Association Between Transcription Factor 7-Like-2 Polymorphisms and Type 2 Diabetes Mellitus in a Ghanaian Population

Supplementary Appendix 1

Text Summary

The supplementary material contains detailed information on the modified and simplified salting-out technique for DNA extraction (pp.2-3). Quality control and troubleshooting procedures for the genotyping of the SNPs have been shown on page 4-5. Figure S1 and S2 shows the results of DNA purity and concentrations. Figure S3 and S4 demonstrate the genotyping results of the two SNPs. Table S1 shows the recipe of the master mix for Quality Control and trouble shooting. Table S2-S5 shows the association between rs12255372 and rs7903146 with cardiometabolic risk factors in both cases and control participants. Supplementary appendix two shows details of logistic regression models used to examine associations.

All images are in Joint Photographic Experts Group (Jpeg) format.

Modified Salting-Out Non-enzymatic DNA extraction Method

Erythrocyte Lysis Buffer

Add 9 volume of 0.155M NH_4Cl (8.291g NH_4Cl into 1L dH_2O) to 1 volume of 0.17M Tris HCL (pH= 7.65)

Wash Buffer

Mix 5 ml of 1.0M NaCl and 10 ml of 0.5M EDTA (pH=8.0) into 985 mL dH2O

TKM 2 (High salt buffer) Preparation (100 ml)

0.121g of Tris HCL (10mM, pH=7.6), 0.074g of KCl (10mM), 1.203g of $MgCl_2$ (10mM), 0.074g of EDTA (2mM), 0.467g of NaCl (0.4M) is dissolved in 100ml of dH_2O.

Saturated Sodium chloride (6M NaCl) solution

Dissolve 8.765g of NaCl in 25 ml of dH_2O

Steps

In a nuclease-free tube (Eppendorf Tube) add 3:1 ratio of Erythrocyte Lysis Buffer to whole blood sample (at 37 ℃ temperature). Incubate the mixture for 5 minutes. Centrifuged the mixture at 8000 rpm for 3 minutes. Discard the supernatant and keep the sediment. To ensure complete removal of haemoglobin stain, add 600 µl of wash buffer to the sediment and centrifuge the mixture at low speed (6000 rpm) for 5 minutes. Discard the supernatant. Resuspend the white cell pellet with 300 µl of TKM-2 buffer and add 40 µl of 10% SDS. Mix thoroughly by 30-secs vertexing and incubate at 37℃ for 5 minutes. At the end of the incubation, add 100 µl of 6M NaCl and vortex for 15 seconds to precipitate the proteins and leave DNA out in solution. Centrifuge the content at 8000 rpm for 5 minutes. Transfer the supernatant into a new Eppendorf tube containing 300 µl of absolute isopropanol (99.9%). Invert the tube slowly several times to precipitate DNA. Centrifuge at 8000 rpm for 10 minutes to pellet down the precipitated DNA. Discard the supernatant and add 70% isopropanol, mix slowly to remove any excess salts. Final centrifugation is conducted at 8000 rpm for 5 minutes to pellet down the DNA. Discard the supernatant. Place Eppendorf tube downward on the tissue paper to drain the ethanol completely. Air-dry the DNA and after thorough drying, add 50 µl of nuclease-free water buffer to dissolve the DNA.

