VARIANTS DISCOVERY IN THE *LPL* AND *CETP* GENES AND THEIR ASSOCIATIONS WITH PLASMA LIPID AND APOLIPOPROTEIN LEVELS

by

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Abstract

Plasma lipid and lipoprotein levels are known to be under strong genetic control and major risk factors for cardiovascular disease (CVD). Identifying novel genetic variants associated with plasma lipoprotein-lipid concentration are of a considerable public health importance because this knowledge may facilitate the design of genetic markers for risk assessment, diagnosis and prognosis of CVD. In this study, we have comprehensively investigated the associations of both common and uncommon/rare variants in two major lipid genes, lipoprotein lipase (*LPL)* and cholesteryl ester transfer protein (*CETP*), in relation to plasma lipoprotein-lipid levels in U.S. non-Hispanic whites (NHWs) and African blacks. We resequenced the entire *LPL* and *CETP* genes plus their flanking regions in 190 individuals presenting extreme high-density lipoprotein cholesterol (HDL-C)/triglyceride (TG) levels selected from two study samples of 623 NHWs and 788 African blacks. We identified a total of 371 and 279 sequence variants in *LPL* and *CETP* genes, respectively, including several novel rare and population-specific variants. Following the discovery stage of resequencing, selected common tagSNPs and uncommon/rare variants from each gene were genotyped in the entire samples of 623 NHWs and 788 African blacks. A total of 171 *LPL* and 184 *CETP* variants passed the quality control and were analyzed for their associations with plasma lipoprotein-lipid levels by using single-site, haplotype and rare variant association analyses. Multiple common variants in the two genes demonstrated significant effects on plasma lipoprotein-lipids levels in both populations. Two putative functional SNPs, *LPL/* rs13702 (*P*=0.006 in NHWs; *P*=0.01 in African blacks) and *CETP/*rs183130 (*P*=1.91E-04 in NHWs; *P*=2.25E-06 in African blacks) exhibited strongest associations with HDL-C in both samples. Rare variant analyses indicated that *CETP* gene harbors rare variants that contribute to plasma lipoprotein-lipid levels in both ethnic groups. However, rare variants in *LPL* revealed associations with plasma lipoprotein-lipid levels only in African blacks. Our data reaffirm the important role of *LPL* and *CETP* genetic variation has in affecting plasma lipoprotein-lipid levels in the general population.

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1.0 BACKGROUND AND SIGNIFICANCE

1.1 INTRODUCTION

The completion of the Human Genome Project and the subsequent HapMap Project paved the way for our understanding of the genetic basis of complex human traits to a great extent. Since the complex traits do not follow clear pattern of Mendelian inheritance, the strategy to identify genetic variants associated with these trait are based on an approach called ‘genetic association’ analysis. The basic idea underlying the genetic association studies is to find a correlation between genetic polymorphisms and a disease status or phenotype and thus identify genetic risk factors by using case-controls, families or unrelated individuals. In the case of association, a particular polymorphism, genotype or haplotype, will be seen more frequently that expected by chance in individuals carrying the trait of interest. Finding such an association implies either the tested variant has a functional effect on the trait (direct association) or it is in linkage disequilibrium (LD) with a functional variant (indirect association). LD is the non-random association of alleles at two or more loci in a population and the principle of the ‘genetic association’ analysis relies on the levels of LD among physically close loci in the genome. Thus, even if a causal variant is not directly observed in the study, a proxy SNP in LD with it may capture its association. Those representatives SNPs are called tag SNPs. Genotyping subset of tag SNPs is useful in genetic association studies in terms of identifying genetic variation without typing each SNP in the region separately and it helps to reduce the cost of genotyping substantially. In this study, we applied genetic association methods to evaluate the role of genetic variation in two major genes, lipoprotein lipase (*LPL*) and cholesteryl ester transfer protein (*CETP*), involved in lipid metabolism in relation to four major plasma lipids [high-density lipoprotein cholesterol (HDL-C), triglycerides (TG), low-density lipoprotein cholesterol (LDL-C) and total cholesterol (TC)] and two apoliporoteins (apoA1 and apoB) by using two genetically discrete well-characterized population-based samples comprising non-Hispanic White (NHW) and African black individuals. This was achieved by using three-step approach; (1) SNP discovery by resequencing the extreme ends of HDL-C and TG distributions (2) screening the entire samples for common SNPs (tagSNPs and reported associations) and selected low-frequency variants identified in the discovery phase; and (3) association testing using gene-based, single-site, haplotype and rare variant analyses.

1.2 CORONARY HEART DISEASE (CHD)

In the United States, coronary heart disease (CHD) is still the leading cause of death and major killer of American males and females; about 600,000 Americans die from heart disease in each year and this accounts for one of every four deaths according to the National Vital Statistics in 2011 (Roger et al. 2012). Based on the Framingham Heart Study (FHS), in 2001 more than half of the total cardiovascular events were due to the CHD in females and males under age 75 (Lloyd-Jones et al. 2010). American Heart Association’s computation based latest available mortality data show that in every twenty five seconds an American will experience a coronary event and it will cause death of one person in about every minute. According to the data of National Health and Nutrition Examination Survey (NHANES) between 2003 and 2006, the prevalence of CHD in the United States was 17,600,000 for adults at age 20 and older. It means 7.9 percent (9.1 percent for males and 7.0 percent for females) of American adults at age 20 and older have CHD (Lloyd-Jones et al. 2010). The latest available data of the American Heart Association estimates that the direct and indirect cost of CHD is $190.3 billion for 2008 (Roger et al. 2012).

1.2.1 Risk factors of CHD

The risk factors for CHD are classified into two categories according to their causative and quantitative contributions to CHD. Low-level serum high-density lipoprotein cholesterol)HDL-C), elevated serum total and low-density lipoprotein cholesterol (LDL-C), elevated blood pressure, cigarette smoking, diabetes mellitus and advancing age are the major and independent risk factors. Several studies, including FHS, have investigated the quantitative relationship between these factors and CHD. Obesity, physical activity, ethnic characteristics, psychosocial factors, family history of premature CHD are predisposing risk factors and elevated serum triglycerides, small LDL particles, elevated serum homocysteine, elevated serum lipoprotein (a), prothrombotic factors and inflammatory markers (e.g., C-reactive protein) are conditional risk factors for CHD (Grundy et al. 1999). The mortality data, prevalence and incidence of CHD show that male gender and blacks has higher risk of developing a CHD (Keil et al. 1989; Cooper et al. 1992; Johnson et al. 1986).

1.3 GENETICS OF PLASMA LIPID LEVELS

1.3.1 Common disease-common variant (CDCV) and common disease-rare variant (CDRV) hypotheses

It has been well established that genetic factors play an important role in determining inter-individual variation in plasma lipid profile. In order to better understand the genotype-phenotype associations and finding genetic basis of common traits such as lipid phenotypes, ongoing efforts have been centered around two parallel hypotheses: common disease-common variant (CDCV) and common disease-rare variant (CDRV) (Robinson et al. 2010). The former suggests that a few common variants account for the majority of the variation in common phenotypes and susceptibility to common diseases whereas the latter states that multiple rare variants determine the susceptibility to common diseases and contribute to the common phenotypic variation cumulatively.

Our understanding of the genetic architecture of interindividual variations in lipid traits has been increased substantially by recent genome wide association studies (GWAS) (Teslovic et al. 2010, Boes et al. 2010). Common variation in a number of genes involved in lipid metabolism has been implicated to confer risk of CHD by revealing strong associations with plasma lipid traits, especially with HDL-C and TG. However, these known genetic variations do not explain all the genetic contributions to the phenotype (Weissglas-Volkov et al. 2010). Most of the loci identified by GWAS have small effect sizes with OR ranging 1.05-1.20 (Prins et al. 2012). Common variants together explain a modest fraction of the underlying genetic basis of inter-individual variation in lipid traits; Peden et al. (2011) reported that these variants explain only ~4% of interindividual variation in disease risk and up to ~13% of the total heritability of coronary disease. This raises the idea of so-called ‘missing heritability’ that is expected to be elucidated by identification of multiple rare variants that have moderate to strong effects on phenotypic variation in complex traits. In recent years, this phenomenon has led to the shift of focus of research from CDCV to CDRV hypothesis. An effective way to understand the role of these rare or low-frequency variants is to resequence the candidate genes in individuals with extreme phenotypes (Cirulli et al. 2010). This strategy has already been successfully employed in candidate genes involved in lipid metabolism *(ABCA1, APOA1, LCAT, APOA5, APOC2, LIPG, LPL, CETP, LIPC)* where multiple rare variants in these genes were found to contribute to the variation in plasma lipid levels (Cohen et al. 2004; Evans et al. 2011; Wang et al. 2007; Johansen et al. 2010; Khovidhunkit et al. 2012; Razzaghi et al. 2000). Cohen et al. (2004) originally report that multiple rare variants in the *ABCA1*, *APOA1* and *LCAT* genes contribute to the variation in plasma HDL-C levels in the general population. Likewise, Johansen et al. (2010) resequenced the *APOA5, GCKR, LPL* and *APOB* genes and found a significant excess of rare variants in individuals with hypertriglyceridemia (HTG) as compared to controls. Furthermore, recently Khovidhunkit et al. (2012) sequenced the exons and exon-intron junctions of the *CETP* gene in 64 Thai individuals with hyperalphalipoproteinemia (HALP) and identified rare *CETP* variants contributing to the HDL-C phenotype.

1.4 SIGNIFICANCE OF THE STUDY

In order to test the association of all common and rare variants in known candidate genes with variation in plasma lipid levels in a comprehensive way, it is important to identify all sequence variations in known candidate genes. In this study we resequenced two biological candidate genes (*LPL* and *CETP*) for CHD in individuals having extreme levels of HDL-C/TG in order to identify both common and rare functional variants that are associated with plasma lipid levels.

The rare variants identified in our study and genetic association results will help to fill the gaps in our understanding of plasma lipoprotein metabolism. Uncovering the functional roles of variants that shows statistical association with lipid traits will eventually have public health impact. Identification of genetic markers may lead to promising future public health interventions, like prognostic tools and therapeutic approaches to alleviate the burden of CHD in the U.S.

The lipoprotein lipase *(LPL)* and cholesterly ester transfer protein *(CETP)* genes are well-known candidate genes for CHD since the key roles of their products in lipoprotein metabolism has been extensively documented. *LPL* encodes lipoprotein lipase enzyme that hydrolyzes triglycerides and functions as ligand/bridging factor for receptor-mediated lipoprotein uptake, *CETP* encodes cholesteryl ester transfer protein which transfers cholestryl esters between lipoproteins and facilitates transport of triglycerides. See **Figure 1.4.1** for schematic diagram showing the roles of LPL and CETP in lipoprotein metabolism.

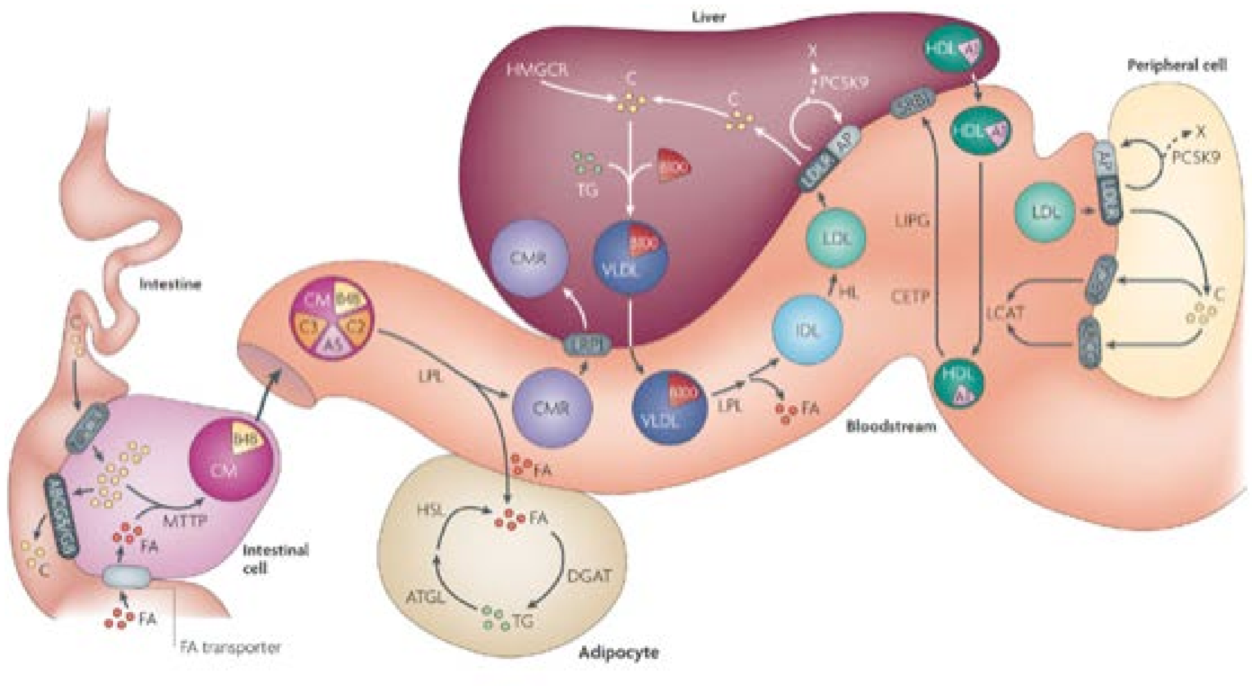

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Figure 1.4.1. Schematic diagram of the LPL and CETP enzymes in lipid metabolism.

(Used by permission from Macmillan Publishers Ltd: Nature Genetics, Hegele et al. 2009)

2.0 LIPOPROTEIN LIPASE (LPL)

2.1 LPL ENZYME

In 1943, Paul Hahn first observed clearance of postprandial lipidemia after injection of heparin injection (Hahn 1943). Subsequent studies focused on understanding the mechanism of so called heparin releasable ‘clearing factor’ and it was revealed that this factor was a lipolytic enzyme which has high activity against the TG component of plasma lipoproteins. The enzyme was called LPL, after discovering its role on breaking down plasma triglycerides of TG-rich lipoproteins (Tsutsumi 2003). LPL is a major rate-limiting enzyme responsible for the hydrolysis of TG-rich particles circulating in the bloodstream, so it has a central role in overall lipid metabolism and transport. ApoCII is required for activation of LPL and there are several factors such as apoCIII, apoE, high salt conditions and fatty acids that inhibit LPL activity (Murthy et al. 1996). It is synthesized by parenchymal cells and then transferred to the luminal surface of endothelial cells where it is anchored to the surface of the cells by heparan sulfate proteoglycans (Goldberg et al. 1996).

LPL enzyme activity has been detected in several extrahepatic tissues and cells, including adipose tissues, heart, skeletal muscle, lung, lactating mammary gland, brain, and kidney (Kirchgessner et al. 1989). LPL enzyme activity has been also identified in differentiated macrophages, placenta, spleen, pancreatic β-cells and steroidgenic tissue, but not in liver of adult animals.

The LPL enzyme is catalytically active in its dimer nascent form which is composed of 55 kDa subunits and it shows a head-to-toe configuration by noncovalent interactions Maturation of nascent LPL starts in the endoplasmic reticulum depending the activity of lipase maturation factor 1 (Wang et al. 1992). LPL is organized into two structurally distinct domains; a larger N-terminal domain (residues 1-312) and a smaller C-terminal domain (residues 312-448) connected by a flexible peptide (Murthy et al. 1996). Interaction of LPL with lipoprotein substrates occurs in the C-domain and it results a conformational change that allows enzyme to conduct its catalytic function by opening of the lid in the N-terminal domain (Santamarina-Fojo et al. 1994).

There are four distinct physiological activities of LPL that have been identified in several studies which all influence the plasma lipoprotein profile and the cellular metabolism of fatty acids and lipids (Preiss-Landl et al 2002). First and major activity of LPL is its hydrolyzing function of TG-rich lipoproteins, including chylomicrons and very-low density lipoprotein (VLDL) to provide fatty acids to underlying tissues (**Figure 2.1.1**). Second, LPL has uncatalytic activity called ‘bridging function’ which allows enzyme to to anchor lipoproteins to the vessel wall so it facilitates TG hydrolysis and lipoprotein uptake (Merkel et al. 2002). Third, LPL has a role in the uptake of lipoproteins by acting as a ligand for the LDL receptors, VLDL receptors, megalin, and LDL receptor related proteins (Medh et al. 1996, Takahashi et al. 1995, Kounnas et al. 1993). Fourth, LPL facilitates the selective uptake of lipoproteins associated lipids (Merkel et al. 2002; Seo et al. 2000) and lipophilic vitamins such as vitamin A and vitamin E (Preiss-Landl et al. 2002; Van Bennekum et al. 1999).

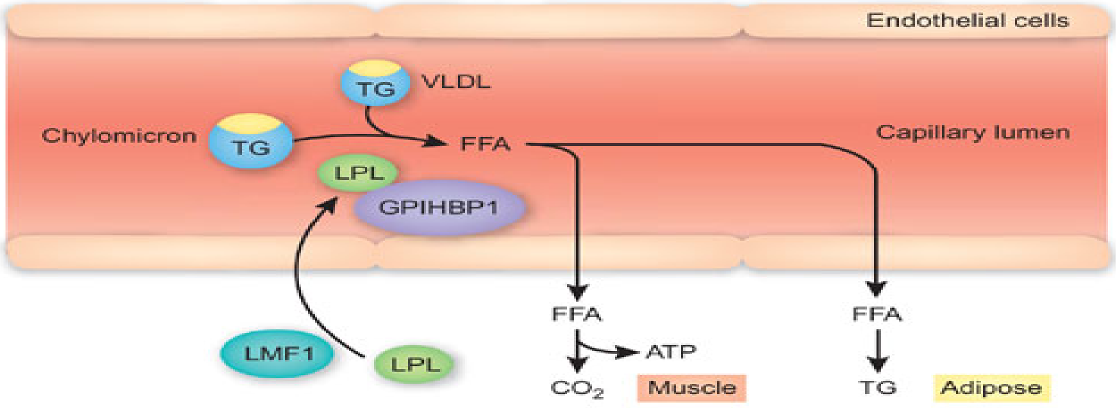


Figure 2.1.1. LPL activity in fatty acid transport to muscle and adipose tissues.

(Used by permission from Macmillan Publishers Ltd: Nature Genetics, Attie et al. 2007)

2.2 *LPL* GENE

The lipoprotein lipase gene is located on chromosome 8p22 in humans (Sparkes et al. 1987). The National Center for Biotechnology Information (NCBI) reference nucleotide sequence is NC_00008.10 (http://www.ncbi.nlm.gov/sites/entrez). It is a member of the TG lipase gene family; the other human genes in the same family are hepatic lipase (HL), pancreatic lipase (PL), and endothelial lipase (EL). The *LPL* gene comprises 10 exons spanning ~30kb (Deeb and Peng 1989). The gene encodes 475 amino acids and it becomes a mature protein of 448 residues after cleavage of a 27-amino-acid signal peptide (Wion et al 1987). 5’- untranslated region, the signal peptide and the first two amino acids are encoded by the first exons. The rest of the 9 exons encode the remaining 446 amino acids. The 10th exon is the largest exon that encodes the long 3’-untranslated region of 1,948 nucleotides and interestingly Intron 1 is the longest intron comprises ~9kb which is almost one third of the gene. It has been shown that *LPL* has a similar gene organization when comparing with the *HL* gene; all exons are almost the same size in both genes. However, the *PL* gene, the other member of the lipase gene family, has a distinct gene structure organization reflecting their molecular evolution and functional divergence (Kirchgessner et al. 1989).

The expression and regulation of *LPL* is regulated at transcriptional, posttranscriptional, translational and posttranslational levels in a tissue specific manner. Hormonal levels and nutritional regulations can also affect the expression of *LPL* by interacting proteins or directly modify the regulation of *LPL* (Wang et al. 1992).

2.2.1 *LPL* genetic variation and plasma lipid levels

LPL is a candidate gene for influencing the risk of CHD due to its central role in lipid metabolism. Several studies have investigated the association of *LPL* polymorphisms with HDL-C levels (Boes et al. 2009). Seven variants have shown significant association with HDL-C levels. Two of them are the common variants (D9N, N291S) that result amino acid changes and lead to decrease in enzymatic activity and so they have been projected to reduce HDL-C levels (Wittrup et al. 1999, Zhang et al. 1996; Mailly et al. 1995). While D9N (rs1801177) results in 3.2 mg/dl decrease in HDL-C levels and 20% increase in TG levels, N291S (rs268) leads to 4.6mg/dl decrease in HDL-C levels (Wittrup et al. 1999). The D9N variant is in near-complete linkage disequilibrium (LD) with the promoter variant (T93G), which may cause decreased LPL activity due to lower promoter activity but the role of the promoter variant is not yet clear (Merkel et al. 2002). The other amino acid substitution, Gly188Glu, decreases HDL-C levels (10mg/dl) and it is most frequent in French Canadians in Quebec (Wittrup et al. 1999; Merkel et al. 2002). It is the major mutation that results nonfunctional LPL protein and has the strongest link with increased risk of CHD among all *LPL* variants (Merkel et al. 2002). The *Hind*III (rs320) polymorphism is located in intron 8 of the *LPL* gene and is in strong LD with the Ser447X variant (Humphries et al. 1998). The *Hind*III polymorphism has been estimated to increase HDL-C levels up to 5.5mg/dl (Senti et al. 2001; Holmer et al. 2000; Ukkola et al. 2001; Radha et al. 2006, Ahn et al. 1993). Ser447X (rs328) is the other common variant that cause stop codon and it is also associated with increased HDL-C levels in several studies (Wittrup et al. 1999; Nettleton et al. 2007; Lee et al. 2004; Komurcu-Bayrak et al. 2007; Pallaud et al. 2001; Constanza et al. 2005; Kathiresan et al. 2008b; Talmud et al. 2002). Two single-nucleotide polymorphisms (SNPs), rs326 and rs13702, have been identified to be in a strong LD with rs320 so they are also associated with HDL-C levels (Boes et al. 2009; Klos et al. 2006).

Genome-wide association (GWA) studies have also identified many SNPs associated with HDL-C levels (Boes et al. 2010). The reported SNPs with the lowest p-values are rs2083637 (Aulchenko et al. 2009), rs10503669 (Willer et al. 2008), rs331 (Chasman et al. 2008), rs328 (Kathiresan et al. 2008b), rs17482753 (Heid et al. 2008), rs17411031 (Wallacee et al. 2008), and rs326 (Kooner et al. 2008).

3.0 CHOLESTERYL ESTER TRANSFER PROTEIN (CETP)

3.1 CETP ENZYME

The *CETP* gene encodes the cholesteryl ester transfer protein which is a member of the lipid transfer/lipopolysaccharide binding protein gene family. Plasma CETP is a glycoprotein (476 amino acids, 74 kDA) which includes four N-glycoslyation sites (Asn88, Asn240, Asn341 and Asn396) (Tall et al. 1993). It is composed of two similar domains (N- and C- domains) which are connnected by a linker. CETP mRNA is found predominantly in liver, spleen and adipose tissue; low levels of expression is also detectable in adrenal gland, small intestine, kidney, heart and skeletal muscle (Tall et al. 1995). The CETP enzyme also observed in several interstitial fluids such as follicular and cerebrospinal fluid. It has been suggested that CETP produced in the brain is secreted into the cerebrosfinal fluid and play a key role in redistribution of the lipids within the central nervous system.

The CETP functions as a key enzyme in lipid metabolism and cellular cholesterol efflux and it has multiple roles in lipid exchange, reverse cholesterol transport (RCT) and HDL conversion. The most widely known function is its ability to transfer cholesterol esters (CEs) from atheroprotective HDL particles to proatherogenic apo-B containing lipoproteins (VLDL and LDL) in exchange for TG from VLDL to HDL. This decreases the plasma levels of HDL and leads to high levels of proatherogenic LDL and VLDL, and hence results atherogenic plasma lipoprotein profile. On the other hand, exchange of TG for CE in HDL results smaller sized TG-enriched HDL which can be more easily hydrolyzed by hepatic lipase and more efficiently contributes to RCT by picking up more cholesterol. Besides the role of CETP in CEs and TG transport, it has been shown that CETP has a role in phospholipid transfer between plasma lipoproteins. **Figure 3.1.1** shows the role of CETP protein in RCT.

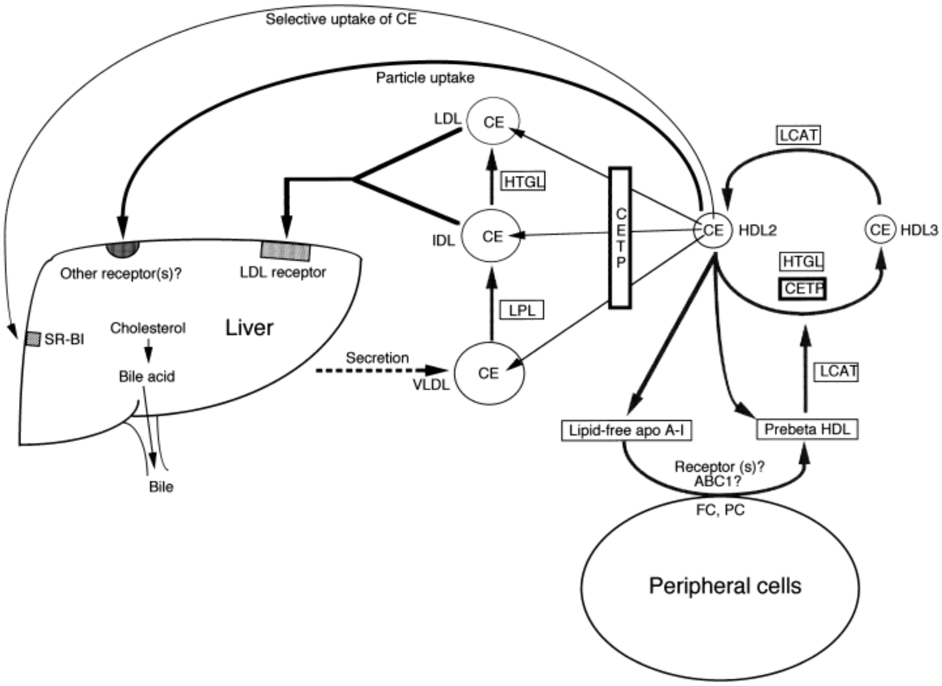


Figure 3.1.1. Roles of CETP in reverse cholesterol transport.

(Used with permission from Elsevier, Yamashita et al. 2000)

3.2 *CETP* GENE

The human *CETP* gene is located on chromosome 16 (16q12-16q21) spanning ~25 kb. It exists in a single copy consisting of 16 exons that range from 32 bp (exon 13) to 250 bp (exon 16) interrupted by 15 introns. The sizes of the introns range from 87 bp (intron 3) to ~6000 bp (intron 2) (Tall et al. 1993). The regulatory sequences located on the upstream of the flanking region are nuclear factor 1, a strerol regulatory element, hepatocyte nuclear factor 1 and a nuclear receptor binding site which requlate by liver X receptors (LXR) (Dullart et al. 2008). The CETP enzyme shares a common pentapeptide sequence within the signal peptide (ValLeuThrLeuAla) with apoA-IV, apo-A-1 and LPL (Agellon et al. 1990). This suggests that this common sequence may have a common conserved role related to translational and post-translation regulation of the gene expressions (Tall et al. 1993).

Inazu et al. (1991) discovered a variant of *CETP* cDNA that lacks exon 9 and suggested that the *CETP* gene expression is modified by alternative splicing of exon 9 which contains 180 nucleotide. This form of the *CETP* mRNA is found in almost all human tissues and it consists of about 20% of the total *CETP* mRNA in liver and 40-60% in spleen (Tall et al. 1993).

3.2.1 *CETP* genetic variation and plasma lipid levels

In 1985, a patient with elevated levels of plasma HDL and very low plasma CE transfer activity was first described due to deficiency in CETP (Koizumu et al. 1985; Brown et al. 1989). This was caused by a homozygous point mutation (G>A) at the first position of intron 14 which resulted splicing defect and lack of CETP in plasma. Since then, several heterozygote or homozygotes mutations in the *CETP* gene have been identified in individuals, mainly among Japanese, manifesting partial or complete CETP deficiency resulting changes in plasma CETP mass, activity and abnormalities of plasma (Dullaart et al. 2008; Yamashita et al. 2000). Patients with CETP deficiency have increased serum levels of HDL-C (3-6 fold increase), Apos A-1, C-III and E, slightly or moderately increases total cholesterol and TG levels (Yamashita et al. 2000). The splicing defect in intron 14 (G+1A/In14) and a missense mutation (D442G) found in exon 15 are the most common mutations in the general Japanese population with a heterozygote frequency of 0.01-0.07 and of 0.05-0.05 among Japanese-Americans. Especially, the G+1A/In14 is most common in Omagari region of Japon with a heterozygous frequency of 27% and homozygous frequency of 0.6% (Boekholdt et al. 2003). The other relatively common mutations are nonsense mutations in exon 10 and exon 6 (G181X) and a splice-site mutation in intron 10. Subjects with G181X mutation show no detectable CETP activity in their plasma. Japanese-American men with *CETP* mutations have shown increased risk of CHD despite having increased HDL-C levels (Zhong et al. 1994). Several noncoding and coding *CETP* variants have been reported in different populations. and their associations with lipid levels and CETP activity have been investigated. *TaqI*B (rs708272), -629C>A (rs1800775) and I405V (rs5882) are the most widely studied common *CETP* variants due to their established effect on plasma lipoprotein profile and plasma CETP levels. Genome-wide associations have been also identified significant SNPs in and around the *CETP* gene which are associated not only with HDL-C levels but also with HDL and LDL particle sizes (Kaess et al. 2011).

4.0 RESEARCH OBJECTIVES

4.1 HYPOTHESIS AND OBJECTIVE

Lipoprotein lipase (*LPL*) and cholesteryl ester transfer (*CETP*) play a central role in lipid metabolism. Common genetic variation in the *LPL* and *CETP* genes has been shown to be associated with interindividual variation in plasma lipid profile. We hypothesize that in addition to the common variation, these biological candidate genes also harbor rare variants that have large effect sizes on plasma lipid levels.

The objective of this study is to test the common disease-common variant (CDCV) and common disease-rare variant (CDRV) hypotheses in two racial groups comprising non-Hispanic whites (NHWs) and African blacks.

4.2 SPECIFIC AIMS

Aim 1: Establish a catalogue of common and rare variations in the *LPL* and *CETP* genes by resequencing the entire genes as well as their flanking regions in individuals falling in the upper (47 NHWs, 48 African blacks) and lower (48 NHWs, 47 African blacks) 10th percentile distribution of plasma HDL-C and TG levels.

Aim 2: Genotype common and low-frequency as well as rare variants in the *LPL* and *CETP* genes in the total sample of NHWs (n=683) and African blacks (n=788) by using TaqMan or Sequenom genotyping methods.

Aim 3: Evaluate the associations of genetic variants in *LPL* and *CETP* in relation to plasma lipoprotein-lipid levels in NHWs and African blacks by using single-site, gene based, haplotype and rare variant association analyses to test the both common disease-common variant and common disease-rare variant hypotheses.

5.0 METHODOLOGY

Our aim to test the association between genetic variants in the *LPL* and *CETP* genes and plasma lipid levels involves three steps: SNP discovery by resequencing, genotyping of the identified variants and association tests using SNPs and haplotypes. These genes were chosen for resequencing based on their significant biological roles in the lipid metabolic pathways. Samples were selected from two genetically discrete groups of 623 Non-Hispanic Whites (NHWs) and 788 African Blacks. The target regions were aimed to resequence in selected 95 NHW and 95 African black individuals with extremely lower HDL-C/higher TG (48 NHWs, 47 African blacks) and the higher HDL-C/ low TG (47 NHWs, 48 African blacks) levels for SNP discovery and identified common and rare variants were screened in our entire NHW (n=623) and African black (n=788) samples. Only those individuals with extreme lipid traits were sequenced in order to reduce the sequencing cost and improve the power to detect rare variants. After extensive genotyping, we performed single-site and haplotype based association tests to assess the effects of common genetic variation in these genes on six lipid and apolipoprotein phenotypes (HDL-C, TG, LDL, TC, apolipoprotein A-1 (ApoA1) and apolipoprotein B (ApoB) Rare variant association tests were also performed to evaluate the associationof rare variants with lipid and apolipoprotein levels.

5.1 SUBJECTS

The study was carried out on two well-characterized and population-based epidemiological samples of 623 NHWs from the US and 788 African blacks from Nigeria. NHWs were collected as a part of the San Luis Valley Diabetes Study, a population-based case-control study of type 2 diabetes in the San Luis Valley, Southern Colorado (Hamman et al. 1989; Rewers et al. 1993). The 623 NHWs subjects used in the current study did not have diabetes and a detailed description of this sample set, including the biometric and quantitative data, can be found elsewhere (Demirci et al. 2010). African black samples are drawn from a study on CHD-related risk factors in Benin City, Nigeria (Bunker et al. 1995; 1996). The characteristics of African black samples have been described in detail in Harris et al. (1998). Biometric and quantitative data of 623 NHWs and 788 African Blacks are summarized in **Table 5.1.1.**

For the resequencing discovery stage, we selected 95 NHWs and 95 African blacks falling in the upper (47 NHWs, 48 African blacks) and lower (48 NHWs, 47 African blacks) 10th percentile distribution of plasma HDL-C and TG levels (see **Table 5.1.2**). This study was approved by the University of Pittsburgh and University of Colorado Denver Institutional Review Boards. All study participants provided written informed consent.

Table 5.1.1. Demographic and characteristics of NHWs and African blacks.

Variable	*NHWs (n=623)* *Mean±sd or percentage*	*African Blacks (n=788)* *Mean±sd or percentage*
Males/Females (%)	47.35/52.64	62.81/37.18
Age (Yrs)	52.8 ± 11.4	42.35 ± 8.62
BMI (kg/m^2)	25.5 ± 4.1	22.03 ± 3.31
LDL-C (mg/dl)	136.9 ± 40.8	104.52 ± 33.71
HDL-C (mg/dl)	50.8 ± 14.4	46.03 ± 12.61
TG (mg/dl)	142.7 ± 93.5	78.72 ± 42.13
TC (mg/dl)	217.0 ± 43.5	166.65 ± 37.37
***ApoB (mg/dl)**	87.7 ± 24.3	65.35 ± 21.71
***ApoA1 (mg/dl)**	149.6 ± 33.3	136.13 ± 29.37

TC: Total cholesterol; LDL-C: Low-density lipoprotein cholesterol; HDL-C; High-density lipoprotein cholesterol; TG: Triglycerides; ApoB: Apolipoprotein B; ApoA1: Apolipoprotein A1

**Data available for only 435 NHWs and 766 Blacks.*

Table 5.1.2. Biometric and quantitative data (mean±SD) of resequencing sample (95 NHWs, 95 African blacks).

	NHWs (n=95)			*Blacks (n=95)*		
	High HDL/Low TG (n=47)	*Low HDL/High TG (n=48)*	*P-value*[a]	*High HDL/ Low TG (n=48)*	*Low HDL/HighTG (n=47)*	*P-value*[a]
Sex (M/F)	24/23	24/24	1	24/24	23/24	1
Age (years)	55.45 ± 9.80	53.03 ± 10.54	0.25	41.29 ± 8.72	40.87 ± 7.12	0.80
BMI (kg/m2)	23.17 ± 3.17	27.35 ± 3.90	1.2E-07	22.06 ± 4.70	23.91 ± 5.51	0.08
TC (mg/dl)	22.734 ± 51.76	208.81± 44.65	0.07	201±39.68	141.68 ± 31.03	2.4E-12
LDL-C (mg/dl)	126.84 ± 46.95	125.54 ± 54.97	0.90	112.55 ± 39.75	95.04 ± 28.28	0.02
HDL-C (mg/dl)	77.68 ± 13.32	31.81 ± 4.37	2.2E-16	76.05 ± 7.53	25.51 ± 5.66	2.2E-16
TG (mg/dl)	114.09 ± 60.88	240.21 ±153.22	1.7E-06	61.98 ± 19.85	95.79 ± 73.21	0.004
ApoB (mg/dl)	87.88 ± 25.49	89.61± 25.18	0.80	66.00 ± 20.22	69.64 ± 21.46	0.40
ApoA1 (mg/dl)	174.08 ± 34.78	130.20 ± 27.08	1.4E-06	166.04 ± 28.19	103.84 ± 27.23	2.2E-16

TC: Total cholesterol; LDL-C: Low-density lipoprotein cholesterol; HDL-C; High-density lipoprotein cholesterol; TG: Triglycerides; ApoB: Apolipoprotein B; ApoA1: Apolipoprotein A1. [a]***P-values were calculated based on the original values by using t-test. No covariates were included.***

5.2 LIPID MEASUREMENTS

Fasting TC was determined by esterase-oxidase method (Richmond et al. 1973). Serum HDL-C and TC concentrations were measured by enzymatic procedures described in Harris et al. 1998. LDL-C was calculated by using the Friedewald equation if triglyceride levels were less than 400 mg/dl (4.5 mmol/l) (Friedewald et al. 1972). ApoB and apoA1 levels were measured using Boehringer Manneheim turbidmetric procedures (Harris et al., 1998). The DNA samples were extracted from blood clots and buffy coats for African black and NHWs sample, respectively by using standard DNA extraction procedures.

5.3 DNA SEQUENCING

The accession numbers of reference sequence used in this study are*:* NC_000008.10 for *LPL*, and NC_000016 for *CETP* that were derived from Genbank in NCBI site (http://www.ncbi.nlm.nih.gov). Although we designed most of the primers for each gene by using Pimer 3 software (http://frodo.wi.mit.edu/primer3/), we also used a subset of primers from a previous study (Nickerson et al. 1998) for *LPL* resequencing and a subset of M13 tagged forward and reverse primers from SeattleSNPs database were used for *CETP* resequencing.

The GeneAMP® PCR System 9700 thermal cycler with a heated lid (Applied Biosystems, Foster City, CA) was used for performing polymerase chain reaction (PCR). The PCR reactions and cycling conditions are presented in **Table 5.3.1** Gel electrophoresis by using 96-well pre-cast agarose E-Gel® 96 2% with SYBR® Safe (Invitrogen Corperation, Carlsbad, CA) was performed following amplification of each of the PCR fragments to check the success of the reaction. Reamplification was done for some of the samples that were failed in the initial amplification and regular 2% agarose gel with ethidium bromide (2µl) was performed after PCR reaction of this subset of reamplified samples to confirm the amplification. All the amplified samples were sent to a commercial sequencing laboratory where automated fluorescence-based cycle sequencing and capillary electrophoresis were performed on ABI 3730x1DNA Analyzers (Genomic Services of Beckman Coulter, Danvers, MA). Sequencing data received from the commercial labortory was analyzed in our laboratory by Variant Reporter version 1.0 (Applied Biosystems) and Sequencher version 4.8 (Gene Codes Corporation, Ann Arbor, MI).

Table 5.3.1. PCR reaction and cycling conditions.

PCR Reaction (Total volume 25 µL)		**PCR conditions**
DNA	3.0 µL	1. 95º C for 5 minutes 2. 95º C for 45 seconds 3. 58-60º C for 45 seconds 4. 72º C for 1 minute - Repeat steps 2-4 for 40 cycles 5. 72º C for 10 minutes 6. Cool to 4º C
dH2O	12.25-13.75 µL	
10x BufferGold	2.5 µL	
MgCl2 (25 mM)	1-3.5 µL	
dNTPs (1.25mM)	3.8 µL	
Forward Primer (20mM)	0.4 µL	
Forward Primer (20mM)	0.4 µL	
AmpliTaqGold (5U/µL)	0.15 µL	

5.3.1 Lipoprotein lipase

The *LPL* gene is located on chromosome 8p22 and comprises 10 exons. A total of 37 overlapping resequencing amplicons were sequenced in both directions and the PCR primers that were used to produce these overlapping amplicons are given in **Table 5.3.2.** These amplicons cover the entire *LPL* gene (27,993 bp) as well as 1,196 bp in the 5’ flanking region and 1kb in the 3’flanking region resulting into a total of 30,189 bp genomic fragment. Although we design most of the primers by using Pimer 3 software (http://frodo.wi.mit.edu/primer3/), we also used a subset of primers from a previous study (Nickerson et al. 1998). That sequenced only a portion of the targeted region (9.7kb), starting 3’ end of intron 3 to 5’ end of intron 9.

Table 5.3.2. *LPL* Polymerase chain reaction (PCR) and sequencing primers.

Amp. #	Amp. size (bp)	Forward Primer	Reverse Primer	Internal Sequencing Primer
1	822	5'-GGGTTGGGGATACACTTCAT-3'	5'-TGTTTTCCAAGGAGGGAAAG-3'	
2	722	5'-TGATCCATCTTGCCAATGTT-3'	5'-AGGGCTTTGCTCTCCATCT-3'	
3	851	5'-GAAAGCTGCCCACTTCTAGC-3'	5'-GTACTTTCTCCACCCCGACA-3'	
4	703	5'-TGACCTGCAGTCACCTCTCT-3'	5'-GCTCTCTATGCTGCTGTTGC-3'	
5	800	5'-GGGGCCAAATGAGAATGTC-3'	5'-AGTTGGCTCCTACCATCTTC-3'	
6	1177	5'-GGATCAGTTTGAAAACACTGGA -3'	5'-CATTTTGATGGCTGGAACAT-3'	
7	1112	5'-TGCCTTATGCCAGATTGTTC-3'	5'-TTGAATGAAGGGCTGTTGAG-3'	
8	1147	5'-ATACCATTCTGGCTTGGATT-3'	5'-ACTGATGTGGTCGATTTGGT-3'	
9	1056	5'-AGCTGCATGTTAGAGAAGTCAA-3'	5'-CCAAACTTCAGTCAGCTCTCC-3'	
10	1093	5'-CTGCCCAATAGCAATCACAG-3'	5'-CAATGGGTAAACACTCCAAGA-3'	
11	1113	5'-TCTTGGTGGATGAATGGAT-3'	5'-ATTACCAGTGTGAGCCATCG-3'	
12	1022	5'-GCCATAGGAGTGGGAACAGT -3'	5'-ACTGGAGGGTTGCTTGATTT-3'	
13	787	5'-TCGAAAACACTTCAGAAACAAAA-3'	5'-AGTAAATGGAGGCCCAGAGA-3'	
14	1090	5'-CTGCGAGGTTGGTAAAGGAT-3'	5'-CCTGCCTGTGCTGAAAATA-3'	
15	1053	5'-TGTGATAAAATCTCAAATTCCTAAA-3'	5'-TCCTACAGTGGCTGACATTTTT-3'	
16	1019	5'-AGGGAGGGCTTCAGTTCAG-3'	5'-TTCACAATGGGAACCCTGTA-3'	
17	1049	5'-AACCCGATTTTCTTGCCTTA-3'	5'-TGAATGCCCCCAGAAAATA-3'	
18	1084	5'-AGAGTTGGGTGCCAAAACTT-3'	5'-GGGTATATATTTTCCCATTATTCC-3'	
19	691	5'-AACCAGGTAATTGGAAGTAAAAA-3'	5'-ACAGTTCTGCCAAAAATAAAACT-3'	
20	1061	5'-TGTTTACGGAAAAGTGAAACAAA-3'	5'-GGGGCTTCTGCATACTCAA-3'	
21 *	475	5'-GGCCAAATGTGTATATGAAAAC-3'	5'-CCATGACTGTAGAATAGGAGC-3'	
22 *	1783	5'-AGAGGACTTGGAGGTAAATATT-3'	5'-GACTCCTTGGTTTCCTTATTTA-3'	5´-ATGTTACTGGAACAGAAGATG-3´ 5´-CTGGTCCACATCTGGGTAAA-3´
23 *	1229	5'-AGGCTGGAGACTGTTGTAAAT-3'	5'-CTCAGGTTTCCATCTGGATTC-3'	5´–CTATCAACTCTGTTATGGTGGC-3´
24	708	5'-CCCTCTATGTGCTCATGCAA-3'	5'-TGGGGCCACTGTTCTTTAAT-3'	
25	1169	5'-GGAATGGTCGGAAAATGAGA-3'	5'-AAGGAAAGGCAGCAGGACTA-3'	
26	915	5'-CCACGCCCAACTAATTTC-3'	5'-CCTAGAAAATGCAGACCTTGAA-3'	
27	1057	5'-TGTTTTGGCCTTCTGATTTG-3'	5'-CATGGTGAGACCCTGTCG-3'	
28	755	5'-AGTAAGAAGTCCATGACAAAGTGT -3'	5'-TTTCCTGGGTTTCCTACAAT-3'	
29*	1881	5'-CATCAATTACAGTCGTACCTAT-3'	5'-TCAGCTTTAGCCCAGAATGC-3'	5´-GAGCAGTCTTATGTTACTGGGC-3´
30*	794	5'-TCATTTGCAGAAAGGAAAGG-3'	5'-AATTCAGAACAGGAGTAGTG-3'	
31	874	5'-TGCCTCTTTCCTACCTGACC-3'	5'-ATTTTTGTAAAGGACGAAAAACAT-3'	
32	1072	5'-AAAAACATGCCTATTAGGAAAAG-3'	5'-CGCATCTGAACATTCTCTGTC-3'	
33	1078	5'-CGGCCCTAGATGCAGTTTTA-3'	5'-AGATTCGCCCAGTTTCTGAG-3'	
34	1049	5'-AGAAGTCATTTGGCCCAGTC-3'	5'-GCTGAGGATTACAGGCTCATT-3'	
35	1046	5'-ACTTGGAGAGGGACGAAGAA-3'	5'-TCACAACCCAAATCCAGAAA-3'	
36	1044	5'-GCATAATTCGGAAGGGAAAA-3'	5'-TTATCAAGGCAACCCAAAGC-3'	
37	754	5'-GCCTGCATAAAGTACACAGGA-3'	5'-CTTCTCCACATCCTCAGCAA-3'	

**Primers from the study of Nickerson et al. (1998)*

5.3.2 Cholesteryl ester transfer protein

The primers for the *CETP* gene were designed to sequence the entire gene without any gap. However, we were unable to sequence ~2kb fragment between positions 6938bp and 8664bp (Intron 2; highlighted yellow in the FASTA sequence). The primers used in the amplification of the *CETP* gene are listed in **Table 5.3.3.**

Table 5.3.3. *CETP* Polymerase chain reaction (PCR) and sequencing primers.

Amp. #	**Amp. size (bp)**	**Forward Primer**	**Reverse Primer**
1	772	AATGTTCAGAGTAGGCAATCCCA	ACTGAGTGAGCATGTACCATCG
2	536	GAGGCCTGGGCTAAAGGGCT	GCTGCCTCCGGGAGAAACTG
3	491	GAGCAAGGCCATCCCGACTC	GGAGAGGGCTTCATGGGTGC
4	582	GAATTGAAATGCCACAGACATTCCC	GCCAGACATTCAACAAGAGCACC
5	478	GCACCCATGAAGCCCTCTCC	GTGTAAGTGGCCCGAGCCGT
6	460	GGTGCTCTTGTTGAATGTCTGGC	TCAGCCCATCTCCCTCCCAG
7	931	ACACTAGCCCAGAGAGAGGAGTG	GCTGCCTTTCCTCCCTGTGG
8	534	CAGCATCGTCTGGGTGAGGC	ACTCACTTGTGCAACCCATACTT
9	699	TCAGAGAGGCTGAGTCATGG	GCGATGGCATTATCCTCTTT
10	989	TCTTATTTCGGGGTGAATGG	ACCGACCCTTGACTGTTACC
11	916	GACCTGGTTGGTCTTAAACTCCT	TGTCTGACCTCTTGCAACACATA
12	808	AGGTAGGAGGATTACCTCAGCC	GAATATGACACAATAGAAGCGGC
13	878	GCACAGTGTGTCATAGTGGCTTA	AAATGAGAAAGTCAGAGCAGGAA
14	955	CACTCCAAGTTTAGTGGCTTAACA	TCTGGTAATAGTTGCGTAAGCTC
15	717	CCTGCAACGTTTTGTCAATC	AAGCCCAAAGCTAGCAGAAG
16	606	GACTGGTAATAATGGCCTTGC	CCAAAATGTCCTCCTAATCCA
17	781	TTTCAAGTTCCATAAGGTGGAAA	TACTCAGCTGTGTGTTGATCTGG
18	1035	ATTCAGAACGTGTCTGTGGTCTT	CAAATCCTACTCCCATCCCTTAG
19	556	TCTGGGCTGGAGGGCTGAAT	CTCAGGTTTGGCCACCCACA
20	850	GTGTGCAAAGCACTATTCCAAG	AGGGTGAAGGAGATGAAATTTGT
21	934	AGTTAATTCTTGGGTCTGAGGCT	TAGAAGGTTGGTTCAGAGCAGAG
22	403	TGAGGCTGGCTGACTCCCTG	GTGTCAGAGCCAGATAGAGCCCA
23	769	CTCAGGACAAATGGGTGATTAAG	TAGAGGATGACAGAAGCCGAATA
24	652	AGACATTGGGGTGGACATTT	CTGTGAGCAGAGTGGGTGTG
25	652	ATTTCCCTCTGTTGCGTTCT	GCCCACTATGTCTCAACCAC
26	818	AACTGGACAGAAGGATCATTTCA	GTCTGGACTTCACTGCTATTGCT
27	1032	GCTGTACTTCTGGTTCTCTGAGC	GAGTCCTACTCTGTCACCCACAC
28	888	GAGGGTCTGTCTCTCTTCTCTCA	TGGAGTAAAGTCCACTCCTCAGA
29	902	AATGCTTAGGTAGTTTCCAGGCT	ATTTGAGGTAGGAGATCATGGGT
30	801	AAAGATAAGGCTCCATTCCCTG	TATTGGAGGGTATCAGGACACAG
31	861	CTCCCTGCACATACACAACTCAC	AATCTCAGTGGGTAAGTAAAC
32	936	GCCATCTCATTCCATTTTCC	GGGGATAGAGCAGCAGAGAG
33	936	AGCCTGGTGTGTCTCTCCTTTA	ATATTACCTAAGCTGTGGAAACC
34	382	CCGGAGCCAGCTTTGTCCTT	CCAGTGCCAGCAGAGGTGGT
35	891	AAGCCTCCAGATCCTTCTCAC	GAAGTTCTGAATTTGGAAACCCT
36	813	TAGAGACAGGGTTTCGCTATGTG	TATTAAGAAATATTGGCCGAGCA
37	967	CTTCCTGGTTCAAGCGATTC	GTCTACATCCACATGAGAAAGCC
38	877	TCGACTAGAGATGTGCACTACCA	TTCTTAGAATAGGAGGCCTGGAC
39	882	AGTGACTTCTCAGGTCCTAACCC	GAGAAGAAGGGTCACAAGAGACA
40	810	AAAGCACTGGCTGCTATTCTTAG	GACCGCTAAGTATCAATGACTGG
41	325	CGGATGGGCATGAGGATGAA	CCAGCAGGGAGAGGAAAGGG
42	929	CTTGTGGGTCACTTCTGTGCT	TCTACCCTGCTAGGAAGGAAACT
43	1027	ACATGGCTTAGGTAGGAGAGGAA	CTTGGATACAGCACTTTAATGCC
44	574	GGGAGAGAGGCCCAGACAGG	CAGGGAGGATCGTGAGTCCCA
45	1069	GAGCTTGAGCTAGAAGTCTCCAA	TGAAATTAGAAGCAAGGGGGCGAA
46	1091	TTAACCCAGCACTCTCCTTGTCTG	TGCAAAGAAATAGCACTCAAACA
47	620	TGCTCTCACCATTGTTCCATCTATGA	AAACCTGGCTCAGAAGATGGTGC

5.4 LINKAGE DISEQUILIBRIUM (LD) AND TAGGER ANALYSES

Haploview (Barrett et al. 2005, www.broadinstitute.org/haploview) was used to determine the LD between variants and selecting tagSNPs of common variants (MAF≥0.05) by performing tagger analyses.

5.5 VARIANT SELECTION AND GENOTYPING

For genotyping the entire sample of 623 NHWs and 788 African black individuals, we used either TaqMan (Applied Biosystems) or iPLEX Gold (Sequenom, San Diego, CA) genotyping methods following manufacturer’s protocols. The 384-well plates containing dried whole genome amplified DNAs were used in both methods. PCR amplification was done by using a PTC-200 MJThermal Cycler (Biorad) or a GeneAmp 9700 (Applied Biosystems). TaqMan reaction and thermal cycler conditions are given in **Table 5.5.1**. After thermal cycling of custom or pre-made TaqMan assays, the ABI Prism 7900HT Sequence Detection Systems was used for endpoint fluorescence reading of the 384-well plates. The iPLEX Gold genotyping was performed in the Genomics and Proteomics Core laboratories of the University of Pittsburgh. We used both TaqMan SNP genotyping assays and Sequenom IPLEX genotyping assays for genotyping variants in the two genes. Overall, the following criteria were considered in selecting the sequencing variants for genotyping in the total samples of 623 NHWs and 788 African blacks: (1) common tagSNPs (MAF ≥0.05, $r^2 \geq 0.9$); (2) all variants located in exons or intron-exon junctions; (3) all uncommon or rare variants (MAF <0.05) present in two or more individuals included in the sequencing, and (4) suspicious rare variants identified in the sequencing. Additionally, we covered all tagSNP bins identified in HAPMAP CEU (Utah residents with Northern and Western European ancestry from the CEPH collection) and YRI (Yoruba in Ibadan, Nigeria) populations. Those SNPs that were not found in our data were selected for genotyping. The discrepancy rate was determined to be 0-0.5% for the genotyped SNPs based on random repeats of 10% of the samples.

Table 5.5.1. TaqMan reaction and thermal cycler conditions.

TaqMan Reaction (Total volume of 5 µL)		**PCR Cycling Conditions**
		1. 95º C for 10 minutes
dH_2O	2.44 µL	2. 95º C for 15 seconds
TaqMan Master Mix	2.50 µL	3. 60º C for 1 minute
TaqMan Assay Mix	0.06 µL	-repeat steps 2-3 50x

5.5.1 Lipoprotein lipase

In NHWs, 43 common tagSNP bins (r^2=0.9) were identified for the common 88 sequencing variants (MAF≥ 0.05) (see **Table 5.5.2).** The SNP genotype data from the HapMap CEU population were used to compare the HapMap tagSNPs with our sequencing-derived tagSNPs. We identified 24 common tagSNP bins (r^2=0.9) capturing 48 HapMap SNPs (MAF ≥0.05) in the same region and all of them were captured by our sequencing-derived tagSNPs. In addiiton to 43 tagSNPs, 43 uncommon/rare variants were selected for subsequent genotyping in the entire sample of 623 NHWs. In African blacks, ninety-two tagSNPs for 130 common SNPs were selected by using Tagger program in Haploview with the following parameters: r^2 ≥0.9, MAF≥0.05 (**Table 5.5.3).** The SNP genotype data from HapMap YRI population was also used to compare the HapMap tagSNPs with ours. Thirty-eight tagSNPs were generated for the same region using HapMap YRI data by applying same parameters and they were all captured by our tagSNPs. In addition to the 92 tagSNPs, we selected 68 uncommon/rare variants for follow-up genotyping in the total sample of 788 individuals. Additionally, three known common *LPL* SNPs (rs1470187, rs328 and rs59184895) that were not detected in our sequencing sample due to low-quality DNA traces in this region were also genotyped.

Table 5.5.2. Tagger results of 88 common variants of *LPL* (MAF ≥ 0.05, r^2=0.09) in the NHWs sequencing sample.

LD Bins	Variants
1	rs75278536, rs145391587, rs325, rs3735964, rs77069344 ,rs117199990,**rs1059611**, rs1803924, rs10645926, rs12679834
2	**rs4921684,** rs11570892, rs331, rs4921683, rs330, rs3866471 ,rs1059507
3	rs3916027, **rs13702,** rs3208305, rs326, rs15285
4	rs3779788**,** rs74304285,12810dup20, **rs3779787**, rs113023641
5	rs291, rs297, rs33936024, **rs295**
6	rs271, rs58935878, rs256**, rs264**
7	rs3200218, rs319, **rs10099160**
8	rs322, rs320, **rs327**
9	rs287, **rs301**, rs289
10	rs252**, rs253**, rs258
11	rs316, **rs312**, rs4922115
12	**rs80181352**, 12853_12854Ins16
13	rs304**, rs305**
14	**rs17410577**, rs34309063
15	rs56321069**, rs8176337**
16	**rs269**, rs263
17	**rs254**, rs255
18	**rs249**
19	**rs314**
20	**rs270**
21	**rs311**
22	**rs57186780**
23	**rs1534649**
24	**rs74746426**
25	**rs13266204**
26	**rs277**
27	**rs11570891**
28	**rs74377536**
29	**rs282**
30	**rs286**
31	**rs113064376**
32	**rs112127208**
33	**rs283**
34	**rs285**
35	**rs294**
36	**rs78031480**
37	**12861del4**
38	**rs117026536**
39	**rs9644636**
40	**rs281**
41	**rs73667472**
42	**rs10104051**
43	**rs278**

43 tagSNP bins were identified. Bold: TagSNPs selected for genotyping

Table 5.5.3. Tagger results of 130 common *LPL* variants identified in African blacks (n=95, MAF≥0.05, r^2=0.9).

LD Bins	Variants
1	rs28689946, **rs28645722**, rs7000460, rs28582042, rs28575919, rs73667468
2	rs304, **rs305**, rs320, rs33936024, rs291, rs297
3	**rs147900112**, rs10283151, rs28439839, rs284, rs28424158
4	18399_18400InsA, **rs247,** rs58670071
5	5772, **rs1031045,** rs73667470
6	**rs255**, rs254
7	**rs1470186**, rs17091742
8	**rs59054859**, rs73601656
9	25272, rs306
10	rs58998793, **rs76707496**
11	**rs6991305**, rs77298438
12	**rs59254395,** 9589
13	rs10099160, **rs319**
14	rs34309063**, rs17410577**
15	**rs13702**, rs15285
16	**rs8176337,** rs56321069
17	rs28681081, **rs313**
18	rs10645926, **rs1059611**
19	**rs10104051**, rs1534649
20	rs287, **rs289**
21	5793, **rs114288334**
22	rs73667469, **rs56043715**
23	rs322, **rs327**
24	rs4922115**, rs4921683**
25	**rs276**
26	**rs7002728**
27	**rs59811201**
28	**rs277**
29	**rs28615996**
30	**rs329**
31	**rs316**
32	**rs3916027**
33	**rs281**
34	**rs140991223**
35	**rs266**
36	**rs261**
37	**rs1121923**
38	**rs79760154**
39	**rs73667472**
40	**rs3208305**
41	**9596insC**
42	**rs260**
43	**rs290**
44	**rs249**
45	**rs73667465**
46	**rs3866471**
47	**rs6999612**
48	**rs259**
49	**rs264**
50	**rs269**
51	**rs1800590**

Table 5.5.3. Continued

52	**rs75026342**
53	**rs145257746**
54	**rs3289**
55	**rs149017698**
56	**rs6997330, rs7016529**
57	**rs272**
58	**rs1801177(D9N)**
59	**rs330**
60	**rs76423146**
61	**rs331**
62	**rs80143795**
63	**rs318**
64	**rs58935878**
65	**rs141390463**
66	**rs75946927**
67	**rs314**
68	**rs74304285**
69	**rs301**
70	**rs252**
71	**rs279**
72	**rs3200218**
73	**rs11570892**
74	**rs263**
75	**rs326**
76	**rs17091815**
77	**rs1059507**
78	**rs312**
79	**rs113064376**
80	**rs251**
81	**rs248(E118E)**
82	**rs28716400**
83	**rs294**
84	**rs283**
85	**rs28445964**
86	**rs253**
87	**rs295**
88	**rs17116619**
89	**rs4921684**
90	**rs115078054**
91	**rs28599962**
92	**rs57186780**

92 TagSNPs were identified for each bin. Bold: TagSNPs

5.5.2 Cholesteryl ester transfer protein (*CETP*)

Single-nucleotide polymorphism (SNP) selection for genotyping in the total samples of 623 NHWs and 788 African blacks was based on our sequencing data plus information obtained from public databases, and literature including candidate and genome-wide association studies (GWAS). (Bansal et al. 2003; Willer et al. 2008; Boes et al. 2009; Teslovich et al. 2010; Spirin et al. 2007; Ridker et al. 2009; Kim et al. 2011: Edmondson et al. 2011). Sequencing-derived SNPs included tagSNPs and uncommon/rare variants which were selected based on their location in the gene and their frequency distribution among seleted individuals with extreme HDL-C/TG included in resequencing. TagSNP selection was performed by tagger and LD analyses (r^2=0.9) in Haploview by using the following parameters: $r^2 \geq 0.9$, MAF≥0.05. Forty-one common tagSNPs in NHWs and 81 tagSNPs in African blacks were identified which capture 81 and 126 common variants (MAF≥0.05) for NHWs and African blacks, respectively (see **Table 5.5.4 and Table 5.5.5).** We compared our sequencing-derived tagSNPs with the tagSNPs of HapMap data for CEU and YRI populations and all of the HapMap SNPs (MAF ≥0.05) in the same region were captured by our tagSNPs so we did not include any SNP from HapMAP. In addition to tagSNPs, 40 uncommon and low frequency (MAF< 0.05) variants in NHWs and 77 in African blacks were selected from our sequencing data**.** Detailed information for selection criteria of SNPs included in association analyses can be found in **Appendix Table B1.5** for NHWs and **Appendix Table B1.6** for African blacks**.** In addition, we selected 16 SNPs for genotyping (8 in NHWs and 8 in African blacks) that were not detected in our sequencing samples but have been previously reported in dbSNP build 137 in European and African descent populations. We also genotyped 26 additional SNPs in NHWs and 7 in African blacks that were not identified tagSNPs in our sequencing cohort but previously they have been shown to be associated with lipid levels in candidate or GWAS. Altogether, 131 variants in NHWs and 175 variants in African blacks were selected for genotyping and 251 of them were successfully genotyped in at least one population (111 SNPs in NHWs and 140 SNPs in African blacks).

Table 5.5.4. Tagger results of 82 common *CETP* variants identified in NHWs (n=95, MAF≥0.05, r^2=0.9).

LD Bin	agSNP ariants	V
1	rs12447620	rs112039804,rs12447620,rs158617,rs289715,rs289742,rs12708985,rs736274,rs11276066,rs158480
2	rs12720926	rs1532625,rs12720926,rs34620476,rs711752,rs11508026,rs1532624,rs7205804,rs708272,rs34145065
3	rs289718	rs289718,rs12720889, rs35874588,rs289719,rs289716
4	rs9939224	rs9939224,rs289713,rs7499892,rs11076175
5	rs2033254	rs2033254,rs11860407,rs12708980
6	rs158478	rs158477,rs158479,rs158478
7	rs4784745	rs291043,rs4784745
8	rs289714	rs289714,rs11076176
9	rs17245715	rs17245715,rs12708968
10	rs4783962	rs12447924,rs4783962
11	rs1864163	rs5817083,rs1864163
12	rs1800774	rs66495554,rs1800774
13	rs12720922	rs12720922,rs8045855
14	rs79398303	rs708273
15	rs3816117	rs1800775,rs3816117
16	rs4784744	rs4784744,rs289717
17	rs71387147	rs71387147
18	rs9923854	rs9923854
19	rs1801706	rs1801706
20	rs289712	rs289712
21	rs17231506	rs17231506, rs36229491
22	rs12720918	rs12720918
23	rs1968905	rs1968905
24	rs9930761	rs9930761
25	rs17231569	rs17231569
26	rs9929488	rs9929488
27	rs289744	rs289744,rs289741,rs5882,rs289743
28	rs5883	rs5883
29	rs12720917	rs12720917
30	rs11076174	rs11076174
31	rs820299	rs820299
32	rs12708974	rs12708974
33	rs9926440	rs9926440
34	rs7203984	rs7203984
35	rs4369653	rs4369653
36	rs7194225	rs7194225
37	rs4587963	rs4587963
38	rs56208677	rs56208677
39	rs4783961	rs4783961
40	rs289745	rs289745
41	rs1800776	rs1800776

Table 5.5.5. Tagger results of 126 common variants of *CETP* in the sequencing sample of African blacks (n=95, MAF≥ 0.05, r^2=0.09).

LD Bin	Variants
1	**rs17231869**
2	**rs13332571**, rs5884, rs13332526, rs12708968, rs13338602
3	**rs12720862**, rs12720860, rs60531466, rs12720861
4	rs5882, rs289741, **rs289743**, rs289744
5	**rs9930761**, rs9923854, rs5883
6	rs1532624, rs1532625, **rs7205804**
7	**rs17231506**, rs36229491
8	rs891143, **rs891142**
9	rs289718, **rs35874588**
10	**rs34620476,** rs34145065
11	rs12597250, **rs12720872**
12	**rs34065661**, rs17231520
13	**rs711752**, rs708272
14	**rs289719**
15	**rs7195984**
16	**rs11076174**
17	**rs9926440**
18	**rs12720903**
19	**rs35585922**
20	**rs11076175**
21	**rs11276066**
22	**rs66495554**
23	**rs12720874**
24	**rs9929488**
25	**CTP3918**
26	**rs7203984**
27	**rs158617**
28	**rs708273**
29	**rs17231569**
30	**rs12447924**
31	**rs11076176**
32	**rs4783962**
33	**rs5886,** rs8045701, rs12720857, rs12598103
34	**rs289714**
35	**rs289713**
36	**rs12720918**
37	rs189327489, rs12720877, rs80180245, rs11076177, rs7196174, rs17238232, rs111754336, rs12720884, rs12596364, rs78603009, rs12708984, rs74678905, rs7192754, rs17238225, rs12708981, rs7197854, **rs7192120,** rs7197340, rs7198026,CTP19607
38	**rs1864163**
39	**rs289745**
40	**rs12720858**
41	**rs291044**
42	**rs12720922**
43	**rs158477**
44	**rs12708985**
45	**rs4369653**
46	**rs142058276**
47	**rs9939224**
48	**rs891141**
49	**rs291043**
50	**rs7194225**
51	**rs7499892**
52	**rs289742**
53	**rs5817083**
54	**rs289716**
55	**rs12720889**
56	**rs1800775**
57	**rs158478**
58	**rs820299**
59	**rs17231534**
60	**rs4587963**
61	**rs112039804**
62	**rs158479**
63	**rs2033254**
64	**rs289740**
65	**rs289712**
66	**rs289715**
67	**rs1800774**

Table 5.5.5. Continued

68	**rs71383212**
69	**rs3816117**
70	**rs12708980**
71	**rs8045855**
72	**rs4783961**
73	**rs4784744**
74	**rs12447620**
75	**rs9935228**
76	**rs67114203**
77	**rs891144**
78	**rs289717**
79	**rs11860407**
80	**rs1968905**
81	**rs4784745**
82	**rs158480**
83	**rs1801706**

Bold: TagSNP

5.6 STATISTICAL ANALYSES

Variants identified by sequencing were analyzed by using Haploview Version 3.32 (Barrett et al. 2005, *www.broadinstitute.org/haploview*) to test the concordance of the genotype distribution with Hardy-Weinberg equilibrium and to determine allele frequencies and their distributions among high and low HDL/TG groups and their linkage disequilibrium (LD) patterns. For those SNPs that were genotyped in the entire sample, the additive linear regression model was used to test for the effects of genotypes on the means of 4 major plasma lipid traits (HDL-C, TG, LDL-C, TC) and apolipoproteins (apoA1 and apoB) levels. In African blacks, all plasma lipid levels were transformed to natural logarithms using Box-Cox transformation to improve normality; in NHWs only HDL-C and TG levels were transformed. Significant covariates were identified using stepwise regression in both directions. The covariates included in the final model were sex, age, BMI and smoking and for NHWs, and sex, age, BMI, waist circumference (waist measurement (cm) at the narrowest point), staff level (junior/senior) and smoking for African blacks. The R statistical software package (version 2.15.2, http://www.r-project.org) was used to perform all computations. A p-value of less than 0.05 was considered as suggestive evidence of association. The versatile gene-based association (VEGA) analyses were performed according to Liu et al. (2010).

It has been shown that haplotype analyses can be advantageous over an analysis based on individual SNPs in the presence of multiple susceptibility alleles, particularly when SNPs are poorly correlated with each other (Morris and Kaplan 2002). We performed the haplotype association analysis by using the generalized linear model (GLM) in "R' software (Lake et al 2002). Including too many haplotypes can make above model inefficient and impractical. To reduce the number of haplotypes considered in association analysis, we used the sliding window, 4 SNPs per window, and assessed evidence for association within each window. Specifically, a global p-value for testing overall effect of the haplotypes with frequency greater than 0.01 was used to assess the association between the traits and haplotypes in each window. Sliding-window haplotype analysis was performed with the haplo.glm function in the Haplo.Stats R package (version 1.5.0).

Rare genetic variants, here defined as alleles with frequency less than <5%, can play key roles in influencing complex disease and traits. Since each rare variant is present in only a small number of individuals, single-marker tests have lower power in association test. Different strategies have been suggested to effectively test the contribution of low-frequency and rare variants on phenotype. In general, kernel-based test and burden tests are two kinds of popular methods. Burden tests collapse all the rare variants within a region and assume that cumulative impact of rare variants increases with the number of rare minor alleles increase in the region (Li. et al. 2008). However, this method has also its own particular limitations that results low power (cause spurious associations or underestimate the real associations) when the region has various non-causal variants or both protective and deleterious variants present together since it considers all the rare variants in the region influence the trait in the same direction with same magnitude (Neale et al., 2011, Wu et al. 2011). Sequence kernel association test (SKAT) which was proposed by Wu et al. (2011), was assumed to boost power of the analysis and to be more efficient statistical method than burden test since it performs multiple regressions of a trait on phenotype and considers the direction and magnitudes of the each variant on phenotype independently. Recently, Lee et al. 2012 proposed SKAT-O, which has been proposed to be the optimal test for rare variant analysis and exceeded the SKAT and burden tests in several ways. Here we applied twot types of burden tests (RV1 and RV2), SKAT and SKAT-O. RV1 and RV1 are two similar burden tests and detailed explaination for these tests can be found in Morris et al. 2012. The analyses were performed by using three different minor allele frequency bin threshold (<1%, <2% and <5%). The SKAT method was implemented using the “SKAT” R package.

5.7 FUNCTIONAL ANNOTATION OF SIGNIFICANT SNPS

We used information from RegulomeDB online database (http://regulome.stanford.edu/) to retrieve the regulatory annotations for the SNPs that were significantly associated with lipid traits (Boyle et al. 2012). Variants were categorized into 1-6 categories as shown in **Table 5.7.1.**

Table 5.7.1. RegulomeDB scores and categories.

CATEGORY	SCORE
Category 1: **Likely to affect binding and linked to expression of a gene target**	➢ **1a-** eQTL + TF binding + matched TF motif + matched DNase Footprint + DNase peak ➢ **1b-** eQTL + TF binding + any motif + DNase Footprint + DNase peak ➢ **1c-** eQTL + TF binding + matched TF motif + DNase peak ➢ **1d-** eQTL + TF binding + any motif + DNase peak ➢ **1e-** eQTL + TF binding + matched TF motif;1f- eQTL + TF binding / DNase peak
Category 2: **Likely to affect binding**	➢ **2a-** TF binding + matched TF motif + matched DNase Footprint + DNase peak ➢ **2b-** TF binding + any motif + DNase Footprint + DNase peak ➢ **2c-** TF binding + matched TF motif + DNase peak
Category 3: **Less likely to affect binding**	➢ **3a-** TF binding + any motif + DNase peak ➢ **3b-** TF binding + matched TF motif
Category 4-6: **Minimal binding evidence**	➢ **4-** TF binding + DNase peak ➢ **5-**TF binding or DNase peak ➢ **6-**Motif hit

6.0 RESULTS

6.1 LIPOPROTEIN LIPASE

6.1.1 Genetic Association Studies in Non-Hispanic Whites (NHWs)

6.1.1.1 DNA resequencing results

Complete resequencing of the *LPL* gene in selected 95 NHW individuals falling in the upper (n=47) and lower (n=48) 10th percentile of HDL-C/TG distribution identified a total of 176 variants, including 159 single nucleotide substitutions and 17 insertions or deletions (indels) (see **Appendix Table A1.1** and **Figure A2.1**). **Figure 6.1.1 and Figure 6.1.2** provide the summary of the resequencing results in NHWs. As expected, most of the identified variants are located in introns and flanking regions of the genes.

Of the 176 variants identified, 148 were previously reported in public databases. Among these 176 variants**,** 88 had a MAF of ≥ 0.05, 52 had a MAF between 0.05-0.01 and 36 had a MAF of < 0.01. Seventeen of these variants were indels, and remaining 159 were single nucleotide substitutions (94 transitions and 65 transversions). The proportions of substitutions were A/G, 23.27%; A/C, 8.33%; A/T, 5.66%; C/T, 35.84%; C/G, 10.06% and G/T, 13.83%. One hundred forty variants were located in introns and 11 in the flanking regions. The remaining 25 variants were exonic, and only 6 of them were located in translated regions of the exons. Of these 6 exonic coding variants, 3 resulted in non-synonymous changes: aspartate to asparagine

(D9N) in exon 2, asparagine to serine (N291S) in exon 6, and serine to stop codon in exon 9 (S447X); and 3 resulted in synonymous changes; valine to valine (V108V) in exon 3, glutamic acid to glutamic acid (E118E) in exon 4 and threonine to threonine (T361T) in exon 8. Of the identified 17 indels, only one of the insertions was located in the exonic region affecting the 3'UTR (untranslated region) in exon 10. The size range of indels was 1-20 bases, except for a 697-nucleotide deletion identified in intron 2.

Of the 28 novel variants that we identified, 3 had MAF ≥ 0.05, 3 had MAF between 0.05-0.01 and 22 had MAF<0.01. Two of them were located in flanking regions, 24 were in introns, 2 were in UTR of exon 1 and exon 10, respectively; 12 of them were transitions, 7 were transversions and 9 were indels. A previously unreported large deletion (12224_12920del697) was observed in intron 2 (see **Appendix Table A1.1; Appendix Figure A2.1)**

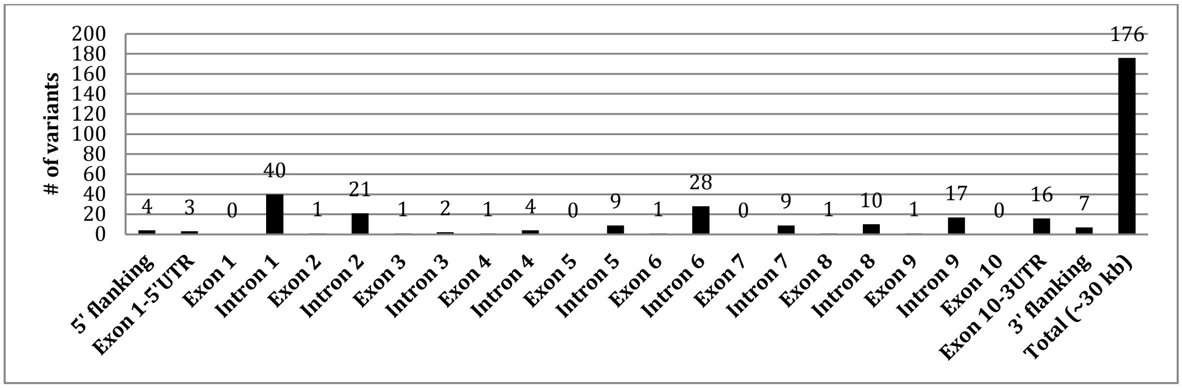
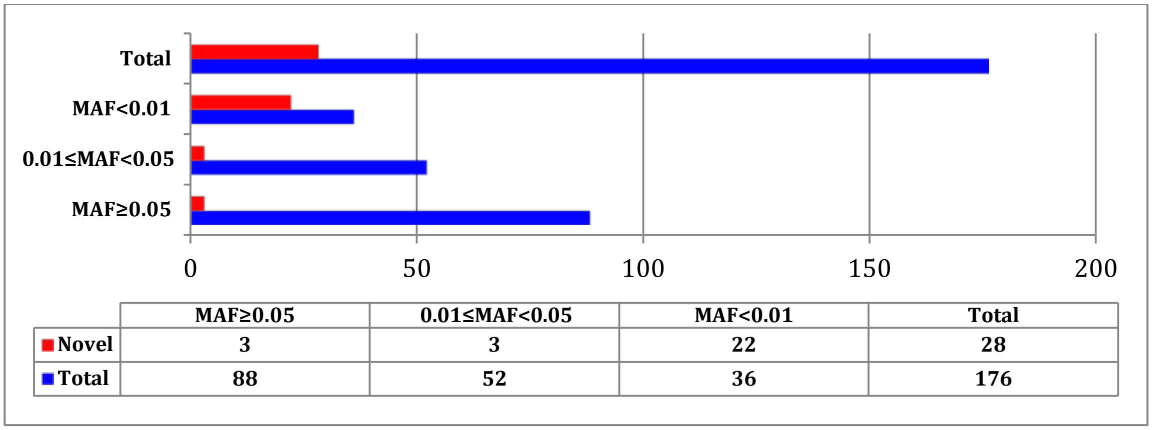


Figure 6.1.1. Number and locations of the identified *LPL* variants in NHWs.



	MAF≥0.05	0.01≤MAF<0.05	MAF<0.01	Total
🟥 Novel	3	3	22	28
🟦 Total	88	52	36	176

Figure 6.1.2. Minor allele frequency distribution of identified *LPL* variants in NHWs.

6.1.1.2 Distribution of identified *LPL* variants in extreme HDL-C/TG groups

Distribution of the 176 identified variants between the two extreme groups is shown in **Appendix Table A3**. Of the 88 uncommon or rare variants (MAF<0.05), 21 were present only in the low HDL-C/high TG group and 22 were present only in the high HDL-C/low TG group; the remaining 45 were present in both groups. Forty of 47 (85.1%) individuals with high HDL-C/low TG carried at least one rare variant versus 35 out of 48 (72.9%) individuals with low HDL-C/high TG. Furthermore, 21 of 47 (44.7%) individuals with high HDL-C/low TG had at least two rare variants versus 16 out of 48 (33.3%) individuals with low HDL-C/high TG; 14 of 47 (29.7%) individuals with high HDL-C/low TG had at least three rare variants versus 7 out of 48 (14.6%) individuals with low HDL-C/high TG.

Among the 25 identified exonic variants, 12 were relatively uncommon or rare (MAF <0.05). Of these 12 variants, three were found only in the high HDL-C/low TG group [1088G>T (rs80351041) in the UTR of exon 1, 24143C>G (rs328, Ser447X) in exon 9 and 27783A>T (novel variant) in the UTR of exon 10] and another three were found only in low HDL-C/high TG group [958G>A (novel variant) and 27688C>T (rs191212278) in the UTR of exon 1, and

28524C>T (novel variant) in the UTR of exon 10]. The remaining 19 exonic variants were found in both the high and low HDL-C/TG groups.

Of the 17 identified indels, four intronic variants were found only in high HDL-C/low TG group [11888_11889insA (rs149017698), 12224_12920del697 (novel variant), 12878_12889del12 (novel variant) and 12884_12887del4 (novel variant)] whereas one intronic and one 3' flanking region variants [21125_21128del4 (novel variant) and 29557_29558insA (novel variant)] were found only in low HDL-C/high TG group.

6.1.1.3 Linkage disequilibrium (LD) and tagger analyses of *LPL* variants identified in sequencing and follow-up genotyping in the entire sample

We selected 86 variants (43 common tagSNPs and 43 uncommon/rare variants) based on LD and tagger analyses. Sixty-five of these variants (35 common tagSNPs and 30 others) were successfully genotyped in the total sample of 623 NHWs using either iPLEX Gold or TaqMan methods; 18 failed genotyping and 3 suspicious rare variants were not confirmed and thus excluded as sequencing artifacts. The genotype call rates and other features of the 65 genotyped variants are shown in **Appendix Table A1.5**. The discrepancy rate was determined to be 0-0.5% for the genotyped variants based on the random repeats of ~10% of the samples. All genotyped variants were in concordance with Hardy-Weinberg equilibrium expectations. We excluded one SNP (rs343) with genotyping efficiency less than 80% and so, a total of 64 variants (40 common and 24 uncommon/rare based on their frequency in the entire sample) were included in subsequent association analyses. The LD groups (r^2 ≥0.80) identified for these 64 SNPs are shown in **Table 6.1.1.**

Table 6.1.1. LD groups ($r^2 \geq 0.80$, MAF ≥ 0.01) of 64 *LPL* SNPs genotyped in the entire NHW sample.

