Supplementary Material

Table S1. Gene symbols, name, GenBank references, GO/pathway and SNPs information in the present study

Symbol	Gene name	BTA	Annotation	SNPs	Databases	Gene function annotation/pathway
Nuclear encoded mitochondrial genes						
ATP5O	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit	1	922635..929993	#1A/G, #2A/G	KEGG/GO	Oxidative phosphorylation/ATP metabolic process
MRPL39	mitochondrial ribosomal protein L39	1	10201965..10217711	#1C/G	GO	Mitochondrial matrix, mitochondrial ribosome
RCAN1	regulator of calcineurin 1	1	351708..362908	#1A/G, #2A/C, #3G/T, #4C/T, #5C/T	GO	Skeletal muscle tissue development, regulation of phoshpoprotein phosphatease activity
SIM2	single-minded homolog 2 (Drosophila)	1	152257720..152309623	#1C/T	GO	Regulation of transcription, DNA-dependent
ALDH4A1	aldehyde dehydrogenase 4 family, member A1	2	138269258..138302514	#1G/T, #2A/G	KEGG	Alanine, aspartate, arginine, proline and glutamate metabolism
FABP3	fatty acid binding protein 3	2	122723225..122783830	#1A/G	KEGG	PPAR signaling pathway
CRP	C-reactive protein, pentraxin-related	3	10100406..10104524	#1C/T, #2A/G	GO	Low-density lipoprotein binding, lipoprotein binding
FABP2	fatty acid binding protein 2	6	7105047..7108888*	#1C/T	KEGG	PPAR signaling pathway
POLRMT	polymerase (RNA) mitochondrial (DNA directed)	7	44851398..44864889*	#1C/T	GO	Transcription from mitochondrial promoter, RNA biosynthetic process
TFB1M	transcription factor B1, mitochondrial	9	93240590..93307575*	#1G/T	GO	rRNA processing, RNA processing, RNA modification
ENY2	enhancer of yellow 2 homolog (Drosophila)	14	57239786..57249241*	#1C/G	GO	Chromatin organization, transcription, regulation of transcription, DNA-dependent
FABP4	fatty acid binding protein 4	14	46833665..46838053*	#1A/G, #2A/G	KEGG	PPAR signaling pathway
MTFR1	mitochondrial fission regulator 1	14	31735268..31794502	#1C/G	GO	plasma membrane, mitochondrion
RAB2A	member RAS oncogene family	14	27864735..27937016	#1A/T	Biocarta	Rab GTPases Mark Targets In The Endocytotic Machinery,
TFB2M	transcription factor B2, mitochondrial	16	31552370..31570750	#1C/T, #2C/T, #3C/G, #4C/T	GO	Regulation of RNA metabolic process, transcription from mitochondrial promoter
UCP1	uncoupling protein 1	17	17467450..17473934	#1C/T	KEGG	PPAR signaling pathway, Huntington's disease
BAK1	BCL2-antagonist/killer 1	23	7655892..7658885*	#1C/T	Biocarta	Role of Mitochondria in Apoptotic Signaling,
SKIV2L	superkiller viralicidic activity 2-like (S. cerevisiae)	23	27130292..27142559	#1C/T	KEGG/GO	RNA degradation/response to nutrient, response to extracellular stimulus
TNF	tumor necrosis factor (TNF superfamily, member 2)	23	27533901..27536674*	#1A/G, #2A/G, #3A/T, #4A/G, #5C/T	KEGG	MAPK signaling pathway, Cytokine-cytokine receptor interaction, Type II diabetes mellitus, Type I diabetes mellitus
TFAM	transcription factor A, mitochondrial	28	46067520..46079446*	#1C/T, #2C/T, #3C/T,	KEGG/GO	Huntington's disease/RNA biosynthetic process
Long chain fatty acids uptake gene complex						
SLC2A2	solute carrier family 2, member 2	1	97220100..97250239	#1A/T	KEGG/GO	Type II diabetes mellitus/glucose transport, transmembrane transport,
SLC27A1	solute carrier family 27, member 1	7	5532596..5571774*	#1G/T	KEGG/GO	PPAR signaling pathway/fatty acid metabolic process
SLC27A2	solute carrier family 27, member 2	10	60221115..60275998*	#1C/T, #2C/T	KEGG/GO	PPAR signaling pathway/very-long chain fatty acid metabolic process
SLC27A4	solute carrier family 27, member 4	11	98959314..98971730	#1C/T, #2C/T, #3C/T, #4C/T	KEGG/GO	PPAR signaling pathway/fatty acid metabolic process
SLC25A27	solute carrier family 25, member 27	23	19860594..19882824	#1C/T	GO	Generation of precursor metabolites and energy, mitochondrial transport
Sauvagine/corticotropin-releasing factor/urotensin I family and related families						
CRH	corticotropin releasing hormone	14	32213670..32214253*	#1C/T, #2A/G, #3C/G, #4C/G	GO	Steroid biosynthetic process, glucocorticoid biosynthetic process, G-protein coupled receptor protein signaling pathway
UTS2	urotensin 2	16	422666610..42672557*	#1A/C, #2A/G	GO	Muscle system process, blood circulation
CRHR1	corticotropin releasing hormone receptor 1	19	46431524..46483532	#1A/G	KEGG/GO	Neuroactive ligand-receptor interaction/G-protein coupled receptor protein signaling pathway
UTS2R	urotensin 2 receptor	19	50814370..50815991*	#1C/T, #2I/D	GO	Regulation of cell growth, cytosolic calcium ion homeostasis
GNG3	Guanine nucleotide binding protein (G protein) gamma 3	29	41722354..41724965	#1A/G, #2G/T	KEGG	Chemokine signaling pathway, Taste transduction,
Lipogene lipogenesis/lipolysis enzymes						
FNDC3B	fibronectin type III domain containing 3B	1	95888014..96173201*	#1C/T	GO	Regulation of fat cell differentiation, positive regulation of developmental process
HMGCL	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase	2	129687547..129705680	#1A/G	GO	Acyl-CoA metabolic process; fatty acid binding, lipid binding
ACAT2	acetyl-Coenzyme A acetyltransferase 2	9	97466440..97481902	#1A/G, #2I/D	KEGG	Fatty acid metabolism
HMGCR	3-hydroxy-3-methylglutaryl-CoA reductase	10	6692478..6713108	#1A/C	KEGG	Terpenoid backbone biosynthesis; steroid biosynthetic process, cholesterol biosynthetic precess
SOAT1	sterol O-acyltransferase 1	16	62068139..62128367	#1C/T	KEGG/GO	Steroid biosynthesis/lipid transport
LIPE	lipase, hormone-sensitive	18	51216019..51227395	#1C/T, #2A/C, #3A/C, #4A/G	KEGG	Insulin signaling pathway,
HMGCS1	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)	20	31451294..31477033	#1A/G	Biocarta	SREBP control of lipid synthesis
ACSL5	acyl-CoA synthetase long-chain family member 5	26	33184653..33234958	#1C/T	KEGG	Fatty acid metabolism, PPAR signaling pathway
SCD1	stearoyl-CoA desaturase (delta-9-desaturase)	26	21137945..21148317*	#1C/T, #2A/G, #3C/T		
DHCR7	7-dehydrocholesterol reductase	29	48930324..48950642*	#1A/G, #2A/G	KEGG/GO	Steroid biosynthesis/cholesterol metabolic process, lipid biosynthetic process
PNPLA2	patatin-like phospholipase domain containing 2	29	50742385..50747161*	#1C/G, #2C/T, #3C/T	GO	Neutral lipid metabolic process, acylglycerol metabolic process, triglyceride metabolic process
FADS1	Fatty acid desaturase 1	29	40938865..40952991*	#1C/T, #2A/G	KEGG	Biosynthesis of unsaturated fatty acids
FADS2	Fatty acid desaturase 2	29	41045232..42082249	#1A/G	KEGG	Biosynthesis of unsaturated fatty acids, PPAR

