	0.1103	0.0856	1.2886	0.2281	2.5416	804	1	0.9993	6.2306	0.0658	0.1229	0.2886	0.0440
L9	rs148137742	2	204787560	C	T	0.0105	-0.5029	0.1147	-4.3845	0.6368	3.2368	855	1	0.6368	3.2368	-0.1323	0.1065	-0.2078	0.0463
L9	rs147450935	2	204984332	G	A	0.0102	-0.5845	0.1167	-5.0086	0.5672	3.1104	1525	1	0.5672	3.1104	-0.1065	0.0989	-0.1878	0.0443
L9	rs231779	2	204734487	C	T	0.382	-0.1722	0.0239	-7.2050	0.4736	2.9471	714	1	0.6777	3.3158	-0.0351	0.0376	-0.0741	0.0100
L9	rs62184059	2	204671864	C	A	0.05	-0.221	0.051	-4.3333	0.2996	2.6243	534	1	0.8077	3.6164	-0.0333	0.0526	-0.1111	0.0246
L9	rs79197498	2	204516679	G	A	0.0285	-0.3071	0.0683	-4.4963	0.2460	2.5066	45	1	0.4360	2.8812	-0.0293	0.0531	-0.1193	0.0270
L9	rs141708670	2	204497841	C	G	0.0194	-0.323	0.0827	-3.9057	0.1676	2.2970	9	1	0.2196	2.4422	-0.0236	0.0543	-0.1409	0.0325
L9	rs190626324	2	204579795	C	G	0.0134	-0.3578	0.1015	-3.5251	0.1501	2.2399	229	1	0.1599	2.2726	-0.0233	0.0575	-0.1554	0.0386
L9	rs78847176	2	204725944	C	T	0.011	-0.4458	0.1106	-4.0307	0.1043	2.0591	695	1	0.1043	2.0591	-0.0200	0.0604	-0.1916	0.0457
L10	rs7090530	10	6110875	C	A	0.405	-0.1855	0.0245	-7.5714	0.2020	2.5818	1269	1	0.2020	2.5818	-0.0095	0.0194	-0.0470	0.0100
L10	rs12722495	10	6097283	T	C	0.1122	0.3145	0.0408	7.7083	0.2018	2.5813	1215	1	0.7264	3.6025	0.0182	0.0369	0.0902	0.0165
L10	rs75252425	10	6217022	G	A	0.0107	0.8593	0.1647	5.2174	0.1831	2.5291	1832	0.9744	0.9625	4.5878	0.0380	0.0823	0.2073	0.0432
L10	rs12722563	10	6069561	G	A	0.1235	0.2993	0.0397	7.5390	0.1729	2.4985	1070	1	0.2614	2.7273	0.0144	0.0323	0.0836	0.0155
L10	rs7893467	10	6079035	G	T	0.0732	0.208	0.043	4.8372	0.1725	2.4975	1131	1	0.1725	2.4975	0.0127	0.0287	0.0734	0.0180
L10	rs7073236	10	6106552	T	C	0.4083	-0.1623	0.0236	-6.8771	0.1657	2.4765	1222	0.9544	0.5746	3.3090	-0.0074	0.0171	-0.0447	0.0095
L10	rs59709453	10	6036079	C	G	0.0244	-0.3049	0.0751	-4.0599	0.1117	2.2779	919	1	0.1277	2.3440	-0.0127	0.0372	-0.1140	0.0291
L10	rs57879330	10	6287926	G	T	0.1151	-0.1464	0.0414	-3.5362	0.0914	2.1811	2202	1	0.0914	2.1811	-0.0048	0.0157	-0.0525	0.0138
L10	rs4147359	10	6108439	G	A	0.34	-0.1574	0.0245	-6.4245	0.0757	2.0920	1257	1	0.1417	2.3960	-0.0034	0.0122	-0.0450	0.0100
L11	rs76132426	10	62177462	T	G	0.1025	0.3369	0.0583	5.7787	0.9992	6.1704	106	1	0.9992	6.1704	0.0799	0.0146	0.0800	0.0145
L11	rs77523242	10	62395516	T	C	0.0623	0.3705	0.0635	5.8347	0.3548	2.8354	927	1	0.3548	2.8354	0.0551	0.0774	0.1554	0.0363
L11	rs10458646	10	62394760	C	T	0.1179	0.2024	0.0387	5.2300	0.3485	2.8236	923	1	0.6899	3.4425	0.0547	0.0766	0.1569	0.0287
