Re-analysis of public genetic data reveals a rare X-chromosomal variant associated with type 2 diabetes

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The reanalysis of existing GWAS data represents a powerful and cost-effective opportunity to gain insights into the genetics of complex diseases. By reanalyzing publicly available type 2 diabetes (T2D) genome-wide association studies (GWAS) data for 70,127 subjects, we identify seven novel associated regions, five driven by common variants (LYPLAL1, NEUROG3, CAMKK2, ABO, and GIP genes), one by a low-frequency (EHMT2), and one driven by a rare variant in chromosome Xq23, rs146662075, associated with a twofold increased risk for T2D in males. rs146662075 is located within an active enhancer associated with the expression of Angiotensin II Receptor type 2 gene (AGTR2), a modulator of insulin sensitivity, and exhibits allelic specific activity in muscle cells. Beyond providing insights into the genetics and pathophysiology of T2D, these results also underscore the value of reanalyzing publicly available data using novel genetic resources and analytical approaches.
During the last decade, hundreds of genome-wide association studies (GWAS) have been performed with the aim of providing a better understanding of the biology of complex diseases, improving their risk prediction, and ultimately discovering novel therapeutic targets. However, the majority of the published GWAS have only reported primary findings, which generally explain a small fraction of the estimated heritability. To examine the missing heritability, most strategies involve generating new genetic and clinical data. Very rarely are new studies based on the revision and reanalysis of existing genetic data by applying more powerful analytic techniques and resources after the primary GWAS findings are published. These cost-effective reanalysis strategies are now possible, given emerging (1) data-sharing initiatives with large amounts of primary genetic data for multiple human genetic diseases, as well as (2) more and improved GWAS methodologies and resources. Notably, genotype imputation with novel sequence-based reference panels can now substantially increase the genetic resolution of GWAS from previously genotyped data sets, reaching good-quality imputation of low-frequency (minor allele frequency [MAF]: 0.01 ≤ MAF < 0.05) and rare variants (MAF < 0.01), increasing the power to identify novel associations, and fine map the known ones. Moreover, the availability of publicly available primary genetic data allows the homogeneous integration of multiple data sets from different origins providing more accurate meta-analysis results, particularly at the low ranges of allele frequency. Finally, the vast majority of reported GWAS analyses omits the X chromosome, despite representing 5% of the genome and coding for more than 1,500 genes. The reanalysis of publicly available data also enables interrogation of this chromosome.

We hypothesized that a unified reanalysis of multiple publicly available data sets, applying homogeneous standardized quality control (QC), genotype imputation, and association methods, as well as novel and denser sequence-based reference panels for imputation would provide new insights into the genetics and the pathophysiology of complex diseases. To test this hypothesis, we focused this study on type 2 diabetes (T2D), one of the most prevalent complex diseases for which many GWAS have been performed during the past decade. These studies have allowed the identification of more than 100 independent loci, most of them driven by common variants, with a few exceptions. Despite these efforts, there is still a large fraction of genetic heritability hidden in the data, and the role of low-frequency variants, although recently proposed to be minor, has still not been fully explored. The availability of large T2D genetic data sets in combination with larger and more comprehensive genetic variation reference panels provides the opportunity to impute a significantly increased fraction of low-frequency and rare variants, and to study their contribution to the risk of developing this disease. This strategy also allows us to fine map known associated loci, increasing the chances of finding causal variants and understanding their functional impact. We therefore gathered publicly available T2D GWAS cohorts with European ancestry, comprising a total of 13,857 T2D cases and 62,126 controls, to which we applied harmonization and quality control protocols covering the whole genome (including the X chromosome). We then performed imputation using 1000 Genomes Project (1000G) and UK10K reference panels, followed by association testing. By using this strategy, we identified novel associated regions driven by common, low-frequency and rare variants, fine mapped and functionally annotated the existing and novel ones, allowing us to describe a regulatory mechanism disrupted by a novel rare and large-effect variant identified at the X chromosome.

**Results**

**Overall analysis strategy.** As shown in Fig. 1, we first gathered all T2D case-control GWAS individual-level data that were available through the EGA and dbGaP databases (i.e., Gene Environment-Association Studies [GENEVA], Wellcome Trust Case Control Consortium [WTCCC], Finland–United States Investigation of NIDDM Genetics [FUSION], Resource for Genetic Epidemiology Research on Aging [GERA], and Northwestern NUGENE project [NuGENE]). We harmonized these cohorts, applied standardized quality control procedures, and filtered out low-quality variants and samples (Methods and Supplementary Notes). After this process, a total of 70,127 subjects (70KforT2D, 12,931 cases, and 57,196 controls, Supplementary Data 1) were retained for downstream analysis. Each of these cohorts was then imputed to the 1000G and UK10K reference panels using an integrative method, which selected the results from the reference panel that provided the highest accuracy for each variant, according to IMPUTE2 info score (Methods). Finally, the results from each of these cohorts were meta-analyzed (Fig. 1), obtaining a total of 15,115,281 variants with good imputation quality (IMPUTE2 info score ≥ 0.7, MAF ≥ 0.001, and I² heterogeneity score < 0.75), across 12,931 T2D cases and 57,196 controls. Of these, 6,845,408 variants were common (MAF ≥ 0.05), 3,100,848 were low-frequency (0.01 ≤ MAF < 0.05), and 5,169,025 were rare (0.001 ≤ MAF < 0.01). Merging the imputation results derived from the two reference panels substantially increased the number of good-quality imputed variants, particularly within the low-frequency and rare spectrum, compared to the imputation results obtained with each of the panels separately. For example, a set of 5,169,025 rare variants with good quality was obtained after integrating 1000G and UK10K results, while only 2,878,263 rare variants were imputed with 1000G and 4,066,210 with UK10K (Supplementary Fig. 1A). This strategy also allowed us to impute 1,357,753 indels with good quality (Supplementary Fig. 1B).