						signaling pathway
FADS3	Fatty acid desaturase 3	29	41087530..41102447*	#1C/T, #2C/T	GO	Fatty acid biosynthetic process, unsaturated fatty acid biosynthetic process
Calpain/calpasatin or related genes						
CAPN7	calpain 7	1	153971502..154022489	#1C/T	GO	Proteolysis, calcium ion binding, acting on L-amino acid peptides, cysteine-type peptidase activity
CAPN10	Calpain 10	3	120330696..120339474*	#1A/G, #2A/C	GO	Proteolysis, response to hormone stimulus, regulation of glucose transport, acting on L-amino acid peptides, cysteine-type peptidase activity
NMU	neuromedin U	6	72732591..72760814*	#1A/C, #2A/G	GO	Regulation of muscle contraction
CAST	calpastatin	7	98444979..98581253	#1A/G, #2C/T, #3G/T	GO	Syncytium formation by plasma membrane fusion, myoblast fusion, myotube differentiation, muscle cell differentiation,
CAPN3	calpain 3	10	37829007..37885645	#1A/G	GO	Proteolysis, muscle organ development, striated muscle cell development
CAPN14	calpain 14	11	68678749..68715047	#1A/G, #2A/G	GO	Proteolysis, calcium ion binding, acting on L-amino acid peptides, cysteine-type peptidase activity
CAPN5	calpain 5	15	57256223..57313832	#1A/C, #2A/G, #3A/G	GO	Proteolysis, calcium ion binding, acting on L-amino acid peptides, cysteine-type peptidase activity
CAPN8	calpain 8	16	27702961..27747884*	#1A/G	GO	Proteolysis, calcium ion binding, acting on L-amino acid peptides, cysteine-type peptidase activity
DPT	dermatopontin	16	37106632..37143040*	#1C/T	GO	Cell adhesion, collagen fibril organization
CAPN12	calpain 12	18	48743599..48755715*	#1I/D, #2A/G	GO	Proteolysis, calcium ion binding, acting on L-amino acid peptides, cysteine-type peptidase activity
CAPNS1	calpain, small subunit 1	18	46987527..46994447	#1A/G, #2C/T	GO	Proteolysis, calcium ion binding, acting on L-amino acid peptides, cysteine-type peptidase activity
TNNT1	troponin T type 1 (skeletal, slow)	18	62725898..62735263	#1C/T, #2A/C	GO	Skeletal muscle contraction, negative regulation of multicellular organismal process
CAPN11	calpain 11	23	17802323..17820479	#1C/T, #2A/G	GO	Proteolysis, calcium ion binding, acting on L-amino acid peptides
CAPN9	calpain 9	28	34723916..34744575*	#1A/G	GO	proteolysis, calcium ion binding, acting on L-amino acid peptides, cysteine-type peptidase activity
CAPN1	calpain 1	29	44063463..44113492	#1C/G, #2C/T, #3A/G, #4C/T, #5A/G	Biocarta/KEGG	mCalpain and friends in Cell motility/apoptosis, Alzheimer's disease
TNNI2	troponin I type 2 (skeletal, fast)	29	50285049..50287648*	#1A/G, #2C/T	GO	Skeletal muscle contraction, negative regulation of multicellular organismal process
Reverse cholesterol transport genes						
PON1	paraoxidase 1	4	12389566..12423459*	#1A/G	GO	Regulation of lipid transport, regulation of sterol transport
ABCA1	ATP binding cassette A1	8	96274035..96390357*	#1G/T, #2A/G, #5A/G, #6C/G, #7A/G, #8C/T	KEGG/ GO	ABC transporters/lipoprotein metabolic process, reverse cholesterol transport
LIPC	hepatic lipase	10	51758867..51921040*	#1C/T, #2A/G	KEGG/GO	Glycerolipid metabolism/reverse cholesterol transport
APOB	apolipoprotein B	11	77953432..78040408	#1A/G, #2 C/T, #3A/G	GO	Lipoprotein metabolic process, Cholesterol homeostasis
PLTP	phospholipid transfer protein	13	75374573..75384734*	#1G/T, #2C/T	KEGG	PPAR signaling pathway,
APOA1	apolipoprotein A1	15	27932198..27934085*	#1G/T, #2A/G	KEGG	PPAR signaling pathway
SCARB1	scavenger receptor B1	17	53180929..53273732	#1A/C, #2C/T	GO	Steroid metabolic process, cholesterol metabolic process
APOC2	apolipoprotein C2	18	53057717..53059957	#1A/G	GO	Triglyceride metabolic process, lipid transport
APOE	apolipoprotein E	18	53040105..53042792	#1C/G, #2C/T, #3A/G, 4#C/T, #5A/G, 6#C/T	KEGG/GO	Alzheimer's disease/lipid homeostasis
LIPG	endothelial lipase	24	49687542..49702609	#1A/G	KEGG/GO	Glycerolipid metabolism/reverse cholesterol transport
Heparan sulfate and heparin metabolism genes						
EXTL1	Exostoses (multiple)-like 1	2	127647570..127665188*	#1C/G	KEGG	Heparan sulfate biosynthesis,
HS6ST1	Heparin sulfate 6-O-sulfotransferase 1	2	4111871..4149372	#1A/T	KEGG	Heparan sulfate biosynthesis,
NDST3	N-deacetylase/N-sulfotransferase (heparin glucosaminyl) 3	6	8124491..8251738*	#1C/T	KEGG	Heparan sulfate biosynthesis
DSEL	Dermatan sulfate epimerase-like	24	9738913..9748901	#1C/T	GO	Integral to membrane, heparan sulfate biosynthesis
Other genes						
PSMG1	proteasome (prosome, macropain) assembly chaperone 1	1	140726627..140739236*	#1A/C	GO	Protein complex assembly, cellular macromolecular complex subunit organization
SCP2	Sterol carrier protein 2	3	93846491..93968364*	#1A/G, #2C/T	KEGG	Primary bile acid biosynthesis, PPAR signaling pathway
GPR37	G protein-coupled receptor 37	4	89805488..89823611*	#1C/T, #2A/G, #3A/G	Biocarta/KEGG	Role of Parkin in the Ubiquitin-Proteasomal Pathway/Parkinson's disease
IGFBP6	Insulin-like growth factor binding protein 6	5	27044008..27047853	#1A/C	GO	Regulation of growth, regulation of cell proliferation
LRPAP1	Low density lipoprotein receptor-related protein associated protein 1	6	107207883..107221545	#1C/T	GO	Regulation of very-low-density lipoprotein particle clearance
PCSK1	Proprotein convertase subtilishin/kexin type 1	7	98155674..98199484*	#1A/C, #2C/T	GO	Response to fatty acid, response to interleukin-1, regulation of hormone levels,
EFEMP1	EGF containing fibulin-like extracellular matrix protein 1	11	38338746..38408288*	#1C/T, #2A/C	GO	Calcium ion binding, growth factor activity
ASB3	ankyrin repeat and SOCS box-containing 3	11	36254029..36371025*	#1G/T, #2C/T	GO	Proteolysis, intracellular signaling cascade, macromolecule catabolic process
ARHGAP1	Rho GTPase activating protein 1	15	77496430..77513093*	#1A/G, #2C/T	Biocarta/GO	Rho cell motility signaling pathway/GTPase activator activity
FTO	Fat mass and obesity associated	18	22118201..22541540	#1A/G, #2A/G, #3C/T, #4C/T, #5G/T, #6G/T, #8C/T, #9C/T	GO	Adipose tissue development, oxidative demethylation, regulation of lipid storage
CHD9	chromodomain helicase DNA binding protein 9	18	21634592..21859834	#1C/T, #2A/C	GO	Chromatin assembly or disassembly, transcription, chromatin modification, regulation of transcription
ASPA	aspartoacylase	19	24825866..24847110	#1C/T, #2C/G	GO	Alanine, aspartate and glutamate metabolism, Histidine metabolism,
GH1	growth hormone 1	19	48768618..48772014*	#1A/G	KEGG/GO	Jak-STAT signaling pathway/positive regulation of

						multicellular organism growth
NEIL1	Nei endonuclease Ⅷ-like 1	21	33855755..33861979*	#1C/T, #2C/T, #3C/G, #4A/G	KEGG/GO	Base excision repair/DNA N-glycosylase activity
HIST1H1C	Histone cluster 1	23	31636903..31639367	#1A/G, #2A/G, #3A/G	GO	DNA packaging, chromatin assembly or disassembly
MTCH1	Mitochondrial carrier 1	23	10854191..10873802*	#1A/G	GO	Apoptosis, activation of caspase activity, transmembrane transport
IGF2	Insulin-like growth factor 2	29	50046626..50065231	#1C/T	KEGG	Insulin signaling pathway, Type II diabetes mellitus, Type I diabetes mellitus

*These genes yielded significant single marker-single trait associations (P<0.05).

Table S2. Gene and genotype frequency of sires and their F_1 offspring

Marker	*G	N	sire	dam	N	F_1	HW (χ2)	P_1	χ2	P_2
Hardy-Weinberg equilibrium markers										
ATP5O#2 A/G	AA	8	0.1860	-	194	0.26	0.5020	0.7780	2.2286	0.3281
	AG	22	0.5116	-	402	0.5296			0.0530	0.8179
	GG	13	0.3023	-	163	0.2148				
	A	38	0.4419	0.5990	790	0.5204			2.0140	0.1561
	G	48	0.5581	0.4010	728	0.4796				
PSMG1#1 A/C	AA	10	0.2326	-	136	0.1785	0.0683	0.9664	1.6106	0.4470
	AC	23	0.5349	-	386	0.5066			0.1306	0.7178
	CC	10	0.2326	-	240	0.3150				
	A	43	0.5000	0.3635	658	0.4318			1.5421	0.2143
	C	43	0.5000	0.6365	866	0.5682				
RCAN1#4 C/T	CC	39	0.9070	-	227	0.3003	0.0002	0.9999	67.4641	0.0000
	CT	4	0.0930	-	505	0.6680			58.1709	0.0000
	TT	0	0.0000	-	24	0.0317				
	C	82	0.9535	0.3150	959	0.6343			36.5196	0.0000
	T	4	0.0465	0.6850	553	0.3657				
RCAN1#5 C/T	CC	0	0.0000	-	45	0.0592	1.7604	0.4147	94.0691	0.0000
	CT	8	0.1860	-	574	0.7553			66.1055	0.0000
	TT	35	0.8140	-	141	0.1855				
	C	8	0.0930	0.7807	664	0.4368			39.5395	0.0000
	T	78	0.9070	0.2193	856	0.5632				
ALDH4A1#1 G/T	GG	6	0.1395	-	96	0.1270	0.0359	0.9822	0.5296	0.7674
	GT	22	0.5116	-	354	0.4683			0.3072	0.5794
	TT	15	0.3488	-	306	0.4048				
	G	34	0.3953	0.3269	546	0.3611			0.4125	0.5207
	T	52	0.6047	0.6731	966	0.6389				
EXTL1#1 C/G	CC	10	0.2326	-	58	0.0786	4.4694	0.1070	12.2232	0.0022
	GCC	15	0.3488	-	288	0.3902			0.2934	0.5881
	GG	18	0.4186	-	392	0.5312				
	C	35	0.4070	0.1404	404	0.2737			7.1425	0.0075
	G	51	0.5930	0.8596	1072	0.7263				
HMGCL#1 A/G	AA	0	0.0000	-	19	0.0245	2.0221	0.3638	17.8617	0.0001
	AG	7	0.1628	-	362	0.4677			15.2922	0.0000
	GG	36	0.8372	-	393	0.5078				
	A	7	0.0814	0.4354	400	0.2584			13.6471	0.0002
	G	79	0.9186	0.5646	1148	0.7416				
SCP2#2 C/T	CC	2	0.0465	-	32	0.0444	1.2216	0.5429	1.7384	0.4193
	CT	21	0.4884	-	281	0.3897			1.6516	0.1987
	TT	20	0.4651	-	408	0.5659				
	C	25	0.2906	0.1878	345	0.2393			1.1706	0.2793
	T	61	0.7093	0.8122	1097	0.7607				
GPR37#2 A/G	AA	22	0.5238	-	199	0.2722	1.4962	0.4733	13.2121	0.0014
	AG	17	0.4048	-	391	0.5349			2.6983	0.1005
	GG	3	0.0714	-	141	0.1929				
	A	61	0.7262	0.3532	789	0.5397			11.1649	0.0008
	G	23	0.2738	0.6468	673	0.4603				
PON1#1 A/G	AA	8	0.1860	-	333	0.4416	0.0380	0.9812	116.3949	0.0000
	AG	23	0.5349	-	412	0.5464			0.0218	0.8825
	GG	12	0.2791	-	9	0.0119				
	A	39	0.4535	0.9762	1078	0.7149			26.5041	0.0000
	G	47	0.5465	0.0238	430	0.2851				
LRPAP1#1 C/T	CC	4	0.0930	-	114	0.1512	2.8641	0.2388	6.6266	0.0364
	CT	14	0.3256	-	350	0.4642			3.1499	0.0759
	TT	25	0.5814	-	290	0.3846				
	C	22	0.2558	0.5108	578	0.3833			5.6325	0.0176
	T	64	0.7442	0.4892	930	0.6167				
CAST#2 C/T	CC	10	0.2326	-	57	0.0743	1.5908	0.4514	14.4982	0.0007
	CT	19	0.4419	-	338	0.4407			0.0002	0.9879
	TT	14	0.3256	-	372	0.4850				
	C	39	0.4535	0.1358	452	0.2947			9.7263	0.0018
	T	47	0.5465	0.8642	1082	0.7053				
PCSK1#2 C/T	CC	6	0.1395	-	196	0.2586	0.0187	0.9907	21.7487	0.0000
	CT	18	0.4186	-	438	0.5778			4.2077	0.0402
	TT	19	0.4419	-	124	0.1636				
	C	30	0.3488	0.7461	830	0.5475			12.9170	0.0003
	T	56	0.6512	0.2539	686	0.4525				
SLC27A1#1 G/T	GG	12	0.2791	-	266	0.3446	0.2009	0.9044	5.7215	0.0572
	GT	18	0.4186	-	381	0.4935			0.9149	0.3388
	TT	13	0.3023	-	125	0.1619				
	G	42	0.4884	0.6943	913	0.5913			3.5585	0.0592
	T	44	0.5116	0.3057	631	0.4087				
ABCA1#2 A/G	AA	5	0.1190	-	65	0.0866	0.1297	0.9372	7.8768	0.0195