Results visualisation of DNA products isolated with MSO method

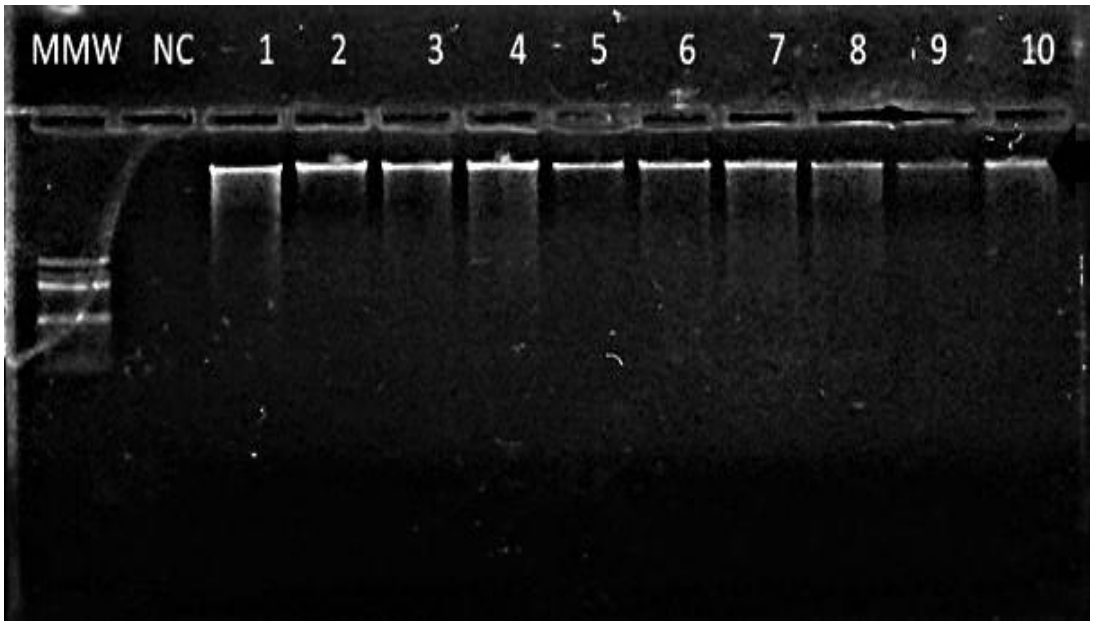

Figure S1: 1% agarose gel electrophoresis of genomic DNA extracted from MSO method

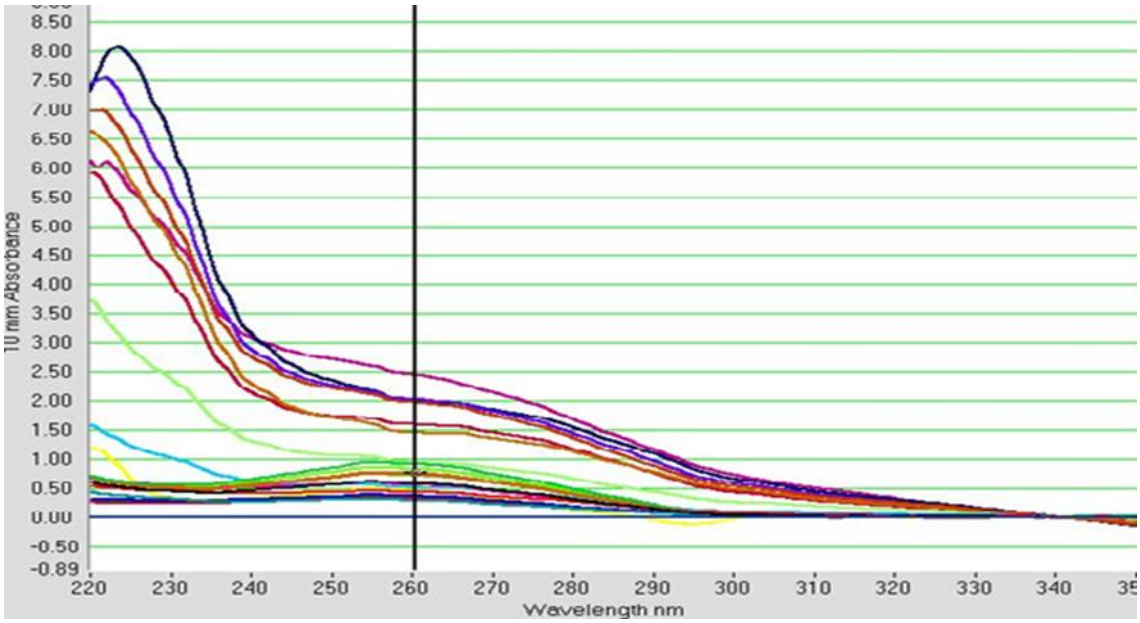

Figure S2: A typical Nanodrop curve of absorbance against the path of light travel (wavelength)

MTPA Quality control and Trouble Shooting

The optimization step of the MTPA solely depends on the primer concentration. Where appropriate, increase the Mg++ concentration of the commercially prepared OneTaq® 2X Master Mix (New England Biolabs) by 0.2 µM during the optimization step.