To take full advantage of publicly available genetic data, we used three main meta-analytic approaches to adapt to the three most common strategies for genetic data sharing: individual-level genotypes, summary statistics, and single-case queries through the Type 2 Diabetes Knowledge Portal (T2D Portal) (http://www.type2diabetesgenetics.org/). We first meta-analyzed all summary statistics results from the DIAGRAM trans-ancestry meta-analysis, selecting 1,918,233 common variants (MAF ≥ 0.05), mostly imputed from HapMap, with the corresponding fraction of non-overlapping samples in our 70KforT2D set, i.e., the GERA and the NuGENE cohorts, comprising a total of 7,522 cases and 50,446 controls (Fig. 1, Supplementary Data 1). Second, the remaining variants (13,197,048), which included mainly non-HapMap variants (MAF < 0.05) or variants not tested above, were meta-analyzed using all five cohorts from the 70KforT2D resource (Supplementary Data 1). Finally, low-frequency variants located in coding regions and with p ≤ 1 × 10⁻⁴ were meta-analyzed using the non-overlapping fraction of samples with the data from the T2D Portal through the interrogation of exome array and whole-exome sequence data from ~80,000 and ~17,000 individuals, respectively.

**Pathway and functional enrichment analysis.** To explore whether our results recapitulate the pathophysiology of T2D, we performed gene-set enrichment analysis with all the variants with p ≤ 1 × 10⁻⁵ using DEPICT® (Methods). This analysis showed enrichment of genes expressed in pancreas (ranked first in tissue enrichment analysis, p = 7.8 × 10⁻⁴, FDR < 0.05, Supplementary Data 2) and cellular response to insulin stimulus (ranked second in gene-set enrichment analysis, p = 3.9 × 10⁻⁵, FDR = 0.05,
Supplementary Data 3, Supplementary Fig. 2, Supplementary Fig. 3), in concordance with the current knowledge of the molecular basis of T2D.

In addition, variant set enrichment analysis of the T2D-associated credible sets across regulatory elements defined in isolated human pancreatic islets showed a significant enrichment for active regulatory enhancers (Supplementary Fig. 4), suggesting that causal SNPs within associated regions have a regulatory function, as previously reported.

Fine-mapping and functional characterization of T2D loci. The three association strategies allowed us to identify 57 genome-wide significant associated loci, of which seven were not previously reported as associated with T2D (Table 1). The remaining 50 loci have been previously reported and included, for example, two low-frequency variants recently discovered in Europeans, one located within one of the CCND2 introns (rs76895963), and a missense variant within the PAM gene. Furthermore, we confirmed that the magnitude and direction of the effect of all the associated variants were highly consistent with those reported previously (ρ = 0.92, p = 1 × 10−248). Supplementary Fig. 5). In addition, the direction of effect was consistent with all 139 previously reported variants, except three that were discovered in east and south Asian populations (Supplementary Data 4).

The high coverage of genetic variation ascertained in this study allowed us to fine-map known and novel loci, providing more candidate causal variants for downstream functional interpretations. We constructed 99% credible variant sets for each of the 71 previously reported loci that we replicated (Supplementary Data 5). As an important improvement over previous T2D genetic studies, we identified several structural variants within the credible sets, consisting mostly of insertions and deletions between 1 and 1,975 nucleotides. In fact, out of the 8,348 variants included within the credible sets for these loci, 927 (11.1%) were indels, of which 105 were genome-wide significant (Supplementary Data 6). Interestingly, by integrating imputed results from 1000G and UK10K reference panels, we gained up to 41% of indels, which were only identified by either one of the two reference panels, confirming the advantage of integrating the results from both reference panels. Interestingly, 15 of the 71 previously reported loci that we replicated (p ≤ 5.3 × 10−4 after correcting for multiple testing) have an indel as the top variant, highlighting the potential role of this type of variation in the susceptibility for T2D. For example, within the IGF2BP2 intron, a well-established and functionally validated locus for T2D, we found that 12 of the 57 variants within its 99% credible set correspond to indels with genome-wide significance (5.6 × 10−16 < p < 2.4 × 10−15), which collectively represented 18.4% posterior probability of being causal.
To prioritize causal variants within all the identified associated loci, we annotated their corresponding credible sets using the Variant Effector Predictor (VEP) for coding variants, and the Combined Annotation-Dependent Depletion (CADD) and LINSIGHT tools for non-coding variation. In addition, we tested the effect of all variants on expression across multiple tissues by interrogating GTEx and RNA-seq gene expression data from pancreatic islets.

### Novel T2D-associated loci driven by common variants

Beyond the detailed characterization of the known T2D-associated regions, we also identified seven novel loci, among which, five were driven by common variants with modest effect sizes (1.06 < OR < 1.12; Table 1, Fig. 2, Supplementary Fig. 6 and 7).

Within the first novel T2D-associated locus in chromosome 1q41 (LYPLAL1-ZC3H11B), several variants have been previously associated with waist-to-hip ratio, height, visceral adipose fat in females, adiponectin levels, fasting insulin, and non-alcoholic fatty liver disease. Among the genes in this locus, LYPLAL1, which encodes for lysophospholipase-1, appears to be the most likely effector gene, as it has been found to be downregulated in mouse models of diet-induced obesity and upregulated during adipogenesis.