LD Bins	Variants
1	rs6999612, rs7000460, rs6997330, rs149017698, rs7016529, rs1801177
2	rs286, rs11570891, rs328, rs117026536, rs1059611
3	rs112127208, rs3779787, rs3779788
4	rs13702,rs327,rs320
5	rs294, rs316, rs312
6	rs10104051 ,rs1534649
7	rs4922115, rs4921684
8	rs73667472, rs249
9	rs13266204 ,rs17410577
10	rs264, rs254 ,rs269
11	rs248, rs80181352
12	rs277 ,rs270
13	rs9644636
15	rs80085105
16	rs74377536
17	rs296
18	rs311
19	rs268
20	rs150252331
21	rs78031480
22	rs282
23	rs117910839
24	rs10099160
25	rs253
26	rs295
27	rs113831503
28	rs283
29	rs8176337
30	rs149477831
31	rs285
32	rs1121923
33	rs343
34	rs11232447
35	rs314
36	rs80351041

6.1.1.4 Gene-based association test

This analysis revealed significant association with HDL-C (*P*=0.023) and TG (*P*=0.005). The best SNP associated with HDL-C was rs295 (*P*=0.002), and for TG it was rs80181352 (*P*=6E-04) (see **Table 6.1.2).** Since gene-based test revealed associations only with HDL-C and TG, these two traits were further examined by single-site, haplotype, and rare variant analyses.

Table 6.1.2. Gene-based association tests on all 64 *LPL* SNPs.

Trait	Chr	Gene	All Variants	Test	P^a	Variants with MAF≥ 0.05	Test	P^a	Smallest P^b
HDL_C	8	*LPL*	64	134.407	**0.023**	40	107.4428	0.02	**0.002** (rs295)
LDL_C	8	*LPL*	64	35.7124	0.885	40	23.06718	0.8	0.063 (rs282)
TG	8	*LPL*	64	167.0369	**0.005**	40	144.957	0.003	**0.0006 (rs80181352)**
TC	8	*LPL*	64	34.59643	0.925	40	17.00418	0.906	0.177 (rs312)
ApoB	8	*LPL*	64	56.21497	0.545	40	25.42954	0.72	0.033 (rs78031480)
ApoA1	8	*LPL*	64	61.24751	0.461	40	46.89066	0.306	0.022 (rs10099160)

^{a}*P*: gene-based, ^{b}Smallest *P* detected for a single SNP

6.1.1.5 Association of common variants (MAF ≥ 0.05) with lipid levels

The detailed results of the single-site analysis for 64 *LPL* variants can be found in Appendix A1 (see **Appendix Tables A1.4-A1.9**). Of 40 common variants, 22 revealed nominal associations ($P<0.05$) with either HDL-C (rs1326624, rs270, rs117026536, rs328, rs11570891, rs1059611) or TG (rs8176337, rs80181352, rs248, rs277, rs294, rs312, rs316, rs4922115, rs4921684) or both (rs282, rs286, rs295, rs314, rs320, rs327, rs13702). There is only one variant (rs10099160) that was associated (β=-5.730; *P*=0.023) with ApoA1 (see **Table 6.1.3**).

Among the 7 SNPs that were significantly associated with both traits, rs295 in intron 6 showed the most significant association with both HDL-C (β=0.021; *P*=0.002) and TG (β=-0.043; *P*=8E-04) and this SNP was in LD with 4 (3 intronic and 1 at 3'-UTR) of the remaining 6 SNPs that also showed associations with both traits (rs314, rs320, rs327 and rs13702 (r^2=0.71-0.74; **Figure 6.1.3**). Among these 4 SNPs, rs320 (*Hind*III polymorphism) has previously been shown to be associated with TG levels (32-34). The other two intronic SNPs (rs282 and rs286) that showed association with both HDL-C (β=0.017; *P*=0.042 and β=0.027; *P*=0.005, respectively) and TG (β=-0.044; *P*=0.006 and β=-0.042; *P*=0.021, respectively) were not in LD with rs295 (r^2=0.088 and r^2=0.36, respectively) or with each other (r^2=0.01). However, rs286 was in LD with a coding SNP, rs328 (Ser447X) (r^2=0.81) that showed a modest association with HDL-C (*P*=0.032) and a trend for association with TG (*P*=0.088), as well as with three other SNPs (rs117026536, rs11570891 and rs1059611) that showed nominal significance for HDL-C. Three SNPs (2 intronic and 1 exonic) were associated with only TG with *P*<0.01: rs80181352 (*P*=6E-04), rs248/E118E (*P*=0.008) and rs294 (*P*=0.005). While rs80181352 and rs248 were in strong LD with each other (r^2=0.88), their association with TG was independent the above mentioned SNPs that showed significant associations with both TG and HDL-C. Four other SNPs (rs312, rs316/T361T, rs4922115 and rs4921684) that showed nominal significance for TG were in moderate to high LD (r^2=0.69-0.96) with rs294. Thus, we have observed five relatively independent (r^2<0.40) signals with *P*<0.01 associated with HDL-C and/or TG, including rs80181352, rs282, rs286, rs294, and rs295. As noted above, two of these SNPs (rs80181352 and rs295) were those the best associated with TG and HDL-C, respectively, according to the gene-based test. Two additional SNPs, albeit less significant, also showed independent association with TG: rs8176337 (*P*=0.027) and rs277 (*P*=0.037, in LD with rs13266204 and rs270 with r^2=0.56-0.81).

Table 6.1.3. Significant association results (*P*<0.05) of common *LPL* variants with plasma lipid levels in NHWs.

				ApoB		**TG**		**ApoA1**		**TC**		**LDL-C**		**HDL-C**		
RefSNP ID	**Genotype**	**MAF**	**Location**	**Beta**	**P**	**Beta**	***P***	**Beta**	***P***	**Beta**	***P***	**Beta**	**P**	**Beta**	***P***	**RegulomeDB Score**
rs13266204	AA/AG/GG	0.214	Intron 1	0.344	0.521	0.028	0.328	-3.912	0.146	0.865	0.764	1.905	0.488	-0.027	0.033	6
rs8176337	CC/CG/GG	0.242	Intron 2	-0.387	0.5	-0.065	0.027	0.525	0.851	-2.182	0.472	-4.055	0.161	0.012	0.387	No data
rs80181352	GG/GT/TT	0.075	Intron 2	-0.312	0.713	-0.148	0.001	5.965	0.163	-0.604	0.892	-5.592	0.187	0.009	0.668	5
rs248	AA/GA/GG	0.067	Exon 4 (E118E)	0.181	0.841	-0.124	0.007	6.873	0.131	-1.487	0.754	-1.495	0.742	0.019	0.375	5
rs270	AA/CA/CC	0.172	Intron 6	0.805	0.161	0.059	0.053	-3.232	0.264	3.949	0.204	5.277	0.076	-0.031	0.025	No data
rs277	CC/CT/TT	0.196	Intron 6	0.363	0.514	0.061	0.036	-4.044	0.139	3.439	0.256	3.654	0.208	-0.02	0.135	No data
rs282	CC/GC/GG	0.135	Intron 6	-1.326	0.04	-0.095	0.006	7.309	0.024	-3.061	0.388	-6.281	0.064	0.032	0.042	5
rs286	AA/TA/TT	0.095	Intron 6	0.793	0.276	-0.09	0.021	3.918	0.285	1.518	0.708	-0.911	0.814	0.051	0.005	6
rs294	AA/AG/GG	0.118	Intron 6	0.124	0.859	-0.102	0.005	1.929	0.582	4.09	0.272	1.943	0.585	0.021	0.205	6
rs295	AA/CA/CC	0.223	Intron 6	0.605	0.263	-0.093	0.001	3.697	0.177	2.561	0.366	2.243	0.407	0.039	0.002	No data
rs312	CC/GC/GG	0.113	Intron 7	0.238	0.739	-0.095	0.01	0.7	0.845	5.092	0.177	2.423	0.501	0.022	0.197	No data
rs314	AA/GA/GG	0.263	Intron 7	0.222	0.672	-0.066	0.015	2.748	0.291	-1.448	0.602	-1.373	0.607	0.026	0.043	No data
rs316	AA/CA/CC	0.113	Exon 8 (T361T)	0.231	0.747	-0.087	0.017	0.972	0.788	4.52	0.23	3.58	0.322	0.024	0.155	1f
rs117026536	GG/GT/TT	0.104	Intron 8	0.708	0.313	-0.06	0.112	4.114	0.247	0.562	0.884	-1.09	0.768	0.034	0.048	6
rs320	GG/GT/TT	0.258	Intron 8	0.336	0.502	-0.068	0.008	0.083	0.974	0.767	0.77	0.897	0.721	0.027	0.026	5
rs327	GG/TG/TT	0.265	Intron 8	0.322	0.518	-0.069	0.007	1.367	0.586	1.181	0.653	0.787	0.755	0.025	0.032	6
rs328	CC/GC/GG	0.103	Exon 9 (S447X)	0.727	0.305	-0.065	0.088	4.585	0.202	-0.011	0.998	-1.907	0.612	0.038	0.032	5
rs10099160	GG/GT/TT	0.260	Intron 9	-0.169	0.736	0.027	0.318	-5.73	0.023	-0.824	0.766	-0.334	0.899	-0.021	0.094	6
rs11570891	CC/TC/TT	0.107	Intron 9	0.831	0.235	-0.058	0.119	4.119	0.246	1.766	0.643	-0.413	0.91	0.039	0.024	5
rs4922115	AA/AG/GG	0.146	3'UTR-exon 10	0.246	0.69	-0.066	0.039	-0.963	0.758	2.024	0.536	2.345	0.454	0.015	0.304	No data
rs13702	CC/CT/TT	0.272	3'UTR -exon 10	0.462	0.342	-0.074	0.003	1.493	0.544	0.724	0.78	0.961	0.698	0.032	0.006	6
rs1059611	CC/TC/TT	0.107	3'UTR -exon 10	0.755	0.28	-0.05	0.176	3.989	0.258	2.049	0.585	-0.243	0.946	0.037	0.03	6
rs4921684	CC/CT/TT	0.149	3' flanking	0.173	0.778	-0.068	0.032	-1.395	0.653	2.131	0.518	1.182	0.707	0.013	0.369	5

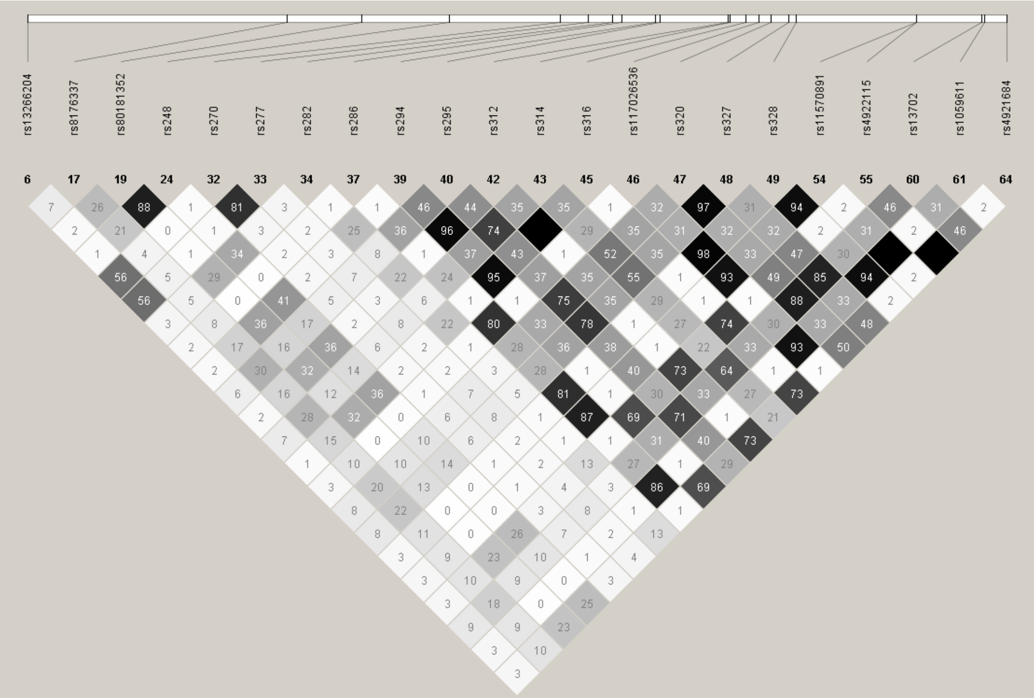


Figure 6.1.3. LD structure of the significant *LPL* SNPs associated with at least one plasma lipid trait in NHWs.

6.1.1.6 Functional annotation of significant SNPs

The regulome scores for 23 significant SNPs are presented in **Table 6.1.4**. Sixteen of the 23 SNPs were located in *LPL* genomic sequences that were predicted to have some regulatory implication. The majority of associated SNPs fell into Category 5 and Category 6, suggesting there was minimal evidence that these variants perturbed TFs (transcription factors) binding sites or disrupted the regulatory motifs, but supporting eQTL (expression quantitative trait loci) data was not available. However, rs316 has a score of 1f. This score indicates that rs316, which is a synonymous variant located in exon 8, is a known cis-eQTL SNP for *LPL* and lies within a TF binding site or a DNase peak based on the experimental evidence. It is important to note that these scores were generated based on the prediction of the “regulatory” function and thus high scores do not rule out the functional significance of these variants; for instance, rs328 (Ser447X) is a well known functional coding variant and is classified in Category 5 in RegulomeDB. Also, the novel rare variant (1130G>C) associated with TG levels appears to be regulatory as indicated by the RegulomeDB score of 2b (likely to affect TF binding) (see **Appendix Table A1)**.

6.1.1.7 Association of uncommon/rare variants (MAF <0.05) with lipid levels

We performed the uncommon/rare variant analysis on 24 variants with MAF<0.05 using SKAT-O. The analysis was performed on three sets of uncommon/rare variants using the MAF thresholds of 1%, 2% and 5%. However, our data revealed no significant association with either HDL-C or TG (see **Table 6.1.4**) Although there was no evidence of cumulative effects of uncommon/rare *LPL* variants on lipid levels, in single site analysis, we observed three individuals with a novel rare variant (1130G>C; MAF=0.002) that was associated with TG levels (*P*=0.017; β=0.556) **(**see **Appendix Table A5).** This variant is located in the 5'UTR and thus may have functional implication as discussed below.

Table 6.1.4. Results of rare variant analysis of *LPL* variants in NHWs.

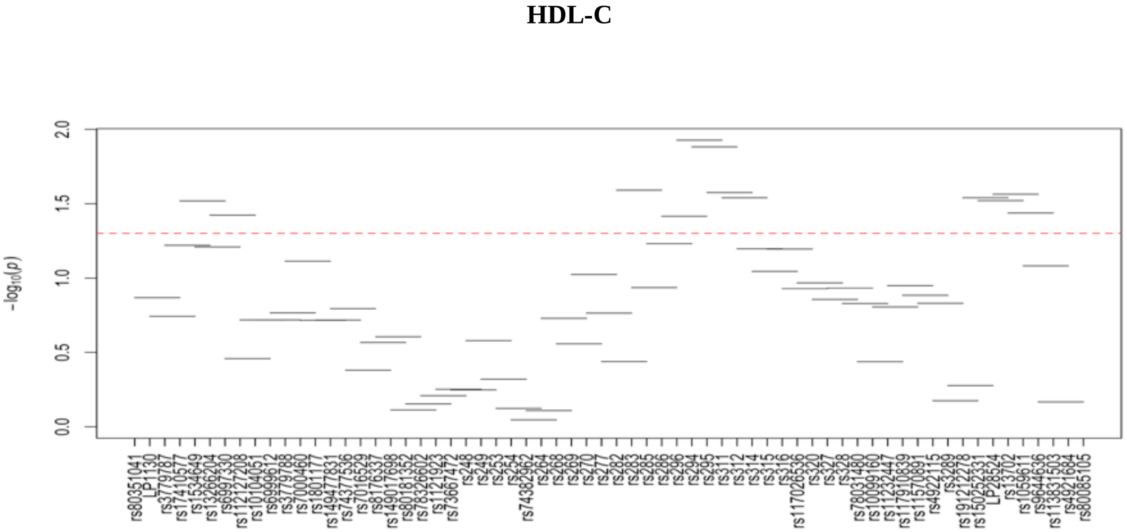
				TG		**TC**		**LDL-C**		**HDL-C**		**APOB**		**ApoA1**	
Bin 1	**N.RV (MAF<0.05)**	**N.Sample_RV**	**N.Sample_NoRV**	**Stat**	**P**	**Stat**	**P**	**Stat**	**P**	**Stat**	**P**	**Stat**	**P**	**Stat**	**P**
RVT1	24	299	324	0.27	0.303	-4.33E+01	0.115	-2.79E+01	0.287	-0.214	0.115	-1.11E+01	0.042	-6.591	0.413
RVT2	24	299	324	0.04	0.177	-4.80E+00	0.154	-2.58E+00	0.422	-0.022	0.179	-1.28E+00	0.041	-0.788	0.395
SKAT	24	299	324	3.50E+04	0.730	3.76E+04	0.681	2.85E+04	0.861	5.24E+04	0.401	4.79E+04	0.183	2.02E+04	0.837
SKAT-O	24	299	324	1.67E+05	0.440	3.26E+05	0.210	2.28E+05	0.334	2.39E+05	0.316	3.43E+05	0.081	4.37E+04	0.694
				TG		**TC**		**LDL-C**		**HDL-C**		**APOB**		**ApoA1**	
Bin 2	**N.RV (MAF<0.02)**	**N.Sample_RV**	**N.Sample_NoRV**	**Stat**	**P**	**Stat**	**P**	**Stat**	**P**	**Stat**	**P**	**Stat**	**P**	**Stat**	**P**
RVT1	15	125	498	3.15E-01	0.282	-3.54E+01	0.243	-3.59E+01	0.215	-0.169	0.259	-12.484	0.038	-1.740	0.844
RVT2	15	125	498	4.03E-02	0.321	-4.87E+00	0.245	-5.83E+00	0.144	-0.014	0.493	-1.877	0.019	-0.064	0.957
SKAT	15	125	498	1.91E+04	0.720	1.96E+04	0.709	1.48E+04	0.853	3.17E+04	0.369	3.08E+04	0.146	8.69E+03	0.905
SKAT-O	15	125	498	7.89E+04	0.391	7.88E+04	0.392	1.03E+05	0.297	7.21E+04	0.423	1.54E+05	0.068	8.69E+03	1.000
				TG		**TC**		**LDL-C**		**HDL-C**		**APOB**		**ApoA1**	
Bin 3	**N.RV (MAF<0.01)**	**N.Sample_RV**	**N.Sample_NoRV**	**Stat**	**P**	**Stat**	**P**	**Stat**	**P**	**Stat**	**P**	**Stat**	**P**	**Stat**	**P**
RVT1	7	37	586	0.189	0.673	-1.92E+01	0.676	-5.47E+01	0.212	0.078	0.732	-7.695	0.342	-10.700	0.369
RVT2	7	37	586	0.013	0.855	-5.63E+00	0.428	-1.05E+01	0.120	0.008	0.811	-1.645	0.198	-1.907	0.311
SKAT	7	37	586	6.19E+03	0.626	6.67E+03	0.599	5.50E+03	0.706	9.74E+03	0.357	5.74E+03	0.533	5.62E+03	0.546
SKAT-O	7	37	586	6.19E+03	0.803	6.67E+03	0.793	1.40E+04	0.358	9.74E+03	0.534	5.74E+03	0.573	5747.754	0.568

N.RV^{a} : Number of rare variants; **N_Sample_RV^{b}:**Number of individuals carrying the rare allele with defined MAF cut offs.; **N.Sample_NoRV^{c}: Number of individuals do not carry any rare alleles with defined MAF cut offs.TG:** Triglycerides; **LDL-C:** Low density lipoproten cholesterol; **HDL-C:** High density lipoprotein cholesterol; **ApoB:** Apolipoprotein B; **ApoA1:** Apolipoprotein A1

6.1.1.8 Haplotype analyses

The haplotype structure of the successfully genotyped 64 variants were constructed by using the sliding window approach that includes 4 SNPs in each window and sliding one SNP at a time; p-values were calculated based on the comparison to the most common haplotype as a reference (R package-Haplostat). As a result, 61 overlapping sliding windows were constructed and examined for association with lipid traits. Four-SNP haplotypes were arranged on the x-axis by the location from the 5' to 3' end of the *LPL* gene. The threshold for statistical significance (*P*=0.05) was shown by a horizontal red line. Overall, the haplotype effects were more significant for TG than HDL-C; 29 significant global p-values for TG versus 12 for HDL-C. Specifically, intron 6-intron 7 region was associated with HDL-C and intron 6-intron 8 region with TG (see **Figure 6.1.4.A** for HDL-C and **Figure 6.1.4B** for TG). We observed no haplotype association with LDL-C (**Figure 6.1.4C**); however, we observed one 4-SNP haplotype window was associated with TC, two windows with both apoA1 and apoB (see **Figures 6.1.4D-6F**). Window 37, which includes rs296, rs294, rs295, and rs311 SNPs revealed the most significant association with HDL-C (global *P*=0.012) and Window 33, which includes rs282, rs283, rs285, and rs286 SNPs, showed the strongest association with TG (global *P*=5E-04) (see **Appendix Tables A10-A15**). Both of these windows harbored variants that showed significant associations with HDL-C and/or TG in single-site analyses.

A


HDL-C
$-\log_{10}(p)$
0.0
0.5
1.0
1.5
2.0
rs80351041
LP1130
rs3779787
rs17410577
rs1534649
rs13266204
rs6997330
rs112127208
rs10104051
rs6996612
rs3779788
rs7000460
rs1801177
rs149477831
rs74377536
rs7016529
rs8176337
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rs270
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rs286
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rs294
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rs11570891
rs4922115
rs3289
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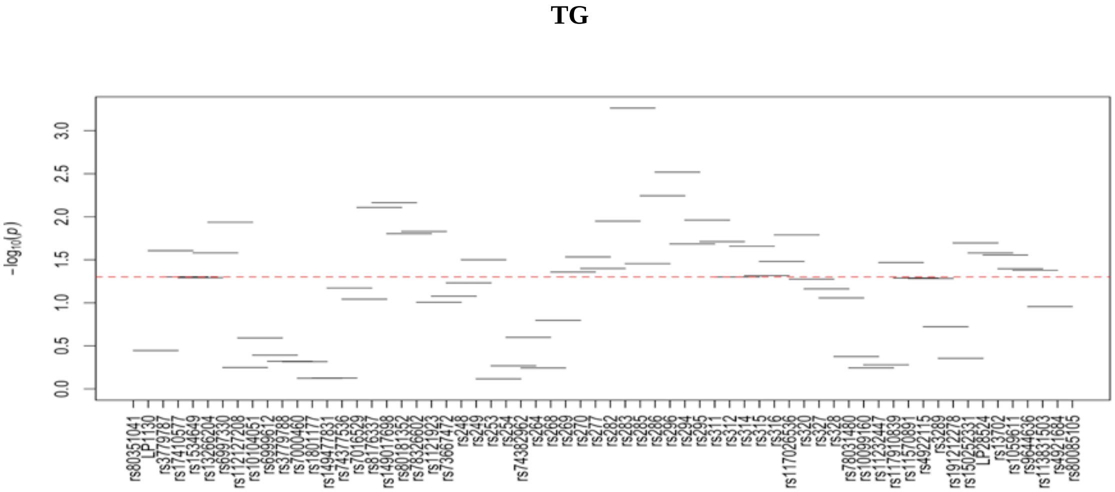
rs4921684
rs80085105

B


TG
$-\log_{10}(p)$
0.0
0.5
1.0
1.5
2.0
2.5
3.0
rs80351041
LP1130
rs3779787
rs17410577
rs1534649
rs13266204
rs6997330
rs112127208
rs10104051
rs6996612
rs3779788
rs7000460
rs1801177
rs149477831
rs74377536
rs7016529
rs8176337
rs149017698
rs80181352
rs78326602
rs1121923
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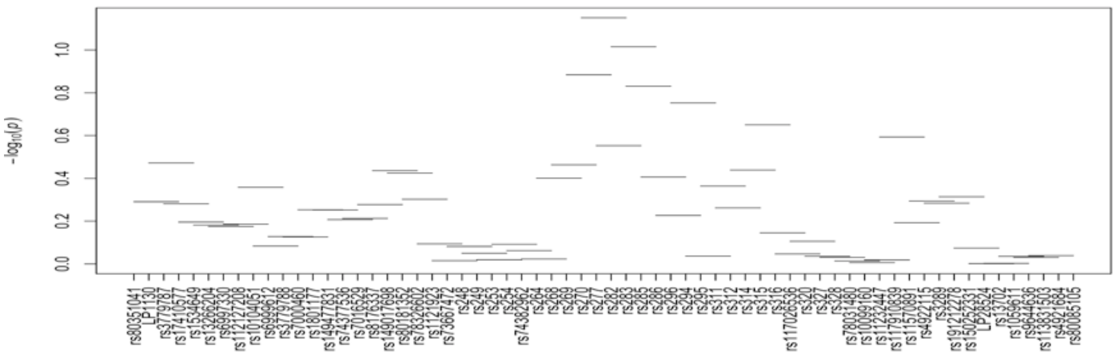
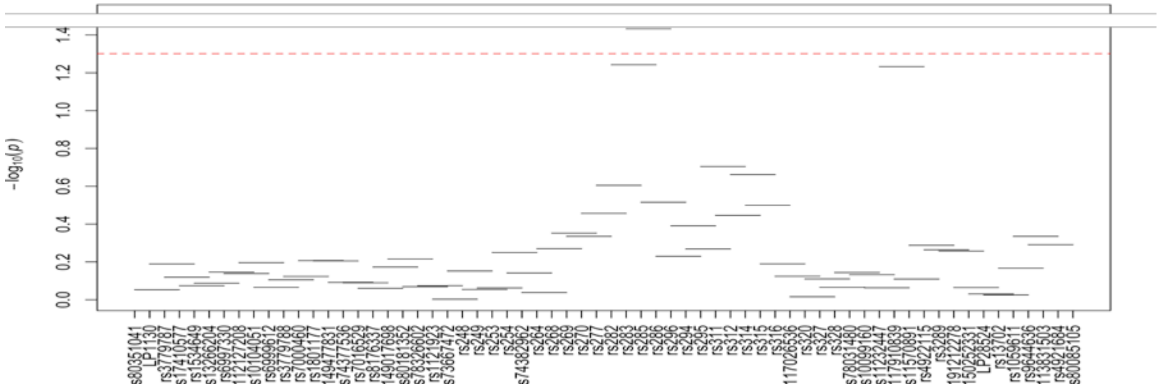
rs248
rs249
rs253
rs254
rs74382962
rs264
rs268
rs269
rs270
rs277
rs282
rs283
rs285
rs286
rs296
rs294
rs295
rs311
rs312
rs314
rs315
rs316
rs117026536
rs320
rs327
rs328
rs78031480
rs10099160
rs11232447
rs117910839
rs11570891
rs4922115
rs3289
rs191212278
rs150252331
LP28524
rs13702
rs1059611
rs9644636
rs113831503
rs4921684
rs80085105

C **LDL-C**

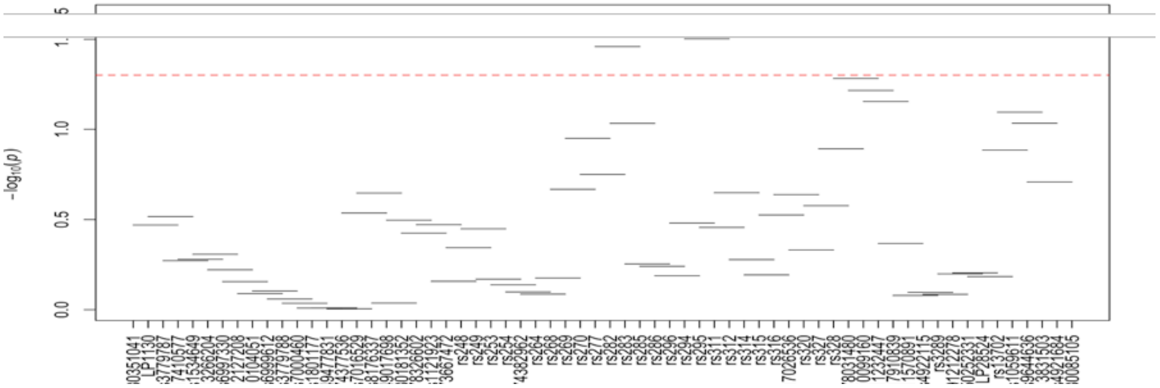


D **TC**



ApoA1

E



ApoB

F

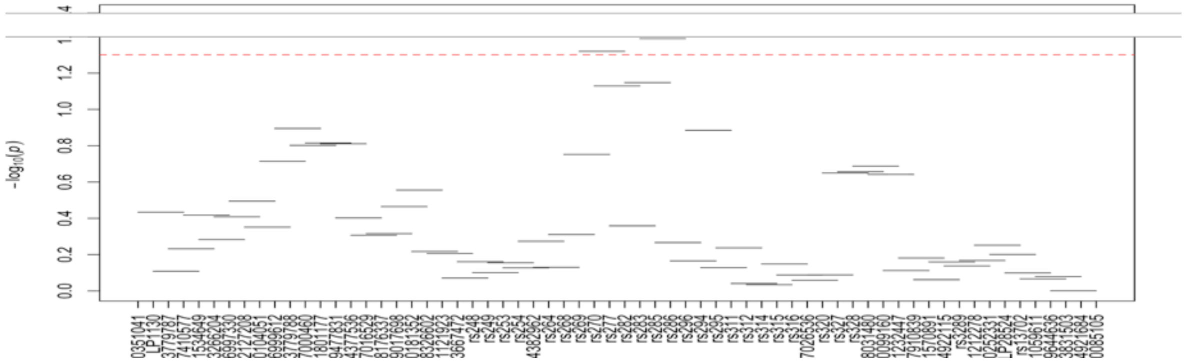


Figure 6.1.4. ***LPL*** **haplotype analysis with plasma lipid levels in NHWs.**
Haplotype windows for HDL-C (A), TG (B), LDL-C (C), TC (D), ApoA1 (E) and ApoB (F)
Horizontal lines represent the window tested, with the corresponding markers along the x-axis and global p-value (in log scale) on the y-axis. Red line shows the threshold for statistical significance (*P*=0.05).

6.1.2 Genetic Association Studies in African Blacks

6.1.2.1 DNA resequencing results

A total of 308 variants, including 69 novel SNPs were identified in resequencing, of which 130 were common (MAF≥0.05), 118 were uncommon (0.01≤MAF<0.05) and 60 were rare variants (MAF<0.01). Eighteen of these variants were indels, 288 were diallelic (182 transitions and 106 transversions) and two were triallelic SNPs (LP13156G/T/A, LP25414T/C/G (see **Appendix A Table A2.1)**. Majority of the identified variants (~80%) were located in intronic regions followed by the 3'UTR-exon 10 (10%), which is the largest exon (~2kb) in the gene. Together, 247 variants were identified in introns, 30 in 3'UTR, 14 in flanking regions, 11 in the coding regions and 6 in 5'UTR **(Figure 6.1.5).** All identified coding variants were known SNPs; six of them resulted in amino acid changes (D36N, rs1801177; A50G, rs148201569; H71Q, rs11542065; R333H, rs144466625; A472T, rs113064376) and 5 were synonymous changes (V135V, rs115589061; E145E, rs248; N152N, rs116678290; I376I, rs299; T388T, rs316).

Of the 18 indels, sixteen were located in intronic regions and two (LP1200_1201Ins2, LP29045_29046Ins2) were located in the UTRs of the gene.

We successfully identified all but three common variants (rs147018794, rs59184895 and rs328) reported in African-ancestry populations (dbSNP build 138); the three variants were not found due to low quality sequence reads in these regions. However, they were successfully genotyped in the entire sample of 788 African blacks and tested for association with lipid levels.

Of the 308 identified variants, 64 have not been reported in any public database to date. These include 2 common (MAF≥0.05) and 62 uncommon/rare variants (MAF<0.05) **(Figure 6.1.6).** Majority of the novel variants (67%) have MAF<0.01 and each of them is carried by only one individual in the entire resequencing sample. Two novel variants were located in flanking regions, 3 in the UTR of exon 1, 7 in the UTR of exon 10 and the remaining 47 variants were located in introns. We identified 8 novel indels that range in size from one base to 15 bases; all were located in introns. Of 8 novel indels, LPL15060_15061del2, LPL9582_9586del5 and LPL18399_18400Ins1, LPL9596_9597Ins1 were common with MAFs of 0.021, 0.032, 0.058 and 0.353, respectively. We identified two trialleleic SNPs [LPL13156G>T (rs7002728); LPL25414T>C (rs28599962)], both of which have been reported as biallelic in dbSNP build 138 (http://www.ncbi.nlm.nih.gov/SNP/), but the third less frequent allele observed at each locus is unique to our sample.

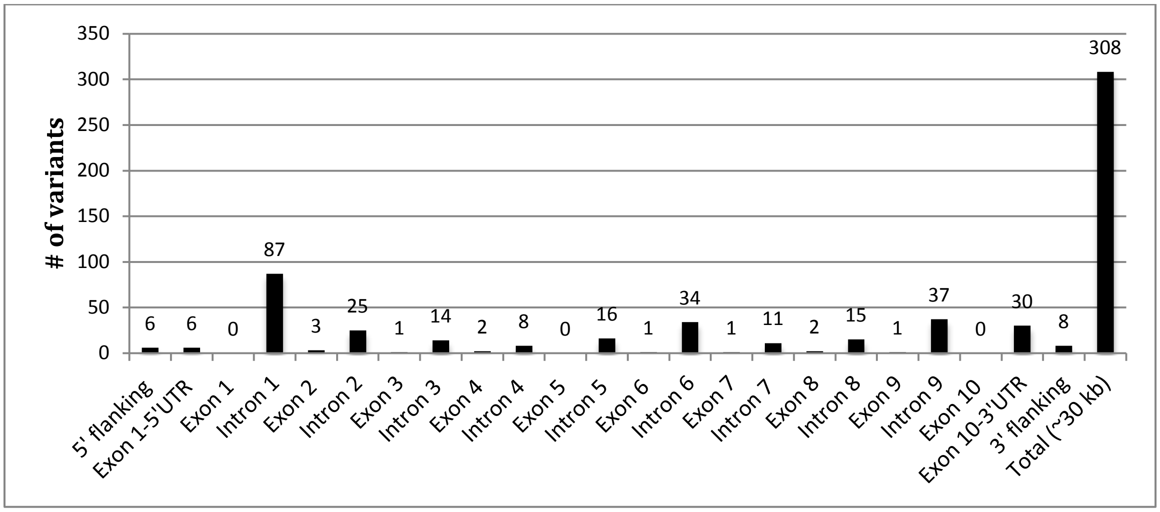
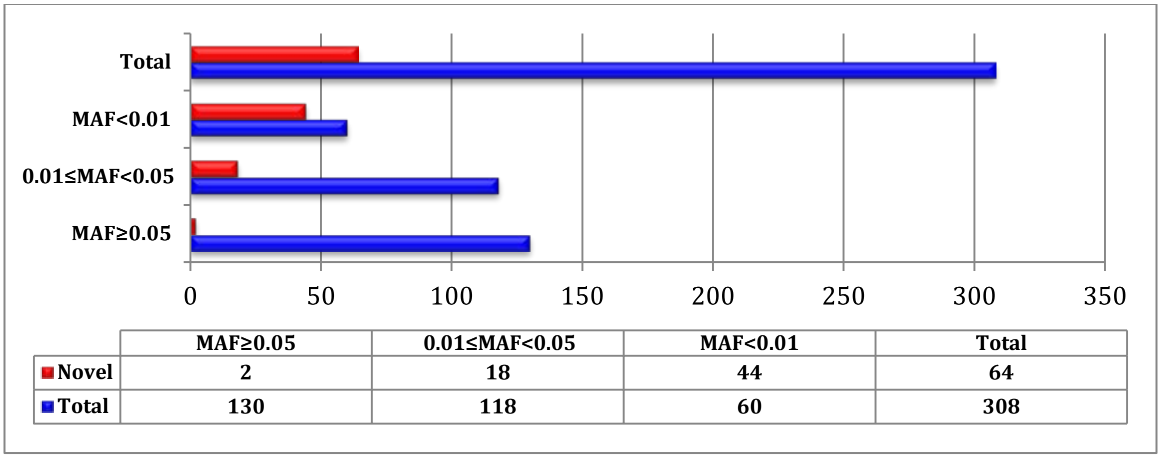


Figure 6.1.5. Number and locations of the identified *LPL* variants in African blacks.



	MAF≥0.05	0.01≤MAF<0.05	MAF<0.01	Total
🟥 **Novel**	**2**	**18**	**44**	**64**
🟦 **Total**	**130**	**118**	**60**	**308**

Figure 6.1.6. Minor allele frequency distribution of identified *LPL* variants in African blacks.

6.1.2.2 Distribution of identified *LPL* variants in extreme HDL-C/TG groups

Distribution of the 308 identified variants between the two extreme HDL-C/TG groups is shown in **Appendix Table A2.1.** We observed 23 variants to be present only in the high HDL-C/low TG group and another set of 54 variants were present only in the low HDL-C/high TG group.

We observed 23 variants to be present only in the high HDL-C/low TG group and another set of 54 variants were present only in the low HDL-C/high TG group.

Of the 23 variants present only in the high HDL-C/low TG group, one was an indel (LPL1977del1; novel variant; MAF=0.005) located in intron 1, 4 were exonic variants (0.005≤ MAF≤ 0.016) located in the UTRs of exon 1 and exon 10, and the remaining were intronic SNPs. Also, the less frequent allele (A) of the triallelic rs7002728 (LPL13156G/T/A) was observed only in two individuals with extreme high HDL-C and low TG levels.

Of the 54 variants present only in the low HDL-C/ high TG group, 3 were novel indels (size range 1-15 bases) and 51 were SNPs. We found 11 exonic SNPs present only in low HDL-C/ high TG group, including 3 in coding region and others in UTRs. Of these 3 coding SNPs, two resulted in amino acid changes (A50G, rs148201569; R333H, rs144466625) and the other was a synonymous variant (N152N, rs116678290).

6.1.2.3 Linkage disequilibrium (LD) and tagger analyses of *LPL* variants identified in sequencing and follow-up genotyping in the entire sample

Of the total 163 (92 tagSNPs; 71 others) variants selected for genotyping, 30 failed in genotyping design and 2 suspicious variants in sequencing turned out to be monomorphic. Thus, a total of 132 variants were successfully genotyped using either Sequenom or TaqMan and their genotype call rates and other features are shown in **Appendix Table A2.3.** Of these 132 variants, one was tri-allelic SNP (rs7002728) and this was excluded from the analysis. As part of quality control, 5 SNPs were also excluded from the analyses; two SNPs (rs171116619, rs143892202) had low call rate (<85%), and three did not meet Hardy-Weinberg equilibrium after Bonferronni correction ($P<10E-04$). Thus, a total of 126 variants (67 common and 59 uncommon/rare based on their frequency in the entire sample) were included in subsequent association analyses. The LD bins ($r^2 \geq 0.80$) of the final 126 QC passed SNPs are listed in **Table 6.1.5.**

Table 6.1.5. LD groups of 126 genotyped *LPL* SNPs in African blacks (r^2 ≥0.80).

LD Bins	Variants
1	rs7016529,rs28615996,rs6999612,rs56043715,rs28645722
2	rs28716400,rs147900112,rs290,rs313
3	rs115064749,rs112943460,rs34513350
4	rs13702,rs3208305
5	rs3779787,rs112127208
6	rs328,rs325
7	rs319,rs3200218
8	rs6991305,rs146786419
9	rs75890454,rs11542065
10	LP15060del,LP10100del1
11	rs280,rs17091775
12	rs266,rs251
13	rs4921683,rs1059507
14	rs80143795,rs75026342
15	rs79760154
16	rs5934
17	rs59184895
18	rs75946927
19	rs282
20	rs17091815
21	rs73667472
22	rs1121923
23	rs252
24	rs318
25	rs141390463
26	rs295
27	rs74304285
28	rs279
29	rs329
30	rs145585712
31	rs260
32	rs59054859
33	rs263
34	rs343
35	rs79756214
36	rs300
37	rs4921684
38	rs1470187
39	rs270
40	rs145257746
41	rs1470186
42	rs73667465
43	rs28445964
44	rs8176337
45	rs261
46	rs326
47	rs139240067
48	rs28599962
49	rs77434393

Table 6.1.5 Continued

50	rs330
51	rs147116359
52	rs58935878
53	rs73601683
54	rs200412008
55	rs17410577
56	rs3916027
57	rs76423146
58	rs185670596
59	rs1031045
60	rs1800590
61	rs181367025
62	rs248
63	rs114236375
64	rs12679834
65	rs314
66	rs277
67	rs76707496
68	rs115668974
69	rs255
70	rs257
71	rs7818177
72	rs259
73	rs59811201
74	rs61274012
75	rs138285812
76	rs316
77	rs301
78	rs276
79	rs258
80	rs11570892
81	rs269
82	rs1801177
83	rs115589061

6.1.2.4 Gene-based association test results

We found no significant result for the gene -based test in theAfrican black sample (**Table 6.1.6).**

Table 6.1.6. Gene-based test based on all 125 *LPL* SNPs in African blacks (n=788).

Trait	All variants	Test	P^a	Best SNP	Smallest P^b	Variants MAF<0.05	Test	P^a	Best SNP	Smallest P^b
HDL-C	125	174.36	0.091	rs316	0.002656	65	95.058	0.125	rs316	0.003
LDL-C	125	138.32	0.304	LP10170	0.000466	65	62.561	0.44	LP15653del	0.002
TG	125	108.99	0.640	LP25579	0.00306	65	32.903	0.923	rs59811201	0.132
TC	125	157.22	0.164	LP10170	0.000276	65	67.490	0.381	LP15653del	0.005
ApoB	125	143.88	0.214	rs328	0.003063	65	65.954	0.405	LP12449	0.010
ApoA1	125	167.58	0.122	LP21299	0.006155	65	84.223	0.194	rs4921683	0.017

6.1.2.5 Association of common variants (MAF ≥ 0.05) with lipid levels

Table 6.1.7 summarizes the significant results from the single-SNP association analyses in 788 African blacks; 17 common variants showed nominal associations (*P*<0.05) with either HDL-C, LDL-C, ApoA1 or ApoB. The results for all 126 SNPs for each lipid trait are summarized in **Appendix Tables A2.4-9.**

The most highly associated SNP, rs252 (located in intron 4), was associated with plasma LDL-C (β=-1.037; *P*=0.002), TC (β=-0.494; *P*=0.005) and ApoB (β=-2.364; *P*=0.012) levels. This association was novel to our study and is independent from other significant SNPs (r^2 ≤0.03), including two functional *LPL* variants [rs1801177 (D9N) and rs13702 (located in 3'UTR; disrupts the microRNA-410 recognition element seed site)]. One additional SNP, rs74304285, also exhibited independent association (r^2 ≤0.11) with both LDL-C (β=0.005; *P*=0.019) and ApoB (β=3.014; *P*=0.010) levels. In addition, four more independent SNPs (rs1801177, rs8176337, rs329 and rs12679834; r^2 ≤0.20) were found to be associated (*P*<0.05) with ApoB levels, of which rs12679834 was also associated (*P*=0.024) with ApoA1 levels. Recently, rs8176337 has been reported to be associated with TG in Alaskan Eskimos (Voruganti et al. 2010), but we did not identified such association in our sample. Even though rs1801177 (D9N) has shown significant associations with TG levels in various studies (Boes et al. 2009), it only exhibited marginal association (*P*=0.153) with TG in our sample which is probably due to its low frequency and relatively small sample size.

The second most highly associated SNP was rs316 (T361T) located in exon 8, which was associated with HDL-C (β=0.68; *P*=0.003) and ApoA1 (β=1.292; *P*=0.022) levels; this was correlated with four intronic SNPs, including rs279 (*P*=0.029; r^2 = 0.59) and rs295 (*P*=0.043; r^2 = 0.46), that showed association with only HDL-C, and rs301 *(P*=0.008; r^2 = 0.69) and rs320 (*P*=0.018; r^2=0.62*)* that showed association with both HDL-C and ApoA1 levels. The latter

SNP, rs320 (*HindIII*), is a well-known *LPL* polymorphism that has been consistently associated with HDL-C and TG in several studies. (Fisher et al. 1997; Boes et al. 2009; Sagoo et al. 2008). There were five more SNPs that yielded significant associations with HDL-C and they are all located in the 3'UTR exon 10: rs1059507 (β=0.689; *P*=0.031), rs13702 (β=-0.490; *P*=0.011), rs3916027 (β=0.421; *P*=0.028), rs4921683 (β=0.757; *P*=0.019) and rs4921684 (β=0.869; *P*=0.016), and are in LD with each other (r^2 = 0.59- 0.72). Overall, ten SNPs yielded significant associations with HDL-C and seven of these (rs301, rs316, rs320, rs1059507, rs13702, rs4921683, rs3916027) exhibited suggestive evidence of association with HDL-C in a recent meta-analysis (Edmondson et al. 2011). Of these HDL-C associated SNPs, rs1059507, rs4921683, rs4921684 also yielded significant associations with ApoA1 levels in our study ($0.017 \leq P \leq 0.026$). The other widely studied functional *LPL* variant, Ser447X (rs328) occurred at lower frequencies (4.2 %) in our African black sample as compared to its frequencies in European populations (~20 %) (Razzaghi et al. 2000; Boes et al. 2009). Furthermore, its well established association with TG and HDL-C observed in European populations was not replicated here; although the minor 447X allele was associated with ApoB (β=3.792; *P*=0.003) (see **Appendix Table A2.8 and Table 6.1.9** lists only significant SNPs with MAF ≥0.05).

All together, we found six significant (*P*<0.05) independent signals (rs1801177, rs8176337, rs74304285, rs252, rs329, rs12670834; r^2< 0.40). To the best of our knowledge, rs74304285 and rs252 have not been tested before for association with any lipid phenotypes. The LD structure of the 17 significant SNPs can be found in **Figure 6.1.7.**

Table 6.1.7. Significant association results (*P*<0.05) of common *LPL* variants with plasma lipid levels in African blacks.

				TG		LDL-C		HDL-C		TC		ApoB		ApoA1		
RefSNP ID	Position[1]	**Location**	**MAF**	**Beta**	***P***	**Beta**	***P***	**Beta**	***P***	**Beta**	***P***	**Beta**	***P***	**Beta**	***P***	**Regulome DB Scores**
rs1801177	**19805707**	Exon 2	0.05	0.023	0.153	0.686	0.112	-0.066	0.877	0.31	0.171	2.715	0.027	0.657	0.536	5
rs8176337	**19806670**	Intron 2	0.313	-0.01	0.177	-0.332	0.103	-0.088	0.663	-0.162	0.13	-1.298	0.021	-0.482	0.333	7
rs74304285	**19808029**	Intron 2	0.056	-0.004	0.788	0.995	0.019	0.232	0.586	0.475	0.034	3.014	0.01	1.724	0.099	7
rs252	**19811233**	Intron 4	0.093	-0.013	0.281	-1.037	0.002	0.03	0.929	-0.494	0.005	-2.364	0.012	-0.832	0.313	7
rs279	**19814695**	Intron 6	0.15	-0.002	0.825	0.078	0.776	0.595	0.029	0.08	0.581	-0.618	0.418	0.67	0.322	7
rs295	**19816237**	Intron 6	0.39	-0.004	0.575	0.32	0.092	0.384	0.043	0.199	0.049	0.534	0.314	0.922	0.05	7
rs301	**19816933**	Intron 7	0.288	-0.006	0.466	0.285	0.176	0.555	0.008	0.173	0.119	0.817	0.164	1.103	0.035	7
rs316	**19818435**	Exon 8	0.225	-0.001	0.891	0.16	0.49	0.68	0.003	0.164	0.179	0.192	0.764	1.292	0.022	1f
rs319	**19818975**	Intron 8	0.082	0.016	0.226	0.078	0.824	-0.083	0.812	0.094	0.617	1.315	0.179	1.692	0.05	4
rs329	**19820085**	Intron 9	0.097	-0.003	0.813	-0.558	0.092	0.405	0.229	-0.123	0.488	-1.806	0.048	-0.537	0.518	4
rs330	**19820395**	Intron 9	0.085	-0.005	0.708	0.354	0.317	0.669	0.055	0.243	0.191	0.886	0.364	2.031	0.019	5
rs12679834	**19820432**	Intron 9	0.058	0.004	0.812	0.424	0.289	0.278	0.487	0.276	0.194	2.711	0.015	2.207	0.024	1f
rs1059507	**19823962**	3'UTR-exon10	0.103	0.001	0.905	0.362	0.267	0.689	0.031	0.253	0.14	0.995	0.267	1.77	0.025	6
rs13702	**19824491**	3'UTR-exon10	0.459	0.004	0.623	-0.209	0.279	-0.49	0.011	-0.178	0.083	-0.08	0.881	-0.386	0.416	6
rs4921683	**19825067**	3'UTR-exon10	0.102	-1.17E-04	0.992	0.438	0.184	0.757	0.019	0.297	0.086	0.856	0.345	1.911	0.017	7
rs4921684	**19825127**	3'UTR-exon10	0.079	-0.012	0.354	0.518	0.154	0.869	0.016	0.298	0.12	0.246	0.807	1.983	0.026	5
rs3916027	**19824867**	3'UTR-exon10	0.413	-0.005	0.523	0.298	0.123	0.421	0.028	0.182	0.076	0.318	0.554	0.814	0.085	5

[1] Chromosomal position is according to the NCBI reference sequence: hg19, NC_00008.10; Bold indicates significant P-value (<0.05); MAF: Minor Allele frequency
TG: Triglycerides; **LDL-C:** Low density lipoproten cholesterol; **HDL-C:** High density lipoprotein cholesterol; **ApoB:** Apolipoprotein B; **ApoA1:** Apolipoprotein A1

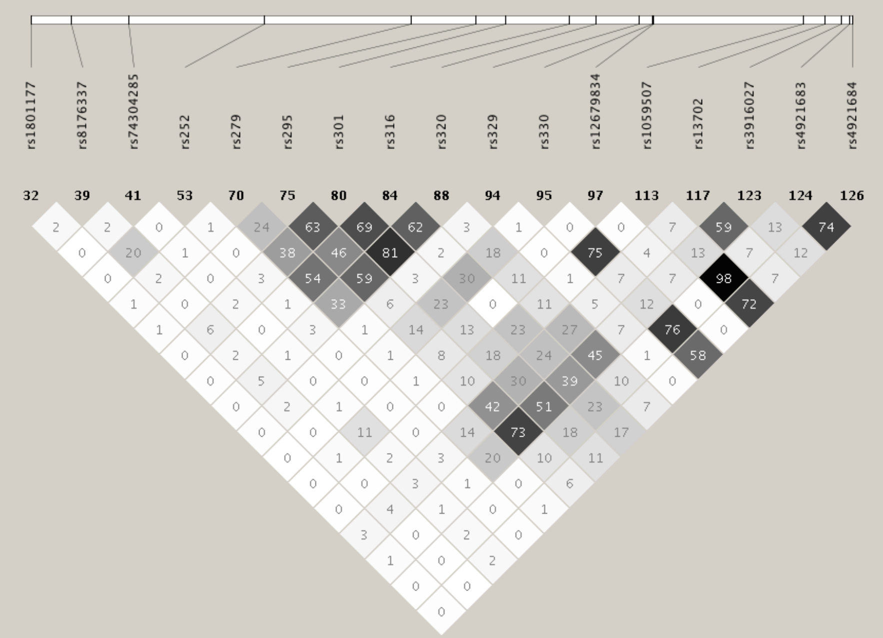


Figure 6.1.7. LD structure of the 17 *LPL* SNPs associated with either HDL-C, LDL-C. ApoA1, or ApoB levels. The values in the cells are the pairwise degree of LD indicated by r^2 × 100.

6.1.2.6 Functional annotation of significant SNPs

The sequences of 10 of the 16 significant SNPs were found to overlap with functional regions (**Table 6.1.7**). Two (rs316 and rs12679834) of the SNPs were classified in Category 1 (score=1f); both are known cis-eQTL (expression quantative trait loci) and overlap with TF binding site or a DNase peak region. The regulomeDB scores for the remaining 8 significant SNPs were 4-6, suggesting there was minimal evidence that these SNPs overlap with functional regions. The two novel rare variants, LPL1300 (MAF=0.005) and LPL25579 (MAF=0.005), showing association in single-SNP analysis and in SKAT-O, had regulomeDB score of 4 and 6, respectively.

6.1.2.7 Association of uncommon/rare variants (MAF< 0.05) with lipid levels

We performed SKAT-O rare variant association analysis to evaluate whether uncommon/rare variants have significant effects on lipid levels. Sixty variants with MAF< 0.05 were included in the analyses and 3 bins were generated by using three different minor allele frequency thresholds [Bin 1 (60 variants with MAF<0.05), Bin 2 (33 variants with MAF=0.02) and Bin 3 (22 variants with MAF< 0.01)] and test statistics were calculated for each bin separately. Only Bin 3 containing 22 rare variants with MAF< 0.01 showed significant association with TG (*P*=0.039) and LDL-C (*P*=0.027) levels (**Table 6.1.8**). The characteristics of the 22 SNPs grouped in significant Bin 3 exhibiting significant association with TG and LDL-C are given in **Table 6.1.9**.

In single-SNP association analyses, 7 of the variants included in Bin 3 also showed association with either TG, HDL-C, LDL-C, or ApoA1 levels, including three novel SNPs (LPL1155, LPL1300 and LPL25579). In addition, 9 uncommon variants with 0.01≤MAF<0.05 also showed associations with all lipid traits examined.

Table 6.1.8. Results of rare variant analysis of *LPL* variants in African blacks.

				TG		TC		LDL		HDL		APOB		APOA1	
Test	**N.RV^a (MAF<0.05)**	**N.Sample_RV^b**	**N.Sample_NoRV^c**	**Stat**	**P**	**Stat**	**P**	**Stat**	**P**	**Stat**	**P**	**Stat**	**P**	**Stat**	**P**
RVT1	60	613	175	-1.50E-01	0.331	-6.27E-02	0.977	-9.46E-01	0.817	1.61E+00	0.692	3.56E+01	0.002	2.04E+01	0.041
RVT2	60	613	175	8.77E-03	0.472	-1.04E-01	0.540	-3.49E-01	0.279	-8.90E-02	0.781	1.56E+00	0.082	1.31E+00	0.100
SKAT	60	613	175	2.16E+05	0.096	1.81E+05	0.236	1.73E+05	0.301	1.96E+05	0.152	2.13E+05	0.102	2.17E+05	0.097
SKAT-O	60	613	175	3.50E+05	0.170	2.02E+05	0.392	2.26E+05	0.487	1.96E+05	0.265	2.08E+06	0.016	7.84E+05	0.128
Test	**N.RV (MAF<0.02)**	**N.Sample_RV**	**N.Sample_NoRV**	**Stat**	**P**	**Stat**	**P**	**Stat**	**P**	**Stat**	**P**	**Stat**	**P**	**Stat**	**P**
RVT1	33	223	565	-1.82E-01	0.293	-4.78E+00	0.052	-8.13E+00	0.076	-3.60E+00	0.439	9.53E+00	0.460	-2.85E+00	0.800
RVT2	33	223	565	-7.63E-03	0.496	-1.12E-01	0.473	-3.28E-01	0.268	1.40E-01	0.634	1.17E-01	0.888	8.98E-01	0.216
SKAT	33	223	565	1.28E+05	0.032	1.22E+05	0.038	7.76E+04	0.338	1.20E+05	0.041	5.45E+04	0.695	1.08E+05	0.092
SKAT-O	33	223	565	1.92E+05	0.059	6.18E+05	0.037	5.07E+05	0.103	1.20E+05	0.075	6.47E+04	0.706	1.08E+05	0.162
Test	**N.RV (MAF<0.01)**	**N.Sample_RV**	**N.Sample_NoRV**	**Stat**	**P**	**Stat**	**P**	**Stat**	**P**	**Stat**	**P**	**Stat**	**P**	**Stat**	**P**
RVT1	22	84	704	-2.39E-01	0.156	-7.03E+00	0.003	-1.05E+01	0.019	-7.81E+00	0.080	1.25E+01	0.326	-5.48E+00	0.618
RVT2	22	84	704	-1.97E-02	0.225	-4.83E-01	0.033	-7.69E-01	0.075	-7.70E-01	0.075	9.23E-01	0.445	-7.13E-01	0.501
SKAT	22	84	704	8.07E+04	0.022	1.01E+05	0.004	6.40E+04	0.065	6.29E+04	0.062	2.63E+04	0.614	4.63E+04	0.209
SKAT-O	22	84	704	1.64E+05	0.039	7.07E+05	0.003	4.57E+05	0.027	2.40E+05	0.086	4.81E+04	0.612	4.63E+04	0.331

N.RV^a : Number of rare variants; **N_Sample_RV^b:**Number of individuals carrying the rare allele with defined MAF cut offs.; **N.Sample_NoRV^c: Number of individuals do not carry any rare alleles with defined MAF cut offs.TG:** Triglycerides; **LDL-C:** Low density lipoproten cholesterol; **HDL-C:** High density lipoprotein cholesterol; **ApoB:** Apolipoprotein B; **ApoA1:** Apolipoprotein A1

Table 6.1.9. The characteristics of the 22 rare variants (MAF< 0.01) contained in significant 'Bin 3' identified in SKAT-O.

LPL variant	RefSNP ID	Alleles^a	MAF	Location	Position^b	RegulomeDB score
LP1155	Novel	A:T	0.001	5' UTR-Exon1	1155	4
LP1264	Novel	G:A	0.008	5' UTR-Exon1	1264	2b
LP1300	Novel	C:G	0.005	5' UTR-Exon1	1300	4
LP9499	rs138110428	G:A	0.007	Intron 1	9499	5
LP10170	rs148201569	C:G	0.003	Exon 2	10170	5
LP10632	Novel	C:T	0.008	Intron 2	10632	No data
LP11895	rs189417962	T:A	0.007	Intron 2	11895	5
LP13691_13693del3	Novel	W:D	0.001	Intron 2	13691	5
LP15266	rs116678290	T:C	0.006	Exon 4	15266	5
LP17993	rs144466625	G:A	0.001	Exon 6	17993	5
LP21299	rs299	C:T	0.007	Exon 7	21299	6
LP23605	rs321	G:C	0.009	Intron 8	23605	5
LP24064	rs149089920	G:A	0.001	Exon 9	24064	5
LP25579	Novel	A:G	0.005	Intron 9	25579	6
LP27629	Novel	C:G	0.001	3'UTR-Exon10	27629	5
LP27695	Novel	G:T	0.001	3'UTR-Exon10	27695	5
LP27706	Novel	G:T	0.001	3'UTR-Exon10	27706	5
LP27928	rs187587525	G:A	0.003	3'UTR-Exon10	27928	5
LP27969	Novel	A:G	0.001	3'UTR-Exon10	27969	No data
LP28669	rs184363931	C:T	0.009	3'UTR-Exon10	28669	No data
LP29047	rs78359368	G:T	0.007	3'UTR-Exon10	29047	6
LP29098	rs187374932	T:C	0.005	3'UTR-Exon10	29098	No data

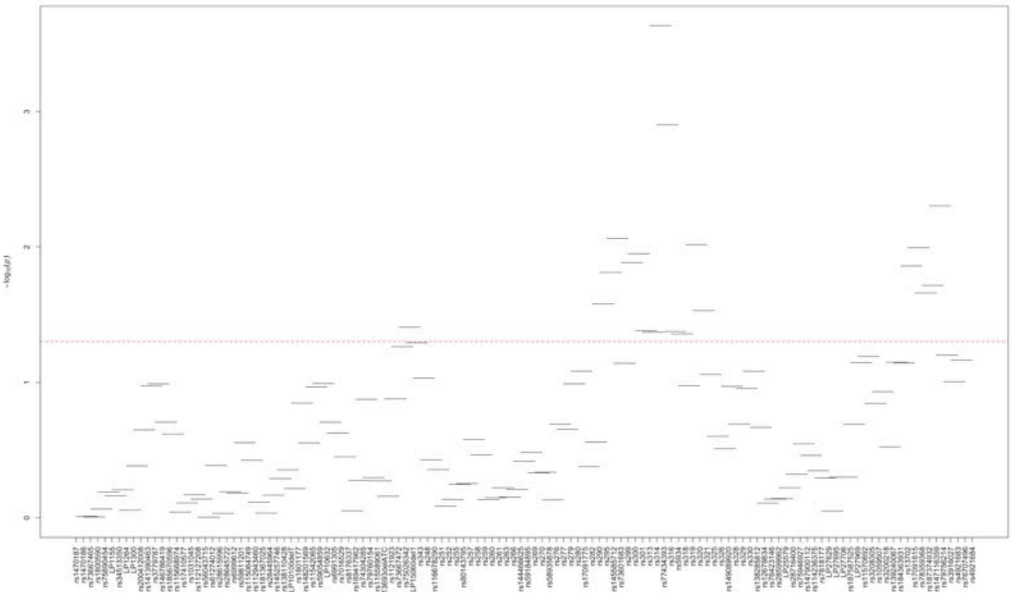
^{a}Major allele:Minor allele; ^{b}Position in the baseline reference sequence

6.1.2.8 Haplotype analyses

A total of 123 overlapping sliding windows, each containing 4 SNPs, were constructed by using the sliding window approach to construct the haplotypes of 126 variants. Analyses were performed by sliding one SNP at a time and *P*-values were calculated based on the comparison to the most common haplotype as a reference in R package-Haplostat. The haplotype plots are presented in **Figures 6.1.10a-10e**. Among the five lipid phenotypes examined, the strongest haplotype effects were observed for ApoB, followed by HDL-C levels revealing 19 and 18 significant ($P<0.05$) global *P*-values, respectively **(see Appendix Tables A2.10-16).** The most significant haplotype window was 'window 81' containing rs313, rs314, rs77434393 and rs316 SNPs, and this was associated with both HDL-C (global $P=0.0002$) and ApoA1 (global $P=0.021$). The only SNP in this window that showed significant association in single-SNP analyses was rs316 ($P=0.008$ with HDL-C; $P=0.035$ with ApoA1). While haplotypes in intron 6-intron 8 region of the gene were associated with HDL-C and ApoA1, haplotypes in intron 8-intron 9 were associated with ApoB. Although, we did not identify any common *LPL* variants yielding association with TG in single-SNP analysis, 7 haplotype windows showed nominal associations with TG. Overall, haplotypes were more informative for associations with TG and LDL-C than the single-SNP analyses.

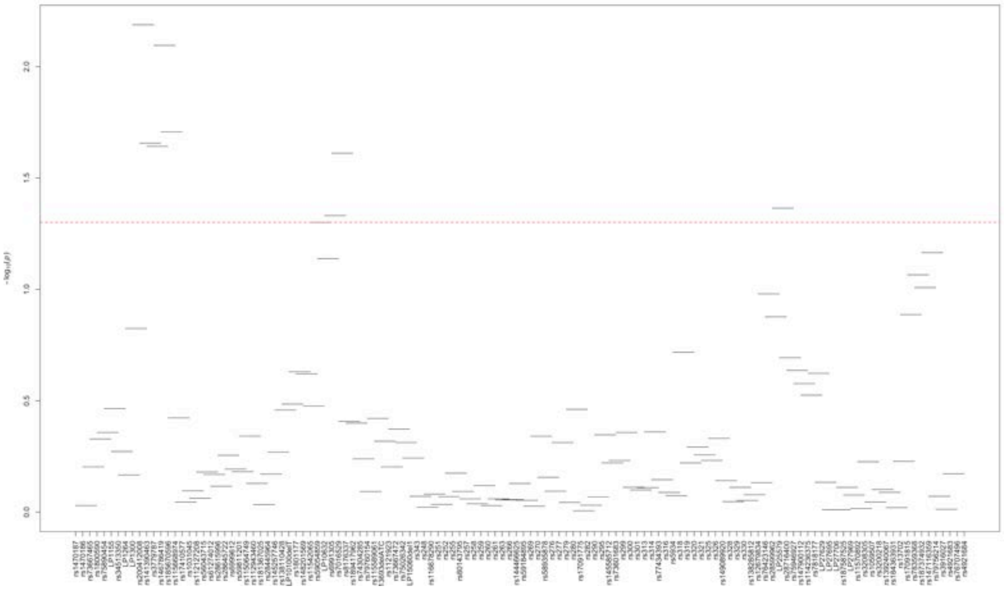
HDL-C

a



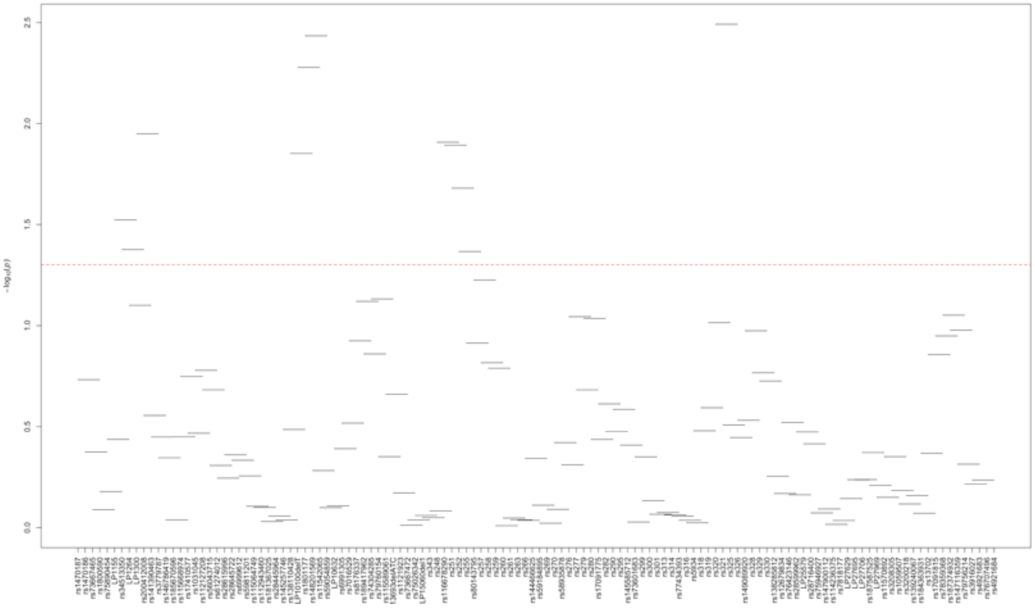
TG

b



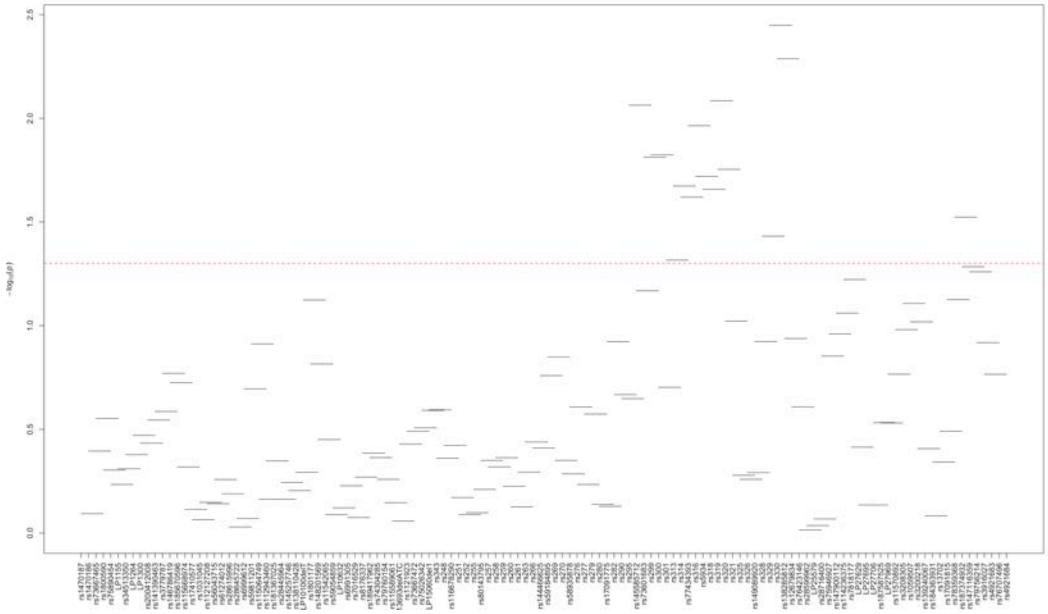
LDL-C

c



ApoA1

d



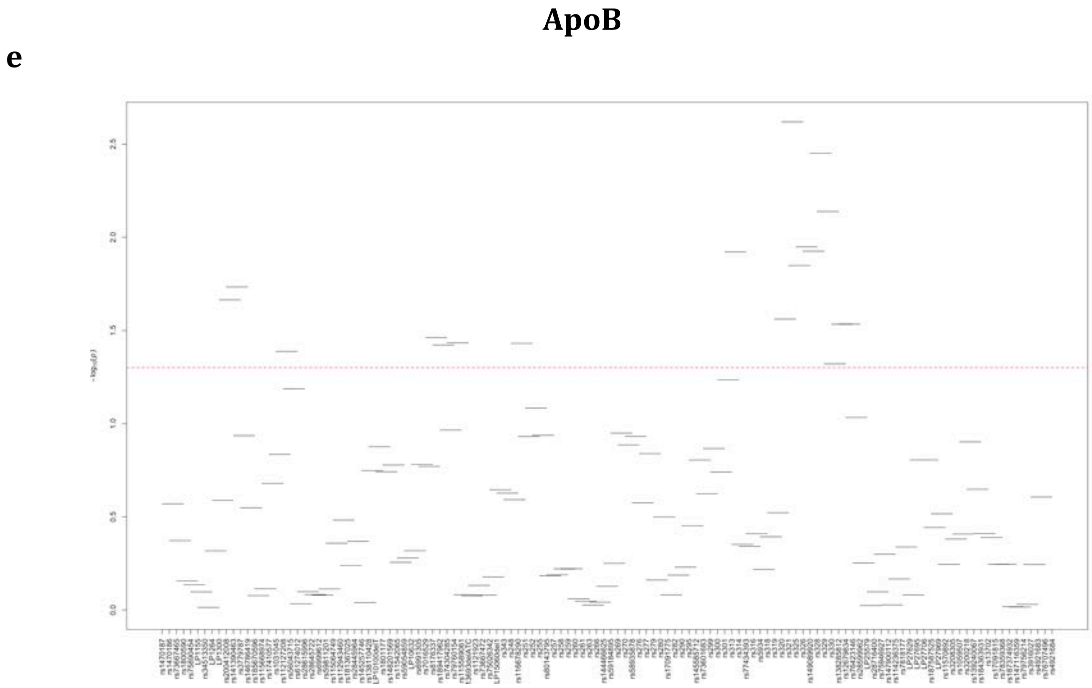


Figure 6.1.8. ***LPL*** **haplotype analysis with plasma lipid levels in African blacks.** **HDL (a), TG (b), LDL-C (b), ApoA1 (d), ApoB (e). The log of the global** ***P*****-value is presented on the y-axis and SNPs are presented across the x-axis in chromosomal order. Horizontal lines are 4-SNP haplotype windows. The red horizontal line shows the significance threshold.**

6.1.3 Discussion

The role of *LPL* genetic variation in relation to lipid levels has been studied extensively (Boes et al. 2009). To the best of our knowledge, the present study is the first of its kind that reports a detailed catalogue of sequence variation in the entire *LPL* gene (~30 kb) in NHWs and African black individuals and its association with major plasma lipid and apolipoprotein traits.

In 95 NHWs with extreme HD-C/TG levels, we identified 176 variants, of which 27 were novel while 308 variants were identified in 95 African blacks of which 69 were novel. Of note, 113 variants were present in both populations. As expected, we observed more variation in African blacks and especially uncommon and low-frequency variants were more common in blacks as compared to NHWs. Previously, Nickerson et al. (1998) sequenced a portion of the

LPL gene (9.7 kb), from 3’ end of intron 3 to 5’ end of intron 9, in 71 individuals randomly selected from three racial groups, including European-Americans from Rochester, Minnesota (n=23), African-Americans from Jackson, Mississippi (n=24) and Europeans from North Karelia, Finland (n=24). Five uncommon variants (MAF ≤0.05) and one common deletion (8538delA; MAF=0.20) reported by Nickerson et al. (1998) in their White sample were not identified in our NHW sample. On the other hand, we identified 17 variants (0.005≤MAF≤0.053) in our NHWsample that were not reported by Nickerson et al. (1998). We also compared our results obtained by resequencing African blacks with those reported by Nickerson et al. (1998) in their African-American sample from Jackson. In our study, more variation (97 variants vs. 78 variants) were observed in this 9.7 kb region of the *LPL* gene than previously reported in Jackson sample including the 10 novel variants (MAF <0.01). Of the 97 variants that we identified in this region, 26 were unique to our study, and of the 78 variants that were identified by Nickerson et al., 7 were unique to their sample; 71 low-frequency or common variants were present in both studies. This difference could be due to the use of different sample criteria (individuals with extreme lipid profile in our study vs. unselected random samples in their study) and/or different software tools and algorithms applied in variant analyses (PolyPhred Program in their study vs. Variant Reporter and Sequencher in our study). Furthermore, different genetic background could also have contributed to this difference.

In NHWs, a total of 64 selected variants (40 common with MAF ≥0.05 and 24 uncommon/rare with MAF <0.05) that passed genotyping QC in the total set of 623 individuals were included in the association analyses. Our initial gene-based analysis including all 64 genotyped variants confirmed the established role of *LPL* in TG and HDL metabolism as it revealed significant associations only with TG (*P*=0.005) and HDL-C (*P*=0.023) levels. Gene-based tests for associations can be more powerful than the single-site tests because they consider all variants within a gene rather than individual markers and also take into account LD between the variants (Liu et al. 2010).

Single-site analysis in NHWs revealed 22 nominally significant associations ($P<0.05$) with either HDL-C or TG or both. Most of the significant SNPs were correlated with each other and/or with 3 known functionally relevant SNPs; rs328 (Ser447X) (Sagoo et al. 2008), rs320 (*Hind*III) (Chen et al. 2008) and rs13702 (Richardson et al. 2012). Overall, we observed 7 relatively independent signals ($P<0.05$; $r^2<0.40$) represented by the following SNPs; rs80181352 (in LD with exonic rs248), rs282, rs286 (in LD with functional rs328), rs294 (in LD with exonic rs316), rs295 (in LD with functional rs320 and exonic rs13702), rs8176337, and rs277. Of these 7 independent SNPs, four (rs80181352, rs282, rs294 and rs277) were never tested before. While no functional data are available for rs8176337 and rs277 in RegulomeDB, rs282 is located in a transcription factor binding site and thus could have regulatory role in affecting the expression of *LPL*.

In African blacks, following the discovery stage, we successfully genotyped 132 variants in the entire sample of 788 African blacks and 126 QC passed variants were included in association analyses with 5 major lipid and apolipoprotein traits (HDL-C, TG, LDL-C, ApoA1 and ApoB). In single-SNP analysis, we observed 9 nominal associations ($P<0.05$) with HDL-C, 2 with LDL-C, 6 with ApoB and 7 with ApoA1 levels. Although, none of the common SNPs were found to be associated with TG in our sample, we identified 8 uncommon *LPL* variants ($0.005\leq$MAF≤0.045) showing associations with TG levels ($0.003 \leq P\leq0.046$).

In Europeans, several SNPs in *LPL* have been reported to be associated with plasma lipid levels, and six common SNPs (rs268 (N291S), rs326, rs320 (*Hind*III), rs328 (Ser447X), rs1801177, rs13702) have consistently shown associations with HDL-C and/or TG (Boes et al. 2009; Wittrup et al. 1999; Ahn et al. 1993; Kathiresan et al. 2008; Komurcu-Bayrak et al. 2007; Klos et al. 2006). Among these, the Ser447X (rs328) polymorphism, located in exon 9, has been shown to increase LPL enzymatic activity and the carriers of 447X have lower TG, higher HDL-C levels and in turn they have reduced risk of CHD (Fisher et al. 1997; Wittrup et al. 1999; Razzaghi et al. 2000; Sagoo et al. 2008). In NHWs, we also observed the same associations with TG and HDL-C. However, rs286 that is in LD with rs328, showed stronger association with both HDL-C (P=0.005) and TG (P=0.021). While the frequency of the 447X minor allele is common in whites (MAF= ~20 %), it is lower in our African black sample (4.2%), which is comparable to the HapMAP YRI population of 3.3%. Also, it was only associated with ApoB levels (β=3.792; P=0.003) in African blacks. In a cross-sectional and longitudinal study, Tang et al. (2010) examined the association of Ser447X with HDL-C and TG in 2405 African Americans and 2116 European Americans and found its significant association with both traits in European Americans but only with TG in African Americans. A recent large GWAS study in African Americans also failed to show association of Ser447X with HDL-C or TG (Lettre et al. 2011). Our findings in an African sample are consistent with the reported findings in African Americans, as we did not observe significant association of this SNP with either HDL-C or TG levels.

The *Hind*III (rs320, G/T) polymorphism located in intron 8 has also been shown to have same effects on TG and HDL-C levels as does rs328 and there has been a debate if the genetic effects of these two polymorphisms are independent from each other (Ahn et al. 1993; Razzaghi et al. 2000; Senti et al. 2001; Holmer et al. 2000; Ukkola et al. 2001). Furthermore, rs320 is predicted to affect the binding of a transcription factor and so it may be functional by itself

(Chen et al. 2008). In NHWs, the effects of rs320 and rs328 are independent as they are in weak LD with each other (r^2=0.32). We also found that rs320 is in LD with rs295 (r^2=0.75) and rs13702 (r^2=0.88) and the latter two SNPs showed even stronger associations with both HDL-C and TG. In African blacks, our data revealed that the association of *HindIII* (rs320) with HDL-C (β=0.485; *P*=0.018) was also independent of rs328 (β=-0.113; *P*=0.804). However, *HindIII* (rs320) was moderately correlated with three other HDL-associated SNPs: rs301 (*P*= 0.008; r^2=0.81), rs316 (*P*=0.003; r^2=0.62) and rs295 (*P*=0.043; r^2=0.59) that previously have also been to be associated with HDL-C (Deo et al. 2009; Edmondson et al. 2011; Heid et al. 2008).

Common SNPs in and around the *LPL* gene have been also reported in several GWAS of lipid phenotypes, which have been conducted mostly in populations of European descent (Kathiresan 2008b; Kooner et al.; Sabatti et al. Willer et al. 2008; Heid et al. 2008; Kraja et al. 2011). In one GWAS in whites (Heid et al. 2008), rs295 has shown a significant association with HDL-C and rs13702 was found to be in strong LD with other reported GWAS significant SNPs (rs326, rs2083637, and rs10105606). Recently, Richardson et al. (2012) have shown that rs13702 is a gain-of-function variant that may affect lipid traits due to its suggested role in allele-specific regulation of *LPL* by miR-410. Although rs13702 was shown to be highly correlated with functionally relevant *HindIII* polymorphism (rs320) in Europeans (Boe et al. 2009) and in our NHW sample, both sites showed weak correlation in our African black sample (r^2=0.24). The significant association of rs13702 with HDL-C has been previously reported in African Americans (Tang et al. 2010; Doe et al. 2009). Replication of the association of rs13702 with HDL-C in multiple independent African or African-derived samples along with its potential significance in disrupting microRNA-410 site supports its functional significance in HDL metabolism. The results of the haplotype associations were largely comparable to the single-SNP association for both populations. Majority of the significant haplotypes, including the most significant ones, contained SNPs that also showed significant association in single-site analysis.

Due to power-related concerns in analyzing rare variants by single site-approach, different strategies have been suggested to effectively test the contribution of low frequency and rare variants. One method is the burden test that collapses all rare variants within a region into a single variable and assumes that cumulative impact of rare variants increases as the number of rare minor alleles increases in the region (Li and Leal 2008). Alternatively, Wu et al. (2011) developed a non-burden sequence kernel association test (SKAT) that is more powerful than burden test when the region has various non-causal variants and/or variants with different directional effects. Since each method has its own particular limitations, Lee et al. (2012) have proposed the SKAT-O, an optimal test for rare variant analyses which performs better than burden tests and SKAT under different scenarios. In NHWs, we found no evidence of association of uncommon/rare *LPL* variants in our sample. On the other hand, we observed an association of a novel rare variant (LP1130) with TG (β=0.556; P=0.017) in the single-site analysis, which awaits confirmation in independent larger samples. This variant appears to affect the binding of transcription factors as suggested by the RegulomeDB score of 2b (see **Table A1.1** for RegulomeDB scores). In African blacks, we obtained some interesting information from rare variant analyses (SKAT-O) with TG and LDL-C levels. For example, SKAT-O analysis with 22 rare variants with MAF< 0.01 showed significant association with TG (P=0.039) and LDL-C (P=0.027). Of these 22 rare variants, 4 are known non-synonymous changes with no previous report of their significant association with lipid levels, and 10 were novel variants. The observed association could represent cumulative effects of the missense mutations and/or novel population specific rare variants in this population. However, further studies are needed to understand the impact of these rare variants on variation in plasma lipid profile in the general population.

