DNA Sequence Variation in *ACVR1C* Encoding the Activin Receptor-Like Kinase 7 Influences Body Fat Distribution and Protects Against Type 2 Diabetes

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GENETICS/GENOMES/PROTEOMICS/METABOLOMICS

A genetic predisposition to higher waist-to-hip ratio adjusted for BMI (WHRadjBMI), a measure of body fat distribution, associates with increased risk for type 2 diabetes. We conducted an exome-wide association study of coding variation in UK Biobank (405,569 individuals) to identify variants that lower WHRadjBMI and protect against type 2 diabetes. We identified four variants in the gene *ACVR1C* (encoding the activin receptor-like kinase 7 receptor expressed on adipocytes and pancreatic β-cells), which independently associated with reduced WHRadjBMI: Asn150His (-0.09 SD, $P = 3.4 \times 10^{-17}$), Ile195Thr (-0.15 SD, $P = 1.0 \times 10^{-9}$), Ile482Val (-0.019 SD, $P = 1.6 \times 10^{-5}$), and rs72927479 (-0.035 SD, $P = 2.6 \times 10^{-12}$). Carriers of these variants exhibited reduced percent abdominal fat in DEXA imaging. Pooling across all four variants, a 0.2 SD decrease in WHRadjBMI through *ACVR1C* was associated with a 30% lower risk of type 2 diabetes (odds ratio [OR] 0.70, 95% CI 0.63, 0.77; $P = 5.6 \times 10^{-13}$). In an analysis of exome sequences from 55,516 individuals, carriers of predicted damaging variants in *ACVR1C* were at 54% lower risk of type 2 diabetes (OR 0.46, 95% CI 0.27, 0.81; $P = 0.006$). These findings indicate that variants predicted to lead to loss of *ACVR1C* gene function influence body fat distribution and protect from type 2 diabetes.

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Discovery of genetic variants that protect against disease can identify novel mechanisms of disease and novel therapeutic targets (1). For example, the discovery of low-frequency coding variants in *PCSK9*, *ANGPTL3*, and *APOC3* that lower blood lipid levels and protect against coronary artery disease catalyzed the development of novel therapeutics for coronary artery disease (2–10). *PCSK9* inhibitors are now approved for treatment of coronary artery disease (4), while inhibitors of *ANGPTL3* (7) and *APOC3* (11) are in clinical development.

Body fat distribution strongly influences the development of type 2 diabetes (12–14). In a Mendelian randomization study of 296,291 individuals, we previously found that a genetic predisposition to increased abdominal fat distribution was associated with elevated triglyceride levels, elevated blood pressure, and an increased risk of coronary artery disease, independent of overall adiposity (12). Furthermore, a genetic predisposition to increased abdominal fat distribution was strongly associated with the development of type 2 diabetes. For each 1 SD genetic increase in waist-to-hip ratio adjusted for BMI (WHRadjBMI) (a measure of body fat distribution), risk of type 2 diabetes increased by 77% (12). These findings were replicated in a separate Mendelian randomization study (14).

These results suggest the hypothesis that genetic variants that influence body fat distribution may also influence the risk of type 2 diabetes (12). Here, we test this hypothesis by analyzing genetic variation in more than 400,000 individuals in UK Biobank to identify novel genetic variants that lower WHRadjBMI and protect against type 2 diabetes. Below, we demonstrate that variants predicted to lead to loss of function of the gene *ACVR1C*, which encodes the activin receptor-like kinase 7 (ALK7), influence body fat distribution and protect against type 2 diabetes.

RESEARCH DESIGN AND METHODS

Study Design
In our discovery analysis, we analyzed the association of 614,042 coding variants with WHRadjBMI in 405,569 individuals in UK Biobank. Coding variants were defined as missense variants or variants predicted to result in loss of function of the protein: *1*) nonsense mutations that resulted in early termination of a protein, *2*) frameshift mutations due to insertions or deletions of DNA, or *2*) splice-site mutations that result in an incorrectly spliced protein. Only variants imputed with a quality score (info score) >0.3 were analyzed. Threshold for significance was defined as $P < 5 \times 10^{-8}$ (genome-wide significance), and analysis was performed using PLINK2 software (15). We reported novel variants as those located more than one megabase away from previously identified loci in the Genetic Investigation of ANthropometric Traits (GIANT) Consortium (16). We reported variants located outside of the MHC locus separately from those within the MHC locus, as variants within the MHC locus typically tag HLA

risk alleles and are thus associated with phenotypes due to linkage disequilibrium with HLA alleles (17). We attempted to replicate the association of novel variants with WHRadjBMI using data from the GIANT Consortium, when the variant was available in the GIANT Consortium (16).

Upon identification of variants in *ACVR1C* as significantly associated with WHRadjBMI, a conditional analysis was conducted to identify additional variants significantly associated ($P < 0.0001$) with WHRadjBMI within the *ACVR1C* locus (± 250 kb of the lead variant rs55920843). To replicate observed associations of *ACVR1C* variants with WHRadjBMI, we examined whether carriers of these variants had reduced WHRadjBMI in a meta-analysis of the GIANT Consortium and two independent cohorts (Atherosclerosis Risk in Communities [ARIC] and Framingham Heart Study). We also examined whether these variants were associated with direct imaging-based measurements of abdominal fat in 4,215 participants who underwent DEXA imaging in UK Biobank.