Second, a novel locus at chromosome 9q34.2 region (ABO, rs505922, OR = 1.06 [1.04–1.09], p = 4.9 × 10^{-8}) includes several variants that have been previously associated with other metabolic traits. For example, the variant rs651007, in linkage disequilibrium (LD) with rs505922 (r^2 = 0.507), has been shown to be associated with fasting glucose, and rs514659 (r^2 with top = 1) is associated with an increased risk for cardiometabolic disorders. One of the variants within the credible set was the single base-pair frame-shift deletion defining the blood group O.

In concordance with previous results that linked O blood type with a lower risk of developing T2D, the frame-shift deletion determining the blood group type O was associated with a protective effect for T2D in our study (rs8176719, p = 3.4 × 10^{-4}, OR = 0.95 [0.91–0.98]). In addition, several variants within this credible set are associated with the expression of the ABO gene in multiple tissues including skeletal muscle, adipose tissue, and pancreatic islets.

### Table 1 Novel T2D-associated loci

| Novel Locus | Chr | rsID—Risk Allele | OR (95% CI) | P-value | Stage1 Discovery Meta-analysis | Stage2 Replication Meta-analysis | Stage1 + Stage2 Combined Meta-analysis | MAF |
|-------------|-----|-----------------|-------------|---------|-------------------------------|-------------------------------|-----------------------------------|------|
| LYPAL1/ZC3H11B (1q41) | 1 | rs2820443-T | 1.08 (1.04–1.13) | 2.94 × 10^{-4} | 2.10 × 10^{-5} | 1.07 (1.04–1.09) | 2.56 × 10^{-8} | 0.28 |
| EHM7 (6p21.33–p21.32) | 6 | rs115884658-A | 1.34 (1.18–1.53) | 1.00 × 10^{-5} | 1.17 (1.09–1.26) | 2.90 × 10^{-6} | 1.21 (1.14–1.29) | 0.02 |
| ABO (9q34.2) | 9 | rs505922-C | 1.07 (1.03–1.11) | 6.93 × 10^{-4} | 1.06 (1.03–1.09) | 1.90 × 10^{-5} | 5.49 × 10^{-8} | 0.34 |
| NEUROG3 (10q22.1) | 10 | rs2642587-G | 1.12 (1.08–1.16) | 8.45 × 10^{-9} | - | - | 2.22 |
| CALCCOCO2/ATPSGI/UBE2Z/SNF8/GIP (17q21.32) | 12 | rs3794205-G | 1.09 (1.05–1.14) | 4.18 × 10^{-5} | 1.06 (1.03–1.09) | 1.60 × 10^{-4} | 1.71 × 10^{-8} | 0.32 |
| AGR2 (Xq23) | X | rs146662075-T | 3.09 (2.06–4.60) | 3.24 × 10^{-8} | 1.57 (1.19–2.07) | 4.12 × 10^{-3} | 1.95 (1.56–2.45) | 0.008 |

Chr: chromosome, OR: odds ratio, MAF: minor allele frequency.

*Imputed based public GWAS discovery meta-analysis (NuGENE + GERA cohort, 7,522 cases and 50,446 controls).
*Transcendence DIAGRAM Consortium (26,488 cases and 83,964 controls).
*Meta-P-value estimated using a weighted Z-score method due to unavailable SE information from Stage 2 replication analysis.
*FUSION + WTCCC, 12,931 cases and 57,196 controls.
*Meta-analysis Impputed based public GWAS meta-analysis (NuGENE + GERA cohort + GENEVA + FUSION + WTCCC, 12,931 cases and 57,196 controls).
*Replication Meta-Cohort (UK10K imputation + InterAct + Danish Cohort (case control and follow-up) + Partners Biobank + UK Biobank (18,370 cases and 88,283 controls older than 55 years and OGTI > 7.8 mmol l^{-1}, when available).
were annotated as altering protein sequences, according to VEP. This resulted in 15 coding variants that were meta-analyzed with exome array and whole-exome sequencing data from a total of ~97,000 individuals6 after excluding the overlapping cohorts between the different data sets. This analysis highlighted a novel genome-wide association driven by a low-frequency missense variant (Ser58Phe) within the EHMT2 gene at chromosome 6p21.33 (rs115884658, OR = 1.21, 95% CI 1.14-1.29, p = 3.00 × 10^{-10}; Fig. 2, Supplementary Figures 6 and 7). EHMT2 is involved in the mediation of FOXO1 translocation induced by insulin36. Since this variant is less than 1 Mb away from HLA-DQA1, a locus reported to be associated with T2D37, we performed a series of reciprocal conditional analyses and excluded the possibility that our analysis was capturing previously reported T2D8,37 or T1D38-40 signals (Supplementary Data 11). Beyond this missense EHMT2 variant, other low-frequency variants within the corresponding credible set may also be causal. For example, rs115333512 (r^2 with lead variant = 0.28) is associated with the expression of CLIC1 in several tissues according to GTEx (multitissue meta-analysis p = 8.9 × 10^{-16}, Supplementary Data 9). In addition, this same variant is associated with the expression of the first and second exon of the CLIC1 mRNA in pancreatic islet donors (p(exon 1) = 1.4 × 10^{-19}, p(exon 2) = 1.9 × 10^{-13}, Supplementary Data 10). Interestingly, CLIC1 has been reported as a direct target of metformin by mediating the antiangirotrophic effect of this drug in human glioblastoma41. All these findings support CLIC1, as an additional possible effector transcript, likely driven by rs115333512. A novel rare X chromosome variant associated with T2D. Similar to other complex diseases, the majority of published large-scale T2D GWAS studies have omitted the analysis of the X chromosome, with the notable exception of the identification of a T2D-associated region near the DUSP9 gene in 201042. To fill this gap, we tested the X chromosome genetic variation for association with T2D. To account for heterogeneity of the effects and for the differences in imputation performance between males and females, the association was stratified by sex and tested separately, and then meta-analyzed. This analysis was able to replicate the DUSP9 locus, not only through the known rs5945326 variant (OR = 1.15, p = 0.049), but also through a three-nucleotide deletion located within a region with several promoter marks in liver (rs61503151 [GCCA/G], OR = 1.29, 95% CI 1.21-1.33, p = 3.5 × 10^{-4}), and in high LD with the first reported variant (r^2 = 0.62). Conditional analyses showed that the originally reported variant was no longer significant (OR = 1.01, p = 0.94) when conditioning on the newly identified variant, rs61503151. On the other hand, when conditioning on the previously reported variant, rs5945326, the effect of the newly identified INDEL remained significant and with a larger effect size (OR = 1.33, p = 0.003), placing this deletion, as a more likely candidate causal variant for this locus (Supplementary Data 14). In addition, we identified a novel genome-wide significant signal in males at the Xq23 locus driven by a rare variant (rs146662075, MAF = 0.008, OR = 2.94 [2.00-4.31], p = 3.5 × 10^{-5}; Fig. 3a). Two other variants in LD with the top variant, rs139246371 (chrX:115329804, OR = 1.65, p = 3.5 × 10^{-5}, r^2 =
0.37 with the top variant) and rs6603744 (chrX:115823966, OR = 1.28, \( p = 1.7 \times 10^{-4} \), \( r^2 = 0.1 \) with the top variant), comprised the 99% credible set and supported the association. We tested in detail the accuracy of the imputation for the rs146662075 variant by comparing the imputed results from the same individuals genotyped by two different platforms (Methods) and found that the imputation was highly accurate in males only when using UK10K, but not in females, nor when using 1000G (\( R^2_{[UK10K,males]} = 0.94 \), \( R^2_{[UK10K,females]} = 0.66 \), \( R^2_{[1000G,males]} = 0.62 \), and \( R^2_{[1000G,females]} = 0.43 \); Supplementary Fig. 8). Whether this association is specific to men, or whether it also affects female carriers, remains to be clarified with datasets that allow accurate imputation on females, or with direct genotyping or sequencing.