In summary, to the best of our knowledge, this the first study that has comprehensively examined the role of *LPL* genetic variation in relation to HDL-C and TG levels. Our gene-based, single-site and haplotype analyses support the well-established role of *LPL* common genetic variation in normal variation of plasma TG and HDL-C levels by confirming previously reported associations and reporting novel additional associations. However, the role of uncommon/rare *LPL* variants in regulation of plasma TG and HDL-C levels remains less clear and warrants additional studies.

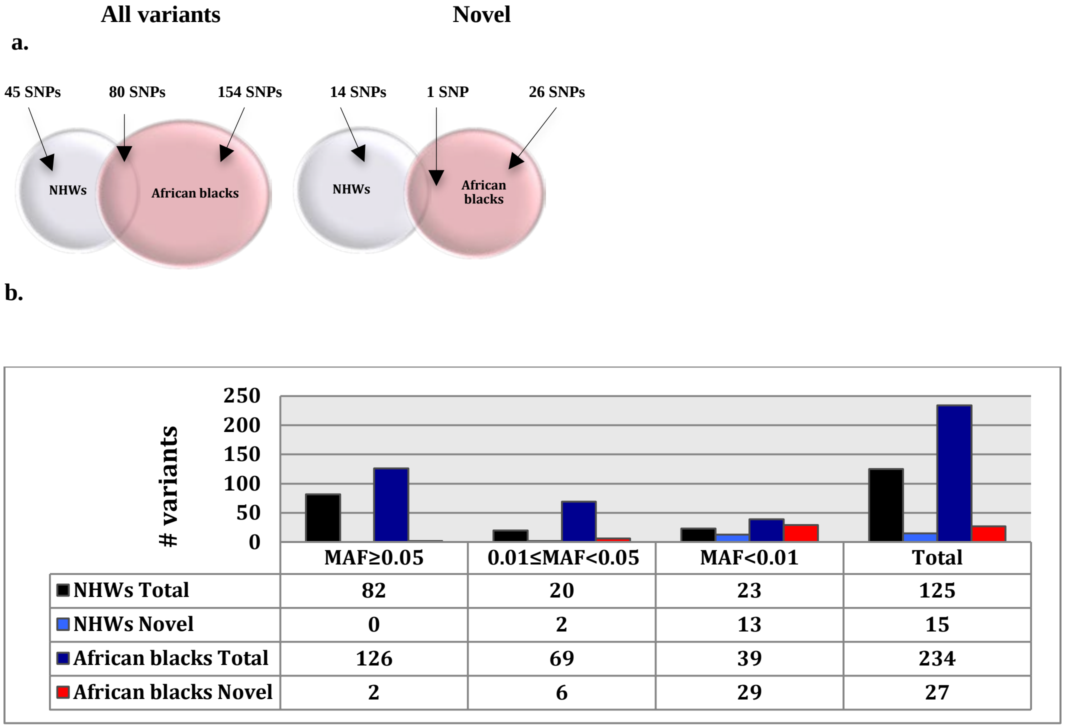
6.2 CHOLESTRYL ESTER TRANSFER PROTEIN

6.2.1 Genetic Association Studies in Non-Hispanic Whites (NHWs) and African Blacks

6.2.1.1 DNA sequencing

We identified a total of 279 variants by resequencing the *CETP* gene in 95 NHWs and 95 African blacks, including 263 biallelic (181 transitions vs. 82 transversions), 2 triallelic and 14 indels. Of 279 variants, 238 are known and 41 are novel. Eighty of these variants were present in both samples, 45 were found only in NHWs and 154 variants were found only in African blacks. The locations of the identified 279 variants are as follows: 224 in introns, 39 in the flanking regions, 1 in the 5'UTR of exon 1, 1 in the 3'UTR of exon 16, and 14 in coding exons. Of the identified 14 coding variants, 7 were non-synonymous and 7 were synonymous. The seven non-synonymous coding variants are: aspartic acid to valine (D6V) and alanine to glycine (A15G) in exon 1, arginine to tryptophan (R154W) in exon 5, alanine to proline (A390P) and valine to methionine (V385M) in exon 12, isoleucine to valine (I405V) in exon 14, and arginine to glutamine (R451Q) in exon 15. We found all 14 indels were located in introns, including two insertions and 12 deletions, ranging in size from one to twelve bases. The characteristics of the identified variants are given in **Figure 6.2.1.**

Of the 125 variants found in NHWs, 82 were common (MAF ≥ 0.05), 20 were uncommon (0.01≤MAF<0.05) and 23 were rare (MAF<0.01) (see **Appendix Table B.1.1).** On the other hand, of the 234 variants identified in African blacks, 126 were common (MAF ≥ 0.05), 69 were uncommon (0.01≤MAF<0.05) and 39 were rare (MAF<0.01). We identified two triallelic SNPs [rs289712 (intron 8) and rs7192120 (exon 12; synonymous)] in African blacks. While rs289712 was diallelic in NHWs and rs7192120 was monomorphic in NHWs **(**see **Appendix Table B1.2).**



	MAF≥0.05	0.01≤MAF<0.05	MAF<0.01	Total
■ NHWs Total	82	20	23	125
■ NHWs Novel	0	2	13	15
■ African blacks Total	126	69	39	234
■ African blacks Novel	2	6	29	27

Figure 6.2.1. Properties of the identified *CETP* variants in NHWS and African blacks.
a. Number of all SNPs identified in each population and number of novel (not present in public databases) SNPs identifeid in each population were showed by venn diagrams. b. Chart showing the distribution of the minor allele frequencies (MAF) of the all and novel SNPs.

6.2.1.2 Distribution of identified *CETP* variants in extreme HDL-C/TG groups

Minor allele frequency distributions of the 125 identified variants in NHWs and 234 variants in African blacks between the two extreme groups are shown in **Appendix Table B1.3** and **Appendix Table B1.4,** respectively**.** In NHWs, 14 variants were present only in the low HDL-C/high TG group vs 11 were present only in the high HDL-C/low TG group; the remaining variants were present in both groups. In African blacks, 27 variants were present only in the low HDL-C/high TG group vs 29 were present only in the high HDL-C/low TG group; the remaining variants were present in both groups.

6.2.1.3 Gene-based association test results

In both populations, gene- based association test revealed significant associations with only HDL-C (*P*=8E-04 for NHWs; *P*=9E-06 for African blacks). The best SNP associated with HDL-C was rs247617 (*P*=7.41E-05) in NHWs and rs3406561 (*P*=6E-06) in African blacks (see **Table 6.2.1 and Table 6.2.2).**

Table 6.2.1. Gene-based association test based on all 100 and 69 with MAF≥0.05 *CETP* variants in NHWs.

Trait	Chr	Gene	All SNPs	Test	[a]*P-value*	Best SNP	[b]SNP *P-value*	SNPs MAF ≥0.05	Test	[a]*P-value*	Best SNP	[b]SNP *P-value*
HDL-C	16	*CETP*	100	322.1438	0.000887	rs247617	7.41E-05	69	260.2633	0.00193	rs247617	7.41E-05
LDL-C	16	*CETP*	100	81.92025	0.639	CTP13868	0.006864	69	34.50891	0.824	CTP13868	0.034344
TG	16	*CETP*	100	52.73295	0.944	rs56208677	0.015627	69	30.4401	0.891	rs56208677	0.015627
TC	16	*CETP*	100	91.41172	0.538	CTP13868	0.000205	69	45.71455	0.712	CTP13868	0.028482
ApoB	16	*CETP*	100	75.7594	0.681	rs289742	0.003514	69	49.67794	0.65	rs289742	0.003514
ApoA1	16	*CETP*	100	122.3072	0.239	rs711752	0.028305	69	96.92092	0.193	rs711752	0.028305

[a]P: gene-based, [b]P detected for the best SNP

Table 6.2.2. Gene-based association test based on all 131 and 86 with MAF≥0.05 *CETP* variants in African blacks.

Trait	Chr	Gene	All SNPs	Test	[a]*P-value*	Best SNP	[b]SNP *P-value*	SNPs MAF ≥0.05	Test	[a]*P-value*	Best SNP	[b]SNP *P-value*
HDL-C	16	*CETP*	131	470.565	9.00E-06	rs34065661	7.88E-10	86	387.1774	6.00E-06	rs34065661	7.88E-10
LDL-C	16	*CETP*	131	150.8933	0.277	rs80296794	0.019748	86	98.07262	0.299	rs4783961	0.040646
TG	16	*CETP*	131	104.4884	0.733	rs114908369	0.003097	86	45.20881	0.927	rs289745	0.056354
TC	16	*CETP*	131	181.023	0.117	rs114203109	0.003057	86	128.8112	0.127	rs66495554	0.005635
APOA1	16	*CETP*	131	170.7475	0.134	rs34065661	0.000114	86	110.1194	0.22	rs34065661	0.000114

[a]P: gene-based, [b]P detected for the best SNP

6.2.1.4 Single-site association analyses

A total of 251 SNPs were successfully genotyped in at least one population group (111 in NHWs and 140 in African blacks) and 51 of them were present in both groups. The genotype call rates, selection criteria and other features of the genotyped SNPs in NHWs (39 tagSNPs; 72 others) and African blacks (73 tagSNPs; 67 others) are shown in **Tables 5.5.4-5.5.5.** The LD bins ($r^2 \geq$

0.80) of the final QC passed SNPs are listed in **Appendix Tables B1.7-B1.8.** Of the 140 SNPs genotyped in African blacks, two triallelic SNPs (rs79398303C/T/A and rs7192120C/G/T) were excluded from analysis. In NHWs, two SNPs (rs247615, rs12720918) which did not meet Hardy-Weinberg equilibrium after Bonferroni correction (*P*<10E-04) were excluded along with five monomorphic SNPs [rs4784741, rs9924087, rs1968905, *CETP*18678 (novel variant), rs5887]. In African blacks 7 SNPs were excluded from the analyses: rs158477 had low call rate (<85 %), and five SNPs (rs71383212, rs11860407, rs12708985, rs12720939, rs17231611) deviated from Hardy-Weinberg equilibrium (*P*<10E-04) and rs9936680 was non-polymorphic. Thus, a total of 104 SNPs (69 common and 35 uncommon/rare based on their MAF in the entire sample) in NHWs and 131 variants (86 common and 45 uncommon/rare) in African blacks were included in subsequent association analyses. The discrepancy rate was determined to be 0-0.5% for the genotyped variants based on the random repeats of ~10% of the samples.

Single-site analyses revealed a total of 55 significant associations (*P*<0.05) with at least one lipid trait in at least one ethnic group, including 30 in NHWs and 37 in African blacks. **Table 6.2.3** and **Table 6.2.4** list the all significant SNPs associated with at least one lipid traits in NHWs and African blacks, respectively.

Table 6.2.3. Significant association results ($P<0.05$) of common *CETP* variants with plasma lipid levels in NHWs (n= 623).

				HDL-C		TG		LDL-C		TC		ApoA1		ApoB		
Ref SNP ID	**[1]Position**	**Locations**	**MAF**	**Beta**	***P***	**Beta**	***P***	**Beta**	***P***	**Beta**	***P***	**Beta**	***P***	**Beta**	***P***	**RegulomeDB Scores**
rs9989419	-8834	5' flanking	0.400	-0.026	0.014	0.027	0.244	0.726	0.749	0.663	0.780	-1.346	0.552	0.065	0.884	1f
rs247617	-3257	5' flanking	0.347	0.043	7.41E-05	-0.024	0.313	2.195	0.342	3.188	0.186	3.941	0.083	-0.268	0.560	5
rs183130	-2610	5' flanking	0.347	0.040	1.91E-04	-0.022	0.340	2.359	0.305	3.240	0.177	3.639	0.115	-0.212	0.643	No data
rs12149545	-812	5' flanking	0.330	0.042	1.66E-04	-0.022	0.356	2.085	0.385	3.614	0.150	4.294	0.074	-0.111	0.817	No data
rs12708967	-762	5' flanking	0.205	-0.034	1.14E-02	0.042	0.150	-2.154	0.451	-4.511	0.131	-1.198	0.668	-0.538	0.334	No data
rs3764261	-648	5' flanking	0.328	0.043	1.63E-04	-0.021	0.405	3.327	0.179	4.856	0.060	3.222	0.189	-0.248	0.609	No data
rs17231506	557	5' flanking	0.343	0.042	1.25E-04	-0.019	0.420	2.249	0.338	3.683	0.134	3.709	0.109	-0.204	0.662	6
rs1800775	1265	5' flanking	0.489	-0.027	1.25E-02	-0.004	0.864	-0.510	0.823	-1.668	0.486	-3.108	0.164	-0.049	0.912	3a
rs3816117	2187	Intron 1	0.488	-0.025	1.84E-02	-0.005	0.842	-0.469	0.835	-1.650	0.485	-3.281	0.142	-0.060	0.894	5
rs711752	2240	Intron 1	0.443	0.033	2.19E-03	-0.016	0.499	-0.312	0.892	0.905	0.706	4.888	0.028	0.155	0.731	5
rs708272	2317	Intron 1	0.442	0.033	2.42E-03	-0.016	0.493	-0.236	0.918	0.964	0.688	4.810	0.032	0.169	0.708	5
rs1864163	3262	Intron 2	0.265	-0.035	3.28E-03	0.025	0.336	0.593	0.816	-1.500	0.575	-2.092	0.413	0.036	0.944	5
rs7203984	5288	Intron 2	0.206	-0.032	0.011	0.025	0.364	-0.228	0.934	-2.298	0.427	-2.829	0.296	-0.243	0.651	5
rs11508026	5358	Intron 2	0.472	0.025	0.012	-0.004	0.859	0.493	0.818	0.627	0.780	4.428	0.036	0.332	0.430	5
rs17231569	5810	Intron 2	0.190	-0.031	0.019	0.023	0.418	-0.301	0.915	-2.293	0.435	-2.143	0.435	-0.187	0.733	5
rs12720922	6914	Intron 2	0.192	-0.030	0.022	0.017	0.541	-1.370	0.621	-3.529	0.224	-1.996	0.463	-0.197	0.717	5
rs12708969	7616	Intron 2	0.439	0.028	0.009	-0.012	0.599	-0.044	0.985	0.970	0.691	4.445	0.054	0.321	0.485	No data
rs9926440	8695	Intron 2	0.302	-0.027	0.019	0.023	0.357	-0.741	0.760	-0.225	0.929	-0.391	0.871	0.009	0.984	4
rs9939224	8764	Intron 2	0.205	-0.034	0.008	0.018	0.521	-1.110	0.685	-2.003	0.483	-1.537	0.568	0.070	0.896	4
rs11076174	9178	Intron 2	0.075	-0.023	0.254	0.022	0.612	1.330	0.754	4.534	0.310	-2.216	0.583	1.950	0.015	5
rs7205804	10921	Intron 5	0.453	0.031	0.004	-0.016	0.484	-0.540	0.814	1.521	0.526	3.903	0.086	0.231	0.610	5
rs1532624	11510	Intron 7	0.452	0.032	0.003	-0.016	0.477	0.046	0.984	1.019	0.668	3.911	0.084	0.212	0.639	5
rs11076175	12409	Intron 8	0.184	-0.034	0.010	0.022	0.430	-0.326	0.907	-1.981	0.499	-2.567	0.351	-0.167	0.761	No data
rs7499892	12621	Intron 8	0.185	-0.033	0.011	0.019	0.496	-0.559	0.842	-2.735	0.352	-2.382	0.387	-0.218	0.692	No data
rs289718	15963	Intron 10	0.304	0.023	0.043	0.002	0.923	-1.187	0.620	-0.037	0.988	2.716	0.262	-0.387	0.423	4
rs289719	15972	Intron 10	0.300	0.023	0.043	0.002	0.932	-1.207	0.622	0.277	0.914	2.493	0.309	-0.425	0.383	5
rs56208677	16263	Intron 10	0.077	0.033	0.096	-0.102	0.016	-4.873	0.244	-4.946	0.258	0.735	0.857	-0.359	0.657	5
rs12720898	17274	Intron 10	0.056	0.015	0.520	-0.003	0.944	-10.214	0.034	-10.098	0.046	6.271	0.199	-0.934	0.335	5
rs12720889	18597	Intron 11	0.290	0.025	0.031	-0.013	0.602	-1.495	0.542	-0.055	0.983	4.078	0.097	-0.130	0.791	No data
rs12447620	20354	Intron 11	0.128	0.021	0.193	-0.010	0.764	-1.869	0.585	-0.415	0.908	-2.180	0.539	-1.918	0.007	2b
rs5880	21126	Exon 12	0.057	-0.032	0.133	-0.004	0.939	-5.642	0.215	-10.436	0.028	-4.504	0.336	-0.679	0.468	4
rs289742	23796	3' flanking	0.127	0.022	0.165	0.003	0.930	-1.870	0.578	0.170	0.962	-0.951	0.787	-2.023	0.004	4
rs289745	25565	3' flanking	0.409	-0.014	0.215	-0.018	0.458	2.792	0.233	0.420	0.864	-4.717	0.037	0.356	0.433	6

[1] Reference sequence: NM_000078

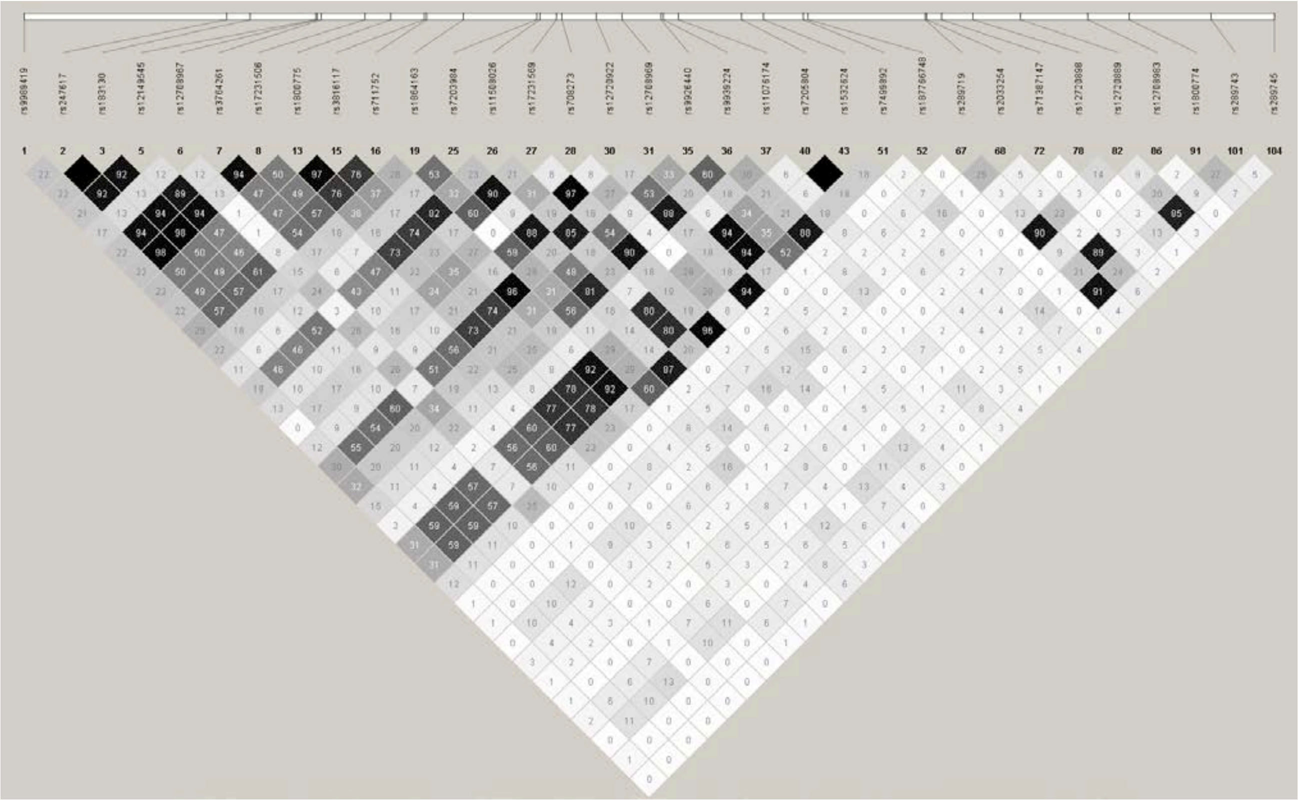


Figure 6.2.2. LD structure of the 33 *CETP* SNPs associated with at least one plasma lipid traits in NHWs (HDL-C, LDL-C, TG, TC, ApoA1, ApoB).
The values in the cells are the pairwise degree of LD indicated by r^2 × 100.

Table 6.2.4. Significant association results (*P*<0.05) of common *CETP* variants with plasma lipid levels in African blacks (n=788).

				HDL-C		**TG**		**LDL-C**		**TC**		**ApoA1**		**ApoB**		
RefSNP ID	**[a]Position**	**Location**	**MAF**	**Beta**	***P***	**Beta**	***P***	**Beta**	***P***	**Beta**	***P***	**Beta**	***P***	**Beta**	***P***	**RegulomeDB Score**
rs183130	-2610	5' flanking	0.244	1.03	2.25E-06	-0.01	0.194	-0.39	0.083	-0.03	0.830	1.44	0.008	-0.77	0.221	No data
rs3764261	-648	5' flanking	0.323	0.62	0.002	-0.01	0.233	-0.37	0.066	-0.09	0.407	0.90	0.073	-0.42	0.455	No data
rs12447924	220	5' flanking	0.224	-0.26	0.269	0.005	0.562	0.46	0.042	0.18	0.141	-0.34	0.547	0.22	0.735	No data
rs4783961	923	5' flanking	0.454	0.64	0.001	0.001	0.924	-0.39	0.041	-0.05	0.616	0.32	0.492	-0.93	0.074	4
rs4783962	1067	5' flanking	0.097	-0.11	0.732	0.02	0.154	0.66	0.042	0.31	0.074	0.12	0.878	-1.27	0.159	3a
rs1800775	1265	5' flanking	0.395	-0.53	0.006	-0.001	0.895	0.27	0.158	0.01	0.955	-0.21	0.666	0.21	0.702	3a
rs17231520	1856	5'UTR-Exon 1	0.090	1.99	1.86E-09	0.01	0.493	-0.48	0.151	0.18	0.294	3.06	1.75E-04	-1.26	0.171	5
rs34065661	1964	Exon 1 (A15G)	0.088	2.07	7.88E-10	0.01	0.542	-0.35	0.295	0.25	0.156	3.19	1.14E-04	-0.96	0.308	5
rs3816117	2187	Intron 1	0.394	-0.54	0.006	-0.001	0.880	0.26	0.188	0.004	0.970	-0.14	0.768	0.37	0.494	5
rs711752	2240	Intron 1	0.232	0.91	3.70E-05	-0.003	0.688	-0.32	0.150	0.03	0.808	1.33	0.016	-0.46	0.460	5
rs708272	2317	Intron 1	0.236	0.88	6.33E-05	-0.003	0.699	-0.35	0.113	0.01	0.938	1.29	0.018	-0.60	0.336	5
rs1864163	3262	Intron 2	0.278	-0.70	0.001	-0.01	0.394	-0.17	0.438	-0.21	0.059	-0.19	0.720	1.11	0.060	5
rs142058276	6022	Intron 2	0.082	1.66	2.06E-06	-0.001	0.920	-0.58	0.106	-0.02	0.914	1.68	0.057	-2.13	0.034	No data
rs9924087	8274	Intron 2	0.207	0.57	0.011	0.003	0.689	0.19	0.403	0.22	0.062	0.04	0.938	0.56	0.378	No data
rs11076174	9178	Intron 2	0.132	-0.71	0.013	-3.33E-04	0.975	-0.27	0.353	-0.29	0.057	-0.93	0.190	-0.08	0.917	5
rs891141	9755	Intron 4	0.130	0.79	0.004	-0.01	0.607	-0.17	0.547	0.05	0.728	0.71	0.298	-1.45	0.062	4
rs891143	10012	Intron 5	0.090	1.29	1.13E-04	-0.003	0.818	-0.25	0.470	0.10	0.583	1.28	0.126	-1.40	0.140	No data
rs7205804	10921	Intron 5	0.097	-0.76	0.015	-0.004	0.746	-0.64	0.043	-0.41	0.014	-0.02	0.980	-0.17	0.848	5
rs1532624	11510	Intron 7	0.097	-0.77	0.014	-0.01	0.511	-0.47	0.143	-0.33	0.051	-0.25	0.745	-0.19	0.834	5
rs11076175	12409	Intron 8	0.243	-0.51	0.020	-0.001	0.877	-0.10	0.652	-0.15	0.200	-0.14	0.797	0.47	0.446	No data
rs9930761	13223	Intron 8	0.148	0.72	0.010	0.01	0.158	0.16	0.571	0.30	0.043	0.40	0.563	0.58	0.447	4
rs5883	13384	Exon 9 (F287F)	0.155	0.65	0.017	0.01	0.336	0.06	0.837	0.22	0.119	0.23	0.729	0.08	0.916	4
rs11076176	13477	Intron 9	0.403	-0.43	0.027	-0.01	0.217	0.01	0.956	-0.11	0.275	-0.84	0.086	0.58	0.291	5
rs289714	13482	Intron 9	0.447	0.24	0.213	-0.001	0.895	0.32	0.106	0.22	0.031	0.53	0.274	0.33	0.541	5
rs289716	15407	Intron 10	0.476	-0.36	0.059	-0.01	0.263	-0.21	0.285	-0.21	0.043	-0.44	0.361	0.04	0.943	No data
rs289718	15963	Intron 10	0.438	-0.40	0.035	-0.01	0.310	-0.31	0.103	-0.26	0.011	-0.52	0.272	0.17	0.747	4
rs289719	15972	Intron 10	0.493	0.41	0.033	0.01	0.164	0.24	0.214	0.23	0.021	0.66	0.164	-0.18	0.744	5
rs2033254	16016	Intron 10	0.317	-0.29	0.145	-0.01	0.420	-0.29	0.146	-0.23	0.034	-0.44	0.375	-0.10	0.863	4
rs1968905	16979	Intron 10	0.360	0.63	0.002	0.004	0.602	-0.03	0.894	0.11	0.298	0.38	0.456	-0.27	0.639	6
rs12708980	18413	Intron 11	0.342	-0.51	0.011	-1.01E-05	0.999	-0.23	0.260	-0.21	0.054	-0.21	0.668	-0.66	0.236	6
rs7195984	21498	Intron 12	0.169	0.72	0.005	0.01	0.323	-0.03	0.918	0.13	0.342	1.35	0.031	-0.29	0.679	4
rs1800774	21580	Intron 12	0.217	-0.51	0.025	-0.01	0.486	-0.43	0.057	-0.32	0.007	-0.61	0.281	-0.48	0.453	4
rs289740	22985	Intron 14	0.117	0.87	0.003	0.01	0.366	-0.10	0.751	0.11	0.490	1.70	0.021	-0.46	0.577	4
rs1801706	23696	3'UTR-Exon 16	0.176	0.57	0.021	0.004	0.641	0.21	0.388	0.24	0.068	0.27	0.660	0.46	0.505	4
rs289743	23830	3'flanking	0.315	-0.39	0.048	-0.004	0.601	-0.28	0.165	-0.22	0.036	-0.29	0.553	0.06	0.913	2b
rs289744	24136	3'flanking	0.306	-0.33	0.105	-0.005	0.487	-0.33	0.108	-0.23	0.030	-0.14	0.781	0.10	0.859	3a
rs66495554	24669	3'flanking	0.193	-0.58	0.015	-0.01	0.259	-0.45	0.061	-0.35	0.006	-1.08	0.067	-0.71	0.286	No data

[a]Position in the baseline reference sequence (NC_000016)

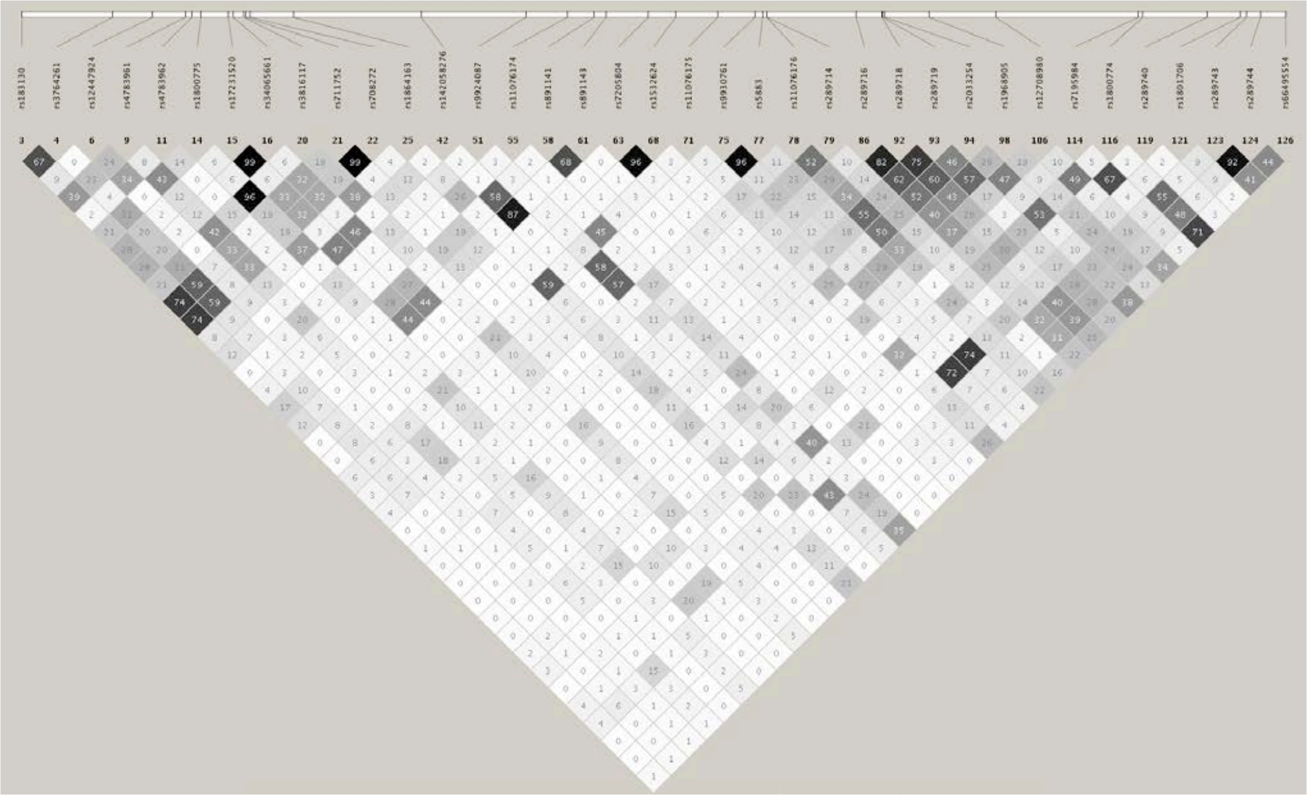


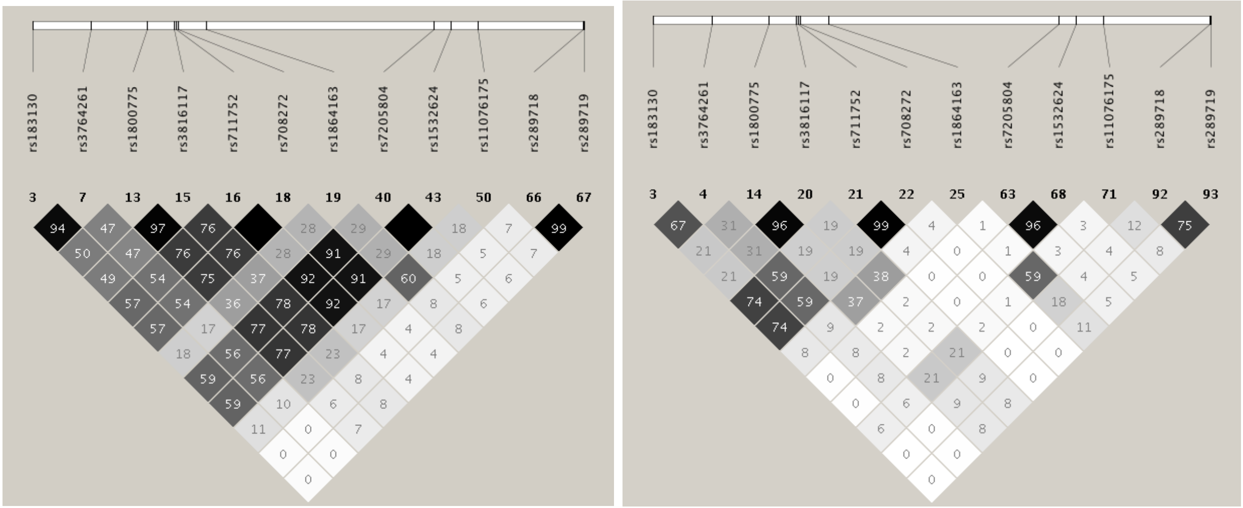
Figure 6.2.3. LD structure of the 37 *CETP* SNPs associated with at least one plasma lipid traits in African blacks.
The values in the cells are the pairwise degree of LD indicated by r^2 × 100.

6.2.1.4.1 Association of common variants (MAF ≥ 0.05) with HDL-C levels

In NHWs, we identified 26 common SNPs exhibiting associations with HDL-C levels (see **Table 6.2.3**). The best SNP was rs247617 (β=0.043; *P*=7.41E-05; located ~3kb upstream of the *CETP* gene) and this was moderately correlated (r^2>0.46) with twelve of the other HDL-C-associated SNPs (see **Figure 6.2.3**) in NHWs. The remaining thirteen SNPs showed independent associations with HDL-C of the top SNP rs247617. On the other hand, 31 SNPs were significantly associated with HDL-C in African blacks; the most significant SNP was a non-synonymous SNP, rs34065661 (β=2.07, *P*=7.88E-10) and this was strongly correlated (r^2=0.99) with a promoter SNP, rs17231520 (β=1.99, *P*=1.86E-09) (see **Table 6.2.4** and **Figure 6.2.4)**.

Detailed results of the association of the **CETP** variants with HDL-C in NHWs and African blacks can be found in **Appendix Table 10 and Appendix Table 15,** respectively.

We identified twelve HDL-associated SNPs which were significant in both populations, including rs183130, rs3764261 (GWAS significant), rs708272 (*Taq1*B), rs1800775 (-629C>A), rs3816117, rs711752, rs1864163, rs289718, rs289719, rs7205804, rs153624 and rs11076175. While the associations of the first 8 SNPs with HDL-C were in the same direction for the same allele in both populations, the latter 4 SNPs showed opposite effect for the same minor allele. The best SNP among the above-listed 12 HDL-associated SNPs was rs183130 (β=1.03; P=2.25E-06 in African blacks and β=0.040; P=1.91E-04 in NHWs) and this was in LD (r^2=0.57-0.94) with 5 significant SNPs in NHWs (rs3764261, rs711752, rs708272, rs7205804, rs1532624) and in LD (r^2=0.67-0.74) with 3 significant SNPs in African blacks (rs3764261, rs711752, rs708272) (see **Figure 6.2.5**). The association of four remaining SNPs in NHWs (rs289719, rs289718, rs1864163 and rs11076175) and 8 remaining SNPs in African blacks (rs1800775, rs3816117, rs1864163, rs7205804, rs1532624, rs11076175, rs289718, rs289719) with HDL-C was independent of rs183130.



a) NHWs

b) African blacks

Figure 6.2.4. LD structure of the 12 *CETP* SNPs associated with HDL-C in both populations.
a) NHWa b) African blacks.
The values in the cells are the pairwise degree of LD indicated by r^2 × 100.

No consistent association was observed between 51 SNPs tested in both populations with other plasma lipid levels [LDL-C, TG ApoA1 and ApoB]. **Appendix Tables B10-B14** and **Appendix Tables B16-20** show detailed single-SNP results of the association analyses for TC, LDL-C and TG in NHWs and African blacks, respectively. In NHWs, 1 SNP (rs56208677) was found to be associated with TG, 1 SNP (rs12720898) with LDL-C, and 2 SNPs (rs12720898 and rs5880; r^2= 0) with TC; associations observed for rs56208677 and rs12720898 were novel in this study. In African blacks, 11 SNPs were associated with TC, 4 with LDL-C, but no association was observed for TG. For LDL-C, we observed association with two weakly correlated promoter SNPs (r^2 =0.34): rs12447924 (β=0.46; *P*=0.042) and rs4783962 (β=0.66, *P*=0.042; plus two independent associations (r^2=0) with rs4783961 (β=-0.39, *P*=0.041; located in promoter) and rs7205804 (β=-0.64; *P*=0.043)] (see **Table 6.2.4** and **Figure 6.2.4**). The top 5 of the 11 SNPs associated with TC (rs66495554, rs289718, rs7205804, rs289714 and rs9930761; *P*-values 6E-03<*P*<0.05) showed independent associations (r^2<0.30).

6.2.1.4.2 Association of uncommon/rare variants (MAF < 0.05) with lipid levels

Rare *CETP* variants with MAF<0.01 in Bin 3 were associated with HDL-C in both NHWs (*P*=0.024) and African blacks (*P*=0.009). We also observed the association of Bin 3 variants with TC in African blacks (*P*=0.026) (see **Table 6.2.5)**

Table 6.2.5. Results of rare variant analysis of *CETP* variants.

NHWs

				HDL-C		TG		LDL-C		TC		ApoA1		ApoB	
Bin 1	**N.RV (MAF<0.01)**	**N.Sample _RV**	**N.Sample _NoRV**	**Stat**	**P**	**Stat**	**P**	**Stat**	**P**	**Stat**	**P**	**Stat**	**P**	**Stat**	**P**
RVT1	26	103	520	-7.12E-01	0.136	5.36E-01	0.577	-1.03E+01	0.911	1.65E+02	0.087	-3.19E+01	0.256	2.07E+01	0.276
RVT2	26	103	520	-2.01E-02	0.368	2.19E-02	0.621	1.08E+00	0.801	7.68E+00	0.089	-7.98E-01	0.525	1.24E+00	0.145
SKAT	26	103	520	5.52E+04	0.011	1.98E+04	0.733	5.34E+04	0.015	3.43E+04	0.221	1.46E+04	0.652	1.21E+04	0.809
SKATO	26	103	520	6.93E+04	0.024	1.98E+04	0.766	5.34E+04	0.030	8.36E+04	0.169	2.42E+04	0.426	1.80E+04	0.523
Bin 2	**N.RV (MAF<0.02)**	**N.Sample_ RV**	**N.Sample _NoRV**	Stat	P	Stat	P	Stat	P	Stat	**P**	**Stat**	**P**	**Stat**	**P**
RVT1	29	147	476	-4.12E-01	0.373	1.26E-02	0.989	9.02E+00	0.919	1.41E+02	0.130	-2.03E+01	0.445	6.05E+00	0.737
RVT2	29	147	476	-6.32E-03	0.747	-2.50E-02	0.516	9.28E-01	0.805	4.62E+00	0.242	-6.04E-01	0.580	4.53E-01	0.540
SKAT	29	147	476	5.94E+04	0.037	2.30E+04	0.839	6.77E+04	0.013	5.25E+04	0.085	1.50E+04	0.866	3.30E+04	0.128
SKATO	29	147	476	5.94E+04	0.072	2.30E+04	1.000	6.77E+04	0.026	9.04E+04	0.129	1.67E+04	0.616	3.30E+04	0.228
Bin 3	**N.RV (MAF<0.05)**	**N.Sample _RV**	**N.Sample_ NoRV**	Stat	P	Stat	P	Stat	P	Stat	**P**	**Stat**	**P**	**Stat**	**P**
RVT1	35	312	311	-5.22E-01	0.139	5.07E-02	0.942	-1.14E+01	0.867	5.73E+01	0.423	-1.83E+01	0.361	-2.57E+00	0.850
RVT2	35	312	311	-2.10E-02	0.207	6.32E-03	0.846	-4.98E-01	0.876	1.46E+00	0.663	-1.07E+00	0.248	-3.29E-01	0.601
SKAT	35	312	311	8.86E+04	0.015	2.88E+04	0.924	7.54E+04	0.057	6.99E+04	0.095	2.21E+04	0.854	3.71E+04	0.296
SKATO	35	312	311	1.10E+05	0.030	2.88E+04	1.000	7.54E+04	0.109	6.99E+04	0.175	4.05E+04	0.425	3.71E+04	0.485

African blacks

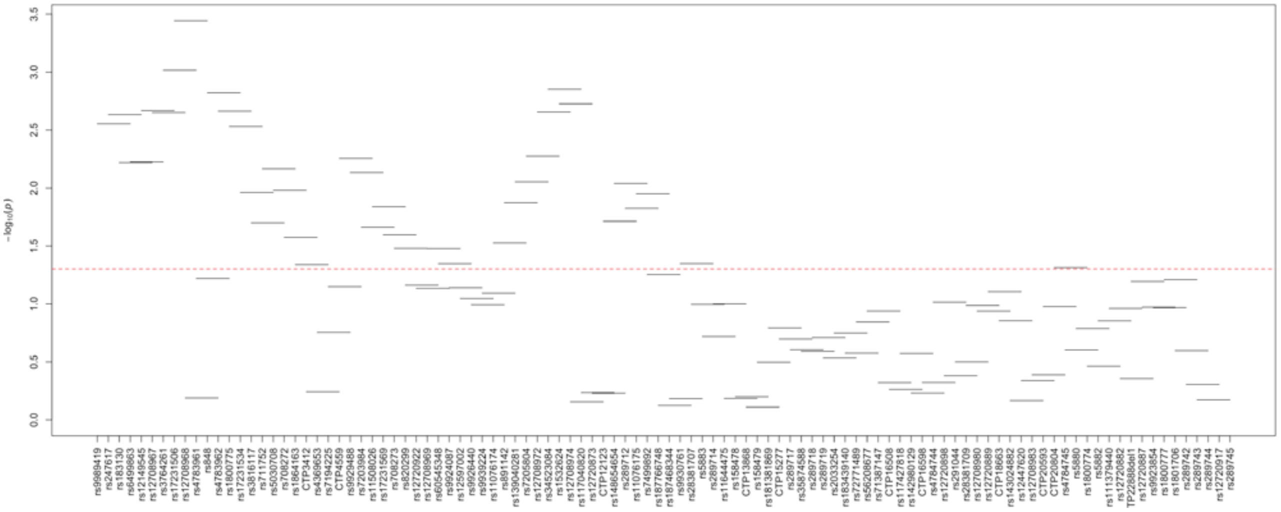
				HDL-C		TG		TC		LDL-C		ApoB		ApoA1	
Bin 1	**N.RV (MAF<0.05)**	**N.Sample _RV**	**N.Sample _NoRV**	**Stat**	**P**	**Stat**	**P**	**Stat**	**P**	**Stat**	**P**	**Stat**	**P**	**Stat**	**P**
RVT1	45	598	190	-1.218	0.681	-0.037	0.739	1.036	0.513	2.081	0.488	5.539	0.501	1.270	0.861
RVT2	45	598	190	-0.325	0.298	-0.013	0.280	-0.042	0.802	0.172	0.583	0.537	0.536	-0.134	0.862
SKAT	45	598	190	2.16E+05	0.042	1.80E+05	0.140	137342.470	0.341	1.45E+05	0.319	1.30E+05	0.437	1.85E+05	0.123
SKATO	45	598	190	2.16E+05	0.077	1.80E+05	0.239	137342.470	0.532	1.45E+05	0.501	1.30E+05	0.647	1.85E+05	0.212
Bin 2	**N.RV (MAF<0.02)**	**N.Sample _RV**	**N.Sample _NoRV**	**Stat**	**P**	**Stat**	**P**	**Stat**	**P**	**Stat**	**P**	**Stat**	**P**	**Stat**	**P**
RVT1	17	195	593	-2.532	0.319	0.008	0.931	0.103	0.939	-0.386	0.880	4.027	0.571	0.627	0.920
RVT2	17	195	593	-0.487	0.114	-0.004	0.705	-0.026	0.874	0.012	0.969	-0.005	0.995	0.216	0.777
SKAT	17	195	593	6.69E+04	0.148	81853.190	0.083	35628.195	0.599	32510.966	0.691	36617.004	0.611	6.89E+04	0.154
SKATO	17	195	593	2.27E+05	0.121	81853.190	0.144	35628.195	0.758	33016.222	0.707	36617.004	0.809	6.89E+04	0.255
Bin 3	**N.RV (MAF<0.01)**	**N.Sample_RV**	**N.Sample_NoRV**	**Stat**	**P**	**Stat**	**P**	**Stat**	**P**	**Stat**	**P**	**Stat**	**P**	**Stat**	**P**
RVT1	6	30	757	-8.234	0.035	0.085	0.557	-5.230	0.013	-8.388	0.037	7.931	0.471	-22.989	0.016
RVT2	6	30	758	-1.968	0.005	0.015	0.553	-0.992	0.008	-1.402	0.050	0.673	0.731	-4.539	0.007
SKAT	6	30	758	27156.591	0.006	7.87E+03	0.352	14614.065	0.070	8.58E+03	0.268	1.15E+04	0.153	14570.580	0.089
SKATO	6	30	758	34737.576	0.009	7.87E+03	0.523	41687.188	0.026	3.03E+04	0.069	1.15E+04	0.248	46934.526	0.023

6.2.1.5 Haplotype anaylses

In both populations, we observed multiple significant haplotype windows in both NHWs and African blacks **(Figure 6.2.8a-8f).** Window 8, (rs17231506, rs12708968, rs4783961 and rs17245715), revealed the most significant signal (global *P*=3.60E-04 for HDL-C) in NHWs. Rs17231506 was the only significant SNP in single-site analysis in this haplotype window with a p-value of 1.25E-05. In African blacks, window 14 (rs180075, rs17231520, rs34065661 and rs5884) had the most significant association with HDL-C (global *P*=1.70E-08). In both populations, the haplotypes in the 5' of the *CETP* gene showed highly significant effect on HDL-C. Details for the haplotype association analyses with plasma lipid traits are shown in **Appendix Tables B21-B26** for NHWs and **Appendix Tables B27-B31** for African blacks.

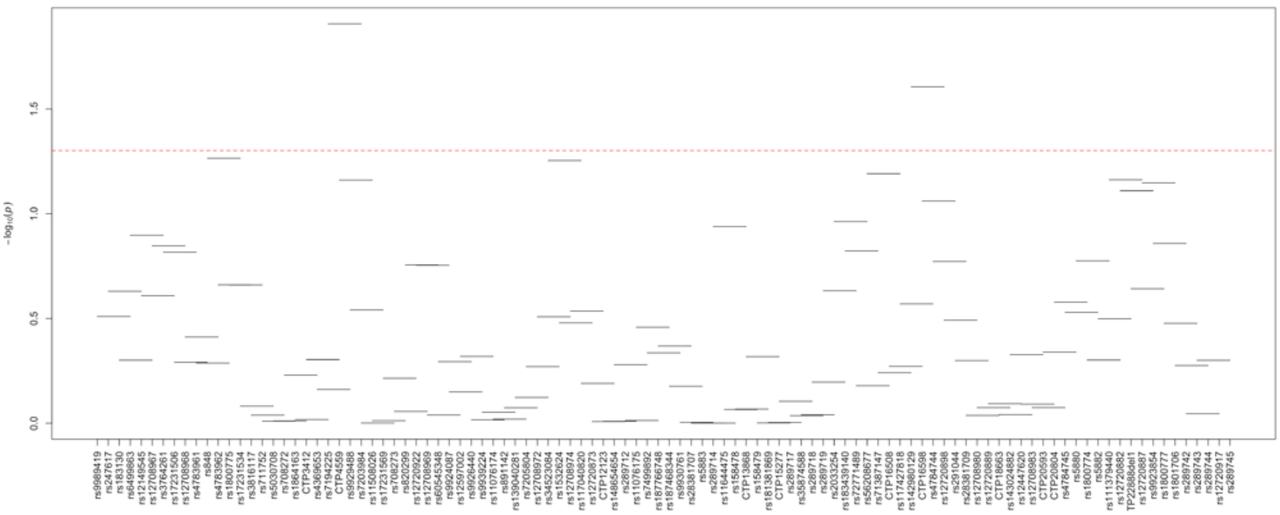
a

HDL-C



LDL-C

b



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1.5
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rs4783962
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rs711752
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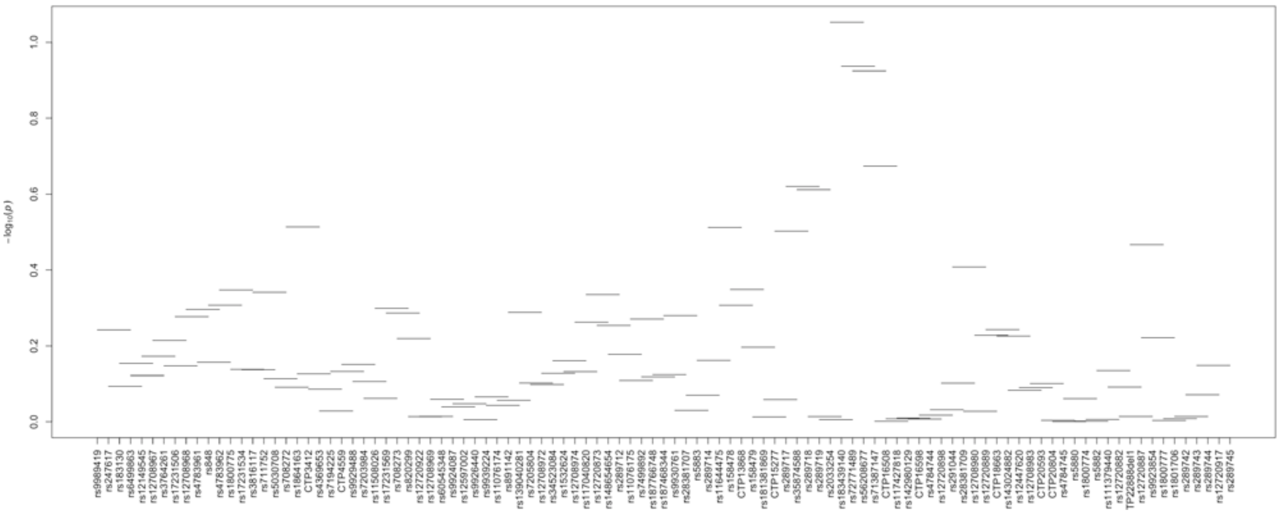
rs289745

TG

c



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rs5880
rs1800774
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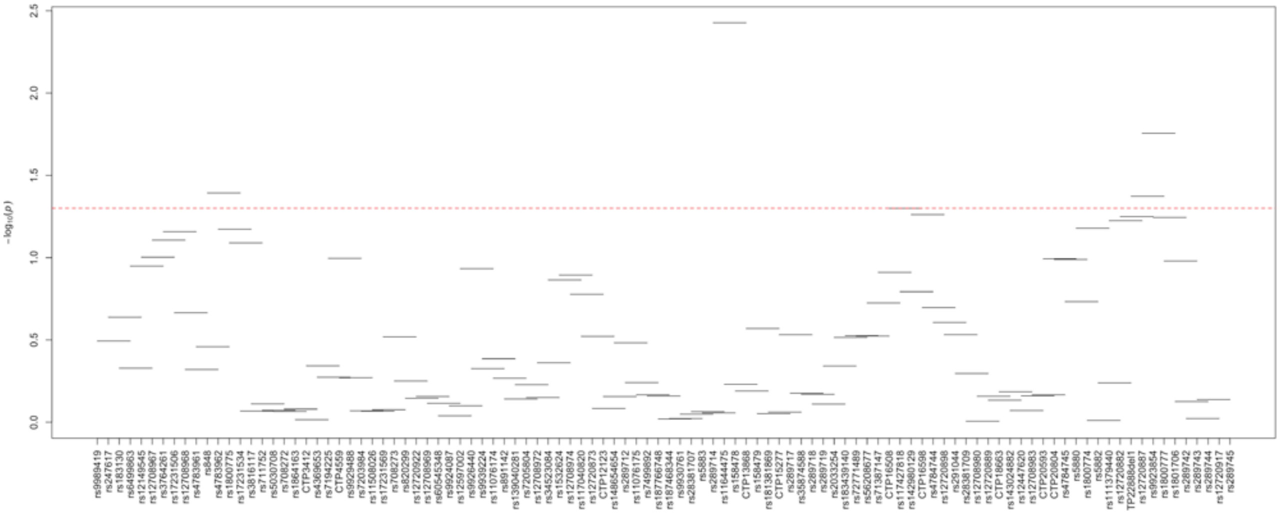
rs289745

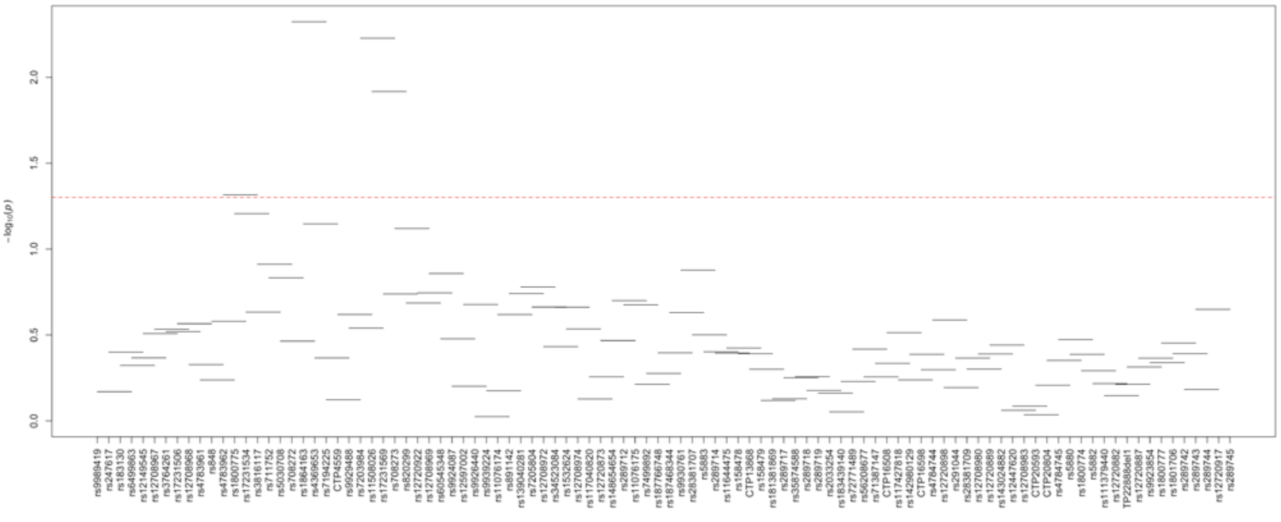
d

TC



ApoA1

e



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ApoB

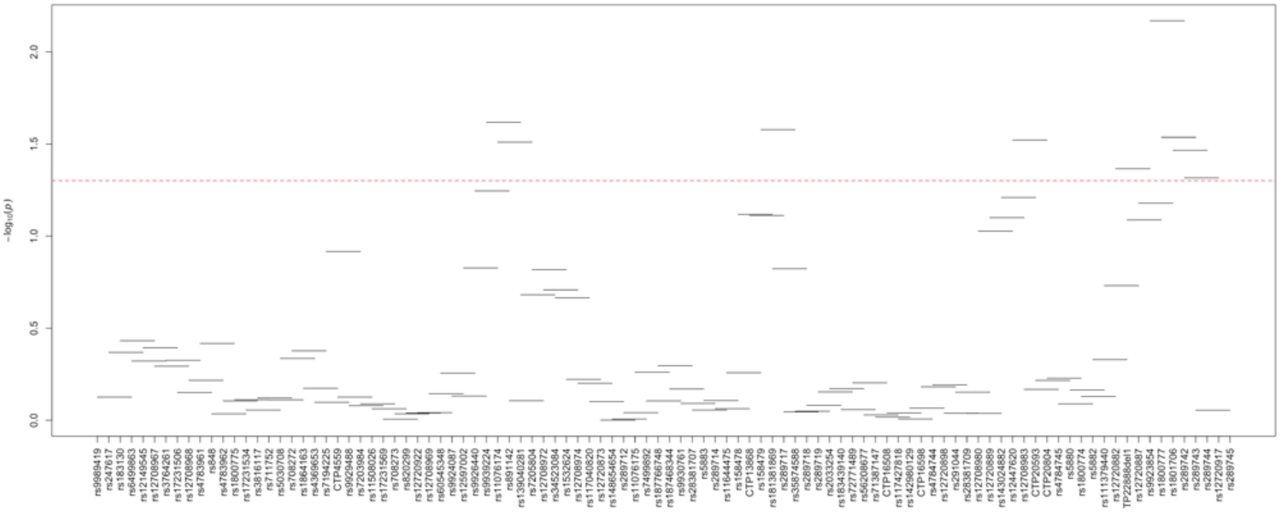
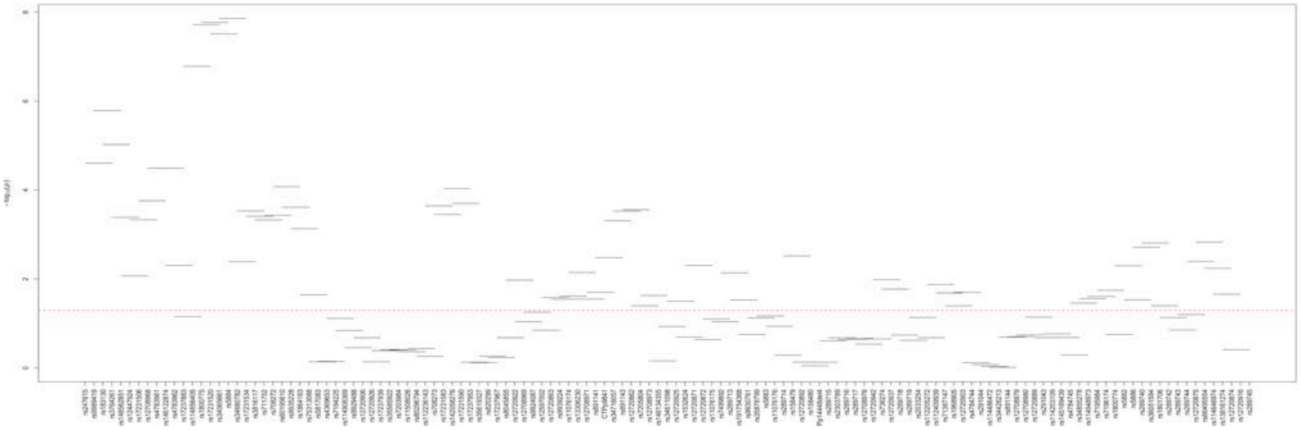


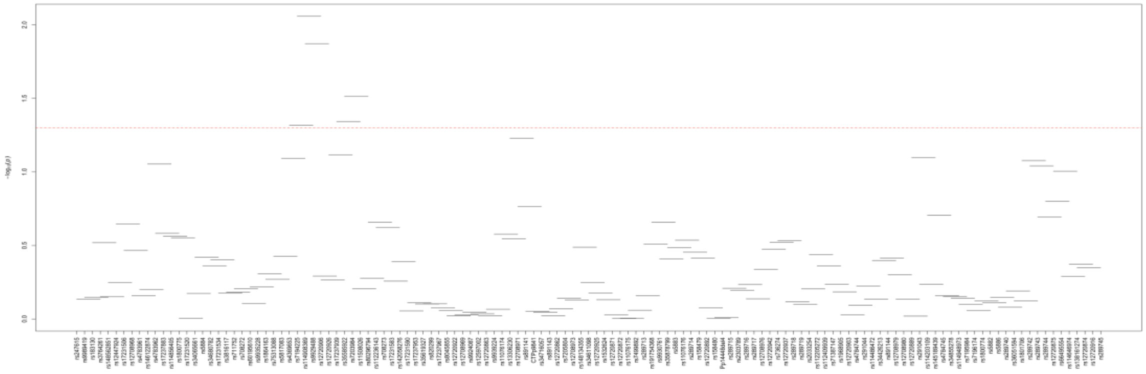
Figure 6.2.5. ***CETP*** **haplotype analysis with plasma lipid levels in NHWs.**
Horizontal lines represent the window tested, with the corresponding markers along the x- axis and global p-value (in log scale) on the y- axis. Red line shows the threshold for statistical significance (*P*=0.05).

HDL-C

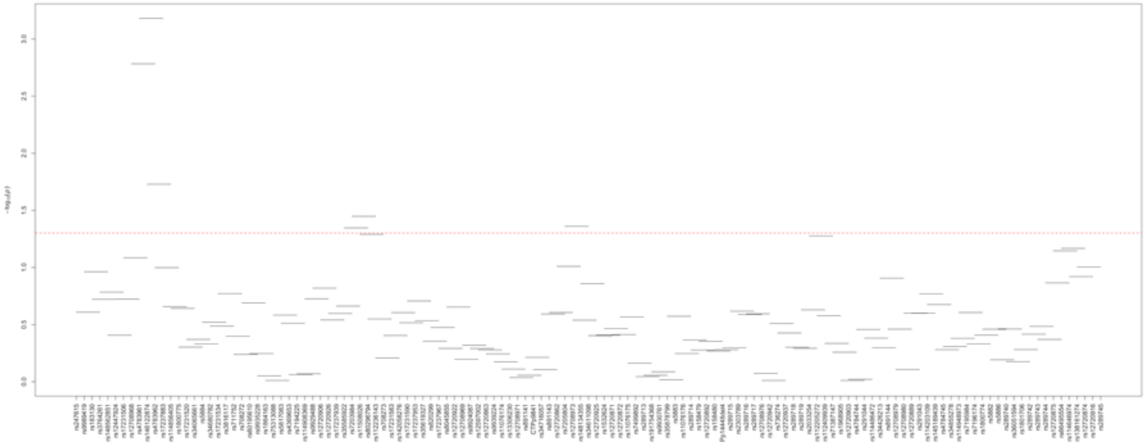
a



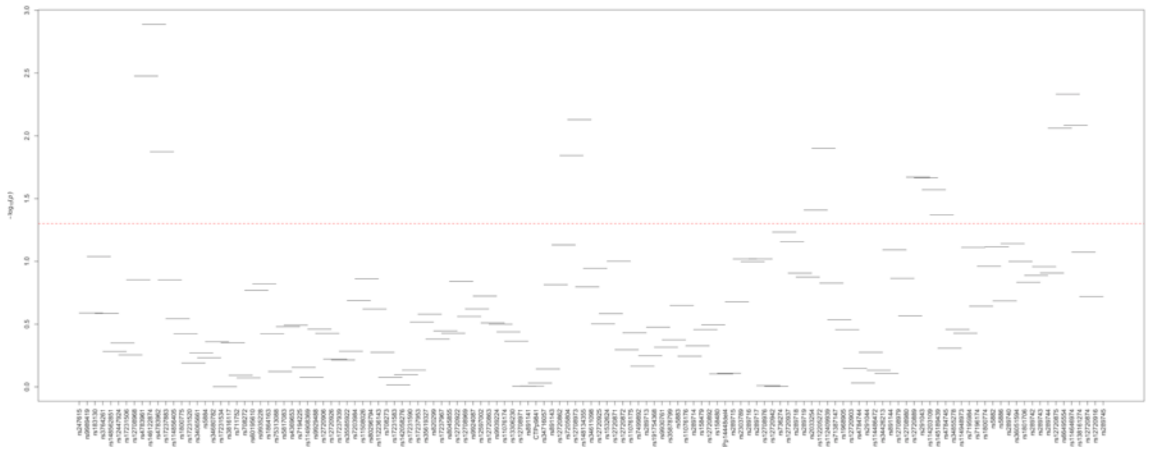
b **TG**



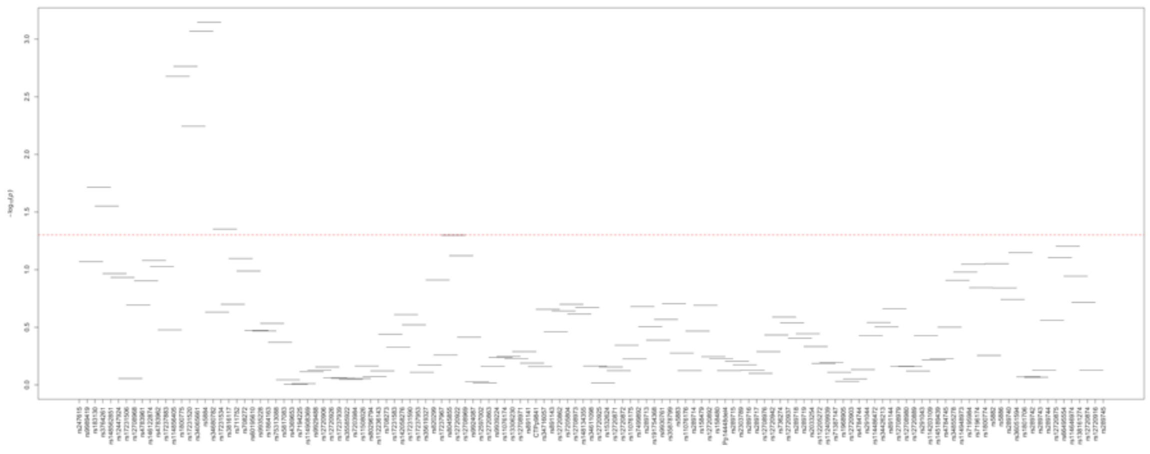
c **LDL-C**



d **TC**



e **ApoA1**



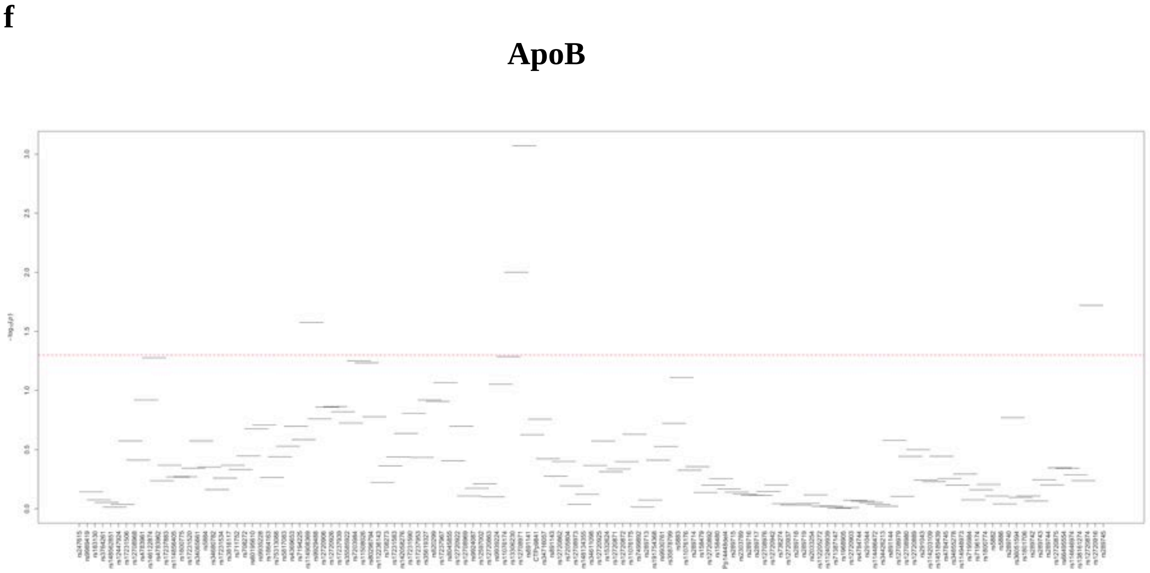


Figure 6.2.6. *CETP* haplotype analysis in African Blacks.
Haplotype windows for HDL-C (a), TG (b), (c) LDL-C, (c) TC, (e) ApoA1 (f) ApoB
Horizontal lines represent the window tested, with the corresponding markers along the x- axis and global p-value (in log scale) on the y- axis. Red line shows the threshold for statistical significance (P=0.05).

6.2.1.6 Functional annotation of significant SNPs

The RegulomeDB scores for all SNPs identified in NHWs and African blacks are listed in **Supplementary Tables 2** and **Supplementary Table 3**, respectively. We identified 22 lipid trait-associated SNPs in NHWs, 26 SNPs in African blacks and 9 SNPs in both populations which were enriched in regions that were described to be associated with a biochemical event in at least one ENCODE cell line. One of our independent signals with HDL-C in NHWs, rs9989419 (located ~8kb upstream of the *CETP* gene) had RegulomeDB score of 1f, indicating this is a known cis-eQTL which lies within a TF binding site or a DNase peak based on the experimental evidence. This SNP had reached genome wide significance for association with HDL-C in a GWAS study (Wang et al. 2007).

6.2.2 Discussion

Previous studies have examined the role of common SNPs and haplotypes in the *CETP* gene in relation to dysplidemia, atherosclerosis and coronary heart disease with inconsistent outcomes. To our knowledge, this is first study that has resequenced the *CETP* gene and its flanking regions in selected individuals with extreme HDL-C/TG levels from two racial groups and then examined the role of identified common and rare variants with lipid level variation in the total samples.

The complete resequencing of the *CETP* gene in 95 NHWs and 95 African blacks revealed a total of 279 variants, of which 80 were found in both populations. We identified all but 16 common variants (8 in NHWs and 8 in African blacks) present in dbSNP (build 137) in populations of European and African descent and also in 1000 genome project. The 16 known variants were missed due to technical issues in resequencing and these SNPs were genotyped in the entire sample of both populations in order to cover the full range of variation in this gene. In addition, we identified 41 low-frequency variants that were not reported in any public databases. In tandem with SNP discovery effort, 200 SNPs including tagSNPs, several low frequency variants (MAF <0.005) and significantly reported variants in and around the *CETP* were successfully genotyped in 623 NHWs and 788 African blacks. A total of 184 QC-passed variants (104 in NHWs and 131 in African blacks) were included in the subsequent association analyses.

In single-SNP association analysis, we identified several nominal significant signals ($P<0.05$) for HDL-C, LDL-C and TC in either NHWs and/or African blacks. In NHWs, 26 SNPs were found to be associated with HDL-C, 1 with LDL-C and 2 with TC In African blacks, 31 SNPs were associated with HDL-C, 11 with TC, and 4 were with LDL-C. Interestingly, no association was observed for TG in either population. This is consistent with published studies in which *CETP* polymorphisms have been reported to influence mostly HDL-C and LDL-C (Schierer et al. 2012, Chasman et al. 2008,Knoblauch et al. 2004). Notably, 12 SNPs (rs183130, rs3764261, rs1800775, rs3816117, rs711752, rs708272, rs1864163, rs7205804, rs1532624, rs11076175, rs289718, rs289719) were significantly associated with HDL-C levels in both populations. In NHWs, the majority of these 12 SNPs were in tighter LD with each other and with the GWAS rs3764261 SNP as well as with -629C>A (rs1800775) and *Taq1B* (rs70272), whereas little LD were observed among these SNPs in African blacks (**Figure 6.2.6a-6b**).

Previously, three SNPs, *TaqIB* (rs708272; located in intron 1), -629C>A (rs1800775; located in promoter) and GWAS significant rs3764261 (5' flanking region), have been shown to be associated with lipid profile and/or CETP mass/activity in several studies (Boekholdt et al. 2003, Thompson et al. 2007). It has been reported that up to 10% of the variation in the HDL-C can be explained by the *Taq*IB polymorphisim (Boekholdt et al. 2003). It has also been shown that *Taq1*B is a marker of promoter variant -629C>A (rs1800775), which is located in Sp2/SP2 binding sites of the proximal promoter (Schierer et al. 2012, Klerkx et al. 2003; Ordovas et al. 2000; Dachet et al. 2000). Although there is a strong LD between these two SNPs, their association with HDL-C has not been consistent in all studies (Dullaart et al. 1991; Boekholdt 2003). In our study, -629C>A was strongly correlated with *Taq1B* in NHWs (r^2=0.75) but not in African blacks (r^2=0.19). Despite this, both *Taq1B* (β=0.033; *P*=2.42E-03 for NHWs; β=0.88; *P*=6.33E-05 for African blacks) and -629C>A (β=-0.027, *P*=1.25E-02 for NHWs; β=-0.53; *P*=0.006 for African blacks) were significantly associated with plasma HDL-C levels in both populations. Recently, Lu et al. (2013) investigated the association of *Taq1*B and -629C>A polymorphisms with CHD and lipid levels in a multiethnic population of Singapore (Lu et al. 2013). They found a weak correlation between the two polymorphisms and *Taq1*B showed stronger association with HDL-C and ApoA1 levels than -629C>A. Hence, they concluded that there could be other functional sites, other than -629C>A, within or around the *CETP* gene which are in LD with *Taq1B* (Lu et al. 2013). In our study, rs183130 (located in ~3kb upstream) was the most significant HDL-associated SNP in both populations and that was also in LD with *Taq1*B and -629C>A. Rs183130 has also shown consistent association with HDL-C across multiple ethnic groups including Europeans, Asians, and African Americans and it appears to be functional since it alters the consensus transcription binding site (Thompson et al. 2007, Spirin et al. 2007)

Furthermore, an uncommon non-synonymous SNP rs1800777 (R451Q) located in exon 15 that was previously reported to be associated with HDL-C levels (Boes et al. 2009), was found only in NHWs with a MAF of 0.035 (MAF= 0.00 % for both HapMAP YRI and our African blacks) and was associated with both HDL-C (*P*=0.023) and TC (*P*=0.027) levels (see Appendix **Table B1.9** and **Appendix Table B1.10).**

Most of the significant SNPs identified in this study are located in the upstream and 5' half of the gene that were strongly correlated with each other, and the majority of these associations have been reported previously (Boekholdt et al. 2003, Willer et al. 2008, Radovica et al. 2013, Spirin et al. 2007, Boes et al. 2009, Heid et al. 2008, Coram et al. 2013, Weissglas-Volkov et al. 2010, Reynolds et al. 2011, Lettre et al. 2011, Ridker et al. 2009, Waterworth et al. 2010, Edmondson et al. 2011). However, we also observed multiple novel independent associations in NHWs (rs56208677 with TG, rs12720898 with TG and LDL-C, and rs5880 with TC) and in African blacks (rs1968905 and rs289740 with HDL-C and rs66495554 with TC).

We also performed haplotype based association analysis to evaluate whether combinations of the C*ETP* SNPs are more strongly associated with plasma lipid profile than the individual SNPs. We mainly observed HDL-C associated significant haplotypes in the 5' region, including the promoter and first ~12kb of the *CETP* gene, and all these significant haplotypes include the HDL-C associated SNPs in single-site analysis. Similar results were obtained by a recent study in 704 Latvians with extreme HDL-C levels (Radovica et al. 2013). They identified a haploblock including SNPs located in ~0.6kb upstream of the *CETP* gene, promoter and first ~10kb of the *CETP* which was significantly associated with HDL-C levels.

In addition to the single-SNP and haplotype association analyses, rare variant analyses also revealed significant results, indicating the importance of rare *CETP* variants (MAF<0.01) in affecting plasma HDL-C and LDL-C levels. Although previous studies have shown the contribution of rare variants in other lipid genes in relation to lipid levels (Cohen et al. 2004, Evans et al. 2011, Johansen et al. 2012, Wang et al. 2007, Razzaghi et al. 2000), to our knowledge, this is first study indicating that rare *CETP* variants make a substantial contribution to the variation of plasma lipid levels in the general white and black populations.

7.0 LIMITATIONS

This study has a few limitations. The discovery sample used in the resequencing stage was relatively small and we may have missed the identification of certain rare functional variants. Also, we did not have costly sequencing data from our entire samples and unknown rare variants in non-sequenced individuals could have affected our rare variant analysis results. However, this was in part compensated by resequencing individuals with extreme phenotypes that resulted in the identification of several novel variants having MAF<0.01. The other weakness of the study is uncorrected p-values, which might have given some false positive associations, as we did not perform multiple testing corrections because we were doing a follow-up comprehensive analysis of a gene already known to be associated with lipid phenotype. Given the relatively small sample size of our study and biological relevance of *LPL* and *CETP* genes, Bonferroni adjustment was considered to be too conservative with possibility of generating false negatives.

8.0 CONCLUSIONS

To the best of our knowledge, this is the first study that has comprehensively evaluated the role of *LPL* and *CETP* genetic variation with 5 major lipid and apolipoprotein phenotypes (HDL-C, TG, LDL-C, ApoA1 and ApoB) in two well-defined and genetically distinct populations. This study suggests that individual and combined effects of both common and rare polymorphisms in the *CETP* and *LPL* genes have significant impact on the complex phenotypic variation of plasma lipid levels among white and/or black population. Further studies are required to better elucidate the role of these variants in affecting interindividual variation in plasma lipid phenotypes.