To test whether identified *ACVR1C* variants were also associated with risk of type 2 diabetes, we pooled data from the DIAbetes Genetics Replication And Meta-analysis (DIAGRAM) Consortium (ExTexT2D exome chip analysis [18]) with UK Biobank. To test whether variation leading to loss of *ACVR1C* function protects against type 2 diabetes, we analyzed the sequences of the nine exons of *ACVR1C* in 55,516 participants (31,672 from the Myocardial Infarction Genetics Consortium [MIGen] [19,20], 5,388 from the ARIC study, and 18,456 from the Type 2 Diabetes Genetic Exploration by Next-generation sequencing in multi-Ethnic Samples [T2D-GENES] Consortium [21]) and examined whether predicted damaging variants in the gene associate with risk of type 2 diabetes.

A phenome-wide association study of *ACVR1C* in UK Biobank was performed using an *ACVR1C* gene risk score (22). Definitions for 31 different diseases analyzed in the phenome-wide association study are provided (Supplementary Table 1). Three metabolic traits available in UK Biobank (urinary albumin-to-creatinine ratio, systolic blood pressure, and diastolic blood pressure) were also analyzed. A *P* value of 0.001 (0.05/34) was used for significance in this analysis.

Data Sources
For the analysis of WHRadjBMI, individual-level data from 405,569 unrelated individuals from the UK Biobank (335,660 individuals of European ancestry and 69,909 individuals of non-European ancestry) were analyzed. UK Biobank received ethical approval from the Research Ethics Committee (reference number 11/NW/0382). Analysis of UK Biobank was approved by the Partners Health Care Institutional Review Board (protocol 2013P001840). Informed consent was obtained from all participants by UK Biobank. For replication, data for WHRadjBMI from the GIANT Consortium (in which the Ile482Val variant was available) were pooled with data from the ARIC and

Framingham Heart Study data sets (in which Asn150His, Ile195Thr, and rs72927479 variants were available). The GIANT Consortium consisted of 224,459 participants (210,088 of European ancestry and 14,371 of non-European ancestry) genotyped using the MetaboChip (16). The ARIC study is a community-based study of 15,792 white and black participants, aged 45 to 64 years (23). The ARIC data set consisted of 10,122 individuals (8,015 of European ancestry and 2,107 of non-European ancestry) who were genotyped and imputed, as previously described (24). For 5,388 participants, exome sequences were also available for analysis. In the Framingham Heart Study, a community–based study of 10,092 individuals of predominantly European ancestry, genotyped data were available from 6,073 individuals of European ancestry.

For the analysis of type 2 diabetes, estimates from UK Biobank were pooled using inverse variance–weighted fixed-effects meta-analysis with estimates from the DIA-GRAM ExTexT2D exome chip analysis of 452,244 participants (81,412 case subjects with diabetes and 370,832 control subjects) (18). In UK Biobank, type 2 diabetes was defined as 1) self-report of type 2 diabetes, followed by a verbal interview with a trained nurse to confirm the diagnosis, or 2) hospitalization for ICD code E11. Because the ExTexT2D analysis included 120,286 participants from UK Biobank (18), these individuals were excluded from the analysis of type 2 diabetes in UK Biobank to prevent analysis of overlapping samples.

Sequence data for *ACVR1C* were extracted from exome sequencing performed in MIGen as previously described (19,20). The Burrows–Wheeler aligner algorithm was used to align reads from participants to the reference genome (hg19). The GATK HaplotypeCaller was used to jointly call variants. Metrics including variant quality score recalibration, quality over depth, and strand bias were then used to filter variants. The Jackson Heart Study (JHS) was excluded from analysis of MIGen, as it was included in the T2D-GENES Consortium. Exome sequences from 5,388 participants in ARIC were analyzed as previously described (25). Phenotype and genotype data were retrieved from the National Center for Biotechnology Information dbGaP server (accession phs000090.v3.p1 and phs000572.v6.p4). Exome sequencing was performed in the T2D-GENES Consortium as previously described (21). To analyze exome sequences from the T2D-GENES Consortium, the online Genetic Association Interactive Tool in the Type 2 Diabetes Knowledge Portal was used (21).

Studies included in MIGen were 1) the Italian Atherosclerosis, Thrombosis, and Vascular Biology (ATVB) study (dbGaP study accession phs000814.v1.p1); 2) the Exome Sequencing Project Early-Onset Myocardial Infarction (ESP-EOMI) study (9); 3) a nested case-control cohort from the JHS; 4) the South German Myocardial Infarction study (dbGaP study accession phs000916.v1.p1); 5) the Ottawa Heart Study (OHS) (dbGaP study accession phs000806.v1.p1); 6) the Precocious Coronary Artery Disease (PROCARDIS) study (dbGaP Study Accession phs000883.v1.p1) ; 7) the Pakistan Risk of Myocardial Infarction Study (PROMIS) (dbGaP study accession phs000917.v1.p1); 8) the Registre Gironí del COR (Gerona Heart Registry or REGICOR) study (dbGaP study accession phs000902.v1.p1); 9) the Leicester Myocardial Infarction study (dbGaP study accession phs001000.v1.p1); 10) the BioImage study (dbGaP study accession phs001058.v1.p1); and 11) the North German Myocardial Infarction study (dbGaP Study Accession phs000990.v1.p1).