To further validate and replicate this association, we next analyzed four independent data sets (SIGMA, INTERACT, Partners Biobank, and UK Biobank), by performing imputation with the UK10K reference panel. In addition, a fifth cohort was genotyped de novo for the rs146662075 variant in several Danish sample sets. The initial meta-analysis, including the five replication data sets did not reach genome-wide significance (OR = 1.57, \( p = 1.2 \times 10^{-5} \); Supplementary Fig. 9A), and revealed a strong degree of heterogeneity (heterogeneity \( p_{het} = 0.004 \), which appeared to be driven by the replication cohorts.

As a complementary replication analysis, within one of the case-control studies, there was a nested prospective cohort study, the Intergenetic study, which consisted of 1,652 non-diabetic male subjects genotyped for rs146662075, of which 158 developed T2D after 11 years of follow-up. Analysis of incident diabetes in this cohort confirmed the association with the same allele, as previously seen in the case-control studies, with carriers of the rare T allele having increased risk of developing incident diabetes, compared to the C carriers (Cox-proportional hazards ratio (HR) = 3.17 [1.3–7.7], \( p = 0.011 \), Fig. 3b). Nearly 30% of carriers of the T risk allele developed incident T2D during 11 years of follow-up, compared to only 10% of noncarriers.

To understand the strong degree of heterogeneity observed after adding the replication datasets, we compared the clinical and demographic characteristics of the discovery and replication cohorts, and found that the majority of the replication datasets contained control subjects that were significantly younger than 55 years, the average age at the onset of T2D reported in this study and in Caucasian populations. This was particularly clear for the Danish cohort (age controls [95%CI] = 46.9 [46.6–47.2] vs. age cases [95%CI] = 60.7 [60.4–61.0]) and for INTERACT (age controls [95%CI] = 51.7 [51.4–52.1] vs. age cases [95%CI] = 54.8 [54.6–55.1]; Supplementary Fig. 10). Given the supporting results, from mouse myoblast cell lines, differentiated myotubes, and human fetal muscle cell line, revealed sequence-specific binding activity of the C allele (Fig. 4b).

Our study complemented other efforts that also aim at unraveling the genetics behind T2D through the generation of new

### Allele-specific enhancer activity of the rs146662075 variant.

We next explored the possible molecular mechanism behind this association, by using different genomic resources and experimental approaches. The credible set of this region contained three variants, with the leading SNP alone (rs146662075), showing 78% posterior probability of being causal (Supplementary Fig. 7, Supplementary Data 5), as well as the highest CADD (scaled C-score = 15.68; Supplementary Data 8), and LINSIGHT score (Supplementary Data 9). rs146662075 lies within a chromosomal region enriched in regulatory (DNase I) and active enhancer (H3K27ac) marks, between the AGTR2 (at 103 kb) and the SLC6A14 (at 150 kb) genes. The closest gene AGTR2, which encodes for the angiotensin II receptor type 2, has been previously associated with insulin secretion and resistance.