APPENDICES

SUPPLEMENTARY TABLES AND FIGURES

APPENDIX A. SUPPLEMENTARY TABLES AND FIGURES FOR *LPL* GENE RESEQUENCING AND ASSOCIATION ANALYSES

APPENDIX A1. Supplementary Tables for *LPL* gene resequencing and association analyses in NHWs

Table A1.1. Variants identified in the sequencing sample of 95 NHW individuals

***LPL* variant/RefSNP ID**	**Position[a]**	**Alleles[b]**	**Location**	**Call rate**	**Amino Acid Change**	**MAF**	**HWE (p-value)**	**[c]RegulomeDB Score**
LP208/rs1470186	208	T>C	5' flanking	98.9		0.016	1	2b
LP351	**351**	**C>A**	**5' flanking**	**98.9**		**0.005**	**1**	**3a**
LP428/rs73667465	428	G>A	5' flanking	98.9		0.016	1	4
LP549/rs17091742	549	C>T	5' flanking	98.9		0.016	1	5
LP1088/rs80351041	1088	G>T	5'UTR-exon1	97.9		0.005	1	2b
LP1090/rs1800590	1090	T>G	5'UTR-exon1	98.9		0.011	1	2b
LP1130	**1130**	**G>C**	**5'UTR-exon1**	**97.9**		**0.005**	**1**	**2b**
LP2335/rs3779787	2335	G>T	Intron 1	98.9		0.122	1	2b
LP2913	**2913**	**T>C**	**Intron 1**	**95.8**		**0.005**	**1**	**No data**
LP3558/rs34309063	3558	G>A	Intron 1	100		0.247	1	5
LP3964/rs17410577	3964	G>C	Intron 1	98.9		0.239	1	No data
LP4060/rs1534649	4060	G>T	Intron 1	97.9		0.43	0.128	No data
LP4424/rs13266204	4424	A>G	Intron 1	97.9		0.263	0.531	6
LP4621/rs182344474	4621	C>G	Intron 1	100		0.021	1	No data
LP4948/rs6997330	4948	C>G	Intron 1	97.9		0.022	1	5
LP5094	**5094**	**C>G**	**Intron 1**	**97.9**		**0.005**	**1**	**5**
LP5107/rs117680193	5107	C>T	Intron 1	96.8		0.005	1	5
LP5200	**5200**	**C>T**	**Intron 1**	**91.6**		**0.006**	**1**	**No data**
LP5531/rs1031045	5531	G>A	Intron 1	96.8		0.016	1	6
LP5772/rs60633545	5772	A>G	Intron 1	98.9		0.016	1	No data
LP5949/rs112127208	5949	T>G	Intron 1	100		0.137	1	6
LP6383	**6383**	**G>T**	**Intron 1**	**100**		**0.005**	**1**	**5**
LP6435/rs181663908	6435	G>C	Intron 1	97.9		0.005	1	5
LP6477	**6477**	**T>C**	**Intron 1**	**98.9**		**0.005**	**1**	**5**
LP6553/rs59254395	6553	C>T	Intron 1	100		0.016	1	6
LP6554/rs56043715	6554	A>G	Intron 1	100		0.016	1	6
LP6821/rs10104051	6821	C>T	Intron 1	98.9		0.426	0.31	No data
LP7130/rs28615996	7130	T>C	Intron 1	73.7		0.021	1	No data
LP7131	**7131**	**T>G**	**Intron 1**	**75.8**		**0.007**	**1**	**No data**
LP7313/rs28645722	7313	G>A	Intron 1	98.9		0.016	1	No data
LP7388/rs28575919	7388	C>G	Intron 1	100		0.016	1	6
LP7503/rs6999612	7503	T>C	Intron 1	100		0.016	1	5
LP7512/rs3779788	7512	C>T	Intron 1	100		0.121	1	5
LP7556/rs59811201	7556	T>C	Intron 1	100		0.016	1	4
LP8221/rs7000460	8221	A>C	Intron 1	89.5		0.018	1	5
LP8250/rs59630933	8250	G>A	Intron 1	84.2		0.019	1	5
LP8415/rs56321069	8415	T>A	Intron 1	97.9		0.183	1	No data
LP8467	**8467**	**C>T**	**Intron 1**	**100**		**0.005**	**1**	**No data**
LP8516	**8516**	**del1**	**Intron 1**	**100**		**0.011**	**1**	**6**
LP9015/rs28445964	9015	A>G	Intron 1	50.5		0.021	1	No data
LP9024	**9024**	**T>C**	**Intron 1**	**68.4**		**0.008**	**1**	**No data**
LP9130/rs13252357	9130	T>A	Intron 1	98.9		0.005	1	6
LP9411/rs28689946	9411	A>C	Intron 1	98.9		0.016	1	5
LP9418/rs28582042	9418	G>A	Intron 1	98.9		0.016	1	5
LP9589	**9589**	**C>T**	**Intron 1**	**98.9**		**0.016**	**1**	**6**
LP9696/rs73667468	9696	G>T	Intron 1	98.9		0.016	1	No data
LP9914/rs73667469	9914	T>G	Intron 1	97.9		0.016	1	No data
LP10127/rs1801177	10127	G>A	Exon 2	100	D9N	0.016	1	5
LP10632	**10632**	**C>T**	**Intron 2**	**100**		**0.005**	**1**	**No data**
LP10912/rs149477831	10912	A>G	Intron 2	94.7		0.022	1	6
LP10987/rs74377536	10987	C>A	Intron 2	94.7		0.122	0.234	No data
LP11050/rs7016529	11050	T>C	Intron 2	96.8		0.016	1	No data
LP11090/rs8176337	11090	C>G	Intron 2	96.8		0.19	1	No data
LP11228/rs192296320	11228	T>C	Intron 2	98.9		0.005	1	6
LP11574/rs34123038	11574	G>A	Intron 2	96.8		0.049	1	No data
LP11600/rs113497343	11600	G>C	Intron 2	100		0.011	1	No data
LP11760/rs73667470	11760	A>C	Intron 2	100		0.016	1	No data
LP11888_11889/rs149017698	11888	ins1	Intron 2	100		0.011	1	5

Table A1.1. Continued

LPL variant/RefSNP ID	Position[a]	Alleles[b]	Location	Call rate	Amino Acid Change	MAF	HWE (p-value)	[c]RegulomeDB Score
LP12224_12920	**12224**	**del697**	**Intron 2**	**95.8**		**0.005**	**1**	**5**
LP12449/rs74304285	12449	G>A	Intron 2	98.9		0.117	1	No data
LP12484/rs144709714	12484	C>A	Intron 2	97.9		0.048	0.367	No data
LP12550/rs113023641	12550	G>A	Intron 2	97.9		0.118	1	6
LP12810_12829	**12810**	**dup20**	**Intron 2**	**95.8**		**0.126**	**1**	**6**
LP12853_12854	**12853**	**Ins16**	**Intron 2**	**95.8**		**0.055**	**0.459**	**6**
LP12861_12864	**12861**	**del4**	**Intron 2**	**95.8**		**0.06**	**0.549**	**6**
LP12878_12889	**12878**	**del12**	**Intron 2**	**95.8**		**0.005**	**1**	**6**
LP12884_12887	**12884**	**del4**	**Intron 2**	**95.8**		**0.016**	**1**	**6**
LP13003/rs80181352	13003	G>T	Intron 2	100		0.053	0.442	5
LP13639/rs78326602	13639	G>A	Intron 2	100		0.011	1	5
LP13854/rs1121923	13854	G>A	Exon 3	100	V108V	0.016	1	No data
LP14114/rs73667472	14114	T>C	Intron 3	98.9		0.08	0.909	5
LP15206/rs343	15206	C>A	Intron 3	100		0.042	1	6
LP15245/rs248	15245	G>A	Exon 4	100	E118E	0.047	0.36	5
LP15425/rs249	15425	T>C	Intron 4	100		0.095	1	No data
LP15448_15449/rs57186780	15448	ins2	Intron 4	100		0.063	1	6
LP15653/rs252	15653	del1	Intron 4	98.9		0.41	0.359	No data
LP15836/rs253	15836	C>T	Intron 4	98.9		0.41	0.359	No data
LP16316/rs254	16316	C>G	Intron 5	92.6		0.074	0.759	No data
LP16320/rs255	16320	T>C	Intron 5	100		0.105	1	No data
LP16386/rs256	16386	C>T	Intron 5	97.9		0.118	1	No data
LP16442/rs74382962	16442	G>C	Intron 5	96.8		0.005	1	No data
LP16563/rs77066732	16563	T>A	Intron 5	97.9		0.016	1	5
LP16671/rs258	16671	G>C	Intron 5	97.9		0.409	0.21	6
LP17231/rs263	17231	C>T	Intron 5	93.7		0.135	1	6
LP17476	**17476**	**A>C**	**Intron 5**	**100**		**0.005**	**1**	**6**
LP17599/rs264	17599	G>A	Intron 5	100		0.116	1	No data
LP17948/rs268	17948	A>G	Exon 6	95.8	N291S	0.033	1	5
LP18065/rs183252580	18065	T>G	Intron 6	60		0.009	1	No data
LP18086/rs269	18086	T>G	Intron 6	92.6		0.119	1	No data
LP18095/rs270	18095	C>A	Intron 6	91.6		0.201	1	No data
LP18121/rs271	18121	G>A	Intron 6	96.8		0.109	1	1f
LP18297/rs144578061	18297	A>C	Intron 6	100		0.005	1	5
LP18395_18396/rs58935878	18395	ins1	Intron 6	100		0.121	1	No data
LP18462	**18462**	**T>G**	**Intron 6**	**97.9**		**0.005**	**1**	**No data**
LP18621/rs187904902	18621	C>T	Intron 6	100		0.005	1	No data
LP18708/rs276	18708	T>C	Intron 6	98.9		0.021	1	6
LP18822/rs277	18822	T>C	Intron 6	100		0.232	0.791	No data
LP18942/rs278	18942	G>A	Intron 6	100		0.211	1	6
LP19442/rs281	19442	A>T	Intron 6	95.8		0.242	0.693	5
LP19445/rs282	19445	C>G	Intron 6	97.9		0.129	0.919	5
LP19517/rs283	19517	C>T	Intron 6	97.9		0.161	0.537	5
LP19608/rs285	19608	C>T	Intron 6	95.8		0.407	0.856	6
LP19675/rs286	19675	A>T	Intron 6	96.8		0.06	0.544	6
LP19815	**19815**	**G>A**	**Intron 6**	**100**		**0.005**	**1**	**No data**
LP19975/rs287	19975	A>G	Intron 6	97.9		0.172	0.525	No data
LP20038/rs289	20038	T>C	Intron 6	95.8		0.159	0.316	6
LP20080	**20080**	**C>T**	**Intron 6**	**97.9**		**0.005**	**1**	**6**
LP20271/rs291	20271	T>C	Intron 6	100		0.163	0.416	No data
LP20363/rs74746426	20363	A>T	Intron 6	100		0.053	0.442	No data
LP20505_20506/rs33936024	20505	ins1	Intron 6	100		0.163	0.416	6
LP20544/rs294	20544	T>C	Intron 6	98.9		0.08	0.909	6
LP20657/rs295	20657	A>C	Intron 6	100		0.163	0.416	No data
LP20663/rs296	20663	G>A	Intron 6	100		0.005	1	No data
LP20790/rs297	20790	T>C	Intron 6	100		0.163	0.416	No data
LP21125_21128	21125	del4	Intron 6	98.9		0.005	1	5
LP21353/rs301	21353	T>C	Intron 7	97.9		0.172	0.525	No data
LP21780/rs304	21780	T>G	Intron 7	91.6		0.103	0.009	6
LP21820/rs305	21820	A>G	Intron 7	87.4		0.108	0.011	6
LP21895/rs308	21895	T>G	Intron 7	86.3		0.012	1	6
LP21965/rs310	21965	C>T	Intron 7	86.3		0.006	1	6
LP22044_22047/rs311	22044	del4	Intron 7	97.9		0.075	0.821	6
LP22416/rs312	22416	G>C	Intron 7	94.7		0.072	0.745	No data
LP22461/rs314	22461	G>A	Intron 7	93.7		0.18	0.587	No data
LP22514/rs315	22514	T>C	Intron 7	92.6		0.011	1	No data
LP22855/rs316	22855	C>A	Exon 8	100	T361T	0.079	0.901	1f
LP23190_23191/rs113064376	23190	del2	Intron 8	92.6		0.5	0.149	6
LP23192/rs117026536	23192	G>T	Intron 8	92.6		0.068	1	6

Table A1.1. Continued

***LPL* variant/RefSNP ID**	**Position^a**	**Alleles^b**	**Location**	**Call rate**	**Amino Acid Change**	**MAF**	**HWE (p-value)**	**^{c}RegulomeDB Score**
LP23388/rs318	23388	C>G	Intron 8	88.4		0.018	1	4
LP23395/rs319	23395	A>C	Intron 8	86.3		0.293	0.451	4
LP23496/rs320	23496	T>G	Intron 8	88.4		0.185	0.576	5
LP23573/rs77243948	23573	T>C	Intron 8	90.5		0.017	1	5
LP23636/rs322	23636	A>C	Intron 8	95.8		0.17	0.468	5
LP23747/rs325	23747	T>C	Intron 8	93.7		0.067	0.655	5
LP23858/rs326	23858	A>G	Intron 8	94.7		0.206	0.593	1f
LP23955/rs327	23955	T>G	Intron 8	95.8		0.192	0.142	6
LP24143/rs328	24143	C>G	Exon9	100	Ser447X	0.005	1	5
LP24505/rs329	24505	A>G	Intron 9	98.9		0.016	1	4
LP24573	**24573**	**T>C**	**Intron 9**	**98.9**		**0.005**	**1**	**5**
LP24815/rs330	24815	G>A	Intron 9	100		0.111	0.025	5
LP24824/rs331	24824	G>A	Intron 9	90.5		0.122	0.036	5
LP24852/rs12679834	24852	T>C	Intron 9	98.9		0.08	0.909	1f
LP24899/rs76423146	24899	C>T	Intron 9	100		0.016	1	5
LP25005/rs184536204	25005	A>G	Intron 9	100		0.005	1	5
LP25049/rs78031480	25049	G>A	Intron 9	100		0.063	1	No data
LP25320	**25320**	**C>T**	**Intron 9**	**100**		**0.005**	**1**	**No data**
LP25335/rs117199990	25335	C>T	Intron 9	100		0.079	0.901	No data
LP25352/rs145391587	25352	A>C	Intron 9	100		0.079	0.901	No data
LP25844/rs75278536	25844	T>G	Intron 9	98.9		0.074	0.813	6
LP26201/rs77069344	26201	T>G	Intron 9	95.8		0.077	0.835	No data
LP26234/rs10099160	26234	T>G	Intron 9	98.9		0.282	0.667	6
LP27000/rs112324447	27000	C>T	Intron 9	91.6		0.029	0.115	No data
LP27160/rs117910839	27160	T>A	Intron 9	95.8		0.027	0.11	5
LP27229/rs11570891	27229	C>T	Intron 9	96.8		0.082	0.924	5
LP27249/rs4922115	27249	G>A	3' UTR-exon10	98.9		0.085	0.247	No data
LP27611/rs3289	27611	T>C	3' UTR-exon10	98.9		0.016	1	5
LP27688/rs191212278	27688	C>T	3' UTR-exon10	98.9		0.005	1	5
LP28036/rs11570892	28036	A>G	3' UTR-exon10	98.9		0.101	0.092	No data
LP28067/rs3208305	28067	A>T	3' UTR-exon10	95.8		0.203	0.574	6
LP28093/rs1803924	28093	C>T	3' UTR-exon10	95.8		0.082	0.932	6
LP28382/rs1059507	28382	C>T	3' UTR-exon10	95.8		0.11	0.135	6
LP28407/rs150252331	28407	C>A	3' UTR-exon10	100		0.026	1	No data
LP28464/rs3735964	28464	C>A	3' UTR-exon10	100		0.079	0.901	No data
LP28490/rs3200218	28490	A>G	3' UTR-exon10	100		0.279	0.697	No data
LP28524	**28524**	**C>T**	**3' UTR-exon10**	**100**		**0.005**	**1**	**No data**
LP28911/rs13702	28911	T>C	3' UTR-exon10	100		0.2	0.594	6
LP28982/rs1059611	28982	T>C	3' UTR-exon10	100		0.079	0.901	6
LP29046_29047/rs10645926	29046	Ins2	3' UTR-exon10	100		0.079	0.901	6
LP29086/rs15285	29086	C>T	3' UTR-exon10	100		0.2	0.594	No data
LP29088/rs3866471	29088	C>A	3' UTR-exon10	100		0.105	0.121	No data
LP29287/rs3916027	29287	G>A	3' flanking	100		0.184	0.347	5
LP29315/rs9644636	29315	T>G	3' flanking	97.9		0.339	0.628	5
LP29474/rs113831503	29474	C>T	3' flanking	100		0.026	0.105	No data
LP29487/rs4921683	29487	T>A	3' flanking	100		0.105	0.121	No data
LP29547/rs4921684	29547	C>T	3' flanking	100		0.105	0.121	5
LP29557_29558	**29557**	**ins1**	**3' flanking**	**100**		**0.005**	**1**	**5**
LP29716/rs80085105	29716	T>C	3' flanking	100		0.026	1	6

MAF: minor allele frequency; Bold: novel variants

[a] Positions in the reference sequence (NC_00008.10).

[b] Variants are reported based on the allele in the reference sequence.

[c] RegulomeDB scores were generated by using http://regulome.stanford.edu/. Scores represents; 1a- eQTL + TF binding + matched TF motif + matched DNase Footprint + DNase peak; 1b- eQTL + TF binding + any motif + DNase Footprint + DNase peak; 1c- eQTL + TF binding + matched TF motif + DNase peak; 1d- eQTL + TF binding + any motif + DNase peak; 1e- eQTL + TF binding + matched TF motif; 1f- eQTL + TF binding / DNase peak; 2a- TF binding + matched TF motif + matched DNase Footprint + DNase peak; 2b- TF binding + any motif + DNase Footprint + DNase peak; 2c- TF binding + matched TF motif + DNase peak; 3a- TF binding + any motif + DNase peak; 3b- TF binding + matched TF motif; 4- TF binding + DNase peak; 5-TF binding or DNase peak; 6-other

Table A1.2. Distrubition of *LPL* variants between extremely high (n=47) and low (n=48) HDL-C/TG groups

#	*LPL* variant/ RefSNP ID	Position[a]	Location	Minor allele	High HDL-C /Low TG group allele counts	Low HDL-C/High TG group allele counts	MAF in High HDL-C/Low TG group	MAF in Low HDL-C/High TG group	MAF in the total sample
1	LP208/rs1470186	208	5' flanking	C	2:92	1:93	0.021	0.011	0.016
2	LP351	351	5' flanking	A	1:93	0:94	0.011	0	0.005
3	LP428/rs73667465	428	5' flanking	A	2:92	1:93	0.021	0.011	0.016
4	LP549/rs17091742	549	5' flanking	T	2:92	1:93	0.021	0.011	0.016
5	LP1088/rs80351041	1088	5'-UTR-exon1	T	1:89	0:96	0.011	0	0.005
6	LP1090/rs1800590	1090	5'-UTR-exon1	G	1:91	1:95	0.011	0.01	0.011
7	LP1130	1130	5'-UTR-exon1	C	90:0	95:1	0	0.01	0.005
8	LP2335/rs3779787	2335	Intron 1	T	15:77	8:88	0.163	0.083	0.122
9	LP2913	2913	Intron 1	C	88:0	93:1	0	0.011	0.005
10	LP3558/rs34309063	3558	Intron 1	A	79:15	64:32	0.16	0.333	0.247
11	LP3964/rs17410577	3964	Intron 1	C	79:15	64:30	0.16	0.319	0.239
12	LP4060/rs1534649	4060	Intron 1	T	58:36	48:44	0.383	0.478	0.43
13	LP4424/rs13266204	4424	Intron 1	G	74:18	63:31	0.196	0.33	0.263
14	LP4621/rs182344474	4621	Intron 1	G	2:92	2:94	0.021	0.021	0.021
15	LP4948/rs6997330	4948	Intron 1	G	3:87	1:95	0.033	0.01	0.022
16	LP5094	5094	Intron 1	G	92:0	93:1	0	0.011	0.005
17	LP5107/rs117680193	5107	Intron 1	T	1:91	0:92	0.011	0	0.005
18	LP5200	5200	Intron 1	T	82:0	91:1	0	0.011	0.006
19	LP5531/rs1031045	5531	Intron 1	A	2:88	1:93	0.022	0.011	0.016
20	LP5772/rs60633545	5772	Intron 1	G	2:90	1:95	0.022	0.01	0.016
21	LP5949/rs112127208	5949	Intron 1	G	15:79	11:85	0.160	0.115	0.137
22	LP6383	6383	Intron 1	T	1:93	0:96	0.011	0	0.005
23	LP6435/rs181663908	6435	Intron 1	C	1:91	0:94	0.011	0	0.005
24	LP6477	6477	Intron 1	C	1:91	0:96	0.011	0	0.005
25	LP6553/rs59254395	6553	Intron 1	T	2:92	1:95	0.021	0.01	0.016
26	LP6554/rs56043715	6554	Intron 1	G	2:92	1:95	0.021	0.01	0.016
27	LP6821/rs10104051	6821	Intron 1	T	56:38	52:42	0.404	0.447	0.426
28	LP7130/rs28615996	7130	Intron 1	C	2:68	1:69	0.029	0.014	0.021
29	LP7131	7131	Intron 1	G	1:73	0:70	0.014	0	0.007
30	LP7313/rs28645722	7313	Intron 1	A	2:90	1:95	0.022	0.01	0.016
31	LP7388/rs28575919	7388	Intron 1	G	2:92	1:95	0.021	0.01	0.016
32	LP7503/rs6999612	7503	Intron 1	C	2:92	1:95	0.021	0.01	0.016
33	LP7512/rs3779788	7512	Intron 1	T	15:79	8:88	0.160	0.083	0.121
34	LP7556/rs59811201	7556	Intron 1	C	2:92	1:95	0.021	0.01	0.016
35	LP8221/rs7000460	8221	Intron 1	C	2:76	1:91	0.026	0.011	0.018
36	LP8250/rs59630933	8250	Intron 1	A	2:74	1:83	0.026	0.012	0.019
37	LP8415/rs56321069	8415	Intron 1	A	21:71	13:81	0.228	0.138	0.183
38	LP8467	8467	Intron 1	T	94:0	95:1	0	0.01	0.005
39	LP8516	8516	Intron 1	del1	1:93	1:95	0.011	0.01	0.011
40	LP9015/rs28445964	9015	Intron 1	G	1:45	1:49	0.022	0.02	0.021
41	LP9024	9024	Intron 1	C	60:0	69:1	0	0.014	0.008
42	LP9130/rs13252357	9130	Intron 1	A	1:93	0:94	0.011	0	0.005
43	LP9411/rs28689946	9411	Intron 1	C	2:92	1:93	0.021	0.011	0.016
44	LP9418/rs28582042	9418	Intron 1	A	2:92	1:93	0.021	0.011	0.016
45	LP9589	9589	Intron 1	T	2:92	1:93	0.021	0.011	0.016
46	LP9696/rs73667468	9696	Intron 1	T	2:90	1:95	0.022	0.01	0.016
47	LP9914/rs73667469	9914	Intron 1	G	2:90	1:93	0.022	0.011	0.016
48	**LP10127/rs1801177 (D9N)**	10127	Exon 2	A	2:92	1:95	0.021	0.01	0.016
49	LP10632	10632	Intron 2	T	94:0	95:1	0	0.01	0.005
50	LP10912/rs149477831	10912	Intron 2	G	86:0	90:4	0	0.043	0.022
51	LP10987/rs74377536	10987	Intron 2	A	12:74	10:84	0.140	0.106	0.122
52	LP11050/rs7016529	11050	Intron 2	C	2:86	1:95	0.023	0.01	0.016
53	LP11090/rs8176337	11090	Intron 2	G	21:67	14:82	0.239	0.146	0.19
54	LP11228/rs192296320	11228	Intron 2	C	1:91	0:96	0.011	0	0.005
55	LP11574/rs34123038	11574	Intron 2	A	5:85	4:90	0.056	0.043	0.049
56	LP11600/rs113497343	11600	Intron 2	C	94:0	94:2	0	0.021	0.011
57	LP11760/rs73667470	11760	Intron 2	C	2:92	1:95	0.021	0.01	0.016
58	LP11888_11889/rs149017698	11888	Intron 2	ins1	2:92	0:96	0.021	0	0.011
59	LP12224_12920	12224	Intron 2	del697	1:91	0:90	0.011	0	0.005
60	LP12449/rs74304285	12449	Intron 2	A	14:78	8:88	0.152	0.083	0.117

Table A1.2. Continued

#	*LPL* variant/ RefSNP ID	Position[a]	Location	Minor allele	High HDL-C /Low TG group allele counts	Low HDL-C/High TG group allele counts	MAF in High HDL-C/Low TG group	MAF in Low HDL-C/High TG group	MAF in the total sample
61	LP12484/rs144709714	12484	Intron 2	A	86:4	91:5	0.044	0.052	0.048
62	LP12550/rs113023641	12550	Intron 2	A	14:76	8:88	0.156	0.083	0.118
63	LP12810_12829	12810	Intron 2	dup20	15:77	8:82	0.163	0.089	0.126
64	LP12853_12854	12853	Intron 2	ins16	87:5	85:5	0.054	0.056	0.055
65	LP12861_12864	12861	Intron 2	del4	87:5	84:6	0.054	0.067	0.06
66	LP12878_12889	12878	Intron 2	del12	1:91	0:90	0.011	0	0.005
67	LP12884_12887	12884	Intron 2	del4	3:89	0:90	0.033	0	0.016
68	LP13003/rs80181352	13003	Intron 2	T	5:89	5:91	0.053	0.052	0.053
69	LP13639/rs78326602	13639	Intron 2	A	2:92	0:96	0.021	0	0.011
70	LP13854/rs1121923	13854	Exon 3	A	2:92	1:95	0.021	0.01	0.016
71	LP14114/rs73667472	14114	Intron 3	C	86:6	87:9	0.065	0.094	0.08
72	LP15206/rs343	15206	Intron 3	A	6:88	2:94	0.064	0.021	0.042
73	LP15245/rs248	15245	Exon 4	A	5:89	4:92	0.053	0.042	0.047
74	LP15425/rs249	15425	Intron 4	C	86:8	86:10	0.085	0.104	0.095
75	LP15448_15449/rs57186780	15448	Intron 4	ins2	9:85	3:93	0.096	0.031	0.063
76	LP15653/rs252	15653	Intron 4	del1	57:37	54:40	0.394	0.426	0.41
77	LP15836/rs253	15836	Intron 4	T	57:37	54:40	0.394	0.426	0.41
78	LP16316/rs254	16316	Intron 5	G	79:5	84:8	0.06	0.087	0.074
79	LP16320/rs255	16320	Intron 5	C	10:84	10:86	0.106	0.104	0.105
80	LP16386/rs256	16386	Intron 5	T	12:78	10:86	0.133	0.104	0.118
81	LP16442/rs74382962	16442	Intron 5	C	88:0	95:1	0	0.01	0.005
82	LP16563/rs77066732	16563	Intron 5	A	89:1	94:2	0.011	0.021	0.016
83	LP16671/rs258	16671	Intron 5	C	57:35	53:41	0.38	0.436	0.409
84	LP17231/rs263	17231	Intron 5	T	13:75	11:79	0.148	0.122	0.135
85	LP17476	17476	Intron 5	C	94:0	95:1	0	0.01	0.005
86	LP17599/rs264	17599	Intron 5	A	12:82	10:86	0.128	0.104	0.116
87	**LP17948/rs268 (N291S)**	17948	Exon 6	G	88:2	88:4	0.022	0.043	0.033
88	LP18065/rs183252580	18065	Intron 6	G	56:0	57:1	0	0.017	0.009
89	LP18086/rs269	18086	Intron 6	G	13:77	8:78	0.144	0.093	0.119
90	LP18095/rs270	18095	Intron 6	A	74:12	65:23	0.14	0.261	0.201
91	LP18121/rs271	18121	Intron 6	A	12:80	8:84	0.130	0.087	0.109
92	LP18297/rs144578061	18297	Intron 6	C	1:93	0:96	0.011	0	0.005
93	LP18395_18396/rs58935878	18395	Intron 6	ins1	13:81	10:86	0.138	0.104	0.121
94	LP18462	18462	Intron 6	G	90:0	95:1	0	0.01	0.005
95	LP18621/rs187904902	18621	Intron 6	T	1:93	0:96	0.011	0	0.005
96	LP18708/rs276	18708	Intron 6	C	2:92	2:92	0.021	0.021	0.021
97	LP18822/rs277	18822	Intron 6	C	77:17	69:27	0.181	0.281	0.232
98	LP18942/rs278	18942	Intron 6	A	78:16	72:24	0.17	0.25	0.211
99	LP19442/rs281	19442	Intron 6	T	73:19	65:25	0.207	0.278	0.242
100	LP19445/rs282	19445	Intron 6	G	12:78	12:84	0.133	0.125	0.129
101	LP19517/rs283	19517	Intron 6	T	15:75	15:81	0.167	0.156	0.161
102	LP19608/rs285	19608	Intron 6	T	40:50	34:58	0.444	0.37	0.407
103	LP19675/rs286	19675	Intron 6	T	10:80	1:93	0.111	0.011	0.06
104	LP19815	19815	Intron 6	A	1:93	0:96	0.011	0	0.005
105	LP19975/rs287	19975	Intron 6	G	22:68	10:86	0.244	0.104	0.172
106	LP20038/rs289	20038	Intron 6	C	19:67	10:86	0.221	0.104	0.159
107	LP20080	20080	Intron 6	T	1:89	0:96	0.011	0	0.005
108	LP20271/rs291	20271	Intron 6	C	22:72	9:87	0.234	0.094	0.163
109	LP20363/rs74746426	20363	Intron 6	T	90:4	90:6	0.043	0.062	0.053
110	LP20505_20506/rs33936024	20505	Intron 6	ins1	22:72	9:87	0.234	0.094	0.163
111	LP20544/rs294	20544	Intron 6	C	8:84	7:89	0.087	0.073	0.08
112	LP20657/rs295	20657	Intron 6	C	22:72	9:87	0.234	0.094	0.163
113	LP20663/rs296	20663	Intron 6	A	94:0	95:1	0	0.01	0.005
114	LP20790/rs297	20790	Intron 6	C	22:72	9:87	0.234	0.094	0.163
115	LP21125_21128	21125	Intron 6	del4	94:0	93:1	0	0.011	0.005
116	LP21353/rs301	21353	Intron 7	C	21:73	11:81	0.223	0.12	0.172
117	LP21780/rs304	21780	Intron 7	G	15:71	3:85	0.174	0.034	0.103
118	LP21820/rs305	21820	Intron 7	G	15:69	3:79	0.179	0.037	0.108
119	LP21895/rs308	21895	Intron 7	G	1:75	1:87	0.013	0.011	0.012
120	LP21965/rs310	21965	Intron 7	T	1:75	0:88	0.013	0	0.006
121	LP22044_22047/rs311	22044	Intron 7	del4	8:84	6:88	0.087	0.064	0.075
122	LP22416/rs312	22416	Intron 7	C	7:81	6:86	0.080	0.065	0.072
123	LP22461/rs314	22461	Intron 7	A	21:65	11:81	0.244	0.12	0.18
124	LP22514/rs315	22514	Intron 7	C	84:0	90:2	0	0.022	0.011
125	LP22855/rs316	22855	Exon 8	A	87:7	88:8	0.074	0.083	0.079
126	LP23190_23191/rs113064376	23190	Intron 8	del4	49:41	39:47	0.456	0.453	0.5
127	LP23192/rs117026536	23192	Intron 8	T	11:79	1:85	0.122	0.012	0.068

Table A1.2. Continued

#	*LPL* variant/ RefSNP ID	Position^a	Location	Minor allele	High HDL-C /Low TG group allele counts	Low HDL-C/High TG group allele counts	MAF in High HDL-C/Low TG group	MAF in Low HDL-C/High TG group	MAF in the total sample
128	LP23388/rs318	23388	Intron 8	G	2:80	1:85	0.024	0.012	0.018
129	LP23395/rs319	23395	Intron 8	C	56:22	60:26	0.282	0.302	0.293
130	LP23496/rs320	23496	Intron 8	G	20:62	11:75	0.244	0.128	0.185
131	LP23573/rs77243948	23573	Intron 8	C	2:82	1:87	0.024	0.011	0.017
132	LP23636/rs322	23636	Intron 8	C	20:68	11:83	0.227	0.117	0.17
133	LP23747/rs325	23747	Intron 8	C	9:79	3:87	0.102	0.033	0.067
134	LP23858/rs326	23858	Intron 8	G	25:65	12:78	0.278	0.133	0.206
135	LP23955/rs327	23955	Intron 8	G	24:68	11:79	0.261	0.122	0.192
136	**LP24143/rs328(Ser447X)**	24143	Exon9	G	96:0	93:1	0	0.01	0.005
137	LP24505/rs329	24505	Intron 9	G	2:92	1:93	0.021	0.011	0.016
138	LP24573	24573	Intron 9	C	94:0	93:1	0	0.011	0.005
139	LP24815/rs330	24815	Intron 9	A	12:82	9:87	0.128	0.094	0.111
140	LP24824/rs331	24824	Intron 9	A	12:66	9:85	0.154	0.096	0.122
141	LP24852/rs12679834	24852	Intron 9	C	13:81	2:92	0.138	0.021	0.08
142	LP24899/rs76423146	24899	Intron 9	T	2:92	1:95	0.021	0.01	0.016
143	LP25005/rs184536204	25005	Intron 9	G	1:93	0:96	0.011	0	0.005
144	LP25049/rs78031480	25049	Intron 9	A	90:4	88:8	0.043	0.083	0.063
145	LP25320	25320	Intron 9	T	1:93	0:96	0.011	0	0.005
146	LP25335/rs117199990	25335	Intron 9	T	13:81	2:94	0.138	0.021	0.079
147	LP25352/rs145391587	25352	Intron 9	C	13:81	2:94	0.138	0.021	0.079
148	LP25844/rs75278536	25844	Intron 9	G	12:80	2:94	0.130	0.021	0.074
149	LP26201/rs77069344	26201	Intron 9	G	12:76	2:92	0.136	0.021	0.077
150	LP26234/rs10099160	26234	Intron 9	G	69:23	66:30	0.25	0.312	0.282
151	LP27000/rs112324447	27000	Intron 9	T	4:86	1:83	0.044	0.012	0.029
152	LP27160/rs117910839	27160	Intron 9	A	5:81	0:96	0.058	0	0.027
153	LP27229/rs11570891	27229	Intron 9	T	13:77	2:92	0.144	0.021	0.082
154	LP27249/rs4922115	27249	3' UTR-exon10	A	8:84	8:88	0.087	0.083	0.085
155	LP27611/rs3289	27611	3' UTR-exon10	C	2:90	1:95	0.022	0.01	0.016
156	LP27688/rs191212278	27688	3' UTR-exon10	T	92:0	95:1	0	0.01	0.005
157	LP28036/rs11570892	28036	3' UTR-exon10	G	11:83	8:86	0.117	0.085	0.101
158	LP28067/rs3208305	28067	3' UTR-exon10	T	25:65	12:80	0.278	0.13	0.203
159	LP28093/rs1803924	28093	3' UTR-exon10	T	13:79	2:88	0.141	0.022	0.082
160	LP28382/rs1059507	28382	3' UTR-exon10	T	11:81	9:81	0.120	0.1	0.11
161	LP28407/rs150252331	28407	3' UTR-exon10	A	92:2	93:3	0.021	0.031	0.026
162	LP28464/rs3735964	28464	3' UTR-exon10	A	13:81	2:94	0.138	0.021	0.079
163	LP28490/rs3200218	28490	3' UTR-exon10	G	70:24	67:29	0.255	0.302	0.279
164	LP28524	28524	3' UTR-exon10	T	94:0	95:1	0	0.01	0.005
165	LP28911/rs13702	28911	3' UTR-exon10	C	26:68	12:84	0.277	0.125	0.2
166	LP28982/rs1059611	28982	3' UTR-exon10	C	13:81	2:94	0.138	0.021	0.079
167	LP29046_29047/rs10645926	29046	3' UTR-exon10	Ins2	13:81	2:94	0.138	0.021	0.079
168	LP29086/rs15285	29086	3' UTR-exon10	T	26:68	12:84	0.277	0.125	0.2
169	LP29088/rs3866471	29088	3' UTR-exon10	A	11:83	9:87	0.117	0.094	0.105
170	LP29287/rs3916027	29287	3' flanking	A	24:70	11:85	0.255	0.115	0.184
171	LP29315/rs9644636	29315	3' flanking	G	32:60	31:63	0.348	0.33	0.339
172	LP29474/rs113831503	29474	3' flanking	T	4:90	1:95	0.043	0.01	0.026
173	LP29487/rs4921683	29487	3' flanking	A	11:83	9:87	0.117	0.094	0.105
174	LP29547/rs4921684	29547	3' flanking	T	11:83	9:87	0.117	0.094	0.105
175	LP29557_29558	29557	3' flanking	ins1	94:0	95:1	0	0.01	0.005
176	LP29716/rs80085105	29716	3' flanking	C	4:90	1:95	0.043	0.01	0.026

MAF: minor allele frequency; ^{a}Positions in the reference sequence (NC_00008.10); Bold: Variant results in amino acid change.

Table A1.3. The genotype call rates and features of the 65 SNPs genotyped in the entire NHW sample

LPL variant	RefSNP ID	Position[a]	ObsHET	PredHET	HWpval	%Geno	MAF	Alleles	Selection criteria[b]
LP1088	rs80351041	1088	0.02	0.02	1.00	96.6	0.01	G:T	2
LP1130	Novel	1130	0.006	0.006	1.00	99.4	0.003	G:C	2
LP2335	rs3779787	2335	0.269	0.26	0.52	99.5	0.154	G:T	1
LP3964	rs17410577	3964	0.322	0.328	0.73	98.6	0.207	G:C	1
LP4060	rs1534649	4060	0.509	0.495	0.57	98.9	0.452	G:T	1
LP4424	rs13266204	4424	0.33	0.336	0.72	99.2	0.213	A:G	1
LP4948	rs6997330	4948	0.037	0.036	1.00	100	0.018	G:C	3
LP5949	rs112127208	5949	0.286	0.272	0.26	99.2	0.162	T:G	1
LP6821	rs10104051	6821	0.503	0.493	0.69	98.7	0.442	C:T	1
LP7503	rs6999612	7503	0.037	0.04	0.44	99.4	0.02	T:C	3
LP7512	rs3779788	7512	0.264	0.252	0.33	99.7	0.148	C:T	3
LP8221	rs7000460	8221	0.037	0.036	1.00	99.4	0.019	A:C	4
LP10127	rs1801177	10127	0.037	0.036	1.00	99.4	0.019	G:A	2
LP10912	rs149477831	10912	0.021	0.021	1.00	99.7	0.01	A:G	3
LP10987	rs74377536	10987	0.204	0.21	0.55	91.2	0.12	C:A	1
LP11050	rs7016529	11050	0.035	0.035	1.00	99.4	0.018	T:C	3
LP11090	rs8176337	11090	0.37	0.366	0.94	88	0.241	C:G	1
LP11888_11889ins1	rs149017698	11888	0.037	0.039	0.44	99.5	0.02	W:I	3
LP13003	rs80181352	13003	0.134	0.139	0.51	99.5	0.075	G:T	1
LP13639	rs78326602	13639	0.014	0.014	1.00	99.5	0.007	G:A	3
LP13854	rs1121923	13854	0.067	0.065	1.00	97.9	0.034	C:T	2
LP14114	rs73667472	14114	0.133	0.144	0.14	99.8	0.078	A:G	1
LP15206	rs343	15206	0.173	0.195	0.04	77.7	0.109	C:A	2
LP15245	rs248	15245	0.127	0.125	0.94	99.5	0.067	G:A	2
LP15425	rs249	15425	0.128	0.139	0.10	99	0.075	T:C	1
LP15836	rs253	15836	0.51	0.495	0.54	100	0.452	C:T	1
LP16316	rs254	16316	0.247	0.245	1.00	97.4	0.143	C:G	1
LP16442	rs74382962	16442	0.005	0.005	1.00	99.5	0.002	G:C	4
LP17599	rs264	17599	0.25	0.245	0.79	97.6	0.143	G:A	1
LP17948	rs268	17948	0.031	0.03	1.00	99.4	0.015	A:G	2
LP18086	rs269	18086	0.295	0.287	0.58	98.7	0.174	T:G	1
LP18095	rs270	18095	0.281	0.284	0.89	99.2	0.171	C:A	1
LP18822	rs277	18822	0.316	0.315	1.00	97.3	0.196	T:C	1
LP19445	rs282	19445	0.246	0.234	0.32	99.8	0.136	G:C	1
LP19517	rs283	19517	0.307	0.32	0.35	99.2	0.2	C:T	1
LP19608	rs285	19608	0.494	0.499	0.86	99.5	0.479	C:T	1
LP19675	rs286	19675	0.17	0.171	0.97	99.8	0.095	T:A	1
LP20363	rs296	20363	0.092	0.094	0.88	99.4	0.049	A:T	3
LP20544	rs294	20544	0.213	0.208	0.69	99.8	0.118	A:G	1
LP20657	rs295	20657	0.348	0.346	1.00	98.6	0.223	A:C	1
LP22044_22047del4	rs311	22044	0.102	0.1	0.97	99	0.053	W:D	1
LP22416	rs312	22416	0.204	0.201	0.92	99.2	0.113	G:C	1
LP22461	rs314	22461	0.376	0.387	0.56	90.7	0.262	G:A	1
LP22514	rs315	22514	0.01	0.01	1.00	99.5	0.005	T:C	3
LP22855	rs316	22855	0.203	0.2	0.96	98.1	0.113	C:A	2
LP23192	rs117026536	23192	0.181	0.185	0.66	99.2	0.103	G:T	1
LP23496	rs320	23496	0.363	0.383	0.23	97.9	0.259	T:G	3
LP23955	rs327	23955	0.376	0.39	0.41	99.4	0.265	T:G	1
LP24143	rs328	24143	0.185	0.184	1.00	99.4	0.102	C:G	2
LP25049	rs78031480	25049	0.09	0.089	1.00	97.8	0.047	G:A	1
LP26234	rs10099160	26234	0.4	0.384	0.37	99.7	0.26	T:G	1
LP27000	rs11232447	27000	0.056	0.058	0.85	100	0.03	C:T	3
LP27160	rs117910839	27160	0.048	0.053	0.14	99.5	0.027	T:A	3
LP27229	rs11570891	27229	0.187	0.191	0.80	99.2	0.107	C:T	1
LP27249	rs4922115	27249	0.242	0.251	0.46	98.7	0.147	G:A	2
LP27611	rs3289	27611	0.051	0.053	0.74	100	0.027	T:C	2
LP27688	rs191212278	27688	0.008	0.008	1.00	99.5	0.004	C:T	2
LP28407	rs150252331	28407	0.035	0.035	1.00	100	0.018	G:T	2
LP28524	Novel	28524	0.002	0.002	1.00	99.5	0.001	C:T	2
LP28911	rs13702	28911	0.382	0.396	0.43	98.9	0.272	T:C	1
LP28982	rs1059611	28982	0.188	0.191	0.82	99.5	0.107	T:C	1
LP29315	rs9644636	29315	0.416	0.411	0.86	99	0.289	T:G	1
LP29474	rs113831503	29474	0.071	0.071	1.00	99.4	0.037	C:T	3
LP29547	rs4921684	29547	0.247	0.254	0.56	99.4	0.149	C:T	1
LP29716	rs80085105	29716	0.027	0.027	1.00	99.4	0.014	T:C	3

[a]Positions in the reference sequence (NC_00008.10). [b]Selection criteria: (1) common tagSNPs (MAF ≥ 0.05, $r^2 \geq 0.9$) (2) all variants located in exons or intron-exon junctions; (3) all uncommon or rare variants (MAF < 0.05) present in two or more individuals included in the sequencing; (4) suspicious rare variants identified in the sequencing. W: Allele in the reference sequence ; D: Deleted base/bases; I: Inserted base/bases

Table A1.4. Association results of HDL-C levels with 64 *LPL* SNPs in NHWs (n=623)

LPL variant	RefSNP ID	Position in Ref NC_00008.10	Chr. Position (hg19)	Genotypes (GTs)	GT Counts	MAF	Adjusted Mean of plasma HDL-C	Standard Deviation	Beta	*P*
LP1088	rs80351041	1088	19796669	GG/GT	588/12	0.010	50.6/53.89	14.15/13.03	0.059	0.285
LP1130	Novel	1130	19796711	GC/GG	3/614	0.002	49.17/50.62	18.5/14.06	-0.029	0.786
LP2335	rs3779787	2335	19797916	GG/GT/TT	439/167/12	0.154	49.94/52.34/48.21	14.18/13.71/11.03	0.029	0.056
LP3964	rs17410577	3964	19799545	CC/GC/GG	28/198/386	0.207	47.05/50.15/51.16	14.07/13.57/14.04	-0.024	0.061
LP4060	rs1534649	4060	19799641	GG/TG/TT	179/313/122	0.453	50.88/50.79/49.91	13.92/14.43/12.24	-0.005	0.613
LP4424	rs13266204	4424	19800005	AA/AG/GG	382/204/30	0.214	50.97/50.25/46.11	14.05/13.76/15.2	-0.027	0.033
LP4948	rs6997330	4948	19800529	CG/GG	23/598	0.018	47.83/50.69	17.55/13.9	-0.057	0.149
LP5949	rs112127208	5949	19801530	GG/TG/TT	12/177/427	0.163	48.16/51.78/50.09	11.12/13.79/14.22	0.019	0.196
LP6821	rs10104051	6821	19802402	CC/TC/TT	187/309/117	0.442	50.75/50.8/50.18	14.12/14.32/13.37	-0.003	0.760
LP7503	rs6999612	7503	19803084	CC/CT/TT	1/23/593	0.020	52.23/47.11/50.72	NA/17.55/13.92	-0.055	0.132
LP7512	rs3779788	7512	19803093	CC/TC/TT	445/164/10	0.148	50.03/52.11/48.04	14.18/13.77/11.14	0.026	0.096
LP8221	rs7000460	8221	19803802	AA/CA	594/23	0.019	50.72/47.84	13.94/17.55	-0.058	0.148
LP10127	rs1801177	10127	19805708	AG/GG	23/594	0.019	47.84/50.72	17.55/13.94	-0.058	0.148
LP10912	rs149477831	10912	19806493	AA/AG	606/13	0.010	50.68/45.3	14.1/12.09	-0.080	0.125
LP10987	rs74377536	10987	19806568	AA/CA/CC	9/116/441	0.120	46.31/51.49/50.46	11.41/16.24/13.8	-0.004	0.833
LP11050	rs7016529	11050	19806631	CT/TT	22/595	0.018	47.5/50.72	17.76/13.92	-0.064	0.117
LP11090	rs8176337	11090	19806671	CC/CG/GG	313/202/31	0.242	50.16/52.23/47.59	14.63/14.34/11.65	0.012	0.387
LP11888_11889ins1	rs149017698	11888	19807469	II/WI/WW	1/23/594	0.020	43.93/48.2/50.72	NA/17.4/13.94	-0.050	0.170
LP13003	rs80181352	13003	19808584	GG/GT/TT	531/82/5	0.075	50.47/50.56/52.9	14.18/12.73/19.35	0.009	0.668
LP13639	rs78326602	13639	19809220	GA/GG	9/609	0.007	52.53/50.47	15.6/13.99	0.028	0.652
LP13854	rs1121923	13854	19809435	CC/TC	567/41	0.034	50.56/50.83	14.02/14.26	0.008	0.781
LP14114	rs73667472	14114	19809695	AA/AG/GG	530/83/7	0.078	50.84/49.46/45.78	14.1/13.91/11.16	-0.026	0.170
LP15245	rs248	15245	19810826	AA/GA/GG	2/78/538	0.067	67.05/50.45/50.53	16.26/12.17/14.21	0.019	0.375
LP15425	rs249	15425	19811006	CC/TC/TT	7/79/529	0.075	45.82/49.76/50.84	11.16/14.17/14.07	-0.023	0.232
LP15836	rs253	15836	19811417	CC/CT/TT	181/317/123	0.453	51.25/50.19/50.6	14.09/14.25/13.43	-0.005	0.623
LP16316	rs254	16316	19811897	CC/CG/GG	443/150/12	0.143	50.31/51.41/47.1	14.17/13.84/9.81	0.009	0.569
LP16442	rs74382962	16442	19812023	CG/GG	3/615	0.002	52.43/50.6	21.83/14.04	0.012	0.915
LP17599	rs264	17599	19813180	AA/GA/GG	11/152/443	0.143	48.53/51.32/50.34	11.18/13.95/14.28	0.011	0.492
LP17948	rs268	17948	19813529	AA/AG	598/19	0.015	50.61/50.33	14.03/15.7	-0.015	0.735
LP18086	rs269	18086	19813667	GG/GT/TT	16/182/415	0.174	48.8/51.72/50.11	10.64/14.37/14.09	0.017	0.239
LP18095	rs270	18095	19813676	AA/CA/CC	19/174/423	0.172	50.29/48.85/51.35	14.11/13.95/13.99	-0.031	0.025
LP18822	rs277	18822	19814403	CC/CT/TT	23/192/389	0.196	50.83/49.53/51.13	14.08/14.37/13.89	-0.020	0.135
LP19445	rs282	19445	19815026	CC/GC/GG	8/151/461	0.135	58.09/51.58/50.07	21.56/13.57/14.01	0.032	0.042
LP19517	rs283	19517	19815098	CC/CT/TT	397/190/29	0.201	50.74/50.46/48.68	13.96/14.55/11.81	-0.009	0.497
LP19608	rs285	19608	19815189	CC/CT/TT	168/307/143	0.480	50.49/50.2/51.19	14.07/14.08/13.76	0.007	0.493
LP19675	rs286	19675	19815256	AA/TA/TT	6/105/509	0.095	53.66/53.55/49.92	17.33/14.78/13.74	0.051	0.005
LP20363	rs296	20363	19815944	AA/TA/TT	558/57/2	0.049	50.74/49.93/37.56	14.03/14.41/12.73	-0.028	0.260
LP20544	rs294	20544	19816125	AA/AG/GG	481/132/7	0.118	50.35/50.72/57.5	14.23/12.93/12.88	0.021	0.205
LP20657	rs295	20657	19816238	AA/CA/CC	369/214/29	0.223	49.52/52/53.57	13.96/13.76/13.93	0.039	0.002
LP22044_22047del4	rs311	22044	19817625	DD/WD/WW	1/62/552	0.052	47.42/53.38/50.35	NA/15.25/13.9	0.040	0.094
LP22416	rs312	22416	19817997	CC/GC/GG	7/125/484	0.113	57.46/50.86/50.45	12.88/12.98/14.36	0.022	0.197
LP22461	rs314	22461	19818042	AA/GA/GG	41/213/309	0.263	52.48/51.41/49.94	14.4/14.09/14.28	0.026	0.043
LP22514	rs315	22514	19818095	CT/TT	6/612	0.005	45.91/50.58	14.78/14.02	-0.106	0.167
LP22855	rs316	22855	19818436	AA/CA/CC	7/123/479	0.113	57.58/51.07/50.51	12.88/12.9/14.38	0.024	0.155
LP23192	rs117026536	23192	19818773	GG/GT/TT	497/111/8	0.104	50.04/52.88/49.83	13.8/14.74/14.03	0.034	0.048
LP23496	rs320	23496	19819077	GG/GT/TT	46/221/341	0.258	51.97/51.56/49.74	13.77/13.72/14.37	0.027	0.026
LP23955	rs327	23955	19819536	GG/TG/TT	47/232/338	0.265	52.41/51.15/49.8	13.89/13.39/14.43	0.025	0.032
LP24143	rs328	24143	19819724	CC/GC/GG	497/114/6	0.103	50.05/52.98/50.36	13.8/14.77/16.17	0.038	0.032
LP25049	rs78031480	25049	19820630	AA/AG/GG	1/55/551	0.047	48.51/48.38/50.8	NA/13.16/14.17	-0.032	0.208
LP26234	rs10099160	26234	19821815	GG/GT/TT	37/248/334	0.260	50.72/49.43/51.39	15.08/13.96/13.99	-0.021	0.094
LP27000	rs11232447	27000	19822581	CC/CT/TT	586/34/1	0.029	50.66/48.38/78.46	14.14/11.86/NA	-0.003	0.927
LP27160	rs117910839	27160	19822741	AA/TA/TT	2/29/587	0.027	60.11/51.67/50.41	31.11/14.62/13.93	0.029	0.360
LP27229	rs11570891	27229	19822810	CC/TC/TT	493/115/8	0.107	50.02/52.88/52.79	13.82/14.51/18.58	0.039	0.024
LP27249	rs4922115	27249	19822830	AA/AG/GG	16/147/450	0.146	57.92/49.61/50.68	13.72/12.14/14.56	0.015	0.304
LP27611	rs3289	27611	19823192	CC/TC/TT	1/32/588	0.027	29.93/50.75/50.61	NA/14.06/14.05	-0.011	0.734
LP27688	rs191212278	27688	19823269	CC/TC	613/5	0.004	50.62/50.15	14.05/15.87	-0.011	0.891
LP28407	rs150252331	28407	19823988	GG/GT	599/22	0.018	50.69/47.69	14.02/14.79	-0.049	0.225
LP28524	Novel	28524	19824105	CC/CT	617/1	0.001	50.64/33.35	14.06/NA	-0.287	0.125
LP28911	rs13702	28911	19824492	CC/CT/TT	49/235/330	0.272	52.79/51.67/49.6	13.44/14.03/14.06	0.032	0.006
LP28982	rs1059611	28982	19824563	CC/TC/TT	8/116/494	0.107	52.82/52.75/50.03	18.58/14.5/13.8	0.037	0.030
LP29315	rs9644636	29315	19824896	GG/GT/TT	50/255/310	0.288	50.25/50.8/50.55	14.54/14.32/13.77	-0.002	0.846
LP29474	rs113831503	29474	19825055	CC/CT/TT	573/43/1	0.036	50.67/47.88/78.29	14.18/11.43/NA	-0.013	0.650
LP29547	rs4921684	29547	19825128	CC/CT/TT	450/151/16	0.149	50.7/49.57/57.85	14.58/12.35/13.72	0.013	0.369
LP29716	rs80085105	29716	19825297	TC/TT	17/600	0.014	53.63/50.44	20.76/13.78	0.027	0.563

W: Allele in the reference sequence ; D: Deleted base/bases; I: Inserted base/bases

Table A1.5. Association results of TG levels with 64 *LPL* SNPs in NHWs (n=623)

LPL Variant	RefSNP ID	Position in Ref NC_000 08.10	Chr. Position (hg19)	Genotypes (GTs)	GT Counts	MAF	Adjusted Mean of plasma TG	Standard Deviation	Beta	*P*
LP1088	rs80351041	1088	19796669	GG/GT	586/12	0.010	137.88/131.03	66.32/47.57	-0.010	0.935
LP1130	Novel	1130	19796711	GC/GG	3/612	0.002	247.29/137.34	114.64/65.07	0.556	0.017
LP2335	rs3779787	2335	19797916	GG/GT/TT	439/165/12	0.154	140.03/133.79/134.48	66.89/63.34/54.08	-0.034	0.300
LP3964	rs17410577	3964	19799545	CC/GC/GG	28/198/386	0.207	149.37/136.58/137.33	65.53/59.1/68.45	0.028	0.312
LP4060	rs1534649	4060	19799641	GG/TG/TT	180/313/121	0.453	142.45/136.83/133.02	70/64.78/61.15	-0.033	0.162
LP4424	rs13266204	4424	19800005	AA/AG/GG	382/204/28	0.214	138.07/136.7/150.67	69.1/58.61/69.14	0.028	0.328
LP4948	rs6997330	4948	19800529	CG/GG	23/596	0.018	151.19/137.42	73.73/65.49	0.061	0.475
LP5949	rs112127208	5949	19801530	GG/TG/TT	12/174/428	0.163	143.78/133.57/139.76	68.37/62.07/67.18	-0.025	0.442
LP6821	rs10104051	6821	19802402	CC/TC/TT	188/308/116	0.442	143.45/136.7/132.79	70.45/63.55/63.65	-0.040	0.091
LP7503	rs6999612	7503	19803084	CC/CT/TT	1/23/591	0.020	92.69/156.81/137.35	NA/74.12/65.47	0.060	0.450
LP7512	rs3779788	7512	19803093	CC/TC/TT	445/162/10	0.148	139.99/133.19/131.93	66.91/62.96/58.36	-0.040	0.231
LP8221	rs7000460	8221	19803802	AA/CA	592/23	0.019	137.36/151.21	65.39/73.73	0.062	0.472
LP10127	rs1801177	10127	19805708	AG/GG	23/592	0.019	151.21/137.36	73.73/65.39	0.062	0.472
LP10912	rs149477831	10912	19806493	AA/AG	604/13	0.010	137.28/143.43	65.55/48.39	0.091	0.417
LP10987	rs74377536	10987	19806568	AA/CA/CC	10/116/438	0.120	156.11/134.91/139.47	62.31/67.59/66.73	-0.002	0.952
LP11050	rs7016529	11050	19806631	CT/TT	22/593	0.018	153.06/137.35	73.35/65.41	0.076	0.384
LP11090	rs8176337	11090	19806671	CC/CG/GG	312/202/30	0.242	142.79/131.64/134.54	67.56/65.05/69.83	-0.065	0.027
LP11888_11889ins1	rs149017698	11888	19807469	II/WI/WW	1/23/592	0.020	204.03/146.38/137.71	NA/72.19/65.56	0.057	0.474
LP13003	rs80181352	13003	19808584	GG/GT/TT	529/83/4	0.075	140.4/124.73/86.8	65.32/67.51/61.33	-0.148	6.10^{-4}
LP13639	rs78326602	13639	19809220	GA/GG	9/607	0.007	129.71/138.07	41.84/66.12	-0.021	0.875
LP13854	rs1121923	13854	19809435	CC/TC	565/41	0.034	137.8/142.14	65.64/68.99	0.018	0.780
LP14114	rs73667472	14114	19809695	AA/AG/GG	530/81/7	0.078	137.23/141.69/157.61	65.8/66.55/58.57	0.043	0.298
LP15245	rs248	15245	19810826	AA/GA/GG	2/79/536	0.067	59.35/129.61/139.56	6.36/71.25/64.89	-0.124	0.007
LP15425	rs249	15425	19811006	CC/TC/TT	7/77/529	0.075	157.45/140.73/137.02	58.57/65.98/66.07	0.040	0.341
LP15836	rs253	15836	19811417	CC/CT/TT	182/316/121	0.453	136.84/138.52/138.04	66.29/67.76/59.74	0.005	0.815
LP16316	rs254	16316	19811897	CC/CG/GG	444/147/12	0.143	139.61/133.39/137.12	67.22/61.97/56.46	-0.027	0.421
LP16442	rs74382962	16442	19812023	CG/GG	3/613	0.002	116.81/137.97	59.54/65.68	-0.111	0.635
LP17599	rs264	17599	19813180	AA/GA/GG	11/149/444	0.143	135.53/135.91/139.94	55.77/63.3/67.26	-0.017	0.619
LP17948	rs268	17948	19813529	AA/AG	596/19	0.015	136.7/163.33	64.41/78.11	0.144	0.125
LP18086	rs269	18086	19813667	GG/GT/TT	16/179/416	0.174	132.58/135.07/139.54	52.34/62.5/67.61	-0.021	0.490
LP18095	rs270	18095	19813676	AA/CA/CC	19/172/423	0.172	133.93/146.22/135.08	50.79/65.7/66.47	0.059	0.053
LP18822	rs277	18822	19814403	CC/CT/TT	23/190/389	0.196	140.41/145.04/134.47	47.83/68.5/65.15	0.061	0.036
LP19445	rs282	19445	19815026	CC/GC/GG	8/151/459	0.135	138.24/128.28/141.24	129.26/62/65.34	-0.095	0.006
LP19517	rs283	19517	19815098	CC/CT/TT	397/188/29	0.201	135.33/144.28/135.35	67.57/64.3/51.44	0.046	0.104
LP19608	rs285	19608	19815189	CC/CT/TT	169/305/142	0.480	140.56/139.46/132.69	71.13/65.5/58.08	-0.021	0.364
LP19675	rs286	19675	19815256	AA/TA/TT	6/105/507	0.095	100.36/130.1/140.13	38.32/62.2/66.51	-0.090	0.021
LP20363	rs296	20363	19815944	AA/TA/TT	556/57/2	0.049	137.71/141.08/126.39	66.61/56.2/23.33	0.044	0.399
LP20544	rs294	20544	19816125	AA/AG/GG	480/131/7	0.118	140.91/130.55/80.5	66.93/60.9/26.86	-0.102	0.005
LP20657	rs295	20657	19816238	AA/CA/CC	368/213/30	0.223	142.94/133.96/107.17	67.76/62.7/46.97	-0.093	8.10^{-4}
LP22044_22047del4	rs311	22044	19817625	DD/WD/WW	1/62/550	0.052	276.39/137.25/136.98	NA/68.06/64.43	0.017	0.738
LP22416	rs312	22416	19817997	CC/GC/GG	7/124/483	0.113	80.33/131.7/140.37	26.86/61.21/66.8	-0.095	0.010
LP22461	rs314	22461	19818042	AA/GA/GG	42/212/308	0.263	121.17/137.3/143.03	59.03/64.63/68.49	-0.066	0.015
LP22514	rs315	22514	19818095	CT/TT	5/611	0.005	132.79/138.19	79.07/65.76	-0.061	0.735
LP22855	rs316	22855	19818436	AA/CA/CC	7/123/478	0.113	81.25/132.13/139.77	26.86/60.95/66.4	-0.087	0.017
LP23192	rs117026536	23192	19818773	GG/GT/TT	495/111/8	0.104	139.51/132.92/113.64	66.36/63.95/39.66	-0.060	0.112
LP23496	rs320	23496	19819077	GG/GT/TT	47/220/340	0.258	128.56/131.65/142.61	63.38/64.2/65.81	-0.068	0.008
LP23955	rs327	23955	19819536	GG/TG/TT	48/230/337	0.265	127.59/132.53/142.84	63.11/64.34/65.92	-0.069	0.007
LP24143	rs328	24143	19819724	CC/GC/GG	495/114/6	0.103	139.45/132.99/102.46	66.36/63.46/28.02	-0.065	0.088
LP25049	rs78031480	25049	19820630	AA/AG/GG	1/55/549	0.047	119.77/134.87/138.41	NA/66.25/65.88	-0.022	0.694
LP26234	rs10099160	26234	19821815	GG/GT/TT	37/246/334	0.260	142.43/139.3/136.26	55.51/67.5/65.82	0.027	0.318
LP27000	rs11232447	27000	19822581	CC/CT/TT	584/34/1	0.029	138.13/135.73/99.63	65.97/63.63/NA	-0.009	0.894
LP27160	rs117910839	27160	19822741	AA/TA/TT	2/30/584	0.027	109.38/126.61/138.62	72.12/53.8/66.34	-0.083	0.218
LP27229	rs11570891	27229	19822810	CC/TC/TT	491/115/8	0.107	139.3/134.79/104.16	66.38/63.62/36.6	-0.058	0.119
LP27249	rs4922115	27249	19822830	AA/AG/GG	16/147/449	0.146	108.82/134/140.58	46.51/64.66/66.53	-0.066	0.039
LP27611	rs3289	27611	19823192	CC/TC/TT	1/32/586	0.027	250.16/149.56/137.11	NA/70.66/65.45	0.103	0.136
LP27688	rs191212278	27688	19823269	CC/TC	611/5	0.004	138/122.3	65.79/28.33	-0.058	0.748
LP28407	rs150252331	28407	19823988	GG/GT	597/22	0.018	137.89/139.16	65.31/78.22	-0.020	0.820
LP28524	Novel	28524	19824105	CC/CT	615/1	0.001	137.61/301.35	65.37/NA	0.864	0.031
LP28911	rs13702	28911	19824492	CC/CT/TT	50/234/329	0.272	121.76/133.5/143.62	53.82/64.65/67.53	-0.074	0.003
LP28982	rs1059611	28982	19824563	CC/TC/TT	8/116/492	0.107	104.24/136.09/139.14	36.6/64.53/66.42	-0.050	0.176
LP29315	rs9644636	29315	19824896	GG/GT/TT	50/254/310	0.288	144.58/139.16/135.72	59.83/69.44/63.52	0.031	0.218
LP29474	rs113831503	29474	19825055	CC/CT/TT	571/43/1	0.036	137.93/139.7/99.4	65.74/68.63/NA	0.005	0.939
LP29547	rs4921684	29547	19825128	CC/CT/TT	449/150/16	0.149	140.4/133.61/108.73	66.32/64.72/46.51	-0.068	0.032
LP29716	rs80085105	29716	19825297	TC/TT	17/598	0.014	134.1/138.03	66/65.9	-0.032	0.749

W: Allele in the reference sequence ; D: Deleted base/bases; I: Inserted base/bases

Table A1.6. Association results of LDL-C levels with 64 *LPL* SNPs in NHWs (n=623)

LPL **Variant**	**RefSNP ID**	**Position in Ref NC_00008.10**	**Chr. Position (hg19)**	**Genotypes (GTs)**	**GT Counts**	**MAF**	**Adjusted Mean of plasma LDL-C**	**Standard Deviation**	**Beta**	***P***
LP1088	rs80351041	1088	19796669	GG/GT	590/12	0.010	137.03/131.79	41.06/32.97	-5.248	0.654
LP1130	Novel	1130	19796711	GC/GG	3/616	0.002	148.97/136.95	23.92/40.91	12.075	0.603
LP2335	rs3779787	2335	19797916	GG/GT/TT	441/167/12	0.154	137.6/134.37/151.22	40.31/41.78/48.56	-0.623	0.846
LP3964	rs17410577	3964	19799545	CC/GC/GG	28/198/388	0.207	142.25/140.39/135.68	33.81/39.99/40.65	4.110	0.135
LP4060	rs1534649	4060	19799641	GG/TG/TT	180/314/122	0.453	137.77/136.94/137.15	40.63/39.33/40.43	-0.366	0.872
LP4424	rs13266204	4424	19800005	AA/AG/GG	384/204/30	0.214	135.64/140.54/131.99	40.55/39.92/48.55	1.905	0.488
LP4948	rs6997330	4948	19800529	CG/GG	23/600	0.018	129.26/137.29	40.64/40.81	-8.075	0.342
LP5949	rs112127208	5949	19801530	GG/TG/TT	12/177/429	0.163	145.03/135.32/137.46	48.24/43.07/39.71	-0.647	0.838
LP6821	rs10104051	6821	19802402	CC/TC/TT	188/310/117	0.442	137.61/136.54/137.19	40.31/40.14/40.82	-0.319	0.889
LP7503	rs6999612	7503	19803084	CC/CT/TT	1/23/595	0.020	142.65/129.2/137.37	NA/40.7/40.86	-6.565	0.403
LP7512	rs3779788	7512	19803093	CC/TC/TT	447/164/10	0.148	137.7/134.07/144.25	40.12/41.09/50.83	-2.062	0.526
LP8221	rs7000460	8221	19803802	AA/CA	596/23	0.019	137.31/129.29	40.85/40.64	-8.061	0.344
LP10127	rs1801177	10127	19805708	AG/GG	23/596	0.019	129.29/137.31	40.64/40.85	-8.061	0.344
LP10912	rs149477831	10912	19806493	AA/AG	608/13	0.010	136.92/139.01	41.09/27.89	2.098	0.852
LP10987	rs74377536	10987	19806568	AA/CA/CC	10/116/442	0.120	140.61/141.09/136.23	38.14/41.84/40.87	4.101	0.256
LP11050	rs7016529	11050	19806631	CT/TT	22/597	0.018	129.81/137.23	41.07/40.82	-7.465	0.391
LP11090	rs8176337	11090	19806671	CC/CG/GG	314/203/31	0.242	139.54/135.9/130.62	40.95/42.02/45.14	-4.055	0.161
LP11888_11889ins1	rs149017698	11888	19807469	II/WI/WW	1/23/596	0.020	113.69/131.33/137.33	NA/40.8/40.89	-6.900	0.379
LP13003	rs80181352	13003	19808584	GG/GT/TT	532/83/5	0.075	137.6/135.07/103.2	40.88/39.06/59.36	-5.592	0.187
LP13639	rs78326602	13639	19809220	GA/GG	9/611	0.007	121.15/137.22	45.32/40.78	-16.143	0.230
LP13854	rs1121923	13854	19809435	CC/TC	569/41	0.034	137.03/137.54	40.97/41.21	0.508	0.938
LP14114	rs73667472	14114	19809695	AA/AG/GG	532/83/7	0.078	137.41/132.85/157.03	39.74/45.08/63.83	-0.690	0.866
LP15245	rs248	15245	19810826	AA/GA/GG	2/79/539	0.067	144.09/135.44/137.46	2.69/39.72/40.69	-1.495	0.742
LP15425	rs249	15425	19811006	CC/TC/TT	7/79/531	0.075	156.88/130.57/137.71	63.83/44.08/40	-2.493	0.549
LP15836	rs253	15836	19811417	CC/CT/TT	182/318/123	0.453	134.91/138.43/136.36	37.94/40.66/45.15	1.009	0.662
LP16316	rs254	16316	19811897	CC/CG/GG	445/150/12	0.143	137.41/135.23/147.35	39.59/43.22/53.92	-0.197	0.952
LP16442	rs74382962	16442	19812023	CG/GG	3/617	0.002	142.07/136.95	14.11/40.91	5.125	0.825
LP17599	rs264	17599	19813180	AA/GA/GG	11/152/445	0.143	151.02/134.47/137.56	53.52/43.03/39.61	-0.563	0.865
LP17948	rs268	17948	19813529	AA/AG	600/19	0.015	137/135.42	40.89/40.77	-1.608	0.864
LP18086	rs269	18086	19813667	GG/GT/TT	16/182/417	0.174	144.05/136.17/136.92	51.92/42.81/39.2	0.578	0.849
LP18095	rs270	18095	19813676	AA/CA/CC	19/174/425	0.172	152.97/138.93/135.55	45.26/40.14/40.37	5.277	0.076
LP18822	rs277	18822	19814403	CC/CT/TT	23/192/391	0.196	147.48/138.14/135.86	44.49/42.65/39.79	3.654	0.208
LP19445	rs282	19445	19815026	CC/GC/GG	8/152/462	0.135	104.4/134.7/138.31	43.97/40.4/40.73	-6.281	0.064
LP19517	rs283	19517	19815098	CC/CT/TT	399/190/29	0.201	137.91/135.15/137.1	41.3/39.84/44.1	-1.708	0.541
LP19608	rs285	19608	19815189	CC/CT/TT	169/307/144	0.480	138.92/136.49/135.01	42.23/38.83/42.31	-1.989	0.378
LP19675	rs286	19675	19815256	AA/TA/TT	6/106/510	0.095	136.61/136.19/137.23	37.56/39.09/41.26	-0.911	0.814
LP20363	rs296	20363	19815944	AA/TA/TT	560/57/2	0.049	136.36/144.35/107.68	40.9/39.91/24.32	5.146	0.324
LP20544	rs294	20544	19816125	AA/AG/GG	482/133/7	0.118	136.54/138.81/137.72	39.97/44.17/36.48	1.943	0.585
LP20657	rs295	20657	19816238	AA/CA/CC	370/214/30	0.223	136.51/136.73/146.07	40.68/39.16/41.69	2.243	0.407
LP22044_22047del4	rs311	22044	19817625	DD/WD/WW	1/62/554	0.052	32.92/140.93/136.63	NA/39.57/40.86	0.707	0.892
LP22416	rs312	22416	19817997	CC/GC/GG	7/126/485	0.113	137.72/139.05/136.2	36.48/45.18/39.53	2.423	0.501
LP22461	rs314	22461	19818042	AA/GA/GG	42/213/310	0.263	138.76/134.83/138.2	39.68/39.03/41.8	-1.373	0.607
LP22514	rs315	22514	19818095	CT/TT	6/614	0.005	122.7/137.04	64.93/40.58	-14.478	0.380
LP22855	rs316	22855	19818436	AA/CA/CC	7/124/480	0.113	137.87/140.7/136.39	36.48/43.37/40.06	3.580	0.322
LP23192	rs117026536	23192	19818773	GG/GT/TT	498/112/8	0.104	137.12/135.13/140.6	40.67/40.56/38.36	-1.090	0.768
LP23496	rs320	23496	19819077	GG/GT/TT	47/221/342	0.258	142.97/135.2/137.02	38.43/41.15/39.95	0.897	0.721
LP23955	rs327	23955	19819536	GG/TG/TT	48/232/339	0.265	142.53/135.36/137.08	38.03/41.87/40.06	0.787	0.755
LP24143	rs328	24143	19819724	CC/GC/GG	498/115/6	0.103	137.1/135.8/128.39	40.67/40.61/32.5	-1.907	0.612
LP25049	rs78031480	25049	19820630	AA/AG/GG	1/55/553	0.047	191.35/134.31/137.12	NA/34.58/41.42	-0.684	0.901
LP26234	rs10099160	26234	19821815	GG/GT/TT	37/249/335	0.260	144.98/134.35/138.13	41.75/40.84/40.66	-0.334	0.899
LP27000	rs11232447	27000	19822581	CC/CT/TT	588/34/1	0.029	137.16/134.02/137.32	40.43/47.68	-2.813	0.674
LP27160	rs117910839	27160	19822741	AA/TA/TT	2/30/588	0.027	150.99/138.94/136.84	40.02/32.29/41.26	3.190	0.632
LP27229	rs11570891	27229	19822810	CC/TC/TT	494/116/8	0.107	136.88/136.79/134.08	40.71/40.56/34.07	-0.413	0.910
LP27249	rs4922115	27249	19822830	AA/AG/GG	16/148/451	0.146	133.36/140.93/136.54	30.79/44.47/39.32	2.345	0.454
LP27611	rs3289	27611	19823192	CC/TC/TT	1/32/590	0.027	126.02/128.1/137.49	NA/38.94/40.89	-9.020	0.187
LP27688	rs191212278	27688	19823269	CC/TC	615/5	0.004	137.13/117.88	40.94/11.68	-19.316	0.282
LP28407	rs150252331	28407	19823988	GG/GT	601/22	0.018	136.97/137.55	40.88/39.52	0.584	0.946
LP28524	Novel	28524	19824105	CC/CT	619/1	0.001	136.95/151.44	40.85/NA	14.516	0.717
LP28911	rs13702	28911	19824492	CC/CT/TT	50/235/331	0.272	142.12/135.9/137.07	38.86/40.77/40.11	0.961	0.698
LP28982	rs1059611	28982	19824563	CC/TC/TT	8/117/495	0.107	134.03/136.64/136.56	34.07/40.47/39.85	-0.243	0.946
LP29315	rs9644636	29315	19824896	GG/GT/TT	50/256/311	0.288	133.55/137.54/136.99	40.85/42.56/38.21	-0.744	0.765
LP29474	rs113831503	29474	19825055	CC/CT/TT	575/43/1	0.036	137.23/133.17/137.45	40.72/43.42/NA	-3.697	0.541
LP29547	rs4921684	29547	19825128	CC/CT/TT	451/152/16	0.149	136.42/138.93/133.56	39.25/46.14/30.79	1.182	0.707
LP29716	rs80085105	29716	19825297	TC/TT	17/602	0.014	133.44/137.07	37.91/40.96	-3.639	0.712

W: Allele in the reference sequence ; D: Deleted base/bases; I: Inserted base/bases

Table A1.7. Association results of TC levels with 64 *LPL* SNPs in NHWs (n=623)

LPL Variant	RefSNP ID	Position in Ref NC_00008.10	Chr. Position (hg19)	Genotypes (GTs)	GT Counts	MAF	Adjusted Mean of plasma TC	Standard Deviation	Beta	*P*
LP1088	rs80351041	1088	19796669	GG/GT	590/12	0.010	217.14/211.75	43.8/37.44	-5.400	0.660
LP1130	Novel	1130	19796711	GC/GG	3/616	0.002	248.29/216.89	15.5/43.64	31.599	0.193
LP2335	rs3779787	2335	19797916	GG/GT/TT	441/167/12	0.154	216.83/216.84/227.36	43.4/43.47/55.29	1.390	0.679
LP3964	rs17410577	3964	19799545	CC/GC/GG	28/198/388	0.207	219.01/217.97/216.56	36/44.26/43.72	1.342	0.647
LP4060	rs1534649	4060	19799641	GG/TG/TT	180/314/122	0.453	217.55/216.6/216.51	45.11/41.95/44.11	-0.565	0.815
LP4424	rs13266204	4424	19800005	AA/AG/GG	384/204/30	0.214	216.5/218.28/215.92	43.71/44.14/38.24	0.865	0.764
LP4948	rs6997330	4948	19800529	CG/GG	23/600	0.018	207.82/217.34	44.39/43.52	-9.594	0.281
LP5949	rs112127208	5949	19801530	GG/TG/TT	12/177/429	0.163	222.66/217.9/216.46	54.17/43.36/43.42	1.871	0.573
LP6821	rs10104051	6821	19802402	CC/TC/TT	188/310/117	0.442	217.46/216.75/214.71	44.94/41.9/42.24	-1.303	0.585
LP7503	rs6999612	7503	19803084	CC/CT/TT	1/23/595	0.020	215.4/208.09/217.46	NA/44.56/43.53	-8.179	0.320
LP7512	rs3779788	7512	19803093	CC/TC/TT	447/164/10	0.148	217.01/216.23/219.6	43.14/42.84/58.52	-0.309	0.928
LP8221	rs7000460	8221	19803802	AA/CA	596/23	0.019	217.4/207.89	43.59/44.39	-9.574	0.283
LP10127	rs1801177	10127	19805708	AG/GG	23/596	0.019	207.89/217.4	44.39/43.59	-9.574	0.283
LP10912	rs149477831	10912	19806493	AA/AG	608/13	0.010	216.93/212.97	43.78/30.18	-3.980	0.734
LP10987	rs74377536	10987	19806568	AA/CA/CC	10/116/442	0.120	222.93/219.83/216.99	48.61/48.1/42.6	2.886	0.447
LP11050	rs7016529	11050	19806631	CT/TT	22/597	0.018	208.26/217.32	44.82/43.59	-9.123	0.317
LP11090	rs8176337	11090	19806671	CC/CG/GG	314/203/31	0.242	219.32/216.77/215.87	44.27/43.27/51.22	-2.182	0.472
LP11888_11889ins1	rs149017698	11888	19807469	II/WI/WW	1/23/596	0.020	196.8/209.2/217.48	NA/44.45/43.58	-8.641	0.293
LP13003	rs80181352	13003	19808584	GG/GT/TT	532/83/5	0.075	217.23/213.58/239.29	43.62/40.3/83.12	-0.604	0.892
LP13639	rs78326602	13639	19809220	GA/GG	9/611	0.007	201.37/217.15	41.33/43.6	-15.900	0.259
LP13854	rs1121923	13854	19809435	CC/TC	569/41	0.034	217.16/216.72	43.75/44.27	-0.443	0.948
LP14114	rs73667472	14114	19809695	AA/AG/GG	532/83/7	0.078	217.11/215.19/235.04	43.41/41.56/72.64	1.014	0.813
LP15245	rs248	15245	19810826	AA/GA/GG	2/79/539	0.067	220.93/215.06/216.93	17.68/40.88/43.53	-1.487	0.754
LP15425	rs249	15425	19811006	CC/TC/TT	7/79/531	0.075	234.9/213.34/217.36	72.64/40.64/43.61	-0.456	0.917
LP15836	rs253	15836	19811417	CC/CT/TT	182/318/123	0.453	213.99/217.98/218.87	42.66/42.97/46.35	2.608	0.281
LP16316	rs254	16316	19811897	CC/CG/GG	445/150/12	0.143	216.56/218.15/223.04	43.09/43.91/61.88	2.068	0.550
LP16442	rs74382962	16442	19812023	CG/GG	3/617	0.002	214.16/217.01	26.46/43.68	-2.872	0.906
LP17599	rs264	17599	19813180	AA/GA/GG	11/152/445	0.143	227.81/217.64/216.83	62.26/42.95/43.08	2.021	0.559
LP17948	rs268	17948	19813529	AA/AG	600/19	0.015	216.86/218.27	43.56/45.13	1.434	0.884
LP18086	rs269	18086	19813667	GG/GT/TT	16/182/417	0.174	220.73/218.77/215.94	59.29/43.16/42.88	2.715	0.394
LP18095	rs270	18095	19813676	AA/CA/CC	19/174/425	0.172	230.14/218.29/216.06	48.08/41.5/43.56	3.949	0.204
LP18822	rs277	18822	19814403	CC/CT/TT	23/192/391	0.196	226.59/218.26/216	45.39/42.7/43.99	3.439	0.256
LP19445	rs282	19445	19815026	CC/GC/GG	8/152/462	0.135	212.31/214.68/217.81	48.39/42.94/43.77	-3.061	0.388
LP19517	rs283	19517	19815098	CC/CT/TT	399/190/29	0.201	217.85/215.88/213.46	44.8/40.85/47.61	-2.095	0.475
LP19608	rs285	19608	19815189	CC/CT/TT	169/307/144	0.480	217.91/216.24/216.66	47.08/40.55/44.49	-0.677	0.775
LP19675	rs286	19675	19815256	AA/TA/TT	6/106/510	0.095	212.37/219.12/216.69	46.25/44.84/43.27	1.518	0.708
LP20363	rs296	20363	19815944	AA/TA/TT	560/57/2	0.049	216.66/222.64/170.31	43.41/45.29/41.72	2.262	0.680
LP20544	rs294	20544	19816125	AA/AG/GG	482/133/7	0.118	215.85/221.42/211.74	43.24/45.11/36.88	4.090	0.272
LP20657	rs295	20657	19816238	AA/CA/CC	370/214/30	0.223	215.65/217.2/223.25	43.26/41.84/45.06	2.561	0.366
LP22044_22047del4	rs311	22044	19817625	DD/WD/WW	1/62/554	0.052	135.8/221.78/216.44	NA/43.13/43.56	2.427	0.655
LP22416	rs312	22416	19817997	CC/GC/GG	7/126/485	0.113	211.52/222.36/215.49	36.88/45.85/42.84	5.092	0.177
LP22461	rs314	22461	19818042	AA/GA/GG	42/213/310	0.263	216.8/215.46/217.95	41.71/42.5/43.62	-1.448	0.602
LP22514	rs315	22514	19818095	CT/TT	6/614	0.005	228.93/216.79	40.57/43.65	12.297	0.476
LP22855	rs316	22855	19818436	AA/CA/CC	7/124/480	0.113	212.01/221.75/215.61	36.88/43.16/43.24	4.520	0.230
LP23192	rs117026536	23192	19818773	GG/GT/TT	498/112/8	0.104	216.63/217.65/214.86	42.68/45.95/49.91	0.562	0.884
LP23496	rs320	23496	19819077	GG/GT/TT	47/221/342	0.258	221.76/214.73/216.44	41.85/43.08/42.6	0.767	0.770
LP23955	rs327	23955	19819536	GG/TG/TT	48/232/339	0.265	221.64/216.01/216.59	41.41/44.57/42.65	1.181	0.653
LP24143	rs328	24143	19819724	CC/GC/GG	498/115/6	0.103	216.6/218.4/201.23	42.68/45.8/46.67	-0.011	0.998
LP25049	rs78031480	25049	19820630	AA/AG/GG	1/55/553	0.047	265.71/209.63/217.66	NA/38.26/44.09	-5.765	0.314
LP26234	rs10099160	26234	19821815	GG/GT/TT	37/249/335	0.260	224.69/213.95/218.4	42.32/42.87/44.2	-0.824	0.766
LP27000	rs11232447	27000	19822581	CC/CT/TT	588/34/1	0.029	217.43/209.09/230.03	43.27/48.55/NA	-6.811	0.330
LP27160	rs117910839	27160	19822741	AA/TA/TT	2/30/588	0.027	234/217.75/216.82	23.33/38.39/43.87	2.602	0.709
LP27229	rs11570891	27229	19822810	CC/TC/TT	494/116/8	0.107	216.31/219.67/209.5	42.72/45.67/44.65	1.766	0.643
LP27249	rs4922115	27249	19822830	AA/AG/GG	16/148/451	0.146	211.73/220.4/216.17	33.82/44.56/42.75	2.024	0.536
LP27611	rs3289	27611	19823192	CC/TC/TT	1/32/590	0.027	202.9/209.07/217.44	NA/44.22/43.53	-8.290	0.247
LP27688	rs191212278	27688	19823269	CC/TC	615/5	0.004	217.18/194.79	43.69/23.53	-22.591	0.231
LP28407	rs150252331	28407	19823988	GG/GT	601/22	0.018	217.08/214.55	43.72/39.16	-2.555	0.779
LP28524	Novel	28524	19824105	CC/CT	619/1	0.001	216.95/248.12	43.62/NA	31.277	0.455
LP28911	rs13702	28911	19824492	CC/CT/TT	50/235/331	0.272	220.2/215.82/216.58	41.92/43.27/42.71	0.724	0.780
LP28982	rs1059611	28982	19824563	CC/TC/TT	8/117/495	0.107	209.18/219.68/215.97	44.65/45.5/42.06	2.049	0.585
LP29315	rs9644636	29315	19824896	GG/GT/TT	50/256/311	0.288	212.7/218.17/215.64	42.7/46.08/40.14	0.261	0.920
LP29474	rs113831503	29474	19825055	CC/CT/TT	575/43/1	0.036	217.51/208.6/229.89	43.5/45.31/NA	-7.607	0.230
LP29547	rs4921684	29547	19825128	CC/CT/TT	451/152/16	0.149	216.06/220.3/212.04	42.78/46.97/33.82	2.131	0.518
LP29716	rs80085105	29716	19825297	TC/TT	17/602	0.014	214.29/217	38.63/43.75	-2.716	0.792

