

Supplementary Table S1. SNP information

ID	Gene	Chromosome position	Functional consequence	Allele (major/minor)	PCR primers
rs822396	ADIPOQ	186566877	intron1	G/A	F: CCCAGGCTGATCGCACCTATTA R: ATAAAGGGTGACGGGGGGCTTA
rs822393	ADIPOQ	186566326	intron1	C/T	F: TCTGACTTCCAAATCGGTGAGCTTT R: GTCGCTAGCATCTTGCGCTCTC
rs10937273	ADIPOQ	186549695	5'-flanking	G/A	F: CACAGCCCGAAGCACTCTCAAT R: GGGACAGCACCCAGAAACATC
rs2236242	VASPIN	94960052	intron4	A/T	F: GAAGGAGGTGCCCTGGAAGAGA R: TCCTCACAGGGACCCAGGATAAC
rs2211651	LEPR	66156021	3'-flanking	G/T	F: TGTAGAGGGATGACGAAGGCTCTC R: TGCAACTGCTTGGTTGCCTCTC
rs3790433	LEPR	65894342	intron2	C/T	F: TGGGAATGGGAGGCTTTCATTAGTGT R: AACTGTTTTCTCCAAATTTCAACAT
rs12037879	LEPR	65942707	intron2	G/A	F: CACACAAGCACACATATGCAGAACA R: CAGGGAATGGAGGTGGGTAAGG
rs11061971	ADIPOR2	1863728	intron2	T/A	F: GGCTCAGAAAAGGGCACCAACT R: ACAAATGTGCAAGTTTCTTCTTACCA

Supplementary Table S2. Comparison of the allele frequencies between the case and control groups

dbSNPID	Genotypes, <i>n</i> (%)			χ^2	<i>P</i>	MAF (%)	HWE- <i>P</i>
rs822396	AA	GA	GG	1.398	0.497	10.50	0.19
Case	194 (81.51)	42 (17.65)	2 (0.84)				
Control	189 (79.41)	44 (18.49)	5 (2.10)				
rs822393	CC	CT	TT	3.710	0.156	37.39	0.50
Case	52 (21.85)	130 (54.62)	56 (23.53)				
Control	68 (28.57)	111 (46.64)	59 (24.79)				
rs10937273	AA	GA	GG	0.254	0.881	39.81	0.59
Case	36 (15.13)	120 (50.42)	82 (34.45)				
Control	36 (15.13)	115 (48.32)	87 (36.55)				
rs2236242	AA	AT	TT	1.261	0.532	27.32	1.00
Case	21 (8.82)	96 (40.33)	120 (50.42)				
Control	15 (6.30)	95 (39.91)	128 (53.78)				
rs2211651	GG	GT	TT	0.990	0.610	27.63	0.26
Case	2 (0.84)	58 (24.37)	178 (74.79)				
Control	1 (0.42)	66 (27.73)	171 (71.85)				
rs3790433	CC	CT	TT	0.668	0.716	12.39	0.88
Case	184 (77.31)	49 (20.58)	5 (2.10)				
Control	182 (76.47)	53 (22.27)	3 (1.26)				
rs12037879	AA	GA	GG	0.650	0.722	20.06	1.00
Case	8 (3.36)	79 (33.19)	151 (63.45)				
Control	11(4.62)	74 (31.09)	153 (64.29)				
rs11061971	AA	TA	TT	1.323	0.516	36.87	0.57
Case	38 (15.97)	103 (43.28)	97 (40.76)				
Control	30 (12.60)	112 (47.06)	96 (40.34)				

Supplementary Table S3. Association of allele frequency with T2DM

SNPID	Alleles	Case, <i>n</i> (%)	Control, <i>n</i> (%)	χ^2	<i>P</i>	OR (95% CI)
rs822393	C	233 (48.90)	249 (52.30)	1.075	0.299	0.874 (0.678, 1.127)
	T	243 (51.10)	227 (47.70)			
rs822396	A	429 (90.10)	423 (88.90)	0.402	0.526	1.142 (0.755, 1.731)
	G	47 (9.90)	53 (11.10)			
rs10937273	A	192 (40.30)	187 (39.30)	0.110	0.741	1.045 (0.806, 1.354)
	G	284 (59.70)	289 (60.70)			
rs2236242	A	143 (30.00)	124 (26.10)	1.879	0.171	1.219 (0.918, 1.618)
	T	333 (70.00)	352 (73.90)			
rs2211651	G	62 (13.00)	69 (14.50)	0.434	0.510	0.883 (0.610, 1.278)
	T	414 (87.00)	407 (85.50)			
rs3790433	C	418 (87.80)	417 (87.60)	0.010	0.921	1.020 (0.692, 1.501)
	T	58 (12.20)	59 (12.40)			
rs12037879	A	95 (20.00)	95 (20.00)	0.000	1.000	1.000 (0.728, 1.374)
	G	381 (80.00)	381 (80.00)			
rs11061971	A	182 (38.20)	172 (36.10)	0.450	0.503	1.094 (0.841, 1.423)
	T	294 (61.80)	304 (63.90)			

Note. *CI*, confidence interval; *OR*, odds ratio.