From the analysis of available epigenomic data sets, we found no evidences of H3K27ac or other enhancer regulatory marks in human pancreatic islets; whereas a significant association was observed between the presence of H3K27ac enhancer marks and the expression of AGTR2 across multiple tissues (Fisher test \( p = 4.45 \times 10^{-5} \), showing the highest signal of both H3K27ac and AGTR2 RNA-seq expression, but not with other genes from the same topologically associated domain (TAD), in fetal muscle (Fig. 4a; Supplementary Figure 11). We next studied whether the region encompassing the rs146662075 variant could act as a transcriptional enhancer and whether its activity was allele-specific. For this, we linked the DNA region with either the T (risk) or the C (non-risk) allele, to a minimal promoter and performed luciferase assays in a mouse myoblast cell line. The luciferase analysis showed an average 4.4-fold increased activity for the disease-associated T allele, compared to the expression measured with the common C allele, suggesting an activating function of the T allele, or a repressive function of the C allele (Fig. 4b). Consistent with these findings, electrophoretic mobility shift assays using nuclear protein extracts from mouse myoblast cell lines, differentiated myotubes, and human fetal muscle cell line, revealed sequence-specific binding activity of the C allele, but not the rare T allele (Fig. 4c).

Our study complemented other efforts that also aim at unraveling the genetics behind T2D through the generation of new
**Fig. 3** Discovery and replication of rs14666075 association signal. 

**a** Forest plot of the discovery of rs146662075 variant. Cohort-specific odds ratios are denoted by boxes proportional to the size of the cohort and 95% CI error bars. The combined OR estimated for all the data sets is represented by a diamond, where the diamond width corresponds to 95% CI bounds. The p-value for the meta-analysis (Meta P) and for the heterogeneity (Het P) of odds ratio is shown.

**b** Kaplan–Meier plot showing the cumulative incidence of T2D for a 11 years follow-up. The red line represents the T carriers and in light blue, C carriers are represented (n = 1,652, cases = 158). 

**c** Forest plot after excluding controls younger than 55 years, OGTT > 7.8 mmol l⁻¹, and controls with family history of T2D in both the discovery and replication cohorts when available.
genetic data. For example, we provided for the first time a comprehensive coverage of structural variants, which point to previously unobserved candidate causal variants in known and novel loci, as well as a comprehensive coverage of the X chromosome through sequence-based imputation.

This study also highlights the importance of a strict classification of both cases and controls, in order to identify rare variants associated with disease. Our initial discovery of the Xq23 locus was only replicated when the control group was restricted to T2D-free individuals who were older than 55 years (average age...
at the onset of T2D), had normal glucose tolerance, and no family history of T2D. This is in line with previous results obtained for a T2D population-specific variant found in Inuit within the TBC1D4 gene, which was only significant when using OGTT as criteria for classifying cases and controls, but not when using HbA1c. Our observation that 30% of the rs146662075-C risk allele carriers developed T2D over 11 years of follow-up, compared to 10% of noncarriers, further supports the association of this variant and suggests that an early identification of these subjects through genotyping may be useful to tailor pharmacological or lifestyle intervention to prevent or delay the onset of T2D.

Using binding and gene-reporter analyses, we demonstrated a functional role of this variant and proposed a possible mechanism behind the pathophysiology of T2D in T risk allele carriers, in which this rare variant could favor a gain of function of AGTR2, previously associated with insulin resistance. AGTR2 appears, therefore, as a potential therapeutic target for this disease, which would be in line with previous studies showing that the blockade of the renin-angiotensin system in mice and in humans presents therapeutic effects of T2D, and T scores.

Overall, beyond our significant contribution toward expanding the number of genetic associations with T2D, our study also highlights the potential of the reanalysis of public data, as a complement to large studies that use newly generated data. This study informs the open debate in favor of data sharing and democratization initiatives, for investigating the genetics and pathophysiology of complex diseases, which may lead to new preventive and therapeutic applications.

**Methods**

**Quality filtering for imputed variants.** In order to assess genotype imputation quality and to determine an accurate post-imputation quality filter, we made use of the Wellcome Trust Case Control Consortium (WTCCC) data available through the European Genotype Archive (EGA, https://www.ebi.ac.uk/ega/studies/EGAS000000000028). The genotyping data and the subjects included in the following tests were filtered according to the guidelines provided by the WTCCC, whose criteria of exclusion are in line with standard quality filters for GWAS. We used the 1958 British Birth cohort (~3,000 samples, 58C) that was genotyped by Affymetrix 6.0 and Illumina IL chips. After applying the quality filtering criteria, 2,706 and 2,699 subjects from the Affymetrix and Illumina platforms, respectively, were available for the 58C samples, leaving an intersection of 2,509 individuals genotyped by both platforms. After variant quality filtering and excluding all the variants with minor allele frequency (MAF) below 0.01, 717,556, and 892,516 variants remained for 58C Affymetrix and Illumina platforms, respectively.

We used a two-step genotype imputation approach based on prephasing the study genotypes into full haplotypes with SHAPEIT to ameliorate the computational burden required for genotype imputation through IMPUTE2. We used the GTOOL software (http://www.well.ox.ac.uk/~freeman/software/gwas/gtool.html, version 0.7.5) to homogenize strand annotation by merging the imputed results obtained from each set of genotyped data. To ensure that there were no strand orientation issues, we excluded all C/G and A/T SNPs. To perform genotype imputation, we used two sequence-based reference panels: the 1000G Phase1 (June 2014) release and the UK10K.

We evaluated genotype imputation for each reference panel considering 2,509 58C individuals that were genotyped by both independent genotyping platforms. Four scenarios were considered: (a) fraction of variants originally genotyped (GT) by both Illumina (IL) and Affymetrix (Affy) platforms (both GT), (b) variants genotyped by Affy, but not present in IL array (Affy GT), (c) variants genotyped by IL, but not present in the Affy array (IL GT), and (d) variants not typed in IL nor in the Affy arrays, and therefore, imputed from IL and Affy data sets (d). This last scenario comprised the largest fraction of variants.