	AG	28	0.6667	-	360	0.4794			5.5844	0.0181
	GG	9	0.2143	-	326	0.4341				
	A	38	0.4524	0.2001	490	0.3262			5.7004	0.0170
	G	46	0.5476	0.7999	1012	0.6738				
ABCA1#5 A/G	AA	1	0.0233	-	31	0.0416	0.1625	0.9220	4.5794	0.1013
	AG	10	0.2326	-	283	0.3794			3.7530	0.0527
	GG	32	0.7442	-	432	0.5791				
	A	12	0.1395	0.3229	345	0.2312			3.9058	0.0481
	G	74	0.8605	0.6771	1147	0.7688				
ABCA1#7 A/G	AA	1	0.0233	-	44	0.0582	0.0400	0.9802	1.9910	0.3695
	AG	20	0.4651	-	283	0.3743			1.4242	0.2327
	GG	22	0.5116	-	429	0.5675				
	A	22	0.2558	0.2349	371	0.2454			0.0479	0.8268
	G	64	0.7442	0.7651	1141	0.7546				
TFB1M#1 G/T	GG	3	0.0714	-	62	0.0832	0.1111	0.9459	0.1743	0.9165
	GT	19	0.4524	-	315	0.4228			0.1422	0.7061
	TT	20	0.4762	-	368	0.4940				
	G	25	0.2976	0.2916	439	0.2946			0.0034	0.9534
	T	59	0.7024	0.7084	1051	0.7054				
CAPN3#1 A/G	AA	0	0.0000	-	48	0.0633	1.4945	0.4737	8.3888	0.0151
	AG	11	0.2558	-	307	0.4050			3.7838	0.0518
	GG	32	0.7442	-	403	0.5317				
	A	11	0.1279	0.4038	403	0.2658			8.0784	0.0045
	G	75	0.8721	0.5962	1113	0.7342				
SLC27A2#1 C/T	CC	6	0.1395	-	73	0.0944	0.0271	0.9866	1.0622	0.5879
	CT	19	0.4419	-	339	0.4386			0.0018	0.9660
	TT	18	0.4186	-	361	0.4670				
	C	31	0.3605	0.2670	485	0.3137			0.8236	0.3641
	T	55	0.6395	0.7330	1061	0.6863				
APOB#2 C/T	CC	28	0.6512	-	106	0.1393	0.0229	0.9886	76.9238	0.0000
	CT	13	0.3023	-	529	0.6951			28.5877	0.0000
	TT	2	0.0465	-	126	0.1656				
	C	69	0.8023	0.1714	741	0.4869			32.4054	0.0000
	T	17	0.1977	0.8286	781	0.5131				
APOB#3 A/G	AA	28	0.6512	-	313	0.4190	1.7287	0.4213	9.1035	0.0105
	AG	11	0.2558	-	343	0.4592			6.7989	0.0091
	GG	4	0.0930	-	91	0.1218				
	A	67	0.7791	0.5181	969	0.6486			6.1320	0.0133
	G	19	0.2209	0.4819	525	0.3514				
ASB3#1 G/T	GG	15	0.3488	-	286	0.3758	1.3127	0.5187	0.2382	0.8877
	GT	23	0.5349	-	378	0.4967			0.2372	0.6263
	TT	5	0.1163	-	97	0.1275				
	G	53	0.6163	0.6321	950	0.6242			0.0216	0.8830
	T	33	0.3837	0.3679	572	0.3758				
ASB3#2 C/T	CC	7	0.1628	-	349	0.4586	4.0773	0.1302	135.7056	0.0000
	CT	27	0.6279	-	410	0.5388			1.3036	0.2536
	TT	9	0.2093	-	2	0.0026				
	C	41	0.4767	0.9792	1108	0.7280			25.1920	0.0000
	T	45	0.5233	0.0208	414	0.2720				
CAPN14#2 A/G	AA	7	0.1628	-	336	0.4375	4.4901	0.1059	28.1118	0.0000
	AG	25	0.5814	-	383	0.4987			1.1140	0.2912
	GG	11	0.2558	-	49	0.0638				
	A	39	0.4535	0.9202	1055	0.6868			20.1997	0.0000
	G	47	0.5465	0.0798	481	0.3132				
EFEMP1#2 A/C	AA	38	0.8837	-	226	0.3100	4.3304	0.1147	59.4805	0.0000
	AC	5	0.1163	-	459	0.6296			44.6244	0.0000
	CC	0	0.0000	-	44	0.0604				
	A	81	0.9419	0.3078	911	0.6248			35.5352	0.0000
	C	5	0.0581	0.6922	547	0.3752				
SLC27A4#2 C/T	CC	26	0.6047	-	294	0.3803	0.9387	0.6254	9.9558	0.0069
	CT	16	0.3721	-	384	0.4968			2.5335	0.1114
	TT	1	0.0233	-	95	0.1229				
	C	68	0.7907	0.4667	972	0.6287			9.2467	0.0024
	T	18	0.2093	0.5333	574	0.3713				
PLTP#2 C/T	CC	16	0.3721	-	220	0.2922	0.5170	0.7722	2.0345	0.3616
	CT	16	0.3721	-	362	0.4807			1.9256	0.1652
	TT	11	0.2558	-	171	0.2271				
	C	48	0.5581	0.5069	802	0.5325			0.2143	0.6434
	T	38	0.4419	0.4931	704	0.4675				
CRH#1 C/T	CC	7	0.1628	-	148	0.1965	0.0000	1.0000	0.4766	0.7880
	CT	21	0.4884	-	374	0.4967			0.0112	0.9156
	TT	15	0.3488	-	231	0.3068				
	C	35	0.4070	0.4828	670	0.4449			0.4739	0.4912
	T	51	0.5930	0.5172	836	0.5551				
CRH#2 A/G	AA	0	0.0000	-	34	0.0439	0.4228	0.8095	2.7342	0.2548