W: Allele in the reference sequence ; D: Deleted base/bases; I: Inserted base/bases

Table A1.8. Association results of apoB levels with 64 *LPL* SNPs in NHWs (n=623)

LPL Variant	RefSNP ID	Position in Ref NC_00008.10	Chr. Position (hg19)	Genotypes (GTs)	GT Counts	MAF	Adjusted Mean of plasma apoB	Standard Deviation	Beta	*P*
LP1088	rs80351041	1088	19796669	GG/GT	408/9	0.010	87.97/78.2	23.86/26.26	-2.788	0.206
LP1130	Novel	1130	19796711	GC/GG	3/427	0.002	84.95/87.98	23.58/23.92	-0.745	0.844
LP2335	rs3779787	2335	19797916	GG/GT/TT	305/118/8	0.154	87.79/87.59/95.88	24.49/23.15/18.16	0.282	0.655
LP3964	rs17410577	3964	19799545	CC/GC/GG	23/133/271	0.207	84.18/90.28/87.02	20.83/23.25/24.41	0.319	0.549
LP4060	rs1534649	4060	19799641	GG/TG/TT	125/218/87	0.453	86.33/89.22/86.35	24.36/24.26/22.47	0.102	0.821
LP4424	rs13266204	4424	19800005	AA/AG/GG	272/137/22	0.214	86.94/90.69/83.05	24.35/23.55/20.56	0.344	0.521
LP4948	rs6997330	4948	19800529	CG/GG	14/420	0.018	78.8/88.22	38.91/23.29	-3.168	0.074
LP5949	rs112127208	5949	19801530	GG/TG/TT	8/123/300	0.163	92.97/87.46/88	19.62/23.15/24.47	0.096	0.878
LP6821	rs10104051	6821	19802402	CC/TC/TT	128/218/82	0.442	86.44/89.08/86.43	24.24/24.19/22.48	0.107	0.814
LP7503	rs6999612	7503	19803084	CC/CT/TT	1/14/415	0.020	125.1/76.3/88.17	NA/37.13/23.3	-1.838	0.242
LP7512	rs3779788	7512	19803093	CC/TC/TT	307/120/6	0.148	87.83/87.65/91.71	24.36/23.1/18.68	0.106	0.870
LP8221	rs7000460	8221	19803802	AA/CA	416/14	0.019	88.27/78.93	23.23/38.91	-3.148	0.076
LP10127	rs1801177	10127	19805708	AG/GG	14/416	0.019	78.93/88.27	38.91/23.23	-3.148	0.076
LP10912	rs149477831	10912	19806493	AA/AG	426/6	0.010	87.63/101.14	24/12.91	3.829	0.152
LP10987	rs74377536	10987	19806568	AA/CA/CC	8/79/312	0.120	87.93/87.18/88.14	17.67/22.76/24.57	-0.128	0.854
LP11050	rs7016529	11050	19806631	CT/TT	13/417	0.018	81.39/88.25	38.91/23.21	-2.433	0.184
LP11090	rs8176337	11090	19806671	CC/CG/GG	217/152/19	0.242	88.52/87.53/85.02	23.58/26.02/19.62	-0.387	0.500
LP11888_11889ins1	rs149017698	11888	19807469	II/WI/WW	1/14/417	0.020	60.51/81.36/88.2	NA/38.93/23.36	-2.755	0.079
LP13003	rs80181352	13003	19808584	GG/GT/TT	368/61/2	0.075	88.36/85.05/114.62	24.2/22.51/14.21	-0.312	0.713
LP13639	rs78326602	13639	19809220	GA/GG	7/424	0.007	79.16/88.16	22.18/24.01	-2.480	0.320
LP13854	rs1121923	13854	19809435	CC/TC	395/30	0.034	88.03/86.22	24.07/24.03	-0.488	0.694
LP14114	rs73667472	14114	19809695	AA/AG/GG	374/57/2	0.078	88.41/83.87/102.33	23.38/27.44/7.14	-0.929	0.286
LP15245	rs248	15245	19810826	AA/GA/GG	1/56/375	0.067	105.97/87.9/88.05	NA/22.77/24.09	0.181	0.841
LP15425	rs249	15425	19811006	CC/TC/TT	2/51/376	0.075	102.47/84.1/88.62	7.14/27.07/23.51	-0.886	0.330
LP15836	rs253	15836	19811417	CC/CT/TT	127/221/86	0.453	85.1/90.37/85.78	25.83/23.53/21.57	0.286	0.525
LP16316	rs254	16316	19811897	CC/CG/GG	309/104/8	0.143	87.79/87.71/92.72	24.29/23.8/21.08	0.193	0.768
LP16442	rs74382962	16442	19812023	CG/GG	2/429	0.002	100.96/87.87	13.51/23.89	3.720	0.421
LP17599	rs264	17599	19813180	AA/GA/GG	7/111/306	0.143	93.57/87.6/87.78	17.79/23.82/24.3	0.176	0.788
LP17948	rs268	17948	19813529	AA/AG	420/10	0.015	88.15/79.23	24.03/15.73	-2.346	0.261
LP18086	rs269	18086	19813667	GG/GT/TT	12/128/288	0.174	87.3/88.82/87.45	22.2/23.61/24.15	0.273	0.645
LP18095	rs270	18095	19813676	AA/CA/CC	16/115/300	0.172	85.92/91.46/86.66	19.01/22.17/24.75	0.805	0.161
LP18822	rs277	18822	19814403	CC/CT/TT	20/122/277	0.196	87.16/89.48/87.25	18.54/23.64/24.66	0.363	0.514
LP19445	rs282	19445	19815026	CC/GC/GG	7/108/319	0.135	80.74/84.37/89.28	18.49/23.99/23.93	-1.326	0.040
LP19517	rs283	19517	19815098	CC/CT/TT	279/128/23	0.201	86.76/90.06/86.12	24.3/22.32/25.12	0.457	0.390
LP19608	rs285	19608	19815189	CC/CT/TT	107/226/100	0.480	86.85/88.36/87.7	25.53/24.35/21.16	0.171	0.705
LP19675	rs286	19675	19815256	AA/TA/TT	5/81/347	0.095	87.32/90.61/87.29	26.74/21.52/24.44	0.793	0.276
LP20363	rs296	20363	19815944	AA/TA/TT	389/40/1	0.049	87.84/88.89/67.75	24.01/22.94/NA	0.025	0.981
LP20544	rs294	20544	19816125	AA/AG/GG	336/92/5	0.118	87.86/88.58/85.55	24.06/24.06/13.02	0.124	0.859
LP20657	rs295	20657	19816238	AA/CA/CC	249/158/20	0.223	87.24/88.33/93.7	24.78/22.43/23.49	0.605	0.263
LP22044_22047del4	rs311	22044	19817625	DD/WD/WW	1/45/383	0.052	32.82/91.5/87.69	NA/25.57/23.59	0.213	0.829
LP22416	rs312	22416	19817997	CC/GC/GG	5/86/338	0.113	85.56/88.85/87.59	13.02/24.43/23.94	0.238	0.739
LP22461	rs314	22461	19818042	AA/GA/GG	31/149/213	0.263	87.91/88.16/87.14	21.25/24.35/24.66	0.222	0.672
LP22514	rs315	22514	19818095	CT/TT	4/429	0.005	94.57/87.84	23.66/23.99	1.918	0.560
LP22855	rs316	22855	19818436	AA/CA/CC	5/85/335	0.113	85.68/88.84/87.62	13.02/24.58/24.04	0.231	0.747
LP23192	rs117026536	23192	19818773	GG/GT/TT	338/85/6	0.104	87.23/90.36/86.67	24.29/22.15/21.23	0.708	0.313
LP23496	rs320	23496	19819077	GG/GT/TT	33/155/235	0.258	90.47/87.89/87.43	25.07/22.19/24.89	0.336	0.502
LP23955	rs327	23955	19819536	GG/TG/TT	33/165/232	0.265	90.34/87.87/87.43	25.07/22.31/25.04	0.322	0.518
LP24143	rs328	24143	19819724	CC/GC/GG	338/87/5	0.103	87.21/90.49/85.02	24.29/21.89/23.22	0.727	0.305
LP25049	rs78031480	25049	19820630	AA/AG/GG	1/35/386	0.047	99.64/78.84/88.72	NA/23.78/23.95	-2.332	0.034
LP26234	rs10099160	26234	19821815	GG/GT/TT	31/166/236	0.260	88.45/86.98/88.52	20.16/23.56/24.75	-0.169	0.736
LP27000	rs11232447	27000	19822581	CC/CT/TT	412/21/1	0.029	88.08/84.5/94.36	23.87/26.25/NA	-0.701	0.601
LP27160	rs117910839	27160	19822741	AA/TA/TT	1/22/408	0.027	116.22/89.9/87.84	NA/16.97/24.3	1.220	0.355
LP27229	rs11570891	27229	19822810	CC/TC/TT	337/86/6	0.107	87.17/90.31/90.24	24.32/21.86/24.89	0.831	0.235
LP27249	rs4922115	27249	19822830	AA/AG/GG	12/97/319	0.146	81.88/90.37/87.41	20.25/24.28/23.87	0.246	0.690
LP27611	rs3289	27611	19823192	CC/TC/TT	1/18/415	0.027	56.58/90.59/87.88	NA/31.46/23.6	-0.318	0.824
LP27688	rs191212278	27688	19823269	CC/TC	427/4	0.004	88.03/77.79	23.94/12.42	-2.672	0.414
LP28407	rs150252331	28407	19823988	GG/GT	419/15	0.018	88.14/81.72	23.93/23.75	-1.874	0.276
LP28524	Novel	28524	19824105	CC/CT	430/1	0.001	87.9/100.91	23.89/NA	3.784	0.561
LP28911	rs13702	28911	19824492	CC/CT/TT	37/162/229	0.272	89.8/88.6/86.95	23.88/22.51/24.86	0.462	0.342
LP28982	rs1059611	28982	19824563	CC/TC/TT	6/87/338	0.107	90.26/89.96/87.17	24.89/22.07/24.38	0.755	0.280
LP29315	rs9644636	29315	19824896	GG/GT/TT	35/182/213	0.288	86.39/88.14/87.85	23.63/24.15/23.71	-0.088	0.858
LP29474	rs113831503	29474	19825055	CC/CT/TT	403/27/1	0.036	87.93/88.96/94.71	23.89/26.24/NA	0.353	0.771
LP29547	rs4921684	29547	19825128	CC/CT/TT	319/100/12	0.149	87.5/90.06/81.8	23.84/24.41/20.25	0.173	0.778
LP29716	rs80085105	29716	19825297	TC/TT	14/416	0.014	87.22/88.01	23.67/24.05	-0.182	0.918

W: Allele in the reference sequence ; D: Deleted base/bases; I: Inserted base/bases

Table A1.9. Association results of apoA1 levels with 64 *LPL* SNPs in NHWs (n=623)

LPL Variant	RefSNP ID	Position	Chr.	Genotype	GT Count	MAF	Adjusted Mean of plasma apoA1	GT_SD	Beta	*P*
LP1088	rs80351041	1088	19796669	GG/GT	409/9	0.010	149.77/146.13	33.11/32.15	-3.639	0.741
LP1130	Novel	1130	19796711	GC/GG	3/428	0.002	164.88/149.48	40.33/33.44	15.416	0.419
LP2335	rs3779787	2335	19797916	GG/GT/TT	306/118/8	0.154	149.98/148.17/163.62	34.18/30.81/13.24	0.346	0.912
LP3964	rs17410577	3964	19799545	CC/GC/GG	23/134/271	0.207	142.07/146.78/151.52	33.96/34.77/32.53	-4.747	0.077
LP4060	rs1534649	4060	19799641	GG/TG/TT	125/219/87	0.453	153.17/148.14/148.17	35.86/31.81/32.65	-2.737	0.227
LP4424	rs13266204	4424	19800005	AA/AG/GG	272/138/22	0.214	151.15/147.45/142.89	32.55/34.73/34.62	-3.912	0.146
LP4948	rs6997330	4948	19800529	CG/GG	14/421	0.018	146.5/149.72	28.33/33.52	-3.23	0.718
LP5949	rs112127208	5949	19801530	GG/TG/TT	8/123/301	0.163	160.62/147.63/150.3	18.24/31.45/33.99	-0.771	0.803
LP6821	rs10104051	6821	19802402	CC/TC/TT	128/219/82	0.442	152.76/148.82/148.35	35.75/31.56/33.12	-2.409	0.289
LP7503	rs6999612	7503	19803084	CC/CT/TT	1/14/416	0.020	137.63/146.64/149.95	NA/28.3/33.62	-3.962	0.616
LP7512	rs3779788	7512	19803093	CC/TC/TT	308/120/6	0.148	150.49/146.25/166.46	33.8/32.6/12.11	-1.853	0.567
LP8221	rs7000460	8221	19803802	AA/CA	417/14	0.019	149.69/146.5	33.65/28.33	-3.206	0.721
LP10127	rs1801177	10127	19805708	AG/GG	14/417	0.019	146.5/149.69	28.33/33.65	-3.206	0.721
LP10912	rs149477831	10912	19806493	AA/AG	427/6	0.010	149.72/151.27	33.31/31.68	1.553	0.908
LP10987	rs74377536	10987	19806568	AA/CA/CC	8/80/312	0.120	145.92/149.4/149.44	52.39/31.83/32.9	-0.591	0.865
LP11050	rs7016529	11050	19806631	CT/TT	13/418	0.018	146.22/149.78	29.45/33.61	-3.574	0.7
LP11090	rs8176337	11090	19806671	CC/CG/GG	218/152/19	0.242	149.81/150.73/149.78	35.59/29.29/27.46	0.525	0.851
LP11888_11889ins1	rs149017698	11888	19807469	II/WI/WW	1/14/418	0.020	124.3/156.88/149.5	NA/40.91/33.12	2.882	0.714
LP13003	rs80181352	13003	19808584	GG/GT/TT	369/61/2	0.075	148.68/153.91/170.65	33.95/30.16/18.1	5.965	0.163
LP13639	rs78326602	13639	19809220	GA/GG	7/425	0.007	132.6/149.8	41.95/33.26	-17.223	0.169
LP13854	rs1121923	13854	19809435	CC/TC	396/30	0.034	149.79/149.43	33.99/26.83	-0.357	0.954
LP14114	rs73667472	14114	19809695	AA/AG/GG	375/57/2	0.078	150.09/147.23/179.48	33.15/32.49/2.19	-0.545	0.9
LP15245	rs248	15245	19810826	AA/GA/GG	1/56/376	0.067	159.12/155.65/148.66	NA/30.9/33.75	6.873	0.131
LP15425	rs249	15425	19811006	CC/TC/TT	2/51/377	0.075	179.56/146.29/150.11	2.19/36.62/33.04	-1.166	0.8
LP15836	rs253	15836	19811417	CC/CT/TT	128/221/86	0.453	150.41/150.4/146.42	37.37/31.73/31.24	-1.804	0.427
LP16316	rs254	16316	19811897	CC/CG/GG	310/104/8	0.143	150.39/146.35/158.41	33.77/28.7/18.25	-1.885	0.552
LP16442	rs74382962	16442	19812023	CG/GG	2/430	0.002	130.57/149.72	20.15/33.47	-19.169	0.411
LP17599	rs264	17599	19813180	AA/GA/GG	7/111/307	0.143	167.54/145.98/150.7	11.98/31.07/34.07	-1.659	0.607
LP17948	rs268	17948	19813529	AA/AG	421/10	0.015	149.5/152.84	33.52/32.37	3.372	0.75
LP18086	rs269	18086	19813667	GG/GT/TT	12/128/289	0.174	155.18/147.05/150.37	21.21/32.23/34.41	-1.478	0.621
LP18095	rs270	18095	19813676	AA/CA/CC	16/115/301	0.172	147.67/146.59/150.94	29.4/33.41/33.54	-3.232	0.264
LP18822	rs277	18822	19814403	CC/CT/TT	20/122/278	0.196	144.21/146.69/151.2	27.72/32.22/33.42	-4.044	0.139
LP19445	rs282	19445	19815026	CC/GC/GG	7/108/320	0.135	149.56/156.5/147.3	22.42/35.1/32.74	7.309	0.024
LP19517	rs283	19517	19815098	CC/CT/TT	280/128/23	0.201	150/149.05/145.24	33.57/33.37/27.2	-1.662	0.534
LP19608	rs285	19608	19815189	CC/CT/TT	108/226/100	0.480	151.77/148.64/149.14	36.33/33.19/30.34	-1.361	0.551
LP19675	rs286	19675	19815256	AA/TA/TT	5/81/348	0.095	149.76/153.46/148.7	22.9/27.5/34.67	3.918	0.285
LP20363	rs296	20363	19815944	AA/TA/TT	390/40/1	0.049	150.32/145.58/142.82	33.9/24.8	-4.684	0.365
LP20544	rs294	20544	19816125	AA/AG/GG	337/92/5	0.118	149.15/150.58/157	33.72/32.85/8.39	1.929	0.582
LP20657	rs295	20657	19816238	AA/CA/CC	250/158/20	0.223	147.95/150.65/157.94	35.79/30.47/24.54	3.697	0.177
LP22044_22047del4	rs311	22044	19817625	DD/WD/WW	1/45/384	0.052	139.17/158.12/148.69	NA/34.22/33.34	8.212	0.098
LP22416	rs312	22416	19817997	CC/GC/GG	5/86/339	0.113	156.84/149.75/149.8	8.39/31.24/34.22	0.7	0.845
LP22461	rs314	22461	19818042	AA/GA/GG	31/149/214	0.263	154.49/150.52/148.27	25.83/32.43/34.92	2.748	0.291
LP22514	rs315	22514	19818095	CT/TT	4/430	0.005	161.74/149.46	19.1/33.45	12.389	0.454
LP22855	rs316	22855	19818436	AA/CA/CC	5/85/336	0.113	157.16/150.11/149.86	8.39/31.31/34.31	0.972	0.788
LP23192	rs117026536	23192	19818773	GG/GT/TT	339/85/6	0.104	148.63/152.12/160.14	34.99/26.2/33.16	4.114	0.247
LP23496	rs320	23496	19819077	GG/GT/TT	33/155/236	0.258	154.07/147.04/149.71	27.97/29.89/36.26	0.083	0.974
LP23955	rs327	23955	19819536	GG/TG/TT	33/165/233	0.265	154.14/148.92/149.06	27.97/30.99/35.69	1.367	0.586
LP24143	rs328	24143	19819724	CC/GC/GG	339/87/5	0.103	148.64/152.27/164.35	34.99/26.07/35.63	4.585	0.202
LP25049	rs78031480	25049	19820630	AA/AG/GG	1/35/387	0.047	168.34/140.68/150.19	NA/28.39/33.1	-7.527	0.162
LP26234	rs10099160	26234	19821815	GG/GT/TT	31/167/236	0.260	137.38/148.3/152.07	39.14/34.71/31.25	-5.73	0.023
LP27000	rs11232447	27000	19822581	CC/CT/TT	413/21/1	0.029	150.09/142.29/110.27	33.1/37.72	-9.888	0.143
LP27160	rs117910839	27160	19822741	AA/TA/TT	1/22/409	0.027	142.87/151.24/149.44	NA/29.32/33.69	1.007	0.88
LP27229	rs11570891	27229	19822810	CC/TC/TT	338/86/6	0.107	148.68/152.09/160.75	35.02/26.39/32.97	4.119	0.246
LP27249	rs4922115	27249	19822830	AA/AG/GG	12/97/320	0.146	154.77/147.6/150.42	31.52/31.03/34.19	-0.963	0.758
LP27611	rs3289	27611	19823192	CC/TC/TT	1/18/416	0.027	95.73/159.72/149.31	NA/37.01/33.15	3.518	0.623
LP27688	rs191212278	27688	19823269	CC/TC	428/4	0.004	149.72/140.71	33.38/44.43	-9.025	0.585
LP28407	rs150252331	28407	19823988	GG/GT	420/15	0.018	149.89/142.02	33.13/39.35	-7.913	0.36
LP28524	Novel	28524	19824105	CC/CT	431/1	0.001	149.69/126.59	33.45/NA	-23.109	0.483
LP28911	rs13702	28911	19824492	CC/CT/TT	37/162/230	0.272	156.73/147.99/149.59	26.42/30.44/36.33	1.493	0.544
LP28982	rs1059611	28982	19824563	CC/TC/TT	6/87/339	0.107	160.75/151.92/148.66	32.97/26.31/34.97	3.989	0.258
LP29315	rs9644636	29315	19824896	GG/GT/TT	35/183/213	0.288	153.53/152.42/146.54	30/35.5/32.04	4.563	0.067
LP29474	rs113831503	29474	19825055	CC/CT/TT	404/27/1	0.036	149.97/144.22/110.16	33.4/33.69	-7.658	0.21
LP29547	rs4921684	29547	19825128	CC/CT/TT	320/100/12	0.149	150.36/146.9/154.75	34.24/30.97/31.52	-1.395	0.653
LP29716	rs80085105	29716	19825297	TC/TT	14/417	0.014	158.49/149.29	38.19/33.25	9.202	0.303

Table A1.10. *LPL* 4-SNP sliding window haplotype association results for HDL-C and TG in NHWs (n=623)

							HDL			TG	
Window	**Window SNP**	**RefSNP ID**	**Location**	**Genotypes**	**MAF**	**Beta**	***P**	****hap_*P***	**Beta**	***P**	****hap_*P***
1	**LP1088**	**rs80351041**	5’ UTR-exon1	GG/GT	0.010	0.059	0.285	0.135	-0.011	0.933	0.358
1	**LP1130**	**Novel**	5’ UTR-exon1	GC/GG	0.002	-0.029	0.786	NA	0.597	0.016	NA
1	**LP2335**	**rs3779787**	Intron 1	GG/GT/TT	0.154	0.029	0.056	NA	-0.036	0.300	NA
1	**LP3964**	**rs17410577**	Intron 1	CC/GC/GG	0.207	-0.024	0.061	NA	0.030	0.315	NA
2	**LP1130**	**Novel**	5’ UTR-exon1	GC/GG	0.002	-0.029	0.786	0.181	0.597	0.016	0.025
2	**LP2335**	**rs3779787**	Intron 1	GG/GT/TT	0.154	0.029	0.056	NA	-0.036	0.300	NA
2	**LP3964**	**rs17410577**	Intron 1	CC/GC/GG	0.207	-0.024	0.061	NA	0.030	0.315	NA
2	**LP4060**	**rs1534649**	Intron 1	GG/TG/TT	0.453	-0.005	0.613	NA	-0.035	0.163	NA
3	**LP2335**	**rs3779787**	Intron 1	GG/GT/TT	0.154	0.029	0.056	0.060	-0.036	0.300	0.050
3	**LP3964**	**rs17410577**	Intron 1	CC/GC/GG	0.207	-0.024	0.061	NA	0.030	0.315	NA
3	**LP4060**	**rs1534649**	Intron 1	GG/TG/TT	0.453	-0.005	0.613	NA	-0.035	0.163	NA
3	**LP4424**	**rs13266204**	Intron 1	AA/AG/GG	0.214	-0.027	0.033	NA	0.029	0.331	NA
4	**LP3964**	**rs17410577**	Intron 1	CC/GC/GG	0.207	-0.024	0.061	0.030	0.030	0.315	0.051
4	**LP4060**	**rs1534649**	Intron 1	GG/TG/TT	0.453	-0.005	0.613	NA	-0.035	0.163	NA
4	**LP4424**	**rs13266204**	Intron 1	AA/AG/GG	0.214	-0.027	0.033	NA	0.029	0.331	NA
4	**LP4948**	**rs6997330**	Intron 1	CG/GG	0.018	-0.057	0.149	NA	0.066	0.471	NA
5	**LP4060**	**rs1534649**	Intron 1	GG/TG/TT	0.453	-0.005	0.613	0.062	-0.035	0.163	0.026
5	**LP4424**	**rs13266204**	Intron 1	AA/AG/GG	0.214	-0.027	0.033	NA	0.029	0.331	NA
5	**LP4948**	**rs6997330**	Intron 1	CG/GG	0.018	-0.057	0.149	NA	0.066	0.471	NA
5	**LP5949**	**rs112127208**	Intron 1	GG/TG/TT	0.163	0.019	0.196	NA	-0.026	0.442	NA
6	**LP4060**	**rs1534649**	Intron 1	AA/AG/GG	0.214	-0.027	0.033	0.038	0.029	0.331	0.012
6	**LP4424**	**rs13266204**	Intron 1	CG/GG	0.018	-0.057	0.149	NA	0.066	0.471	NA
6	**LP4948**	**rs6997330**	Intron 1	GG/TG/TT	0.163	0.019	0.196	NA	-0.026	0.442	NA
6	**LP6821**	**rs10104051**	Intron 1	CC/TC/TT	0.442	-0.003	0.760	NA	-0.042	0.091	NA
7	**LP4948**	**rs6997330**	Intron 1	CG/GG	0.018	-0.057	0.149	0.348	0.066	0.471	0.565
7	**LP5949**	**rs112127208**	Intron 1	GG/TG/TT	0.163	0.019	0.196	NA	-0.026	0.442	NA
7	**LP6821**	**rs10104051**	Intron 1	CC/TC/TT	0.442	-0.003	0.760	NA	-0.042	0.091	NA
7	**LP7503**	**rs6999612**	Intron 1	CC/CT/TT	0.020	-0.055	0.132	NA	0.065	0.446	NA
8	**LP5949**	**rs112127208**	Intron 1	GG/TG/TT	0.163	0.019	0.196	0.191	-0.026	0.442	0.256
8	**LP6821**	**rs10104051**	Intron 1	CC/TC/TT	0.442	-0.003	0.760	NA	-0.042	0.091	NA
8	**LP7503**	**rs6999612**	Intron 1	CC/CT/TT	0.020	-0.055	0.132	NA	0.065	0.446	NA
8	**LP7512**	**rs3779788**	Intron 1	CC/TC/TT	0.148	0.026	0.096	NA	-0.043	0.231	NA
9	**LP6821**	**rs10104051**	Intron 1	CC/TC/TT	0.442	-0.003	0.760	0.191	-0.042	0.091	0.406
9	**LP7503**	**rs6999612**	Intron 1	CC/CT/TT	0.020	-0.055	0.132	NA	0.065	0.446	NA
9	**LP7512**	**rs3779788**	Intron 1	CC/TC/TT	0.148	0.026	0.096	NA	-0.043	0.231	NA
9	**LP8221**	**rs7000460**	Intron 1	AA/CA	0.019	-0.058	0.148	NA	0.067	0.468	NA
10	**LP7503**	**rs6999612**	Intron 1	CC/CT/TT	0.020	-0.055	0.132	0.171	0.065	0.446	0.478
10	**LP7512**	**rs3779788**	Intron 1	CC/TC/TT	0.148	0.026	0.096	NA	-0.043	0.231	NA
10	**LP8221**	**rs7000460**	Intron 1	AA/CA	0.019	-0.058	0.148	NA	0.067	0.468	NA
10	**LP10127**	**rs1801177**	Intron 1	AG/GG	0.019	-0.058	0.148	NA	0.067	0.468	NA
11	**LP7512**	**rs3779788**	Intron 1	CC/TC/TT	0.148	0.026	0.096	0.077	-0.043	0.231	0.483
11	**LP8221**	**rs7000460**	Intron 1	AA/CA	0.019	-0.058	0.148	NA	0.067	0.468	NA
11	**LP10127**	**rs1801177**	Intron 1	AG/GG	0.019	-0.058	0.148	NA	0.067	0.468	NA
11	**LP10912**	**rs149477831**	Intron 1	AA/AG	0.010	-0.080	0.125	NA	0.097	0.421	NA
12	**LP8221**	**rs7000460**	Intron 1	AA/CA	0.019	-0.058	0.148	0.192	0.067	0.468	0.752
12	**LP10127**	**rs1801177**	Exon 2	AG/GG	0.019	-0.058	0.148	NA	0.067	0.468	NA
12	**LP10912**	**rs149477831**	Intron 1	AA/AG	0.010	-0.080	0.125	NA	0.097	0.421	NA
12	**LP10987**	**rs74377536**	Intron 2	AA/CA/CC	0.120	-0.004	0.833	NA	-0.002	0.951	NA
13	**LP10127**	**rs1801177**	Exon 2	AG/GG	0.019	-0.058	0.148	0.192	0.067	0.468	0.749
13	**LP10912**	**rs149477831**	Intron 1	AA/AG	0.010	-0.080	0.125	NA	0.097	0.421	NA
13	**LP10987**	**rs74377536**	Intron 2	AA/CA/CC	0.120	-0.004	0.833	NA	-0.002	0.951	NA
13	**LP11050**	**rs7016529**	Intron 2	CT/TT	0.018	-0.064	0.117	NA	0.082	0.381	NA
14	**LP10912**	**rs149477831**	Intron 1	AA/AG	0.010	-0.080	0.125	0.160	0.097	0.421	0.067
14	**LP10987**	**rs74377536**	Intron 2	AA/CA/CC	0.120	-0.004	0.833	NA	-0.002	0.951	NA
14	**LP11050**	**rs7016529**	Intron 2	CT/TT	0.018	-0.064	0.117	NA	0.082	0.381	NA
14	**LP11090**	**rs8176337**	Intron 2	CC/CG/GG	0.242	0.012	0.387	NA	-0.069	0.027	NA
15	**LP10987**	**rs74377536**	Intron 2	AA/CA/CC	0.120	-0.004	0.833	0.417	-0.002	0.951	0.091
15	**LP11050**	**rs7016529**	Intron 2	CT/TT	0.018	-0.064	0.117	NA	0.082	0.381	NA
15	**LP11090**	**rs8176337**	Intron 2	CC/CG/GG	0.242	0.012	0.387	NA	-0.069	0.027	NA
15	**LP11888_11889ins1**	**rs149017698**	Intron 2	II/WI/WW	0.020	-0.050	0.170	NA	0.061	0.471	NA
16	**LP11050**	**rs7016529**	Intron 2	CT/TT	0.018	-0.064	0.117	0.271	0.082	0.381	0.008

Table A1.10. Continued

						HDL			TG		
Window	**Window SNP**	**RefSNP ID**	**Location**	**Genotypes**	**MAF**	**Beta**	***P**	****hap_P**	**Beta**	***P**	****hap_P**
16	**LP11090**	**rs8176337**	Intron 2	CC/CG/GG	0.242	0.012	0.387	NA	-0.069	0.027	NA
16	**LP11888_11889ins1**	**rs149017698**	Intron 2	II/WI/WW	0.020	-0.050	0.170	NA	0.061	0.471	NA
16	**LP13003**	**rs80181352**	Intron 2	GG/GT/TT	0.075	0.009	0.668	NA	-0.158	0.001	NA
17	**LP11090**	**rs8176337**	Intron 2	CC/CG/GG	0.242	0.012	0.387	0.248	-0.069	0.027	0.007
17	**LP11888_11889ins1**	**rs149017698**	Intron 2	II/WI/WW	0.020	-0.050	0.170	NA	0.061	0.471	NA
17	**LP1300**	**rs80181352**	Intron 2	GG/GT/TT	0.075	0.009	0.668	NA	-0.158	0.001	NA
17	**LP13639**	**rs78326602**	Intron 2	GA/GG	0.007	0.028	0.652	NA	-0.023	0.872	NA
18	**LP11888_11889ins1**	**rs149017698**	Intron 2	II/WI/WW	0.020	-0.050	0.170	0.771	0.061	0.471	0.016
18	**LP1300**	**rs80181352**	Intron 2	GG/GT/TT	0.075	0.009	0.668	NA	-0.158	0.001	NA
18	**LP13639**	**rs78326602**	Intron 2	GA/GG	0.007	0.028	0.652	NA	-0.023	0.872	NA
18	**LP13854**	**rs1121923**	Intron 2	CC/TC	0.034	0.008	0.781	NA	0.020	0.778	NA
19	**LP1300**	**rs80181352**	Intron 2	GG/GT/TT	0.075	0.009	0.668	0.700	-0.158	0.001	0.015
19	**LP13639**	**rs78326602**	Intron 2	GA/GG	0.007	0.028	0.652	NA	-0.023	0.872	NA
19	**LP13854**	**rs1121923**	Exon 3	CC/TC	0.034	0.008	0.781	NA	0.020	0.778	NA
19	**LP14114**	**rs73667472**	Intron 3	AA/AG/GG	0.078	-0.026	0.170	NA	0.046	0.298	NA
20	**LP13639**	**rs78326602**	Intron 2	GA/GG	0.007	0.028	0.652	0.617	-0.023	0.872	0.099
20	**LP13854**	**rs1121923**	Exon 3	CC/TC	0.034	0.008	0.781	NA	0.020	0.778	NA
20	**LP14114**	**rs73667472**	Intron 3	AA/AG/GG	0.078	-0.026	0.170	NA	0.046	0.298	NA
20	**LP15245**	**rs248**	Exon 4	AA/GA/GG	0.067	0.019	0.375	NA	-0.132	0.008	NA
21	**LP13854**	**rs1121923**	Exon 3	CC/TC	0.034	0.008	0.781	0.559	0.020	0.778	0.084
21	**LP14114**	**rs73667472**	Intron 3	AA/AG/GG	0.078	-0.026	0.170	NA	0.046	0.298	NA
21	**LP15245**	**rs248**	Exon 4	AA/GA/GG	0.067	0.019	0.375	NA	-0.132	0.008	NA
21	**LP15425**	**rs249**	Intron 4	CC/TC/TT	0.075	-0.023	0.232	NA	0.043	0.341	NA
22	**LP14114**	**rs73667472**	Intron 3	AA/AG/GG	0.078	-0.026	0.170	0.564	0.046	0.298	0.059
22	**LP15245**	**rs248**	Exon 4	AA/GA/GG	0.067	0.019	0.375	NA	-0.132	0.008	NA
22	**LP15425**	**rs249**	Intron 4	CC/TC/TT	0.075	-0.023	0.232	NA	0.043	0.341	NA
22	**LP15836**	**rs253**	Intron 4	CC/CT/TT	0.453	-0.005	0.623	NA	0.006	0.814	NA
23	**LP15245**	**rs248**	Exon 4	AA/GA/GG	0.067	0.019	0.375	0.263	-0.132	0.008	0.032
23	**LP15425**	**rs249**	Intron 4	CC/TC/TT	0.075	-0.023	0.232	NA	0.043	0.341	NA
23	**LP15836**	**rs253**	Intron 4	CC/CT/TT	0.453	-0.005	0.623	NA	0.006	0.814	NA
23	**LP16316**	**rs254**	Intron 5	CC/CG/GG	0.143	0.009	0.569	NA	-0.029	0.419	NA
24	**LP15425**	**rs249**	Intron 4	CC/TC/TT	0.075	-0.023	0.232	0.479	0.043	0.341	0.765
24	**LP15836**	**rs253**	Intron 4	CC/CT/TT	0.453	-0.005	0.623	NA	0.006	0.814	NA
24	**LP16316**	**rs254**	Intron 5	CC/CG/GG	0.143	0.009	0.569	NA	-0.029	0.419	NA
24	**LP16442**	**rs74382962**	Intron 5	CG/GG	0.002	0.012	0.915	NA	-0.119	0.634	NA
25	**LP15836**	**rs253**	Intron 4	CC/CT/TT	0.453	-0.005	0.623	0.751	0.006	0.814	0.540
25	**LP16316**	**rs254**	Intron 5	CC/CG/GG	0.143	0.009	0.569	NA	-0.029	0.419	NA
25	**LP16442**	**rs74382962**	Intron 5	CG/GG	0.002	0.012	0.915	NA	-0.119	0.634	NA
25	**LP17599**	**rs264**	Intron 5	AA/GA/GG	0.143	0.011	0.492	NA	-0.018	0.616	NA
26	**LP16316**	**rs254**	Intron 5	CC/CG/GG	0.143	0.009	0.569	0.898	-0.029	0.419	0.252
26	**LP16442**	**rs74382962**	Intron 5	CG/GG	0.002	0.012	0.915	NA	-0.119	0.634	NA
26	**LP17599**	**rs264**	Intron 5	AA/GA/GG	0.143	0.011	0.492	NA	-0.018	0.616	NA
26	**LP17948**	**rs268**	Exon 6	AA/AG	0.015	-0.015	0.735	NA	0.155	0.124	NA
27	**LP16442**	**rs74382962**	Intron 5	CG/GG	0.002	0.012	0.915	0.778	-0.119	0.634	0.572
27	**LP17599**	**rs264**	Intron 5	AA/GA/GG	0.143	0.011	0.492	NA	-0.018	0.616	NA
27	**LP17948**	**rs268**	Exon 6	AA/AG	0.015	-0.015	0.735	NA	0.155	0.124	NA
27	**LP18086**	**rs269**	Intron 6	GG/GT/TT	0.174	0.017	0.239	NA	-0.023	0.489	NA
28	**LP17599**	**rs264**	Intron 5	AA/GA/GG	0.143	0.011	0.492	0.187	-0.018	0.616	0.160
28	**LP17948**	**rs268**	Exon 6	AA/AG	0.015	-0.015	0.735	NA	0.155	0.124	NA
28	**LP18086**	**rs269**	Intron 6	GG/GT/TT	0.174	0.017	0.239	NA	-0.023	0.489	NA
28	**LP18095**	**rs270**	Intron 6	AA/CA/CC	0.172	-0.031	0.025	NA	0.063	0.053	NA
29	**LP17948**	**rs268**	Exon 6	AA/AG	0.015	-0.015	0.735	0.276	0.155	0.124	0.044
29	**LP18086**	**rs269**	Intron 6	GG/GT/TT	0.174	0.017	0.239	NA	-0.023	0.489	NA
29	**LP18095**	**rs270**	Intron 6	AA/CA/CC	0.172	-0.031	0.025	NA	0.063	0.053	NA
29	**LP18822**	**rs277**	Intron 6	CC/CT/TT	0.196	-0.020	0.135	NA	0.065	0.037	NA
30	**LP18086**	**rs269**	Intron 6	GG/GT/TT	0.174	0.017	0.239	0.094	-0.023	0.489	0.029
30	**LP18095**	**rs270**	Intron 6	AA/CA/CC	0.172	-0.031	0.025	NA	0.063	0.053	NA
30	**LP18822**	**rs277**	Intron 6	CC/CT/TT	0.196	-0.020	0.135	NA	0.065	0.037	NA
30	**LP19445**	**rs282**	Intron 6	CC/GC/GG	0.135	0.032	0.042	NA	-0.101	0.006	NA
31	**LP18095**	**rs270**	Intron 6	AA/CA/CC	0.172	-0.031	0.025	0.172	0.063	0.053	0.040
31	**LP18822**	**rs277**	Intron 6	CC/CT/TT	0.196	-0.020	0.135	NA	0.065	0.037	NA
31	**LP19445**	**rs282**	Intron 6	CC/GC/GG	0.135	0.032	0.042	NA	-0.101	0.006	NA
31	**LP19517**	**rs283**	Intron 6	CC/CT/TT	0.201	-0.009	0.497	NA	0.049	0.105	NA
32	**LP18822**	**rs277**	Intron 6	CC/CT/TT	0.196	-0.020	0.135	0.364	0.065	0.037	0.011
32	**LP19445**	**rs282**	Intron 6	CC/GC/GG	0.135	0.032	0.042	NA	-0.101	0.006	NA

Table A1.10. Continued

						HDL			TG		
Window	**Window SNP**	**RefSNP ID**	**Location**	**Genotypes**	**MAF**	**Beta**	***P**	****hap_*P***	**Beta**	***P**	****hap_*P***
32	**LP19517**	**rs283**	Intron 6	CC/CT/TT	0.201	-0.009	0.497	NA	0.049	0.105	NA
32	**LP19608**	**rs285**	Intron 6	CC/CT/TT	0.480	0.007	0.493	NA	-0.022	0.363	NA
33	**LP19445**	**rs282**	Intron 6	CC/GC/GG	0.135	0.032	0.042	0.026	-0.101	0.006	5.10^{-4}
33	**LP19517**	**rs283**	Intron 6	CC/CT/TT	0.201	-0.009	0.497	NA	0.049	0.105	NA
33	**LP19608**	**rs285**	Intron 6	CC/CT/TT	0.480	0.007	0.493	NA	-0.022	0.363	NA
33	**LP19675**	**rs286**	Intron 6	AA/TA/TT	0.095	0.051	0.005	NA	-0.096	0.021	NA
34	**LP19517**	**rs283**	Intron 6	CC/CT/TT	0.201	-0.009	0.497	0.116	0.049	0.105	0.035
34	**LP19608**	**rs285**	Intron 6	CC/CT/TT	0.480	0.007	0.493	NA	-0.022	0.363	NA
34	**LP19675**	**rs286**	Intron 6	AA/TA/TT	0.095	0.051	0.005	NA	-0.096	0.021	NA
34	**LP20363**	**rs296**	Intron 6	AA/TA/TT	0.049	-0.028	0.260	NA	0.047	0.403	NA
35	**LP19608**	**rs285**	Intron 6	CC/CT/TT	0.480	0.007	0.493	0.059	-0.022	0.363	0.006
35	**LP19675**	**rs286**	Intron 6	AA/TA/TT	0.095	0.051	0.005	NA	-0.096	0.021	NA
35	**LP20363**	**rs296**	Intron 6	AA/TA/TT	0.049	-0.028	0.260	NA	0.047	0.403	NA
35	**LP20544**	**rs294**	Intron 6	AA/AG/GG	0.118	0.021	0.205	NA	-0.109	0.005	NA
36	**LP19675**	**rs286**	Intron 6	AA/TA/TT	0.095	0.051	0.005	0.038	-0.096	0.021	0.003
36	**LP20363**	**rs296**	Intron 6	AA/TA/TT	0.049	-0.028	0.260	NA	0.047	0.403	NA
36	**LP20544**	**rs294**	Intron 6	AA/AG/GG	0.118	0.021	0.205	NA	-0.109	0.005	NA
36	**LP20657**	**rs295**	Intron 6	AA/CA/CC	0.223	0.039	0.002	NA	-0.100	0.001	NA
37	**LP20363**	**rs296**	Intron 6	AA/TA/TT	0.049	-0.028	0.260	0.012	0.047	0.403	0.021
37	**LP20544**	**rs294**	Intron 6	AA/AG/GG	0.118	0.021	0.205	NA	-0.109	0.005	NA
37	**LP20657**	**rs295**	Intron 6	AA/CA/CC	0.223	0.039	0.002	NA	-0.100	0.001	NA
37	**LP22044_22047 del4**	**rs311**	Intron 7	DD/WD/WW	0.052	0.040	0.094	NA	0.019	0.735	NA
38	**LP20544**	**rs294**	Intron 6	AA/AG/GG	0.118	0.021	0.205	0.013	-0.109	0.005	0.011
38	**LP20657**	**rs295**	Intron 6	AA/CA/CC	0.223	0.039	0.002	NA	-0.100	0.001	NA
38	**LP22044_22047 del4**	**rs311**	Intron 7	DD/WD/WW	0.052	0.040	0.094	NA	0.019	0.735	NA
38	**LP22416**	**rs312**	Intron 7	CC/GC/GG	0.113	0.022	0.197	NA	-0.101	0.010	NA
39	**LP20657**	**rs295**	Intron 6	AA/CA/CC	0.223	0.039	0.002	0.027	-0.100	0.001	0.019
39	**LP22044_22047 del4**	**rs311**	Intron 7	DD/WD/WW	0.052	0.040	0.094	NA	0.019	0.735	NA
39	**LP22416**	**rs312**	Intron 7	CC/GC/GG	0.113	0.022	0.197	NA	-0.101	0.010	NA
39	**LP22461**	**rs314**	Intron 6	AA/GA/GG	0.263	0.026	0.043	NA	-0.070	0.015	NA
40	**LP22044_22047 del4**	**rs311**	Intron 7	DD/WD/WW	0.052	0.040	0.094	0.029	0.019	0.735	0.050
40	**LP22416**	**rs312**	Intron 7	CC/GC/GG	0.113	0.022	0.197	NA	-0.101	0.010	NA
40	**LP22461**	**rs314**	Intron 7	AA/GA/GG	0.263	0.026	0.043	NA	-0.070	0.015	NA
40	**LP22514**	**rs315**	Intron 7	CT/TT	0.005	-0.106	0.167	NA	-0.065	0.737	NA
41	**LP22416**	**rs312**	Intron 7	CC/GC/GG	0.113	0.022	0.197	0.063	-0.101	0.010	0.022
41	**LP22461**	**rs314**	Intron 7	AA/GA/GG	0.263	0.026	0.043	NA	-0.070	0.015	NA
41	**LP22514**	**rs315**	Intron 7	CT/TT	0.005	-0.106	0.167	NA	-0.065	0.737	NA
41	**LP22855**	**rs316**	Exon 8	AA/CA/CC	0.113	0.024	0.155	NA	-0.093	0.017	NA
42	**LP22461**	**rs314**	Intron 7	AA/GA/GG	0.263	0.026	0.043	0.090	-0.070	0.015	0.048
42	**LP22514**	**rs315**	Intron 7	CT/TT	0.005	-0.106	0.167	NA	-0.065	0.737	NA
42	**LP22855**	**rs316**	Exon 8	AA/CA/CC	0.113	0.024	0.155	NA	-0.093	0.017	NA
42	**LP23192**	**rs117026536**	Intron 8	GG/GT/TT	0.104	0.034	0.048	NA	-0.064	0.112	NA
43	**LP22514**	**rs315**	Intron 7	CT/TT	0.005	-0.106	0.167	0.064	-0.065	0.737	0.033
43	**LP22855**	**rs316**	Exon 8	AA/CA/CC	0.113	0.024	0.155	NA	-0.093	0.017	NA
43	**LP23192**	**rs117026536**	Intron 8	GG/GT/TT	0.104	0.034	0.048	NA	-0.064	0.112	NA
43	**LP23496**	**rs320**	Intron 8	GG/GT/TT	0.258	0.027	0.026	NA	-0.073	0.008	NA
44	**LP22855**	**rs316**	Exon 8	AA/CA/CC	0.113	0.024	0.155	0.118	-0.093	0.017	0.016
44	**LP23192**	**rs117026536**	Intron 8	GG/GT/TT	0.104	0.034	0.048	NA	-0.064	0.112	NA
44	**LP23496**	**rs320**	Intron 8	GG/GT/TT	0.258	0.027	0.026	NA	-0.073	0.008	NA
44	**LP22855**	**rs327**	Intron 8	GG/TG/TT	0.265	0.025	0.032	NA	-0.073	0.007	NA
45	**LP23192**	**rs117026536**	Intron 8	GG/GT/TT	0.104	0.034	0.048	0.108	-0.064	0.112	0.053
45	**LP23496**	**rs320**	Intron 8	GG/GT/TT	0.258	0.027	0.026	NA	-0.073	0.008	NA
45	**LP22855**	**rs327**	Intron 8	GG/TG/TT	0.265	0.025	0.032	NA	-0.073	0.007	NA
45	**LP24143**	**rs328**	Intron 8	CC/GC/GG	0.103	0.038	0.032	NA	-0.069	0.088	NA
46	**LP23496**	**rs320**	Intron 8	GG/GT/TT	0.258	0.027	0.026	0.139	-0.073	0.008	0.069
46	**LP22855**	**rs327**	Intron 8	GG/TG/TT	0.265	0.025	0.032	NA	-0.073	0.007	NA
46	**LP24143**	**rs328**	Exon 9	CC/GC/GG	0.103	0.038	0.032	NA	-0.069	0.088	NA
46	**LP25049**	**rs78031480**	Intron 9	AA/AG/GG	0.047	-0.032	0.208	NA	-0.023	0.692	NA
47	**LP22855**	**rs327**	Intron 8	GG/TG/TT	0.265	0.025	0.032	0.117	-0.073	0.007	0.088
47	**LP24143**	**rs328**	Exon 9	CC/GC/GG	0.103	0.038	0.032	NA	-0.069	0.088	NA
47	**LP25049**	**rs78031480**	Intron 9	AA/AG/GG	0.047	-0.032	0.208	NA	-0.023	0.692	NA
47	**LP26234**	**rs10099160**	Intron 9	GG/GT/TT	0.260	-0.021	0.094	NA	0.029	0.319	NA
48	**LP24143**	**rs328**	Exon 9	CC/GC/GG	0.103	0.038	0.032	0.148	-0.069	0.088	0.421
48	**LP25049**	**rs78031480**	Intron 9	AA/AG/GG	0.047	-0.032	0.208	NA	-0.023	0.692	NA

Table A1.10. Continued

						HDL			TG		
Window	**Window SNP**	**RefSNP ID**	**Location**	**Genotypes**	**MAF**	**Beta**	***P**	****hap_P**	**Beta**	***P**	****hap_P**
48	**LP26234**	**rs10099160**	Intron 9	GG/GT/TT	0.260	-0.021	0.094	NA	0.029	0.319	NA
48	**LP27000**	**rs11232447**	Intron 9	CC/CT/TT	0.029	-0.003	0.927	NA	-0.010	0.890	NA
49	**LP25049**	**rs78031480**	Intron 9	AA/AG/GG	0.047	-0.032	0.208	0.365	-0.023	0.692	0.570
49	**LP26234**	**rs10099160**	Intron 9	GG/GT/TT	0.260	-0.021	0.094	NA	0.029	0.319	NA
49	**LP27000**	**rs11232447**	Intron 9	CC/CT/TT	0.029	-0.003	0.927	NA	-0.010	0.890	NA
49	**LP27160**	**rs117910839**	Intron 9	AA/TA/TT	0.027	0.029	0.360	NA	-0.089	0.218	NA
50	**LP26234**	**rs10099160**	Intron 9	GG/GT/TT	0.260	-0.021	0.094	0.156	0.029	0.319	0.524
50	**LP27000**	**rs11232447**	Intron 9	CC/CT/TT	0.029	-0.003	0.927	NA	-0.010	0.890	NA
50	**LP27160**	**rs117910839**	Intron 9	AA/TA/TT	0.027	0.029	0.360	NA	-0.089	0.218	NA
50	**LP27229**	**rs11570891**	Intron 9	CC/TC/TT	0.107	0.039	0.024	NA	-0.062	0.119	NA
51	**LP27000**	**rs11232447**	Intron 9	CC/CT/TT	0.029	-0.003	0.927	0.112	-0.010	0.890	0.034
51	**LP27160**	**rs117910839**	Intron 9	AA/TA/TT	0.027	0.029	0.360	NA	-0.089	0.218	NA
51	**LP27229**	**rs11570891**	Intron 9	CC/TC/TT	0.107	0.039	0.024	NA	-0.062	0.119	NA
51	**LP27249**	**rs4922115**	3’ UTR-exon10	AA/AG/GG	0.146	0.015	0.304	NA	-0.070	0.039	NA
52	**LP27160**	**rs117910839**	Intron 9	AA/TA/TT	0.027	0.029	0.360	0.131	-0.089	0.218	0.052
52	**LP27229**	**rs11570891**	Intron 9	CC/TC/TT	0.107	0.039	0.024	NA	-0.062	0.119	NA
52	**LP27249**	**rs4922115**	3’ UTR-exon10	AA/AG/GG	0.146	0.015	0.304	NA	-0.070	0.039	NA
52	**LP27611**	**rs3289**	3’ UTR-exon10	CC/TC/TT	0.027	-0.011	0.734	NA	0.110	0.135	NA
53	**LP27229**	**rs11570891**	Intron 9	CC/TC/TT	0.107	0.039	0.024	0.148	-0.062	0.119	0.052
53	**LP27249**	**rs4922115**	3’ UTR-exon10	AA/AG/GG	0.146	0.015	0.304	NA	-0.070	0.039	NA
53	**LP27611**	**rs3289**	3’ UTR-exon10	CC/TC/TT	0.027	-0.011	0.734	NA	0.110	0.135	NA
53	**LP27688**	**rs191212278**	3’ UTR-exon10	CC/TC	0.004	-0.011	0.891	NA	-0.063	0.744	NA
54	**LP27249**	**rs4922115**	3’ UTR-exon10	AA/AG/GG	0.146	0.015	0.304	0.667	-0.070	0.039	0.190
54	**LP27611**	**rs3289**	3’ UTR-exon10	CC/TC/TT	0.027	-0.011	0.734	NA	0.110	0.135	NA
54	**LP27688**	**rs191212278**	3’ UTR-exon10	CC/TC	0.004	-0.011	0.891	NA	-0.063	0.744	NA
54	**LP28407**	**rs150252331**	3’ UTR-exon10	GG/GT	0.018	-0.049	0.225	NA	-0.021	0.822	NA
55	**LP27611**	**rs3289**	3’ UTR-exon10	CC/TC/TT	0.027	-0.011	0.734	0.528	0.110	0.135	0.440
55	**LP27688**	**rs191212278**	3’ UTR-exon10	CC/TC	0.004	-0.011	0.891	NA	-0.063	0.744	NA
55	**LP28407**	**rs150252331**	3’ UTR-exon10	GG/GT	0.018	-0.049	0.225	NA	-0.021	0.822	NA
55	**LP28524**	**Novel**	3’ UTR-exon10	CC/CT	0.001	-0.287	0.125	NA	0.927	0.031	NA
56	**LP27688**	**rs191212278**	3’ UTR-exon10	CC/TC	0.004	-0.011	0.891	0.029	-0.063	0.744	0.020
56	**LP28407**	**rs150252331**	3’ UTR-exon10	GG/GT	0.018	-0.049	0.225	NA	-0.021	0.822	NA
56	**LP28524**	**Novel**	3’ UTR-exon10	CC/CT	0.001	-0.287	0.125	NA	0.927	0.031	NA
56	**LP28911**	**rs13702**	3’ UTR-exon10	CC/CT/TT	0.272	0.032	0.006	NA	-0.079	0.003	NA
57	**LP28407**	**rs150252331**	3’ UTR-exon10	GG/GT	0.018	-0.049	0.225	0.030	-0.021	0.822	0.026
57	**LP28524**	**Novel**	3’ UTR-exon10	CC/CT	0.001	-0.287	0.125	NA	0.927	0.031	NA
57	**LP28911**	**rs13702**	3’ UTR-exon10	CC/CT/TT	0.272	0.032	0.006	NA	-0.079	0.003	NA
57	**LP28982**	**rs1059611**	3’ UTR-exon10	CC/TC/TT	0.107	0.037	0.030	NA	-0.054	0.176	NA
58	**LP28524**	**Novel**	3’ UTR-exon10	CC/CT	0.001	-0.287	0.125	0.027	0.927	0.031	0.028
58	**LP28911**	**rs13702**	3’ UTR-exon10	CC/CT/TT	0.272	0.032	0.006	NA	-0.079	0.003	NA
58	**LP28982**	**rs1059611**	3’ UTR-exon10	CC/TC/TT	0.107	0.037	0.030	NA	-0.054	0.176	NA
58	**LP29315**	**rs9644636**	3’ UTR-exon10	GG/GT/TT	0.288	-0.002	0.846	NA	0.034	0.219	NA
59	**LP28911**	**rs13702**	3’ UTR-exon10	CC/CT/TT	0.272	0.032	0.006	0.036	-0.079	0.003	0.040
59	**LP28982**	**rs1059611**	3’ UTR-exon10	CC/TC/TT	0.107	0.037	0.030	NA	-0.054	0.176	NA
59	**LP29315**	**rs9644636**	3’ UTR-exon10	GG/GT/TT	0.288	-0.002	0.846	NA	0.034	0.219	NA
59	**LP29474**	**rs113831503**	3’ UTR-exon10	CC/CT/TT	0.036	-0.013	0.650	NA	0.005	0.941	NA
60	**LP28982**	**rs1059611**	3’ UTR-exon10	CC/TC/TT	0.107	0.037	0.030	0.083	-0.054	0.176	0.042
60	**LP29315**	**rs9644636**	3’ UTR-exon10	GG/GT/TT	0.288	-0.002	0.846	NA	0.034	0.219	NA
60	**LP29474**	**rs113831503**	3’ UTR-exon10	CC/CT/TT	0.036	-0.013	0.650	NA	0.005	0.941	NA
60	**LP29547**	**rs4921684**	3’ flanking	CC/CT/TT	0.149	0.013	0.369	NA	-0.073	0.032	NA
61	**LP29315**	**rs9644636**	3’ UTR-exon10	GG/GT/TT	0.288	-0.002	0.846	0.679	0.034	0.219	0.111
61	**LP29474**	**rs113831503**	3’ UTR-exon10	CC/CT/TT	0.036	-0.013	0.650	NA	0.005	0.941	NA
61	**LP29547**	**rs4921684**	3’ flanking	CC/CT/TT	0.149	0.013	0.369	NA	-0.073	0.032	NA
61	**LP29716**	**rs8008515**	3’ flanking	TC/TT	0.014	0.027	0.563	NA	-0.034	0.750	NA

*P: Single-SNP p-value, **hap_P: Global haplotype p-value, W: Allele in the reference sequence ; D: Deleted base/bases; I: Inserted base/bases

Table A1.11. ***LPL*** **4-SNP sliding window haplotype association results for TC and LDL-C in NHWs (n=623)**

							TC			LDL	
Window	**Window SNP**	**RefSNP ID**	**Location**	**Genotypes**	**MAF**	**Beta**	**P****	***hap_P**	**Beta**	**P****	***hap_P**
1	**LP1088**	**rs80351041**	5' UTR-exon1	GG/GT	0.01	-5.4	0.66	0.886	-5.25	0.65	0.512
1	**LP1130**	**Novel**	5' UTR-exon1	GC/GG	0	31.6	0.19	NA	12.08	0.6	NA
1	**LP2335**	**rs3779787**	Intron 1	GG/GT/TT	0.15	1.39	0.68	NA	-0.62	0.85	NA
1	**LP3964**	**rs17410577**	Intron 1	CC/GC/GG	0.21	1.342	0.65	NA	4.11	0.14	NA
2	**LP1130**	**Novel**	5' UTR-exon1	GC/GG	0	31.6	0.19	0.647	12.08	0.6	0.337
2	**LP2335**	**rs3779787**	Intron 1	GG/GT/TT	0.15	1.39	0.68	NA	-0.62	0.85	NA
2	**LP3964**	**rs17410577**	Intron 1	CC/GC/GG	0.21	1.342	0.65	NA	4.11	0.14	NA
2	**LP4060**	**rs1534649**	Intron 1	GG/TG/TT	0.45	-0.57	0.82	NA	-0.37	0.87	NA
3	**LP2335**	**rs3779787**	Intron 1	GG/GT/TT	0.15	1.39	0.68	0.76	-0.62	0.85	0.524
3	**LP3964**	**rs17410577**	Intron 1	CC/GC/GG	0.21	1.342	0.65	NA	4.11	0.14	NA
3	**LP4060**	**rs1534649**	Intron 1	GG/TG/TT	0.45	-0.57	0.82	NA	-0.37	0.87	NA
3	**LP4424**	**rs13266204**	Intron 1	AA/AG/GG	0.21	0.865	0.76	NA	1.905	0.49	NA
4	**LP3964**	**rs17410577**	Intron 1	CC/GC/GG	0.21	1.342	0.65	0.843	4.11	0.14	0.637
4	**LP4060**	**rs1534649**	Intron 1	GG/TG/TT	0.45	-0.57	0.82	NA	-0.37	0.87	NA
4	**LP4424**	**rs13266204**	Intron 1	AA/AG/GG	0.21	0.865	0.76	NA	1.905	0.49	NA
4	**LP4948**	**rs6997330**	Intron 1	CG/GG	0.02	-9.59	0.28	NA	-8.08	0.34	NA
5	**LP4060**	**rs1534649**	Intron 1	GG/TG/TT	0.45	-0.57	0.82	0.818	-0.37	0.87	0.658
5	**LP4424**	**rs13266204**	Intron 1	AA/AG/GG	0.21	0.865	0.76	NA	1.905	0.49	NA
5	**LP4948**	**rs6997330**	Intron 1	CG/GG	0.02	-9.59	0.28	NA	-8.08	0.34	NA
5	**LP5949**	**rs112127208**	Intron 1	GG/TG/TT	0.16	1.871	0.57	NA	-0.65	0.84	NA
6	**LP4060**	**rs1534649**	Intron 1	AA/AG/GG	0.21	0.865	0.76	0.714	1.905	0.49	0.668
6	**LP4424**	**rs13266204**	Intron 1	CG/GG	0.02	-9.59	0.28	NA	-8.08	0.34	NA
6	**LP4948**	**rs6997330**	Intron 1	GG/TG/TT	0.16	1.871	0.57	NA	-0.65	0.84	NA
6	**LP6821**	**rs10104051**	Intron 1	CC/TC/TT	0.44	-1.3	0.59	NA	-0.32	0.89	NA
7	**LP4948**	**rs6997330**	Intron 1	CG/GG	0.02	-9.59	0.28	0.726	-8.08	0.34	0.652
7	**LP5949**	**rs112127208**	Intron 1	GG/TG/TT	0.16	1.871	0.57	NA	-0.65	0.84	NA
7	**LP6821**	**rs10104051**	Intron 1	CC/TC/TT	0.44	-1.3	0.59	NA	-0.32	0.89	NA
7	**LP7503**	**rs6999612**	Intron 1	CC/CT/TT	0.02	-8.18	0.32	NA	-6.57	0.4	NA
8	**LP5949**	**rs112127208**	Intron 1	GG/TG/TT	0.16	1.871	0.57	0.637	-0.65	0.84	0.438
8	**LP6821**	**rs10104051**	Intron 1	CC/TC/TT	0.44	-1.3	0.59	NA	-0.32	0.89	NA
8	**LP7503**	**rs6999612**	Intron 1	CC/CT/TT	0.02	-8.18	0.32	NA	-6.57	0.4	NA
8	**LP7512**	**rs3779788**	Intron 1	CC/TC/TT	0.15	-0.31	0.93	NA	-2.06	0.53	NA
9	**LP6821**	**rs10104051**	Intron 1	CC/TC/TT	0.44	-1.3	0.59	0.86	-0.32	0.89	0.825
9	**LP7503**	**rs6999612**	Intron 1	CC/CT/TT	0.02	-8.18	0.32	NA	-6.57	0.4	NA
9	**LP7512**	**rs3779788**	Intron 1	CC/TC/TT	0.15	-0.31	0.93	NA	-2.06	0.53	NA
9	**LP8221**	**rs7000460**	Intron 1	AA/CA	0.02	-9.57	0.28	NA	-8.06	0.34	NA
10	**LP7503**	**rs6999612**	Intron 1	CC/CT/TT	0.02	-8.18	0.32	0.784	-6.57	0.4	0.745
10	**LP7512**	**rs3779788**	Intron 1	CC/TC/TT	0.15	-0.31	0.93	NA	-2.06	0.53	NA
10	**LP8221**	**rs7000460**	Intron 1	AA/CA	0.02	-9.57	0.28	NA	-8.06	0.34	NA
10	**LP10127**	**rs1801177**	Intron 1	AG/GG	0.02	-9.57	0.28	NA	-8.06	0.34	NA
11	**LP7512**	**rs3779788**	Intron 1	CC/TC/TT	0.15	-0.31	0.93	0.753	-2.06	0.53	0.748
11	**LP8221**	**rs7000460**	Intron 1	AA/CA	0.02	-9.57	0.28	NA	-8.06	0.34	NA
11	**LP10127**	**rs1801177**	Intron 1	AG/GG	0.02	-9.57	0.28	NA	-8.06	0.34	NA
11	**LP10912**	**rs149477831**	Intron 1	AA/AG	0.01	-3.98	0.73	NA	2.098	0.85	NA
12	**LP8221**	**rs7000460**	Intron 1	AA/CA	0.02	-9.57	0.28	0.621	-8.06	0.34	0.558
12	**LP10127**	**rs1801177**	Exon 2	AG/GG	0.02	-9.57	0.28	NA	-8.06	0.34	NA
12	**LP10912**	**rs149477831**	Intron 1	AA/AG	0.01	-3.98	0.73	NA	2.098	0.85	NA
12	**LP10987**	**rs74377536**	Intron 2	AA/CA/CC	0.12	2.886	0.45	NA	4.101	0.26	NA
13	**LP10127**	**rs1801177**	Exon 2	AG/GG	0.02	-9.57	0.28	0.624	-8.06	0.34	0.56
13	**LP10912**	**rs149477831**	Intron 1	AA/AG	0.01	-3.98	0.73	NA	2.098	0.85	NA
13	**LP10987**	**rs74377536**	Intron 2	AA/CA/CC	0.12	2.886	0.45	NA	4.101	0.26	NA
13	**LP11050**	**rs7016529**	Intron 2	CT/TT	0.02	-9.12	0.32	NA	-7.47	0.39	NA
14	**LP10912**	**rs149477831**	Intron 1	AA/AG	0.01	-3.98	0.73	0.809	2.098	0.85	0.62
14	**LP10987**	**rs74377536**	Intron 2	AA/CA/CC	0.12	2.886	0.45	NA	4.101	0.26	NA
14	**LP11050**	**rs7016529**	Intron 2	CT/TT	0.02	-9.12	0.32	NA	-7.47	0.39	NA
14	**LP11090**	**rs8176337**	Intron 2	CC/CG/GG	0.24	-2.18	0.47	NA	-4.06	0.16	NA
15	**LP10987**	**rs74377536**	Intron 2	AA/CA/CC	0.12	2.886	0.45	0.814	4.101	0.26	0.613
15	**LP11050**	**rs7016529**	Intron 2	CT/TT	0.02	-9.12	0.32	NA	-7.47	0.39	NA
15	**LP11090**	**rs8176337**	Intron 2	CC/CG/GG	0.24	-2.18	0.47	NA	-4.06	0.16	NA
15	**LP11888_11889ins1**	**rs149017698**	Intron 2	II/WI/WW	0.02	-8.64	0.29	NA	-6.9	0.38	NA
16	**LP11050**	**rs7016529**	Intron 2	CT/TT	0.02	-9.12	0.32	0.87	-7.47	0.39	0.528
16	**LP11090**	**rs8176337**	Intron 2	CC/CG/GG	0.24	-2.18	0.47	NA	-4.06	0.16	NA

Table A1.11. Continued

							TC			LDL	
Window	**Window SNP**	**RefSNP ID**	**Location**	**Genotypes**	**MAF**	**Beta**	**P****	***hap_P**	**Beta**	**P****	***hap_P**
16	**LP11888_11889ins1**	**rs149017698**	Intron 2	II/WI/WW	0.02	-8.64	0.29	NA	-6.9	0.38	NA
16	**LP13003**	**rs80181352**	Intron 2	GG/GT/TT	0.08	-0.6	0.89	NA	-5.59	0.19	NA
17	**LP11090**	**rs8176337**	Intron 2	CC/CG/GG	0.24	-2.18	0.47	0.671	-4.06	0.16	0.366
17	**LP11888_11889ins1**	**rs149017698**	Intron 2	II/WI/WW	0.02	-8.64	0.29	NA	-6.9	0.38	NA
17	**LP1300**	**rs80181352**	Intron 2	GG/GT/TT	0.08	-0.6	0.89	NA	-5.59	0.19	NA
17	**LP13639**	**rs78326602**	Intron 2	GA/GG	0.01	-15.9	0.26	NA	-16.1	0.23	NA
18	**LP11888_11889ins1**	**rs149017698**	Intron 2	II/WI/WW	0.02	-8.64	0.29	0.609	-6.9	0.38	0.376
18	**LP1300**	**rs80181352**	Intron 2	GG/GT/TT	0.08	-0.6	0.89	NA	-5.59	0.19	NA
18	**LP13639**	**rs78326602**	Intron 2	GA/GG	0.01	-15.9	0.26	NA	-16.1	0.23	NA
18	**LP13854**	**rs1121923**	Intron 2	CC/TC	0.03	-0.44	0.95	NA	0.508	0.94	NA
19	**LP1300**	**rs80181352**	Intron 2	GG/GT/TT	0.08	-0.6	0.89	0.852	-5.59	0.19	0.498
19	**LP13639**	**rs78326602**	Intron 2	GA/GG	0.01	-15.9	0.26	NA	-16.1	0.23	NA
19	**LP13854**	**rs1121923**	Exon 3	CC/TC	0.03	-0.44	0.95	NA	0.508	0.94	NA
19	**LP14114**	**rs73667472**	Intron 3	AA/AG/GG	0.08	1.014	0.81	NA	-0.69	0.87	NA
20	**LP13639**	**rs78326602**	Intron 2	GA/GG	0.01	-15.9	0.26	0.843	-16.1	0.23	0.806
20	**LP13854**	**rs1121923**	Exon 3	CC/TC	0.03	-0.44	0.95	NA	0.508	0.94	NA
20	**LP14114**	**rs73667472**	Intron 3	AA/AG/GG	0.08	1.014	0.81	NA	-0.69	0.87	NA
20	**LP15245**	**rs248**	Exon 4	AA/GA/GG	0.07	-1.49	0.75	NA	-1.5	0.74	NA
21	**LP13854**	**rs1121923**	Exon 3	CC/TC	0.03	-0.44	0.95	0.993	0.508	0.94	0.965
21	**LP14114**	**rs73667472**	Intron 3	AA/AG/GG	0.08	1.014	0.81	NA	-0.69	0.87	NA
21	**LP15245**	**rs248**	Exon 4	AA/GA/GG	0.07	-1.49	0.75	NA	-1.5	0.74	NA
21	**LP15425**	**rs249**	Intron 4	CC/TC/TT	0.08	-0.46	0.92	NA	-2.49	0.55	NA
22	**LP14114**	**rs73667472**	Intron 3	AA/AG/GG	0.08	1.014	0.81	0.705	-0.69	0.87	0.828
22	**LP15245**	**rs248**	Exon 4	AA/GA/GG	0.07	-1.49	0.75	NA	-1.5	0.74	NA
22	**LP15425**	**rs249**	Intron 4	CC/TC/TT	0.08	-0.46	0.92	NA	-2.49	0.55	NA
22	**LP15836**	**rs253**	Intron 4	CC/CT/TT	0.45	2.608	0.28	NA	1.009	0.66	NA
23	**LP15245**	**rs248**	Exon 4	AA/GA/GG	0.07	-1.49	0.75	0.883	-1.5	0.74	0.892
23	**LP15425**	**rs249**	Intron 4	CC/TC/TT	0.08	-0.46	0.92	NA	-2.49	0.55	NA
23	**LP15836**	**rs253**	Intron 4	CC/CT/TT	0.45	2.608	0.28	NA	1.009	0.66	NA
23	**LP16316**	**rs254**	Intron 5	CC/CG/GG	0.14	2.068	0.55	NA	-0.2	0.95	NA
24	**LP15425**	**rs249**	Intron 4	CC/TC/TT	0.08	-0.46	0.92	0.866	-2.49	0.55	0.956
24	**LP15836**	**rs253**	Intron 4	CC/CT/TT	0.45	2.608	0.28	NA	1.009	0.66	NA
24	**LP16316**	**rs254**	Intron 5	CC/CG/GG	0.14	2.068	0.55	NA	-0.2	0.95	NA
24	**LP16442**	**rs74382962**	Intron 5	CG/GG	0	-2.87	0.91	NA	5.125	0.83	NA
25	**LP15836**	**rs253**	Intron 4	CC/CT/TT	0.45	2.608	0.28	0.563	1.009	0.66	0.809
25	**LP16316**	**rs254**	Intron 5	CC/CG/GG	0.14	2.068	0.55	NA	-0.2	0.95	NA
25	**LP16442**	**rs74382962**	Intron 5	CG/GG	0	-2.87	0.91	NA	5.125	0.83	NA
25	**LP17599**	**rs264**	Intron 5	AA/GA/GG	0.14	2.021	0.56	NA	-0.56	0.87	NA
26	**LP16316**	**rs254**	Intron 5	CC/CG/GG	0.14	2.068	0.55	0.722	-0.2	0.95	0.867
26	**LP16442**	**rs74382962**	Intron 5	CG/GG	0	-2.87	0.91	NA	5.125	0.83	NA
26	**LP17599**	**rs264**	Intron 5	AA/GA/GG	0.14	2.021	0.56	NA	-0.56	0.87	NA
26	**LP17948**	**rs268**	Exon 6	AA/AG	0.02	1.434	0.88	NA	-1.61	0.86	NA
27	**LP16442**	**rs74382962**	Intron 5	CG/GG	0	-2.87	0.91	0.916	5.125	0.83	0.948
27	**LP17599**	**rs264**	Intron 5	AA/GA/GG	0.14	2.021	0.56	NA	-0.56	0.87	NA
27	**LP17948**	**rs268**	Exon 6	AA/AG	0.02	1.434	0.88	NA	-1.61	0.86	NA
27	**LP18086**	**rs269**	Intron 6	GG/GT/TT	0.17	2.715	0.39	NA	0.578	0.85	NA
28	**LP17599**	**rs264**	Intron 5	AA/GA/GG	0.14	2.021	0.56	0.537	-0.56	0.87	0.397
28	**LP17948**	**rs268**	Exon 6	AA/AG	0.02	1.434	0.88	NA	-1.61	0.86	NA
28	**LP18086**	**rs269**	Intron 6	GG/GT/TT	0.17	2.715	0.39	NA	0.578	0.85	NA
28	**LP18095**	**rs270**	Intron 6	AA/CA/CC	0.17	3.949	0.2	NA	5.277	0.08	NA
29	**LP17948**	**rs268**	Exon 6	AA/AG	0.02	1.434	0.88	0.444	-1.61	0.86	0.344
29	**LP18086**	**rs269**	Intron 6	GG/GT/TT	0.17	2.715	0.39	NA	0.578	0.85	NA
29	**LP18095**	**rs270**	Intron 6	AA/CA/CC	0.17	3.949	0.2	NA	5.277	0.08	NA
29	**LP18822**	**rs277**	Intron 6	CC/CT/TT	0.2	3.439	0.26	NA	3.654	0.21	NA
30	**LP18086**	**rs269**	Intron 6	GG/GT/TT	0.17	2.715	0.39	0.462	0.578	0.85	0.131
30	**LP18095**	**rs270**	Intron 6	AA/CA/CC	0.17	3.949	0.2	NA	5.277	0.08	NA
30	**LP18822**	**rs277**	Intron 6	CC/CT/TT	0.2	3.439	0.26	NA	3.654	0.21	NA
30	**LP19445**	**rs282**	Intron 6	CC/GC/GG	0.14	-3.06	0.39	NA	-6.28	0.06	NA
31	**LP18095**	**rs270**	Intron 6	AA/CA/CC	0.17	3.949	0.2	0.349	5.277	0.08	0.071
31	**LP18822**	**rs277**	Intron 6	CC/CT/TT	0.2	3.439	0.26	NA	3.654	0.21	NA
31	**LP19445**	**rs282**	Intron 6	CC/GC/GG	0.14	-3.06	0.39	NA	-6.28	0.06	NA
31	**LP19517**	**rs283**	Intron 6	CC/CT/TT	0.2	-2.1	0.48	NA	-1.71	0.54	NA
32	**LP18822**	**rs277**	Intron 6	CC/CT/TT	0.2	3.439	0.26	0.248	3.654	0.21	0.28
32	**LP19445**	**rs282**	Intron 6	CC/GC/GG	0.14	-3.06	0.39	NA	-6.28	0.06	NA
32	**LP19517**	**rs283**	Intron 6	CC/CT/TT	0.2	-2.1	0.48	NA	-1.71	0.54	NA
32	**LP19608**	**rs285**	Intron 6	CC/CT/TT	0.48	-0.68	0.78	NA	-1.99	0.38	NA
33	**LP19445**	**rs282**	Intron 6	CC/GC/GG	0.14	-3.06	0.39	0.057	-6.28	0.06	0.097
33	**LP19517**	**rs283**	Intron 6	CC/CT/TT	0.2	-2.1	0.48	NA	-1.71	0.54	NA
33	**LP19608**	**rs285**	Intron 6	CC/CT/TT	0.48	-0.68	0.78	NA	-1.99	0.38	NA
33	**LP19675**	**rs286**	Intron 6	AA/TA/TT	0.1	1.518	0.71	NA	-0.91	0.81	NA
34	**LP19517**	**rs283**	Intron 6	CC/CT/TT	0.2	-2.1	0.48	0.037	-1.71	0.54	0.148
34	**LP19608**	**rs285**	Intron 6	CC/CT/TT	0.48	-0.68	0.78	NA	-1.99	0.38	NA
34	**LP19675**	**rs286**	Intron 6	AA/TA/TT	0.1	1.518	0.71	NA	-0.91	0.81	NA