As the individuals typed (and imputed) using Affy and IL SNPs as backbones were the same, we expected no statistical differences when comparing the allele and genotype frequencies with any of the variants. The quality of the imputed variants was evaluated using the allelic dosage $R^2$ correlation coefficient, between the genotype dosages estimated when imputing using Affy or IL as the backbone. The Affy GT and IL GT SNPs were used to evaluate the correspondence between the allelic dosage $R^2$ scores and the IMPUTE2 INFO scores for the imputed genotypes. The linear model, between the allelic dosage $R^2$ and the IMPUTE2 INFO, was used to set an info score threshold of 0.7, which corresponds to an allelic dosage $R^2$ of 0.5. The correlation between $R^2$ and INFO score was uniform across all reference panels and platforms.

**The 70KforT2D resource.** We collected genetic individual-level data for T2D case/control studies from five independent datasets, Gene Environment Association Studies initiative [GENEVA], Wellcome Trust Case Control Consortium [WTCCC], Finland–United States Investigation of NIDDM Genetics [FUSION], Resource for Genetic Epidemiology Research on Aging [GERA], and the Northwestern NUgene project [NuGENE] publicly available in the dbGaP (http://www.ncbi.nlm.nih.gov/gap) and EGA (https://www.ebi.ac.uk/ega/home) public repositories, comprising a total of 13,201 cases and 59,656 controls (for the description of each cohort, see Supplementary Note 1 and Supplementary Data 1).

Each dataset was independently harmonized and quality controlled with a three-step protocol, including two stages of SNP removal and an intermediate stage of sample exclusion. The exclusion criterion for variants were (i) missing call rate $\geq 0.05$, (ii) significant deviation from Hardy–Weinberg equilibrium (HWE) $p \leq 1 \times 10^{-6}$ for controls and $p \leq 1 \times 10^{-7}$ for the entire cohort, (iii) significant differences in the proportion of missingness between cases and controls $p \leq 1 \times 10^{-7}$, and (iv) MAF $< 0.01$ (for the GERA cohort, we considered a MAF of 0.001). The exclusion criteria for samples were i) genotype quality scores were not imputed from IL and Affy arrays, ii) variants were not typed in IL and Affy arrays, iii) variants were not typed in both platforms. We removed the individuals with the highest proportion of missingness, (iii) missing call rates per sample $\geq 0.02$, and (iv) population structure showing more than four standard deviations within the distribution of the study population according to the first four principal components.

We performed genotype imputation independently for each cohort by prephasing the genotypes to whole haplotypes with SHAPEIT2 and then, we performed genotype imputation with IMPUTE2. We tested for association with additive logistic regression using SNPTAST, seven derived principal component sets with body-mass index as covariate, and except for WTCCC and Affy datasets, they were not available (Supplementary Data 1). To maximize power and accuracy, we combined the association results from 1000G Phase1 integrated haplotypes (June, 2014) and UK10K (http://www.uk10k.org/) reference panels by choosing for each variant, the reference panel that provided the best IMPUTE2 info score. For 1000G-based genotype imputation in chromosome X (chrX), we used the V3. macGT1 release (August, 2012). For chrX, we restricted the analysis to non-pseudoautosomal (non-PAR) regions and stratified the association analysis by sex to account for hemizygosity for males, while for females, we followed an autosomal model. Also, we did not apply HWE filtering in the X chromosome variants.

Finally, for the GERA cohort due to the large computational burden that comprises the whole genotype imputation process in such a large sample size, we randomly split this cohort into two homogeneous subsets of ~30,000 individuals each, in order to minimize the memory requirements.

We included variants with IMPUTE2 info score $\geq 0.7$, MAF $\geq 0.01$, and for nonpandemic variants, HWE controls $p > 1 \times 10^{-5}$. Further details about genotype imputation and covariate information used in association testing are summarized in Supplementary Data 1.

**70KforT2D and inclusion of previous summary statistics data.** We meta-analyzed the different sets from the 70KforT2D data set with METAL, using the inverse variance-weighted fixed effect model. We included variants with $I^2$ heterogeneity $< 75$. This filter was not applied to the final X chromosome data set, after meta-analyzing the results from males and females separately (which were already filtered by $I^2 < 75$).

For the meta-analysis with the DIAGRAM trans-ethnic study, we excluded from the whole 70KforT2D datasets those cohorts that overlapped with the DIAGRAM data. Therefore, we meta-analyzed the GERA and NuGENE cohorts (75,446 and 59,446 controls), the 70KforT2D datasets, and the EuroCGP cohorts. The 70KforT2D cohort was also combined with the neutral and ethnic summary statistics results. As standard errors were not provided for the
DIAGRAM trans-ethnic meta-analysis, we performed a sample size based meta-analysis, which converts the direction of the effect and the p-value into a Z-score. In addition, we also performed an inverse variance-weighted fixed effect meta-analysis to estimate the final effect sizes. This approach required the estimation of the beta and standard errors from the summary statistics (p-value and odds ratio).

For the meta-analysis of coding low-frequency variants with the Type 2 Diabetes Knowledge Portal (T2D Portal),7 we included the 70KorfT2D data set the NuGENE and GERA cohorts (7,522 cases and 50,446 controls), to avoid overlapping samples. Like in the previous scenario, standard errors were not provided for the T2D Portal data and we used a sample size based meta-analysis with METAL. However, to estimate the effect sizes, we also calculated the standard errors from the p-values and odds ratios, and we performed an inverse variance-weighted fixed effect meta-analysis.

See further details about the cohorts in Supplementary Note 1.