Amplification of common product

Amplification of common primers was performed in a total volume of 25µL containing ≥50 ng of DNA template, 0.4 µM each of forward and reverse outer primers and 1X of OneTaq® 2X Master Mix (New England Biolabs).

MTPA reaction

Allele-specific Amplification

Forward outer vs reverse inner primers; and Forward inner vs reverse outer primer combinations were used to optimise the allele-specific amplification conditions. The reaction was completed with 0.4 µM each of forward-outer vs reverse-inner primers in 25 uL reaction volume using the 1X of OneTaq® 2X Master Mix (New England Biolabs).

Table S1: Recipe for the master mix for Quality Control

Component	Initial Conc.	Final conc.	Volume (µL) Per Sample
Amplification of common Primers			
FOP	10 µM	0.4 µM	1
ROP	10 µM	0.4 µM	1
MTPA reaction			
FIP	10 µM	0.2 µM	0.5
RIP	10 µM	0.2 µM	0.5
FOP	10 µM	0.2 µM	0.5
ROP	10 µM	0.2 µM	0.5
Amplification of mutant Allele			
FIP	10 µM	0.4 µM	1
ROP	10 µM	0.4 µM	1
Amplification of ancestral Allele			
RIP	10 µM	0.2 µM	1
FOP	10 µM	0.4 µM	1
Onetaq® 2x Master Mix	2X	1X	12.5
Nuclease Free water	-	-	
DNA sample	>50 ng/ **µL**	>50 ng/ **µL**	1

FIP- forward inner primer; RIP- reverse inner primer; FOP; forward outer primer; ROP: reverse outer primer