Table A1.11. Continued

						TC			LDL		
Window	**Window SNP**	**RefSNP ID**	**Location**	**Genotypes**	**MAF**	**Beta**	**P****	***hap_P**	**Beta**	**P****	***hap_P**
34	**LP20363**	**rs296**	Intron 6	AA/TA/TT	0.05	2.262	0.68	NA	5.146	0.32	NA
35	**LP19608**	**rs285**	Intron 6	CC/CT/TT	0.48	-0.68	0.78	0.305	-1.99	0.38	0.393
35	**LP19675**	**rs286**	Intron 6	AA/TA/TT	0.1	1.518	0.71	NA	-0.91	0.81	NA
35	**LP20363**	**rs296**	Intron 6	AA/TA/TT	0.05	2.262	0.68	NA	5.146	0.32	NA
35	**LP20544**	**rs294**	Intron 6	AA/AG/GG	0.12	4.09	0.27	NA	1.943	0.59	NA
36	**LP19675**	**rs286**	Intron 6	AA/TA/TT	0.1	1.518	0.71	0.589	-0.91	0.81	0.593
36	**LP20363**	**rs296**	Intron 6	AA/TA/TT	0.05	2.262	0.68	NA	5.146	0.32	NA
36	**LP20544**	**rs294**	Intron 6	AA/AG/GG	0.12	4.09	0.27	NA	1.943	0.59	NA
36	**LP20657**	**rs295**	Intron 6	AA/CA/CC	0.22	2.561	0.37	NA	2.243	0.41	NA
37	**LP20363**	**rs296**	Intron 6	AA/TA/TT	0.05	2.262	0.68	0.406	5.146	0.32	0.177
37	**LP20544**	**rs294**	Intron 6	AA/AG/GG	0.12	4.09	0.27	NA	1.943	0.59	NA
37	**LP20657**	**rs295**	Intron 6	AA/CA/CC	0.22	2.561	0.37	NA	2.243	0.41	NA
37	**LP22044_22047del4**	**rs311**	Intron 7	DD/WD/WW	0.05	2.427	0.66	NA	0.707	0.89	NA
38	**LP20544**	**rs294**	Intron 6	AA/AG/GG	0.12	4.09	0.27	0.539	1.943	0.59	0.92
38	**LP20657**	**rs295**	Intron 6	AA/CA/CC	0.22	2.561	0.37	NA	2.243	0.41	NA
38	**LP22044_22047del4**	**rs311**	Intron 7	DD/WD/WW	0.05	2.427	0.66	NA	0.707	0.89	NA
38	**LP22416**	**rs312**	Intron 7	CC/GC/GG	0.11	5.092	0.18	NA	2.423	0.5	NA
39	**LP20657**	**rs295**	Intron 6	AA/CA/CC	0.22	2.561	0.37	0.198	2.243	0.41	0.433
39	**LP22044_22047del4**	**rs311**	Intron 7	DD/WD/WW	0.05	2.427	0.66	NA	0.707	0.89	NA
39	**LP22416**	**rs312**	Intron 7	CC/GC/GG	0.11	5.092	0.18	NA	2.423	0.5	NA
39	**LP22461**	**rs314**	Intron 6	AA/GA/GG	0.26	-1.45	0.6	NA	-1.37	0.61	NA
40	**LP22044_22047del4**	**rs311**	Intron 7	DD/WD/WW	0.05	2.427	0.66	0.358	0.707	0.89	0.547
40	**LP22416**	**rs312**	Intron 7	CC/GC/GG	0.11	5.092	0.18	NA	2.423	0.5	NA
40	**LP22461**	**rs314**	Intron 7	AA/GA/GG	0.26	-1.45	0.6	NA	-1.37	0.61	NA
40	**LP22514**	**rs315**	Intron 7	CT/TT	0.01	12.3	0.48	NA	-14.5	0.38	NA
41	**LP22416**	**rs312**	Intron 7	CC/GC/GG	0.11	5.092	0.18	0.218	2.423	0.5	0.364
41	**LP22461**	**rs314**	Intron 7	AA/GA/GG	0.26	-1.45	0.6	NA	-1.37	0.61	NA
41	**LP22514**	**rs315**	Intron 7	CT/TT	0.01	12.3	0.48	NA	-14.5	0.38	NA
41	**LP22855**	**rs316**	Exon 8	AA/CA/CC	0.11	4.52	0.23	NA	3.58	0.32	NA
42	**LP22461**	**rs314**	Intron 7	AA/GA/GG	0.26	-1.45	0.6	0.317	-1.37	0.61	0.224
42	**LP22514**	**rs315**	Intron 7	CT/TT	0.01	12.3	0.48	NA	-14.5	0.38	NA
42	**LP22855**	**rs316**	Exon 8	AA/CA/CC	0.11	4.52	0.23	NA	3.58	0.32	NA
42	**LP23192**	**rs117026536**	Intron 8	GG/GT/TT	0.1	0.562	0.88	NA	-1.09	0.77	NA
43	**LP22514**	**rs315**	Intron 7	CT/TT	0.01	12.3	0.48	0.646	-14.5	0.38	0.716
43	**LP22855**	**rs316**	Exon 8	AA/CA/CC	0.11	4.52	0.23	NA	3.58	0.32	NA
43	**LP23192**	**rs117026536**	Intron 8	GG/GT/TT	0.1	0.562	0.88	NA	-1.09	0.77	NA
43	**LP23496**	**rs320**	Intron 8	GG/GT/TT	0.26	0.767	0.77	NA	0.897	0.72	NA
44	**LP22855**	**rs316**	Exon 8	AA/CA/CC	0.11	4.52	0.23	0.752	3.58	0.32	0.898
44	**LP23192**	**rs117026536**	Intron 8	GG/GT/TT	0.1	0.562	0.88	NA	-1.09	0.77	NA
44	**LP23496**	**rs320**	Intron 8	GG/GT/TT	0.26	0.767	0.77	NA	0.897	0.72	NA
44	**LP22855**	**rs327**	Intron 8	GG/TG/TT	0.27	1.181	0.65	NA	0.787	0.76	NA
45	**LP23192**	**rs117026536**	Intron 8	GG/GT/TT	0.1	0.562	0.88	0.965	-1.09	0.77	0.784
45	**LP23496**	**rs320**	Intron 8	GG/GT/TT	0.26	0.767	0.77	NA	0.897	0.72	NA
45	**LP22855**	**rs327**	Intron 8	GG/TG/TT	0.27	1.181	0.65	NA	0.787	0.76	NA
45	**LP24143**	**rs328**	Intron 8	CC/GC/GG	0.1	-0.01	1	NA	-1.91	0.61	NA
46	**LP23496**	**rs320**	Intron 8	GG/GT/TT	0.26	0.767	0.77	0.776	0.897	0.72	0.921
46	**LP22855**	**rs327**	Intron 8	GG/TG/TT	0.27	1.181	0.65	NA	0.787	0.76	NA
46	**LP24143**	**rs328**	Exon 9	CC/GC/GG	0.1	-0.01	1	NA	-1.91	0.61	NA
46	**LP25049**	**rs78031480**	Intron 9	AA/AG/GG	0.05	-5.77	0.31	NA	-0.68	0.9	NA
47	**LP22855**	**rs327**	Intron 8	GG/TG/TT	0.27	1.181	0.65	0.86	0.787	0.76	0.932
47	**LP24143**	**rs328**	Exon 9	CC/GC/GG	0.1	-0.01	1	NA	-1.91	0.61	NA
47	**LP25049**	**rs78031480**	Intron 9	AA/AG/GG	0.05	-5.77	0.31	NA	-0.68	0.9	NA
47	**LP26234**	**rs10099160**	Intron 9	GG/GT/TT	0.26	-0.82	0.77	NA	-0.33	0.9	NA
48	**LP24143**	**rs328**	Exon 9	CC/GC/GG	0.1	-0.01	1	0.718	-1.91	0.61	0.968
48	**LP25049**	**rs78031480**	Intron 9	AA/AG/GG	0.05	-5.77	0.31	NA	-0.68	0.9	NA
48	**LP26234**	**rs10099160**	Intron 9	GG/GT/TT	0.26	-0.82	0.77	NA	-0.33	0.9	NA
48	**LP27000**	**rs11232447**	Intron 9	CC/CT/TT	0.03	-6.81	0.33	NA	-2.81	0.67	NA
49	**LP25049**	**rs78031480**	Intron 9	AA/AG/GG	0.05	-5.77	0.31	0.737	-0.68	0.9	0.986
49	**LP26234**	**rs10099160**	Intron 9	GG/GT/TT	0.26	-0.82	0.77	NA	-0.33	0.9	NA
49	**LP27000**	**rs11232447**	Intron 9	CC/CT/TT	0.03	-6.81	0.33	NA	-2.81	0.67	NA
49	**LP27160**	**rs117910839**	Intron 9	AA/TA/TT	0.03	2.602	0.71	NA	3.19	0.63	NA
50	**LP26234**	**rs10099160**	Intron 9	GG/GT/TT	0.26	-0.82	0.77	0.865	-0.33	0.9	0.958
50	**LP27000**	**rs11232447**	Intron 9	CC/CT/TT	0.03	-6.81	0.33	NA	-2.81	0.67	NA
50	**LP27160**	**rs117910839**	Intron 9	AA/TA/TT	0.03	2.602	0.71	NA	3.19	0.63	NA
50	**LP27229**	**rs11570891**	Intron 9	CC/TC/TT	0.11	1.766	0.64	NA	-0.41	0.91	NA
51	**LP27000**	**rs11232447**	Intron 9	CC/CT/TT	0.03	-6.81	0.33	0.059	-2.81	0.67	0.255
51	**LP27160**	**rs117910839**	Intron 9	AA/TA/TT	0.03	2.602	0.71	NA	3.19	0.63	NA
51	**LP27229**	**rs11570891**	Intron 9	CC/TC/TT	0.11	1.766	0.64	NA	-0.41	0.91	NA
51	**LP27249**	**rs4922115**	3’ UTR-exon10	AA/AG/GG	0.15	2.024	0.54	NA	2.345	0.45	NA
52	**LP27160**	**rs117910839**	Intron 9	AA/TA/TT	0.03	2.602	0.71	0.777	3.19	0.63	0.642
52	**LP27229**	**rs11570891**	Intron 9	CC/TC/TT	0.11	1.766	0.64	NA	-0.41	0.91	NA
52	**LP27249**	**rs4922115**	3’ UTR-exon10	AA/AG/GG	0.15	2.024	0.54	NA	2.345	0.45	NA
52	**LP27611**	**rs3289**	3’ UTR-exon10	CC/TC/TT	0.03	-8.29	0.25	NA	-9.02	0.19	NA

Table A1.11. Continued

							TC			LDL	
Window	**Window SNP**	**RefSNP ID**	**Location**	**Genotypes**	**MAF**	**Beta**	**P****	***hap_P**	**Beta**	**P****	***hap_P**
53	**LP27229**	**rs11570891**	Intron 9	CC/TC/TT	0.11	1.766	0.64	0.515	-0.41	0.91	0.508
53	**LP27249**	**rs4922115**	3’ UTR-exon10	AA/AG/GG	0.15	2.024	0.54	NA	2.345	0.45	NA
53	**LP27611**	**rs3289**	3’ UTR-exon10	CC/TC/TT	0.03	-8.29	0.25	NA	-9.02	0.19	NA
53	**LP27688**	**rs191212278**	3’ UTR-exon10	CC/TC	0	-22.6	0.23	NA	-19.3	0.28	NA
54	**LP27249**	**rs4922115**	3’ UTR-exon10	AA/AG/GG	0.15	2.024	0.54	0.544	2.345	0.45	0.52
54	**LP27611**	**rs3289**	3’ UTR-exon10	CC/TC/TT	0.03	-8.29	0.25	NA	-9.02	0.19	NA
54	**LP27688**	**rs191212278**	3’ UTR-exon10	CC/TC	0	-22.6	0.23	NA	-19.3	0.28	NA
54	**LP28407**	**rs150252331**	3’ UTR-exon10	GG/GT	0.02	-2.56	0.78	NA	0.584	0.95	NA
55	**LP27611**	**rs3289**	3’ UTR-exon10	CC/TC/TT	0.03	-8.29	0.25	0.553	-9.02	0.19	0.485
55	**LP27688**	**rs191212278**	3’ UTR-exon10	CC/TC	0	-22.6	0.23	NA	-19.3	0.28	NA
55	**LP28407**	**rs150252331**	3’ UTR-exon10	GG/GT	0.02	-2.56	0.78	NA	0.584	0.95	NA
55	**LP28524**	**Novel**	3’ UTR-exon10	CC/CT	0	31.28	0.46	NA	14.52	0.72	NA
56	**LP27688**	**rs191212278**	3’ UTR-exon10	CC/TC	0	-22.6	0.23	0.862	-19.3	0.28	0.844
56	**LP28407**	**rs150252331**	3’ UTR-exon10	GG/GT	0.02	-2.56	0.78	NA	0.584	0.95	NA
56	**LP28524**	**Novel**	3’ UTR-exon10	CC/CT	0	31.28	0.46	NA	14.52	0.72	NA
56	**LP28911**	**rs13702**	3’ UTR-exon10	CC/CT/TT	0.27	0.724	0.78	NA	0.961	0.7	NA
57	**LP28407**	**rs150252331**	3’ UTR-exon10	GG/GT	0.02	-2.56	0.78	0.932	0.584	0.95	0.997
57	**LP28524**	**Novel**	3’ UTR-exon10	CC/CT	0	31.28	0.46	NA	14.52	0.72	NA
57	**LP28911**	**rs13702**	3’ UTR-exon10	CC/CT/TT	0.27	0.724	0.78	NA	0.961	0.7	NA
57	**LP28982**	**rs1059611**	3’ UTR-exon10	CC/TC/TT	0.11	2.049	0.59	NA	-0.24	0.95	NA
58	**LP28524**	**Novel**	3’ UTR-exon10	CC/CT	0	31.28	0.46	0.943	14.52	0.72	0.995
58	**LP28911**	**rs13702**	3’ UTR-exon10	CC/CT/TT	0.27	0.724	0.78	NA	0.961	0.7	NA
58	**LP28982**	**rs1059611**	3’ UTR-exon10	CC/TC/TT	0.11	2.049	0.59	NA	-0.24	0.95	NA
58	**LP29315**	**rs9644636**	3’ UTR-exon10	GG/GT/TT	0.29	0.261	0.92	NA	-0.74	0.77	NA
59	**LP28911**	**rs13702**	3’ UTR-exon10	CC/CT/TT	0.27	0.724	0.78	0.681	0.961	0.7	0.921
59	**LP28982**	**rs1059611**	3’ UTR-exon10	CC/TC/TT	0.11	2.049	0.59	NA	-0.24	0.95	NA
59	**LP29315**	**rs9644636**	3’ UTR-exon10	GG/GT/TT	0.29	0.261	0.92	NA	-0.74	0.77	NA
59	**LP29474**	**rs113831503**	3’ UTR-exon10	CC/CT/TT	0.04	-7.61	0.23	NA	-3.7	0.54	NA
60	**LP28982**	**rs1059611**	3’ UTR-exon10	CC/TC/TT	0.11	2.049	0.59	0.462	-0.24	0.95	0.932
60	**LP29315**	**rs9644636**	3’ UTR-exon10	GG/GT/TT	0.29	0.261	0.92	NA	-0.74	0.77	NA
60	**LP29474**	**rs113831503**	3’ UTR-exon10	CC/CT/TT	0.04	-7.61	0.23	NA	-3.7	0.54	NA
60	**LP29547**	**rs4921684**	3’ flanking	CC/CT/TT	0.15	2.131	0.52	NA	1.182	0.71	NA
61	**LP29315**	**rs9644636**	3’ UTR-exon10	GG/GT/TT	0.29	0.261	0.92	0.512	-0.74	0.77	0.915
61	**LP29474**	**rs113831503**	3’ UTR-exon10	CC/CT/TT	0.04	-7.61	0.23	NA	-3.7	0.54	NA
61	**LP29547**	**rs4921684**	3’ flanking	CC/CT/TT	0.15	2.131	0.52	NA	1.182	0.71	NA
61	**LP29716**	**rs8008515**	3’ flanking	TC/TT	0.01	-2.72	0.79	NA	-3.64	0.71	NA

Table A1.12. *LPL* 4-SNP sliding window haplotype association results for ApoA1 and ApoB1 in NHWs (n=623)

						ApoA1			ApoB		
Window	**Window SNP**	**RefSNP ID**	**Location**	**Genotypes**	**MAF**	**Beta**	**P****	***hap_P**	**Beta**	**P****	***hap_P**
1	**LP1088**	**rs80351041**	5’ UTR-exon1	GG/GT	0.01	-3.639	0.74	0.339	-2.79	0.21	0.368
1	**LP1130**	**Novel**	5’ UTR-exon1	GC/GG	0.002	15.42	0.42	NA	-0.75	0.84	NA
1	**LP2335**	**rs3779787**	Intron 1	GG/GT/TT	0.154	0.346	0.91	NA	0.282	0.66	NA
1	**LP3964**	**rs17410577**	Intron 1	CC/GC/GG	0.207	-4.747	0.08	NA	0.319	0.55	NA
2	**LP1130**	**Novel**	5’ UTR-exon1	GC/GG	0.002	15.42	0.42	0.305	-0.75	0.84	0.78
2	**LP2335**	**rs3779787**	Intron 1	GG/GT/TT	0.154	0.346	0.91	NA	0.282	0.66	NA
2	**LP3964**	**rs17410577**	Intron 1	CC/GC/GG	0.207	-4.747	0.08	NA	0.319	0.55	NA
2	**LP4060**	**rs1534649**	Intron 1	GG/TG/TT	0.453	-2.737	0.23	NA	0.102	0.82	NA
3	**LP2335**	**rs3779787**	Intron 1	GG/GT/TT	0.154	0.346	0.91	0.535	0.282	0.66	0.585
3	**LP3964**	**rs17410577**	Intron 1	CC/GC/GG	0.207	-4.747	0.08	NA	0.319	0.55	NA
3	**LP4060**	**rs1534649**	Intron 1	GG/TG/TT	0.453	-2.737	0.23	NA	0.102	0.82	NA
3	**LP4424**	**rs13266204**	Intron 1	AA/AG/GG	0.214	-3.912	0.15	NA	0.344	0.52	NA
4	**LP3964**	**rs17410577**	Intron 1	CC/GC/GG	0.207	-4.747	0.08	0.525	0.319	0.55	0.382
4	**LP4060**	**rs1534649**	Intron 1	GG/TG/TT	0.453	-2.737	0.23	NA	0.102	0.82	NA
4	**LP4424**	**rs13266204**	Intron 1	AA/AG/GG	0.214	-3.912	0.15	NA	0.344	0.52	NA
4	**LP4948**	**rs6997330**	Intron 1	CG/GG	0.018	-3.23	0.72	NA	-3.17	0.07	NA
5	**LP4060**	**rs1534649**	Intron 1	GG/TG/TT	0.453	-2.737	0.23	0.493	0.102	0.82	0.521
5	**LP4424**	**rs13266204**	Intron 1	AA/AG/GG	0.214	-3.912	0.15	NA	0.344	0.52	NA
5	**LP4948**	**rs6997330**	Intron 1	CG/GG	0.018	-3.23	0.72	NA	-3.17	0.07	NA
5	**LP5949**	**rs112127208**	Intron 1	GG/TG/TT	0.163	-0.771	0.8	NA	0.096	0.88	NA
6	**LP4060**	**rs1534649**	Intron 1	AA/AG/GG	0.214	-3.912	0.15	0.601	0.344	0.52	0.39
6	**LP4424**	**rs13266204**	Intron 1	CG/GG	0.018	-3.23	0.72	NA	-3.17	0.07	NA
6	**LP4948**	**rs6997330**	Intron 1	GG/TG/TT	0.163	-0.771	0.8	NA	0.096	0.88	NA
6	**LP6821**	**rs10104051**	Intron 1	CC/TC/TT	0.442	-2.409	0.29	NA	0.107	0.81	NA
7	**LP4948**	**rs6997330**	Intron 1	CG/GG	0.018	-3.23	0.72	0.699	-3.17	0.07	0.32
7	**LP5949**	**rs112127208**	Intron 1	GG/TG/TT	0.163	-0.771	0.8	NA	0.096	0.88	NA
7	**LP6821**	**rs10104051**	Intron 1	CC/TC/TT	0.442	-2.409	0.29	NA	0.107	0.81	NA
7	**LP7503**	**rs6999612**	Intron 1	CC/CT/TT	0.02	-3.962	0.62	NA	-1.84	0.24	NA
8	**LP5949**	**rs112127208**	Intron 1	GG/TG/TT	0.163	-0.771	0.8	0.814	0.096	0.88	0.445
8	**LP6821**	**rs10104051**	Intron 1	CC/TC/TT	0.442	-2.409	0.29	NA	0.107	0.81	NA
8	**LP7503**	**rs6999612**	Intron 1	CC/CT/TT	0.02	-3.962	0.62	NA	-1.84	0.24	NA
8	**LP7512**	**rs3779788**	Intron 1	CC/TC/TT	0.148	-1.853	0.57	NA	0.106	0.87	NA
9	**LP6821**	**rs10104051**	Intron 1	CC/TC/TT	0.442	-2.409	0.29	0.788	0.107	0.81	0.193
9	**LP7503**	**rs6999612**	Intron 1	CC/CT/TT	0.02	-3.962	0.62	NA	-1.84	0.24	NA
9	**LP7512**	**rs3779788**	Intron 1	CC/TC/TT	0.148	-1.853	0.57	NA	0.106	0.87	NA
9	**LP8221**	**rs7000460**	Intron 1	AA/CA	0.019	-3.206	0.72	NA	-3.15	0.08	NA
10	**LP7503**	**rs6999612**	Intron 1	CC/CT/TT	0.02	-3.962	0.62	0.872	-1.84	0.24	0.127
10	**LP7512**	**rs3779788**	Intron 1	CC/TC/TT	0.148	-1.853	0.57	NA	0.106	0.87	NA
10	**LP8221**	**rs7000460**	Intron 1	AA/CA	0.019	-3.206	0.72	NA	-3.15	0.08	NA
10	**LP10127**	**rs1801177**	Intron 1	AG/GG	0.019	-3.206	0.72	NA	-3.15	0.08	NA
11	**LP7512**	**rs3779788**	Intron 1	CC/TC/TT	0.148	-1.853	0.57	0.921	0.106	0.87	0.158
11	**LP8221**	**rs7000460**	Intron 1	AA/CA	0.019	-3.206	0.72	NA	-3.15	0.08	NA
11	**LP10127**	**rs1801177**	Intron 1	AG/GG	0.019	-3.206	0.72	NA	-3.15	0.08	NA
11	**LP10912**	**rs149477831**	Intron 1	AA/AG	0.01	1.553	0.91	NA	3.829	0.15	NA
12	**LP8221**	**rs7000460**	Intron 1	AA/CA	0.019	-3.206	0.72	0.979	-3.15	0.08	0.153
12	**LP10127**	**rs1801177**	Exon 2	AG/GG	0.019	-3.206	0.72	NA	-3.15	0.08	NA
12	**LP10912**	**rs149477831**	Intron 1	AA/AG	0.01	1.553	0.91	NA	3.829	0.15	NA
12	**LP10987**	**rs74377536**	Intron 2	AA/CA/CC	0.12	-0.591	0.87	NA	-0.13	0.85	NA
13	**LP10127**	**rs1801177**	Exon 2	AG/GG	0.019	-3.206	0.72	0.979	-3.15	0.08	0.155
13	**LP10912**	**rs149477831**	Intron 1	AA/AG	0.01	1.553	0.91	NA	3.829	0.15	NA
13	**LP10987**	**rs74377536**	Intron 2	AA/CA/CC	0.12	-0.591	0.87	NA	-0.13	0.85	NA
13	**LP11050**	**rs7016529**	Intron 2	CT/TT	0.018	-3.574	0.7	NA	-2.43	0.18	NA
14	**LP10912**	**rs149477831**	Intron 1	AA/AG	0.01	1.553	0.91	0.989	3.829	0.15	0.396
14	**LP10987**	**rs74377536**	Intron 2	AA/CA/CC	0.12	-0.591	0.87	NA	-0.13	0.85	NA
14	**LP11050**	**rs7016529**	Intron 2	CT/TT	0.018	-3.574	0.7	NA	-2.43	0.18	NA
14	**LP11090**	**rs8176337**	Intron 2	CC/CG/GG	0.242	0.525	0.85	NA	-0.39	0.5	NA
15	**LP10987**	**rs74377536**	Intron 2	AA/CA/CC	0.12	-0.591	0.87	0.291	-0.13	0.85	0.494
15	**LP11050**	**rs7016529**	Intron 2	CT/TT	0.018	-3.574	0.7	NA	-2.43	0.18	NA
15	**LP11090**	**rs8176337**	Intron 2	CC/CG/GG	0.242	0.525	0.85	NA	-0.39	0.5	NA
15	**LP11888_11889ins1**	**rs149017698**	Intron 2	II/WI/WW	0.02	2.882	0.71	NA	-2.76	0.08	NA
16	**LP11050**	**rs7016529**	Intron 2	CT/TT	0.018	-3.574	0.7	0.225	-2.43	0.18	0.484
16	**LP11090**	**rs8176337**	Intron 2	CC/CG/GG	0.242	0.525	0.85	NA	-0.39	0.5	NA
16	**LP11888_11889ins1**	**rs149017698**	Intron 2	II/WI/WW	0.02	2.882	0.71	NA	-2.76	0.08	NA
16	**LP13003**	**rs80181352**	Intron 2	GG/GT/TT	0.075	5.965	0.16	NA	-0.31	0.71	NA
17	**LP11090**	**rs8176337**	Intron 2	CC/CG/GG	0.242	0.525	0.85	0.919	-0.39	0.5	0.343
17	**LP11888_11889ins1**	**rs149017698**	Intron 2	II/WI/WW	0.02	2.882	0.71	NA	-2.76	0.08	NA
17	**LP1300**	**rs80181352**	Intron 2	GG/GT/TT	0.075	5.965	0.16	NA	-0.31	0.71	NA
17	**LP13639**	**rs78326602**	Intron 2	GA/GG	0.007	-17.22	0.17	NA	-2.48	0.32	NA

Table A1.12. Continued

						ApoA1			ApoB		
Window	**Window SNP**	**RefSNP ID**	**Location**	**Genotypes**	**MAF**	**Beta**	**P****	***hap_P**	**Beta**	**P****	***hap_P**
18	**LP11888_11889ins1**	**rs149017698**	Intron 2	II/WI/WW	0.02	2.882	0.71	0.319	-2.76	0.08	0.278
18	**LP1300**	**rs80181352**	Intron 2	GG/GT/TT	0.075	5.965	0.16	NA	-0.31	0.71	NA
18	**LP13639**	**rs78326602**	Intron 2	GA/GG	0.007	-17.22	0.17	NA	-2.48	0.32	NA
18	**LP13854**	**rs1121923**	Intron 2	CC/TC	0.034	-0.357	0.95	NA	-0.49	0.69	NA
19	**LP1300**	**rs80181352**	Intron 2	GG/GT/TT	0.075	5.965	0.16	0.376	-0.31	0.71	0.607
19	**LP13639**	**rs78326602**	Intron 2	GA/GG	0.007	-17.22	0.17	NA	-2.48	0.32	NA
19	**LP13854**	**rs1121923**	Exon 3	CC/TC	0.034	-0.357	0.95	NA	-0.49	0.69	NA
19	**LP14114**	**rs73667472**	Intron 3	AA/AG/GG	0.078	-0.545	0.9	NA	-0.93	0.29	NA
20	**LP13639**	**rs78326602**	Intron 2	GA/GG	0.007	-17.22	0.17	0.338	-2.48	0.32	0.622
20	**LP13854**	**rs1121923**	Exon 3	CC/TC	0.034	-0.357	0.95	NA	-0.49	0.69	NA
20	**LP14114**	**rs73667472**	Intron 3	AA/AG/GG	0.078	-0.545	0.9	NA	-0.93	0.29	NA
20	**LP15245**	**rs248**	Exon 4	AA/GA/GG	0.067	6.873	0.13	NA	0.181	0.84	NA
21	**LP13854**	**rs1121923**	Exon 3	CC/TC	0.034	-0.357	0.95	0.696	-0.49	0.69	0.849
21	**LP14114**	**rs73667472**	Intron 3	AA/AG/GG	0.078	-0.545	0.9	NA	-0.93	0.29	NA
21	**LP15245**	**rs248**	Exon 4	AA/GA/GG	0.067	6.873	0.13	NA	0.181	0.84	NA
21	**LP15425**	**rs249**	Intron 4	CC/TC/TT	0.075	-1.166	0.8	NA	-0.89	0.33	NA
22	**LP14114**	**rs73667472**	Intron 3	AA/AG/GG	0.078	-0.545	0.9	0.453	-0.93	0.29	0.69
22	**LP15245**	**rs248**	Exon 4	AA/GA/GG	0.067	6.873	0.13	NA	0.181	0.84	NA
22	**LP15425**	**rs249**	Intron 4	CC/TC/TT	0.075	-1.166	0.8	NA	-0.89	0.33	NA
22	**LP15836**	**rs253**	Intron 4	CC/CT/TT	0.453	-1.804	0.43	NA	0.286	0.53	NA
23	**LP15245**	**rs248**	Exon 4	AA/GA/GG	0.067	6.873	0.13	0.356	0.181	0.84	0.793
23	**LP15425**	**rs249**	Intron 4	CC/TC/TT	0.075	-1.166	0.8	NA	-0.89	0.33	NA
23	**LP15836**	**rs253**	Intron 4	CC/CT/TT	0.453	-1.804	0.43	NA	0.286	0.53	NA
23	**LP16316**	**rs254**	Intron 5	CC/CG/GG	0.143	-1.885	0.55	NA	0.193	0.77	NA
24	**LP15425**	**rs249**	Intron 4	CC/TC/TT	0.075	-1.166	0.8	0.677	-0.89	0.33	0.699
24	**LP15836**	**rs253**	Intron 4	CC/CT/TT	0.453	-1.804	0.43	NA	0.286	0.53	NA
24	**LP16316**	**rs254**	Intron 5	CC/CG/GG	0.143	-1.885	0.55	NA	0.193	0.77	NA
24	**LP16442**	**rs74382962**	Intron 5	CG/GG	0.002	-19.17	0.41	NA	3.72	0.42	NA
25	**LP15836**	**rs253**	Intron 4	CC/CT/TT	0.453	-1.804	0.43	0.727	0.286	0.53	0.746
25	**LP16316**	**rs254**	Intron 5	CC/CG/GG	0.143	-1.885	0.55	NA	0.193	0.77	NA
25	**LP16442**	**rs74382962**	Intron 5	CG/GG	0.002	-19.17	0.41	NA	3.72	0.42	NA
25	**LP17599**	**rs264**	Intron 5	AA/GA/GG	0.143	-1.659	0.61	NA	0.176	0.79	NA
26	**LP16316**	**rs254**	Intron 5	CC/CG/GG	0.143	-1.885	0.55	0.797	0.193	0.77	0.533
26	**LP16442**	**rs74382962**	Intron 5	CG/GG	0.002	-19.17	0.41	NA	3.72	0.42	NA
26	**LP17599**	**rs264**	Intron 5	AA/GA/GG	0.143	-1.659	0.61	NA	0.176	0.79	NA
26	**LP17948**	**rs268**	Exon 6	AA/AG	0.015	3.372	0.75	NA	-2.35	0.26	NA
27	**LP16442**	**rs74382962**	Intron 5	CG/GG	0.002	-19.17	0.41	0.82	3.72	0.42	0.742
27	**LP17599**	**rs264**	Intron 5	AA/GA/GG	0.143	-1.659	0.61	NA	0.176	0.79	NA
27	**LP17948**	**rs268**	Exon 6	AA/AG	0.015	3.372	0.75	NA	-2.35	0.26	NA
27	**LP18086**	**rs269**	Intron 6	GG/GT/TT	0.174	-1.478	0.62	NA	0.273	0.65	NA
28	**LP17599**	**rs264**	Intron 5	AA/GA/GG	0.143	-1.659	0.61	0.667	0.176	0.79	0.489
28	**LP17948**	**rs268**	Exon 6	AA/AG	0.015	3.372	0.75	NA	-2.35	0.26	NA
28	**LP18086**	**rs269**	Intron 6	GG/GT/TT	0.174	-1.478	0.62	NA	0.273	0.65	NA
28	**LP18095**	**rs270**	Intron 6	AA/CA/CC	0.172	-3.232	0.26	NA	0.805	0.16	NA
29	**LP17948**	**rs268**	Exon 6	AA/AG	0.015	3.372	0.75	0.215	-2.35	0.26	0.177
29	**LP18086**	**rs269**	Intron 6	GG/GT/TT	0.174	-1.478	0.62	NA	0.273	0.65	NA
29	**LP18095**	**rs270**	Intron 6	AA/CA/CC	0.172	-3.232	0.26	NA	0.805	0.16	NA
29	**LP18822**	**rs277**	Intron 6	CC/CT/TT	0.196	-4.044	0.14	NA	0.363	0.51	NA
30	**LP18086**	**rs269**	Intron 6	GG/GT/TT	0.174	-1.478	0.62	0.112	0.273	0.65	0.048
30	**LP18095**	**rs270**	Intron 6	AA/CA/CC	0.172	-3.232	0.26	NA	0.805	0.16	NA
30	**LP18822**	**rs277**	Intron 6	CC/CT/TT	0.196	-4.044	0.14	NA	0.363	0.51	NA
30	**LP19445**	**rs282**	Intron 6	CC/GC/GG	0.135	7.309	0.02	NA	-1.33	0.04	NA
31	**LP18095**	**rs270**	Intron 6	AA/CA/CC	0.172	-3.232	0.26	0.178	0.805	0.16	0.074
31	**LP18822**	**rs277**	Intron 6	CC/CT/TT	0.196	-4.044	0.14	NA	0.363	0.51	NA
31	**LP19445**	**rs282**	Intron 6	CC/GC/GG	0.135	7.309	0.02	NA	-1.33	0.04	NA
31	**LP19517**	**rs283**	Intron 6	CC/CT/TT	0.201	-1.662	0.53	NA	0.457	0.39	NA
32	**LP18822**	**rs277**	Intron 6	CC/CT/TT	0.196	-4.044	0.14	0.035	0.363	0.51	0.438
32	**LP19445**	**rs282**	Intron 6	CC/GC/GG	0.135	7.309	0.02	NA	-1.33	0.04	NA
32	**LP19517**	**rs283**	Intron 6	CC/CT/TT	0.201	-1.662	0.53	NA	0.457	0.39	NA
32	**LP19608**	**rs285**	Intron 6	CC/CT/TT	0.48	-1.361	0.55	NA	0.171	0.71	NA
33	**LP19445**	**rs282**	Intron 6	CC/GC/GG	0.135	7.309	0.02	0.093	-1.33	0.04	0.071
33	**LP19517**	**rs283**	Intron 6	CC/CT/TT	0.201	-1.662	0.53	NA	0.457	0.39	NA
33	**LP19608**	**rs285**	Intron 6	CC/CT/TT	0.48	-1.361	0.55	NA	0.171	0.71	NA
33	**LP19675**	**rs286**	Intron 6	AA/TA/TT	0.095	3.918	0.29	NA	0.793	0.28	NA
34	**LP19517**	**rs283**	Intron 6	CC/CT/TT	0.201	-1.662	0.53	0.558	0.457	0.39	0.041
34	**LP19608**	**rs285**	Intron 6	CC/CT/TT	0.48	-1.361	0.55	NA	0.171	0.71	NA
34	**LP19675**	**rs286**	Intron 6	AA/TA/TT	0.095	3.918	0.29	NA	0.793	0.28	NA
34	**LP20363**	**rs296**	Intron 6	AA/TA/TT	0.049	-4.684	0.37	NA	0.025	0.98	NA
35	**LP19608**	**rs285**	Intron 6	CC/CT/TT	0.48	-1.361	0.55	0.574	0.171	0.71	0.542
35	**LP19675**	**rs286**	Intron 6	AA/TA/TT	0.095	3.918	0.29	NA	0.793	0.28	NA
35	**LP20363**	**rs296**	Intron 6	AA/TA/TT	0.049	-4.684	0.37	NA	0.025	0.98	NA
35	**LP20544**	**rs294**	Intron 6	AA/AG/GG	0.118	1.929	0.58	NA	0.124	0.86	NA
36	**LP19675**	**rs286**	Intron 6	AA/TA/TT	0.095	3.918	0.29	0.648	0.793	0.28	0.684

Table A1.12. Continued

						ApoA1			ApoB		
Window	**Window SNP**	**RefSNP ID**	**Location**	**Genotypes**	**MAF**	**Beta**	**P****	***hap_P**	**Beta**	**P****	***hap_P**
36	**LP20363**	**rs296**	Intron 6	AA/TA/TT	0.049	-4.684	0.37	NA	0.025	0.98	NA
36	**LP20544**	**rs294**	Intron 6	AA/AG/GG	0.118	1.929	0.58	NA	0.124	0.86	NA
36	**LP20657**	**rs295**	Intron 6	AA/CA/CC	0.223	3.697	0.18	NA	0.605	0.26	NA
37	**LP20363**	**rs296**	Intron 6	AA/TA/TT	0.049	-4.684	0.37	0.331	0.025	0.98	0.13
37	**LP20544**	**rs294**	Intron 6	AA/AG/GG	0.118	1.929	0.58	NA	0.124	0.86	NA
37	**LP20657**	**rs295**	Intron 6	AA/CA/CC	0.223	3.697	0.18	NA	0.605	0.26	NA
37	**LP22044_22047del4**	**rs311**	Intron 7	DD/WD/WW	0.052	8.212	0.1	NA	0.213	0.83	NA
38	**LP20544**	**rs294**	Intron 6	AA/AG/GG	0.118	1.929	0.58	0.031	0.124	0.86	0.744
38	**LP20657**	**rs295**	Intron 6	AA/CA/CC	0.223	3.697	0.18	NA	0.605	0.26	NA
38	**LP22044_22047del4**	**rs311**	Intron 7	DD/WD/WW	0.052	8.212	0.1	NA	0.213	0.83	NA
38	**LP22416**	**rs312**	Intron 7	CC/GC/GG	0.113	0.7	0.85	NA	0.238	0.74	NA
39	**LP20657**	**rs295**	Intron 6	AA/CA/CC	0.223	3.697	0.18	0.35	0.605	0.26	0.579
39	**LP22044_22047del4**	**rs311**	Intron 7	DD/WD/WW	0.052	8.212	0.1	NA	0.213	0.83	NA
39	**LP22416**	**rs312**	Intron 7	CC/GC/GG	0.113	0.7	0.85	NA	0.238	0.74	NA
39	**LP22461**	**rs314**	Intron 6	AA/GA/GG	0.263	2.748	0.29	NA	0.222	0.67	NA
40	**LP22044_22047del4**	**rs311**	Intron 7	DD/WD/WW	0.052	8.212	0.1	0.224	0.213	0.83	0.91
40	**LP22416**	**rs312**	Intron 7	CC/GC/GG	0.113	0.7	0.85	NA	0.238	0.74	NA
40	**LP22461**	**rs314**	Intron 7	AA/GA/GG	0.263	2.748	0.29	NA	0.222	0.67	NA
40	**LP22514**	**rs315**	Intron 7	CT/TT	0.005	12.39	0.45	NA	1.918	0.56	NA
41	**LP22416**	**rs312**	Intron 7	CC/GC/GG	0.113	0.7	0.85	0.528	0.238	0.74	0.924
41	**LP22461**	**rs314**	Intron 7	AA/GA/GG	0.263	2.748	0.29	NA	0.222	0.67	NA
41	**LP22514**	**rs315**	Intron 7	CT/TT	0.005	12.39	0.45	NA	1.918	0.56	NA
41	**LP22855**	**rs316**	Exon 8	AA/CA/CC	0.113	0.972	0.79	NA	0.231	0.75	NA
42	**LP22461**	**rs314**	Intron 7	AA/GA/GG	0.263	2.748	0.29	0.641	0.222	0.67	0.71
42	**LP22514**	**rs315**	Intron 7	CT/TT	0.005	12.39	0.45	NA	1.918	0.56	NA
42	**LP22855**	**rs316**	Exon 8	AA/CA/CC	0.113	0.972	0.79	NA	0.231	0.75	NA
42	**LP23192**	**rs117026536**	Intron 8	GG/GT/TT	0.104	4.114	0.25	NA	0.708	0.31	NA
43	**LP22514**	**rs315**	Intron 7	CT/TT	0.005	12.39	0.45	0.298	1.918	0.56	0.817
43	**LP22855**	**rs316**	Exon 8	AA/CA/CC	0.113	0.972	0.79	NA	0.231	0.75	NA
43	**LP23192**	**rs117026536**	Intron 8	GG/GT/TT	0.104	4.114	0.25	NA	0.708	0.31	NA
43	**LP23496**	**rs320**	Intron 8	GG/GT/TT	0.258	0.083	0.97	NA	0.336	0.5	NA
44	**LP22855**	**rs316**	Exon 8	AA/CA/CC	0.113	0.972	0.79	0.23	0.231	0.75	0.874
44	**LP23192**	**rs117026536**	Intron 8	GG/GT/TT	0.104	4.114	0.25	NA	0.708	0.31	NA
44	**LP23496**	**rs320**	Intron 8	GG/GT/TT	0.258	0.083	0.97	NA	0.336	0.5	NA
44	**LP22855**	**rs327**	Intron 8	GG/TG/TT	0.265	1.367	0.59	NA	0.322	0.52	NA
45	**LP23192**	**rs117026536**	Intron 8	GG/GT/TT	0.104	4.114	0.25	0.467	0.708	0.31	0.816
45	**LP23496**	**rs320**	Intron 8	GG/GT/TT	0.258	0.083	0.97	NA	0.336	0.5	NA
45	**LP22855**	**rs327**	Intron 8	GG/TG/TT	0.265	1.367	0.59	NA	0.322	0.52	NA
45	**LP24143**	**rs328**	Intron 8	CC/GC/GG	0.103	4.585	0.2	NA	0.727	0.31	NA
46	**LP23496**	**rs320**	Intron 8	GG/GT/TT	0.258	0.083	0.97	0.265	0.336	0.5	0.224
46	**LP22855**	**rs327**	Intron 8	GG/TG/TT	0.265	1.367	0.59	NA	0.322	0.52	NA
46	**LP24143**	**rs328**	Exon 9	CC/GC/GG	0.103	4.585	0.2	NA	0.727	0.31	NA
46	**LP25049**	**rs78031480**	Intron 9	AA/AG/GG	0.047	-7.527	0.16	NA	-2.33	0.03	NA
47	**LP22855**	**rs327**	Intron 8	GG/TG/TT	0.265	1.367	0.59	0.128	0.322	0.52	0.22
47	**LP24143**	**rs328**	Exon 9	CC/GC/GG	0.103	4.585	0.2	NA	0.727	0.31	NA
47	**LP25049**	**rs78031480**	Intron 9	AA/AG/GG	0.047	-7.527	0.16	NA	-2.33	0.03	NA
47	**LP26234**	**rs10099160**	Intron 9	GG/GT/TT	0.26	-5.73	0.02	NA	-0.17	0.74	NA
48	**LP24143**	**rs328**	Exon 9	CC/GC/GG	0.103	4.585	0.2	0.052	0.727	0.31	0.205
48	**LP25049**	**rs78031480**	Intron 9	AA/AG/GG	0.047	-7.527	0.16	NA	-2.33	0.03	NA
48	**LP26234**	**rs10099160**	Intron 9	GG/GT/TT	0.26	-5.73	0.02	NA	-0.17	0.74	NA
48	**LP27000**	**rs11232447**	Intron 9	CC/CT/TT	0.029	-9.888	0.14	NA	-0.7	0.6	NA
49	**LP25049**	**rs78031480**	Intron 9	AA/AG/GG	0.047	-7.527	0.16	0.061	-2.33	0.03	0.228
49	**LP26234**	**rs10099160**	Intron 9	GG/GT/TT	0.26	-5.73	0.02	NA	-0.17	0.74	NA
49	**LP27000**	**rs11232447**	Intron 9	CC/CT/TT	0.029	-9.888	0.14	NA	-0.7	0.6	NA
49	**LP27160**	**rs117910839**	Intron 9	AA/TA/TT	0.027	1.007	0.88	NA	1.22	0.36	NA
50	**LP26234**	**rs10099160**	Intron 9	GG/GT/TT	0.26	-5.73	0.02	0.07	-0.17	0.74	0.772
50	**LP27000**	**rs11232447**	Intron 9	CC/CT/TT	0.029	-9.888	0.14	NA	-0.7	0.6	NA
50	**LP27160**	**rs117910839**	Intron 9	AA/TA/TT	0.027	1.007	0.88	NA	1.22	0.36	NA
50	**LP27229**	**rs11570891**	Intron 9	CC/TC/TT	0.107	4.119	0.25	NA	0.831	0.24	NA
51	**LP27000**	**rs11232447**	Intron 9	CC/CT/TT	0.029	-9.888	0.14	0.429	-0.7	0.6	0.659
51	**LP27160**	**rs117910839**	Intron 9	AA/TA/TT	0.027	1.007	0.88	NA	1.22	0.36	NA
51	**LP27229**	**rs11570891**	Intron 9	CC/TC/TT	0.107	4.119	0.25	NA	0.831	0.24	NA
51	**LP27249**	**rs4922115**	3’ UTR-exon10	AA/AG/GG	0.146	-0.963	0.76	NA	0.246	0.69	NA
52	**LP27160**	**rs117910839**	Intron 9	AA/TA/TT	0.027	1.007	0.88	0.834	1.22	0.36	0.867
52	**LP27229**	**rs11570891**	Intron 9	CC/TC/TT	0.107	4.119	0.25	NA	0.831	0.24	NA
52	**LP27249**	**rs4922115**	3’ UTR-exon10	AA/AG/GG	0.146	-0.963	0.76	NA	0.246	0.69	NA
52	**LP27611**	**rs3289**	3’ UTR-exon10	CC/TC/TT	0.027	3.518	0.62	NA	-0.32	0.82	NA
53	**LP27229**	**rs11570891**	Intron 9	CC/TC/TT	0.107	4.119	0.25	0.801	0.831	0.24	0.692
53	**LP27249**	**rs4922115**	3’ UTR-exon10	AA/AG/GG	0.146	-0.963	0.76	NA	0.246	0.69	NA
53	**LP27611**	**rs3289**	3’ UTR-exon10	CC/TC/TT	0.027	3.518	0.62	NA	-0.32	0.82	NA
53	**LP27688**	**rs191212278**	3’ UTR-exon10	CC/TC	0.004	-9.025	0.59	NA	-2.67	0.41	NA
54	**LP27249**	**rs4922115**	3’ UTR-exon10	AA/AG/GG	0.146	-0.963	0.76	0.822	0.246	0.69	0.729
54	**LP27611**	**rs3289**	3’ UTR-exon10	CC/TC/TT	0.027	3.518	0.62	NA	-0.32	0.82	NA

Table A1.12. Continued

						ApoA1			ApoB		
Window	**Window SNP**	**RefSNP ID**	**Location**	**Genotypes**	**MAF**	**Beta**	**P****	***hap_P**	**Beta**	**P****	***hap_P**
54	**LP27688**	**rs191212278**	3' UTR-exon10	CC/TC	0.004	-9.025	0.59	NA	-2.67	0.41	NA
54	**LP28407**	**rs150252331**	3' UTR-exon10	GG/GT	0.018	-7.913	0.36	NA	-1.87	0.28	NA
55	**LP27611**	**rs3289**	3' UTR-exon10	CC/TC/TT	0.027	3.518	0.62	0.633	-0.32	0.82	0.68
55	**LP27688**	**rs191212278**	3' UTR-exon10	CC/TC	0.004	-9.025	0.59	NA	-2.67	0.41	NA
55	**LP28407**	**rs150252331**	3' UTR-exon10	GG/GT	0.018	-7.913	0.36	NA	-1.87	0.28	NA
55	**LP28524**	**Novel**	3' UTR-exon10	CC/CT	0.001	-23.11	0.48	NA	3.784	0.56	NA
56	**LP27688**	**rs191212278**	3' UTR-exon10	CC/TC	0.004	-9.025	0.59	0.625	-2.67	0.41	0.56
56	**LP28407**	**rs150252331**	3' UTR-exon10	GG/GT	0.018	-7.913	0.36	NA	-1.87	0.28	NA
56	**LP28524**	**Novel**	3' UTR-exon10	CC/CT	0.001	-23.11	0.48	NA	3.784	0.56	NA
56	**LP28911**	**rs13702**	3' UTR-exon10	CC/CT/TT	0.272	1.493	0.54	NA	0.462	0.34	NA
57	**LP28407**	**rs150252331**	3' UTR-exon10	GG/GT	0.018	-7.913	0.36	0.655	-1.87	0.28	0.63
57	**LP28524**	**Novel**	3' UTR-exon10	CC/CT	0.001	-23.11	0.48	NA	3.784	0.56	NA
57	**LP28911**	**rs13702**	3' UTR-exon10	CC/CT/TT	0.272	1.493	0.54	NA	0.462	0.34	NA
57	**LP28982**	**rs1059611**	3' UTR-exon10	CC/TC/TT	0.107	3.989	0.26	NA	0.755	0.28	NA
58	**LP28524**	**Novel**	3' UTR-exon10	CC/CT	0.001	-23.11	0.48	0.13	3.784	0.56	0.796
58	**LP28911**	**rs13702**	3' UTR-exon10	CC/CT/TT	0.272	1.493	0.54	NA	0.462	0.34	NA
58	**LP28982**	**rs1059611**	3' UTR-exon10	CC/TC/TT	0.107	3.989	0.26	NA	0.755	0.28	NA
58	**LP29315**	**rs9644636**	3' UTR-exon10	GG/GT/TT	0.288	4.563	0.07	NA	-0.09	0.86	NA
59	**LP28911**	**rs13702**	3' UTR-exon10	CC/CT/TT	0.272	1.493	0.54	0.08	0.462	0.34	0.858
59	**LP28982**	**rs1059611**	3' UTR-exon10	CC/TC/TT	0.107	3.989	0.26	NA	0.755	0.28	NA
59	**LP29315**	**rs9644636**	3' UTR-exon10	GG/GT/TT	0.288	4.563	0.07	NA	-0.09	0.86	NA
59	**LP29474**	**rs113831503**	3' UTR-exon10	CC/CT/TT	0.036	-7.658	0.21	NA	0.353	0.77	NA
60	**LP28982**	**rs1059611**	3' UTR-exon10	CC/TC/TT	0.107	3.989	0.26	0.092	0.755	0.28	0.834
60	**LP29315**	**rs9644636**	3' UTR-exon10	GG/GT/TT	0.288	4.563	0.07	NA	-0.09	0.86	NA
60	**LP29474**	**rs113831503**	3' UTR-exon10	CC/CT/TT	0.036	-7.658	0.21	NA	0.353	0.77	NA
60	**LP29547**	**rs4921684**	3' flanking	CC/CT/TT	0.149	-1.395	0.65	NA	0.173	0.78	NA
61	**LP29315**	**rs9644636**	3' UTR-exon10	GG/GT/TT	0.288	4.563	0.07	0.196	-0.09	0.86	0.998
61	**LP29474**	**rs113831503**	3' UTR-exon10	CC/CT/TT	0.036	-7.658	0.21	NA	0.353	0.77	NA
61	**LP29547**	**rs4921684**	3' flanking	CC/CT/TT	0.149	-1.395	0.65	NA	0.173	0.78	NA
61	**LP29716**	**rs8008515**	3' flanking	TC/TT	0.014	9.202	0.3	NA	-0.18	0.92	NA

Table A1.13. Summary of *LPL* 4-SNP sliding haplotypes for TG and HDL-C in NHWs

						TG					HDL-C				
	Window	loc1	loc2	loc3	loc4	Hap.freq.[1]	Coef.[2]	S.E.[3]	T.stat.[4]	*P*	Hap.freq[1]	Coef.[2]	S.E.[3]	T.stat.[4]	*P*
Geno.2	1	G	G	G	C	0.207	0.027	0.031	0.860	0.390	0.208	-0.021	0.013	-1.564	0.118
Geno.5	1	G	G	T	G	0.143	-0.031	0.037	-0.844	0.399	0.145	0.021	0.016	1.299	0.194
Geno.rare	1	*	*	*	*	0.012	0.142	0.121	1.173	0.241	0.012	0.018	0.052	0.354	0.723
haplo.base	1	G	G	G	G	0.637	NA	NA	NA	NA	0.636	NA	NA	NA	NA
Geno.4	2	G	G	C	T	0.207	0.010	0.031	0.310	0.757	0.207	-0.022	0.014	-1.567	0.118
Geno.6	2	G	G	G	T	0.092	-0.103	0.044	-2.379	0.018	0.092	-0.008	0.019	-0.430	0.667
Geno.7	2	G	T	G	T	0.154	-0.047	0.036	-1.313	0.190	0.155	0.022	0.016	1.417	0.157
Geno.rare1	2	*	*	*	*	0.003	0.389	0.255	1.527	0.127	0.003	-0.028	0.107	-0.263	0.792
haplo.base1	2	G	G	G	G	0.543	NA	NA	NA	NA	0.542	NA	NA	NA	NA
Geno.21	3	G	C	T	G	0.207	0.009	0.031	0.279	0.781	0.210	-0.025	0.014	-1.827	0.068
Geno.51	3	G	G	T	A	0.091	-0.116	0.044	-2.654	0.008	0.090	-0.009	0.019	-0.460	0.646
Geno.71	3	T	G	T	A	0.154	-0.048	0.036	-1.344	0.179	0.155	0.020	0.015	1.281	0.201
Geno.rare2	3	*	*	*	*	0.005	0.105	0.193	0.541	0.589	0.005	-0.113	0.091	-1.249	0.212
haplo.base2	3	G	G	G	A	0.543	NA	NA	NA	NA	0.539	NA	NA	NA	NA
Geno.22	4	C	T	G	G	0.207	0.009	0.031	0.296	0.767	0.210	-0.025	0.014	-1.861	0.063
Geno.52	4	G	T	A	C	0.019	0.054	0.091	0.588	0.557	0.019	-0.062	0.040	-1.573	0.116
Geno.61	4	G	T	A	G	0.227	-0.082	0.031	-2.656	0.008	0.228	0.013	0.013	0.985	0.325
Geno.rare3	4	*	*	*	*	0.005	0.121	0.175	0.691	0.490	0.005	-0.122	0.083	-1.464	0.144
haplo.base3	4	G	G	A	G	0.542	NA	NA	NA	NA	0.539	NA	NA	NA	NA
Geno.62	5	T	A	C	T	0.019	0.055	0.091	0.601	0.548	0.019	-0.062	0.040	-1.578	0.115
Geno.72	5	T	A	G	G	0.154	-0.046	0.036	-1.279	0.201	0.155	0.018	0.016	1.174	0.241
Geno.8	5	T	A	G	T	0.073	-0.154	0.048	-3.209	0.001	0.073	0.002	0.021	0.117	0.907
Geno.10	5	T	G	G	T	0.207	0.008	0.031	0.266	0.790	0.209	-0.023	0.014	-1.674	0.095
Geno.rare4	5	*	*	*	*	0.009	0.038	0.135	0.283	0.777	0.010	-0.091	0.058	-1.575	0.116
haplo.base4	5	G	A	G	T	0.539	NA	NA	NA	NA	0.536	NA	NA	NA	NA
Geno.1	6	A	C	T	T	0.019	0.057	0.091	0.631	0.529	0.019	-0.063	0.039	-1.598	0.111
Geno.3	6	A	G	G	T	0.149	-0.051	0.036	-1.401	0.162	0.150	0.021	0.016	1.337	0.182
Geno.53	6	A	G	T	T	0.073	-0.155	0.048	-3.207	0.001	0.072	0.004	0.021	0.177	0.859
Geno.9	6	G	G	T	T	0.200	0.003	0.032	0.093	0.926	0.202	-0.021	0.014	-1.503	0.133
Geno.rare5	6	*	*	*	*	0.020	0.111	0.093	1.199	0.231	0.020	-0.078	0.039	-1.967	0.050
haplo.base5	6	A	G	T	C	0.540	NA	NA	NA	NA	0.537	NA	NA	NA	NA
Geno.23	7	C	T	T	C	0.019	0.045	0.093	0.487	0.627	0.019	-0.057	0.040	-1.433	0.152
Geno.31	7	G	G	C	T	0.011	0.005	0.145	0.033	0.974	0.011	-0.040	0.065	-0.623	0.534
Geno.41	7	G	G	T	T	0.151	-0.044	0.036	-1.194	0.233	0.152	0.018	0.016	1.116	0.265
Geno.73	7	G	T	T	T	0.273	-0.046	0.029	-1.576	0.115	0.273	-0.013	0.013	-1.033	0.302
Geno.rare6	7	*	*	*	*	0.002	0.081	0.307	0.262	0.793	0.002	-0.065	0.133	-0.487	0.626
haplo.base6	7	G	T	C	T	0.546	NA	NA	NA	NA	0.544	NA	NA	NA	NA
Geno.11	8	G	C	T	C	0.011	0.074	0.127	0.584	0.559	0.011	-0.051	0.054	-0.951	0.342
Geno.54	8	G	T	T	T	0.149	-0.054	0.036	-1.488	0.137	0.150	0.018	0.016	1.170	0.242
Geno.81	8	T	T	C	C	0.018	0.038	0.095	0.399	0.690	0.018	-0.059	0.042	-1.403	0.161
Geno.91	8	T	T	T	C	0.273	-0.041	0.029	-1.431	0.153	0.274	-0.014	0.013	-1.123	0.262
Geno.rare7	8	*	*	*	*	0.005	0.258	0.210	1.229	0.220	0.005	-0.065	0.103	-0.630	0.529
haplo.base7	8	T	C	T	C	0.545	NA	NA	NA	NA	0.542	NA	NA	NA	NA
Geno.42	9	T	C	C	C	0.019	0.046	0.092	0.496	0.620	0.019	-0.057	0.040	-1.419	0.156
Geno.63	9	T	T	C	A	0.276	-0.040	0.029	-1.400	0.162	0.277	-0.014	0.012	-1.091	0.276
Geno.74	9	T	T	T	A	0.148	-0.055	0.036	-1.496	0.135	0.149	0.020	0.016	1.259	0.208
Geno.rare8	9	*	*	*	*	0.002	0.080	0.307	0.261	0.794	0.002	-0.064	0.132	-0.482	0.630
haplo.base8	9	C	T	C	A	0.556	NA	NA	NA	NA	0.554	NA	NA	NA	NA
Geno.24	10	C	C	C	A	0.017	0.026	0.103	0.257	0.797	0.017	-0.048	0.042	-1.128	0.260
Geno.55	10	T	T	A	G	0.146	-0.044	0.036	-1.249	0.212	0.148	0.025	0.015	1.629	0.104
Geno.rare9	10	*	*	*	*	0.003	0.208	0.244	0.850	0.396	0.003	-0.072	0.114	-0.628	0.530
haplo.base9	10	T	C	A	G	0.834	NA	NA	NA	NA	0.832	NA	NA	NA	NA
Geno.25	11	C	A	G	G	0.011	0.091	0.121	0.754	0.451	0.010	-0.077	0.052	-1.473	0.141
Geno.32	11	C	C	A	A	0.018	0.055	0.095	0.575	0.566	0.018	-0.056	0.040	-1.382	0.167
Geno.43	11	T	A	G	A	0.147	-0.041	0.035	-1.170	0.242	0.148	0.023	0.015	1.531	0.126
haplo.base10	11	C	A	G	A	0.824	NA	NA	NA	NA	0.823	NA	NA	NA	NA
Geno.12	12	A	G	A	A	0.120	0.001	0.039	0.031	0.976	0.118	-0.006	0.017	-0.349	0.727
Geno.64	12	C	A	A	C	0.019	0.069	0.092	0.756	0.450	0.019	-0.060	0.039	-1.521	0.129
Geno.rare10	12	*	*	*	*	0.010	0.101	0.124	0.813	0.416	0.010	-0.083	0.054	-1.537	0.125
haplo.base11	12	A	G	A	C	0.851	NA	NA	NA	NA	0.853	NA	NA	NA	NA
Geno.26	13	A	A	C	C	0.019	0.070	0.092	0.766	0.444	0.019	-0.060	0.039	-1.523	0.128
Geno.33	13	G	A	A	T	0.120	0.001	0.039	0.031	0.975	0.118	-0.006	0.017	-0.349	0.727
Geno.rare11	13	*	*	*	*	0.010	0.101	0.124	0.814	0.416	0.010	-0.083	0.054	-1.537	0.125
haplo.base12	13	G	A	C	T	0.851	NA	NA	NA	NA	0.853	NA	NA	NA	NA
Geno.13	14	A	A	T	C	0.121	-0.020	0.039	-0.518	0.605	0.118	-0.002	0.017	-0.131	0.896
Geno.27	14	A	C	C	G	0.018	0.070	0.093	0.752	0.452	0.018	-0.063	0.040	-1.566	0.118
Geno.44	14	A	C	T	G	0.222	-0.086	0.032	-2.697	0.007	0.223	0.017	0.014	1.205	0.229
Geno.65	14	G	C	T	C	0.011	0.078	0.121	0.649	0.517	0.011	-0.078	0.052	-1.493	0.136
haplo.base13	14	A	C	T	C	0.629	NA	NA	NA	NA	0.630	NA	NA	NA	NA
Geno.14	15	A	T	C	W	0.120	-0.021	0.039	-0.523	0.601	0.118	-0.002	0.017	-0.096	0.924
Geno.45	15	C	C	G	I	0.019	0.048	0.093	0.519	0.604	0.018	-0.056	0.040	-1.378	0.169
Geno.75	15	C	T	G	W	0.219	-0.087	0.032	-2.736	0.006	0.221	0.018	0.014	1.285	0.199
Geno.rare12	15	*	*	*	*	0.002	0.003	0.401	0.008	0.994	0.002	0.025	0.167	0.150	0.881
haplo.base14	15	C	T	C	W	0.640	NA	NA	NA	NA	0.642	NA	NA	NA	NA
Geno.28	16	C	G	I	G	0.019	0.046	0.093	0.492	0.623	0.018	-0.055	0.040	-1.372	0.170
Geno.76	16	T	G	W	G	0.144	-0.050	0.037	-1.368	0.172	0.145	0.027	0.016	1.706	0.089
Geno.82	16	T	G	W	T	0.073	-0.165	0.047	-3.544	4.24E-04	0.074	0.012	0.020	0.578	0.564
Geno.rare13	16	*	*	*	*	0.002	0.008	1.04E-16	8.00E+13	0.000	0.002	0.027	5.54E-17	4.78E+14	0.000
haplo.base15	16	T	C	W	G	0.762	NA	NA	NA	NA	0.761	NA	NA	NA	NA
Geno.34	17	G	I	G	G	0.019	0.051	0.086	0.590	0.555	0.019	-0.050	0.037	-1.350	0.177
Geno.66	17	G	W	G	G	0.144	-0.050	0.037	-1.361	0.174	0.144	0.028	0.016	1.729	0.084
Geno.83	17	G	W	T	G	0.073	-0.166	0.047	-3.556	4.06E-04	0.074	0.012	0.020	0.575	0.566
Geno.rare14	17	*	*	*	*	0.008	-0.051	0.146	-0.348	0.728	0.008	0.034	0.068	0.498	0.618
haplo.base16	17	C	W	G	G	0.755	NA	NA	NA	NA	0.755	NA	NA	NA	NA

Table A1.13. Continued

						TG					HDL-C				
	Window	**loc1**	**loc2**	**loc3**	**loc4**	**Hap.freq.[1]**	**Coef.[2]**	**S.E.[3]**	**T.stat.[4]**	***P***	**Hap.freq[1]**	**Coef.[2]**	**S.E.[3]**	**T.stat.[4]**	***P***
Geno.15	18	I	G	G	C	0.019	0.057	0.094	0.605	0.545	0.019	-0.047	0.040	-1.182	0.238
Geno.67	18	W	G	G	T	0.032	0.012	0.071	0.162	0.871	0.032	0.014	0.031	0.443	0.658
Geno.84	18	W	T	G	C	0.074	-0.158	0.046	-3.414	6.83E-04	0.074	0.008	0.020	0.381	0.703
Geno.rare15	18	*	*	*	*	0.009	-0.024	0.135	-0.176	0.861	0.009	0.006	0.061	0.104	0.917
haplo.base17	18	W	G	G	C	0.866	NA	NA	NA	NA	0.866	NA	NA	NA	NA
Geno.35	19	G	G	C	G	0.077	0.034	0.044	0.780	0.436	0.078	-0.025	0.019	-1.308	0.191
Geno.46	19	G	G	T	A	0.034	0.010	0.069	0.142	0.887	0.034	0.007	0.030	0.235	0.814
Geno.77	19	T	G	C	A	0.074	-0.155	0.046	-3.348	8.65E-04	0.074	0.006	0.020	0.319	0.750
Geno.rare16	19	*	*	*	*	0.007	-0.024	0.143	-0.164	0.870	0.007	0.024	0.064	0.382	0.703
haplo.base18	19	G	G	C	A	0.808	NA	NA	NA	NA	0.806	NA	NA	NA	NA
Geno.36	20	G	C	A	A	0.067	-0.127	0.049	-2.574	0.010	0.066	0.016	0.022	0.755	0.450
Geno.56	20	G	C	G	G	0.077	0.036	0.044	0.805	0.421	0.078	-0.024	0.019	-1.261	0.208
Geno.78	20	G	T	A	G	0.034	0.014	0.069	0.200	0.841	0.034	0.008	0.030	0.257	0.798
Geno.rare17	20	*	*	*	*	0.007	-0.021	0.145	-0.149	0.882	0.007	0.025	0.064	0.389	0.697
haplo.base19	20	G	C	A	G	0.815	NA	NA	NA	NA	0.814	NA	NA	NA	NA
Geno.29	21	C	A	A	T	0.066	-0.129	0.050	-2.598	0.010	0.065	0.016	0.022	0.755	0.451
Geno.68	21	C	G	G	C	0.072	0.031	0.045	0.678	0.498	0.073	-0.028	0.020	-1.406	0.160
Geno.92	21	T	A	G	T	0.034	0.015	0.069	0.220	0.826	0.034	0.008	0.030	0.252	0.801
Geno.rare18	21	*	*	*	*	0.009	0.088	0.137	0.645	0.519	0.009	0.017	0.061	0.270	0.787
haplo.base20	21	C	A	G	T	0.819	NA	NA	NA	NA	0.819	NA	NA	NA	NA
Geno.210	22	A	A	T	T	0.067	-0.120	0.050	-2.385	0.017	0.066	0.014	0.022	0.618	0.537
Geno.69	22	A	G	T	T	0.310	0.026	0.028	0.935	0.350	0.312	-0.003	0.012	-0.289	0.773
Geno.85	22	G	G	C	T	0.072	0.041	0.047	0.881	0.379	0.073	-0.029	0.020	-1.461	0.145
Geno.rare19	22	*	*	*	*	0.009	0.098	0.135	0.724	0.469	0.009	0.016	0.060	0.259	0.795
haplo.base21	22	A	G	T	C	0.542	NA	NA	NA	NA	0.540	NA	NA	NA	NA
Geno.211	23	A	T	T	C	0.067	-0.121	0.050	-2.420	0.016	0.067	0.018	0.022	0.807	0.420
Geno.47	23	G	C	T	C	0.016	0.120	0.107	1.120	0.263	0.015	-0.063	0.053	-1.206	0.228
Geno.57	23	G	C	T	G	0.057	0.015	0.052	0.280	0.780	0.059	-0.021	0.023	-0.927	0.354
Geno.79	23	G	T	T	C	0.223	0.054	0.031	1.754	0.080	0.224	-0.014	0.013	-1.071	0.285
Geno.86	23	G	T	T	G	0.087	-0.040	0.046	-0.885	0.376	0.088	0.024	0.020	1.228	0.220
Geno.rare20	23	*	*	*	*	0.001	0.419	0.431	0.972	0.331	0.002	0.226	0.158	1.426	0.154
haplo.base22	23	G	T	C	C	0.548	NA	NA	NA	NA	0.545	NA	NA	NA	NA
Geno.212	24	C	T	C	G	0.015	0.119	0.113	1.053	0.293	0.015	-0.053	0.050	-1.068	0.286
Geno.37	24	C	T	G	G	0.058	0.017	0.053	0.318	0.751	0.059	-0.021	0.023	-0.946	0.345
Geno.87	24	T	T	C	G	0.289	0.013	0.028	0.475	0.635	0.290	-0.007	0.012	-0.538	0.591
Geno.101	24	T	T	G	G	0.086	-0.040	0.046	-0.869	0.385	0.087	0.022	0.020	1.109	0.268
Geno.rare21	24	*	*	*	*	0.004	0.005	0.263	0.018	0.986	0.004	0.064	0.116	0.553	0.580
haplo.base23	24	T	C	C	G	0.548	NA	NA	NA	NA	0.545	NA	NA	NA	NA
Geno.58	25	T	C	G	G	0.302	0.015	0.028	0.530	0.596	0.302	-0.011	0.012	-0.871	0.384
Geno.710	25	T	G	G	A	0.141	-0.019	0.037	-0.522	0.602	0.143	0.006	0.016	0.382	0.703
Geno.rare22	25	*	*	*	*	0.008	0.174	0.165	1.058	0.290	0.008	-0.012	0.070	-0.165	0.869
haplo.base24	25	C	C	G	G	0.549	NA	NA	NA	NA	0.547	NA	NA	NA	NA
Geno.48	26	C	G	G	G	0.015	0.149	0.101	1.484	0.138	0.015	-0.013	0.043	-0.289	0.773
Geno.610	26	G	G	A	A	0.142	-0.022	0.035	-0.633	0.527	0.144	0.010	0.015	0.681	0.496
Geno.rare23	26	*	*	*	*	0.008	0.169	0.161	1.049	0.295	0.008	-0.007	0.070	-0.095	0.925
haplo.base25	26	C	G	G	A	0.835	NA	NA	NA	NA	0.833	NA	NA	NA	NA
Geno.38	27	G	A	A	G	0.141	-0.017	0.035	-0.483	0.629	0.143	0.011	0.015	0.734	0.463
Geno.59	27	G	G	A	G	0.033	0.002	0.071	0.024	0.981	0.033	0.033	0.031	1.078	0.281
Geno.88	27	G	G	G	T	0.015	0.156	0.103	1.517	0.130	0.015	-0.013	0.044	-0.306	0.760
Geno.rare24	27	*	*	*	*	0.003	-0.126	0.277	-0.452	0.651	0.003	0.024	0.127	0.191	0.849
haplo.base26	27	G	G	A	T	0.808	NA	NA	NA	NA	0.806	NA	NA	NA	NA
Geno.16	28	A	A	G	C	0.142	-0.004	0.036	-0.104	0.917	0.144	0.006	0.016	0.373	0.709
Geno.39	28	G	A	G	C	0.033	0.014	0.070	0.201	0.841	0.033	0.028	0.030	0.914	0.361
Geno.49	28	G	A	T	A	0.170	0.067	0.033	2.031	0.043	0.172	-0.030	0.014	-2.079	0.038
Geno.89	28	G	G	T	C	0.015	0.188	0.110	1.715	0.087	0.015	-0.017	0.043	-0.394	0.694
haplo.base27	28	G	A	T	C	0.640	NA	NA	NA	NA	0.636	NA	NA	NA	NA
Geno.213	29	A	G	C	T	0.173	-0.007	0.033	-0.212	0.832	0.175	0.012	0.014	0.795	0.427
Geno.310	29	A	T	A	C	0.169	0.074	0.033	2.235	0.026	0.171	-0.026	0.014	-1.818	0.070
Geno.510	29	A	T	C	C	0.029	0.032	0.071	0.448	0.654	0.029	0.029	0.031	0.938	0.349
Geno.93	29	G	T	C	T	0.015	0.221	0.107	2.076	0.038	0.015	-0.012	0.044	-0.270	0.787
Geno.rare25	29	*	*	*	*	0.003	-0.549	0.300	-1.828	0.068	0.002	-0.078	0.130	-0.600	0.549
haplo.base28	29	A	T	C	T	0.611	NA	NA	NA	NA	0.608	NA	NA	NA	NA
Geno.410	30	G	C	T	G	0.170	-0.025	0.035	-0.730	0.466	0.171	0.018	0.015	1.161	0.246
Geno.511	30	T	A	C	G	0.170	0.046	0.034	1.371	0.171	0.171	-0.019	0.015	-1.315	0.189
Geno.711	30	T	C	C	G	0.029	0.013	0.071	0.177	0.860	0.029	0.033	0.031	1.081	0.280
Geno.810	30	T	C	T	C	0.132	-0.095	0.039	-2.434	0.015	0.131	0.033	0.017	1.906	0.057
Geno.rare26	30	*	*	*	*	0.005	-0.261	0.222	-1.176	0.240	0.006	0.013	0.095	0.133	0.895
haplo.base29	30	T	C	T	G	0.494	NA	NA	NA	NA	0.492	NA	NA	NA	NA
Geno.214	31	A	C	G	C	0.052	0.110	0.056	1.948	0.052	0.052	-0.022	0.025	-0.876	0.381
Geno.311	31	A	C	G	T	0.118	0.038	0.039	0.993	0.321	0.119	-0.024	0.017	-1.463	0.144
Geno.611	31	C	C	G	T	0.020	0.006	0.082	0.079	0.937	0.020	0.052	0.036	1.442	0.150
Geno.712	31	C	T	C	C	0.133	-0.084	0.038	-2.220	0.027	0.133	0.027	0.017	1.656	0.098
Geno.102	31	C	T	G	T	0.061	0.068	0.052	1.298	0.195	0.060	0.002	0.023	0.092	0.927
Geno.rare27	31	*	*	*	*	0.012	-0.001	0.118	-0.011	0.991	0.012	-0.008	0.052	-0.158	0.874
haplo.base30	31	C	T	G	C	0.603	NA	NA	NA	NA	0.603	NA	NA	NA	NA
Geno.215	32	C	G	C	C	0.013	0.176	0.126	1.396	0.163	0.013	-0.060	0.057	-1.050	0.294
Geno.312	32	C	G	C	T	0.047	0.089	0.060	1.473	0.141	0.047	-0.008	0.027	-0.295	0.768
Geno.512	32	C	G	T	T	0.134	0.016	0.038	0.426	0.670	0.135	-0.005	0.016	-0.323	0.747
Geno.612	32	T	C	C	C	0.064	-0.048	0.060	-0.792	0.428	0.064	0.037	0.025	1.491	0.136
Geno.713	32	T	C	C	T	0.069	-0.144	0.054	-2.694	0.007	0.069	0.030	0.023	1.297	0.195
Geno.103	32	T	G	C	T	0.168	-0.049	0.038	-1.301	0.194	0.170	0.022	0.016	1.377	0.169
Geno.121	32	T	G	T	T	0.057	0.046	0.056	0.835	0.404	0.057	0.001	0.024	0.041	0.967
Geno.rare28	32	*	*	*	*	0.009	0.186	0.156	1.188	0.235	0.009	0.061	0.067	0.915	0.361
haplo.base31	32	T	G	C	C	0.438	NA	NA	NA	NA	0.437	NA	NA	NA	NA
Geno.216	33	C	C	C	T	0.064	-0.030	0.057	-0.531	0.596	0.064	0.043	0.024	1.788	0.074
Geno.313	33	C	C	T	T	0.070	-0.157	0.052	-3.007	0.003	0.069	0.031	0.022	1.373	0.170
Geno.714	33	G	C	T	A	0.089	-0.113	0.045	-2.548	0.011	0.088	0.053	0.019	2.763	0.006

Table A1.13. Continued

						TG					HDL-C				
	Window	**loc1**	**loc2**	**loc3**	**loc4**	**Hap.freq.[1]**	**Coef.[2]**	**S.E.[3]**	**T.stat.[4]**	***P***	**Hap.freq[1]**	**Coef.[2]**	**S.E.[3]**	**T.stat.[4]**	***P***
Geno.811	33	G	C	T	T	0.126	0.061	0.040	1.524	0.128	0.127	-0.005	0.017	-0.264	0.792
Geno.104	33	G	T	T	T	0.192	0.022	0.033	0.688	0.492	0.192	0.001	0.014	0.065	0.948
Geno.rare29	33	*	*	*	*	0.015	0.187	0.115	1.627	0.104	0.015	0.069	0.050	1.388	0.166
haplo.base32	33	G	C	C	T	0.445	NA	NA	NA	NA	0.444	NA	NA	NA	NA
Geno.314	34	C	C	T	T	0.049	0.040	0.057	0.704	0.481	0.049	-0.024	0.025	-0.955	0.340
Geno.411	34	C	T	A	A	0.088	-0.105	0.045	-2.353	0.019	0.088	0.045	0.019	2.329	0.020
Geno.513	34	C	T	T	A	0.196	-0.007	0.033	-0.211	0.833	0.197	-0.001	0.014	-0.048	0.962
Geno.105	34	T	T	T	A	0.193	0.030	0.032	0.909	0.364	0.194	-0.006	0.014	-0.403	0.687
Geno.rare30	34	*	*	*	*	0.013	0.230	0.122	1.884	0.060	0.013	0.050	0.053	0.944	0.346
haplo.base33	34	C	C	T	A	0.460	NA	NA	NA	NA	0.458	NA	NA	NA	NA
Geno.315	35	C	T	A	G	0.013	-0.214	0.129	-1.656	0.098	0.013	0.016	0.055	0.295	0.768
Geno.412	35	C	T	T	A	0.050	0.034	0.057	0.594	0.553	0.049	-0.023	0.025	-0.911	0.363
Geno.514	35	T	A	A	A	0.089	-0.111	0.045	-2.473	0.014	0.088	0.046	0.019	2.378	0.018
Geno.613	35	T	T	A	A	0.285	0.030	0.030	1.020	0.308	0.287	-0.012	0.013	-0.917	0.360
Geno.715	35	T	T	A	G	0.104	-0.094	0.043	-2.171	0.030	0.105	0.024	0.019	1.269	0.205
Geno.rare31	35	*	*	*	*	0.006	0.061	0.194	0.316	0.752	0.006	0.070	0.079	0.882	0.378
haplo.base34	35	C	T	A	A	0.453	NA	NA	NA	NA	0.451	NA	NA	NA	NA
Geno.17	36	A	A	A	C	0.095	-0.108	0.042	-2.604	0.009	0.094	0.052	0.018	2.887	0.004
Geno.316	36	T	A	A	C	0.010	0.131	0.123	1.072	0.284	0.010	-0.036	0.054	-0.670	0.503
Geno.413	36	T	A	G	C	0.117	-0.118	0.038	-3.094	0.002	0.117	0.027	0.017	1.585	0.113
Geno.515	36	T	T	A	A	0.049	0.017	0.056	0.303	0.762	0.047	-0.017	0.025	-0.672	0.502
Geno.rare32	36	*	*	*	*	0.001	0.464	0.369	1.256	0.209	0.002	-0.040	0.175	-0.227	0.820
haplo.base35	36	T	A	A	A	0.728	NA	NA	NA	NA	0.729	NA	NA	NA	NA
Geno.18	37	A	A	A	D	0.051	-0.021	0.058	-0.357	0.722	0.049	0.034	0.026	1.339	0.181
Geno.414	37	A	A	C	W	0.106	-0.078	0.040	-1.971	0.049	0.105	0.047	0.017	2.709	0.007
Geno.614	37	A	G	C	W	0.117	-0.117	0.038	-3.048	0.002	0.118	0.029	0.017	1.760	0.079
Geno.812	37	T	A	A	W	0.049	0.019	0.056	0.329	0.743	0.047	-0.028	0.025	-1.118	0.264
Geno.rare33	37	*	*	*	*	0.001	0.659	0.000	8.5E+15	0.000	0.003	0.196	0.127	1.550	0.122
haplo.base36	37	A	A	A	W	0.675	NA	NA	NA	NA	0.678	NA	NA	NA	NA
Geno.19	38	A	A	D	G	0.052	0.003	0.056	0.045	0.964	0.052	0.047	0.024	1.966	0.050
Geno.415	38	A	C	W	G	0.106	-0.079	0.039	-2.010	0.045	0.105	0.048	0.017	2.819	0.005
Geno.615	38	G	C	W	C	0.113	-0.112	0.039	-2.858	0.004	0.113	0.029	0.017	1.718	0.086
Geno.rare34	38	*	*	*	*	0.004	-0.303	0.190	-1.593	0.112	0.004	0.033	0.083	0.396	0.692
haplo.base37	38	A	A	W	G	0.725	NA	NA	NA	NA	0.725	NA	NA	NA	NA
Geno.217	39	A	D	G	G	0.052	0.006	0.056	0.101	0.920	0.052	0.046	0.024	1.888	0.060
Geno.317	39	A	W	G	A	0.047	0.058	0.059	0.984	0.326	0.047	0.001	0.026	0.048	0.962
Geno.813	39	C	W	C	A	0.112	-0.106	0.039	-2.701	0.007	0.113	0.030	0.017	1.771	0.077
Geno.94	39	C	W	G	A	0.106	-0.093	0.040	-2.353	0.019	0.105	0.047	0.017	2.725	0.007
Geno.rare35	39	*	*	*	*	0.005	0.050	0.200	0.251	0.802	0.005	0.073	0.087	0.846	0.398
haplo.base38	39	A	W	G	G	0.678	NA	NA	NA	NA	0.679	NA	NA	NA	NA
Geno.318	40	D	G	G	T	0.052	0.003	0.056	0.053	0.958	0.052	0.046	0.024	1.899	0.058
Geno.516	40	W	C	A	T	0.112	-0.113	0.040	-2.852	0.004	0.112	0.030	0.017	1.746	0.081
Geno.616	40	W	G	A	T	0.150	-0.053	0.034	-1.537	0.125	0.149	0.031	0.015	2.063	0.040
Geno.rare36	40	*	*	*	*	0.004	-0.094	0.193	-0.489	0.625	0.005	-0.088	0.093	-0.941	0.347
haplo.base39	40	W	G	G	T	0.682	NA	NA	NA	NA	0.682	NA	NA	NA	NA
Geno.218	41	C	A	T	A	0.111	-0.112	0.039	-2.840	0.005	0.112	0.028	0.017	1.617	0.106
Geno.416	41	G	A	T	C	0.151	-0.058	0.034	-1.679	0.094	0.150	0.028	0.015	1.919	0.055
Geno.rare37	41	*	*	*	*	0.004	-0.097	0.192	-0.504	0.614	0.005	-0.093	0.076	-1.225	0.221
haplo.base40	41	G	G	T	C	0.734	NA	NA	NA	NA	0.734	NA	NA	NA	NA
Geno.219	42	A	T	A	G	0.112	-0.104	0.040	-2.609	0.009	0.112	0.029	0.017	1.704	0.089
Geno.319	42	A	T	C	G	0.053	-0.002	0.057	-0.032	0.974	0.053	0.013	0.024	0.552	0.581
Geno.417	42	A	T	C	T	0.101	-0.078	0.040	-1.939	0.053	0.101	0.038	0.018	2.154	0.032
Geno.rare38	42	*	*	*	*	0.006	-0.017	0.162	-0.108	0.914	0.007	-0.065	0.066	-0.988	0.323
haplo.base41	42	G	T	C	G	0.728	NA	NA	NA	NA	0.728	NA	NA	NA	NA
Geno.320	43	T	A	G	G	0.111	-0.112	0.039	-2.849	0.005	0.111	0.030	0.017	1.732	0.084
Geno.418	43	T	C	G	G	0.045	0.013	0.060	0.213	0.831	0.045	-0.010	0.025	-0.392	0.695
Geno.617	43	T	C	T	G	0.104	-0.072	0.040	-1.805	0.072	0.104	0.037	0.017	2.131	0.034
Geno.rare39	43	*	*	*	*	0.004	-0.093	0.192	-0.485	0.628	0.005	-0.095	0.076	-1.246	0.213
haplo.base42	43	T	C	G	T	0.736	NA	NA	NA	NA	0.736	NA	NA	NA	NA
Geno.110	44	A	G	G	G	0.112	-0.114	0.039	-2.914	0.004	0.111	0.030	0.017	1.758	0.079
Geno.321	44	C	G	G	G	0.045	0.021	0.059	0.359	0.720	0.045	-0.009	0.025	-0.347	0.729
Geno.716	44	C	T	G	G	0.104	-0.072	0.040	-1.813	0.070	0.104	0.038	0.017	2.191	0.029
Geno.rare40	44	*	*	*	*	0.006	-0.217	0.177	-1.224	0.221	0.006	-0.013	0.075	-0.169	0.866
haplo.base43	44	C	G	T	T	0.734	NA	NA	NA	NA	0.735	NA	NA	NA	NA
Geno.111	45	G	G	G	C	0.157	-0.069	0.033	-2.071	0.039	0.156	0.018	0.014	1.226	0.221
Geno.618	45	T	G	G	G	0.103	-0.077	0.041	-1.891	0.059	0.102	0.040	0.018	2.263	0.024
Geno.rare41	45	*	*	*	*	0.007	-0.128	0.153	-0.838	0.403	0.007	-0.018	0.066	-0.273	0.785
haplo.base44	45	G	T	T	C	0.733	NA	NA	NA	NA	0.734	NA	NA	NA	NA
Geno.220	46	G	G	C	G	0.158	-0.069	0.033	-2.068	0.039	0.158	0.016	0.014	1.091	0.276
Geno.322	46	G	G	G	G	0.103	-0.081	0.041	-1.973	0.049	0.102	0.037	0.018	2.112	0.035
Geno.717	46	T	T	C	A	0.047	-0.037	0.060	-0.612	0.541	0.046	-0.025	0.026	-0.994	0.321
Geno.rare42	46	*	*	*	*	0.006	-0.217	0.200	-1.088	0.277	0.006	-0.015	0.080	-0.183	0.855
haplo.base45	46	T	T	C	G	0.687	NA	NA	NA	NA	0.688	NA	NA	NA	NA
Geno.323	47	G	C	G	T	0.164	-0.071	0.034	-2.082	0.038	0.163	0.014	0.015	0.929	0.353
Geno.419	47	G	G	G	T	0.103	-0.078	0.042	-1.838	0.067	0.102	0.035	0.018	1.894	0.059
Geno.517	47	T	C	A	G	0.047	-0.037	0.059	-0.632	0.528	0.047	-0.029	0.026	-1.120	0.263
Geno.619	47	T	C	G	G	0.212	0.009	0.032	0.292	0.770	0.213	-0.009	0.014	-0.616	0.538
haplo.base46	47	T	C	G	T	0.475	NA	NA	NA	NA	0.475	NA	NA	NA	NA
Geno.112	48	C	A	G	C	0.047	-0.020	0.059	-0.346	0.730	0.047	-0.034	0.026	-1.325	0.186
Geno.324	48	C	G	G	C	0.212	0.025	0.031	0.801	0.423	0.213	-0.012	0.014	-0.883	0.378
Geno.518	48	C	G	T	T	0.028	-0.016	0.074	-0.215	0.830	0.028	-0.006	0.032	-0.171	0.864
Geno.620	48	G	G	T	C	0.102	-0.066	0.042	-1.575	0.116	0.102	0.032	0.018	1.786	0.075
haplo.base47	48	C	G	T	C	0.610	NA	NA	NA	NA	0.610	NA	NA	NA	NA
Geno.113	49	A	G	C	T	0.047	-0.012	0.059	-0.196	0.845	0.047	-0.040	0.026	-1.536	0.125
Geno.420	49	G	G	C	T	0.212	0.034	0.031	1.119	0.263	0.213	-0.017	0.013	-1.279	0.201
Geno.519	49	G	T	C	A	0.028	-0.085	0.072	-1.181	0.238	0.027	0.023	0.031	0.723	0.470
Geno.718	49	G	T	T	T	0.029	0.001	0.073	0.011	0.991	0.028	-0.012	0.032	-0.364	0.716