Pathway and enrichment analysis. Summary statistics that resulted from the 70KorfT2D meta-analysis were analyzed by Data-driven Expression-Prioritized Integration for Complex Traits (DEPICT)10 to prioritize likely causal genes, to highlight enriched pathways, and to identify the most relevant tissues/cell types. DEPICT relies on publicly available gene sets (including molecular pathways) and leverages gene expression data from 77,840 gene expression arrays, to perform gene prioritization and gene-set enrichment based on predicted gene function and the so-called reconstituted gene sets. A reconstituted gene set contains a membership probability for each gene and conversely, each gene is functionally characterized by its membership across 14,461 reconstituted gene sets. As input to DEPICT, we used all summary statistics from autosomal variants with p < 1 × 10−5 in the 70KorfT2D meta-analysis. We used an updated version of DEPICT, which handled 1000G Phase1-integrated haplotypes (June 2014, www.broadinstitute.org/depict). DEPICT was run using 3,412 associated SNPs (p < 1 × 10−7), from which we identified independent SNPs using PLINK and the following parameters: --clump-p1 5e-8, --clump-p2 1e-5, --clump-r2 0.6, and --clump-kb 250. We used LD r2 ≥ 0.5 distance to define locus limits yielding 70 autosomal loci comprising 119 genes (note that this is not the same locus definition that we used elsewhere in the text). We ran DEPICT with default settings, i.e., using 500 permutations to adjust for bias to estimate false discovery rate (FDR). We tested normalized expression data from 77,840 Affymetrix microarrays to reconstitute gene sets. The resulting 14,461 reconstituted gene sets were tested for enrichment analysis. A total of 209 tissue or cell type expression data sets assembled from 37,427 Affymetrix U133 Plus 2.0 Array samples were used for enrichment in tissue/cell type expression data and 18 different discovery factors (FDR). We used normalized expression data from 77,840 Affymetrix microarrays to locate expression data for 119 genes. To find the fine limits of each gene, we used the coordinates of variants within 99% credible sets and the corresponding alleles, as described in Supplementary Data8. We also used the LINSIGHT score to prioritize functional variants, which are defined as those with a p-value ≤ 0.04. The LINSIGHT score represents the sum of all the fine limits of each gene, as described in Supplementary Data8. We also used the LINSIGHT score to prioritize functional variants, which are defined as those with a p-value ≤ 0.04. The LINSIGHT score represents the sum of all the fine limits of each gene, as described in Supplementary Data8.

Characterization of indels. We examined whether indels from the 99% credible sets were present or absent in the 1000G Phase1 or UK10K reference panels, and also checked whether they were present or not in the 1000G Phase3 reference panel. All the information has been summarized in Supplementary Data 6. We also visualized the aligned reads from the most variant indels from both projects to discard that they could be alignment artifacts.

Functional annotation of the 99% credible set variants. To determine the effect of 99% credible set variants on genes, transcripts, and protein sequence, we used the variant effect predictor (VEP, GRCh37.p13 assembly)13. The VEP application determines the effect of variants (SNPs, insertions, deletions, CNVs, or structural variants) on genes, transcripts, proteins, and regulatory regions. We used as input the coordinates of variants within 99% credible sets and the corresponding alleles, to find out the affected genes and RefSeq transcripts and the consequence on the protein sequence by using the GRCh37.p13 assembly. We also manually checked all these annotations with the Ensembl Aggregation Consortium data set (EnAAG, http://exac.broadinstitute.org) and the most updated VEP server based on the GRCh38.p7 assembly. All these annotations are provided in Supplementary Data 7.

We used combined annotation-dependent depletion (CADD) scoring function to prioritize functional, deleterious, and disease causal variants. We obtained the scaled C-score (PHRED-like scaled C-score ranking each variant with respect to all possible substitutions of the human genome) metric for each 99% credible set variant, as it has been shown to distinguish causal variants within individual genome sequences14 (Supplementary Data 8). We also used the LINSIGHT score to prioritize functional variants, which measures the probability of negative selection on noncoding sites by combining a generalized linear model for functional genomic data with a probabilistic model of molecular evolution.15 For each credible set variant, we retrieved the precomputed LINSIGHT score at that particular nucleotide site, as well as the mean LINSIGHT precomputed score for a region of 20 bp centered on each credible set variant, respectively (https://github.com/CshlSiepelLab/LINSIGHT). These metrics are summarized in Supplementary Data 9.

In order to prioritize functional regulatory variants, we used the V6 release from the GTEx data that provides gene-level expression quantifications and eQTLs based on the annotation with GENCODE v19. This release included 450 genotyped donors, 8,555 RNA-seq samples across 51 tissues, and two cell lines, which led to the identification of eQTLs across 44 tissues16. Moreover, RNA-seq data from human pancreatic islets from 89 deceased donors cataloged as eQTLs and exon use (sQTL) were also integrated with the GWAS data to prioritize candidate regulatory variants17 but in pancreatic islets, which is a target tissue for T2D. Both analyses are summarized in Supplementary Data 10 and Supplementary Data 11, respectively.

Conditional analysis. To confirm the independence between novel loci and previously known T2D signals, we performed reciprocal conditional analyses (Supplementary Data 5, Supplementary Data 12, Supplementary Data 13, and Supplementary Data 14). We included the conditioning SNP as a covariate in the
logistic regression model, assuming that every residual signal that arises corresponds to a secondary signal independent from this conditioning SNP. We applied this approach to the E13 T2D locus (less than 1MB away from the T2D and T1D signal have been identified), to confirm that this association was independent of previously reported T2D signals and also to discard that this association is also driven by possible contamination of T1D diagnosed as T2D cases. We conditioned on the variant top identified in this study and the top variant from the 99% credible set analysis, but also on the top variants previously described for T2D and T1D.38–40. For this purpose, we used the full 70KforT2D resource (NuGENE, GERA, FUSION, GENEA, and WTCCC cohorts imputed with 1000G and UK10K reference panels). Finally, all the results were meta-analyzed as explained in previous sections. These analyses are provided in Supplementary Data 13. This approach was also applied to confirm that the novel CAMKK2 signal at rs3794205 is independent of known T2D signals at the HNF1A locus (rs169288, rs1800574, and chr12:121440833D)34, which is summarized in Supplementary Data 12.