Results of TCF7L2- rs7903146 and rs12255372 genotyping

Figure S3: 2% agarose gel electrophoresis of TCF7L2- rs7903146

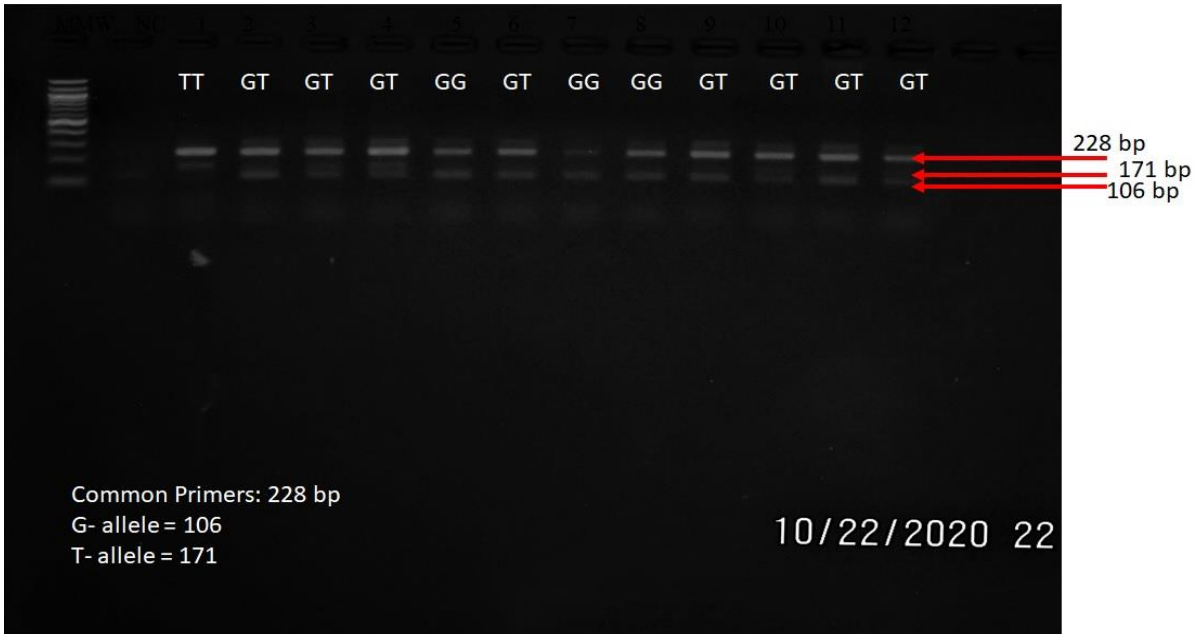

Figure S4: 2% agarose gel electrophoresis of *TCF7L2*- rs12255372

Table S2: Association of TCF7L2 SNPs with Anthropometric and biochemical markers

Variables	Wild type	Mutant type	P-value
	rs7903146		
Controls (N=110)			
BMI (Kg/m^2)	26.14 ±5.40	26.07 ±3.45	0.924
Systolic BP (mmHg)	120.96 ±19.15	121..49 ±17.96	0.142
Diastolic BP (mmHg)	75.57 ±11.11	76.74 ±11.28	0.403
Triglycerides (mmol/l)	1.31 ±0.33	1.27 ±0.61	**0.048**
T. Chol (mmol/l)	4.52 ±0.98	4.76 ±1.13	0.465
HDL-C(mmol/l)	1.24 ±0.23	1.22 ±0.30	0.163
LDL-C (mmol/l)	3.19 ±0.50	3.42 ±0.85	**0.001**
FPG (mmol/l)	4.63 ±0.75	5.02 ±0.98	0.069
HbA1c (%)	4.81 ±0.52	4.85 ±0.66	0.981
Cases (N=106)			
BMI (Kg/m^2)	28.62 ±5.71	28.04 ±5.49	0.160
Systolic BP (mmHg)	138.19 ±21.46	131.78 ±19.05	**0.015**
Diastolic BP (mmHg)	84.65 ±12.93	83.36 ±11.39	0.450
Triglycerides (mmol/l)	1.53 ±0.46	1.74 ±0.68	0.284
T. Chol (mmol/l)	4.95 ±0.94	5.35 ±1.04	0.110
HDL-C(mmol/l)	1.06 ±0.22	0.98 ±0.24	0.283
LDL-C (mmol/l)	3.31 ±0.72	3.48 ±1.01	**0.046**
FPG (mmol/l)	7.38 ±4.52	9.16 ±4.64	0.414
HbA1c (%)	6.23 ±1.49	7.24 ±1.92	0.099
	rs12255372		
Controls (N=110)			
BMI (Kg/m^2)	25.72 ±4.64	27.17 ±3.53	0.493
Systolic BP (mmHg)	121.56 ±17.90	120.41 ±21.10	0.145
Diastolic BP (mmHg)	76.00 ±11.29	76.83 ±10.98	0.402
Triglycerides (mmol/l)	1.20 ±0.36	1.54 ±0.72	**0.003**
T. Chol (mmol/l)	4.51 ±1.03	5.04 ±1.07	**0.048**
HDL-C(mmol/l)	1.24 ±0.26	1.21 ±0.31	0.122
LDL-C (mmol/l)	3.27 ±0.61	3.45 ±0.99	**0.001**
FPG (mmol/l)	4.67 ±0.71	5.34 ±1.19	**0.005**
HbA1c (%)	4.72 ±0.55	5.17 ±0.63	**<0.001**
Cases (N=106)			
BMI (Kg/m^2)	27.54 ±6.00	29.05 ±4.75	**0.044**
Systolic BP (mmHg)	128.57 ±17.09	139.82 ±21.41	**0.003**
Diastolic BP (mmHg)	81.61 ±10.69	86.49 ±12.60	0.077
Triglycerides (mmol/l)	1.63 ±0.57	1.77 ±0.71	0.476
T. Chol (mmol/l)	5.30 ±1.09	5.18 ±0.95	0.339
HDL-C(mmol/l)	1.02 ±0.26	0.96 ±0.19	0.459
LDL-C (mmol/l)	3.48 ±0.99	3.38 ±0.89	0.061
FPG (mmol/l)	8.47 ±4.31	9.06 ±5.12	0.935
HbA1c (%)	6.69 ±1.52	7.40 ±2.21	0.078

Mt- mutant type, Wt- wild type. Highlighted P-values are statistically significant.

