SUPPLEMENTARY DATA

Supplementary Table 1: Rationale for categorizing 30 T2D-associated single-nucleotide polymorphisms (SNP) as affecting β-cell function or insulin resistance, based on known gene function or specific metabolic phenotypes in the Meta-Analysis of Glucose and Insulin-related traits Consortium (MAGIC).

								Physiology based on MAGIC analyses				
	SNP	**Locus**	**Chr**	**Risk allele**	**T2D effect**	**HOMA-β effect**	***p***	**HOMA-β effect <-0.008**	**IGI *p*<0.05**	**AIR *p*<0.05**	**Proinsulin *p*<0.05**	**Physiology clustering**
β-cell function	rs10830963	*MTNR1B*	11	G	0.0414	-0.0394	8.6E-23	xx	xx			
	rs10203174	*THADA*	2	C	0.0569	-0.0262	9.8E-06	x				x
	rs6819243	*MAEA*	4	T	0.0294	-0.0249	9.5E-03	x				
	rs7903146	*TCF7L2*	10	T	0.1399	-0.0200	1.4E-07	x	x		x	x
	rs11717195	*ADCY5*	3	T	0.0492	-0.0181	2.7E-05	x			x	x
	rs1552224	*ARAP1*	11	A	0.0374	-0.0166	9.4E-05	x	x		xx	
	rs3802177	*SLC30A8*	8	G	0.0531	-0.0160	2.0E-05	x	x	x	x	x
	rs10758593	*GLIS3*	9	A	0.0253	-0.0145	1.3E-05	x				
	rs10278336	*GCK*	7	A	0.0374	-0.0128	2.1E-04	x	x			
	rs17168486	*DGKB*	7	T	0.0374	-0.0126	3.0E-03	x	x			x
	rs2075423	*PROX1*	1	G	0.0294	-0.0125	3.9E-04	x	x			x
	rs4402960	*IGF2BP2*	3	T	0.0531	-0.0115	1.2E-03	x	x	x		
	rs4502156	*VPS13C*	15	T	0.0212	-0.0099	3.6E-03	x				
	rs7756992	*CDKAL1*	6	G	0.0607	-0.0095	7.5E-03	x	xx	x		x
	rs11257655	*CDC123*	10	T	0.0334	-0.0091	2.5E-02	x	x			
	rs1496653	*UBE2E2*	3	A	0.0374	-0.0088	1.9E-02	x				
	rs163184	*KCNQ1*	11	G	0.0374	-0.0086	1.6E-02	x		x		
	rs10811661	*CDKN2A/B*	9	T	0.0755	-0.0085	5.1E-02	x	x	x		x
	rs1111875	*HHEX/IDE*	10	C	0.0374	-0.0042	2.0E-01		xx	x		x
	rs5215	*KCNJ11*	11	C	0.0294	0.0009	7.8E-01			x		
						HOMA-IR effect	***p***	**HOMA-IR *p*<0.05**	**FI $p<10^{-8}$**	**Obesity $p<10^{-8}$**	**IR lipid profile**	**Physiology clustering**
Insulin resistance	rs12970134	*MC4R*	18	A	0.0334	0.0084	7.6E-02			x		x
	rs13233731	*KLF14*	7	G	0.0043	0.0077	5.1E-02	x			x	
	rs13389219	*GRB14*	2	C	0.0374	0.0124	2.2E-03	x	x			
	rs1801282	*PPARG*	3	C	0.0453	0.0161	5.6E-03	x	x		x	
	rs2261181	*HMGA2*	12	T	0.0414	0.0135	4.9E-02	x				
	rs2943640	*IRS1*	2	C	0.0414	0.0086	3.6E-02	x	x		x	
	rs459193	*ANKRD55*	5	G	0.0414	0.0115	1.1E-02	x				
	rs780094	*GCKR*	2	C	0.0334	0.0201	7.6E-07	x	x		x	
	rs8182584	*PEPD*	19	T	0.0212	0.0122	3.9E-03	x	x			
	rs9936385	*FTO*	16	C	0.0531	0.0148	3.3E-04	x		x		x

Physiology clustering as β-cell function or insulin resistance based on MAGIC analyses(1). Fasting insulin (FI) *p*-values based on body-mass index*gene analyses in (2). Obesity defined as association with risk of increased body-mass index in Genetic Investigation of ANthropometric Traits (GIANT) data(3). Insulin resistance (IR) lipid profile defined as

high triglyceride and low HDL levels as reported in (2). AIR—acute insulin response; Chr—chromosome; FI: fasting insulin; HOMA—homeostasis model of assessment; IGI—insulinogenic index; MAGIC—Meta-Analysis of Glucose and Insulin-related traits Consortium; SNP—single-nucleotide polymorphism; T2D—type 2 diabetes.