Moreover, this approach confirmed known secondary signals in the 9p21 locus45 which allowed us to build 99% credible sets based on the results from the conditional analyses (included in Supplementary Data 5), and allowed us to identify the most likely causal variant for the DUSP9 locus (Supplementary Data 14).

Replication of the rare variant association at Xq23. To replicate the association of the rs146662075 variant, we performed genotype imputation with the UK10K reference panel in four independent data sets: the InterAct case-cohort study43, the European Health Care Professionals Partners (InterAct) study44, and the UK Biobank cohort45. Phasing was performed with SHAPEIT2 and the IMPUTE2 software was used for genotype imputation.

The current UK Biobank data release did not contain imputed data for the X chromosome, for which phasing and imputation had to be analyzed in-house. The data released covered the X chromosome markers of 488,243 participants, which were assayed using two arrays sharing 95% of marker content (Applied Biosystems™ UK BiLEVE Axion™ Array and the Applied Biosystems™ UK Biobank Axion™ Array). We included samples and markers that were used as input for phasing by UK Biobank investigators. At the sample level, we excluded individuals, who were phasing and association were not available and showed missing call rate > 5%. This gender discordance between the reported and the genetically predicted sex. At the variant level, we excluded markers with MAF < 0.1% and with missing call rate > 5%. The final set of 16,463 X chromosome markers and 222,725 male individuals was split into six subsets due to the huge computational burden that would require phasing the entire cohort. Therefore, the overall meta-analysis was excluded to included individuals with MAF < 1%, and variants showing deviation of Hardy–Weinberg equilibrium with p < 1 × 10−20 before the imputation step. In addition, from those pairs of relatives reported to be third degree or higher according to UK Biobank, we excluded from each pair the individual with the lowest call rate. We then tested the rs146662075 variant for association with type 2 diabetes using SNPTESTv2.5.1 and the threshold method. To avoid contamination from other types of diabetes mellitus, we excluded from the entire sample data set, individuals with ICD10 codes falling in any of these categories: E10 (insulin-dependent diabetes mellitus), E13 (other specified diabetes mellitus), and E14 (unspecified diabetes mellitus). Then, we excluded those individuals with E11 (non-insulin dependent diabetes mellitus) ICD10 codes, and the rest as controls. Moreover, we only kept as control subjects those individuals without reported family history of diabetes mellitus and older than 55 years, which is the average age at the onset of T2D.

We also genotyped de novo the rs146662075 variant with KASPar SNP genotyping system (LGCG Genomics, Hoddesdon, UK) in the Danish cohort, which comprises data from five sample sets (Supplementary Note 2 also for the genotyping and QC analysis for this variant).

We used Cox-proportional hazard regression models to assess the association of the variant with the risk of incident T2D in 1,652 nondiabetic male subjects (Experiments) and the human myoblast cell line (ATCC CRL-1772) were obtained as described before.89 Double stranded oligonucleotides containing either the common or rare variants of rs146662075 were labeled using dCTP and the GK® (New England BioLabs). Findings were confirmed by repeating binding assays on separate days.

In silico functional characterization of rs146662075. This variant is located in an intergenic region, flanked by AGTR2 and SLC6A14 genes, and within several DNase I hypersensitive sites. We searched for regulatory marks (i.e., H3K4me1 and H3K27ac marks) through the HaploReg web server (http://archive.broadinstitute.org/mammals/haploreg/haploreg.php), in order to assess which type of regulatory element was associated with the rs146662075 variant.

To further evaluate the putative regulatory role of rs146662075, we used the WashU Epigenome Browser (http://epigenomegateway.wustl.edu/browser/), last access on June 2016). We used the following public data hubs: (1) the reference human epigenomes from the Roadmap Epigenomics Consortium track hubs and (2) the Roadmap Epigenomics Integrative Analysis Hub. The data were released as described above.34,35 RNAsig was used to evaluate whether gene expression of any of the closest genes (AGTR2 and SLC6A14 genes, fixed scale at 80 RPMK) correlated with the presence of the H3K27ac enhancer marks (a more strict mark for active enhancers in contrast with H3K4me1, which we highlighted by the HaploReg search) at the rs146662075 location. For visualizing the H3K27ac marks around rs146662075, we focused on a region of 8 kb and we used a fixed scale at 40−log10 Poisson p-value of the counts relative to the expected background counts (i.e., background).

The NIH Roadmap Epigenomics Consortium data from standardized epigenomes also allowed us to further interrogate which target gene within the same topologically associating domain (TAD) was more likely to be regulated by this rs146662075 enhancer. We used H3K27ac narrow peaks from 59 tissues called using MACS2 with a p-value threshold of 0.01 from 98 consolidated epigenomes to seek for enhancer marks in a given tissue (the presence of H3K27ac peak). To assess gene expression for any of the putative target genes within TAD, we used the RPMK expression matrix for 57 consolidated epigenomes (https://www.epigenencode.org/). With this, we were able to test for each of the genes, the association between gene expression and enhancer activity in 31 tissues with a Fisher’s exact test.
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