Predicted damaging *ACVR1C* variants in the exome sequencing analysis were defined as those that resulted in loss of function of the protein (nonsense mutations that resulted in early termination of *ACVR1C*, frameshift mutations due to insertions or deletions of DNA, or splice-site mutations that result in an incorrectly spliced protein) or those labeled as damaging by each of five different algorithms (LRT score, MutationTaster, PolyPhen-2 HumDiv, PolyPhen-2 HumVar, and SIFT), as previously described (19,26). The Variant Effect Predictor algorithm was used to annotate predicted damaging variants (27).

Statistical Analysis

In UK Biobank, WHRadjBMI was derived through inverse normal transformation of waist-to-hip ratio after adjustment for age, sex, and BMI (as in the GIANT Consortium [16]). In UK Biobank, linear regression was used to estimate the association of variants with WHRadjBMI. All UK Biobank analyses included adjustment for age, sex, 10 principal components of ancestry, and a dummy variable for the array type used in genotyping. Logistic regression was used to estimate the association of variants with type 2 diabetes. Estimates of the association of each variant with type 2 diabetes in UK Biobank were pooled with estimates from the ExTexT2D Consortium using inverse variant–weighted fixed-effects meta-analysis.

In the primary analysis of 405,569 individuals for WHRadjBMI, we had 80% power to detect a minimum effect of 0.05 SD with a minor allele frequency of 5% at genome-wide significance ($P < 5 \times 10^{-8}$). In the primary analysis of 95,978 case subjects with type 2 diabetes and 646,985 control subjects, we had 80% power to detect a minimum odds ratio (OR) of 1.05 at $P < 5 \times 10^{-8}$. With a minor allele frequency of 1%, we had 80% power to detect a minimum effect of 0.1 SD for WHRadjBMI and an OR of 1.10 for type 2 diabetes at $P < 5 \times 10^{-8}$.

To estimate the overall association of variation in *ACVR1C* with WHRadjBMI, we pooled across all variants using a gene risk score, weighted by the square root of allele frequency (estimating a weighted mean effect of *ACVR1C* variants on WHRadjBMI) (28). To estimate the overall association of variation in *ACVR1C* with type 2 diabetes, we pooled across all variants in a gene risk score, weighted by the association of each variant with WHRadjBMI (29).

For analysis of exome sequencing data, logistic regression was performed with adjustment for sex, five principal components of ancestry, and a dummy variable for each

Table 1—Baseline characteristics of participants in UK Biobank

	All participants (N = 405,569)	Type 2 diabetes case subjects (N = 20,458)	Control subjects without diabetes (N = 385,111)
Age, years	57 ± 8.1	61 ± 6.9	57 ± 8.1
Female	218,376 (54)	7,801 (38)	210,575 (55)
UK BiLEVE array	48,625 (12.0)	3,097 (15)	45,528 (12)
BMI, kg/m²	27 ± 4.8	32 ± 5.9	27 ± 4.6
Waist-to-hip ratio	0.87 ± 0.09	0.95 ± 0.08	0.87 ± 0.09

Data are mean ± SD or n (%).

cohort to estimate the association of predicted damaging variants with type 2 diabetes. Estimates from MIGen were pooled with estimates from the T2D-GENES Consortium using inverse variance–weighted fixed-effects meta-analysis.

For the phenome-wide association study, all four *ACVR1C* variants were pooled in a gene risk score in UK Biobank, as previously described (25,30). For each individual in UK Biobank, the *ACVR1C* variants associated with lower WHRadjBMI were weighted by their effect on WHRadjBMI and summed. The association of this gene risk score with 31 different diseases in UK Biobank and three metabolic traits was tested using logistic regression with adjustment for age, sex, 10 principal components of ancestry, and a dummy variable for the array type used in genotyping. Although exploratory due to the low number of case subjects for certain diseases (e.g., 1,707 case subjects for cervical cancer), we conducted this analysis to detect possible adverse associations of *ACVR1C* with diseases that could allow for prediction of adverse effects of pharmacologic inhibition of *ACVR1C*.

Analyses were performed using R version 3.2.3 (R Project for Statistical Computing).

RESULTS

Exome-Wide Association Study of Body Fat Distribution in UK Biobank

Among 405,569 participants in UK Biobank, 54% were female, the median age was 57 years, and the median waist-to-hip ratio, measured at enrollment, was 0.87 (Table 1). One SD in waist-to-hip ratio corresponded to an absolute change of 0.09. In an analysis of 614,012 coding variants in UK Biobank, no evidence of genomic inflation was observed (λ 1.08) (Supplementary Fig. 1).