	AG	12	0.2791	-	254	0.3277			0.4398	0.5072
	GG	31	0.7209	-	487	0.6284				
	A	12	0.1395	0.2759	322	0.2077			2.3330	0.1267
	G	74	0.8605	0.7241	1228	0.7923				
CRH#3 C/G	CC	12	0.2857	-	98	0.1268	0.0652	0.9679	10.5148	0.0052
	CG	22	0.5238	-	402	0.5201			0.0023	0.9621
	GG	8	0.1905	-	273	0.3532				
	C	46	0.5476	0.2260	598	0.3868			8.6211	0.0033
	G	38	0.4524	0.7740	948	0.6132				
FABP4#1 A/G	AA	6	0.1395	-	160	0.2105	1.5320	0.4649	1.9858	0.3705
	AG	23	0.5349	-	412	0.5421			0.0085	0.9263
	GG	14	0.3256	-	188	0.2474				
	A	35	0.4070	0.5562	732	0.4816			1.8157	0.1778
	G	51	0.5930	0.4438	788	0.5184				
MTFR1#1 C/G	CC	12	0.2791	-	170	0.2199	0.5640	0.7543	1.3870	0.4998
	CG	23	0.5349	-	407	0.5265			0.0114	0.9149
	GG	8	0.1860	-	196	0.2536				
	C	47	0.5465	0.4199	747	0.4832			1.3079	0.2528
	G	39	0.4535	0.5801	799	0.5168				
APOA1#2 A/G	AA	0	0.0000	-	14	0.0186	2.0098	0.3661	11.1555	0.0038
	AG	3	0.0714	-	222	0.2952			9.8096	0.0017
	GG	39	0.9286	-	516	0.6862				
	A	3	0.0357	0.2967	250	0.1662			10.1171	0.0015
	G	81	0.9643	0.7033	1254	0.8338				
ARHGAP1#1 A/G	AA	26	0.6047	-	356	0.4740	0.0000	1.0000	3.7517	0.1532
	AG	16	0.3721	-	332	0.4421			0.8091	0.3684
	GG	1	0.0233	-	63	0.0839				
	A	68	0.7907	0.5994	1044	0.6951			3.5436	0.0598
	G	18	0.2093	0.4006	458	0.3049				
CAPN5#3 A/G	AA	20	0.4651	-	394	0.5253	0.0108	0.9946	0.6826	0.7109
	AG	19	0.4419	-	302	0.4027			0.2593	0.6106
	GG	4	0.0930	-	54	0.0720				
	A	59	0.6860	0.7673	1090	0.7267				
	G	27	0.3140	0.2327	410	0.2733			0.6723	0.4122
SOAT1#1 C/T	CC	9	0.2093	-	118	0.1559	0.8956	0.6390	1.5172	0.4683
	CT	18	0.4186	-	384	0.5073			1.2794	0.2580
	TT	16	0.3721	-	255	0.3369				
	C	36	0.4186	0.4004	620	0.4095			0.0278	0.8675
	T	50	0.5814	0.5996	894	0.5905				
TFB2M#1 C/T	CC	14	0.3256	-	275	0.3647	0.0008	0.9996	1.0412	0.5942
	CT	20	0.4651	-	364	0.4828			0.0507	0.8218
	TT	9	0.2093	-	115	0.1525				
	C	48	0.5581	0.6541	914	0.6061			0.7821	0.3765
	T	38	0.4419	0.3459	594	0.3939				
TFB2M#2 C/T	CC	13	0.3095	-	196	0.2678	0.2481	0.8833	2.9679	0.2267
	CT	24	0.5714	-	365	0.4986			0.8420	0.3588
	TT	5	0.1190	-	171	0.2336				
	C	50	0.5952	0.4389	757	0.5171			1.9449	0.1631
	T	34	0.4048	0.5611	707	0.4829				
SCARB1#2 C/T	CC	27	0.6279	-	377	0.5007	0.3544	0.8376	2.6525	0.2655
	CT	14	0.3256	-	324	0.4303			1.8250	0.1767
	TT	2	0.0465	-	52	0.0691				
	C	68	0.7907	0.6409	1078	0.7158			2.2628	0.1325
	T	18	0.2093	0.3591	428	0.2842				
APOE#4 C/T	CC	0	0.0000	-	45	0.0597	4.9620	0.0837	28.9271	0.0000
	CT	12	0.2791	-	465	0.6167			19.2992	0.0000
	TT	31	0.7209	-	244	0.3236				
	C	12	0.1395	0.5965	555	0.3680			18.5360	0.0000
	T	74	0.8605	0.4035	953	0.6320				
APOE#5 A/G	AA	10	0.2326	-	71	0.0940	5.2715	0.0717	8.7258	0.0127
	AG	21	0.4884	-	409	0.5417			0.4660	0.4948
	GG	12	0.2791	-	275	0.3642				
	A	41	0.4767	0.2531	551	0.3649			4.3619	0.0368
	G	45	0.5233	0.7469	959	0.6351				
CAPN12#1 I/D	II	3	0.0698	-	87	0.1154	0.0119	0.9941	10.6666	0.0048
	ID	13	0.3023	-	382	0.5066			6.7926	0.0092
	DD	27	0.6279	-	285	0.3780				
	I	19	0.2209	0.5165	556	0.3687			7.7040	0.0055
	D	67	0.7791	0.4835	952	0.6313				
CHD9#1 C/T	CC	0	0.0000	-	48	0.0623	0.3174	0.8533	16.2467	0.0003
	CT	10	0.2326	-	370	0.4799			10.0105	0.0016
	TT	33	0.7674	-	353	0.4578				
	C	10	0.1163	0.4881	466	0.3022			13.6100	0.0002
	T	76	0.8837	0.5119	1076	0.6978				
FTO#2 A/G	AA	14	0.3256	-	371	0.4920	1.2929	0.5239	11.8373	0.0027

	AG	20	0.4651	-	328	0.4350			0.1499	0.6987
	GG	9	0.2093	-	55	0.0729				
	A	48	0.5581	0.8610	1070	0.7095			8.9052	0.0028
	G	38	0.4419	0.1390	438	0.2905				
FTO#3 C/T	CC	24	0.5581	-	277	0.3688	0.6816	0.7112	6.2499	0.0439
	CT	16	0.3721	-	387	0.5153			3.3377	0.0677
	TT	3	0.0698	-	87	0.1158				
	C	64	0.7442	0.5088	941	0.6265			4.8490	0.0277
	T	22	0.2558	0.4912	561	0.3735				
FTO#8 C/T	CC	18	0.4186	-	365	0.4809	0.7422	0.6900	7.8222	0.0200
	CT	17	0.3953	-	341	0.4493			0.4789	0.4889
	TT	8	0.1860	-	53	0.0698				
	C	53	0.6163	0.7948	1071	0.7055			3.0919	0.0787
	T	33	0.3837	0.2052	447	0.2945				
FTO#9 C/T	CC	31	0.7209	-	289	0.3848	0.1689	0.9190	19.1478	0.0000
	CT	10	0.2326	-	400	0.5326			14.6637	0.0001
	TT	2	0.0465	-	62	0.0826				
	C	72	0.8372	0.4651	978	0.6511			12.5729	0.0004
	T	14	0.1628	0.5349	524	0.3489				
LIPE#1 C/T	CC	0	0.0000	-	33	0.0435	0.0037	0.9981	43.4202	0.0000
	CT	6	0.1395	-	454	0.5982			34.9951	0.0000
	TT	37	0.8605	-	272	0.3584				
	C	6	0.0698	0.6153	520	0.3426			27.4804	0.0000
	T	80	0.9302	0.3847	998	0.6574				
CRHR1#1 A/G	AA	29	0.6744	-	194	0.2563	0.5680	0.7528	35.4657	0.0000
	AG	12	0.2791	-	458	0.6050			17.8379	0.0000
	GG	2	0.0465	-	105	0.1387				
	A	70	0.8140	0.3036	846	0.5588			21.6495	0.0000
	G	16	0.1860	0.6964	668	0.4412				
UTS2R#2 I/D	II	34	0.7907	-	348	0.4496	3.3254	0.1896	19.5891	0.0000
	ID	9	0.2093	-	370	0.4780			11.8294	0.0006
	DD	0	0.0000	-	56	0.0724				
	I	77	0.8953	0.4819	1066	0.6886			16.5635	0.0000
	D	9	0.1047	0.5181	482	0.3114				
HMGCS1#1 A/G	AA	8	0.1860	-	296	0.3834	4.0762	0.1303	13.4929	0.0012
	AG	22	0.5116	-	378	0.4896			0.0788	0.7789
	GG	13	0.3023	-	98	0.1269				
	A	38	0.4419	0.8146	970	0.6282			11.9914	0.0005
	G	48	0.5581	0.1854	574	0.3718				
NEIL1#2 C/T	CC	38	0.8837	-	464	0.6129	0.0141	0.9930	12.8566	0.0016
	CT	5	0.1163	-	277	0.3659			11.1097	0.0009
	TT	0	0.0000	-	16	0.0211				
	C	81	0.9419	0.6499	1205	0.7959			10.9904	0.0009
	T	5	0.0581	0.3501	309	0.2041				
NEIL1#4 A/G	AA	37	0.8605	-	284	0.3782	1.1102	0.5740	39.4163	0.0000
	AG	6	0.1395	-	428	0.5699			30.3966	0.0000
	GG	0	0.0000	-	39	0.0519				
	A	80	0.9302	0.3960	996	0.6631			26.5668	0.0000
	G	6	0.0698	0.6040	506	0.3369				
BAK1#1 C/T	CC	16	0.3721	-	247	0.3199	4.0949	0.1291	0.8049	0.6687
	CT	20	0.4651	-	413	0.5350			0.7982	0.3716
	TT	7	0.1628	-	112	0.1451				
	C	52	0.6047	0.5702	907	0.5874			0.0997	0.7522
	T	34	0.3953	0.4298	637	0.4126				
SKIV2L#1 C/T	CC	10	0.2326	-	222	0.2872	2.5078	0.2854	8.6932	0.0130
	CT	15	0.3488	-	378	0.4890			3.2055	0.0734
	TT	18	0.4186	-	173	0.2238				
	C	35	0.4070	0.6564	822	0.5317			5.0816	0.0242
	T	51	0.5930	0.3436	724	0.4683				
TNF#3 A/T	AA	3	0.0698	-	107	0.1388	5.9736	0.0504	3.6704	0.1596
	AT	15	0.3488	-	323	0.4189			0.8242	0.3639
	TT	25	0.5814	-	341	0.4423				
	A	21	0.2442	0.4523	537	0.3482			3.9157	0.0478
	T	65	0.7558	0.5477	1005	0.6518				
DSEL#1 C/T	CC	12	0.2791	-	262	0.3479	1.7455	0.4178	1.1155	0.5725
	CT	23	0.5349	-	344	0.4568			0.9971	0.3180
	TT	8	0.1860	-	147	0.1952				
	C	47	0.5465	0.6062	868	0.5764			0.2966	0.5860
	T	39	0.4535	0.3938	638	0.4236				
ACSL5#1 C/T	CC	16	0.3721	-	286	0.3773	0.2311	0.8909	1.5022	0.4718
	CT	23	0.5349	-	353	0.4657			0.7820	0.3765
	TT	4	0.0930	-	119	0.1570				
	C	55	0.6395	0.5808	925	0.6102			0.2957	0.5866
	T	31	0.3605	0.4192	591	0.3898				
SCD1#2 A/G	AA	8	0.1860	-	41	0.0543	0.0405	0.9800	12.3224	0.0021

