

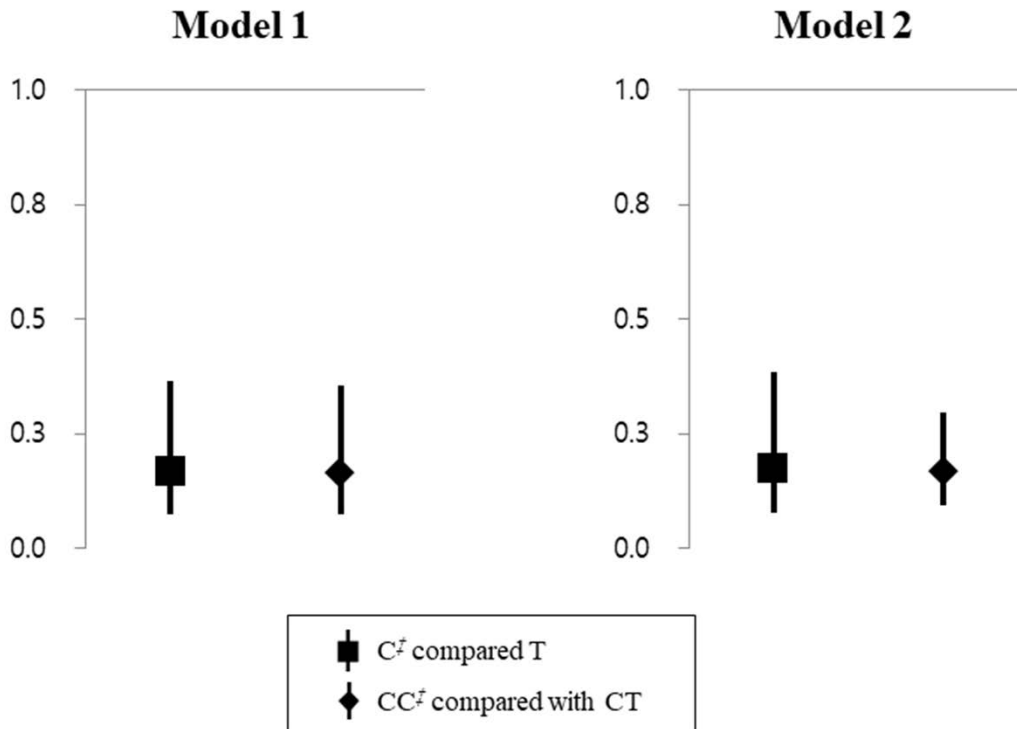
Supplementary Data 1. Affymetrix Axiom™ KORV1.0-96 array hybridization and SNP selection

A total of 2,167 samples were genotyped using the Axiom® 2.0 Reagent Kit (Affymetrix Axiom® 2.0 Assay User Guide; Affymetrix, Santa Clara, CA, USA) according to the manufacturer's protocol. Approximately 200 ng of genomic DNA (gDNA) was amplified and randomly fragmented into 25- to 125-base pair (bp) fragments. The gDNA was initially amplified in a 40- μ L reaction containing 20 μ L of a 10-ng/ μ L genomic DNA stock and 20 μ L of a master mix. The initial amplification reaction conditions consisted of a 10-min initial amplification at room temperature, followed by amplification with 130 μ L of Axiom 2.0 Neutral Solution, 225 μ L of Axiom 2.0 Amp Solution and 5 μ L of Axiom 2.0 Amp Enzyme. The amplification reactions were performed for 23 \pm 1 h at 37°C. The amplification products were analyzed in an optimized reaction to amplify fragments between 200 and 1100 bp in length. A fragmentation step reduced the amplified products into segments of approximately 25-50 bp in length, which were end-labeled using biotinylated nucleotides. After hybridization, the bound target was washed under stringent conditions to remove the non-specific background and to minimize the background noise caused by random ligation events. Each polymorphic nucleotide was queried in a multicolor ligation event conducted on the array surface. After ligation, the arrays were stained and imaged using a GeneTitan MC Instrument (Affymetrix, Santa Clara, CA, USA). The images were analyzed using the Genotyping Console™ Software (Affymetrix, Santa Clara, CA, USA). The genotype data were produced using the K-CHIP available through the K-CHIP consortium. The K-CHIP was designed by the Center for Genome Science at the Korea National Institute of Health (4845-301, 3000-3031). Samples with the following inclusion thresholds were excluded: sex inconsistency, markers with a high missing rate (>5%), individuals with a high missing rate (>10%), minor allele frequency <0.01, and a significant deviation from the Hardy-Weinberg equilibrium (HWE) (p <0.001). SNPs in linkage disequilibrium with each other were excluded.

Supplementary Data 2. Clinical characteristics and frequencies of *PPARD* rs7770619 in NFG controls and patients with IFG or newly diagnosed T2D

	NFG control (n=1210)	IFG + T2D (n=588)	<i>p</i>^a	<i>p</i>^b
Sex distribution (n, male/female)	415/795	314/274	<0.001	-
Age (year)	47.9±0.30	53.6±0.41	<0.001	-
BMI (kg/m ²)	23.8±0.08	24.9±0.12	<0.001	-
Systolic BP (mmHg)	119.6±0.44	127.0±0.67	<0.001	<0.001
Diastolic BP (mmHg)	75.5±0.33	79.0±0.43	<0.001	0.094
Triglyceride (mg/dL) [↯]	118.1±2.02	143.3±3.39	<0.001	<0.001
Total-cholesterol (mg/dL) [↯]	198.9±1.02	200.5±1.53	0.445	0.315
HDL-cholesterol (mg/dL) [↯]	54.6±0.39	51.6±0.53	<0.001	0.526
LDL-cholesterol (mg/dL) [↯]	121.2±0.93	122.0±1.42	0.854	0.075
Glucose (mg/dL) [↯]	86.9±0.21	118.2±1.01	<0.001	<0.001
Insulin (μIU/dL) [↯]	9.01±0.12	9.25±0.25	0.603	0.282
HOMA-IR [↯]	1.94±0.03	2.71±0.09	<0.001	<0.001
HbA _{1c} (%) [↯]	5.69±0.02	6.42±0.05	<0.001	<0.001
hs-CRP (mg/dL) [↯]	1.25±0.09	1.55±0.12	0.081	0.082
Malondialdehyde (nmol/mL) [↯]	8.23±0.07	10.9±0.23	<0.001	<0.001
<i>PPARD</i> rs7770619, n (%)				
CC	1,127 (93.1)	581 (98.8)		
CT	83 (6.9)	7 (1.2)	<0.001	
TT	0 (0)	0 (0)		
T allele frequency	83 (3.4)	7 (0.6)	<0.001	

Mean ± SE. [↯] tested by logarithmic transformation. *p*-values derived from an independent *t*-test. *p*^a; Unadjusted. *p*^b; Adjusted for age, sex, BMI, smoking and drinking.



Supplementary Data 3. Unadjusted and adjusted odds ratios for all patients with impaired fasting glucose and type 2 diabetes according to the *PPARD* rs7770619 genotypes.

#Reference. CI, confidence interval. Model 1: unadjusted; Model 2: adjusted for age, sex, BMI, smoking status, and drinking status.