Table S3: Logistic regression analysis of TCF7L2 SNPs associated with cardiometabolic risk factors

Variables	Wild type (C-allele)	Mutant type (T-allele)	aOR (95%CI)	P-value
		rs7903146		
Controls (N=110)				
High BP	4 (8.2)	6 (9.8)	0.991 (0.25-3.96)	0.990
High TC	1 (2.0)	5 (8.2)	5.14 (0.57-46.67)	0.146
High TG	7 (14.3)	9 (14.8)	0.93 (0.31-2.77)	0.890
Low HDL-C	24 (49.0)	28 (45.9)	1.12 (0.46-2.73)	0.800
High LDL-C	11 (22.4)	25 (41.0)	2.98 (1.23-7.30)	**0.017**
Atherogenic dyslipidaemia	1 (2.0)	4 (6.6)	3.71 (0.39-35.43)	0.254
Overweight/Obesity	23 (46.9)	37 (60.7)	1.73 (0.78-3.76)	0.164
MetS	6 (12.2)	8 (13.1)	1.02 (0.32-3.28)	0.969
Cases (N=106)				
High BP	11 (42.3)	25 (31.3)	0.62 (0.25-1.55)	0.307
High TC	1 (3.8)	12 (15.0)	4.46 (0.55-36.17)	0.162
High TG	10 (38.5)	51 (63.7)	2.95 (1.16-7.50)	**0.023**
Low HDL-C	18 (69.2)	63 (78.8)	1.73 (0.62-4.83)	0.299
High LDL-C	13 (50.0)	51 (63.7)	1.95 (0.75-5.10)	0.174
Atherogenic dyslipidaemia	7 (26.9)	37 (46.3)	2.67 (0.95-7.52)	0.063
Overweight/Obesity	16 (61.5)	56 (70.0)	1.48 (0.58-3.79)	0.405
MetS	15 (57.7)	55 (68.8)	1.70 (0.66-4.39)	0.272
		rs12255372		
Controls (N=110)				
High BP	6 (7.4)	4 (13.8)	1.48 (0.35-6.45)	0.597
High TC	2 (2.5)	4 (13.8)	14.0 (1.43-137.32)	**0.023**
High TG	9 (11.1)	7 (24.1)	1.96 (0.64-6.02)	0.239
Low HDL-C	39 (48.1)	13 (44.8)	1.41 (0.48-4.18)	0.533
High LDL-C	23 (28.4)	13 (44.8)	3.12 (1.14-8.56)	**0.027**
Atherogenic dyslipidaemia	4 (4.9)	1 (3.4)	0.65 (0.08-6.30)	0.710
Overweight/Obesity	42 (51.9)	18 (62.1)	1.55 (0.62-3.84)	0.348
MetS	7 (8.6)	7 (24.1)	2.91 (0.88-9.59)	0.080
Cases (N=106)				
High BP	15 (24.6)	21 (46.7)	3.01 (1.27-7.18)	**0.013**
High TC	8 (13.1)	5 (11.1)	0.91 (0.27-3.09)	0.883
High TG	31 (50.8)	30 (66.7)	1.89 (0.83-4.32)	0.131
Low HDL-C	45 (73.8)	36 (80.0)	1.46 (0.56-3.88)	0.439
High LDL-C	36 (41.0)	28 (62.2)	1.24 (0.53-2.94)	0.622
Atherogenic dyslipidaemia	21 (34.4)	23 (51.1)	2.17 (0.91-5.17)	0.082
Overweight/Obesity	36 (59.0)	36 (80.0)	3.33 (1.30-8.53)	**0.012**
MetS	37 (60.7)	33 (73.3)	2.04 (0.84-4.97)	0.117

Mt- mutant type, Wt- wild type. Highlighted P-values are statistically significant. aOR-adjusted for age and sex

Supplementary Appendix 2

Logistic regression analysis to test association between rs7903146 and T2DM

Block 0: Beginning Block

Classification Table[a,b]

			Predicted		
			T2DM Status		Percentage
	Observed		0	1	Correct
Step 0	T2DM Status	0	110	0	100.0
		1	106	0	.0
	Overall Percentage				50.9

a. Constant is included in the model.
b. The cut value is .500

Variables in the Equation

		B	S.E.	Wald	df	Sig.	Exp(B)
Step 0	Constant	-.037	.136	.074	1	.786	.964

Variables not in the Equation

			Score	df	Sig.
Step 0	Variables	rs7903146	12.066	2	.002
		rs7903146(1)	2.832	1	.092
		rs7903146(2)	5.049	1	.025
	Overall Statistics		12.066	2	.002

Block 1: Method = Enter

Omnibus Tests of Model Coefficients

		Chi-square	df	Sig.
Step 1	Step	12.354	2	.002
	Block	12.354	2	.002
	Model	12.354	2	.002

Model Summary

Step	-2 Log likelihood	Cox & Snell R Square	Nagelkerke R Square
1	287.012[a]	.056	.074

a. Estimation terminated at iteration number 4 because parameter estimates changed by less than .001.