We identified 16 low-frequency variants (<5%) associated with WHRadjBMI outside of known loci (Supplementary Table 2) (16). We identified an additional 43 novel common variants (frequency >5%) associated with WHRadjBMI (Supplementary Table 3). We identified 94 independent variants in total, including variants at known loci (Supplementary Data). Of 59 novel coding variants, 34 variants were available in the GIANT Consortium for replication (16). A strong correlation in the effect sizes of the association of variants with WHRadjBMI in UK Biobank and GIANT was observed (R^2 = 0.87). A total of 24 variants were independently associated with

WHRadjBMI in GIANT ($P < 0.05$) (Supplementary Table 4). Of the 10 variants that were not significantly associated with WHRadjBMI in GIANT ($P > 0.05$), only 3 variants exhibited evidence of heterogeneity between estimates in UK Biobank and GIANT, with the remaining 7 variants showing similar estimates of association in UK Biobank and GIANT (although not reaching significance in GIANT) (Supplementary Table 4).

The lead novel low-frequency variant was a missense variant in *PNPLA2* (rs140201358, Asn252Lys) that associated with elevated WHRadjBMI (0.09 SD, $P = 3.2 \times 10^{-19}$). *PNPLA2* encodes adipocyte triglyceride lipase, which hydrolyzes triglycerides in adipose tissue to mobilize fat stores (31). Two low-frequency missense variants in *ABHD15*, which encodes alpha/beta hydrolase domain-containing protein 15, were found to be associated with elevated WHRadjBMI. *ABHD15* is also highly expressed in adipocytes and has been reported to mediate insulin-induced suppression of lipolysis in adipocytes (32). We also identified a low-frequency variant in a known locus (*CALCRL* Leu87Pro, 0.1% frequency) associated with lower WHRadjBMI (-0.14 SD, $P = 1.9 \times 10^{-11}$). A common noncoding variant in the *CALCRL* locus, encoding calcitonin receptor-like receptor, was previously identified in the GIANT Consortium as associated with WHRadjBMI (16). The identification of an independent low-frequency missense variant in the gene suggests that *CALCRL* may be the causal gene at this locus.

Variation Leading to Lower WHRadjBMI: The *ACVR1C* Locus

We next focused on novel variant alleles leading to lower WHRadjBMI. The lead novel low-frequency variant associated with lower WHRadjBMI lay within the gene *ACVR1C*. *ACVR1C* Asn150His (allele frequency 1.1%) associated with 0.09 SD lower WHRadjBMI ($P = 3.4 \times 10^{-17}$). An independent missense variant in *ACVR1C*, Ile195Thr (AF 0.4%), also associated with lower WHRadjBMI (0.15 SD, $P = 1.0 \times 10^{-9}$).

Upon conditioning on these two variants, we identified an additional coding variant: Ile482Val (AF 7%), which associated with 0.019 SD lower WHRadjBMI ($P = 1.6 \times 10^{-5}$), and rs72927479, a noncoding variant, for which the minor G allele (AF 5%) was associated with 0.035 SD lower WHRadjBMI ($P = 2.6 \times 10^{-12}$) (Table 2). Despite being an

independent signal for WHRadjBMI, the noncoding variant rs72927479 is nominally correlated with Ile482Val ($r^2 = 0.06$ in UK Biobank). No other variants were correlated with one another in UK Biobank (all $r^2 < 0.001$).

Pooling across all four variants with weighting by square root of allele frequency, *ACVR1C* variation was associated with lower WHRadjBMI in UK Biobank (-0.07 SD, $P = 2.6 \times 10^{-35}$). To replicate this finding, we pooled data from the GIANT Consortium (in which the Ile482Val variant was available, $n = 224,156$) with data from ARIC and Framingham Heart Study data sets (in which Asn150His, Ile195Thr, and rs72927479 variants were available, $n = 13,704$). Pooling across all four variants in these three replication studies, variation in *ACVR1C* was associated with reduced WHRadjBMI (-0.07 SD, $P = 0.0005$) (Supplementary Table 5).

Examining other anthropometric traits in UK Biobank, variation in *ACVR1C* was associated with elevated hip circumference (0.035 SD, $P = 3 \times 10^{-8}$) and nominally elevated BMI (0.02 SD, $P = 0.002$) and was unassociated with waist circumference (-0.007 SD, $P = 0.20$) or height (0.005 SD, $P = 0.23$). In the Meta-Analyses of Glucose and Insulin-related traits Consortium (MAGIC) analysis of insulin resistance (HOMA-IR), Ile482Val (the only *ACVR1C* variant available for analysis) was unassociated with HOMA-IR (-1.1%, $P = 0.17$) (33).

We examined whether *ACVR1C* variation also associated with direct imaging measurement of abdominal obesity. A total of 4,215 participants in UK Biobank underwent DEXA imaging to estimate abdominal fat mass. Carriers of *ACVR1C* variants had lower percent abdominal fat ($P = 0.008$) (Fig. 1). When one outlying individual with four *ACVR1C* variants was excluded (Fig. 1), carriers of *ACVR1C* continued to have significantly lower percent abdominal fat ($P = 0.009$).

