

Supplementary material

Szczerbiński Ł, Gościk J, Bauer W, et al. Efficacy of family history, genetic risk score, and physical activity in assessing the prevalence of type 2 diabetes. *Pol Arch Intern Med.* 2019; 129: 442-450. doi:10.20452/pamw.14866

Please note that the journal is not responsible for the scientific accuracy or functionality of any supplementary material submitted by the authors. Any queries (except missing content) should be directed to the corresponding author of the article.

Table S1 Single nucleotide polymorphisms used in constructing genetic risk scores

Gene	rs number	Odds ratio	Risk allele frequency	Weight	Effect allele	Other allele	Source reference
<i>PROX1</i>	rs340874	1.09	0.477	0.09	C	T	[18]
<i>GCKR</i>	rs780094	1.07	0.363	0.07	C	T	[18]
<i>ADCY5</i>	rs11708067	0.88	0.211	-0.12	G	A	[18]
<i>CDKAL1</i>	rs10946398	1.13	0.336	0.13	C	A	[18]
<i>DGKB / TMEM195</i>	rs2191349	1.09	0.485	0.09	T	G	[18]
<i>SLC30A8</i>	rs11558471	0.89	0.332	-0.11	G	A	[18]
<i>CDKN2B</i>	rs10811661	0.84	0.154	-0.16	C	T	[20]
<i>HHEX</i>	rs7923837	0.90	0.376	-0.10	A	G	[18]
<i>TCF7L2</i>	rs7903146	1.37	0.269	0.37	T	C	[18]
<i>MC4R</i>	rs17782313	1.08	0.265	0.08	C	T	[20]
<i>HHEX</i>	rs5015480	0.89	0.425	-0.11	T	C	[18]
<i>KCNJ11</i>	rs5215	1.07	0.402	0.07	C	T	[18]
<i>MTNR1B</i>	rs10830963	1.09	0.295	0.09	G	C	[18]
<i>FTO</i>	rs8050136	1.15	0.412	0.15	A	C	[18]
<i>FTO</i>	rs8044769	0.90	0.480	-0.10	T	C	[20]
<i>PPARG</i>	rs1801282	0.88	0.136	-0.12	G	C	[20]
<i>IGF2BP2</i>	rs4402960	1.12	0.316	0.12	T	G	[18]
<i>COBLL1</i>	rs13389219	0.92	0.391	-0.08	T	C	[18]
<i>COBLL2</i>	rs7607980	0.88	0.117	-0.12	C	T	[18]

Table describes the single nucleotide polymorphisms (rs number) from which type 2 diabetes genetic risk scores were calculated. These single nucleotide polymorphisms were selected from two large-scale genome-wide association studies [18,20] that estimated the effect size of each single nucleotide polymorphism is explaining the variation in type 2 diabetes prevalence in very large patient populations.