Hosmer and Lemeshow Test

Step	Chi-square	df	Sig.
1	.000	1	1.000

Contingency Table for Hosmer and Lemeshow Test

		T2DM Status = 0		T2DM Status = 1		
		Observed	Expected	Observed	Expected	Total
Step 1	1	49	49.000	26	26.000	75

	2	56	56.000	66	66.000	122
	3	5	5.000	14	14.000	19

Classification Table[a]

			Predicted		
			T2DM Status		Percentage
	Observed		0	1	Correct
Step 1	T2DM Status	0	49	61	44.5
		1	26	80	75.5
	Overall Percentage				59.7

a. The cut value is .500

Variables in the Equation

		B	S.E.	Wald	df	Sig.	Exp(B)
Step 1[a]	rs7903146			11.467	2	.003	
	rs7903146(1)	.798	.303	6.931	1	.008	2.221
	rs7903146(2)	1.663	.575	8.376	1	.004	5.277
	Constant	**-.634**	**.243**	**6.822**	**1**	**.009**	**.531**

Variables in the Equation

		95% C.I.for EXP(B)	
		Lower	Upper
Step 1[a]	rs7903146		
	rs7903146(1)	1.226	4.023
	rs7903146(2)	1.711	16.277
	Constant		

a. Variable(s) entered on step 1: rs7903146.

Block 2: Method = Enter

Omnibus Tests of Model Coefficients

		Chi-square	df	Sig.
Step 1	Step	1.468	1	.226
	Block	1.468	1	.226
	Model	13.821	3	.003

Model Summary

Step	-2 Log likelihood	Cox & Snell R Square	Nagelkerke R Square
1	285.544[a]	.062	.083

a. Estimation terminated at iteration number 4 because parameter estimates changed by less than .001.

Hosmer and Lemeshow Test

Step	Chi-square	df	Sig.
1	.255	3	.968

Contingency Table for Hosmer and Lemeshow Test

		T2DM Status = 0		T2DM Status = 1		
		Observed	Expected	Observed	Expected	Total
Step 1	1	35	34.007	15	15.993	50
	2	14	14.993	11	10.007	25
	3	36	36.043	37	36.957	73

	4	20	19.957	29	29.043	49
	5	5	5.000	14	14.000	19

Classification Table[a]

			Predicted		
			T2DM Status		Percentage
	Observed		0	1	Correct
Step 1	T2DM Status	0	49	61	44.5
		1	26	80	75.5
	Overall Percentage				59.7

Variables in the Equation

		B	S.E.	Wald	df	Sig.	Exp(B)
Step 1[a]	rs7903146			10.856	2	.004	
	rs7903146(1)	.779	.304	6.560	1	.010	2.180
	rs7903146(2)	1.625	.577	7.940	1	.005	5.081
	Sex(1)	**-.350**	**.289**	**1.464**	**1**	**.226**	**.705**
	Constant	**-.404**	**.307**	**1.739**	**1**	**.187**	**.667**

Variables in the Equation

		95% C.I.for EXP(B)	
		Lower	Upper
Step 1[a]	rs7903146		
	rs7903146(1)	1.201	3.959
	rs7903146(2)	1.640	15.738
	Sex(1)	.400	1.242
	Constant		

Block 3: Method = Forward Stepwise (Conditional)

Omnibus Tests of Model Coefficients

		Chi-square	df	Sig.
Step 1	Step	6.700	1	.010
	Block	6.700	1	.010
	Model	20.521	4	.000

Model Summary

Step	-2 Log likelihood	Cox & Snell R Square	Nagelkerke R Square
1	278.845[a]	.091	.121

a. Estimation terminated at iteration number 4 because parameter estimates changed by less than .001.