Supplementary Table 2: Mean β-cell (GRS_{β}) and insulin resistance (GRS_{IR}) genotype risk scores in the Framingham Offspring and CARDIA Studies

	Total	BMI<30 kg/m^2	BMI≥30 kg/m^2
GRS_{β}			
FOS	21.6 (3.0)	21.6 (3.0)	21.6 (2.9)
T2D	22.6 (3.0)	23.2 (3.1)	22.4 (2.6)
No T2D	21.6 (3.0)	21.6 (3.0)	21.6 (2.9)
CARDIA Whites	21.2 (3.1)	21.2 (3.1)	21.0 (3.2)
T2D	22.1 (3.3)	22.3 (3.4)	21.6 (2.9)
No T2D	21.2 (3.1)	21.2 (3.1)	20.7 (3.3)
CARDIA Blacks	21.3 (2.4)	21.4 (2.4)	21.1 (2.4)
T2D	21.6 (2.5)	21.6 (2.5)	21.7 (2.5)
No T2D	21.3 (2.4)	21.3 (2.4)	20.8 (2.3)
GRS_{IR}			
FOS	10.4 (2.0)	10.4 (2.0)	10.5 (2.0)
T2D	10.3 (2.4)	10.3 (2.3)	10.3 (2.7)
No T2D	10.4 (2.0)	10.4 (2.0)	10.5 (2.0)
CARDIA Whites	10.4 (2.0)	10.4 (2.0)	10.3 (2.1)
T2D	10.6 (1.9)	10.5 (1.9)	10.8 (2.0)
No T2D	10.4 (2.0)	10.4 (2.0)	10.1 (2.1)
CARDIA Blacks	11.1 (1.9)	11.1 (1.9)	11.0 (1.8)
T2D	11.4 (1.8)	11.5 (1.8)	11.3 (1.7)
No T2D	11.0 (1.9)	11.0 (1.9)	10.9 (1.9)

Data are mean (SD) weighted genotype risk scores (GRS) consisting of 20 single-nucleotide polymorphisms (SNP) associated with β-cell dysfunction (GRS_{β}) and 10 SNP associated with insulin resistance (GRS_{IR}) in the overall FOS and CARDIA cohorts and in participants with and without type 2 diabetes (T2D). Among FOS and CARDIA whites, GRS are weighted by the effects sizes from the DIAGRAM v3 meta-analysis(4). GRS are unweighted among CARDIA blacks.

Supplementary Table 3: Odds ratios for GRS_{β} and GRS_{IR} in prediction models for incident type 2 diabetes in the Framingham Offspring Study

	GRS_{β} model	GRS_{IR} model	GRS_{β} + GRS_{IR} model
Demographic model			
GRS_{β}	1.11 (1.08, 1.15)*	---	1.11 (1.08, 1.15)*
GRS_{IR}	---	1.04 (1.00, 1.10)	1.05 (1.00, 1.10)
Clinical model			
GRS_{β}	1.10 (1.06, 1.14)*	---	1.10 (1.06, 1.14)*
GRS_{IR}	---	0.98 (0.93, 1.04)	0.99 (0.93, 1.04)

Data are odds ratios from pooled logistic regression models for incident type 2 diabetes and correspond to a 1-allele increase in the GRS. Demographic models are adjusted for age and sex. Clinical models are adjusted for age, sex, parental history of diabetes (yes vs. no), body-mass index, systolic blood pressure, fasting plasma glucose, high-density lipoprotein (HDL), and fasting triglycerides. GRS_{β} and GRS_{IR} models include only the GRS_{β} and GRS_{IR}, respectively. The GRS_{β} + GRS_{IR} model contains both terms. *$p<0.001$

Supplementary Table 4: Hazard ratios for GRS_{β} and GRS_{IR} in prediction models for incident type 2 diabetes among whites in the CARDIA Study