L11	rs2028564	10	62384372	A	G	0.1406	0.0215	0.0341	0.6305	0.1629	2.3843	811	0.9948	0.5897	3.2528	-0.0164	0.0383	-0.1006	0.0234
L11	rs117040459	10	62508952	G	A	0.0367	-0.0577	0.0647	-0.8918	0.1438	2.3202	1371	1	0.2185	2.5418	-0.0197	0.0494	-0.1372	0.0300
L11	10_62486467_T_C	10	62486467	T	C	0.1389	0.0016	0.0341	0.0469	0.1147	2.2075	1307	0.9951	0.2371	2.5878	-0.0090	0.0259	-0.0781	0.0213
L12	rs3741206	11	2169864	T	C	0.3802	-0.2046	0.0264	-7.7500	0.9690	4.6447	954	1	0.9711	4.6758	-0.0710	0.0192	-0.0733	0.0146
L12	rs689	11	2182224	A	T	0.2891	-0.7004	0.0354	-19.7853	0.9297	4.2715	996	1	1.0000	8.5680	-0.1148	0.0350	-0.1235	0.0156
L12	rs6356	11	2190951	C	T	0.3651	-0.3058	0.0273	-11.2015	0.9113	4.1613	1017	1	0.9798	4.8364	-0.0740	0.0269	-0.0812	0.0144
L12	rs4320932	11	2171601	T	C	0.2036	-0.2123	0.0297	-7.1482	0.2921	2.7655	962	1	0.3069	2.7960	-0.0150	0.0243	-0.0513	0.0126
L12	rs74918256	11	2161159	G	A	0.2186	-0.1993	0.029	-6.8724	0.0956	2.1739	940	0.9133	0.1112	2.2471	-0.0046	0.0145	-0.0476	0.0125
L13	rs10830227	11	88890822	G	A	0.4259	-0.1582	0.0233	-6.7897	1.0000	12.9259	648	1	1.0000	12.9259	-0.1611	0.0198	-0.1611	0.0198
L13	rs11018520	11	88903115	T	C	0.3422	0.0279	0.0248	1.1250	0.6715	3.2365	642	0.9329	0.9915	4.9927	-0.0815	0.0592	-0.1214	0.0195
L13	rs10830229	11	88891267	A	G	0.0852	-0.0703	0.0426	-1.6502	0.4419	2.8245	649	0.9089	0.7756	3.4644	0.0515	0.0599	0.1166	0.0228
L14	rs77724586	12	9848457	A	C	0.4033	-0.1522	0.0265	-5.7434	0.0848	2.0435	528	1	0.0848	2.0435	-0.0032	0.0111	-0.0382	0.0107
L15	rs75639074	12	56367901	C	G	0.067	-0.0872	0.0481	-1.8129	0.3586	2.4413	271	1	0.4434	2.5951	-0.0256	0.0359	-0.0715	0.0181
L15	rs1131017	12	56435929	C	G	0.4197	0.2461	0.0238	10.3403	0.3467	2.4187	395	1	0.7025	3.0670	0.0304	0.0426	0.0877	0.0149
L16	rs74094155	12	60969507	G	T	0.0065	-0.8633	0.112	-7.7080	0.9963	5.4574	867	1	0.9963	5.4574	-0.5185	0.1254	-0.5204	0.1216
L16	rs2654669	12	60984151	C	T	0.4206	-0.088	0.0226	-3.8938	0.3418	2.7383	930	1	0.3453	2.7451	-0.0321	0.0461	-0.0940	0.0197
L16	rs143161882	12	60883999	T	C	0.0066	-0.0724	0.1407	-0.5146	0.1771	2.3557	1001	0.9403	0.8622	3.8194	0.0583	0.1302	0.3292	0.0813
L16	rs7312791	12	60885641	T	A	0.4326	0.0161	0.0235	0.6851	0.1042	2.0887	591	0.9245	0.2999	2.6547	0.0093	0.0279	0.0892	0.0182
L17	rs6490029	12	111698457	G	A	0.2146	0.1822	0.0298	6.1141	0.7271	3.1443	219	1	0.7341	3.1597	0.0868	0.0572	0.1194	0.0246
L17	rs10774624	12	111833788	G	A	0.4963	0.2556	0.0244	10.4754	0.4303	2.5969	537	1	0.9517	4.0130	0.0367	0.0428	0.0854	0.0106
