ESM Table 2. Availability of specific categories of family history data by country: The EPIC-InterAct study.

	Family History Variables					
Country	Any 1st degree relative	Maternal	Paternal	Sibling		
France	765	710	710	0		
UK	1,746	1619	1548	1544		
Netherlands	2,271	1956	1745	1121		
Germany	1,699	1512	1339	1292		
Swedena	4,320	1959	1724	1574		
Denmark	3,068	2623	2465	2294		
Total	13,869	10379	9531	7825		

^a In Sweden, one centre (Umea) asked a single question about family history in any first degree relative. They were therefore included only in analyses of any first degree family member, and not in those requiring information on further degrees of family history.

ESM Table. 3 SNPs included in the genetic risk score and quality metrics in the InterAct subcohort (N=11,400^a)

Gene	SNP#	Strand HapMap	Effect/ Risk Allele	Other Allele	Effect Allele Freq HapMap (%)	Effect Allele Freq InterAct (%)	Call Rate	HWE p- value
ADAMTS9	rs4607103	+	С	T	81	73	0.997	0.59
ADCY5	rs11708067	+	A	G	77	80	0.980	0.002
BCL11A	rs243021	+	A	G	48	45	0.997	0.003
CDC123	rs12779790	+	G	A	23	18	0.968	< 0.001
CDKAL1	rs10946398	+	C	A	34	31	0.990	0.14
CDKN2A/B	rs10811661	+	T	C	80	81	0.995	0.29
CDKN2A/B	rs564398	+	T	C	57	59	0.999	0.20
ARAP1	rs1552224	+	A	C	87	85	0.999	0.17
CHCHD9	rs13292136	+	C	T	93	94	0.999	0.007
DGKB	rs2191349	+	T	G	48	55	0.987	0.59
GCK	rs4607517	+	A	G	20	18	0.999	0.08
GCKR	rs780093	+	C	T	61	58	0.999	0.04
HHEX	rs1111875	+	C	T	58	60	0.998	0.70
HMGA2	rs1531343	+	C	G	12	11	0.999	0.33
HNF1A	rs7957197	+	T	A	85	39	0.998	0.11
HNF1B_TCF2	rs4430796	+	G	A	51	50	0.999	0.39
IGF2BP2	rs4402960	+	T	G	30	30	0.988	0.85
IRS1	rs7578326	+	A	G	65	64	0.999	0.77
JAZF1	rs864745	+	T	C	49	50	0.991	85
KCNJ11	rs757110	+	C	A	39	37	0.984	0.40
KCNQ1	rs163184	+	G	T	44	48	0.999	0.50
KCNQ1	rs2237892	+	C	T	93	94	0.998	< 0.001
KLF14	rs972283	+	G	A	55	55	0.978	0.65
MTNR1B	rs10830963	+	G	C	30	28	0.976	0.21
NOTCH2	rs10923931	+	T	G	9	11	0.998	0.53
PPARg	rs1801282	+	С	G	90	88	0.999	0.007
PRC1 [°]	rs8042680	+	A	C	26	33	0.998	0.04
PROX1	rs340874	+	C	T	56	54	0.983	0.95
SLC30A8	rs13266634	+	C	T	75	70	0.990	0.05
TCF7L2	rs7903146	+	T	Č	28	30	0.980	0.73
THADA	rs7578597	+	T	Č	88	90	0.985	0.28
TSPAN8	rs7961581	+	Ċ	T	25	29	0.993	0.77
WFS1	rs10010131	+	Ğ	Ā	68	60	0.941	0.53
ZBED3	rs4457053	+	Ğ	A	26	30	0.995	0.47
ZFAND6	rs11634397	+	Ğ	A	64	65	0.999	0.09

^a Descriptives were produced on the InterAct subcohort after exclusion of individuals from Denmark (who had no DNA available) and those from other countries who were not included in the genetic risk score (i.e. were not successfully genotyped for at least 30 of the 35 polymorphisms). #Genotyped SNPs represent published index SNPs, except for KCNJ11 (index rs5215, proxy rs757110; r^2 =0.97); CDKAL1 (index rs7754840, proxy rs10946398; r^2 =1); IGF2BP2 (index rs1470579, proxy rs4402960; r^2 =1); GCKR (index rs780094, proxy rs780093; r^2 =1); HNF1B/TCF2 (index rs757210, DIAGRAM better meta-analysis SNP rs4430796); IRS1 (index rs2943641, DIAGRAM better meta-analysis SNP rs7578326).

ESM Table 4. Proportion of individuals reporting a family history of diabetes in each country in the subcohort: the EPIC-InterAct study.

	Family	y history in relat	any first degree		
	+	-		Missing family history data N (% of total N)	
Country	Sub	cohort	Overall Total reporting family history	` ,	
France	475	53	765	102 (12%)	
%	90	10		102 (1270)	
UK	874	114	1,746	1 (0.1%)	
%	88	12		1 (0.170)	
Netherlands	1,127	366	2,271	19 (0.8%)	
%	75	25		19 (0.8%)	
Germany	767	261	1,699	261 (120/)	
%	75	25		261 (13%)	
Sweden	1,906	460	4,320	1001 (200/)	
%	81	19		1081 (20%)	
Denmark	1,392	249	3,068	0.60 (2.40/.)	
%	85	15		969 (24%)	
Total	6,541	1,503	13,869	Total N=16,302	

ESM Table 6. Association of family history with T2D risk in BMI, physical activity and genetic risk strata

	Family History in ar	$P_{interaction}^{a}$		
BMI group (kg/m ²)	-	+		
18.5-24.9	1	2.91 (2.48, 3.43)		
25-29.9	3.81 (2.85, 5.10)	9.18 (6.30, 13.37)	0.08	
>=30	10.98 (7.77, 15.51)	22.00 (16.89, 28.65)		
Physical activity group				
Active	1	3.27 (2.73, 3.92)		
Moderately active	1.17 (1.03, 1.33)	3.24 (2.45, 4.29)	0.049	
Moderately inactive	1.30 (1.12, 1.51)	3.50 (2.84, 4.31)	0.048	
Inactive	1.82 (1.54, 2.16)	4.33 (3.58, 5.25)		
Genetic score tertile				
Low genetic risk	1	2.56 (2.14, 3.06)		
Medium genetic risk	1.40 (1.21, 1.63)	3.83 (3.18, 4.61)	0.81	
High genetic risk	1.88 (1.61, 2.19)	4.83 (4.02, 5.80)		

^aInteraction is with BMI, PA index and genetic score treated as continuous variables.