	GRS_{β} model	**GRS_{IR} model**	**GRS_{β} + GRS_{IR} model**
Demographic model			
GRS_{β}	1.09 (1.02, 1.16)*	---	1.09 (1.02, 1.16)**
GRS_{IR}	---	1.06 (0.96, 1.17)	1.06 (0.96, 1.17)
Clinical model			
GRS_{β}	1.09 (1.02, 1.17)**	---	1.09 (1.02, 1.17)**
GRS_{IR}	---	1.01 (0.91, 1.12)	1.01 (0.91, 1.11)

Data are hazard ratios from Cox regression models for incident type 2 diabetes and correspond to a 1-allele increase in the GRS. Demographic models are adjusted for age and sex. Clinical models are adjusted for age, sex, parental history of diabetes (yes vs. no), body-mass index, systolic blood pressure, fasting plasma glucose, log-transformed high-density lipoprotein (HDL), and log-transformed fasting triglycerides. GRS_{β} and GRS_{IR} models include only the GRS_{β} and GRS_{IR}, respectively. The GRS_{β} + GRS_{IR} model contains both terms. *p<0.05, **p<0.01

Supplementary Table 5: Hazard ratios for GRS_{β} and GRS_{IR} in prediction models for incident type 2 diabetes among blacks in the CARDIA Study

	GRS_{β} model	GRS_{IR} model	GRS_{β} + GRS_{IR} model
Demographic model			
GRS_{β}	1.06 (0.98, 1.14)	---	1.06 (0.98, 1.14)
GRS_{IR}	---	1.09 (1.00, 1.20)	1.10 (1.00, 1.20)
Clinical model			
GRS_{β}	1.06 (0.99, 1.15)	---	1.07 (0.99, 1.15)
GRS_{IR}	---	1.05 (0.96, 1.15)	1.05 (0.96, 1.16)

Data are hazard ratios from Cox regression models for incident type 2 diabetes and correspond to a 1-allele increase in the GRS. Demographic models are adjusted for age and sex. Clinical models are adjusted for age, sex, parental history of diabetes (yes vs. no), body-mass index, systolic blood pressure, fasting plasma glucose, log-transformed high-density lipoprotein (HDL), and log-transformed fasting triglycerides. GRS_{β} and GRS_{IR} models include only the GRS_{β} and GRS_{IR}, respectively. The GRS_{β} + GRS_{IR} model contains both terms.

Supplementary Table 6: Racial differences in the associations between GRS and incident type 2 diabetes

	GRS_t	GRS_β	GRS_{IR}
Demographic model			
Whites	1.077 (1.059, 1.095)	1.109 (1.079, 1.139)	1.047 (1.003, 1.093)
Blacks	1.046 (1.005, 1.088)	1.058 (0.982, 1.140)	1.095 (0.997, 1.202)
p	0.19	0.25	0.39
Clinical model			
Whites	1.060 (1.040, 1.080)	1.098 (1.063, 1.133)	0.990 (0.945, 1.038)
Blacks	1.046 (1.003, 1.090)	1.063 (0.986, 1.147)	1.049 (0.957, 1.151)
p	0.57	0.45	0.28

Data are effect sizes of the association between each GRS and incident T2D among FOS and CARDIA whites (meta-analyzed) and CARDIA blacks. Demographic models are adjusted for age and sex. Clinical models are adjusted for age, sex, parental history of diabetes (yes vs. no), body-mass index, systolic blood pressure, fasting plasma glucose, log-transformed high-density lipoprotein (HDL), and log-transformed fasting triglycerides. *P* values correspond to *t*-tests comparing the effect sizes between whites and blacks.

Supplementary Table 7: *P*-values for GRS_{β} and GRS_{IR} regression terms in prediction models for incident type 2 diabetes in the Framingham Offspring Study, stratified by body-mass index (BMI)

	GRS_{β} model	GRS_{IR} model	GRS_{β} + GRS_{IR} model
BMI≥30 kg/m^2			
GRS_{β}	<0.001	---	<0.001
GRS_{IR}	---	0.427	0.426
BMI<30 kg/m^2			
GRS_{β}	<0.001	---	<0.001
GRS_{IR}	---	0.223	0.199

Data are *p*-values from pooled logistic regression models for incident type 2 diabetes, stratified by BMI category. Models are adjusted for age and sex. GRS_{β} and GRS_{IR} models include only the GRS_{β} and GRS_{IR}, respectively. The GRS_{β} + GRS_{IR} model contains both terms.