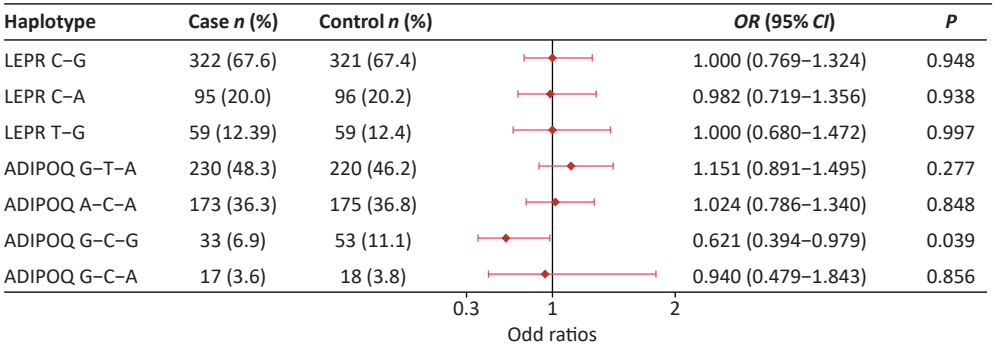
Supplementary Table S4. Association of genetic models with T2DM

SNPs	Genetic models	<i>P</i>	OR (95% CI)	Adjusted OR (95% CI)
rs822396	AA vs. GA+GG	0.563	1.143 (0.726, 1.799)	0.783 (0.506, 1.212)
	GG vs. GA+AA	0.253	0.395 (0.076, 2.056)	0.823 (0.526, 1.289)
rs822393	CC vs. CT+TT	0.091	0.699 (0.461, 1.060)	0.889 (0.551, 1.436)
	TT vs. CT+CC	0.748	0.934 (0.613, 1.421)	0.441 (0.077, 2.522)
rs10937273	AA vs. GA+GG	1.000	1.000 (0.606, 1.651)	0.946 (0.561, 1.594)
	GG vs. GA+AA	0.632	0.912 (0.627, 1.328)	0.826 (0.556, 1.229)
rs2236242	AA vs. AT+TT	0.292	1.445 (0.726, 2.877)	1.639 (0.806, 3.335)
	TT vs. AT+AA	0.492	0.881 (0.615, 1.264)	0.799 (0.548, 1.167)
rs2211651	GG vs. GT+TT	0.562	2.008 (0.181, 22.300)	2.445 (0.218, 27.486)
	TT vs. GT+GG	0.468	1.162 (0.774, 1.746)	1.066 (0.696, 1.632)
rs3790433	CC vs. CT+TT	0.828	1.048 (0.685, 1.606)	1.066 (0.681, 1.669)
	TT vs. CT+CC	0.476	1.681 (0.397, 7.115)	1.733 (0.381, 7.877)
rs12037879	AA vs. GA+GG	0.482	0.718 (0.283, 1.817)	0.533 (0.196, 1.450)
	GG vs. GA+AA	0.849	0.964 (0.663, 1.402)	0.888 (0.599, 1.315)
rs11061971	AA vs. AT+TT	0.295	1.317 (0.786, 2.208)	1.081 (0.628, 1.862)
	TT vs. AT+AA	0.926	1.018 (0.706, 1.467)	1.074 (0.731, 1.578)

Note. Adjusted for BMI; *CI*, confidence interval; *OR*, odds ratio.

Supplementary Table S5. Linkage disequilibrium analyses of the eight SNP Loci

SNP	<i>D'</i>	<i>r</i> ²
rs822396-rs822393	0.968	0.108
rs822396-rs10937273	0.632	0.031
rs822393-rs10937273	0.896	0.520
rs2211651-rs3790433	0.399	0.142
rs2211651-rs12037879	0.424	0.007
rs12037879-rs3790433	1.000	0.036



Supplementary Figure S1. Haplotype distribution of the Gene SNPs. *CI*, confidence interval; *OR*, odds ratio.