Association of Variants in *ACVR1C* With Type 2 Diabetes

Genetic predisposition to increased WHRadjBMI strongly predisposes to type 2 diabetes (12). We therefore examined whether variants in *ACVR1C* that lower WHRadjBMI adiposity protect against type 2 diabetes. In a combined analysis of UK Biobank and the DIAGRAM Consortium, all four *ACVR1C* variants were found to independently protect against type 2 diabetes (OR 0.88, $P = 8.7 \times 10^{-5}$ for
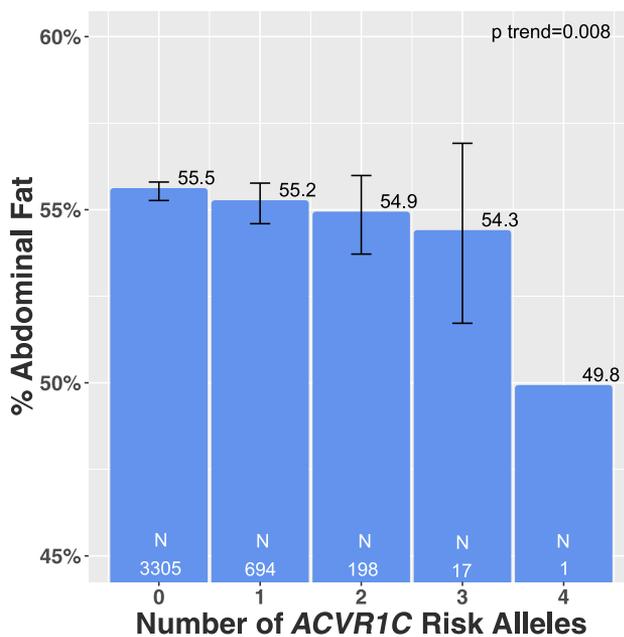

Figure 1—Across four *ACVR1C* genetic variants, association of number of WHRadjBMI-lowering alleles with mean directly measured abdominal fat (percent abdominal fat of total body fat) in 4,215 participants who underwent DEXA scan in UK Biobank, adjusted for age, sex, 10 principal components of ancestry, and array type. Number of participants in each group is displayed in white for each bar.

Asn150His; OR 0.79, $P = 0.005$ for Ile195Thr; OR 0.95, $P = 4.8 \times 10^{-6}$ for Ile482Val; OR 0.93, $P = 0.0006$ for rs72927479) (Table 1). Pooling across all four variants, a 0.2 SD decrease in WHRadjBMI through *ACVR1C* was associated with a 30% lower risk of type 2 diabetes (OR 0.70, 95% CI 0.63, 0.77; $P = 5.6 \times 10^{-13}$) (Fig. 2). When we excluded the noncoding variant rs72927479, which is nominally correlated with Ile482Val ($r^2 = 0.06$ in UK Biobank), the *ACVR1C* gene risk score remained associated with risk of type 2 diabetes (OR 0.71, 95% CI 0.64, 0.79; $P = 1.8 \times 10^{-10}$)

In three independent data sets with exome sequence data—MIGen, ARIC, and the T2D-GENES Consortium—we examined whether variants predicted to damage *ACVR1C* gene function protect against type 2 diabetes. The nine exons of the *ACVR1C* gene were sequenced in

Table 2—Association of variants in *ACVR1C* with WHRadjBMI and with type 2 diabetes

Variant	Minor allele frequency (%)	WHRadjBMI		Type 2 diabetes	
		β (95% CI)	*P* value	OR (95% CI)	*P* value
Asn150His	1.1	-0.089 (-0.11, -0.067)	3.4×10^{-17}	0.88 (0.83, 0.94)	8.7×10^{-5}
Ile195Thr	0.2	-0.15 (-0.09, 0.19)	1.0×10^{-9}	0.79 (0.67, 0.93)	0.005
Ile482Val	7.2	-0.019 (-0.01, -0.027)	1.6×10^{-5}	0.95 (0.93, 0.97)	4.8×10^{-6}
rs72927479	5.1	-0.035 (-0.045, -0.025)	2.6×10^{-12}	0.93 (0.89, 0.97)	6.0×10^{-4}

Estimates for WHRadjBMI were derived through linear regression analysis in UK Biobank. Estimates for type 2 diabetes were derived through meta-analysis of UK Biobank and the DIAGRAM ExTexT2D Consortium.
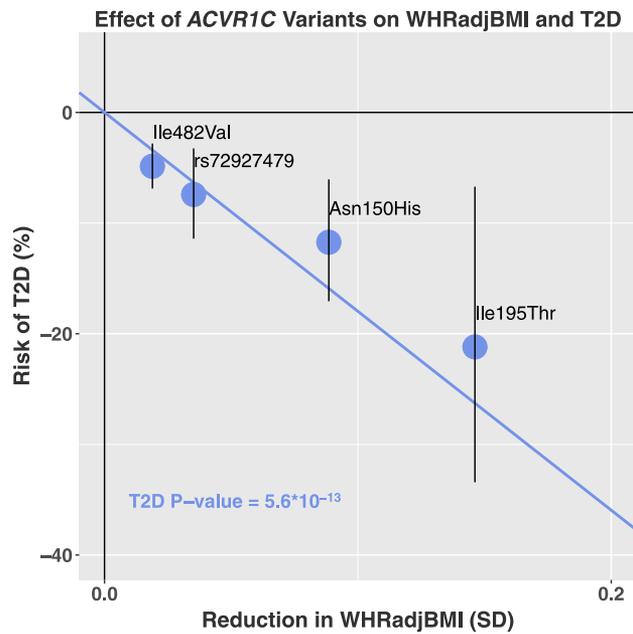
Figure 2—Association of four variants in *ACVR1C* with WHRadjBMI (*x*-axis) and type 2 diabetes (T2D) (*y*-axis).