Hosmer and Lemeshow Test

Step	Chi-square	df	Sig.
1	1.640	6	.950

Contingency Table for Hosmer and Lemeshow Test

		T2DM Status = 0		T2DM Status = 1		
		Observed	Expected	Observed	Expected	Total
Step 1	1	27	27.041	10	9.959	37
	2	11	12.384	8	6.616	19
	3	30	30.499	26	25.501	56
	4	8	6.932	5	6.068	13

	5	18	16.720	19	20.280	37
	6	9	8.334	14	14.666	23
	7	4	5.410	15	13.590	19
	8	3	2.680	9	9.320	12

Classification Table[a]

			Predicted		
			T2DM Status		Percentage
	Observed		0	1	Correct
Step 1	T2DM Status	0	76	34	69.1
		1	49	57	53.8
	Overall Percentage				61.6

Variables in the Equation

		B	S.E.	Wald	df	Sig.	Exp(B)
Step 1[a]	rs7903146			11.494	2	.003	
	rs7903146(1)	.820	.311	6.966	1	.008	2.270
	rs7903146(2)	1.701	.584	8.471	1	.004	5.479
	Sex(1)	**-.372**	**.294**	**1.600**	**1**	**.206**	**.689**
	Age (1)	**.866**	**.341**	**6.449**	**1**	**.011**	**2.377**
	Constant	**-.627**	**.325**	**3.727**	**1**	**.054**	**.534**

Variables in the Equation

		95% C.I.for EXP(B)	
		Lower	Upper
Step 1[a]	rs7903146		
	rs7903146(1)	1.235	4.174
	rs7903146(2)	1.743	17.222
	Sex(1)	.387	1.227
	Age (1)	1.218	4.636
	Constant		

Model if Term Removed[a]

Variable		Model Log Likelihood	Change in -2 Log Likelihood	df	Sig. of the Change
Step 1	Age	-142.779	6.714	1	.010

a. Based on conditional parameter estimates

Logistic regression analysis to test association between rs12255372 and T2DM

Block 0: Beginning Block

Classification Table[a,b]

			Predicted		
			T2DM Status		
	Observed		0	1	Percentage Correct
Step 0	T2DM Status	0	110	0	100.0
		1	106	0	.0
	Overall Percentage				50.9

a. Constant is included in the model.
b. The cut value is .500

Variables in the Equation

		B	S.E.	Wald	df	Sig.	Exp(B)
Step 0	Constant	-.037	.136	.074	1	.786	.964

Variables not in the Equation

			Score	df	Sig.
Step 0	Variables	rs12255372	6.240	2	.044
		rs12255372(1)	5.193	1	.023
		rs12255372(2)	.436	1	.509
	Overall Statistics		6.240	2	.044

Block 1: Method = Enter

Omnibus Tests of Model Coefficients

		Chi-square	df	Sig.
Step 1	Step	6.276	2	.043
	Block	6.276	2	.043
	Model	6.276	2	.043

Model Summary

Step	-2 Log likelihood	Cox & Snell R Square	Nagelkerke R Square
1	293.090[a]	.029	.038

a. Estimation terminated at iteration number 3 because parameter estimates changed by less than .001.

Hosmer and Lemeshow Test

Step	Chi-square	df	Sig.
1	.000	1	1.000

Contingency Table for Hosmer and Lemeshow Test

		T2DM Status = 0		T2DM Status = 1		
		Observed	Expected	Observed	Expected	Total
Step 1	1	81	81.000	61	61.000	142
	2	5	5.000	7	7.000	12
	3	24	24.000	38	38.000	62

Classification Table[a]

			Predicted		
			T2DM Status		
	Observed		0	1	Percentage Correct
Step 1	T2DM Status	0	81	29	73.6
		1	61	45	42.5
	Overall Percentage				58.3

a. The cut value is .500

Variables in the Equation

		B	S.E.	Wald	df	Sig.	Exp(B)
Step 1[a]	rs12255372			6.148	2	.046	
	rs12255372(1)	.743	.311	5.709	1	.017	2.102
	rs12255372(2)	.620	.610	1.035	1	.309	1.859
	Constant	-.284	.170	2.798	1	.094	.753

Variables in the Equation

		95% C.I.for EXP(B)	
		Lower	Upper
Step 1[a]	rs12255372		
	rs12255372(1)	1.143	3.868
	rs12255372(2)	.563	6.140
	Constant		

a. Variable(s) entered on step 1: rs12255372.