Table A1.13. Continued

						TG					HDL-C				
	Window	**loc1**	**loc2**	**loc3**	**loc4**	**Hap.freq.[1]**	**Coef.[2]**	**S.E.[3]**	**T.stat.[4]**	***P***	**Hap.freq[1]**	**Coef.[2]**	**S.E.[3]**	**T.stat.[4]**	***P***
haplo.base48	49	G	T	C	T	0.685	NA	NA	NA	NA	0.685	NA	NA	NA	NA
Geno.221	50	G	C	T	C	0.259	0.019	0.029	0.632	0.528	0.260	-0.015	0.013	-1.142	0.254
Geno.325	50	T	C	A	T	0.028	-0.087	0.072	-1.210	0.227	0.027	0.028	0.031	0.900	0.369
Geno.520	50	T	C	T	T	0.078	-0.045	0.047	-0.962	0.336	0.079	0.037	0.020	1.810	0.071
Geno.621	50	T	T	T	C	0.028	-0.016	0.074	-0.210	0.833	0.028	-0.002	0.032	-0.069	0.945
haplo.base49	50	T	C	T	C	0.605	NA	NA	NA	NA	0.605	NA	NA	NA	NA
Geno.114	51	C	A	T	G	0.026	-0.138	0.074	-1.860	0.063	0.027	0.038	0.031	1.203	0.229
Geno.222	51	C	T	C	A	0.118	-0.100	0.038	-2.616	0.009	0.118	0.026	0.017	1.550	0.122
Geno.521	51	C	T	T	G	0.077	-0.073	0.046	-1.583	0.114	0.078	0.048	0.020	2.418	0.016
Geno.719	51	T	T	C	A	0.027	-0.060	0.076	-0.791	0.429	0.027	0.012	0.033	0.377	0.706
Geno.rare43	51	*	*	*	*	0.003	0.535	0.463	1.155	0.249	0.002	-0.129	0.153	-0.843	0.399
haplo.base50	51	C	T	C	G	0.749	NA	NA	NA	NA	0.749	NA	NA	NA	NA
Geno.223	52	A	T	G	T	0.028	-0.102	0.071	-1.426	0.154	0.027	0.036	0.031	1.137	0.256
Geno.326	52	T	C	A	T	0.146	-0.075	0.035	-2.167	0.031	0.146	0.020	0.015	1.352	0.177
Geno.421	52	T	C	G	C	0.027	0.086	0.074	1.154	0.249	0.027	-0.003	0.032	-0.083	0.933
Geno.814	52	T	T	G	T	0.079	-0.058	0.046	-1.261	0.208	0.079	0.044	0.020	2.226	0.026
haplo.base51	52	T	C	G	T	0.720	NA	NA	NA	NA	0.721	NA	NA	NA	NA
Geno.115	53	C	A	T	C	0.146	-0.074	0.035	-2.154	0.032	0.146	0.020	0.015	1.318	0.188
Geno.327	53	C	G	C	C	0.027	0.086	0.074	1.158	0.247	0.027	-0.003	0.032	-0.098	0.922
Geno.720	53	T	G	T	C	0.105	-0.073	0.040	-1.832	0.067	0.105	0.041	0.017	2.383	0.017
Geno.rare44	53	*	*	*	*	0.004	-0.077	0.200	-0.387	0.699	0.004	-0.004	0.089	-0.047	0.962
haplo.base52	53	C	G	T	C	0.717	NA	NA	NA	NA	0.718	NA	NA	NA	NA
Geno.116	54	A	T	C	G	0.146	-0.067	0.034	-1.950	0.052	0.146	0.014	0.015	0.908	0.364
Geno.328	54	G	C	C	G	0.027	0.091	0.074	1.229	0.219	0.027	-0.007	0.032	-0.223	0.824
Geno.622	54	G	T	C	T	0.018	-0.038	0.094	-0.404	0.686	0.018	-0.045	0.041	-1.105	0.270
Geno.rare45	54	*	*	*	*	0.004	-0.056	0.193	-0.290	0.772	0.004	-0.016	0.083	-0.198	0.843
haplo.base53	54	G	T	C	G	0.805	NA	NA	NA	NA	0.805	NA	NA	NA	NA
Geno.117	55	C	C	G	C	0.027	0.109	0.074	1.482	0.139	0.027	-0.010	0.032	-0.327	0.744
Geno.522	55	T	C	T	C	0.017	-0.021	0.094	-0.225	0.822	0.017	-0.048	0.041	-1.166	0.244
Geno.rare46	55	*	*	*	*	0.005	0.117	0.193	0.603	0.547	0.005	-0.066	0.083	-0.795	0.427
haplo.base54	55	T	C	G	C	0.950	NA	NA	NA	NA	0.950	NA	NA	NA	NA
Geno.118	56	C	G	C	C	0.270	-0.083	0.027	-3.074	0.002	0.269	0.031	0.012	2.636	0.009
Geno.523	56	C	T	C	T	0.018	-0.047	0.093	-0.507	0.612	0.018	-0.039	0.040	-0.977	0.329
Geno.rare47	56	*	*	*	*	0.005	0.076	0.194	0.392	0.695	0.005	-0.050	0.083	-0.599	0.550
haplo.base55	56	C	G	C	T	0.707	NA	NA	NA	NA	0.708	NA	NA	NA	NA
Geno.119	57	G	C	C	C	0.107	-0.068	0.039	-1.722	0.085	0.107	0.040	0.017	2.342	0.020
Geno.224	57	G	C	C	T	0.164	-0.090	0.033	-2.701	0.007	0.164	0.025	0.014	1.712	0.087
Geno.623	57	T	C	T	T	0.018	-0.049	0.093	-0.522	0.602	0.018	-0.040	0.040	-0.983	0.326
haplo.base56	57	G	C	T	T	0.710	NA	NA	NA	NA	0.711	NA	NA	NA	NA
Geno.120	58	C	C	C	T	0.107	-0.068	0.041	-1.653	0.099	0.107	0.047	0.018	2.610	0.009
Geno.329	58	C	C	T	T	0.165	-0.090	0.035	-2.581	0.010	0.164	0.031	0.015	2.049	0.041
Geno.422	58	C	T	T	G	0.287	-0.002	0.029	-0.076	0.939	0.287	0.014	0.013	1.121	0.263
haplo.base57	58	C	T	T	T	0.440	NA	NA	NA	NA	0.441	NA	NA	NA	NA
Geno.122	59	C	C	T	C	0.107	-0.065	0.041	-1.567	0.118	0.107	0.046	0.018	2.598	0.010
Geno.423	59	C	T	T	C	0.129	-0.105	0.039	-2.715	0.007	0.129	0.038	0.017	2.277	0.023
Geno.524	59	C	T	T	T	0.037	-0.009	0.065	-0.131	0.896	0.036	-0.003	0.028	-0.090	0.928
Geno.624	59	T	T	G	C	0.288	0.004	0.029	0.132	0.895	0.288	0.012	0.013	0.986	0.324
haplo.base58	59	T	T	T	C	0.440	NA	NA	NA	NA	0.441	NA	NA	NA	NA
Geno.123	60	C	T	C	C	0.107	-0.065	0.041	-1.579	0.115	0.107	0.045	0.018	2.507	0.012
Geno.424	60	T	G	C	C	0.288	0.005	0.029	0.163	0.871	0.287	0.011	0.013	0.881	0.379
Geno.815	60	T	T	C	T	0.112	-0.109	0.041	-2.693	0.007	0.112	0.031	0.018	1.780	0.076
Geno.95	60	T	T	T	T	0.037	-0.004	0.065	-0.066	0.948	0.036	-0.005	0.028	-0.171	0.864
haplo.base59	60	T	T	C	C	0.457	NA	NA	NA	NA	0.457	NA	NA	NA	NA
Geno.225	61	G	C	C	T	0.288	0.019	0.028	0.687	0.492	0.288	0.001	0.012	0.095	0.924
Geno.330	61	T	C	C	C	0.014	-0.040	0.105	-0.379	0.705	0.014	0.029	0.046	0.624	0.533
Geno.525	61	T	C	T	T	0.112	-0.097	0.040	-2.417	0.016	0.112	0.023	0.017	1.307	0.192
Geno.721	61	T	T	T	T	0.037	0.006	0.065	0.088	0.930	0.036	-0.012	0.028	-0.415	0.679
haplo.base60	61	T	C	C	T	0.549	NA	NA	NA	NA	0.549	NA	NA	NA	NA

W: Allele in the referecne sequence ; D: Deleted base/bases; I: Inserted base/bases.

[1] Haplotype frequency; [2]Coefficient; [3]Standard error; [4]Test statistic

Table A1.14. Summary of 4-SNP sliding window haplotype analysis for TC and LDL-C in NHWs

						TC					LDL-C				
	Win	loc1	loc2	loc3	loc4	hap.freq	coef	se	t.stat	pval	hap.freq	coef	se	t.stat	pval
Geno.2	1	G	G	G	C	0.207	1.74	2.979	0.584	0.559	0.207	4.261	2.89	1.474	0.141
Geno.5	1	G	G	T	G	0.144	2.342	3.541	0.661	0.509	0.144	0.821	3.388	0.242	0.809
Geno.rare	1	*	*	*	*	0.012	-0.186	0.146	-1.274	0.203	0.012	-2.663	0.143	-18.664	0
haplo.base	1	G	G	G	G	0.637	NA	NA	NA	NA	0.638	NA	NA	NA	NA
Geno.4	2	G	G	C	T	0.207	1.224	3.065	0.399	0.69	0.206	3.507	2.975	1.179	0.239
Geno.6	2	G	G	G	T	0.093	-4.152	4.209	-0.986	0.324	0.093	-5.884	4.128	-1.425	0.155
Geno.7	2	G	T	G	T	0.155	1.159	3.473	0.334	0.739	0.155	-0.427	3.324	-0.128	0.898
Geno.rare1	2	*	*	*	*	0.003	20.105	0.07	287.083	0	0.003	7.554	0.071	107.088	0
haplo.base1	2	G	G	G	G	0.543	NA	NA	NA	NA	0.543	NA	NA	NA	NA
Geno.21	3	G	C	T	G	0.209	0.788	3.021	0.261	0.794	0.209	1.252	2.894	0.433	0.665
Geno.51	3	G	G	T	A	0.091	-4.943	4.219	-1.172	0.242	0.091	-6.14	4.034	-1.522	0.129
Geno.71	3	T	G	T	A	0.155	1.003	3.468	0.289	0.773	0.155	-0.913	3.317	-0.275	0.783
Geno.rare2	3	*	*	*	*	0.005	3.609	0.118	30.468	0	0.005	7.805	0.102	76.785	0
haplo.base2	3	G	G	G	A	0.54	NA	NA	NA	NA	0.54	NA	NA	NA	NA
Geno.22	4	C	T	G	G	0.209	0.658	3.001	0.219	0.826	0.209	1.144	2.903	0.394	0.694
Geno.52	4	G	T	A	C	0.018	-9.497	0.402	-23.643	0	0.018	-8.171	8.524	-0.959	0.338
Geno.61	4	G	T	A	G	0.228	-0.921	2.995	-0.307	0.759	0.228	-2.71	2.887	-0.939	0.348
Geno.rare3	4	*	*	*	*	0.005	3.208	0.052	62.207	0	0.005	8.017	0.146	55.057	0
haplo.base3	4	G	G	A	G	0.539	NA	NA	NA	NA	0.539	NA	NA	NA	NA
Geno.62	5	T	A	C	T	0.018	-9.269	0.532	-17.432	0	0.018	-7.969	0.507	-15.715	0
Geno.72	5	T	A	G	G	0.154	1.026	3.475	0.295	0.768	0.154	-0.935	3.319	-0.282	0.778
Geno.8	5	T	A	G	T	0.073	-3.249	4.63	-0.702	0.483	0.073	-5.157	4.433	-1.163	0.245
Geno.10	5	T	G	G	T	0.208	0.956	3.041	0.314	0.753	0.208	2.118	2.908	0.728	0.467
Geno.rare4	5	*	*	*	*	0.01	6.185	0.2	30.846	0	0.01	-3.139	0.199	-15.742	0
haplo.base4	5	G	A	G	T	0.536	NA	NA	NA	NA	0.536	NA	NA	NA	NA
Geno.1	6	A	C	T	T	0.018	-9.474	8.904	-1.064	0.288	0.018	-7.846	8.525	-0.92	0.358
Geno.3	6	A	G	G	T	0.15	0.335	3.557	0.094	0.925	0.15	-1.071	3.401	-0.315	0.753
Geno.53	6	A	G	T	T	0.072	-5.382	4.74	-1.136	0.257	0.072	-3.79	4.557	-0.832	0.406
Geno.9	6	G	G	T	T	0.201	1.213	3.123	0.389	0.698	0.201	2.859	2.989	0.956	0.339
Geno.rare5	6	*	*	*	*	0.02	1.33	9.2	0.145	0.885	0.02	-4.123	8.834	-0.467	0.641
haplo.base5	6	A	G	T	C	0.538	NA	NA	NA	NA	0.538	NA	NA	NA	NA
Geno.23	7	C	T	T	C	0.018	-9.556	8.855	-1.079	0.281	0.018	-7.735	8.471	-0.913	0.362
Geno.31	7	G	G	C	T	0.011	19.021	0.414	45.985	0	0.011	19.209	0.488	39.385	0
Geno.41	7	G	G	T	T	0.152	0.212	3.572	0.059	0.953	0.152	-1.711	3.386	-0.505	0.614
Geno.73	7	G	T	T	T	0.273	-0.571	2.812	-0.203	0.839	0.273	1.413	2.69	0.525	0.6
Geno.rare6	7	*	*	*	*	0.002	7.348	0.385	19.094	0	0.002	9.223	0.369	25.01	0
haplo.base6	7	G	T	C	T	0.544	NA	NA	NA	NA	0.544	NA	NA	NA	NA
Geno.11	8	G	C	T	C	0.011	16.633	0.712	23.376	0	0.011	22.651	12.194	1.858	0.064
Geno.54	8	G	T	T	T	0.149	0.005	3.535	0.001	0.999	0.149	-1.14	3.387	-0.337	0.736
Geno.81	8	T	T	C	C	0.018	-10.092	9.098	-1.109	0.268	0.018	-5.373	8.693	-0.618	0.537
Geno.91	8	T	T	T	C	0.274	-0.441	2.81	-0.157	0.875	0.274	1.436	2.694	0.533	0.594
Geno.rare7	8	*	*	*	*	0.005	8.578	0.807	10.634	0	0.005	-28.659	0.797	-35.954	0
haplo.base7	8	T	C	T	C	0.543	NA	NA	NA	NA	0.543	NA	NA	NA	NA
Geno.42	9	T	C	C	C	0.018	-10.08	8.882	-1.135	0.257	0.018	-8.341	8.505	-0.981	0.327
Geno.63	9	T	T	C	A	0.277	-0.706	2.82	-0.25	0.802	0.277	0.7	2.699	0.259	0.795
Geno.74	9	T	T	T	A	0.148	-0.683	3.558	-0.192	0.848	0.148	-1.926	3.404	-0.566	0.572
Geno.rare8	9	*	*	*	*	0.002	6.83	0.385	17.726	0	0.002	8.658	0.369	23.46	0
haplo.base8	9	C	T	C	A	0.555	NA	NA	NA	NA	0.555	NA	NA	NA	NA
Geno.24	10	C	C	C	A	0.018	-9.514	9.022	-1.054	0.292	0.018	-8.286	8.594	-0.964	0.335
Geno.55	10	T	T	A	G	0.148	-0.431	3.435	-0.126	0.9	0.148	-2.153	3.285	-0.655	0.512
Geno.rare9	10	*	*	*	*	0.002	1.642	0.43	3.818	0	0.002	3.516	0.405	8.684	0
haplo.base9	10	T	C	A	G	0.832	NA	NA	NA	NA	0.832	NA	NA	NA	NA
Geno.25	11	C	A	G	G	0.01	-4.405	11.695	-0.377	0.707	0.01	1.305	11.18	0.117	0.907
Geno.32	11	C	C	A	A	0.018	-9.451	9.049	-1.044	0.297	0.018	-7.952	8.654	-0.919	0.358
Geno.43	11	T	A	G	A	0.148	-0.518	3.443	-0.15	0.881	0.148	-2.125	3.294	-0.645	0.519
haplo.base10	11	C	A	G	A	0.823	NA	NA	NA	NA	0.823	NA	NA	NA	NA
Geno.12	12	A	G	A	A	0.119	2.586	3.741	0.691	0.49	0.119	3.842	3.59	1.07	0.285
Geno.64	12	C	A	A	C	0.019	-9.056	8.851	-1.023	0.307	0.019	-7.2	8.476	-0.849	0.396
Geno.rare10	12	*	*	*	*	0.01	-4.002	12.135	-0.33	0.742	0.01	2.244	11.597	0.193	0.847
haplo.base11	12	A	G	A	C	0.852	NA	NA	NA	NA	0.852	NA	NA	NA	NA
Geno.26	13	A	A	C	C	0.019	-9.018	8.867	-1.017	0.31	0.019	-7.182	8.492	-0.846	0.398
Geno.33	13	G	A	A	T	0.119	2.589	3.741	0.692	0.489	0.119	3.843	3.59	1.071	0.285
Geno.rare11	13	*	*	*	*	0.01	-3.999	12.136	-0.33	0.742	0.01	2.246	11.598	0.194	0.847
haplo.base12	13	G	A	C	T	0.852	NA	NA	NA	NA	0.852	NA	NA	NA	NA
Geno.13	14	A	A	T	C	0.12	2.099	3.805	0.552	0.581	0.12	2.908	3.649	0.797	0.426
Geno.27	14	A	C	C	G	0.018	-8.805	9.055	-0.972	0.331	0.018	-7.116	8.67	-0.821	0.412
Geno.44	14	A	C	T	G	0.223	-0.813	3.087	-0.263	0.792	0.223	-2.722	2.951	-0.922	0.357
Geno.65	14	G	C	T	C	0.01	-4.288	11.714	-0.366	0.714	0.01	1.348	11.202	0.12	0.904
haplo.base13	14	A	C	T	C	0.629	NA	NA	NA	NA	0.629	NA	NA	NA	NA
Geno.14	15	A	T	C	W	0.119	2.095	3.779	0.554	0.58	0.119	2.755	3.624	0.76	0.447
Geno.45	15	C	C	G	I	0.018	-9.217	0.383	-24.076	0	0.018	-8.061	0.368	-21.902	0
Geno.75	15	C	T	G	W	0.221	-0.637	3.07	-0.207	0.836	0.221	-2.685	2.934	-0.915	0.361
Geno.rare12	15	*	*	*	*	0.002	0.063	0.023	2.672	0.008	0.002	2.906	0.023	128.826	0
haplo.base14	15	C	T	C	W	0.64	NA	NA	NA	NA	0.64	NA	NA	NA	NA
Geno.28	16	C	G	I	G	0.018	-9.674	9.061	-1.068	0.286	0.018	-8.895	8.664	-1.027	0.305
Geno.76	16	T	G	W	G	0.144	-0.464	3.587	-0.129	0.897	0.144	-0.916	3.427	-0.267	0.789
Geno.82	16	T	G	W	T	0.074	-1.225	4.474	-0.274	0.784	0.074	-6.41	4.279	-1.498	0.135
Geno.rare13	16	*	*	*	*	0.002	0.067	0	1.59E+13	0	0.002	3.043	NA	NA	NA
haplo.base15	16	T	C	W	G	0.761	NA	NA	NA	NA	0.761	NA	NA	NA	NA
Geno.34	17	G	I	G	G	0.019	-9.58	8.34	-1.149	0.251	0.019	-8.971	7.974	-1.125	0.261
Geno.66	17	G	W	G	G	0.144	-0.624	3.59	-0.174	0.862	0.144	-1.097	3.429	-0.32	0.749
Geno.83	17	G	W	T	G	0.074	-1.252	4.48	-0.28	0.78	0.074	-6.542	4.277	-1.53	0.127
Geno.rare14	17	*	*	*	*	0.008	-13.487	14.904	-0.905	0.366	0.008	-12.777	13.879	-0.921	0.358
haplo.base16	17	C	W	G	G	0.754	NA	NA	NA	NA	0.754	NA	NA	NA	NA

Table A1.14. Continued

						TC					LDL-C				
	Win	loc1	loc2	loc3	loc4	hap.freq	coef	se	t.stat	pval	hap.freq	coef	se	t.stat	pval
Geno.15	18	I	G	G	C	0.019	-7.318	8.812	-0.83	0.407	0.019	-6.48	8.397	-0.772	0.441
Geno.67	18	W	G	G	T	0.032	0.335	6.869	0.049	0.961	0.032	0.368	6.537	0.056	0.955
Geno.84	18	W	T	G	C	0.075	-0.704	4.422	-0.159	0.874	0.075	-5.811	4.217	-1.378	0.169
Geno.rare15	18	*	*	*	*	0.009	-17.636	0.49	-35.97	0	0.009	-16.464	0.423	-38.894	0
haplo.base17	18	W	G	G	C	0.866	NA	NA	NA	NA	0.865	NA	NA	NA	NA
Geno.35	19	G	G	C	G	0.078	0.704	4.278	0.165	0.869	0.078	-1.401	4.088	-0.343	0.732
Geno.46	19	G	G	T	A	0.034	-0.627	6.718	-0.093	0.926	0.034	-0.304	6.43	-0.047	0.962
Geno.77	19	T	G	C	A	0.075	-0.572	4.437	-0.129	0.898	0.075	-5.803	4.234	-1.371	0.171
Geno.rare16	19	*	*	*	*	0.007	-15.793	14.303	-1.104	0.27	0.007	-16.549	13.366	-1.238	0.216
haplo.base18	19	G	G	C	A	0.806	NA	NA	NA	NA	0.806	NA	NA	NA	NA
Geno.36	20	G	C	A	A	0.067	-1.297	4.878	-0.266	0.79	0.067	-1.495	4.689	-0.319	0.75
Geno.56	20	G	C	G	G	0.078	0.639	4.283	0.149	0.881	0.078	-1.051	4.099	-0.256	0.798
Geno.78	20	G	T	A	G	0.034	-0.659	6.718	-0.098	0.922	0.034	0.156	6.447	0.024	0.981
Geno.rare17	20	*	*	*	*	0.007	-15.866	14.438	-1.099	0.272	0.007	-16.397	13.967	-1.174	0.241
haplo.base19	20	G	C	A	G	0.814	NA	NA	NA	NA	0.814	NA	NA	NA	NA
Geno.29	21	C	A	A	T	0.066	-1.482	4.901	-0.302	0.762	0.066	-1.722	4.711	-0.365	0.715
Geno.68	21	C	G	G	C	0.073	-0.557	4.385	-0.127	0.899	0.073	-2.306	4.196	-0.55	0.583
Geno.92	21	T	A	G	T	0.034	-0.458	6.712	-0.068	0.946	0.034	0.339	6.434	0.053	0.958
Geno.rare18	21	*	*	*	*	0.009	4.442	0.226	19.628	0	0.009	4.594	0.229	20.057	0
haplo.base20	21	C	A	G	T	0.819	NA	NA	NA	NA	0.818	NA	NA	NA	NA
Geno.210	22	A	A	T	T	0.066	0.304	5.004	0.061	0.952	0.067	-1.331	4.836	-0.275	0.783
Geno.69	22	A	G	T	T	0.311	3.762	2.679	1.404	0.161	0.311	2.353	2.574	0.914	0.361
Geno.85	22	G	G	C	T	0.073	1.026	4.499	0.228	0.82	0.073	-1.406	4.31	-0.326	0.744
Geno.rare19	22	*	*	*	*	0.009	5.994	0.227	26.43	0	0.009	5.582	0.229	24.402	0
haplo.base21	22	A	G	T	C	0.54	NA	NA	NA	NA	0.54	NA	NA	NA	NA
Geno.211	23	A	T	T	C	0.067	-0.106	4.951	-0.021	0.983	0.067	-1.416	4.762	-0.297	0.766
Geno.47	23	G	C	T	C	0.016	-4.628	10.232	-0.452	0.651	0.016	-6.228	10.246	-0.608	0.544
Geno.57	23	G	C	T	G	0.059	2.081	5.025	0.414	0.679	0.059	-0.362	4.88	-0.074	0.941
Geno.79	23	G	T	T	C	0.224	3.509	2.994	1.172	0.242	0.223	2.479	2.885	0.859	0.391
Geno.86	23	G	T	T	G	0.088	3.528	4.467	0.79	0.43	0.088	0.499	4.341	0.115	0.909
Geno.rare20	23	*	*	*	*	0.001	-10.106	0.28	-36.147	0	0.001	-32.208	0.1	-323.524	0
haplo.base22	23	G	T	C	C	0.546	NA	NA	NA	NA	0.546	NA	NA	NA	NA
Geno.212	24	C	T	C	G	0.015	-5.321	0.409	-13.017	0	0.015	-6.877	0.388	-17.709	0
Geno.37	24	C	T	G	G	0.059	2.177	5.023	0.433	0.665	0.059	-0.399	4.847	-0.082	0.934
Geno.87	24	T	T	C	G	0.29	2.811	2.689	1.045	0.296	0.289	1.66	2.592	0.641	0.522
Geno.101	24	T	T	G	G	0.087	3.173	4.445	0.714	0.476	0.087	0.358	4.288	0.083	0.934
Geno.rare21	24	*	*	*	*	0.004	-2.49	0.129	-19.319	0	0.004	-2.906	0.125	-23.225	0
haplo.base23	24	T	C	C	G	0.546	NA	NA	NA	NA	0.546	NA	NA	NA	NA
Geno.58	25	T	C	G	G	0.302	2.36	2.683	0.879	0.379	0.302	1.329	2.572	0.517	0.606
Geno.710	25	T	G	G	A	0.143	2.662	3.533	0.754	0.451	0.143	-0.038	3.385	-0.011	0.991
Geno.rare22	25	*	*	*	*	0.008	15.656	0.115	135.741	0	0.008	11.816	0.111	106.043	0
haplo.base24	25	C	C	G	G	0.547	NA	NA	NA	NA	0.547	NA	NA	NA	NA
Geno.48	26	C	G	G	G	0.015	1.959	9.7	0.202	0.84	0.015	-1.455	9.292	-0.157	0.876
Geno.610	26	G	G	A	A	0.143	1.891	3.4	0.556	0.578	0.143	-0.515	3.256	-0.158	0.874
Geno.rare23	26	*	*	*	*	0.008	14.312	0.214	66.826	0	0.008	11.105	0.206	53.852	0
haplo.base25	26	C	G	G	A	0.834	NA	NA	NA	NA	0.834	NA	NA	NA	NA
Geno.38	27	G	A	A	G	0.143	1.918	3.456	0.555	0.579	0.143	-0.719	3.303	-0.218	0.828
Geno.59	27	G	G	A	G	0.033	5.566	6.925	0.804	0.422	0.033	5.062	6.593	0.768	0.443
Geno.88	27	G	G	G	T	0.015	2.496	9.857	0.253	0.8	0.015	-1.294	9.375	-0.138	0.89
Geno.rare24	27	*	*	*	*	0.003	-4.915	0.07	-70.381	0	0.003	3.52	0.066	53.498	0
haplo.base26	27	G	G	A	T	0.807	NA	NA	NA	NA	0.807	NA	NA	NA	NA
Geno.16	28	A	A	G	C	0.143	2.995	3.511	0.853	0.394	0.143	0.514	3.351	0.153	0.878
Geno.39	28	G	A	G	C	0.033	6.268	6.909	0.907	0.365	0.033	5.989	6.578	0.91	0.363
Geno.49	28	G	A	T	A	0.171	4.829	3.224	1.498	0.135	0.171	5.675	3.08	1.842	0.066
Geno.89	28	G	G	T	C	0.015	2.953	9.773	0.302	0.763	0.015	-0.531	9.307	-0.057	0.955
haplo.base27	28	G	A	T	C	0.637	NA	NA	NA	NA	0.637	NA	NA	NA	NA
Geno.213	29	A	G	C	T	0.174	3.29	3.255	1.011	0.312	0.174	1.223	3.112	0.393	0.695
Geno.310	29	A	T	A	C	0.17	5.041	3.212	1.569	0.117	0.17	5.562	3.072	1.81	0.071
Geno.510	29	A	T	C	C	0.029	-4.77	6.935	-0.688	0.492	0.029	-8.244	6.62	-1.245	0.213
Geno.93	29	G	T	C	T	0.015	2.56	9.697	0.264	0.792	0.015	-0.801	9.299	-0.086	0.931
Geno.rare25	29	*	*	*	*	0.002	-26.482	0.087	-304.201	0	0.002	-9.493	0.085	-111.144	0
haplo.base28	29	A	T	C	T	0.609	NA	NA	NA	NA	0.609	NA	NA	NA	NA
Geno.410	30	G	C	T	G	0.171	3.218	3.378	0.953	0.341	0.171	0.683	3.254	0.21	0.834
Geno.511	30	T	A	C	G	0.17	4.623	3.288	1.406	0.16	0.17	4.444	3.142	1.415	0.158
Geno.711	30	T	C	C	G	0.029	-5.028	6.967	-0.722	0.471	0.029	-9.278	6.637	-1.398	0.163
Geno.810	30	T	C	T	C	0.131	-1.598	3.775	-0.423	0.672	0.131	-5.252	3.646	-1.441	0.15
Geno.rare26	30	*	*	*	*	0.005	-14.297	0.122	-117.588	0	0.005	-17.073	0.114	-150.167	0
haplo.base29	30	T	C	T	G	0.493	NA	NA	NA	NA	0.493	NA	NA	NA	NA
Geno.214	31	A	C	G	C	0.052	9.303	5.484	1.696	0.09	0.052	9.541	5.237	1.822	0.069
Geno.311	31	A	C	G	T	0.119	1.003	3.714	0.27	0.787	0.119	1.376	3.544	0.388	0.698
Geno.611	31	C	C	G	T	0.02	-9.675	8.105	-1.194	0.233	0.02	-11.65	7.683	-1.516	0.13
Geno.712	31	C	T	C	C	0.133	-3.124	3.689	-0.847	0.397	0.133	-6.277	3.524	-1.781	0.075
Geno.102	31	C	T	G	T	0.06	-4.514	5.064	-0.891	0.373	0.06	-4.905	4.855	-1.01	0.313
Geno.rare27	31	*	*	*	*	0.012	-2.005	0.488	-4.11	0	0.012	-8.418	0.49	-17.183	0
haplo.base30	31	C	T	G	C	0.604	NA	NA	NA	NA	0.604	NA	NA	NA	NA
Geno.215	32	C	G	C	C	0.013	27.546	12.939	2.129	0.034	0.013	17.26	12.745	1.354	0.176
Geno.312	32	C	G	C	T	0.047	4.165	6.019	0.692	0.489	0.047	3.738	5.918	0.632	0.528
Geno.512	32	C	G	T	T	0.134	-0.256	3.658	-0.07	0.944	0.134	-1.087	3.519	-0.309	0.758
Geno.612	32	T	C	C	C	0.064	-4.839	5.489	-0.882	0.378	0.063	-8.91	5.412	-1.646	0.1
Geno.713	32	T	C	C	T	0.069	-0.538	5.07	-0.106	0.916	0.07	-5.149	4.893	-1.052	0.293
Geno.103	32	T	G	C	T	0.17	1.102	3.519	0.313	0.754	0.169	-2.197	3.45	-0.637	0.524
Geno.121	32	T	G	T	T	0.057	-6.871	5.399	-1.272	0.204	0.057	-7.868	5.207	-1.511	0.131
Geno.rare28	32	*	*	*	*	0.009	20.217	0.397	50.935	0	0.009	8.955	14.888	0.602	0.548
haplo.base31	32	T	G	C	C	0.437	NA	NA	NA	NA	0.437	NA	NA	NA	NA
Geno.216	33	C	C	C	T	0.064	-4.111	5.341	-0.77	0.442	0.063	-7.762	5.263	-1.475	0.141
Geno.313	33	C	C	T	T	0.07	-1.511	4.914	-0.307	0.759	0.07	-5.897	4.803	-1.228	0.22
Geno.714	33	G	C	T	A	0.089	-2.07	4.365	-0.474	0.636	0.089	-4.81	4.185	-1.15	0.251

Table A1.14. Continued

						TC					LDL-C			
	Win	**loc1**	**loc2**	**loc3**	**loc4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**
Geno.811	33	G	C	T	T	0.127	5.315	3.826	1.389	0.165	0.127	3.08	3.744	0.823	0.411
Geno.104	33	G	T	T	T	0.192	-2.514	3.15	-0.798	0.425	0.192	-3.181	3.044	-1.045	0.297
Geno.rare29	33	*	*	*	*	0.015	33.939	0.555	61.176	0	0.015	22.392	11.064	2.024	0.043
haplo.base32	33	G	C	C	T	0.444	NA	NA	NA	NA	0.444	NA	NA	NA	NA
Geno.314	34	C	C	T	T	0.049	1.981	5.562	0.356	0.722	0.049	4.442	5.31	0.837	0.403
Geno.411	34	C	T	A	A	0.089	-1.35	4.348	-0.311	0.756	0.089	-3.4	4.173	-0.815	0.415
Geno.513	34	C	T	T	A	0.197	3.543	3.175	1.116	0.265	0.197	1.295	3.05	0.425	0.671
Geno.105	34	T	T	T	A	0.194	-1.891	3.137	-0.603	0.547	0.194	-1.94	3.013	-0.644	0.52
Geno.rare30	34	*	*	*	*	0.013	38.414	12.243	3.138	0.002	0.013	28.193	11.753	2.399	0.017
haplo.base33	34	C	C	T	A	0.459	NA	NA	NA	NA	0.459	NA	NA	NA	NA
Geno.315	35	C	T	A	G	0.013	-2.998	12.141	-0.247	0.805	0.013	4.258	12.203	0.349	0.727
Geno.412	35	C	T	T	A	0.049	2.295	5.551	0.413	0.679	0.049	4.936	5.324	0.927	0.354
Geno.514	35	T	A	A	A	0.089	-1.334	4.416	-0.302	0.763	0.089	-3.402	4.231	-0.804	0.422
Geno.613	35	T	T	A	A	0.286	-1.296	2.854	-0.454	0.65	0.286	-1.029	2.746	-0.375	0.708
Geno.715	35	T	T	A	G	0.106	5.071	4.146	1.223	0.222	0.106	1.429	3.999	0.357	0.721
Geno.rare31	35	*	*	*	*	0.006	41.409	17.72	2.337	0.02	0.006	36.77	17.321	2.123	0.034
haplo.base34	35	C	T	A	A	0.452	NA	NA	NA	NA	0.452	NA	NA	NA	NA
Geno.17	36	A	A	A	C	0.095	2.379	4.062	0.586	0.558	0.095	-0.143	3.887	-0.037	0.971
Geno.316	36	T	A	A	C	0.01	16.909	0.18	94.187	0	0.01	17.648	0.183	96.538	0
Geno.413	36	T	A	G	C	0.117	4.55	3.748	1.214	0.225	0.118	2.159	3.572	0.605	0.546
Geno.515	36	T	T	A	A	0.047	3.372	5.593	0.603	0.547	0.048	5.822	5.28	1.103	0.271
Geno.rare32	36	*	*	*	*	0.002	-2.872	0.025	-115.373	0	0.001	-13.004	0.032	-412.211	0
haplo.base35	36	T	A	A	A	0.728	NA	NA	NA	NA	0.727	NA	NA	NA	NA
Geno.18	37	A	A	A	D	0.051	5.955	5.58	1.067	0.286	0.051	4.933	5.335	0.925	0.355
Geno.414	37	A	A	C	W	0.106	2.037	3.931	0.518	0.604	0.106	1.95	3.75	0.52	0.603
Geno.614	37	A	G	C	W	0.118	4.532	3.74	1.212	0.226	0.118	2.392	3.573	0.669	0.503
Geno.812	37	T	A	A	W	0.048	4.499	5.508	0.817	0.414	0.048	7.36	5.231	1.407	0.16
Geno.rare33	37	*	*	*	*	0.001	-56.311	0.068	-833.657	0	0.001	-99.953	0	-1.51X10^{16}	0
haplo.base36	37	A	A	A	W	0.676	NA	NA	NA	NA	0.676	NA	NA	NA	NA
Geno.19	38	A	A	D	G	0.052	2.993	5.415	0.553	0.581	0.052	1.052	5.193	0.203	0.84
Geno.415	38	A	C	W	G	0.106	1.849	3.91	0.473	0.637	0.106	1.518	3.749	0.405	0.686
Geno.615	38	G	C	W	C	0.114	5.137	3.781	1.359	0.175	0.114	2.599	3.628	0.717	0.474
Geno.rare34	38	*	*	*	*	0.004	-16.843	0.095	-177.839	0	0.004	-9.057	0.09	-100.139	0
haplo.base37	38	A	A	W	G	0.724	NA	NA	NA	NA	0.724	NA	NA	NA	NA
Geno.217	39	A	D	G	G	0.051	2.177	5.488	0.397	0.692	0.051	0.712	5.224	0.136	0.892
Geno.317	39	A	W	G	A	0.047	-7.773	5.77	-1.347	0.178	0.047	-8.334	5.566	-1.497	0.135
Geno.813	39	C	W	C	A	0.113	4.7	3.808	1.234	0.218	0.113	1.928	3.659	0.527	0.598
Geno.94	39	C	W	G	A	0.105	-0.846	3.94	-0.215	0.83	0.106	-0.286	3.765	-0.076	0.939
Geno.rare35	39	*	*	*	*	0.006	35.964	0.106	337.989	0	0.005	25.138	0.106	236.159	0
haplo.base38	39	A	W	G	G	0.678	NA	NA	NA	NA	0.678	NA	NA	NA	NA
Geno.318	40	D	G	G	T	0.052	2.565	5.415	0.474	0.636	0.052	0.257	5.189	0.05	0.961
Geno.516	40	W	C	A	T	0.113	4.551	3.84	1.185	0.236	0.113	1.642	3.662	0.448	0.654
Geno.616	40	W	G	A	T	0.149	-4.23	3.385	-1.25	0.212	0.149	-4.339	3.243	-1.338	0.181
Geno.rare36	40	*	*	*	*	0.005	11.635	0.141	82.313	0	0.005	-15.4	0.13	-118.807	0
haplo.base39	40	W	G	G	T	0.682	NA	NA	NA	NA	0.682	NA	NA	NA	NA
Geno.218	41	C	A	T	A	0.112	4.556	3.825	1.191	0.234	0.112	1.727	3.649	0.473	0.636
Geno.416	41	G	A	T	C	0.15	-4.536	3.352	-1.353	0.177	0.15	-4.422	3.215	-1.375	0.17
Geno.rare37	41	*	*	*	*	0.005	11.293	0.092	122.776	0	0.005	-15.436	0.083	-185.702	0
haplo.base40	41	G	G	T	C	0.733	NA	NA	NA	NA	0.733	NA	NA	NA	NA
Geno.219	42	A	T	A	G	0.112	4.08	3.868	1.055	0.292	0.112	3.003	3.663	0.82	0.413
Geno.319	42	A	T	C	G	0.053	-9.309	5.476	-1.7	0.09	0.053	-9.438	5.276	-1.789	0.074
Geno.417	42	A	T	C	T	0.101	1.378	3.962	0.348	0.728	0.101	-0.379	3.796	-0.1	0.921
Geno.rare38	42	*	*	*	*	0.007	4.93	0.156	31.622	0	0.007	-17.269	0.136	-126.897	0
haplo.base41	42	G	T	C	G	0.727	NA	NA	NA	NA	0.727	NA	NA	NA	NA
Geno.320	43	T	A	G	G	0.111	4.463	3.863	1.155	0.248	0.111	3.542	3.669	0.965	0.335
Geno.418	43	T	C	G	G	0.044	-4.215	5.778	-0.73	0.466	0.044	-2.557	5.528	-0.462	0.644
Geno.617	43	T	C	T	G	0.104	1.15	3.886	0.296	0.767	0.104	-1.06	3.72	-0.285	0.776
Geno.rare39	43	*	*	*	*	0.005	12.513	0.129	97.321	0	0.005	-14.337	0.12	-119.69	0
haplo.base42	43	T	C	G	T	0.735	NA	NA	NA	NA	0.735	NA	NA	NA	NA
Geno.110	44	A	G	G	G	0.112	3.52	3.808	0.924	0.356	0.112	3.292	3.646	0.903	0.367
Geno.321	44	C	G	G	G	0.044	-3.67	5.739	-0.639	0.523	0.044	-1.68	5.486	-0.306	0.759
Geno.716	44	C	T	G	G	0.104	0.873	3.89	0.224	0.823	0.104	-0.91	3.726	-0.244	0.807
Geno.rare40	44	*	*	*	*	0.006	-11.42	0.093	-122.426	0	0.006	-1.396	0.096	-14.516	0
haplo.base43	44	C	G	T	T	0.734	NA	NA	NA	NA	0.734	NA	NA	NA	NA
Geno.111	45	G	G	G	C	0.156	1.67	3.21	0.52	0.603	0.156	2.009	3.069	0.655	0.513
Geno.618	45	T	G	G	G	0.103	0.124	3.92	0.032	0.975	0.103	-1.798	3.75	-0.479	0.632
Geno.rare41	45	*	*	*	*	0.007	-0.208	0.068	-3.079	0.002	0.007	8.241	0.065	126.595	0
haplo.base44	45	G	T	T	C	0.733	NA	NA	NA	NA	0.733	NA	NA	NA	NA
Geno.220	46	G	G	C	G	0.158	1.728	3.256	0.531	0.596	0.158	2.38	3.118	0.763	0.446
Geno.322	46	G	G	G	G	0.103	-0.28	3.989	-0.07	0.944	0.103	-1.732	3.82	-0.453	0.65
Geno.717	46	T	T	C	A	0.046	-5.079	5.744	-0.884	0.377	0.046	-0.276	5.51	-0.05	0.96
Geno.rare42	46	*	*	*	*	0.006	-11.997	0.085	-141.177	0	0.006	-1.613	0.08	-20.267	0
haplo.base45	46	T	T	C	G	0.687	NA	NA	NA	NA	0.687	NA	NA	NA	NA
Geno.323	47	G	C	G	T	0.164	1.595	3.346	0.477	0.634	0.164	2.21	3.202	0.69	0.49
Geno.419	47	G	G	G	T	0.103	-0.071	4.134	-0.017	0.986	0.103	-1.754	3.957	-0.443	0.658
Geno.517	47	T	C	A	G	0.047	-5.451	5.807	-0.939	0.348	0.047	-0.654	5.564	-0.118	0.906
Geno.619	47	T	C	G	G	0.213	0.519	3.13	0.166	0.868	0.213	-0.129	2.999	-0.043	0.966
haplo.base46	47	T	C	G	T	0.474	NA	NA	NA	NA	0.474	NA	NA	NA	NA
Geno.112	48	C	A	G	C	0.047	-6.011	5.748	-1.046	0.296	0.047	-1.255	5.513	-0.228	0.82
Geno.324	48	C	G	G	C	0.213	-0.202	3.047	-0.066	0.947	0.213	-0.779	2.922	-0.267	0.79
Geno.518	48	C	G	T	T	0.028	-7.452	7.125	-1.046	0.296	0.029	-3.369	6.773	-0.497	0.619
Geno.620	48	G	G	T	C	0.102	-0.721	4.083	-0.177	0.86	0.102	-2.331	3.906	-0.597	0.551
haplo.base47	48	C	G	T	C	0.609	NA	NA	NA	NA	0.609	NA	NA	NA	NA
Geno.113	49	A	G	C	T	0.047	-5.757	5.718	-1.007	0.314	0.047	-0.373	5.519	-0.068	0.946
Geno.420	49	G	G	C	T	0.213	-0.012	2.976	-0.004	0.997	0.213	-0.251	2.854	-0.088	0.93
Geno.519	49	G	T	C	A	0.027	1.824	6.949	0.263	0.793	0.027	3.012	6.665	0.452	0.652
Geno.718	49	G	T	T	T	0.029	-6.774	6.989	-0.969	0.333	0.029	-2.429	6.773	-0.359	0.72

Table A1.14. Continued

						TC					LDL-C			
	Win	**loc1**	**loc2**	**loc3**	**loc4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**
haplo.base48	49	G	T	C	T	0.684	NA	NA	NA	NA	0.684	NA	NA	NA	NA
Geno.221	50	G	C	T	C	0.26	-0.912	2.856	-0.319	0.75	0.26	-0.681	2.737	-0.249	0.804
Geno.325	50	T	C	A	T	0.027	2.107	6.96	0.303	0.762	0.027	2.616	6.671	0.392	0.695
Geno.520	50	T	C	T	T	0.079	0.901	4.57	0.197	0.844	0.079	-2.11	4.366	-0.483	0.629
Geno.621	50	T	T	T	C	0.028	-7.155	7.077	-1.011	0.312	0.029	-3.104	6.762	-0.459	0.646
haplo.base49	50	T	C	T	C	0.605	NA	NA	NA	NA	0.605	NA	NA	NA	NA
Geno.114	51	C	A	T	G	0.027	1.765	6.946	0.254	0.8	0.027	1.958	6.696	0.292	0.77
Geno.222	51	C	T	C	A	0.117	2.849	3.691	0.772	0.44	0.117	1.793	3.601	0.498	0.619
Geno.521	51	C	T	T	G	0.077	-1.115	4.458	-0.25	0.803	0.077	-3.568	4.318	-0.826	0.409
Geno.719	51	T	T	C	A	0.028	-7.339	6.959	-1.055	0.292	0.028	-3.635	6.706	-0.542	0.588
Geno.rare43	51	*	*	*	*	0.002	115.14	0.085	1360.036	0	0.002	88.579	0.068	1296.618	0
haplo.base50	51	C	T	C	G	0.748	NA	NA	NA	NA	0.748	NA	NA	NA	NA
Geno.223	52	A	T	G	T	0.027	2.627	6.945	0.378	0.705	0.027	2.989	6.649	0.45	0.653
Geno.326	52	T	C	A	T	0.146	1.614	3.383	0.477	0.633	0.146	1.91	3.228	0.592	0.554
Geno.421	52	T	C	G	C	0.027	-7.759	7.247	-1.071	0.285	0.027	-8.7	6.979	-1.247	0.213
Geno.814	52	T	T	G	T	0.079	1.529	4.466	0.342	0.732	0.079	-1.68	4.278	-0.393	0.695
haplo.base51	52	T	C	G	T	0.72	NA	NA	NA	NA	0.72	NA	NA	NA	NA
Geno.115	53	C	A	T	C	0.146	1.503	3.379	0.445	0.657	0.146	1.838	3.227	0.57	0.569
Geno.327	53	C	G	C	C	0.027	-7.909	7.175	-1.102	0.271	0.027	-8.664	6.871	-1.261	0.208
Geno.720	53	T	G	T	C	0.106	1.976	3.88	0.509	0.611	0.106	-0.135	3.713	-0.036	0.971
Geno.rare44	53	*	*	*	*	0.004	-22.303	0.103	-217.554	0	0.004	-19.331	0.098	-196.673	0
haplo.base52	53	C	G	T	C	0.717	NA	NA	NA	NA	0.717	NA	NA	NA	NA
Geno.116	54	A	T	C	G	0.146	1.472	3.38	0.436	0.663	0.146	1.861	3.224	0.577	0.564
Geno.328	54	G	C	C	G	0.027	-8.129	7.185	-1.131	0.258	0.027	-8.715	6.877	-1.267	0.206
Geno.622	54	G	T	C	T	0.018	-2.548	9.094	-0.28	0.779	0.018	0.672	8.704	0.077	0.938
Geno.rare45	54	*	*	*	*	0.004	-21.894	0.151	-145.229	0	0.004	-18.632	0.144	-129.374	0
haplo.base53	54	G	T	C	G	0.805	NA	NA	NA	NA	0.805	NA	NA	NA	NA
Geno.117	55	C	C	G	C	0.027	-8.578	7.154	-1.199	0.231	0.027	-9.328	6.85	-1.362	0.174
Geno.522	55	T	C	T	C	0.017	-3.037	9.108	-0.333	0.739	0.017	0.004	8.721	0	1
Geno.rare46	55	*	*	*	*	0.005	-12.846	0.132	-97.461	0	0.005	-12.569	0.126	-99.566	0
haplo.base54	55	T	C	G	C	0.951	NA	NA	NA	NA	0.951	NA	NA	NA	NA
Geno.118	56	C	G	C	C	0.27	0.532	2.672	0.199	0.842	0.27	0.927	2.555	0.363	0.717
Geno.523	56	C	T	C	T	0.018	-2.488	9.073	-0.274	0.784	0.018	0.747	8.688	0.086	0.931
Geno.rare47	56	*	*	*	*	0.005	-13.32	0.139	-95.684	0	0.005	-13.192	0.133	-98.97	0
haplo.base55	56	C	G	C	T	0.708	NA	NA	NA	NA	0.708	NA	NA	NA	NA
Geno.119	57	G	C	C	C	0.107	2.328	3.904	0.596	0.551	0.107	0.109	3.757	0.029	0.977
Geno.224	57	G	C	C	T	0.164	0.049	3.301	0.015	0.988	0.164	0.7	3.171	0.221	0.825
Geno.623	57	T	C	T	T	0.018	-2.325	9.08	-0.256	0.798	0.018	0.761	8.699	0.088	0.93
haplo.base56	57	G	C	T	T	0.71	NA	NA	NA	NA	0.71	NA	NA	NA	NA
Geno.120	58	C	C	C	T	0.108	2.529	4.09	0.618	0.537	0.107	-0.142	3.935	-0.036	0.971
Geno.329	58	C	C	T	T	0.165	0.228	3.449	0.066	0.947	0.165	0.473	3.311	0.143	0.886
Geno.422	58	C	T	T	G	0.287	0.475	2.894	0.164	0.87	0.287	-0.497	2.773	-0.179	0.858
haplo.base57	58	C	T	T	T	0.44	NA	NA	NA	NA	0.44	NA	NA	NA	NA
Geno.122	59	C	C	T	C	0.107	2.145	4.041	0.531	0.596	0.107	-0.603	3.87	-0.156	0.876
Geno.423	59	C	T	T	C	0.129	3.236	3.82	0.847	0.397	0.129	2.34	3.653	0.641	0.522
Geno.524	59	C	T	T	T	0.036	-6.834	6.386	-1.07	0.285	0.036	-3.538	6.126	-0.578	0.564
Geno.624	59	T	T	G	C	0.288	0.677	2.89	0.234	0.815	0.288	-0.423	2.772	-0.153	0.879
haplo.base58	59	T	T	T	C	0.44	NA	NA	NA	NA	0.44	NA	NA	NA	NA
Geno.123	60	C	T	C	C	0.107	2.549	4.044	0.63	0.529	0.107	-0.489	3.875	-0.126	0.9
Geno.424	60	T	G	C	C	0.287	0.917	2.867	0.32	0.749	0.287	-0.172	2.754	-0.062	0.95
Geno.815	60	T	T	C	T	0.113	5.586	3.935	1.419	0.156	0.113	2.379	3.78	0.629	0.529
Geno.95	60	T	T	T	T	0.036	-6.731	6.367	-1.057	0.291	0.036	-3.523	6.113	-0.576	0.565
haplo.base59	60	T	T	C	C	0.456	NA	NA	NA	NA	0.456	NA	NA	NA	NA
Geno.225	61	G	C	C	T	0.288	0.561	2.753	0.204	0.839	0.288	-0.359	2.642	-0.136	0.892
Geno.330	61	T	C	C	C	0.014	-2.1	10.228	-0.205	0.837	0.014	-3.453	9.811	-0.352	0.725
Geno.525	61	T	C	T	T	0.113	5.13	3.86	1.329	0.184	0.113	2.327	3.707	0.628	0.531
Geno.721	61	T	T	T	T	0.036	-7.078	6.339	-1.117	0.265	0.036	-3.557	6.085	-0.585	0.559
haplo.base60	61	T	C	C	T	0.549	NA	NA	NA	NA	0.549	NA	NA	NA	NA

Table A1.15. Summary of 4-SNP sliding window haplotype analysis for ApoB and ApoA1 in NHWs

							ApoA1					apoB		
Win	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**
1	G	G	G	C	0.209	0.383	0.545	0.704	0.482	0.210	-4.943	2.714	-1.821	0.069
1	G	G	T	G	0.145	0.612	0.661	0.926	0.355	0.144	-0.553	3.409	-0.162	0.871
1	*	*	*	*	0.013	-2.600	1.976	-1.316	0.189	0.013	-3.064	0.167	-18.353	0.000
1	G	G	G	G	0.633	NA	NA	NA	NA	0.632	NA	NA	NA	NA
2	G	G	C	T	0.209	0.350	0.560	0.624	0.533	0.210	-4.831	2.812	-1.718	0.087
2	G	G	G	T	0.092	-0.710	0.799	-0.889	0.375	0.092	1.583	4.046	0.391	0.696
2	G	T	G	T	0.156	0.273	0.652	0.418	0.676	0.156	-0.825	3.298	-0.250	0.803
2	*	*	*	*	0.005	-0.920	3.372	-0.273	0.785	0.005	17.950	0.115	155.760	0.000
2	G	G	G	G	0.538	NA	NA	NA	NA	0.538	NA	NA	NA	NA
3	G	C	T	G	0.210	0.323	0.556	0.582	0.561	0.210	-4.355	2.800	-1.555	0.121
3	G	G	T	A	0.090	-0.899	0.796	-1.129	0.259	0.090	1.295	4.069	0.318	0.750
3	T	G	T	A	0.157	0.268	0.650	0.412	0.681	0.156	-0.649	3.297	-0.197	0.844
3	*	*	*	*	0.002	3.400	4.612	0.737	0.461	0.002	12.433	0.060	205.916	0.000
3	G	G	G	A	0.541	NA	NA	NA	NA	0.541	NA	NA	NA	NA
4	C	T	G	G	0.209	0.338	0.557	0.607	0.544	0.210	-4.548	2.808	-1.619	0.106
4	G	T	A	C	0.016	-3.044	1.770	-1.720	0.086	0.016	-4.153	8.931	-0.465	0.642
4	G	T	A	G	0.230	0.066	0.570	0.115	0.908	0.230	-0.208	2.879	-0.072	0.942
4	*	*	*	*	0.003	3.498	4.632	0.755	0.451	0.003	12.526	0.090	138.482	0.000
4	G	G	A	G	0.542	NA	NA	NA	NA	0.542	NA	NA	NA	NA
5	T	A	C	T	0.016	-3.055	1.773	-1.723	0.086	0.016	-4.423	8.927	-0.495	0.621
5	T	A	G	G	0.157	0.178	0.653	0.272	0.786	0.156	-0.945	3.298	-0.286	0.775
5	T	A	G	T	0.075	-0.205	0.877	-0.234	0.815	0.075	2.371	4.491	0.528	0.598
5	T	G	G	T	0.208	0.400	0.563	0.710	0.478	0.208	-3.792	2.831	-1.339	0.181
5	*	*	*	*	0.006	-1.614	2.920	-0.553	0.581	0.006	-19.815	0.283	-69.915	0.000
5	G	A	G	T	0.538	NA	NA	NA	NA	0.538	NA	NA	NA	NA
6	A	C	T	T	0.016	-3.072	1.771	-1.735	0.083	0.016	-4.343	8.944	-0.486	0.628
6	A	G	G	T	0.155	0.151	0.659	0.229	0.819	0.154	-0.477	3.378	-0.141	0.888
6	A	G	T	T	0.074	-0.209	0.884	-0.237	0.813	0.074	1.952	4.523	0.431	0.666
6	G	G	T	T	0.201	0.548	0.576	0.952	0.342	0.202	-3.811	2.905	-1.312	0.190
6	*	*	*	*	0.014	-1.955	1.996	-0.979	0.328	0.014	-10.641	10.126	-1.051	0.294
6	A	G	T	C	0.540	NA	NA	NA	NA	0.540	NA	NA	NA	NA
7	C	T	T	C	0.016	-3.248	1.775	-1.830	0.068	0.016	-3.300	8.888	-0.371	0.711
7	G	G	T	T	0.156	0.128	0.657	0.194	0.846	0.156	-1.528	3.351	-0.456	0.649
7	G	T	T	T	0.275	0.344	0.527	0.653	0.514	0.276	-3.090	2.660	-1.162	0.246
7	*	*	*	*	0.008	3.298	3.025	1.090	0.276	0.007	-13.744	0.747	-18.391	0.000
7	G	T	C	T	0.545	NA	NA	NA	NA	0.545	NA	NA	NA	NA
8	G	T	T	T	0.153	0.206	0.662	0.312	0.755	0.153	-2.695	3.344	-0.806	0.421
8	T	T	C	C	0.016	-3.189	1.822	-1.751	0.081	0.015	-4.034	9.206	-0.438	0.661
8	T	T	T	C	0.276	0.315	0.526	0.598	0.550	0.277	-2.775	2.660	-1.043	0.297
8	*	*	*	*	0.011	1.627	2.229	0.730	0.466	0.011	-3.445	11.009	-0.313	0.754
8	T	C	T	C	0.544	NA	NA	NA	NA	0.544	NA	NA	NA	NA
9	T	C	C	C	0.016	-3.570	1.792	-1.992	0.047	0.016	-3.393	8.897	-0.381	0.703
9	T	T	C	A	0.279	0.317	0.522	0.608	0.543	0.279	-2.643	2.641	-1.001	0.318
9	T	T	T	A	0.152	0.173	0.662	0.262	0.793	0.152	-2.867	3.343	-0.857	0.392
9	*	*	*	*	0.002	7.519	4.653	1.616	0.107	0.002	-12.386	0.683	-18.126	0.000
9	C	T	C	A	0.550	NA	NA	NA	NA	0.550	NA	NA	NA	NA
10	C	C	C	A	0.016	-3.641	1.787	-2.037	0.042	0.016	-2.795	8.866	-0.315	0.753
10	T	T	A	G	0.152	0.065	0.637	0.102	0.919	0.152	-1.963	3.221	-0.609	0.543
10	*	*	*	*	0.002	7.320	4.647	1.575	0.116	0.002	-10.888	0.704	-15.458	0.000
10	T	C	A	G	0.829	NA	NA	NA	NA	0.830	NA	NA	NA	NA
11	C	C	A	A	0.016	-3.071	1.760	-1.745	0.082	0.016	-3.471	8.895	-0.390	0.697
11	T	A	G	A	0.152	0.101	0.639	0.159	0.874	0.152	-1.899	3.231	-0.588	0.557
11	*	*	*	*	0.007	3.750	2.661	1.409	0.159	0.007	0.834	13.554	0.062	0.951
11	C	A	G	A	0.824	NA	NA	NA	NA	0.825	NA	NA	NA	NA
12	A	G	A	A	0.119	-0.185	0.687	-0.270	0.788	0.120	-0.788	3.523	-0.224	0.823
12	C	A	A	C	0.016	-3.126	1.757	-1.779	0.076	0.016	-3.266	8.895	-0.367	0.714
12	*	*	*	*	0.007	3.695	2.701	1.368	0.172	0.007	1.354	14.202	0.095	0.924
12	A	G	A	C	0.858	NA	NA	NA	NA	0.857	NA	NA	NA	NA
13	A	A	C	C	0.016	-3.125	1.762	-1.773	0.077	0.016	-3.314	8.912	-0.372	0.710
13	G	A	A	T	0.119	-0.185	0.687	-0.269	0.788	0.120	-0.789	3.523	-0.224	0.823
13	*	*	*	*	0.007	3.695	2.701	1.368	0.172	0.007	1.353	14.202	0.095	0.924
13	G	A	C	T	0.858	NA	NA	NA	NA	0.857	NA	NA	NA	NA
14	A	A	T	C	0.119	-0.212	0.700	-0.303	0.762	0.120	-0.410	3.591	-0.114	0.909
14	A	C	C	G	0.015	-2.537	1.838	-1.380	0.168	0.015	-3.475	9.225	-0.377	0.707
14	A	C	T	G	0.229	-0.169	0.579	-0.292	0.770	0.229	1.050	3.032	0.346	0.729
14	*	*	*	*	0.007	3.682	2.664	1.382	0.168	0.007	1.675	13.579	0.123	0.902
14	A	C	T	C	0.629	NA	NA	NA	NA	0.629	NA	NA	NA	NA
15	A	T	C	W	0.118	-0.274	0.703	-0.389	0.697	0.119	-1.637	3.595	-0.456	0.649
15	C	C	G	I	0.016	-3.085	1.862	-1.657	0.098	0.016	-6.898	8.886	-0.776	0.438
15	C	T	G	W	0.226	-0.160	0.580	-0.276	0.782	0.225	0.297	3.026	0.098	0.922
15	*	*	*	*	0.002	-1.479	6.563	-0.225	0.822	0.002	50.208	0.644	77.962	0.000
15	C	T	C	W	0.638	NA	NA	NA	NA	0.638	NA	NA	NA	NA
16	C	G	I	G	0.016	-3.045	1.814	-1.679	0.094	0.016	-6.440	8.843	-0.728	0.467
16	T	G	W	G	0.148	0.045	0.670	0.068	0.946	0.148	-0.185	3.485	-0.053	0.958
16	T	G	W	T	0.074	-0.407	0.857	-0.475	0.635	0.074	4.029	4.309	0.935	0.350
16	*	*	*	*	0.002	-1.379	4.804	-0.287	0.774	0.002	50.734	0.690	73.500	0.000
16	T	C	W	G	0.759	NA	NA	NA	NA	0.759	NA	NA	NA	NA
17	G	I	G	G	0.017	-3.060	1.610	-1.901	0.058	0.017	-3.492	8.228	-0.424	0.671

Table A1.15. Continued

							ApoA1					apoB		
Win	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**
17	G	W	G	G	0.148	0.062	0.672	0.093	0.926	0.147	-0.128	3.526	-0.036	0.971
17	G	W	T	G	0.074	-0.336	0.863	-0.389	0.697	0.074	3.658	4.374	0.836	0.403
17	*	*	*	*	0.009	-2.029	2.465	-0.823	0.411	0.009	-0.610	0.157	-3.875	0.000
17	C	W	G	G	0.752	NA	NA	NA	NA	0.753	NA	NA	NA	NA
18	I	G	G	C	0.015	-3.723	1.883	-1.977	0.049	0.016	9.549	9.327	1.024	0.307
18	W	G	G	T	0.033	-0.765	1.275	-0.600	0.549	0.033	0.386	6.305	0.061	0.951
18	W	T	G	C	0.074	-0.296	0.855	-0.347	0.729	0.074	6.642	4.286	1.550	0.122
18	*	*	*	*	0.011	-1.500	2.392	-0.627	0.531	0.011	-19.299	11.662	-1.655	0.099
18	W	G	G	C	0.866	NA	NA	NA	NA	0.866	NA	NA	NA	NA
19	G	G	C	G	0.069	-0.966	0.888	-1.089	0.277	0.069	0.313	4.600	0.068	0.946
19	G	G	T	A	0.035	-0.638	1.231	-0.518	0.605	0.035	-0.174	6.163	-0.028	0.978
19	T	G	C	A	0.074	-0.284	0.869	-0.327	0.744	0.073	6.663	4.414	1.509	0.132
19	*	*	*	*	0.009	-2.833	2.609	-1.086	0.278	0.010	-18.982	12.130	-1.565	0.118
19	G	G	C	A	0.812	NA	NA	NA	NA	0.813	NA	NA	NA	NA
20	G	C	A	A	0.065	0.269	0.927	0.290	0.772	0.065	7.778	4.730	1.644	0.101
20	G	C	G	G	0.070	-0.922	0.879	-1.049	0.295	0.069	0.417	4.596	0.091	0.928
20	G	T	A	G	0.035	-0.564	1.236	-0.457	0.648	0.035	-0.181	6.156	-0.029	0.977
20	*	*	*	*	0.009	-2.905	2.683	-1.083	0.279	0.010	-19.695	12.357	-1.594	0.112
20	G	C	A	G	0.821	NA	NA	NA	NA	0.821	NA	NA	NA	NA
21	C	A	A	T	0.065	0.162	0.918	0.177	0.860	0.065	5.781	4.583	1.261	0.208
21	C	G	G	C	0.063	-0.965	0.907	-1.064	0.288	0.063	-1.949	4.558	-0.428	0.669
21	T	A	G	T	0.035	-0.535	1.232	-0.435	0.664	0.035	0.044	6.171	0.007	0.994
21	*	*	*	*	0.009	0.113	2.435	0.046	0.963	0.009	7.030	0.236	29.829	0.000
21	C	A	G	T	0.827	NA	NA	NA	NA	0.827	NA	NA	NA	NA
22	A	A	T	T	0.066	0.376	0.940	0.399	0.690	0.066	4.537	4.698	0.966	0.335
22	A	G	T	T	0.322	0.499	0.491	1.016	0.310	0.321	-2.850	2.462	-1.158	0.248
22	G	G	C	T	0.063	-0.763	0.923	-0.827	0.409	0.063	-3.079	4.633	-0.665	0.507
22	*	*	*	*	0.009	0.348	2.374	0.146	0.884	0.009	6.552	0.215	30.508	0.000
22	A	G	T	C	0.539	NA	NA	NA	NA	0.540	NA	NA	NA	NA
23	A	T	T	C	0.067	0.361	0.934	0.387	0.699	0.066	5.918	4.742	1.248	0.213
23	G	C	T	C	0.011	-1.149	2.233	-0.515	0.607	0.010	17.293	13.915	1.243	0.215
23	G	C	T	G	0.053	-0.638	1.002	-0.637	0.525	0.053	-4.560	5.008	-0.911	0.363
23	G	T	T	C	0.227	0.348	0.542	0.641	0.522	0.227	-2.850	2.732	-1.043	0.298
23	G	T	T	G	0.095	0.832	0.802	1.038	0.300	0.095	-2.801	4.114	-0.681	0.496
23	G	T	C	C	0.547	NA	NA	NA	NA	0.548	NA	NA	NA	NA
24	C	T	C	G	0.011	-1.119	2.239	-0.500	0.618	0.011	12.212	11.990	1.019	0.309
24	C	T	G	G	0.053	-0.625	1.003	-0.623	0.534	0.053	-4.785	5.041	-0.949	0.343
24	T	T	C	G	0.292	0.340	0.504	0.674	0.500	0.291	-1.203	2.536	-0.474	0.635
24	T	T	G	G	0.095	0.847	0.803	1.056	0.292	0.094	-3.346	4.143	-0.807	0.420
24	*	*	*	*	0.002	3.958	4.643	0.852	0.394	0.002	-20.585	0.197	-104.724	0.000
24	T	C	C	G	0.547	NA	NA	NA	NA	0.548	NA	NA	NA	NA
25	T	C	G	G	0.300	0.255	0.500	0.509	0.611	0.299	-1.409	2.514	-0.560	0.576
25	T	G	G	A	0.148	0.286	0.660	0.433	0.665	0.147	-2.327	3.350	-0.694	0.488
25	*	*	*	*	0.005	3.194	3.262	0.979	0.328	0.005	-14.875	0.077	-194.415	0.000
25	C	C	G	G	0.547	NA	NA	NA	NA	0.548	NA	NA	NA	NA
26	C	G	G	G	0.011	-2.378	2.125	-1.119	0.264	0.011	2.974	0.077	38.552	0.000
26	G	G	A	A	0.147	0.158	0.631	0.250	0.802	0.147	-1.762	3.225	-0.546	0.585
26	*	*	*	*	0.005	2.909	3.240	0.898	0.370	0.005	-13.287	0.015	-908.594	0.000
26	C	G	G	A	0.836	NA	NA	NA	NA	0.836	NA	NA	NA	NA
27	G	A	A	G	0.147	0.147	0.637	0.230	0.818	0.147	-2.502	3.212	-0.779	0.436
27	G	G	A	G	0.032	0.275	1.293	0.213	0.832	0.032	2.478	6.615	0.375	0.708
27	G	G	G	T	0.011	-2.339	2.113	-1.107	0.269	0.012	3.091	10.458	0.296	0.768
27	*	*	*	*	0.003	3.523	4.625	0.762	0.447	0.002	-19.567	0.097	-200.801	0.000
27	G	G	A	T	0.807	NA	NA	NA	NA	0.807	NA	NA	NA	NA
28	A	A	G	C	0.148	0.308	0.647	0.476	0.634	0.147	-3.154	3.267	-0.965	0.335
28	G	A	G	C	0.032	0.408	1.294	0.316	0.752	0.032	1.840	6.639	0.277	0.782
28	G	A	T	A	0.170	0.842	0.585	1.441	0.150	0.170	-3.633	2.945	-1.234	0.218
28	G	G	T	C	0.012	-2.142	2.076	-1.032	0.303	0.012	2.549	10.460	0.244	0.808
28	G	A	T	C	0.638	NA	NA	NA	NA	0.639	NA	NA	NA	NA
29	A	G	C	T	0.178	0.339	0.599	0.567	0.571	0.177	-2.578	3.008	-0.857	0.392
29	A	T	A	C	0.171	0.780	0.583	1.337	0.182	0.171	-4.085	2.940	-1.390	0.165
29	A	T	C	C	0.027	-2.073	1.277	-1.624	0.105	0.027	-12.909	6.471	-1.995	0.047
29	G	T	C	T	0.012	-2.278	2.068	-1.102	0.271	0.012	1.512	10.420	0.145	0.885
29	A	T	C	T	0.612	NA	NA	NA	NA	0.613	NA	NA	NA	NA
30	G	C	T	G	0.175	0.332	0.615	0.539	0.590	0.175	-1.520	3.100	-0.490	0.624
30	T	A	C	G	0.171	0.558	0.595	0.937	0.349	0.171	-2.814	3.022	-0.931	0.352
30	T	C	C	G	0.027	-2.310	1.274	-1.813	0.070	0.027	-11.649	6.486	-1.796	0.073
30	T	C	T	C	0.138	-0.934	0.688	-1.357	0.176	0.138	5.813	3.472	1.674	0.095
30	*	*	*	*	0.003	-12.147	5.421	-2.241	0.026	0.002	7.382	0.052	141.012	0.000
30	T	C	T	G	0.485	NA	NA	NA	NA	0.486	NA	NA	NA	NA
31	A	C	G	C	0.048	0.411	1.043	0.394	0.694	0.048	-4.745	5.283	-0.898	0.370
31	A	C	G	T	0.124	0.512	0.669	0.765	0.445	0.123	-1.089	3.381	-0.322	0.748
31	C	C	G	T	0.021	-1.545	1.415	-1.092	0.276	0.021	-11.465	7.104	-1.614	0.107
31	C	T	C	C	0.139	-1.249	0.672	-1.859	0.064	0.138	6.677	3.406	1.961	0.051
31	C	T	G	T	0.056	0.208	0.967	0.215	0.830	0.055	3.049	4.894	0.623	0.534
31	*	*	*	*	0.008	-6.076	2.707	-2.245	0.025	0.008	-5.604	13.563	-0.413	0.680
31	C	T	G	C	0.605	NA	NA	NA	NA	0.606	NA	NA	NA	NA
32	C	G	C	T	0.046	0.070	1.118	0.063	0.950	0.044	-10.806	6.177	-1.749	0.081
32	C	G	T	T	0.142	0.045	0.662	0.068	0.946	0.142	-2.599	3.263	-0.796	0.426
32	T	C	C	C	0.068	-2.601	1.052	-2.473	0.014	0.068	3.402	5.067	0.671	0.502
32	T	C	C	T	0.069	-0.314	1.000	-0.314	0.754	0.070	8.939	4.913	1.819	0.070
32	T	G	C	T	0.180	-0.248	0.672	-0.369	0.713	0.180	1.722	3.417	0.504	0.614

Table A1.15. Continued

							ApoA1					apoB		
Win	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**
32	T	G	T	T	0.053	-0.530	1.047	-0.506	0.613	0.052	-1.395	5.059	-0.276	0.783
32	*	*	*	*	0.014	0.346	2.504	0.138	0.890	0.015	40.668	11.439	3.555	0.000
32	T	G	C	C	0.430	NA	NA	NA	NA	0.429	NA	NA	NA	NA
33	C	C	C	T	0.067	-2.180	1.016	-2.145	0.033	0.066	3.685	5.512	0.669	0.504
33	C	C	T	T	0.069	-0.466	0.972	-0.480	0.632	0.070	7.056	4.833	1.460	0.145
33	G	C	T	A	0.101	0.447	0.773	0.578	0.564	0.101	3.693	3.887	0.950	0.343
33	G	C	T	T	0.123	-0.159	0.760	-0.210	0.834	0.121	-5.507	3.766	-1.462	0.144
33	G	T	T	T	0.196	0.103	0.593	0.173	0.862	0.195	-2.284	3.051	-0.749	0.455
33	*	*	*	*	0.011	6.238	2.696	2.314	0.021	0.011	25.325	17.275	1.466	0.143
33	G	C	C	T	0.433	NA	NA	NA	NA	0.436	NA	NA	NA	NA
34	C	C	T	T	0.049	0.416	1.040	0.400	0.689	0.049	-5.098	5.361	-0.951	0.342
34	C	T	A	A	0.101	0.679	0.777	0.873	0.383	0.101	2.390	3.915	0.610	0.542
34	C	T	T	A	0.193	0.142	0.611	0.232	0.817	0.192	-2.335	3.111	-0.751	0.453
34	T	T	T	A	0.199	0.461	0.579	0.797	0.426	0.198	-2.821	2.944	-0.958	0.338
34	*	*	*	*	0.008	10.124	2.912	3.476	0.001	0.007	13.047	15.577	0.838	0.403
34	C	C	T	A	0.451	NA	NA	NA	NA	0.453	NA	NA	NA	NA
35	C	T	A	G	0.012	-0.728	2.549	-0.286	0.775	0.013	-2.537	12.044	-0.211	0.833
35	C	T	T	A	0.049	0.240	1.056	0.228	0.820	0.049	-5.957	5.397	-1.104	0.270
35	T	A	A	A	0.099	0.374	0.802	0.467	0.641	0.100	2.378	3.956	0.601	0.548
35	T	T	A	A	0.288	0.186	0.535	0.347	0.729	0.287	-4.195	2.699	-1.554	0.121
35	T	T	A	G	0.106	0.426	0.797	0.535	0.593	0.105	1.190	4.044	0.294	0.769
35	*	*	*	*	0.007	7.880	3.296	2.391	0.017	0.006	-1.518	17.287	-0.088	0.930
35	C	T	A	A	0.440	NA	NA	NA	NA	0.442	NA	NA	NA	NA
36	A	A	A	C	0.105	0.854	0.729	1.171	0.242	0.105	4.029	3.674	1.097	0.273
36	T	A	G	C	0.115	0.276	0.713	0.387	0.699	0.114	2.566	3.582	0.716	0.474
36	T	T	A	A	0.045	0.142	1.090	0.131	0.896	0.045	-3.951	5.547	-0.712	0.477
36	*	*	*	*	0.011	2.189	2.339	0.936	0.350	0.011	5.874	11.558	0.508	0.612
36	T	A	A	A	0.724	NA	NA	NA	NA	0.724	NA	NA	NA	NA
37	A	A	A	D	0.054	1.150	1.026	1.121	0.263	0.053	9.185	5.133	1.790	0.074
37	A	A	C	W	0.114	0.905	0.707	1.280	0.201	0.114	4.492	3.542	1.268	0.205
37	A	G	C	W	0.118	0.277	0.700	0.396	0.692	0.115	2.993	3.575	0.837	0.403
37	T	A	A	W	0.048	0.662	1.044	0.634	0.526	0.045	-3.385	5.562	-0.609	0.543
37	*	*	*	*	0.001	-17.213	6.748	-2.551	0.011	0.004	-3.123	0.129	-24.120	0.000
37	A	A	A	W	0.666	NA	NA	NA	NA	0.670	NA	NA	NA	NA
38	A	A	D	G	0.054	0.299	0.991	0.301	0.763	0.053	8.297	5.149	1.611	0.108
38	A	C	W	G	0.114	0.884	0.711	1.243	0.215	0.112	4.601	3.578	1.286	0.199
38	G	C	W	C	0.113	0.365	0.713	0.512	0.609	0.113	1.765	3.552	0.497	0.620
38	*	*	*	*	0.005	-1.434	3.252	-0.441	0.660	0.006	39.305	15.095	2.604	0.010
38	A	A	W	G	0.714	NA	NA	NA	NA	0.716	NA	NA	NA	NA
39	A	D	G	G	0.050	-0.438	1.156	-0.379	0.705	0.054	8.500	4.987	1.705	0.089
39	A	W	G	A	0.043	-0.526	1.089	-0.483	0.629	0.043	-0.311	5.597	-0.056	0.956
39	C	W	C	A	0.109	0.199	0.738	0.270	0.787	0.112	1.833	3.622	0.506	0.613
39	C	W	G	A	0.114	0.421	0.737	0.571	0.568	0.115	6.151	3.570	1.723	0.086
39	*	*	*	*	0.008	6.513	2.942	2.214	0.027	0.004	-1.151	0.065	-17.741	0.000
39	A	W	G	G	0.676	NA	NA	NA	NA	0.672	NA	NA	NA	NA
40	D	G	G	T	0.050	-0.336	1.240	-0.271	0.787	0.055	9.021	4.936	1.828	0.068
40	W	C	A	T	0.110	0.091	0.740	0.122	0.903	0.112	1.575	3.605	0.437	0.662
40	W	G	A	T	0.151	0.030	0.633	0.048	0.962	0.152	4.621	3.121	1.481	0.139
40	*	*	*	*	0.010	4.270	3.042	1.404	0.161	0.005	14.770	17.481	0.845	0.399
40	W	G	G	T	0.680	NA	NA	NA	NA	0.676	NA	NA	NA	NA
41	C	A	T	A	0.111	0.248	0.716	0.346	0.729	0.111	1.359	3.611	0.376	0.707
41	G	A	T	C	0.155	0.114	0.610	0.187	0.852	0.154	3.975	3.112	1.278	0.202
41	*	*	*	*	0.005	1.953	3.477	0.562	0.575	0.005	13.597	17.699	0.768	0.443
41	G	G	T	C	0.730	NA	NA	NA	NA	0.730	NA	NA	NA	NA
42	A	T	A	G	0.112	0.307	0.714	0.430	0.668	0.112	1.220	3.598	0.339	0.735
42	A	T	C	G	0.049	-0.763	1.034	-0.738	0.461	0.049	3.415	5.337	0.640	0.523
42	A	T	C	T	0.111	0.800	0.712	1.124	0.262	0.111	4.167	3.552	1.173	0.241
42	*	*	*	*	0.006	1.232	3.044	0.405	0.686	0.006	13.762	0.133	103.232	0.000
42	G	T	C	G	0.721	NA	NA	NA	NA	0.722	NA	NA	NA	NA
43	T	A	G	G	0.111	0.324	0.715	0.453	0.651	0.110	1.253	3.596	0.348	0.728
43	T	C	G	G	0.040	-0.271	1.102	-0.246	0.806	0.040	-9.109	5.534	-1.646	0.100
43	T	C	T	G	0.114	0.708	0.705	1.005	0.316	0.114	4.019	3.530	1.139	0.255
43	*	*	*	*	0.005	2.064	3.477	0.594	0.553	0.005	12.538	17.685	0.709	0.479
43	T	C	G	T	0.731	NA	NA	NA	NA	0.732	NA	NA	NA	NA
44	A	G	G	G	0.110	0.302	0.717	0.422	0.674	0.110	1.913	3.586	0.533	0.594
44	C	G	G	G	0.039	-0.310	1.104	-0.281	0.779	0.039	-9.037	5.532	-1.634	0.103
44	C	T	G	G	0.114	0.671	0.706	0.950	0.343	0.114	4.214	3.519	1.197	0.232
44	*	*	*	*	0.007	-0.696	2.683	-0.259	0.795	0.007	14.529	0.194	74.844	0.000
44	C	G	T	T	0.730	NA	NA	NA	NA	0.730	NA	NA	NA	NA
45	G	G	G	C	0.150	0.126	0.606	0.208	0.835	0.149	-1.315	3.042	-0.432	0.666
45	T	G	G	G	0.113	0.676	0.712	0.949	0.343	0.113	4.218	3.577	1.179	0.239
45	*	*	*	*	0.008	-0.293	2.472	-0.118	0.906	0.008	10.761	0.121	89.072	0.000
45	G	T	T	C	0.729	NA	NA	NA	NA	0.730	NA	NA	NA	NA
46	G	G	C	G	0.151	0.009	0.606	0.015	0.988	0.150	-1.810	3.041	-0.595	0.552
46	G	G	G	G	0.113	0.500	0.715	0.699	0.485	0.113	3.783	3.586	1.055	0.292
46	T	T	C	A	0.043	-2.372	1.099	-2.159	0.031	0.043	-8.389	5.745	-1.460	0.145
46	*	*	*	*	0.007	-0.838	2.907	-0.288	0.773	0.007	14.172	0.179	79.082	0.000
46	T	T	C	G	0.686	NA	NA	NA	NA	0.687	NA	NA	NA	NA
47	G	C	G	T	0.157	0.118	0.629	0.187	0.852	0.157	-2.587	3.160	-0.819	0.413
47	G	G	G	T	0.113	0.669	0.747	0.895	0.371	0.113	1.779	3.746	0.475	0.635
47	T	C	A	G	0.045	-2.104	1.096	-1.919	0.056	0.045	-10.454	5.739	-1.822	0.069
47	T	C	G	G	0.219	0.383	0.573	0.669	0.504	0.219	-5.023	2.905	-1.729	0.085