Figure 3—Association of predicted damaging variants in *ACVR1C* with type 2 diabetes (T2D) from sequences in MIGen, ARIC, and the T2D-GENES Consortium (T2D Genes).

55,516 individuals. A total of 105 predicted damaging variants were identified (Supplementary Tables 6–8). Among 16,452 case subjects with type 2 diabetes, the frequency of predicted damaging variants in *ACVR1C* was 0.1% (17) compared with 0.2% (88) among 39,064 control subjects without diabetes. Overall, carrying a predicted damaging variant in *ACVR1C* was associated with 54% lower risk of type 2 diabetes (OR 0.46, 95% CI 0.27, 0.81; *P* = 0.006) (Fig. 3). When we excluded 47 carriers of I195T (annotated as a predicted damaging variant by five of five algorithms) in the exome sequencing analysis, carriers of predicted damaging variants in *ACVR1C* remained protected from type 2 diabetes (OR 0.48, 95% CI 0.24, 0.97; *P* = 0.04).

To further examine whether loss of *ACVR1C* function lowers WHRadjBMI, we examined whether the noncoding variant rs72927479 associates with *ACVR1C* expression. The minor allele of rs72927479 (G, frequency 5%) associated with lower WHRadjBMI (β −0.035, $P = 2.6 \times 10^{-12}$) and type 2 diabetes (OR 0.93, *P* = 0.0006). In the Genotype-Tissue Expression (GTEx) data set (34), the minor allele of rs72927479 associated with reduced expression of *ACVR1C* in subcutaneous adipose tissue (*P* = 0.02) and pancreas (*P* = 0.02) (Supplementary Fig. 2).

Phenome-Wide Association Study of *ACVR1C* in UK Biobank

To anticipate whether *ACVR1C* inhibition may be associated with on-target adverse effects, we conducted a phenome-wide association study of 31 disease phenotypes in UK Biobank. We did not observe any significant associations between the *ACVR1C* gene risk score and the
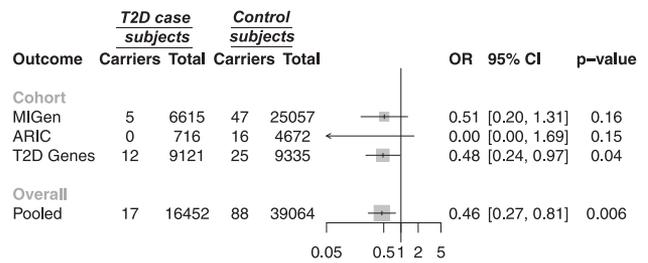
31 diseases analyzed (Fig. 4). The *ACVR1C* gene risk score was unassociated with coronary artery disease (OR 1.01, *P* = 0.86). We also examined whether *ACVR1C* variation associates with three metabolic traits currently available in UK Biobank: urinary albumin, systolic blood pressure, and diastolic blood pressure. While the *ACVR1C* gene risk score did not significantly associate with urinary albumin levels, it associated with significantly lower diastolic blood pressure (−0.6 mmHg, *P* = 0.0004) and nominally lower systolic blood pressure (−0.6 mmHg, *P* = 0.03).

DISCUSSION

In this study, four genetic variants in *ACVR1C*, ranging in frequency from 0.2 to 7.2%, independently associated with lower WHRadjBMI and protected against type 2 diabetes. Furthermore, damaging variants in *ACVR1C* protected against type 2 diabetes in an analysis of exome sequences from 55,516 individuals. An *ACVR1C* gene risk score did not associate with any of 31 additional diseases in UK Biobank but did nominally associate with lower blood pressure.