	AG	14	0.3256	-	303	0.4013			0.9748	0.3235
	GG	21	0.4884	-	411	0.5444				
	A	30	0.3488	0.1611	385	0.2550			3.7262	0.0536
	G	56	0.6512	0.8389	1125	0.7450				
TFAM#2 C/T	CC	6	0.1429	-	137	0.1869	0.2227	0.8946	7.1960	0.0274
	CT	15	0.3571	-	374	0.5102			3.7240	0.0536
	TT	21	0.5000	-	222	0.3029				
	C	27	0.3214	0.5626	648	0.4420			4.6996	0.0302
	T	57	0.6786	0.4374	818	0.5580				
TFAM#3 C/T	CC	21	0.4884	-	265	0.3552	0.9488	0.6223	3.1696	0.2050
	CT	18	0.4186	-	383	0.5134			1.4619	0.2266
	TT	4	0.0930	-	98	0.1314				
	C	60	0.6977	0.5262	913	0.6119			2.5288	0.1118
	T	26	0.3023	0.4738	579	0.3881				
CAPN1#1 C/G	CC	13	0.3023	-	310	0.4079	0.0461	0.9772	2.9879	0.2245
	CG	22	0.5116	-	363	0.4776			0.1885	0.6642
	GG	8	0.1860	-	87	0.1145				
	C	48	0.5581	0.7353	983	0.6467			2.7781	0.0956
	G	38	0.4419	0.2647	537	0.3533				
CAPN1#2 C/T	CC	27	0.6429	-	322	0.4242	0.0325	0.9839	7.7864	0.0204
	CT	13	0.3095	-	367	0.4835			4.8327	0.0279
	TT	2	0.0476	-	70	0.0922				
	C	67	0.7976	0.5344	1011	0.6660			6.2640	0.0123
	T	17	0.2024	0.4656	507	0.3340				
CAPN1#3 A/G	AA	6	0.1429	-	61	0.0810	2.0909	0.3515	1.9785	0.3719
	AG	18	0.4286	-	351	0.4661			0.2257	0.6347
	GG	18	0.4286	-	341	0.4529				
	A	30	0.3571	0.2710	473	0.3141			0.6823	0.4088
	G	54	0.6429	0.7290	1033	0.6859				
CAPN1#5 A/G	AA	8	0.1860	-	116	0.1541	1.7936	0.4079	0.5362	0.7648
	AG	23	0.5349	-	393	0.5219			0.0274	0.8684
	GG	12	0.2791	-	244	0.3240				
	A	39	0.4535	0.3765	625	0.4150			0.4955	0.4815
	G	47	0.5465	0.6235	881	0.5850				
DHCR7#1 A/G	AA	0	0.0000	-	12	0.0155	0.1197	0.9419	10.0614	0.0065
	AG	4	0.0930	-	238	0.3067			8.9360	0.0028
	GG	39	0.9070	-	526	0.6778				
	A	4	0.0465	0.2911	262	0.1688			8.9607	0.0028
	G	82	0.9535	0.7089	1290	0.8312				
DHCR7#2 A/G	AA	38	0.8837	-	339	0.4357	0.4880	0.7835	33.0099	0.0000
	AG	5	0.1163	-	410	0.5270			27.4976	0.0000
	GG	0	0.0000	-	29	0.0373				
	A	81	0.9419	0.4566	1088	0.6992			23.3938	0.0000
	G	5	0.0581	0.5434	468	0.3008				
FADS1#1 C/T	CC	40	0.9302	-	444	0.5896	0.1557	0.9251	19.8216	0.0000
	CT	3	0.0698	-	297	0.3944			18.2565	0.0000
	TT	0	0.0000	-	12	0.0159				
	C	83	0.9651	0.6086	1185	0.7869			15.9488	0.0000
	T	3	0.0349	0.3914	321	0.2131				
FADS2#1 A/G	AA	23	0.5349	-	272	0.3622	0.2407	0.8866	9.0196	0.0110
	AG	20	0.4651	-	381	0.5073			0.2898	0.5903
	GG	0	0.0000	-	98	0.1305				
	A	66	0.7674	0.4642	925	0.6158			7.9680	0.0048
	G	20	0.2326	0.5358	577	0.3842				
GNG3#2 G/T	GG	14	0.3256	-	67	0.0898	0.9516	0.6214	25.1735	0.0000
	GT	12	0.2791	-	340	0.4558			5.1369	0.0234
	TT	17	0.3953	-	339	0.4544				
	G	40	0.4651	0.1703	474	0.3177			8.0463	0.0046
	T	46	0.5349	0.8297	1018	0.6823				
IGF2#1 C/T	CC	6	0.1395	-	215	0.2909	1.1465	0.5637	6.2748	0.0434
	CT	23	0.5349	-	374	0.5061			0.1348	0.7135
	TT	14	0.3256	-	150	0.2030				
	C	35	0.4070	0.6810	804	0.5440			6.1342	0.0133
	T	51	0.5930	0.3190	674	0.4560				
PNPLA2#1 C/G	CC	14	0.3333	-	204	0.2649	0.7393	0.6910	2.1521	0.3403
	CG	17	0.4048	-	401	0.5208			2.1462	0.1429
	GG	11	0.2619	-	165	0.2143				
	C	45	0.5357	0.5149	809	0.5253			0.0345	0.8527
	G	39	0.4643	0.4851	731	0.4747				
PNPLA2#2 C/T	CC	29	0.6744	-	440	0.5714	0.0967	0.9528	1.8155	0.4034
	CT	12	0.2791	-	290	0.3766			1.6600	0.1976
	TT	2	0.0465	-	40	0.0519				
	C	70	0.8140	0.7055	1170	0.7597			1.3223	0.2502
	T	16	0.1860	0.2945	370	0.2403				
PNPLA2#3 C/T	CC	13	0.3023	-	168	0.2182	0.6905	0.7080	6.8753	0.0321

	CT	26	0.6047	-	394	0.5117			1.4094	0.2352
	TT	4	0.0930	-	208	0.2701				
	C	52	0.6047	0.3434	730	0.4740			5.5673	0.0183
	T	34	0.3953	0.6566	810	0.5260				
CAPN7#1 C/T	CC	2	0.0465	-	1	0.0013	0.6952	0.7064	22.4748	0.0000
	CT	7	0.1628	-	115	0.1511			0.0431	0.8356
	TT	34	0.7907	-	645	0.8476				
	C	11	0.1279	0.0258	117	0.0769			2.8937	0.0889
	T	75	0.8721	0.9742	1405	0.9231				
FNDC3B#1 C/T	CC	0	0.0000	-	1	0.0014	0.0340	0.9832	5.7990	0.0550
	CT	1	0.0233	-	116	0.1572			5.7220	0.0168
	TT	42	0.9767	-	621	0.8415				
	C	1	0.0116	0.1483	118	0.0799			5.3892	0.0203
	T	85	0.9884	0.8517	1358	0.9201				
RCAN1#1 A/G	AA	39	0.9070	-	231	0.3004	0.0060	0.9970	67.5393	0.0000
	AG	4	0.0930	-	513	0.6671			58.0201	0.0000
	GG	0	0.0000	-	25	0.0325				
	A	82	0.9535	0.3144	975	0.6339			36.5978	0.0000
	G	4	0.0465	0.6856	563	0.3661				
RCAN1#3 A/C	AA	39	0.9070	-	206	0.2930	2.8352	0.2423	69.2929	0.0000
	AC	4	0.0930	-	463	0.6586			55.3648	0.0000
	CC	0	0.0000	-	34	0.0484				
	A	82	0.9535	0.2912	875	0.6223			38.6412	0.0000
	C	4	0.0465	0.7088	531	0.3777				
RCAN1#4 G/T	GG	39	0.9070	-	232	0.3021	0.0085	0.9958	66.9932	0.0000
	GT	4	0.0930	-	511	0.6654			57.5522	0.0000
	TT	0	0.0000	-	25	0.0326				
	G	82	0.9535	0.3160	975	0.6348			36.4454	0.0000
	T	4	0.0465	0.6840	561	0.3652				
SIM2#1 C/T	CC	43	1.0000	-	573	0.7403	3.0974	0.2125	14.8103	0.0006
	CT	0	0.0000	-	198	0.2558			14.5186	0.0000
	TT	0	0.0000	-	3	0.0039				
	C	86	1.0000	0.7364	1344	0.8682			12.9501	0.0003
	T	0	0.0000	0.2636	204	0.1318				
ALDH4A1#2 A/G	AA	6	0.1395	-	93	0.1245	0.0006	0.9997	0.7353	0.6924
	AG	22	0.5116	-	344	0.4605			0.4273	0.5133
	GG	15	0.3488	-	310	0.4150				
	A	34	0.3953	0.3142	530	0.3548			0.5839	0.4448
	G	52	0.6047	0.6858	964	0.6452				
CAPN10#2 A/C	AA	0	0.0000	-	0	0.0000	0.0000	1.0000	3.8469	0.0498
	AC	0	0.0000	-	71	0.0923			3.8469	0.0498
	CC	38	1.0000	-	698	0.9077				
	A	0	0.0000	0.0923	71	0.0462			3.6699	0.0554
	C	76	1.0000	0.9077	1467	0.9538				
SCP2#1 A/G	AA	2	0.0476	-	31	0.0411	3.2099	0.2009	0.9985	0.6070
	AG	20	0.4762	-	305	0.4040			0.8592	0.3540
	GG	20	0.4762	-	419	0.5550				
	A	24	0.2857	0.2004	367	0.2430			0.7825	0.3764
	G	60	0.7143	0.7996	1143	0.7570				
GPR37#1 C/T	CC	0	0.0000	-	0	0.0000	0.0000	1.0000	2.9335	0.0868
	CT	0	0.0000	-	48	0.0641			2.9335	0.0868
	TT	43	1.0000	-	701	0.9359				
	C	0	0.0000	0.0641	48	0.0320			2.8418	0.0918
	T	86	1.0000	0.9359	1450	0.9680				
GPR37#3 A/G	AA	21	0.5000	-	181	0.2500	1.2157	0.5445	14.0073	0.0009
	AG	18	0.4286	-	394	0.5442			2.1352	0.1440
	GG	3	0.0714	-	149	0.2058				
	A	60	0.7143	0.3299	756	0.5221			11.7801	0.0006
	G	24	0.2857	0.6701	692	0.4779				
IGFBP6#1 A/C	AA	42	0.9767	-	530	0.7057	0.6515	0.7220	14.8316	0.0006
	AC	1	0.0233	-	220	0.2929			14.7266	0.0001
	CC	0	0.0000	-	1	0.0013				
	A	85	0.9884	0.7160	1280	0.8522			12.4962	0.0004
	C	1	0.0116	0.2840	222	0.1478				
NDST3#1 C/T	CC	29	0.6905	-	628	0.8464	2.2595	0.3231	7.7505	0.0207
	CT	13	0.3095	-	111	0.1496			7.6358	0.0057
	TT	0	0.0000	-	3	0.0040				
	C	71	0.8452	0.9971	1367	0.9212			6.0267	0.0141
	T	13	0.1548	0.0029	117	0.0788				
CAST#1 A/G	AA	14	0.3256	-	371	0.4947	2.9315	0.2309	14.5882	0.0007
	AG	19	0.4419	-	323	0.4307			0.0208	0.8854
	GG	10	0.2326	-	56	0.0747				
	A	47	0.5465	0.8735	1065	0.7100			10.3749	0.0013
	G	39	0.4535	0.1265	435	0.2900				
CAST#3 G/T	GG	14	0.3256	-	376	0.4941	2.9204	0.2322	14.5331	0.0007