L17	rs73197980	12	111674121	T	C	0.0667	-0.0307	0.0467	-0.6574	0.3956	2.5346	177	1	0.7340	3.1595	-0.0554	0.0705	-0.1401	0.0267
L17	rs4766561	12	111673244	C	T	0.1454	0.1054	0.0341	3.0909	0.3620	2.4725	159	0.9847	0.6093	2.9117	-0.0365	0.0501	-0.1008	0.0211
L18	rs61944716	12	118915240	C	A	0.1912	-0.2126	0.0308	-6.9026	0.2634	2.5742	715	1	0.9980	5.7123	-0.0198	0.0337	-0.0752	0.0114
L19	rs194749	14	69273905	T	C	0.2455	0.1638	0.0281	5.8292	0.0853	2.0448	972	0.9097	0.8266	3.7535	0.0048	0.0162	0.0568	0.0108
L20	rs200639691	14	89616782	A	G	0.0718	0.4653	0.0697	6.6758	1.0000	8.3811	286	1	1.0000	8.3811	0.1085	0.0170	0.1085	0.0170
L20	rs17125653	14	89771348	T	A	0.077	-0.2355	0.0402	-5.8582	0.9280	4.1370	773	1	0.9716	4.5609	-0.0912	0.0347	-0.0983	0.0245
L21	rs200494724	15	49049214	G	A	0.0749	0.4582	0.0701	6.5364	1.0000	7.7416	189	1	1.0000	7.7416	0.1028	0.0166	0.1028	0.0166
L21	15_49217859_T_C	15	49217859	T	C	0.2647	-0.013	0.0265	-0.4906	0.9997	6.4238	629	0.9785	1.0000	7.4045	0.1599	0.0183	0.1599	0.0181
L21	rs4566101	15	49219631	T	C	0.2697	-0.1755	0.0255	-6.8824	0.9804	4.6171	642	1	1.0000	12.9173	-0.1942	0.0326	-0.1981	0.0177
L22	rs35342456	16	11401503	A	C	0.1905	0.1474	0.0309	4.7702	0.1228	2.2262	1641	1	0.9867	4.9505	0.0070	0.0190	0.0567	0.0115
L22	rs741172	16	11200798	C	T	0.3205	0.2034	0.0258	7.8837	0.0892	2.0713	839	1	0.5752	3.2118	0.0064	0.0207	0.0715	0.0114
L23	16_28536519_A_G	16	28536519	A	G	0.1026	-0.2411	0.0399	-6.0426	0.4825	2.5511	240	1	0.5782	2.7187	-0.0369	0.0407	-0.0765	0.0200
L24	rs8056814	16	75252327	G	A	0.0793	-0.2641	0.0415	-6.3639	0.1416	2.3561	988	1	0.8927	4.0588	-0.0140	0.0351	-0.0991	0.0169
L24	rs72802342	16	75234872	C	A	0.0738	-0.2692	0.043	-6.2605	0.0772	2.0609	850	1	0.0772	2.0609	-0.0077	0.0272	-0.1000	0.0182
L25	rs34536443	19	10463118	G	C	0.0515	0.4139	0.0665	6.2241	0.9858	4.8063	702	1	0.9858	4.8063	0.1157	0.0251	0.1174	0.0210
L25	rs12720356	19	10469975	A	C	0.1069	0.1551	0.0429	3.6154	0.1013	2.0184	721	1	0.1137	2.0746	0.0054	0.0168	0.0536	0.0144
L26	rs4471947	20	1608021	T	G	0.3573	-0.1046	0.0256	-4.0859	0.3501	2.7839	580	1	0.3501	2.7839	-0.0133	0.0189	-0.0379	0.0093
L26	rs202525	20	1673775	G	A	0.2774	0.1574	0.0256	6.1484	0.2213	2.5063	888	1	0.9676	4.5273	0.0129	0.0246	0.0582	0.0102
L27	rs2128344	21	22096544	T	A	0.0055	-0.7827	0.1271	-6.1581	0.8348	3.8898	1382	1	0.9909	5.2251	-0.3847	0.1865	-0.4608	0.0810
L27	rs34997358	21	22088371	A	G	0.0925	0.16	0.0407	3.9312	0.1218	2.3284	1349	1	0.8827	4.0626	0.0097	0.0267	0.0797	0.0160