These results permit several conclusions. First, pharmaceutical inhibition of *ACVR1C* may be useful in the treatment of type 2 diabetes. *ACVR1C* encodes ALK7, a transforming growth factor-β family receptor highly expressed on pancreatic islet cells (35,36) and adipocytes (37). Overexpression of AKL7 induces growth inhibition and apoptosis of pancreatic β-cells (36,38), suggesting that it is a negative regulator of β-cell mass. A number of findings from model systems also suggest that ALK7 may be useful as a therapeutic target for abdominal obesity, type 2 diabetes, and other metabolic diseases. *ACVR1C*-deficient mice have been reported to have reduced body fat when fed a high-fat diet (37,39) and have improved glucose tolerance and insulin sensitivity when obese (37). Chemical inhibition of *ACVR1C* has also been shown to reduce fat accumulation and increase lipolysis in mice (40). Rats with streptozocin-induced diabetes show elevated ALK7 expression, and shRNA knockdown of *ACVR1C* reduces arterial stiffness in this model (41). In combination with the human genetic results presented here, these findings suggest that inhibition of *ACVR1C* may prove useful to modify body fat distribution and lower risk for type 2 diabetes.
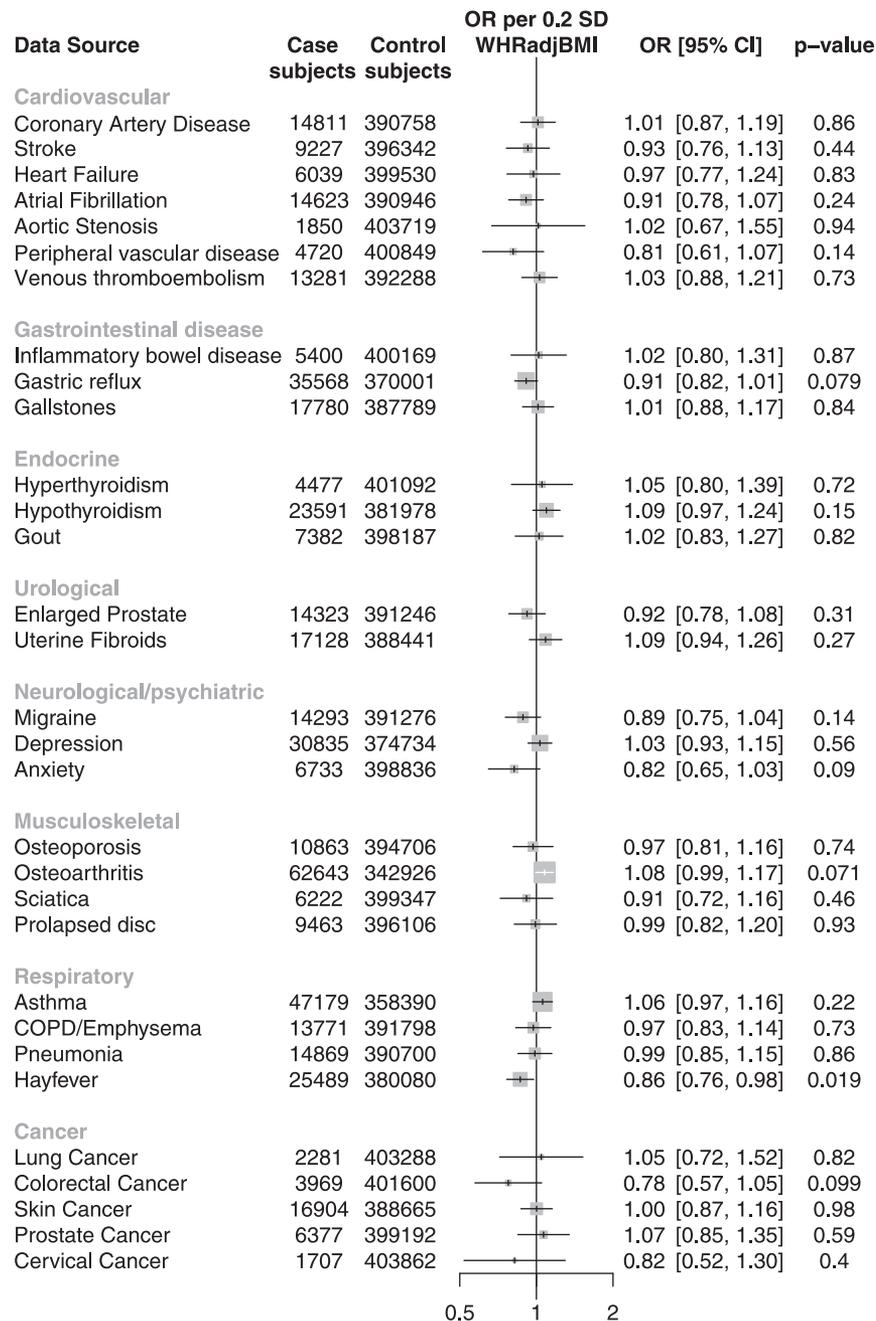
Data Source	Case subjects	Control subjects	OR per 0.2 SD WHRadjBMI	OR [95% CI]	p–value
Cardiovascular					
Coronary Artery Disease	14811	390758		1.01 [0.87, 1.19]	0.86
Stroke	9227	396342		0.93 [0.76, 1.13]	0.44
Heart Failure	6039	399530		0.97 [0.77, 1.24]	0.83
Atrial Fibrillation	14623	390946		0.91 [0.78, 1.07]	0.24
Aortic Stenosis	1850	403719		1.02 [0.67, 1.55]	0.94
Peripheral vascular disease	4720	400849		0.81 [0.61, 1.07]	0.14
Venous thromboembolism	13281	392288		1.03 [0.88, 1.21]	0.73
Gastrointestinal disease					
Inflammatory bowel disease	5400	400169		1.02 [0.80, 1.31]	0.87
Gastric reflux	35568	370001		0.91 [0.82, 1.01]	0.079
Gallstones	17780	387789		1.01 [0.88, 1.17]	0.84
Endocrine					
Hyperthyroidism	4477	401092		1.05 [0.80, 1.39]	0.72
Hypothyroidism	23591	381978		1.09 [0.97, 1.24]	0.15
Gout	7382	398187		1.02 [0.83, 1.27]	0.82
Urological					
Enlarged Prostate	14323	391246		0.92 [0.78, 1.08]	0.31
Uterine Fibroids	17128	388441		1.09 [0.94, 1.26]	0.27
Neurological/psychiatric					
Migraine	14293	391276		0.89 [0.75, 1.04]	0.14
Depression	30835	374734		1.03 [0.93, 1.15]	0.56
Anxiety	6733	398836		0.82 [0.65, 1.03]	0.09
Musculoskeletal					
Osteoporosis	10863	394706		0.97 [0.81, 1.16]	0.74
Osteoarthritis	62643	342926		1.08 [0.99, 1.17]	0.071
Sciatica	6222	399347		0.91 [0.72, 1.16]	0.46
Prolapsed disc	9463	396106		0.99 [0.82, 1.20]	0.93
Respiratory					
Asthma	47179	358390		1.06 [0.97, 1.16]	0.22
COPD/Emphysema	13771	391798		0.97 [0.83, 1.14]	0.73
Pneumonia	14869	390700		0.99 [0.85, 1.15]	0.86
Hayfever	25489	380080		0.86 [0.76, 0.98]	0.019
Cancer					
Lung Cancer	2281	403288		1.05 [0.72, 1.52]	0.82
Colorectal Cancer	3969	401600		0.78 [0.57, 1.05]	0.099
Skin Cancer	16904	388665		1.00 [0.87, 1.16]	0.98
Prostate Cancer	6377	399192		1.07 [0.85, 1.35]	0.59
Cervical Cancer	1707	403862		0.82 [0.52, 1.30]	0.4