	GT	19	0.4419	-	328	0.4310			0.0195	0.8889
	TT	10	0.2326	-	57	0.0749				
	G	47	0.5465	0.8727	1080	0.7096			10.3261	0.0013
	T	39	0.4535	0.1273	442	0.2904				
POLRMT#1 C/T	CC	38	0.8837	-	552	0.7380	0.2269	0.8928	5.1920	0.0746
	CT	4	0.0930	-	183	0.2447			5.1789	0.0229
	TT	1	0.0233	-	13	0.0174				
	C	80	0.9302	0.7904	1287	0.8603			3.3874	0.0657
	T	6	0.0698	0.2096	209	0.1397				
ABCA1#1 G/T	GG	41	0.9535	-	678	0.9088	1.2205	0.5432	1.0021	0.3168
	GT	2	0.0465	-	68	0.0912			1.0021	0.3168
	TT	0	0.0000	-	0	0.0000				
	G	84	0.9767	0.9321	1424	0.9544			0.9556	0.3283
	T	2	0.0233	0.0679	68	0.0456				
ABCA1#8 C/T	CC	22	0.5116	-	428	0.5669	0.0437	0.9784	1.9785	0.3719
	CT	20	0.4651	-	283	0.3748			1.4079	0.2354
	TT	1	0.0233	-	44	0.0583				
	C	64	0.7442	0.7644	1139	0.7543			0.0449	0.8322
	T	22	0.2558	0.2356	371	0.2457				
ACAT2#1 A/G	AA	0	0.0000	-	0	0.0000	0.0000	1.0000	3.1971	0.0738
	AG	0	0.0000	-	53	0.0695			3.1971	0.0738
	GG	43	1.0000	-	710	0.9305				
	A	0	0.0000	0.0695	53	0.0347			3.0884	0.0789
	G	86	1.0000	0.9305	1473	0.9653				
LIPC#1 C/T	CC	38	0.8837	-	588	0.7830	0.1155	0.9439	3.9629	0.1379
	CT	4	0.0930	-	156	0.2077			3.3254	0.0682
	TT	1	0.0233	-	7	0.0093				
	C	80	0.9302	0.8434	1332	0.8868			1.5558	0.2123
	T	6	0.0698	0.1566	170	0.1132				
LIPC#2 A/G	AA	0	0.0000	-	0	0.0000	0.0000	1.0000	1.2267	0.2681
	AG	0	0.0000	-	21	0.0278			1.2267	0.2681
	GG	43	1.0000	-	735	0.9722				
	A	0	0.0000	0.0278	21	0.0139			1.2104	0.2713
	G	86	1.0000	0.9722	1491	0.9861				
SLC27A2#2 C/T	CC	6	0.1395	-	73	0.0944	0.0271	0.9866	1.0622	0.5879
	CT	19	0.4419	-	339	0.4386			0.0018	0.9660
	TT	18	0.4186	-	361	0.4670				
	C	31	0.3605	0.2670	485	0.3137			0.8236	0.3641
	T	55	0.6395	0.7330	1061	0.6863				
APOB#1 A/G	AA	28	0.6667	-	313	0.4140	2.6750	0.2625	10.6202	0.0049
	AG	10	0.2381	-	348	0.4603			7.9435	0.0048
	GG	4	0.0952	-	95	0.1257				
	A	66	0.7857	0.5026	974	0.6442			7.0223	0.0081
	G	18	0.2143	0.4974	538	0.3558				
CAPN14#1 A/G	AA	11	0.2558	-	50	0.0663	4.1848	0.1234	26.8121	0.0000
	AG	25	0.5814	-	376	0.4987			1.1135	0.2913
	GG	7	0.1628	-	328	0.4350				
	A	47	0.5465	0.0848	476	0.3156			19.6698	0.0000
	G	39	0.4535	0.9152	1032	0.6844				
SLC27A4#1 C/T	CC	27	0.6279	-	297	0.3842	1.6574	0.4366	11.2451	0.0036
	CT	15	0.3488	-	382	0.4942			3.4444	0.0635
	TT	1	0.0233	-	94	0.1216				
	C	69	0.8023	0.4603	976	0.6313			10.3458	0.0013
	T	17	0.1977	0.5397	570	0.3687				
SLC27A4#3 C/T	CC	1	0.0233	-	100	0.1326	1.5426	0.4624	11.7870	0.0028
	CT	16	0.3721	-	382	0.5066			2.9453	0.0861
	TT	26	0.6047	-	272	0.3607				
	C	18	0.2093	0.5626	582	0.3859			10.8150	0.0010
	T	68	0.7907	0.4374	926	0.6141				
SLC27A4#4 C/T	CC	26	0.6047	-	292	0.3862	1.1518	0.5622	9.5006	0.0086
	CT	16	0.3721	-	371	0.4907			2.2932	0.1299
	TT	1	0.0233	-	93	0.1230				
	C	68	0.7907	0.4725	955	0.6316			8.9400	0.0028
	T	18	0.2093	0.5275	557	0.3684				
CRH#4 C/G	CC	15	0.3488	-	231	0.3008	0.1856	0.9114	0.5160	0.7726
	CG	21	0.4884	-	390	0.5078			0.0616	0.8040
	GG	7	0.1628	-	147	0.1914				
	C	51	0.5930	0.5164	852	0.5547			0.4850	0.4862
	G	35	0.4070	0.4836	684	0.4453				
FABP4#2 A/G	AA	6	0.1395	-	164	0.2172	0.9132	0.6334	2.1715	0.3377
	AG	23	0.5349	-	405	0.5364			0.0004	0.9843
	GG	14	0.3256	-	186	0.2464				
	A	35	0.4070	0.5639	733	0.4854			2.0061	0.1567
	G	51	0.5930	0.4361	777	0.5146				
RAB2A#1 A/T	AA	0	0.0000	-	5	0.0066	2.1710	0.3377	0.6694	0.7156

	AT	8	0.1860	-	171	0.2250			0.3565	0.5505
	TT	35	0.8140	-	584	0.7684				
	A	8	0.0930	0.1451	181	0.1191			0.5322	0.4657
	T	78	0.9070	0.8549	1339	0.8809				
ARHGAP1#2 C/T	CC	40	0.9302	-	683	0.9011	1.7743	0.4118	0.3941	0.5301
	CT	3	0.0698	-	75	0.0989			0.3941	0.5301
	TT	0	0.0000	-	0	0.0000				
	C	83	0.9651	0.9359	1441	0.9505			0.3739	0.5409
	T	3	0.0349	0.0641	75	0.0495				
CAPN5#2 A/G	AA	0	0.0000	-	5	0.0066	4.7712	0.0920	0.9301	0.6281
	AG	1	0.0233	-	38	0.0500			0.6299	0.4274
	GG	42	0.9767	-	717	0.9434				
	A	1	0.0116	0.0515	48	0.0316			1.0953	0.2953
	G	85	0.9884	0.9485	1472	0.9684				
CAPN8#1 A/G	AA	27	0.6279	-	633	0.8508	3.6211	0.0571	14.9240	0.0001
	AG	16	0.3721	-	111	0.1492			14.9240	0.0001
	GG	0	0.0000	-	0	0.0000				
	A	70	0.8140	1.0000	1377	0.9254			13.6142	0.0002
	G	16	0.1860	0.0000	111	0.0746				
DPT#1 C/T	CC	0	0.0000	-	1	0.0013	1.0267	0.5985	4.9549	0.0840
	CT	0	0.0000	-	76	0.1026			4.8837	0.0271
	TT	43	1.0000	-	664	0.8961				
	C	0	0.0000	0.1053	78	0.0526			4.7633	0.0291
	T	86	1.0000	0.8947	1404	0.9474				
TFB2M#4 C/T	CC	13	0.3023	-	203	0.2721	0.2870	0.8663	3.1373	0.2083
	CT	25	0.5814	-	370	0.4960			1.1865	0.2760
	TT	5	0.1163	-	173	0.2319				
	C	51	0.5930	0.4472	776	0.5201			1.7333	0.1880
	T	35	0.4070	0.5528	716	0.4799				
UCP#1 C/T	CC	0	0.0000	-	10	0.0130	0.0104	0.9948	0.6408	0.7259
	CT	8	0.1860	-	155	0.2008			0.0552	0.8142
	TT	35	0.8140	-	607	0.7863				
	C	8	0.0930	0.1337	175	0.1133			0.3374	0.5613
	T	78	0.9070	0.8663	1369	0.8867				
APOE#2 C/T	CC	31	0.7209	-	243	0.3223	5.0360	0.0806	29.1646	0.0000
	CT	12	0.2791	-	466	0.6180			19.4713	0.0000
	TT	0	0.0000	-	45	0.0597				
	C	74	0.8605	0.4021	952	0.6313			18.6290	0.0000
	T	12	0.1395	0.5979	556	0.3687				
APOE#3 A/G	AA	0	0.0000	-	45	0.0598	5.0621	0.0796	29.4856	0.0000
	AG	12	0.2791	-	466	0.6197			19.6827	0.0000
	GG	31	0.7209	-	241	0.3205				
	A	12	0.1395	0.5998	556	0.3697			18.7651	0.0000
	G	74	0.8605	0.4002	948	0.6303				
APOE#6 C/T	CC	0	0.0000	-	45	0.0597	5.0360	0.0806	29.1646	0.0000
	CT	12	0.2791	-	466	0.6180			19.4713	0.0000
	TT	31	0.7209	-	243	0.3223				
	C	12	0.1395	0.5979	556	0.3687			18.6290	0.0000
	T	74	0.8605	0.4021	952	0.6313				
CAPNS1#1 A/G	AA	0	0.0000	-	0	0.0000	0.0245	0.8757	3.7177	0.0538
	AG	7	0.1667	-	61	0.0811			3.7177	0.0538
	GG	35	0.8333	-	691	0.9189				
	A	7	0.0833	0.0000	61	0.0406			3.5514	0.0595
	G	77	0.9167	1.0000	1443	0.9594				
CHD9#2 A/C	AA	33	0.7674	-	350	0.4617	0.3406	0.8434	15.8367	0.0004
	AC	10	0.2326	-	361	0.4763			9.7190	0.0018
	CC	0	0.0000	-	47	0.0620				
	A	76	0.8837	0.5160	1061	0.6999			13.3533	0.0003
	C	10	0.1163	0.4840	455	0.3001				
FTO#1 A/G	AA	24	0.5581	-	556	0.7374	0.0589	0.9710	6.6996	0.0351
	AG	18	0.4186	-	190	0.2520			5.8553	0.0155
	GG	1	0.0233	-	8	0.0106				
	A	66	0.7674	0.9593	1302	0.8634			6.1562	0.0131
	G	20	0.2326	0.0407	206	0.1366				
FTO#4 C/T	CC	18	0.4186	-	365	0.4822	0.7820	0.6764	8.0788	0.0176
	CT	17	0.3953	-	340	0.4491			0.4765	0.4900
	TT	8	0.1860	-	52	0.0687				
	C	53	0.6163	0.7972	1070	0.7067			3.1823	0.0744
	T	33	0.3837	0.2028	444	0.2933				
FTO#5 G/T	GG	24	0.5581	-	551	0.7356	0.1340	0.9352	6.4731	0.0393
	GT	18	0.4186	-	189	0.2523			5.8233	0.0158
	TT	1	0.0233	-	9	0.0120				
	G	66	0.7674	0.9562	1291	0.8618			5.9002	0.0151
	T	20	0.2326	0.0438	207	0.1382				
FTO#6 G/T	GG	43	1.0000	-	684	0.9060	1.0289	0.5978	4.4386	0.1087