Block 2: Method = Enter

Omnibus Tests of Model Coefficients

		Chi-square	df	Sig.
Step 1	Step	1.562	1	.211
	Block	1.562	1	.211
	Model	7.838	3	.049

Model Summary

Step	-2 Log likelihood	Cox & Snell R Square	Nagelkerke R Square
1	291.527[a]	.036	.048

a. Estimation terminated at iteration number 3 because parameter estimates changed by less than .001.

Hosmer and Lemeshow Test

Step	Chi-square	df	Sig.
1	.442	2	.802

Contingency Table for Hosmer and Lemeshow Test

		T2DM Status = 0		T2DM Status = 1		
		Observed	Expected	Observed	Expected	Total
Step 1	1	57	55.888	36	37.112	93
	2	24	25.112	25	23.888	49
	3	16	17.112	24	22.888	40
	4	13	11.888	21	22.112	34

Classification Table[a]

			Predicted		
			T2DM Status		
	Observed		0	1	Percentage Correct
Step 1	T2DM Status	0	81	29	73.6
		1	61	45	42.5
	Overall Percentage				58.3

a. The cut value is .500

Variables in the Equation

		B	S.E.	Wald	df	Sig.	Exp(B)
Step 1[a]	rs12255372			5.560	2	.062	
	rs12255372(1)	.722	.312	5.340	1	.021	2.058
	rs12255372(2)	.508	.618	.677	1	.411	1.663
	Sex(1)	-.359	.288	1.558	1	.212	.698
	Constant	-.050	.252	.039	1	.843	.951

Variables in the Equation

		95% C.I.for EXP(B)	
		Lower	Upper
Step 1[a]	rs12255372		
	rs12255372(1)	1.116	3.797
	rs12255372(2)	.495	5.581
	Sex(1)	.397	1.227
	Constant		

a. Variable(s) entered on step 1: Sex.

Block 3: Method = Forward Stepwise (Conditional)

Omnibus Tests of Model Coefficients

		Chi-square	df	Sig.
Step 1	Step	5.639	1	.018
	Block	5.639	1	.018
	Model	13.477	4	.009

Model Summary

Step	-2 Log likelihood	Cox & Snell R Square	Nagelkerke R Square
1	285.888[a]	.060	.081

a. Estimation terminated at iteration number 3 because parameter estimates changed by less than .001.

Hosmer and Lemeshow Test

Step	Chi-square	df	Sig.
1	9.794	4	.044

Contingency Table for Hosmer and Lemeshow Test

		T2DM Status = 0		T2DM Status = 1		
		Observed	Expected	Observed	Expected	Total
Step 1	1	43	46.516	29	25.484	72
	2	19	20.575	18	16.425	37
	3	16	13.414	12	14.586	28
	4	14	9.544	7	11.456	21
	5	13	10.494	14	16.506	27
	6	5	9.456	26	21.544	31

Classification Table[a]

			Predicted		
			T2DM Status		
	Observed		0	1	Percentage Correct
Step 1	T2DM Status	0	62	48	56.4
		1	47	59	55.7
	Overall Percentage				56.0

a. The cut value is .500

Variables in the Equation

		B	S.E.	Wald	df	Sig.	Exp(B)
Step 1[a]	rs12255372			5.272	2	.072	
	rs12255372(1)	.694	.317	4.812	1	.028	2.002
	rs12255372(2)	.632	.625	1.025	1	.311	1.882
	Sex(1)	-.376	.292	1.666	1	.197	.686
	Age (1)	.784	.335	5.473	1	.019	2.191
	Constant	-.225	.265	.721	1	.396	.798

Variables in the Equation

		95% C.I.for EXP(B)	
		Lower	Upper
Step 1[a]	rs12255372		
	rs12255372(1)	1.077	3.724
	rs12255372(2)	.553	6.401

	Sex(1)	.387	1.216
	Age (1)	1.136	4.227
	Constant		

a. Variable(s) entered on step 1: Age .

Model if Term Removed[a]

Variable		Model Log Likelihood	Change in -2 Log Likelihood	df	Sig. of the Change
Step 1	Age	-145.767	5.645	1	.018

a. Based on conditional parameter estimates