Supplementary Table 8: *P*-values for GRS_{β} and GRS_{IR} regression terms in prediction models for incident type 2 diabetes in the overall CARDIA Study, stratified by body-mass index (BMI)

	GRS_{β} model	GRS_{IR} model	GRS_{β} + GRS_{IR} model
BMI≥30 kg/m^2			
GRS_{β}	0.018	---	0.021
GRS_{IR}	---	0.221	0.263
BMI<30 kg/m^2			
GRS_{β}	0.015	---	0.013
GRS_{IR}	---	0.084	0.070

Data are *p*-values from Cox regression models for incident type 2 diabetes, stratified by BMI category. Models are adjusted for age, sex, and race. GRS_{β} and GRS_{IR} models include only the GRS_{β} and GRS_{IR}, respectively. The GRS_{β} + GRS_{IR} model contains both terms.

Supplementary Table 9: Prediction models for incident type 2 diabetes in the Framingham Offspring Study, examining the interaction between genotype risk score and obesity

	GRS model	GRS + obesity model	GRS*obesity interaction model
GRS_t model			
GRS_t	1.08 (1.06, 1.10)	1.08 (1.06, 1.10)	1.09 (1.07, 1.12)
Obesity	---	4.46 (3.66, 5.43)	22.39 (1.66, 301.34)
GRS_t*obesity interaction	---	---	0.98 (0.94, 1.01)
GRS_β model			
GRS_β	1.11 (1.08,1.15)	1.13 (1.09, 1.16)	1.14 (1.09, 1.19)
Obesity	---	4.46 (3.66, 5.43)	8.44 (1.97, 36.16)
GRS_β*obesity interaction	---	---	0.97 (0.91, 1.04)
GRS_{IR} model			
GRS_{IR}	1.04 (1.00, 1.10)	1.03 (0.98, 1.09)	1.04 (0.98, 1.11)
Obesity	---	4.31 (3.54, 5.25)	5.11 (1.82, 14.36)
GRS_{IR}*obesity interaction	---	---	0.98 (0.89, 1.08)

Data are odds ratios (OR) from pooled logistic regression models for type 2 diabetes per weighted allele increase in 62-SNP GRS (GRS_t), β-cell GRS (GRS_β), and insulin resistance GRS (GRS_{IR}), or for obesity (BMI≥30 kg/m^2). All models are adjusted for age and sex. The GRS models include the corresponding GRS. GRS + obesity models include both the corresponding GRS and a term for obesity. GRS*obesity interaction models include the corresponding GRS, an obesity term, and an interaction term between GRS and obesity.

Supplementary Table 10: Prediction models for incident type 2 diabetes in the overall CARDIA Study, examining the interaction between genotype risk score and obesity

	GRS model	GRS + obesity model	GRS*obesity interaction model
GRS_t model			
GRS_t	1.06 (1.03, 1.09)	1.07 (1.04, 1.10)	1.07 (1.03, 1.10)
Obesity	---	6.11 (4.52, 8.26)	9.99 (0.19, 517.69)
GRS_t*obesity interaction	---	---	0.99 (0.94, 1.05)
GRS_β model			
GRS_β	1.09 (1.02, 1.16)	1.09 (1.04, 1.14)	1.07 (1.01, 1.14)
Obesity	---	6.17 (4.56, 8.34)	2.60 (0.28, 23.81)
GRS_β*obesity interaction	---	---	1.04 (0.94, 1.15)
GRS_{IR} model			
GRS_{IR}	1.08 (1.01, 1.15)	1.08 (1.01, 1.15)	1.10 (1.01, 1.19)
Obesity	---	5.94 (4.40, 8.02)	9.61 (2.01, 45.85)
GRS_{IR}*obesity interaction	---	---	0.96 (0.83, 1.10)

Data are odds ratios (OR) from Cox regression models for type 2 diabetes per weighted allele increase in 62-SNP GRS (GRS_t), β-cell GRS (GRS_β), and insulin resistance GRS (GRS_{IR}), or for obesity (BMI≥30 kg/m^2). All models are adjusted for age, sex, and race. The GRS models include the corresponding GRS. GRS + obesity models include both the corresponding GRS and a term for obesity. GRS*obesity interaction models include the corresponding GRS, an obesity term, and an interaction term between GRS and obesity.

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