	GT	0	0.0000	-	70	0.0927			4.3701	0.0366
	TT	0	0.0000	-	1	0.0013				
	G	86	1.0000	0.9046	1438	0.9523			4.2944	0.0382
	T	0	0.0000	0.0954	72	0.0477				
LIPE#3 A/C	AA	41	0.9535	-	299	0.4079	3.1988	0.2020	49.1190	0.0000
	AC	2	0.0465	-	415	0.5662			44.1198	0.0000
	CC	0	0.0000	-	19	0.0259				
	A	84	0.9767	0.4052	1013	0.6910			32.0091	0.0000
	C	2	0.0233	0.5948	453	0.3090				
LIPE#4 A/G	AA	0	0.0000	-	35	0.0465	1.0325	0.5967	45.8761	0.0000
	AG	5	0.1190	-	448	0.5950			36.7561	0.0000
	GG	37	0.8810	-	270	0.3586				
	A	5	0.0595	0.6284	518	0.3440			29.1607	0.0000
	G	79	0.9405	0.3716	988	0.6560				
TNNT1#1 C/T	CC	41	0.9535	-	748	0.9881	2.8328	0.0924	3.5967	0.0579
	CT	2	0.0465	-	9	0.0119			3.5967	0.0579
	TT	0	0.0000	-	0	0.0000				
	C	84	0.9767	1.0000	1505	0.9941			3.5718	0.0588
	T	2	0.0233	0.0000	9	0.0059				
ASPA#2 C/G	CC	0	0.0000	-	5	0.0067	0.0833	0.9592	0.4204	0.8104
	CG	8	0.1860	-	123	0.1638			0.1463	0.7021
	GG	35	0.8140	-	623	0.8296				
	C	8	0.0930	0.0841	133	0.0885			0.0201	0.8872
	G	78	0.9070	0.9159	1369	0.9115				
NEIL1#1 C/T	CC	43	1.0000	-	691	0.9201	0.0000	1.0000	3.7162	0.0539
	CT	0	0.0000	-	60	0.0799			3.7162	0.0539
	TT	0	0.0000	-	0	0.0000				
	C	86	1.0000	0.9201	1442	0.9601			3.5703	0.0588
	T	0	0.0000	0.0799	60	0.0399				
NEIL1#3 C/G	CC	42	0.9767	-	559	0.7658	1.7522	0.4164	12.4539	0.0020
	CG	0	0.0000	-	163	0.2233			12.1670	0.0005
	GG	1	0.0233	-	8	0.0110				
	C	84	0.9767	0.7781	1281	0.8774			7.7546	0.0054
	G	2	0.0233	0.2219	179	0.1226				
CAPN11#1 C/T	CC	42	0.9767	-	559	0.7213	2.4662	0.2914	13.6400	0.0002
	CT	1	0.0233	-	216	0.2787			13.6400	0.0002
	TT	0	0.0000	-	0	0.0000				
	C	85	0.9884	0.7329	1334	0.8606			11.5541	0.0007
	T	1	0.0116	0.2671	216	0.1394				
CAPN11#3 A/G	AA	0	0.0000	-	1	0.0013	1.0293	0.5977	4.3263	0.1150
	AG	0	0.0000	-	69	0.0906			4.2587	0.0390
	GG	43	1.0000	-	692	0.9081				
	A	0	0.0000	0.0932	71	0.0466			4.1914	0.0406
	G	86	1.0000	0.9068	1453	0.9534				
HIST1H1C#2 A/G	AA	42	0.9767	-	708	0.9328	0.5001	0.7788	1.2957	0.2550
	AG	1	0.0233	-	51	0.0672			1.2957	0.2550
	GG	0	0.0000	-	0	0.0000				
	A	85	0.9884	0.9444	1467	0.9664			1.2523	0.2631
	G	1	0.0116	0.0556	51	0.0336				
TNF#4 A/G	AA	19	0.4524	-	478	0.6176	2.7730	0.2499	34.9337	0.0000
	AG	15	0.3571	-	277	0.3579			0.0001	0.9922
	GG	8	0.1905	-	19	0.0245				
	A	53	0.6310	0.9621	1233	0.7965			13.0725	0.0003
	G	31	0.3690	0.0379	315	0.2035				
LIPG#1 A/G	AA	2	0.0465	-	13	0.0172	1.0739	0.5845	2.6658	0.2637
	AG	11	0.2558	-	156	0.2063			0.6021	0.4378
	GG	30	0.6977	-	587	0.7765				
	A	15	0.1744	0.0663	182	0.1204			2.1993	0.1381
	G	71	0.8256	0.9337	1330	0.8796				
CAPN9#1 A/G	AA	5	0.1163	-	0	0.0000	2.1273	0.3452	89.6818	0.0000
	AG	14	0.3256	-	219	0.2889			0.2652	0.6066
	GG	24	0.5581	-	539	0.7111				
	A	24	0.2791	0.0098	219	0.1445			11.4602	0.0007
	G	62	0.7209	0.9902	1297	0.8555				
CAPN1#4 C/T	CC	13	0.3023	-	239	0.3149	1.5461	0.4616	0.1384	0.9331
	CT	22	0.5116	-	395	0.5204			0.0126	0.9106
	TT	8	0.1860	-	125	0.1647				
	C	48	0.5581	0.5921	873	0.5751			0.0957	0.7570
	T	38	0.4419	0.4079	645	0.4249				
FADS1#2 A/G	AA	0	0.0000	-	0	0.0000	1.1170	0.2906	8.9819	0.0027
	AG	12	0.2791	-	91	0.1212			8.9819	0.0027
	GG	31	0.7209	-	660	0.8788				
	A	12	0.1395	0.0000	91	0.0606			8.3589	0.0038
	G	74	0.8605	1.0000	1411	0.9394				
FADS3#1 C/T	CC	37	0.8605	-	677	0.8920	0.4191	0.8109	0.5060	0.7765

	CT	6	0.1395	-	81	0.1067			0.4531	0.5009
	TT	0	0.0000	-	1	0.0013				
	C	80	0.9302	0.9604	1435	0.9453			0.3536	0.5521
	T	6	0.0698	0.0396	83	0.0547				
FADS3#2 C/T	CC	28	0.6512	-	619	0.8242	0.3186	0.8527	8.2800	0.0159
	CT	15	0.3488	-	131	0.1744			8.2435	0.0041
	TT	0	0.0000	-	1	0.0013				
	C	71	0.8256	0.9973	1369	0.9115			7.0970	0.0077
	T	15	0.1744	0.0027	133	0.0885				
Not Hardy-Weinberg equilibrium markers										
ATP5O#1 A/G	AA	14	0.3256	-	337	0.4434	34.3631	0.0000	215.3166	0.0000
	AG	17	0.3953	-	423	0.5566			4.2710	0.0388
	GG	12	0.2791	-	0	0.0000				
	A	45	0.5233	0.9202	1097	0.7217			15.6037	0.0000
	G	41	0.4767	0.0798	423	0.2783				
MRPL39#1 C/G	CC	35	0.8140	-	187	0.2490	9.4634	0.0088	64.7971	0.0000
	CG	8	0.1860	-	485	0.6458			36.5238	0.0000
	GG	0	0.0000	-	79	0.1052				
	C	78	0.9070	0.2368	859	0.5719			37.7551	0.0000
	G	8	0.0930	0.7632	643	0.4281				
FABP3#1 A/G	AA	17	0.3953	-	552	0.7321	24.4706	0.0000	23.8964	0.0000
	AG	25	0.5814	-	185	0.2454			23.6709	0.0000
	GG	1	0.0233	-	17	0.0225				
	A	59	0.6860	1.0000	1289	0.8548			17.7475	0.0000
	G	27	0.3140	0.0000	219	0.1452				
HS6ST1#1 A/T	AA	2	0.0465	-	2	0.0027	8.3818	0.0151	26.0617	0.0000
	AT	16	0.3721	-	132	0.1789			9.8779	0.0017
	TT	25	0.5814	-	604	0.8184				
	A	20	0.2326	0.0000	136	0.0921			17.8237	0.0000
	T	66	0.7674	1.0000	1340	0.9079				
CAPN10#1 A/G	AA	0	0.0000	-	49	0.0657	114.8836	0.0000	4.7772	0.0918
	AG	0	0.0000	-	26	0.0349			1.5497	0.2132
	GG	43	1.0000	-	671	0.8995				
	A	0	0.0000	0.1662	124	0.0831			7.7570	0.0054
	G	86	1.0000	0.8338	1368	0.9169				
CRP#1 C/T	CC	13	0.3023	-	473	0.6111	16.1997	0.0003	16.1969	0.0003
	CT	26	0.6047	-	265	0.3424			12.2198	0.0005
	TT	4	0.0930	-	36	0.0465				
	C	52	0.6047	0.9599	1211	0.7823			14.6510	0.0001
	T	34	0.3953	0.0401	337	0.2177				
CRP#2 A/G	AA	17	0.3953	-	558	0.7256	19.3555	0.0000	22.0831	0.0000
	AG	25	0.5814	-	197	0.2562			21.6818	0.0000
	GG	1	0.0233	-	14	0.0182				
	A	59	0.6860	1.0000	1313	0.8537			17.4640	0.0000
	G	27	0.3140	0.0000	225	0.1463				
NMU#1 A/C	AA	10	0.2326	-	381	0.5094	40.4530	0.0000	52.9519	0.0000
	AC	20	0.4651	-	334	0.4465			0.0568	0.8115
	CC	13	0.3023	-	33	0.0441				
	A	40	0.4651	1.0000	1096	0.7326			28.7464	0.0000
	C	46	0.5349	0.0000	400	0.2674				
NMU#2 A/G	AA	10	0.2326	-	386	0.5126	39.9624	0.0000	55.0268	0.0000
	AG	20	0.4651	-	335	0.4449			0.0674	0.7952
	GG	13	0.3023	-	32	0.0425				
	A	40	0.4651	1.0000	1107	0.7351			29.4367	0.0000
	G	46	0.5349	0.0000	399	0.2649				
PCSK1#1 A/C	AA	11	0.2558	-	382	0.5107	29.0918	0.0000	44.0353	0.0000
	AC	19	0.4419	-	327	0.4372			0.0036	0.9519
	CC	13	0.3023	-	39	0.0521				
	A	41	0.4767	0.9818	1091	0.7293			25.4810	0.0000
	C	45	0.5233	0.0182	405	0.2707				
HMGCR#1 A/C	AA	0	0.0000	-	19	0.0246	57.2424	0.0000	1.0821	0.2982
	AC	0	0.0000	-	0	0.0000			-	-
	CC	43	1.0000	-	754	0.9754				
	A	0	0.0000	0.0492	38	0.0246			2.1642	0.1413
	C	86	1.0000	0.9508	1508	0.9754				
EFEMP1#1 C/T	CC	4	0.0930	-	384	0.5134	71.9364	0.0000	153.7810	0.0000
	CT	21	0.4884	-	346	0.4626			0.1089	0.7414
	TT	18	0.4186	-	18	0.0241				
	C	29	0.3372	1.0000	1114	0.7447			67.3379	0.0000
	T	57	0.6628	0.0000	382	0.2553				
ENY2#1 C/G	CC	0	0.0000	-	358	0.4619	1326.2357	0.0000	44.2895	0.0000
	CG	0	0.0000	-	46	0.0594			2.7043	0.1001
	GG	43	1.0000	-	371	0.4787				
	C	0	0.0000	0.9832	762	0.4916			79.1396	0.0000