0.5   1   2

Figure 4—Association of *ACVR1C* gene risk score with 31 disease phenotypes in UK Biobank. COPD, chronic obstructive pulmonary disease.

Second, the lack of association of the *ACVR1C* gene risk score with 31 different diseases in UK Biobank suggests that therapeutic *ACVR1C* inhibition may not have adverse on-target effects. In the Exome Aggregation Consortium (ExAC), *ACVR1C* is tolerant of loss-of-function variants, with 18 of 66,720 individuals of European ancestry carrying an early stop codon (Leu32Ter) in *ACVR1C* (42). In combination with the phenome-wide association study presented here, these findings suggest that *ACVR1C* could be safely inhibited. However, due to the small number of case subjects for many of the analyzed diseases

and the multiple diseases tested in the phenome-wide association study, modest associations of *ACVR1C* variation with the analyzed phenotypes cannot excluded. Furthermore, many common adverse effects of therapeutics, such as elevations in liver function enzymes, could not be analyzed due to a lack of available data in UK Biobank. In particular, ALK7-deficient mice have been reported to have lengthened QT intervals (43), a phenotype that was unavailable for analysis in UK Biobank. The association of the *ACVR1C* gene risk score with nominally lower diastolic and systolic blood pressure suggests that *ACVR1C*

inhibition may have the additional benefit of lowering blood pressure. However, this finding, which did not reach genome-wide significance, requires replication in independent data sets.

The primary strength of the analysis is the use of multiple data sources to replicate the association of *ACVR1C* variation with WHRadjBMI and type 2 diabetes. We demonstrated associations of *ACVR1C* with WHRadjBMI and type 2 diabetes to greater than genome-wide significance ($P = 2.6 \times 10^{-35}$ for WHRadjBMI and $P = 5.6 \times 10^{-13}$ for type 2 diabetes). We further showed that variants leading to loss of *ACVR1C* function protected against diabetes in an analysis of predicted damaging variants in exome sequences of 55,516 individuals. A primary limitation of the analysis is that we did not experimentally characterize the analyzed variants. The consistent protective associations observed with three different *ACVR1C* missense variants, with a noncoding variant that reduces *ACVR1C* expression, and with variants predicted to truncate the *ACVR1C* protein or predicted to damage *ACVR1C* function by five different algorithms suggest that variants leading to loss of *ACVR1C* function protect against type 2 diabetes. However, experimental demonstration that *ACVR1C* variants that lower WHRadjBMI and protect against type 2 diabetes actually reduce ALK7 receptor function is necessary before it can be concluded that *ACVR1C* deficiency will protect against type 2 diabetes. A second limitation is that pharmacological *ACVR1C* inhibition may be associated with off-target effects that cannot be characterized in a human genetic study.

In summary, variants predicted to damage *ACVR1C* gene function lower WHRadjBMI and protect against type 2 diabetes. These findings provide human genetic validation for the *ACVR1C* gene as a therapeutic target for type 2 diabetes.

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