Table S2 Characteristics of the participants by unweighted Genetic Risk Score

	Low uGRS	High uGRS	P-
--	----------	-----------	----

	Median	IQR	Median	IQR	value
Age, years	37.67	26.12–52.64	37.85	27.30–52.91	0.97
BMI, kg/m ²	26.74	23.78–31.84	27.16	24.45–31.87	0.33
BFM, kg	21.91	14.80–34.24	24.00	16.72–32.18	0.23
PBF, %	28.75	21.04–37.15	30.00	22.71–38.04	0.23
SMM, kg	32.60	25.08–38.32	31.00	25.11–38.64	0.77
SM%, %	39.43	34.33–44.09	38.93	34.04–43.22	0.29
FPG, mg/dl	91.00	83.00–99.00	94.00	89.00–105.00	0.002
2-h PG, mg/dl	86.20	73.75–106.00	91.00	74.50–111.00	0.09
Fasting insulin, μ U/ml	9.49	6.25–15.56	9.81	7.18–16.02	0.58
HOMA- β , %	125.29	81.23–214.25	115.45	80.06–173.06	0.09
HOMA-IR	2.15	1.46–3.77	2.30	1.60–3.69	0.18
HbA1c, %	5.40	5.10–5.60	5.40	5.10–5.70	0.24
CHOL, mg/dl	187.00	156.0–217.0	186.00	164.0–211.5	0.91
LDL, mg/dl	104.60	80.75–134.50	106.50	82.56–129.05	0.73
HDL, mg/dl	58.00	50.00–68.00	58.00	49.00–67.00	0.78
TG, mg/dl	91.00	65.75–137.18	94.50	67.48–134.85	0.50
DEI, kcal/day	1728.61	1385–2412	1607.09	1324–2223	0.17
Protein intake, g/day	81.39	62.12–109.77	81.88	60.34–96.87	0.58
Fat intake, g/day	57.84	44.29–84.12	58.23	43.87–81.99	0.45
Carbohydrates intake, g/day	220.80	171.3–286.3	218.72	170.8–283.4	0.72
Physical activity, MET min/week	7464	3412–14340	7587	3588–12980	0.88

Table shows median values and interquartile ranges (IQR). The *P*-value describes significance of difference between participants with high and low unweighted genetic risk score (high uGRS and low uGRS, respectively) using Wilcoxon rank-sum test. Abbreviations: BFM, body fat mass; BMI, body mass index; CHOL, total cholesterol concentration; DEI, average daily energy intake; FPG, fasting plasma glucose; HbA1c, haemoglobin A1c concentration; HDL, HDL-cholesterol concentration; HOMA- β , homeostatic model assessment of beta cell function; HOMA-IR, homeostatic model assessment of insulin resistance; IQR, interquartile ranges; LDL, LDL-cholesterol concentration; n, sample size; PBF, percent body fat; SMM, skeletal muscle mass; SM%, skeletal muscle percentage; TG, triglycerides concentration; uGRS, unweighted genetic risk score; 2-h PG, 2-hour plasma glucose

SI conversion factors: to convert glucose to mmol/l, multiply by 0.0555; insulin to pmol/l, multiply by 6.0; CHOL to mmol/l, multiply by 0.0259; HDL-cholesterol to mmol/l, multiply by 0.0259; LDL-cholesterol to mmol/l, multiply by 0.0259; TG to mmol/l, multiply by 0.0113.

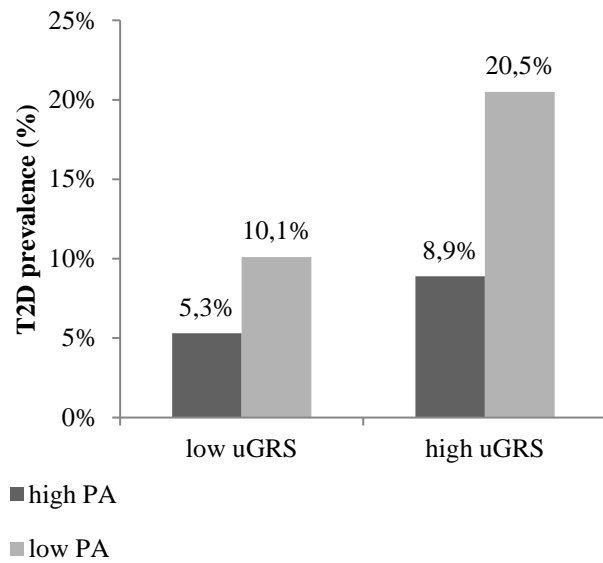


Figure S1 Type 2 diabetes prevalence (%) in unweighted genetic risk score and physical activity groups

References

- 1 Fuchsberger C, Flannick J, Teslovich TM, et al. The genetic architecture of type 2 diabetes. *Nature*. 2016; 536: 41–47.
- 2 Morris AP, Voight BF, Teslovich TM, et al. Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. *Nat Genet*. 2012; 44: 981–990.