	G	86	1.0000	0.0168	788	0.5084				
CAPN5#1 A/C	AA	4	0.0930	-	34	0.0453	19.6702	0.0000	4.6861	0.0960
	AC	13	0.3023	-	157	0.2091			2.1028	0.1470
	CC	26	0.6047	-	560	0.7457				
	A	21	0.2442	0.0554	225	0.1498			5.5353	0.0186
	C	65	0.7558	0.9446	1277	0.8502				
UTS2#1 A/C	AA	14	0.3256	-	346	0.4701	22.4624	0.0000	43.2816	0.0000
	AC	22	0.5116	-	380	0.5163			0.0036	0.9524
	CC	7	0.1628	-	10	0.0136				
	A	50	0.5814	0.8751	1072	0.7283			8.6963	0.0032
	C	36	0.4186	0.1249	400	0.2717				
UTS2#2 A/G	AA	14	0.3256	-	371	0.4869	25.0823	0.0000	45.1158	0.0000
	AG	23	0.5349	-	384	0.5039			0.1559	0.6929
	GG	6	0.1395	-	7	0.0092				
	A	51	0.5930	0.8847	1126	0.7388			8.8042	0.0030
	G	35	0.4070	0.1153	398	0.2612				
APOC2#1 A/G	AA	9	0.2093	-	12	0.0165	25.8587	0.0000	56.8956	0.0000
	AG	18	0.4186	-	386	0.5309			2.0546	0.1517
	GG	16	0.3721	-	329	0.4525				
	A	36	0.4186	0.1454	410	0.2820			7.3669	0.0066
	G	50	0.5814	0.8546	1044	0.7180				
APOE#1 C/G	CC	27	0.6279	-	486	0.6463	26.5425	0.0000	52.7926	0.0000
	CG	13	0.3023	-	266	0.3537			0.4717	0.4922
	GG	3	0.0698	-	0	0.0000				
	C	67	0.7791	0.8672	1238	0.8231			1.0739	0.3001
	G	19	0.2209	0.1328	266	0.1769				
CAPN12#2 A/G	AA	15	0.3488	-	397	0.5265	18.5631	0.0000	94.8931	0.0000
	AG	21	0.4884	-	355	0.4708			0.0503	0.8226
	GG	7	0.1628	-	2	0.0027				
	A	51	0.5930	0.9308	1149	0.7619			12.4749	0.0004
	G	35	0.4070	0.0692	359	0.2381				
CAPNS1#2 C/T	CC	39	0.9070	-	325	0.4265	28.9540	0.0000	38.0473	0.0000
	CT	4	0.0930	-	376	0.4934			26.1859	0.0000
	TT	0	0.0000	-	61	0.0801				
	C	82	0.9535	0.3930	1026	0.6732			29.7981	0.0000
	T	4	0.0465	0.6070	498	0.3268				
LIPE#2 A/C	AA	41	0.9535	-	285	0.3765	1283.0836	0.0000	56.1162	0.0000
	AC	0	0.0000	-	26	0.0343			1.5265	0.2166
	CC	2	0.0465	-	446	0.5892				
	A	82	0.9535	0.0000	596	0.3937			104.4467	0.0000
	C	4	0.0465	1.0000	918	0.6063				
TNNT1#3 A/C	AA	0	0.0000	-	61	0.0806	7.7604	0.0206	24.9588	0.0000
	AC	8	0.1860	-	372	0.4914			15.2148	0.0000
	CC	35	0.8140	-	324	0.4280				
	A	8	0.0930	0.5596	494	0.3263			20.5654	0.0000
	C	78	0.9070	0.4404	1020	0.6737				
ASPA#1 C/T	CC	41	0.9535	-	358	0.4767	64.9353	0.0000	37.0251	0.0000
	CT	2	0.0465	-	325	0.4328			25.0489	0.0000
	TT	0	0.0000	-	68	0.0905				
	C	84	0.9767	0.4094	1041	0.6931			31.6889	0.0000
	T	2	0.0233	0.5906	461	0.3069				
UTS2R#1 C/T	CC	2	0.0465	-	194	0.2510	9.2560	0.0098	373.0554	0.0000
	CT	15	0.3488	-	572	0.7400			30.8690	0.0000
	TT	26	0.6047	-	7	0.0091				
	C	19	0.2209	1.0000	960	0.6210			54.3139	0.0000
	T	67	0.7791	0.0000	586	0.3790				
HIST1H1C#1 A/G	AA	30	0.6977	-	83	0.1070	89.0879	0.0000	120.5101	0.0000
	AG	12	0.2791	-	497	0.6405			22.6202	0.0000
	GG	1	0.0233	-	196	0.2526				
	A	72	0.8372	0.0172	663	0.4272			55.3778	0.0000
	G	14	0.1628	0.9828	889	0.5728				
HIST1H1C#3 A/G	AA	43	1.0000	-	760	0.9896	11.2665	0.0036	0.4524	0.7976
	AG	0	0.0000	-	3	0.0039			0.1686	0.6814
	GG	0	0.0000	-	5	0.0065				
	A	86	1.0000	0.9831	1523	0.9915			0.7337	0.3917
	G	0	0.0000	0.0169	13	0.0085				
MTCH1#2 A/G	AA	17	0.3953	-	548	0.7316	23.0847	0.0000	23.6034	0.0000
	AG	25	0.5814	-	185	0.2470			23.3380	0.0000
	GG	1	0.0233	-	16	0.0214				
	A	59	0.6860	1.0000	1281	0.8551			17.8454	0.0000
	G	27	0.3140	0.0000	217	0.1449				
TNF#1 A/G	AA	9	0.2093	-	6	0.0079	9.7618	0.0076	91.2400	0.0000
	AG	15	0.3488	-	253	0.3333			0.0440	0.8339
	GG	19	0.4419	-	500	0.6588				
	A	33	0.3837	0.0000	265	0.1746			23.5357	0.0000

	G	53	0.6163	1.0000	1253	0.8254				
TNF#2 A/G	AA	19	0.4419	-	470	0.6184	7.5663	0.0228	39.8212	0.0000
	AG	15	0.3488	-	270	0.3553			801.6591	0.0000
	GG	9	0.2093	-	20	0.0263				
	A	53	0.6163	0.9758	1210	0.7961			15.6618	0.0000
	G	33	0.3837	0.0242	310	0.2039				
TNF#5 C/T	CC	19	0.4419	-	507	0.6550	11.1314	0.0038	108.0168	0.0000
	CT	14	0.3256	-	261	0.3372			0.0247	0.8752
	TT	10	0.2326	-	6	0.0078				
	C	52	0.6047	1.0000	1275	0.8236			25.6076	0.0000
	T	34	0.3953	0.0000	273	0.1764				
GNG3#1 A/G	AA	25	0.5952	-	103	0.1359	88.6436	0.0000	63.3775	0.0000
	AG	13	0.3095	-	395	0.5211			7.1290	0.0076
	GG	4	0.0952	-	260	0.3430				
	A	63	0.7500	0.0429	601	0.3964			40.9813	0.0000
	G	21	0.2500	0.9571	915	0.6036				
TNNI2#2 C/T	CC	38	0.9268	-	460	0.5974	11.1601	0.0038	18.1059	0.0000
	CT	2	0.0488	-	275	0.3571			16.4588	0.0000
	TT	1	0.0244	-	35	0.0455				
	C	78	0.9512	0.6007	1195	0.7760			14.1588	0.0002
	T	4	0.0488	0.3993	345	0.2240				

*G represents genotypes. For the chi-square test and P_2 value, the first row of every marker shows the significance between sires and F_1 genotypes. The second row of every marker shows the significance of heterozygote frequency between sires and the F_1. The fourth row of every marker shows the significance between sires and F_1 gene frequencies. Tag SNPs are identified by underline.