Table A1.15. Continued

							ApoA1					apoB		
Win	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**
47	T	C	G	T	0.466	NA	NA	NA	NA	0.466	NA	NA	NA	NA
48	C	A	G	C	0.045	-2.138	1.085	-1.970	0.049	0.044	-10.049	5.690	-1.766	0.078
48	C	G	G	C	0.219	0.324	0.551	0.589	0.556	0.219	-4.993	2.788	-1.791	0.074
48	C	G	T	T	0.026	-0.558	1.341	-0.416	0.678	0.026	-11.475	6.771	-1.695	0.091
48	G	G	T	C	0.113	0.658	0.728	0.904	0.367	0.113	2.215	3.630	0.610	0.542
48	C	G	T	C	0.597	NA	NA	NA	NA	0.597	NA	NA	NA	NA
49	A	G	C	T	0.045	-2.195	1.080	-2.033	0.043	0.044	-10.581	5.686	-1.861	0.063
49	G	G	C	T	0.219	0.234	0.536	0.436	0.663	0.219	-5.422	2.714	-1.998	0.046
49	G	T	C	A	0.028	1.059	1.309	0.809	0.419	0.028	-0.812	6.560	-0.124	0.902
49	G	T	T	T	0.026	-0.613	1.340	-0.457	0.648	0.026	-11.822	6.795	-1.740	0.083
49	G	T	C	T	0.683	NA	NA	NA	NA	0.683	NA	NA	NA	NA
50	G	C	T	C	0.263	-0.069	0.520	-0.133	0.894	0.264	-5.865	2.604	-2.252	0.025
50	T	C	A	T	0.028	1.263	1.313	0.962	0.336	0.028	-0.171	6.574	-0.026	0.979
50	T	C	T	T	0.086	0.593	0.822	0.722	0.471	0.086	2.412	4.081	0.591	0.555
50	T	T	T	C	0.026	-0.681	1.346	-0.505	0.613	0.026	-11.686	6.734	-1.735	0.083
50	T	C	T	C	0.596	NA	NA	NA	NA	0.596	NA	NA	NA	NA
51	C	A	T	G	0.028	1.354	1.312	1.032	0.303	0.028	1.691	6.613	0.256	0.798
51	C	T	C	A	0.117	0.543	0.708	0.768	0.443	0.116	1.731	3.543	0.489	0.625
51	C	T	T	G	0.086	0.704	0.811	0.868	0.386	0.085	4.930	4.031	1.223	0.222
51	T	T	C	A	0.026	-0.754	1.372	-0.549	0.583	0.026	-9.788	6.806	-1.438	0.151
51	C	T	C	G	0.744	NA	NA	NA	NA	0.744	NA	NA	NA	NA
52	A	T	G	T	0.028	1.293	1.320	0.980	0.328	0.027	0.658	6.730	0.098	0.922
52	T	C	A	T	0.141	0.326	0.632	0.515	0.607	0.141	-0.312	3.159	-0.099	0.921
52	T	C	G	C	0.022	-0.227	1.466	-0.155	0.877	0.022	2.537	7.342	0.346	0.730
52	T	T	G	T	0.085	0.721	0.809	0.891	0.373	0.086	4.851	4.024	1.206	0.229
52	*	*	*	*	0.001	1.157	NA	NA	NA	0.001	39.368	NA	NA	NA
52	T	C	G	T	0.723	NA	NA	NA	NA	0.723	NA	NA	NA	NA
53	C	A	T	C	0.141	0.318	0.632	0.503	0.615	0.141	-0.525	3.165	-0.166	0.868
53	C	G	C	C	0.022	-0.215	1.452	-0.148	0.883	0.022	3.467	7.330	0.473	0.636
53	T	G	T	C	0.113	0.876	0.708	1.237	0.217	0.113	3.800	3.543	1.073	0.284
53	*	*	*	*	0.005	-2.177	3.702	-0.588	0.557	0.005	-6.536	0.078	-83.527	0.000
53	C	G	T	C	0.718	NA	NA	NA	NA	0.719	NA	NA	NA	NA
54	A	T	C	G	0.141	0.143	0.630	0.228	0.820	0.140	-1.294	3.148	-0.411	0.681
54	G	C	C	G	0.023	-0.361	1.428	-0.253	0.800	0.023	2.817	7.196	0.391	0.696
54	G	T	C	T	0.017	-1.855	1.719	-1.079	0.281	0.017	-8.183	8.668	-0.944	0.346
54	*	*	*	*	0.005	-2.756	3.431	-0.803	0.422	0.005	-9.278	0.157	-59.255	0.000
54	G	T	C	G	0.814	NA	NA	NA	NA	0.815	NA	NA	NA	NA
55	C	C	G	C	0.023	-0.393	1.416	-0.277	0.782	0.023	3.123	7.133	0.438	0.662
55	T	C	T	C	0.017	-1.888	1.708	-1.105	0.270	0.017	-7.859	8.605	-0.913	0.362
55	*	*	*	*	0.006	-1.470	2.926	-0.502	0.616	0.006	-11.937	0.211	-56.510	0.000
55	T	C	G	C	0.954	NA	NA	NA	NA	0.954	NA	NA	NA	NA
56	C	G	C	C	0.274	0.384	0.487	0.788	0.431	0.273	1.177	2.442	0.482	0.630
56	C	T	C	T	0.017	-1.730	1.715	-1.008	0.314	0.017	-7.583	8.644	-0.877	0.381
56	*	*	*	*	0.006	-1.332	3.164	-0.421	0.674	0.006	-11.751	0.147	-79.972	0.000
56	C	G	C	T	0.703	NA	NA	NA	NA	0.704	NA	NA	NA	NA
57	G	C	C	C	0.115	0.758	0.697	1.087	0.277	0.115	3.745	3.508	1.068	0.286
57	G	C	C	T	0.160	0.081	0.606	0.134	0.894	0.159	-0.453	3.035	-0.149	0.882
57	T	C	T	T	0.017	-1.803	1.726	-1.045	0.297	0.017	-7.956	8.739	-0.910	0.363
57	*	*	*	*	0.001	3.787	6.526	0.580	0.562	0.001	-19.458	0.043	-450.244	0.000
57	G	C	T	T	0.707	NA	NA	NA	NA	0.708	NA	NA	NA	NA
58	C	C	C	T	0.115	0.824	0.730	1.129	0.260	0.115	6.316	3.645	1.733	0.084
58	C	C	T	T	0.160	0.191	0.630	0.303	0.762	0.160	1.960	3.132	0.626	0.532
58	C	T	T	G	0.291	0.111	0.535	0.208	0.835	0.292	6.150	2.655	2.316	0.021
58	*	*	*	*	0.001	4.198	6.543	0.642	0.521	0.001	-17.334	0.056	-307.434	0.000
58	C	T	T	T	0.432	NA	NA	NA	NA	0.432	NA	NA	NA	NA
59	C	C	T	C	0.115	0.802	0.731	1.097	0.273	0.114	6.373	3.650	1.746	0.081
59	C	T	T	C	0.128	0.145	0.703	0.206	0.837	0.128	3.948	3.497	1.129	0.260
59	C	T	T	T	0.033	0.485	1.221	0.397	0.692	0.033	-5.268	6.106	-0.863	0.389
59	T	T	G	C	0.293	0.126	0.534	0.235	0.814	0.293	6.092	2.654	2.296	0.022
59	T	T	T	C	0.431	NA	NA	NA	NA	0.431	NA	NA	NA	NA
60	C	T	C	C	0.115	0.842	0.734	1.147	0.252	0.115	6.321	3.664	1.725	0.085
60	T	G	C	C	0.293	0.158	0.532	0.296	0.767	0.293	5.943	2.644	2.248	0.025
60	T	T	C	T	0.110	0.303	0.743	0.408	0.683	0.110	3.464	3.695	0.938	0.349
60	T	T	T	T	0.033	0.494	1.220	0.405	0.686	0.033	-5.458	6.101	-0.894	0.372
60	T	T	C	C	0.449	NA	NA	NA	NA	0.449	NA	NA	NA	NA
61	G	C	C	T	0.293	-0.053	0.509	-0.105	0.916	0.294	4.628	2.530	1.829	0.068
61	T	C	C	C	0.016	-0.135	1.771	-0.076	0.939	0.016	9.573	8.874	1.079	0.281
61	T	C	T	T	0.110	0.094	0.728	0.129	0.898	0.110	2.333	3.627	0.643	0.520
61	T	T	T	T	0.033	0.352	1.218	0.289	0.773	0.033	-6.094	6.098	-0.999	0.318
61	T	C	C	T	0.547	NA	NA	NA	NA	0.547	NA	NA	NA	NA

APPENDIX A2. Supplementary Tables for *LPL* gene resequencing and association analyses in African Blacks

Table A2.1. Chracteristics of 308 *LPL* variants identified in the sequencing sample of 95 African black individuals

LPL variant/RefSNP ID	Position[a]	Chr. position[b]	Location	Alleles[c]	Amino acid change[d]	High HDL-C/Low TG MAF (n=48)	Low HDL-C/High TG MAF (n=47)	MAF In the total sample (n=95)	HWE (*P*-value)	Call rate (%)	RegulomeDB score[e]
LP208/rs1470186	208	19795789	5' flanking	T>C		0.23	0.234	0.232	0.755	100	2b
LP308/rs114637785	308	19795889	5' flanking	T>C		0.02	0.022	0.021	1.000	98.9	4
LP428/rs73667465	428	19796009	5' flanking	G>A		0.38	0.348	0.362	0.552	98.9	4
LP549/rs17091742	549	19796130	5' flanking	C>T		0.23	0.234	0.232	0.755	100	5
LP847	847	19796428	5' flanking	A>T		0.011	0	0.005	1.000	96.8	3a
LP957	957	19796538	5' flanking	A>G		0.01	0.011	0.011	1.000	96.8	5
LP1090/rs1800590	1090	19796671	5'UTR-Exon 1	G>T		0.48	0.489	0.495	0.156	95.8	2b
LP1107/rs75890454	1107	19796688	5'UTR-Exon 1	T>A		0.02	0.023	0.022	1.000	95.8	4
LP1155	1155	19796736	5'UTR-Exon 1	A>T		0	0.011	0.005	1.000	95.8	4
LP1200_1201ins2/rs34513350	1200	19796781	5'UTR-Exon 1	-/CC		0.02	0.047	0.033	1.000	94.7	2b
LP1264	1264	19796845	5'UTR-Exon 1	G>A		0.021	0	0.011	1.000	94.7	2b
LP1300	1300	19796881	5'UTR-Exon 1	C>G		0	0.021	0.011	1.000	100	4
LP1488/rs200412008	1488	19797069	Intron 1	C>T		0.052	0.021	0.037	1.000	100	2b
LP1498/rs141390463	1498	19797079	Intron 1	G>A		0.073	0.064	0.068	0.712	100	3a
LP1729/rs185205408	1729	19797310	Intron 1	C>A		0.01	0.011	0.011	1.000	98.9	4
LP1737	1737	19797318	Intron 1	C>T		0.01	0.011	0.011	1.000	98.9	4
LP1977del1	1977	19797558	Intron 1	C/-		0.01	0	0.005	1.000	100	5
LP2005	2005	19797586	Intron 1	C>T		0.01	0	0.005	1.000	100	5
LP2053/rs7839976	2053	19797634	Intron 1	C>G		0.01	0.022	0.016	1.000	98.9	5
LP2335/rs3779787	2335	19797916	Intron 1	G>T		0.031	0.011	0.021	1.000	98.9	2b
LP2758/rs146786419	2758	19798339	Intron 1	C>T		0.064	0.032	0.048	0.364	98.9	5
LP2830/rs185670596	2830	19798411	Intron 1	G>C		0.02	0.022	0.021	1.000	98.9	6
LP2931	2931	19798512	Intron 1	A>G		0.01	0	0.005	1.000	98.9	No data
LP3253	3253	19798834	Intron 1	T>C		0	0.011	0.005	1.000	98.9	4
LP3434/rs192170805	3434	19799015	Intron 1	G>A		0	0.011	0.005	1.000	100	5
LP3505	3505	19799086	Intron 1	T>G		0	0.011	0.005	1.000	100	5
LP3558/rs34309063	3558	19799139	Intron 1	G>A		0.094	0.076	0.085	0.997	98.9	5
LP3725/rs115668974	3725	19799306	Intron 1	C>T		0.042	0.011	0.026	1.000	100	No data
LP3783	3783	19799364	Intron 1	A>T		0.01	0	0.005	1.000	100	No data
LP3964/rs17410577	3964	19799545	Intron 1	G>C		0.09	0.106	0.1	1.000	100	No data
LP4060/rs1534649	4060	19799641	Intron 1	T>G		0.07	0.111	0.092	0.887	96.8	No data
LP4424/rs13266204	4424	19800005	Intron 1	A>G		0.02	0.023	0.022	1.000	95.8	6
LP4717/rs114624068	4717	19800298	Intron 1	G>T		0.02	0.023	0.022	1.000	96.8	5
LP4760/rs10503668	4760	19800341	Intron 1	G>A		0.01	0.011	0.011	1.000	96.8	5
LP4799/rs147151973	4799	19800380	Intron 1	T>C		0.01	0.023	0.016	1.000	96.8	5
LP4803	4803	19800384	Intron 1	T>C		0	0.011	0.005	1.000	96.8	5
LP4948/rs6997330	4948	19800529	Intron 1	G>C		0.375	0.352	0.364	1.000	96.8	5
LP4999/rs114288334	4999	19800580	Intron 1	G>A		0.03	0.083	0.056	1.000	94.7	5
LP5394/rs149233602	5394	19800975	Intron 1	T>C		0	0.012	0.005	1.000	95.8	6
LP5457/rs116448989	5457	19801038	Intron 1	G>C		0.042	0.035	0.038	0.226	95.8	No data
LP5488/rs115851910	5488	19801069	Intron 1	T>A		0.02	0.076	0.048	1.000	97.9	No data
LP5531/rs1031045	5531	19801112	Intron 1	A>G		0.45	0.467	0.457	0.218	98.9	6
LP5723	5723	19801304	Intron 1	G>A		0.01	0	0.005	1.000	98.9	No data
LP5772/rs60633545	5772	19801353	Intron 1	G>A		0.45	0.489	0.468	0.171	97.9	No data
LP5793/rs144495763	5793	19801374	Intron 1	T>C		0.03	0.089	0.059	1.000	97.9	6
LP5871	5871	19801452	Intron 1	C>G		0	0.011	0.005	1.000	97.9	No data
LP5890/rs372372026	5890	19801471	Intron 1	G>A		0.01	0.011	0.011	1.000	97.9	6
LP5949/rs112127208	5949	19801530	Intron 1	T>G		0.031	0.011	0.021	1.000	98.9	6
LP6111	6111	19801692	Intron 1	G>A		0	0.012	0.006	1.000	94.7	6
LP6351	6351	19801932	Intron 1	A>C		0	0.011	0.005	1.000	97.9	5
LP6553/rs59254395	6553	19802134	Intron 1	C>T		0.323	0.272	0.298	0.885	98.9	6
LP6554/rs56043715	6554	19802135	Intron 1	A>G		0.396	0.391	0.394	1.000	98.9	6
LP6590	6590	19802171	Intron 1	C>T		0	0.011	0.005	1.000	98.9	No data
LP6762/rs61274012	6762	19802343	Intron 1	T>C		0.052	0.022	0.037	1.000	98.9	No data
LP6821/rs10104051	6821	19802402	Intron 1	T>C		0.07	0.109	0.09	0.904	98.9	No data
LP6835	6835	19802416	Intron 1	C>A		0	0.011	0.005	1.000	97.9	6
LP6838/rs73667467	6838	19802419	Intron 1	G>A		0.02	0.022	0.022	1.000	97.9	6
LP7069	7069	19802650	Intron 1	T>A		0.027	0.024	0.026	1.000	82.1	5
LP7130/rs28615996	7130	19802711	Intron 1	T>C		0.429	0.36	0.391	1.000	48.4	No data
LP7245/rs114636902	7245	19802826	Intron 1	G>A		0.031	0.021	0.026	1.000	100	No data
LP7313/rs28645722	7313	19802894	Intron 1	G>A		0.365	0.311	0.339	1.000	97.9	No data
LP7388/rs28575919	7388	19802969	Intron 1	C>G		0.354	0.283	0.319	0.978	98.9	6
LP7407/rs114437971	7407	19802988	Intron 1	T>G		0.04	0.043	0.042	1.000	100	6
LP7503/rs6999612	7503	19803084	Intron 1	T>C		0.302	0.239	0.271	2.00E-	98.9	5

Table A2.1. Continued

LPL variant/RefSNP ID	Position[a]	Chr. position[b]	Location	Alleles[c]	Amino acid change[d]	High HDL-C/Low TG MAF (n=48)	Low HDL-C/High TG MAF (n=47)	MAF In the total sample (n=95)	HWE (*P*-value)	Call rate (%)	RegulomeDB score[e]
									04		
LP7512/rs3779788	7512	19803093	Intron 1	C>T		0.031	0.021	0.026	1.000	100	5
LP7556/rs59811201	7556	19803137	Intron 1	T>C		0.188	0.163	0.176	0.344	98.9	4
LP7611	7611	19803192	Intron 1	T>G		0.01	0	0.005	1.000	100	2b
LP7907/rs115064749	7907	19803488	Intron 1	A>G		0.03	0.068	0.049	1.000	95.8	6
LP8097/rs143892202	8097	19803678	Intron 1	G>A		0	0.023	0.011	1.000	93.7	5
LP8221/rs7000460	8221	19803802	Intron 1	A>C		0.411	0.297	0.35	0.468	63.2	5
LP8415/rs56321069	8415	19803996	Intron 1	A>T		0.22	0.283	0.25	0.487	98.9	No data
LP8441_8442del2/rs112943460	8441	19804022	Intron 1	-/CT		0.02	0.064	0.042	1.000	100	No data
LP8463/rs146866595	8463	19804044	Intron 1	C>G		0.02	0.022	0.022	1.000	97.9	No data
LP8518/rs116640183	8518	19804099	Intron 1	G>A		0.02	0.054	0.037	1.000	98.9	6
LP8582/rs114186305	8582	19804163	Intron 1	C>T		0.01	0.022	0.016	1.000	98.9	5
LP8614/rs114997087	8614	19804195	Intron 1	T>A		0.04	0.043	0.043	0.288	98.9	5
LP8766/rs181367025	8766	19804347	Intron 1	T>C		0	0.022	0.011	1.000	98.9	No data
LP8778/rs77436400	8778	19804359	Intron 1	C>T		0.042	0.022	0.032	1.000	98.9	No data
LP9003/rs73601656	9003	19804584	Intron 1	G>A		0.134	0.09	0.112	0.682	84.2	No data
LP9015/rs28445964	9015	19804596	Intron 1	A>G		0.4	0.31	0.359	0.273	48.4	No data
LP9130/rs13252357	9130	19804711	Intron 1	A>T		0.022	0.022	0.022	1.000	94.7	6
LP9232/rs145257746	9232	19804813	Intron 1	T>G		0.07	0.087	0.081	1.000	97.9	No data
LP9252	9252	19804833	Intron 1	T>C		0	0.011	0.005	1.000	98.9	No data
LP9307/rs146991585	9307	19804888	Intron 1	T>C		0.03	0.065	0.048	1.000	98.9	No data
LP9369/rs79822715	9369	19804950	Intron 1	C>T		0.02	0.021	0.021	1.000	100	6
LP9411/rs28689946	9411	19804992	Intron 1	A>C		0.375	0.3	0.339	0.657	97.9	5
LP9418/rs28582042	9418	19804999	Intron 1	G>A		0.375	0.304	0.34	0.735	98.9	5
LP9499/rs138110428	9499	19805080	Intron 1	G>A		0.021	0	0.011	1.000	100	5
LP9582_9586del5	9582	19805163	Intron 1	AACAA/-		0.042	0.021	0.032	1.000	100	6
LP9589/rs371696656	9589	19805170	Intron 1	C>T		0.33	0.272	0.301	0.920	97.9	6
LP9596delC	9596	19805177	Intron 1	-/C		0.32	0.383	0.353	0.000	100	6
LP9609	9609	19805190	Intron 1	C>T		0	0.011	0.005	1.000	98.9	6
LP9615	9615	19805196	Intron 1	T>C		0.01	0	0.005	1.000	97.9	No data
LP9663/rs146174239	9663	19805244	Intron 1	C>T		0.01	0.011	0.011	1.000	98.9	No data
LP9696/rs73667468	9696	19805277	Intron 1	G>T		0.365	0.315	0.34	0.426	98.9	No data
LP9798/rs74339584	9798	19805379	Intron 1	C>T		0.01	0.022	0.016	1.000	97.9	6
LP9914/rs73667469	9914	19805495	Intron 1	T>G		0.402	0.372	0.388	0.909	93.7	No data
LP9955/rs77298438	9955	19805536	Intron 1	C>G		0.076	0.033	0.055	0.459	95.8	No data
LP10100del1	10100	19805681	Intron 1	T/-		0.042	0.011	0.016	0.105	100	5
LP10127/rs1801177	10127	19805708	Exon 2	G>A	D36N	0.06	0.064	0.063	1.000	100	5
LP10170/rs148201569	10170	19805751	Exon 2	C>G	A50G	0	0.011	0.005	1.000	100	5
LP10234/rs11542065	10234	19805815	Exon 2	C>G	H71Q	0.02	0.021	0.021	1.000	100	5
LP10348/rs59054859	10348	19805929	Intron 2	A>G		0.135	0.096	0.116	0.506	100	No data
LP10599/rs138877694	10599	19806180	Intron 2	G>A		0	0.011	0.005	1.000	100	No data
LP10632	10632	19806213	Intron 2	C>T		0	0.021	0.011	1.000	100	No data
LP10800/rs6991305	10800	19806381	Intron 2	G>A		0.073	0.033	0.053	0.446	98.9	5
LP10958/rs114795370	10958	19806539	Intron 2	G>T		0	0.011	0.005	1.000	96.8	6
LP11050/rs7016529	11050	19806631	Intron 2	T>C		0.394	0.344	0.37	0.674	96.8	No data
LP11090/rs8176337	11090	19806671	Intron 2	G>C		0.22	0.3	0.261	0.733	96.8	No data
LP11476/rs140135149	11476	19807057	Intron 2	G>A		0.052	0.023	0.038	1.000	96.8	6
LP11659del1	11659	19807240	Intron 2	C/-		0	0.022	0.011	1.000	98.9	No data
LP11760/rs73667470	11760	19807341	Intron 2	C>A		0.43	0.466	0.445	0.496	95.8	No data
LP11888_11889Ins1/rs149017698	11888	19807469	Intron 2	A/-		0.48	0.424	0.473	1.000	98.9	5
LP11895/rs189417962	11895	19807476	Intron 2	T>A		0.021	0	0.011	1.000	98.9	5
LP12382/rs188863293	12382	19807963	Intron 2	A>C		0	0.011	0.005	1.000	98.9	6
LP12417	12417	19807998	Intron 2	C>T		0	0.011	0.005	1.000	98.9	No data
LP12449/rs74304285	12449	19808030	Intron 2	G>A		0.094	0.033	0.064	0.624	98.9	No data
LP12457/rs57357723	12457	19808038	Intron 2	C>T		0	0.022	0.011	1.000	98.9	No data
LP12550/rs113023641	12550	19808131	Intron 2	G>A		0.031	0.011	0.021	1.000	98.9	6
LP13003/rs80181352	13003	19808584	Intron 2	G>T		0.031	0.022	0.027	0.106	98.9	5
LP13102/rs79760154	13102	19808683	Intron 2	A>C		0.13	0.185	0.154	0.155	98.9	5
LP13106/rs80341714	13106	19808687	Intron 2	C>T		0.042	0.022	0.032	1.000	98.9	5
*LP13156/rs7002728	13156	19808737	Intron 2	G>A		0.021	0	0.011	0.997	98.9	5
*LP13156/rs7002728	13156	19808737	Intron 2	G>T		0.146	0.12	0.133	1.000	98.9	5
LP13311/rs114236319	13311	19808892	Intron 2	G>A		0.04	0.043	0.043	0.288	98.9	6
LP13321	13321	19808902	Intron 2	A>G		0.01	0	0.005	1.000	98.9	No data
LP13443/rs115589061	13443	19809024	Intron 2	C>G		0.01	0.054	0.032	1.000	98.9	No data
LP13691_13693del3	13691	19809272	Intron 2	ATC/-		0	0.011	0.005	1.000	97.9	5
LP13854/rs1121923	13854	19809435	Exon 3	G>A	V135V	0.146	0.138	0.142	0.037	100	No data
LP14114/rs73667472	14114	19809695	Intron 3	T>C		0.229	0.202	0.216	0.895	100	5

Table A2.1. Continued

LPL variant/RefSNP ID	Position[a]	Chr. position[b]	Location	Alleles[c]	Amino acid change[d]	High HDL-C/Low TG MAF (n=48)	Low HDL-C/High TG MAF (n=47)	MAF In the total sample (n=95)	HWE (*P*-value)	Call rate (%)	RegulomeDB score[e]
LP14213/rs58670071	14213	19809794	Intron 3	C>A		0.062	0.053	0.058	1.000	100	No data
LP14241/rs75026342	14241	19809822	Intron 3	C>T		0.06	0.085	0.074	0.806	100	No data
LP14314	14314	19809895	Intron 3	G>A		0.01	0	0.005	1.000	100	5
LP14530	14530	19810111	Intron 3	T>G		0	0.011	0.005	1.000	98.9	5
LP14790/rs113443162	14790	19810371	Intron 3	T>C		0	0.011	0.005	1.000	100	6
LP14829	14829	19810410	Intron 3	T>G		0.031	0.011	*0.021*	1.000	*100*	*6*
LP14886	14886	19810467	Intron 3	G>A		0.031	0.011	*0.021*	1.000	*100*	No data
LP14898/rs193260945	14898	19810479	Intron 3	G>T		0.01	0	0.005	1.000	100	6
LP14997	14997	19810578	Intron 3	C>A		0	0.011	0.005	1.000	100	No data
LP15060_15061del2	15060	19810641	Intron 3	AA/-		0.031	0.011	0.021	1.000	100	No data
LP15115/rs57345602	15115	19810696	Intron 3	A>C		0.02	0.021	0.021	1.000	100	No data
LP15206/rs343	15206	19810787	Intron 3	C>A		0.022	0.022	0.022	1.000	94.7	6
LP15210/rs247	15210	19810791	Intron 3	A>C		0.056	0.056	0.056	1.000	94.7	No data
LP15245/rs248	15245	19810826	Exon 4	G>A	E145E	0.089	0.056	0.072	1.000	94.7	5
LP15266/rs116678290	15266	19810847	Exon 4	T>C	N152N	0	0.011	0.006	1.000	94.7	5
LP15425/rs249	15425	19811006	Intron 4	T>C		0.163	0.156	0.159	0.591	95.8	No data
LP15448_15449Ins2/rs397963556	15448	19811029	Intron 4	-/TG		0.46	0.5	0.479	0.227	98.9	6
LP15540_15554del15	15540	19811121	Intron 4	TTACTATCCACTGGC/-		0	0.012	0.006	1.000	88.4	5
LP15579/rs251	15579	19811160	Intron 4	T>C		0.23	0.238	0.232	0.226	88.4	5
LP15650del1/rs252	15650	19811231	Intron 4	-/A		0.09	0.133	0.113	1.000	97.9	No data
LP15836/rs253	15836	19811417	Intron 4	T>C		0.22	0.261	0.239	0.483	98.9	No data
LP15884/rs139426179	15884	19811465	Intron 4	C>T		0.02	0.033	0.027	1.000	98.9	No data
LP15920/rs144254368	15920	19811501	Intron 4	C>A		0.01	0	0.005	1.000	98.9	No data
LP16316/rs254	16316	19811897	Intron 5	C>G		0.21	0.277	0.242	0.969	100	No data
LP16320/rs255	16320	19811901	Intron 5	T>C		0.21	0.266	0.237	1.000	100	No data
LP16363/rs80143795	16363	19811944	Intron 5	A>G		0.07	0.096	0.084	0.995	100	No data
LP16386/rs256	16386	19811967	Intron 5	C>T		0.02	0.022	0.021	1.000	98.9	No data
LP16392/rs148719093	16392	19811973	Intron 5	G>A		0.02	0.033	0.027	1.000	98.9	No data
LP16421/rs111255464	16421	19812002	Intron 5	A>G		0.01	0.022	0.016	1.000	98.9	6
LP16647/rs257	16647	19812228	Intron 5	A>C		0.062	0.033	0.048	0.364	98.9	No data
LP16671/rs258	16671	19812252	Intron 5	C>G		0.052	0.043	0.048	1.000	98.9	6
LP16856/rs259	16856	19812437	Intron 5	A>T		0.062	0.054	0.059	1.000	98.9	No data
LP16928/rs260	16928	19812509	Intron 5	C>G		0.07	0.076	0.075	0.821	97.9	6
LP17039/rs261	17039	19812620	Intron 5	A>G		0.15	0.17	0.158	0.343	100	6
LP17061/rs262	17061	19812642	Intron 5	A>T		0.01	0.012	0.011	1.000	95.8	No data
LP17229	17229	19812810	Intron 5	C>G		0	0.011	0.005	1.000	100	6
LP17231/rs263	17231	19812812	Intron 5	C>T		0.391	0.359	0.376	1.000	89.5	6
LP17599/rs264	17599	19813180	Intron 5	G>A		0.083	0.056	0.07	0.725	97.9	No data
LP17718/rs266	17718	19813299	Intron 5	A>G		0.19	0.233	0.21	0.345	97.9	No data
LP17993/rs144466625	17993	19813574	Exon 6	G>A	R333H	0	0.023	0.012	1.000	43.2	5
LP18086/rs269	18086	19813667	Intron 6	T>G		0.447	0.42	0.434	0.837	95.8	No data
LP18095/rs270	18095	19813676	Intron 6	C>A		0.064	0.022	0.043	1.000	96.8	No data
LP18121/rs271	18121	19813702	Intron 6	G>A		0.02	0.022	0.021	1.000	98.9	1f
LP18347/rs272	18347	19813928	Intron 6	C>G		0.083	0.043	0.064	1.000	98.9	5
LP18395_18396Ins1/rs58935878	18395	19813976	Intron 6	-/T		0.083	0.053	0.068	1.000	100	No data
LP18399_18400Ins1	18399	19813980	Intron 6	-/A		0.062	0.053	0.058	1.000	100	No data
LP18600	18600	19814181	Intron 6	T>G		0.01	0	0.005	1.000	100	6
LP18652/rs275	18652	19814233	Intron 6	C>T		0.02	0.043	0.032	1.000	98.9	No data
LP18708/rs276	18708	19814289	Intron 6	T>C		0.21	0.245	0.229	0.442	98.9	6
LP18822/rs277	18822	19814403	Intron 6	T>C		0.117	0.106	0.112	1.000	98.9	No data
LP18942/rs278	18942	19814523	Intron 6	G>A		0.053	0.022	0.038	1.000	97.9	6
LP18992	18992	19814573	Intron 6	G>A		0.01	0.011	0.011	1.000	97.9	6
LP19115/rs279	19115	19814696	Intron 6	C>G		0.149	0.109	0.129	1.000	97.9	No data
LP19301/rs280	19301	19814882	Intron 6	G>A		0.042	0.011	0.027	1.000	97.9	6
LP19407/rs17091775	19407	19814988	Intron 6	G>A		0.062	0.011	0.038	0.223	96.8	5
LP19442/rs281	19442	19815023	Intron 6	A>T		0.45	0.478	0.484	0.108	97.9	5
LP19445/rs282	19445	19815026	Intron 6	C>G		0.02	0.044	0.032	1.000	97.9	5
LP19517/rs283	19517	19815098	Intron 6	T>C		0.458	0.411	0.435	0.401	97.9	5
LP19525/rs284	19525	19815106	Intron 6	T>C		0.15	0.167	0.156	1.000	97.9	5
LP19608/rs285	19608	19815189	Intron 6	T>C		0.042	0.023	0.033	1.000	96.8	6
LP19975/rs287	19975	19815556	Intron 6	A>G		0.26	0.2	0.231	0.698	97.9	No data
LP20038/rs289	20038	19815619	Intron 6	T>C		0.25	0.189	0.22	0.505	97.9	6
LP20042/rs140991223	20042	19815623	Intron 6	C>T		0.06	0.067	0.065	0.079	97.9	6
LP20109	20109	19815690	Intron 6	C>G		0	0.011	0.005	1.000	97.9	6
LP20188/rs290	20188	19815769	Intron 6	G>A		0.13	0.16	0.142	0.820	100	6
LP20271/rs291	20271	19815852	Intron 6	T>C		0.302	0.277	0.289	0.870	100	No data

Table A2.1. Continued

LPL variant/RefSNP ID	Position[a]	Chr. position[b]	Location	Alleles[c]	Amino acid change[d]	High HDL-C/Low TG MAF (n=48)	Low HDL-C/High TG MAF (n=47)	MAF In the total sample (n=95)	HWE (*P*-value)	Call rate (%)	RegulomeDB score[e]
LP20474/rs292	20474	19816055	Intron 6	G>A		0.02	0.032	0.026	1.000	100	No data
LP20505_20506Ins1/rs33936024	20505	19816086	Intron 6	-/A		0.302	0.277	0.289	0.870	100	6
LP20544/rs294	20544	19816125	Intron 6	T>C		0.188	0.096	0.142	0.820	100	6
LP20657/rs295	20657	19816238	Intron 6	A>C		0.365	0.362	0.363	1.000	100	No data
LP20670/rs145585712	20670	19816251	Intron 6	G>A		0.042	0.011	0.026	1.000	100	No data
LP20790/rs297	20790	19816371	Intron 6	T>C		0.302	0.277	0.289	0.870	100	No data
LP20884	20884	19816465	Intron 6	G>T		0	0.022	0.011	1.000	98.9	No data
LP21136/rs73601683	21136	19816717	Intron 6	G>A		0.01	0.021	0.016	1.000	100	5
LP21299/rs299	21299	19816880	Exon 7	C>T	I376I	0.01	0.021	0.016	1.000	100	6
LP21306/rs300	21306	19816887	Intron 7	A>G		0.021	0.011	0.016	1.000	100	6
LP21353/rs301	21353	19816934	Intron 7	T>C		0.271	0.245	0.258	0.712	100	No data
LP21548	21548	19817129	Intron 7	T>G		0.011	0	0.005	1.000	97.9	6
LP21596/rs183821381	21596	19817177	Intron 7	G>T		0	0.011	0.005	1.000	95.8	No data
LP21780/rs304	21780	19817361	Intron 7	T>G		0.302	0.297	0.3	0.761	84.2	6
LP21820/rs305	21820	19817401	Intron 7	A>G		0.291	0.289	0.29	0.921	85.3	6
LP21862/rs306	21862	19817443	Intron 7	G>A		0.05	0.098	0.075	0.150	97.9	No data
LP22416/rs312	22416	19817997	Intron 7	G>C		0.244	0.225	0.235	0.968	89.5	No data
LP22445/rs313	22445	19818026	Intron 7	A>G		0.13	0.171	0.151	0.788	90.5	6
LP22461/rs314	22461	19818042	Intron 7	A>G		0.273	0.268	0.271	1.000	89.5	No data
LP22774/rs77434393	22774	19818355	Intron 7	G>A		0.052	0.023	0.038	1.000	96.8	6
LP22855/rs316	22855	19818436	Exon 8	C>A	T388T	0.25	0.167	0.21	0.345	97.9	1f
LP22970/rs5934	22970	19818551	Exon 8	G>A	A472T	0.031	0.022	0.027	1.000	97.9	5
LP23190_23191del2/rs113064376	23190	19818771	Intron 8	-/AG		0.15	0.182	0.163	0.376	96.8	6
LP23192/rs117026536	23192	19818773	Intron 8	G>T		0.041	0.041	0.041	1.000	77.9	6
LP23388/rs318	23388	19818969	Intron 8	C>G		0.17	0.226	0.197	0.891	93.7	4
LP23395/rs319	23395	19818976	Intron 8	A>C		0.096	0.06	0.079	0.851	93.7	4
LP23496/rs320	23496	19819077	Intron 8	T>G		0.287	0.274	0.281	0.838	93.7	5
LP23573/rs77243948	23573	19819154	Intron 8	T>C		0.02	0.024	0.022	1.000	93.7	5
LP23593	23593	19819174	Intron 8	A>G		0	0.012	0.006	1.000	94.7	5
LP23605/rs321	23605	19819186	Intron 8	G>C		0.01	0.036	0.022	1.000	94.7	5
LP23632/rs182033043	23632	19819213	Intron 8	C>A		0.01	0.024	0.017	1.000	94.7	5
LP23636/rs322	23636	19819217	Intron 8	A>C		0.396	0.366	0.382	0.871	93.7	5
LP23747/rs325	23747	19819328	Intron 8	T>C		0.031	0.012	0.022	1.000	95.8	5
LP23858/rs326	23858	19819439	Intron 8	G>A		0.391	0.384	0.388	0.314	93.7	1f
LP23866/rs7005541	23866	19819447	Intron 8	C>G		0.032	0.023	0.028	1.000	94.7	5
LP23919	23919	19819500	Intron 8	G>A		0.01	0.012	0.011	1.000	91.6	6
LP23955/rs327	23955	19819536	Intron 8	T>G		0.375	0.369	0.372	0.553	90.5	6
LP24064/rs149089920	24064	19819645	Exon 9	G>A	E448K	0.012	0.012	0.012	1.000	86.3	5
LP24373/rs370324129	24373	19819954	Intron 9	G>A		0	0.011	0.005	1.000	97.9	4
LP24505/rs329	24505	19820086	Intron 9	A>G		0.167	0.13	0.149	0.230	98.9	4
LP24815/rs330	24815	19820396	Intron 9	G>A		0.115	0.064	0.089	0.912	100	5
LP24824/rs331	24824	19820405	Intron 9	G>A		0.3	0.351	0.324	0.416	98.9	5
LP24829/rs138285812	24829	19820410	Intron 9	G>A		0.01	0.043	0.027	1.000	98.9	5
LP24852/rs12679834	24852	19820433	Intron 9	T>C		0.053	0.022	0.038	1.000	97.9	1f
LP24863	24863	19820444	Intron 9	T>C		0	0.011	0.005	1.000	100	5
LP24899/rs76423146	24899	19820480	Intron 9	C>T		0.13	0.138	0.132	0.324	100	5
LP24957	24957	19820538	Intron 9	G>A		0	0.011	0.005	1.000	100	5
LP25080/rs28681081	25080	19820661	Intron 9	G>A		0.12	0.16	0.137	0.914	100	No data
LP25272/rs150647190	25272	19820853	Intron 9	G>A		0.06	0.096	0.079	0.901	100	No data
LP25335/rs117199990	25335	19820916	Intron 9	C>T		0.031	0.022	0.027	1.000	98.9	No data
LP25352/rs145391587	25352	19820933	Intron 9	A>C		0.022	0.022	0.022	1.000	96.8	No data
LP25380/rs190629324	25380	19820961	Intron 9	C>A		0.033	0	0.018	1.000	86.3	6
*LP25414/rs28599962	25414	19820995	Intron 9	T>C		0.105	0.097	0.101	1.000	83.2	No data
*LP25414/rs28599962	25414	19820995	Intron 9	T>G		0.01	0.069	0.038	1.000	83.2	No data
LP25460/rs183689105	25460	19821041	Intron 9	T>C		0.031	0.011	0.021	1.000	100	6
LP25579	25579	19821160	Intron 9	A>G		0	0.032	0.016	0.032	100	6
LP25652/rs17116619	25652	19821233	Intron 9	A>G		0.09	0.117	0.105	0.527	100	No data
LP25666/rs28439839	25666	19821247	Intron 9	G>A		0.12	0.181	0.147	1.000	100	6
LP25805/rs28424158	25805	19821386	Intron 9	C>T		0.12	0.181	0.147	1.000	100	5
LP25844/rs75278536	25844	19821425	Intron 9	T>G		0.03	0.043	0.037	1.000	100	6
LP25869	25869	19821450	Intron 9	T>C		0	0.011	0.005	1.000	100	6
LP25886/rs28716400	25886	19821467	Intron 9	C>A		0.11	0.141	0.124	0.272	97.9	6
LP26054/rs115078054	26054	19821635	Intron 9	G>A		0.078	0.078	0.078	1.000	94.7	6
LP26057	26057	19821638	Intron 9	T>C		0	0.011	0.006	1.000	94.7	6
LP26183	26183	19821764	Intron 9	T>C		0	0.011	0.005	1.000	96.8	No data
LP26201/rs77069344	26201	19821782	Intron 9	T>G		0.033	0.033	0.033	1.000	96.8	No data
LP26220/rs80307903	26220	19821801	Intron 9	A>T		0	0.011	0.005	1.000	98.9	6

Table A2.1. Continued

LPL variant/RefSNP ID	Position[a]	Chr. position[b]	Location	Alleles[c]	Amino acid change[d]	High HDL-C/Low TG MAF (n=48)	Low HDL-C/High TG MAF (n=47)	MAF In the total sample (n=95)	HWE (*P*-value)	Call rate (%)	RegulomeDB score[e]
LP26234/rs10099160	26234	19821815	Intron 9	T>G		0.106	0.053	0.08	0.909	98.9	6
LP26377	26377	19821958	Intron 9	T>C		0	0.011	0.005	1.000	98.9	No data
LP26460/rs75946927	26460	19822041	Intron 9	T>G		0.083	0.053	0.068	1.000	100	6
LP27033del1/rs147900112	27033	19822614	Intron 9	C/-		0.1	0.189	0.145	1.000	90.5	No data
LP27050/rs114236375	27050	19822631	Intron 9	T>G		0.022	0	0.011	1.000	97.9	No data
LP27075	27075	19822656	Intron 9	A>G		0	0.011	0.005	1.000	97.9	5
LP27076/rs114991789	27076	19822657	Intron 9	T>C		0.011	0	0.005	1.000	97.9	5
LP27113/rs10283151	27113	19822694	Intron 9	T>C		0.12	0.191	0.158	0.306	96.8	5
LP27229/rs11570891	27229	19822810	Intron 9	C>T		0.02	0.033	0.027	1.000	98.9	5
LP27249/rs4922115	27249	19822830	3'UTR-Exon10	G>A		0.125	0.054	0.09	0.904	98.9	No data
LP27268/rs375896929	27268	19822849	3'UTR-Exon10	C>T		0.01	0	0.005	1.000	98.9	6
LP27269/rs7818177	27269	19822850	3'UTR-Exon10	G>A		0.031	0.011	0.021	1.000	98.9	6
LP27611/rs3289	27611	19823192	3'UTR-Exon10	T>C		0.12	0.117	0.116	1.000	100	5
LP27629	27629	19823210	3'UTR-Exon10	C>G		0	0.011	0.005	1.000	100	5
LP27695	27695	19823276	3'UTR-Exon10	C>A		0.01	0	0.005	1.000	100	5
LP27706	27706	19823287	3'UTR-Exon10	C>A		0	0.011	0.005	1.000	100	5
LP27928/rs187587525	27928	19823509	3'UTR-Exon10	G>A		0.01	0.011	0.005	1.000	100	5
LP27969	27969	19823550	3'UTR-Exon10	A>G		0	0.011	0.005	1.000	100	No data
LP28036/rs11570892	28036	19823617	3'UTR-Exon10	A>G		0.271	0.196	0.234	0.370	98.9	No data
LP28062	28062	19823643	3'UTR-Exon10	A>G		0.01	0.011	0.011	1.000	98.9	6
LP28067/rs3208305	28067	19823648	3'UTR-Exon10	T>A		0.43	0.43	0.428	1.000	94.7	6
LP28093/rs1803924	28093	19823674	3'UTR-Exon10	C>T		0.02	0.023	0.022	1.000	96.8	6
LP28382/rs1059507	28382	19823963	3'UTR-Exon10	C>T		0.115	0.078	0.097	0.805	97.9	6
LP28464/rs3735964	28464	19824045	3'UTR-Exon10	C>A		0.01	0.022	0.016	1.000	97.9	No data
LP28490/rs3200218	28490	19824071	3'UTR-Exon10	A>G		0.083	0.078	0.081	0.917	97.9	No data
LP28531/rs139240067	28531	19824112	3'UTR-Exon10	G>A		0.02	0.022	0.022	1.000	97.9	No data
LP28656/rs58998793	28656	19824237	3'UTR-Exon10	T>C		0.07	0.076	0.074	1.000	98.9	6
LP28669/rs184363931	28669	19824250	3'UTR-Exon10	C>T		0.01	0.021	0.016	1.000	100	No data
LP28911/rs13702	28911	19824492	3'UTR-Exon10	C>T		0.458	0.446	0.452	0.864	98.9	6
LP28982/rs1059611	28982	19824563	3'UTR-Exon10	T>C		0.15	0.174	0.16	0.844	98.9	6
LP29023/rs17091815	29023	19824604	3'UTR-Exon10	A>T		0.06	0.065	0.064	1.000	98.9	No data
LP29045_29046Ins2/rs10645926	29045	19824626	3'UTR-Exon10	-/TT		0.14	0.17	0.153	0.731	100	6
LP29047/rs188554527	29047	19824628	3'UTR-Exon10	G>T		0	0.021	0.011	1.000	100	No data
LP29086/rs15285	29086	19824667	3'UTR-Exon10	C>T		0.458	0.447	0.453	0.630	100	No data
LP29088/rs3866471	29088	19824669	3'UTR-Exon10	C>A		0.24	0.191	0.216	0.256	100	No data
LP29098/rs187374932	29098	19824679	3'UTR-Exon10	A>G		0	0.021	0.011	1.000	100	No data
LP29110	29110	19824691	3'UTR-Exon10	A>C		0	0.011	0.005	1.000	100	6
LP29126/rs147116359	29126	19824707	3'UTR-Exon10	G>A		0.031	0	0.016	1.000	100	No data
LP29168/rs79756214	29168	19824749	3'UTR-Exon10	T>C		0.02	0.053	0.037	1.000	100	6
LP29287/rs3916027	29287	19824868	3' flanking	G>A		0.385	0.359	0.372	0.858	98.9	5
LP29315/rs9644636	29315	19824896	3' flanking	T>G		0.021	0.011	0.016	1.000	98.9	5
LP29487/rs4921683	29487	19825068	3' flanking	T>A		0.135	0.053	0.095	0.823	100	No data
LP29543/rs76707496	29543	19825124	3' flanking	G>A		0.07	0.085	0.079	1.000	100	5
LP29547/rs4921684	29547	19825128	3' flanking	C>T		0.104	0.021	0.063	1.000	100	5
LP29826	29826	19825407	3' flanking	G>A		0	0.021	0.011	1.000	100	No data
LP29847	29847	19825428	3' flanking	C>T		0	0.011	0.005	1.000	100	6
LP30050/rs77004748	30050	19825631	3' flanking	T>A		0.02	0.043	0.032	1.000	98.9	No data

MAF: minor allele frequency; * Tri-allelic SNPs (LP13156, LP25414); MAF was calculated for each minor allele.

[a] Nucleotide positions in the reference sequence (hg19, NC_000008 .10)

[b] Chromosomal position in the NCBI reference sequence: NC_000008 .10, [c] Variants are reported based on the allele in the reference sequence.

[d] amino acid positions are reported based on dbSNP build 138 and known names of the variants were showin in paranthesis

[e] RegulomeDB scores were generated by using http://regulome.stanford.edu/. Scores represents; 1a- eQTL + TF binding + matched TF motif + matched DNase Footprint + DNase peak; 1b- eQTL + TF binding + any motif + DNase Footprint + DNase peak; 1c- eQTL + TF binding + matched TF motif + DNase peak; 1d- eQTL + TF binding + any motif + DNase peak; 1e- eQTL + TF binding + matched TF motif; 1f- eQTL + TF binding / DNase peak; 2a- TF binding + matched TF motif + matched DNase Footprint + DNase peak; 2b- TF binding + any motif + DNase Footprint + DNase peak; 2c- TF binding + matched TF motif + DNase peak; 3a- TF binding + any motif + DNase peak; 3b- TF binding + matched TF motif; 4- TF binding + DNase peak; 5-TF binding or DNase peak; 6-other

Table A2.2. Tagger results of 130 common variants of *LPL* (MAF≥ 0.05, r^2=0.90) in the sequencing sample.

LD Bins	Variants
1	rs28689946, **rs28645722**, rs7000460, rs28582042, rs28575919, rs73667468
2	rs304, **rs305**, rs320, rs33936024, rs291, rs297
3	**rs147900112**, rs10283151, rs28439839, rs284, rs28424158

Table A2.2. Continued

4	18399_18400Ins1, **rs247,** rs58670071
5	5772, **rs1031045,** rs73667470
6	**rs255**, rs254
7	**rs1470186**, rs17091742
8	**rs59054859**, rs73601656
9	25272, rs306
10	rs58998793, **rs76707496**
11	**rs6991305**, rs77298438
12	**rs59254395,** 9589
13	rs10099160, **rs319**
14	rs34309063, **rs17410577**
15	**rs13702**, rs15285
16	**rs8176337,** rs56321069
17	rs28681081, **rs313**
18	rs10645926, **rs1059611**
19	**rs10104051**, rs1534649
20	rs287, **rs289**
21	5793, **rs114288334**
22	rs73667469, **rs56043715**
23	rs322, **rs327**
24	rs4922115, **rs4921683**
25	**rs276**
26	**rs7002728**
27	**rs59811201**
28	**rs277**
29	**rs28615996**
30	**rs329**
31	**rs316(T361T)**
32	**rs3916027**
33	**rs281**
34	**rs140991223**
35	**rs266**
36	**rs261**
37	**rs1121923**
38	**rs79760154**
39	**rs73667472**
40	**rs3208305**
41	**9596ins1**
42	**rs260**
43	**rs290**
44	**rs249**
45	**rs73667465**
46	**rs3866471**
47	**rs6999612**
48	**rs259**
49	**rs264**
50	**rs269**
51	**rs1800590**
52	**rs75026342**
53	**rs145257746**
54	**rs3289**
55	**rs149017698**
56	**rs6997330, rs7016529**
57	**rs272**
58	**rs1801177**
59	**rs330**
60	**rs76423146**
61	**rs331**
62	**rs80143795**
63	**rs318**

Table A2.2. Continued

64	**rs58935878**
65	**rs141390463**
66	**rs75946927**
67	**rs314**
68	**rs74304285**
69	**rs301**
70	**rs252**
71	**rs279**
72	**rs3200218**
73	**rs11570892**
74	**rs263**
75	**rs326**
76	**rs17091815**
77	**rs1059507**
78	**rs312**
79	**rs113064376**
80	**rs251**
81	**rs248(E118E)**
82	**rs28716400**
83	**rs294**
84	**rs283**
85	**rs28445964**
86	**rs253**
87	**rs295**
88	**rs17116619**
89	**rs4921684**
90	**rs115078054**
91	**rs28599962**
92	**rs57186780**

92 TagSNPs were identified for each bin. Bold: TagSNPs

Table A2.3. The genotype call rates and features of the 130 SNPs genotyped in the entire sample (n=788)

LPL variant	RefSNP ID	Alleles[a]	MAF	Selection criteria	Location	Position[b]	ObsHET	PredHET	HWpval	%Geno
rs1470187*	rs1470187	G:T	0.112	Database	5'flanking	-94	0.198	0.199	0.9469	95.7
LP208	rs1470186	T:C	0.225	TagSNPs	5'flanking	208	0.336	0.348	0.4006	94.7
LP428	rs73667465	G:A	0.314	TagSNPs	5'flanking	428	0.384	0.431	0.0042	94.8
LP1090	rs1800590	T:G	0.468	TagSNPs	5' UTR-Exon1	1090	0.471	0.498	0.1575	94.5
LP1107	rs75890454	T:A	0.02	Uncommon/Rare	5' UTR-Exon1	1107	0.039	0.039	1	96.4
LP1155	Novel	A:T	0.001	Suspicious rare	5' UTR-Exon1	1155	0.001	0.001	1	96.7
LP12001201insCC	rs34513350	W:I	0.029	5' UTR	5' UTR-Exon1	1200	0.054	0.055	0.9201	95.7
LP1264	Novel	G:A	0.008	5' UTR	5' UTR-Exon1	1264	0.015	0.015	1	98.9
LP1300	Novel	C:G	0.005	5' UTR	5' UTR-Exon1	1300	0.01	0.01	1	96.8
LP1488	rs200412008	C:T	0.029	Exon/Intron Junction	Intron 1	1488	0.059	0.057	1	96.8
LP1498	rs141390463	G:A	0.041	TagSNPs	Intron 1	1498	0.068	0.078	0.0112	94.8
LP2335	rs3779787	G:T	0.023	Uncommon/Rare	Intron 1	2335	0.045	0.044	1	95.6
LP2758	rs146786419	C:T	0.039	Uncommon/rare	Intron 1	2758	0.076	0.075	1	95.3
LP2830	rs185670596	G:C	0.022	Suspicious rare	Intron 1	2830	0.045	0.044	1	96.7
LP3725	rs115668974	C:T	0.042	Uncommon/Rare	Intron 1	3725	0.07	0.08	0.0145	95.6
LP3964	rs17410577	G:C	0.12	TagSNPs	Intron 1	3964	0.203	0.211	0.3928	98
LP5531	rs1031045	G:A	0.451	TagSNPs	Intron 1	5531	0.459	0.495	0.0543	95.3
LP5949	rs112127208	T:G	0.025	Uncommon/Rare	Intron 1	5949	0.047	0.048	0.7672	99.6
LP6554	rs56043715	A:G	0.307	TagSNPs	Intron 1	6554	0.413	0.426	0.4667	94.5
LP6762	rs61274012	T:C	0.03	Uncommon/Rare	Intron 1	6762	0.057	0.058	0.9786	96.3
LP7130	rs28615996	T:C	0.333	TagSNPs	Intron 1	7130	0.44	0.444	0.8602	95.7
LP7313	rs28645722	G:A	0.281	TagSNPs	Intron 1	7313	0.381	0.404	0.132	94.9
LP7503	rs6999612	A:G	0.284	TagSNPs	Intron 1	7503	0.393	0.406	0.3985	99.1
LP7556	rs59811201	T:C	0.166	TagSNPs	Intron 1	7556	0.281	0.277	0.775	95.7
LP7907	rs115064749	A:G	0.03	Uncommon	Intron 1	7907	0.058	0.059	1	96.4
LP8097	**rs143892202**	**G:A**	**0.004**	**Uncommon/Rare**	**Intron 1**	**8097**	**0.008**	**0.008**	**1**	**83.8**
LP8441_8442del2	rs112943460	W:D	0.029	Uncommon/Rare	Intron 1	8441	0.056	0.057	0.9536	95.4
LP8766	rs181367025	T:C	0.013	Uncommon/Rare	Intron 1	8766	0.025	0.025	1	96.3
LP9015	rs28445964	A:G	0.247	TagSNPs	Intron 1	9015	0.355	0.372	0.2423	95.2
LP9232	rs145257746	A:C	0.052	TagSNPs	Intron 1	9232	0.099	0.099	1	94.5
LP9499	rs138110428	G:A	0.007	Uncommon/Rare	Intron 1	9499	0.014	0.014	1	97.7
LP10100delT	Novel	W:D	0.022	Exon/Intron Junction	Intron 1	10100	0.045	0.044	1	96.6
LP10127	rs1801177	G:A	0.05	TagSNPs/D9N	Exon 2	10127	0.091	0.094	0.5812	98.5
LP10170	rs148201569	C:G	0.003	Non-syn	Exon 2	10170	0.005	0.005	1	96.7
LP10234	rs11542065	G:C	0.018	Non-syn	Exon 2	10234	0.035	0.035	1	97.2
LP10348	rs59054859	A:G	0.118	TagSNPs	Intron 2	10348	0.211	0.208	0.8027	94.9
LP10632	Novel	C:T	0.008	Uncommon/Rare	Intron 2	10632	0.017	0.017	1	97.1
LP10800	rs6991305	G:A	0.045	TagSNPs	Intron 2	10800	0.088	0.087	1	96.4
LP11050	rs7016529	T:C	0.295	TagSNPs	Intron 2	11050	0.404	0.416	0.4799	97
LP11090	rs8176337	G:C	0.313	TagSNPs	Intron 2	11090	0.411	0.43	0.2584	97.2
LP11895	rs189417962	T:A	0.007	Uncommon/Rare	Intron 2	11895	0.014	0.014	1	99.5
LP12449	rs74304285	G:A	0.056	TagSNPs	Intron 2	12449	0.107	0.106	1	95.1
LP13102	rs79760154	A:C	0.091	TagSNPs	Intron 2	13102	0.169	0.165	0.78	96.2
LP13156**	**rs7002728**	**G:A**	**0.006**	**Triallelic SNP**	**Intron 2**	**13156**	**0.012**	**0.012**	**1**	**95.9**
LP13156**	**rs7002728**	**G:T**	**0.144**	**Triallelic SNP**	**Intron 2**	**13156**	**0.251**	**0.247**	**0.7506**	**95.9**
LP13443	rs115589061	C:G	0.023	Uncommon/Rare	Intron 2	13443	0.046	0.045	1	96.8
LP13691_13693del2	Novel	W:D	0.001	Exon/Intron Junction	Intron 2	19809272	13691	0.003	1	90.6
LP13854	rs1121923	G:A	0.111	TagSNPs/Syn	Exon 3	13854	0.189	0.198	0.2701	97.5
LP14114	rs73667472	A:G	0.203	TagSNPs	Intron 3	14114	0.321	0.323	0.9094	99.2
LP14241	rs75026342	C:T	0.109	TagSNPs	Intron 3	14241	0.181	0.194	0.1027	96.7
LP15060del1	Novel	G:A	0.022	Uncommon/Rare	Intron 3	15060	0.044	0.043	1	98.2
LP15206	rs343	C:A	0.031	Exon	Intron 3	15206	0.059	0.059	1	93.3
LP15245	rs248	G:A	0.034	TagSNPs/Syn	Exon 4	15245	0.068	0.066	0.8026	99.1
LP15266	rs116678290	T:C	0.006	Non-syn	Exon 4	15266	0.012	0.012	1	95.4
LP15448ins2	**rs57186780**	**W:I**	**0.444**	**TagSNPs**	**Intron 4**	**15448**	**0.41**	**0.494**	**2.05E-05**	**82.9**
LP15579	rs251	T:C	0.192	TagSNPs	Intron 4	15579	0.32	0.31	0.4574	95.4
LP15650_15651Ins1	rs252	W:I	0.093	TagSNPs	Intron 4	15650	0.175	0.168	0.3854	97.2
LP16320	rs255	T:C	0.244	TagSNPs	Intron 4	16320	0.353	0.369	0.2853	94.5
LP16363	rs80143795	A:G	0.115	TagSNPs	Intron 4	16363	0.191	0.204	0.1225	96.2
LP16647	rs257	A:C	0.034	Uncommon	Intron 4	16647	0.058	0.066	0.0179	96.6
LP16671	rs258	C:G	0.035	Uncommon	Intron 4	16671	0.067	0.067	1	96.7
LP16856	rs259	A:T	0.053	TagSNPs	Intron 4	16856	0.105	0.1	0.2101	98.7
LP16928	rs260	C:G	0.076	TagSNPs	Intron 4	16928	0.151	0.14	0.0196	95.7
LP17039	rs261	A:G	0.195	TagSNPs	Intron 4	17039	0.293	0.314	0.0932	94.3
LP17231	rs263	C:T	0.359	TagSNPs	Intron 4	17231	0.44	0.46	0.2503	94.9
LP17718	rs266	A:G	0.17	TagSNPs	Intron 4	17718	0.277	0.282	0.6343	95.4
LP17993	rs144466625	G:A	0.001	Non-syn	Exon 6	17993	0.003	0.003	1	96.7
rs59184895*	rs59184895	T:C	0.052	Database	Intron 6	18029	0.095	0.098	0.6385	95.9
LP18086	rs269	T:G	0.479	TagSNPs	Intron 6	18086	0.49	0.499	0.6627	97.8

Table A2.3. Continued

***LPL* variant**	**RefSNP ID**	**Alleles[a]**	**MAF**	**Selection criteria**	**Location**	**Position[b]**	**ObsHET**	**PredHET**	**HWpval**	**%Geno**
LP18095	rs270	C:A	0.069	Uncommon/Rare	Intron 6	18095	0.126	0.129	0.5927	97
LP18395_18396ins1	rs58935878	W:I	0.042	TagSNPs	Intron 6	18395	0.082	0.081	1	96.2
LP18708	rs276	T:C	0.19	TagSNPs	Intron 6	18708	0.304	0.308	0.769	96.1
LP18822	rs277	T:C	0.11	TagSNPs	Intron 6	18822	0.189	0.197	0.3822	95.9
LP19115	rs279	C:G	0.15	TagSNPs	Intron 6	19115	0.257	0.255	0.9716	94.9
LP19301	rs280	G:A	0.058	Uncommon/Rare	Intron 6	19301	0.108	0.109	0.9377	96.4
LP19407	rs17091775	G:A	0.056	Suspicious rare	Intron 6	19407	0.104	0.105	0.827	95.4
LP19442	rs282	A:T	0.477	TagSNPs	Intron 6	19442	0.467	0.499	0.0856	95.2
LP20188	rs290	G:A	0.145	TagSNPs	Intron 6	20188	0.238	0.248	0.3431	87.6
LP20657	rs295	A:C	0.39	TagSNPs	Intron 6	20657	0.445	0.476	0.0837	97
LP20670	rs145585712	G:A	0.016	Uncommon/Rare	Intron 6	20670	0.033	0.032	1	96.7
LP21136	rs73601683	G:A	0.012	Exon/Intron Junction	Intron 6	21136	0.024	0.023	1	96.8
LP21299	rs299	C:T	0.007	Syn	Exon 7	21299	0.011	0.013	0.0589	96.2
LP21306	rs300	A:G	0.011	Exon/Intron Junction	Intron 7	21306	0.021	0.021	1	95.6
LP21353	rs301	T:C	0.288	TagSNPs	Intron 7	21353	0.407	0.41	0.8496	97.1
LP22445	rs313	A:G	0.15	TagSNPs	Intron 7	22445	0.251	0.255	0.7886	94.4
LP22461	rs314	A:G	0.248	TagSNPs	Intron 7	22461	0.335	0.373	0.0091	93.5
LP22774	rs77434393	C:T	0.024	Uncommon/Rare	Intron 7	22774	0.047	0.046	1	99.4
LP22855	rs316	C:A	0.225	TagSNPs	Intron 7	22855	0.343	0.349	0.7	96.8
LP22970	rs5934	G:A	0.033	Non-syn	Exon 8	22970	0.065	0.063	0.8593	99
LP23388	rs318	C:G	0.139	TagSNPs	Intron 8	23388	0.234	0.24	0.561	96.1
LP23395	rs319	A:C	0.082	TagSNPs	Intron 8	23395	0.151	0.15	1	96.1
LP23605	rs321	G:C	0.009	Uncommon/Rare	Intron 8	23605	0.017	0.017	1	96.6
LP23747	rs325	T:C	0.043	Uncommon/Rare	Intron 8	23747	0.079	0.083	0.3254	96.4
LP23858	rs326	G:A	0.398	TagSNPs	Intron 8	23858	0.504	0.479	0.1827	98
LP24064	rs149089920	G:A	0.001	Non-syn	Exon 9	24064	0.003	0.003	1	97.1
rs328*	rs328	C:G	0.042	Database	Intron 9	24143	0.077	0.081	0.2951	97.8
LP24505	rs329	A:G	0.097	TagSNPs	Intron 9	24505	0.165	0.175	0.2155	89.8
LP24815	rs330	G:A	0.085	TagSNPs	Intron 9	24815	0.162	0.155	0.369	96.4
LP24829	rs138285812	G:A	0.025	Uncommon/Rare	Intron 9	24829	0.05	0.049	1	96.2
LP24852	rs12679834	T:C	0.058	Uncommon/Rare	Intron 9	24852	0.102	0.109	0.2046	97.8
LP24899	rs76423146	C:T	0.157	TagSNPs	Intron 9	24899	0.243	0.265	0.0385	96.4
LP25380	rs28599962	G:T	0.021	Uncommon/Rare	Intron 9	25380	0.041	0.04	1	98.4
LP25579	Novel	A:G	0.005	Uncommon/Rare	Intron 9	25579	0.01	0.01	1	96.7
LP25652	**rs17116619**	**A:G**	**0.107**	**TagSNPs**	**Intron 9**	**25652**	**0.187**	**0.19**	**0.7762**	**78**
LP25886del1	rs28716400	W:D	0.152	TagSNPs	Intron 9	25886	0.253	0.257	0.701	95.4
LP26460	rs75946927	T:G	0.087	TagSNPs	Intron 9	26460	0.155	0.158	0.687	97.5
LP27033del1	rs147900112	G:A	0.157	TagSNPs	Intron 9	27033	0.257	0.265	0.4453	96.3
LP27050	rs114236375	T:G	0.012	Uncommon/Rare	Intron 9	27050	0.024	0.023	1	96.2
LP27269	rs7818177	G:A	0.015	3'UTR	3'UTR-Exon10	27269	0.031	0.03	1	95.7
LP27629	Novel	C:G	0.001	3'UTR	3'UTR-Exon10	27629	0.003	0.003	1	96.7
LP27695	Novel	G:T	0.001	3'UTR	3'UTR-Exon10	27695	0.001	0.001	1	96.3
LP27706	Novel	G:T	0.001	3'UTR	3'UTR-Exon10	27706	0.003	0.003	1	99.5
LP27928	rs187587525	G:A	0.003	3'UTR	3'UTR-Exon10	27928	0.007	0.007	1	96.6
LP27969	Novel	A:G	0.001	3'UTR	3'UTR-Exon10	27969	0.003	0.003	1	96.6
LP28036	rs11570892	A:G	0.24	TagSNPs	3'UTR-Exon10	28036	0.361	0.364	0.8615	94.5
LP28067	rs3208305	A:T	0.443	TagSNPs	3'UTR-Exon10	28067	0.494	0.493	1	97.3
LP28093	**rs1803924**	**C:T**	**0.04**	**3'UTR**	**3'UTR-Exon10**	**28093**	**0.058**	**0.076**	**1.33E-05**	**95.7**
LP28382	rs1059507	C:T	0.103	TagSNPs	3'UTR-Exon10	28382	0.192	0.184	0.3319	96.4
LP28464	**rs3735964**	**C:A**	**0.037**	**Exon**	**3'UTR-Exon10**	**28464**	**0.052**	**0.071**	**3.12E-06**	**95.2**
LP28490	rs3200218	A:G	0.093	TagSNPs	3'UTR-Exon10	28490	0.172	0.168	0.7149	95.9
LP28531	rs139240067	G:A	0.013	Exon	3'UTR-Exon10	28531	0.026	0.026	1	95.9
LP28669	rs184363931	C:T	0.009	Exon	3'UTR-Exon10	28669	0.018	0.018	1	96.4
LP28911	rs13702	C:T	0.459	TagSNP-Exon	3'UTR-Exon10	28911	0.501	0.497	0.8948	97.8
LP29023	rs17091815	A:T	0.084	TagSNPs	3'UTR-Exon10	29023	0.162	0.153	0.1737	95.6
LP29047	rs78359368	G:T	0.007	Exon	3'UTR-Exon10	29047	0.013	0.013	1	96.7
LP29098	rs187374932	T:C	0.005	Exon	3'UTR-Exon10	29098	0.01	0.01	1	99
LP29126	rs147116359	G:A	0.011	Uncommon/Rare	3'UTR-Exon10	29126	0.02	0.022	0.1754	95.1
LP29168	rs79756214	T:C	0.016	3'UTR	3'UTR-Exon10	29168	0.032	0.031	1	96.4
LP29287	rs3916027	G:A	0.413	TagSNPs	3' flanking	29287	0.465	0.485	0.2755	95.3
LP29487	rs4921683	T:A	0.102	TagSNPs	3' flanking	29487	0.194	0.184	0.1659	96.2
LP29543	rs76707496	G:A	0.09	TagSNPs	3' flanking	29543	0.162	0.164	0.847	97.2
LP29547	rs4921684	C:T	0.079	TagSNPs	3' flanking	29547	0.155	0.145	0.0734	99.4

*database SNP; ** triallelic SNP (position: 13156)-MAFs for two minor alleles were listed seperately; Bold: excluded SNPs; Syn: Synonymous variant; Non-syn: Non-synonymous variant
[a] Major allele:Minor allele; [b] Position in the baseline reference sequence; W: Allele in the referecne sequence (NC_00008.10); D: Deleted base/bases; I: Inserted base/bases

Table A2.4. Association results of TG levels with 125 *LPL* SNPs in African blacks (n=788)

LPL variant	RefSNP ID[a]	Chr. Position (hg19)	Genotypes	GT Counts	MAF	Adjusted Mean of plasma TG	Standard Deviation	Beta	*P*
rs147018794	rs147018794	19795467	GG/GT/TT	585/145/10	0.112	70.04/69.6/83.08	30.29/30.7/42.14	0.005	0.628
LP208	rs1470186	19795581	CC/CT/TT	42/244/445	0.225	73.58/70.11/70.02	35.17/29.67/30.62	0.004	0.601
LP428	rs73667465	19796009	AA/AG/GG	91/279/362	0.314	72.78/69.48/70.39	32.76/30.67/30.52	0.001	0.848
LP1090	rs1800590	19796671	GG/GT/TT	171/342/217	0.468	71.24/70.36/69.51	30.49/32.31/28.24	0.002	0.753
LP1107	rs75890454	19796688	TA/TT	29/716	0.02	62.37/70.41	24.9/30.74	-0.039	0.139
LP1155	Novel	19796736	AA/TA	745/1	0.001	70.19/64.42	30.66/NA	0.002	0.991
LP1200_1201ins2	rs34513350	19796781	II/WI/WW	1/40/697	0.029	57.89/68.92/70.32	NA/22.9/31.23	0.006	0.778
LP1264	Novel	19796845	GA/GG	12/744	0.008	79.3/70.15	40.9/30.5	0.032	0.431
LP1300	Novel	19796881	CC/CG	739/8	0.005	70.45/48.66	30.67/21.72	-0.135	0.006
LP1488	rs200412008	19797069	CC/CT	702/45	0.029	70.15/71.31	30.75/29.02	0.008	0.692
LP1498	rs141390463	19797079	AA/GA/GG	5/51/676	0.041	83.66/77.71/69.69	32.53/37.23/29.98	0.034	0.046
LP2335	rs3779787	19797916	GG/GT	704/34	0.023	70.3/66.22	30.67/26.73	-0.022	0.372
LP2758	rs146786419	19798339	CC/TC/TT	681/53/1	0.039	70.77/62.36/68.67	30.75/26.98/NA	-0.049	0.009
LP2830	rs185670596	19798411	GC/GG	33/713	0.022	67.38/70.39	27.24/30.78	-0.013	0.599
LP3725	rs115668974	19799306	CC/CT/TT	682/51/5	0.042	70.03/73.27/53.49	30.83/27.77/9.91	0.003	0.858
LP3964	rs17410577	19799545	CC/GC/GG	13/153/585	0.12	62.01/70.06/70.48	16.48/30.13/31.14	-0.004	0.707
LP5531	rs1031045	19801112	AA/AG/GG	163/338/235	0.451	72.59/69.34/69.2	29.98/32.95/27.42	0.006	0.373
LP5949	rs112127208	19801530	GG/TG/TT	1/35/726	0.025	78.14/68.23/70.48	NA/28.98/30.83	-0.01	0.672
LP6554	rs56043715	19802135	AA/GA/GG	355/301/74	0.307	69.75/68.51/75.86	29.53/31.19/31.71	0.007	0.388
LP6762	rs61274012	19802343	CC/CT/TT	1/43/700	0.03	74.59/65.85/70.5	NA/26.32/30.85	-0.013	0.517
LP7130	rs28615996	19802711	CC/TC/TT	84/325/330	0.333	75.91/69.36/69.53	32.07/31.49/29.27	0.01	0.200
LP7313	rs28645722	19802894	AA/GA/GG	67/279/388	0.281	75.9/69.67/69.45	32.61/32.02/29.22	0.008	0.318
LP7503	rs6999612	19803084	AA/AG/GG	396/296/66	0.284	70.3/69.22/75.76	29.71/30.57/33.55	0.004	0.609
LP7556	rs59811201	19803137	CC/CT/TT	19/207/513	0.166	81.21/71.37/69.49	36.48/31.79/30.04	0.015	0.132
LP7907	rs115064749	19803488	AA/AG/GG	693/43/1	0.03	70.35/68.14/57.76	31.13/20.33/NA	0.005	0.818
LP8441_8442del2	rs112943460	19804022	DD/WD/WW	1/42/695	0.029	57.91/68.45/70.29	NA/22.08/31	0.005	0.805
LP8766	rs181367025	19804347	CT/TT	19/725	0.013	66.67/70.04	16.63/30.53	0.007	0.831
LP9015	rs28445964	19804596	AA/GA/GG	425/259/51	0.247	69.4/70.56/76.1	28.95/33.17/31.59	0.008	0.340
LP9232	rs145257746	19804813	AA/AC/CC	650/72/2	0.052	69.96/71.58/63.14	30.21/31.71/38.18	0.005	0.737
LP9499	rs138110428	19805080	GA/GG	11/736	0.007	81.78/69.94	40.62/30.21	0.048	0.252
LP10100del1	Novel	19805681	WD/WW	34/712	0.022	71.19/70.21	26.15/30.84	0.02	0.413
LP10127	rs1801177	19805708	AA/AG/GG	3/70/681	0.05	89.81/73.47/69.94	28.36/32.73/30.49	0.023	0.153
LP10170	rs148201569	19805751	CC/CG	743/4	0.003	70.06/77.31	30.37/69.19	-0.028	0.690
LP10234	rs11542065	19805815	GC/GG	27/717	0.018	59.65/70.59	19.53/30.9	-0.049	0.071
LP10348	rs59054859	19805929	AA/AG/GG	571/153/9	0.118	69.52/72.24/70.22	29.75/33.43/33.01	0.006	0.620
LP10632	Novel	19806213	CC/CT	736/13	0.008	70.26/63.7	30.8/16.88	-0.012	0.747
LP10800	rs6991305	19806381	AA/AG/GG	1/64/680	0.045	68.99/63.36/70.97	NA/26.13/30.93	-0.041	0.018
LP11050	rs7016529	19806631	CC/CT/TT	71/299/374	0.295	74.46/70.37/69.93	31.63/31.93/29.64	0.007	0.392
LP11090	rs8176337	19806671	CC/CG/GG	80/305/360	0.313	66.37/69.37/71.73	24.58/30.4/31.95	-0.01	0.177
LP11895	rs189417962	19807476	TA/TT	11/750	0.007	81.89/70.29	40.62/30.58	0.047	0.261
LP12449	rs74304285	19808030	AA/GA/GG	2/79/649	0.056	71.12/68.75/70.68	9.9/27.84/31.41	-0.004	0.788
LP13102	rs79760154	19808683	AA/CA/CC	612/126/5	0.091	69.98/71.25/63.67	30.91/29.74/24.47	0.009	0.482
LP13443	rs115589061	19809024	CC/GC	717/31	0.023	70.22/68.1	30.53/31.65	-0.012	0.627
LP13691_13693del3	Novel	19809272	WD/WW	2/698	0.001	48.28/70.6	7.78/30.99	-0.129	0.185
LP13854	rs1121923	19809435	AA/GA/GG	13/139/595	0.111	70.12/72.69/69.7	25.16/34.7/29.66	0.006	0.562
LP14114	rs73667472	19809695	AA/AG/GG	481/245/33	0.203	69.55/72.59/65.75	29.65/33.27/23.69	0.005	0.599
LP14241	rs75026342	19809822	CC/CT/TT	597/135/14	0.109	69.67/70.78/83.17	30.62/29.54/38.7	0.014	0.213
LP15060del2	Novel	19810641	WD/WW	34/718	0.022	71.44/70.33	25.83/30.9	0.022	0.375
LP15206	rs343	19810787	AA/CA/CC	1/42/671	0.031	46.6/70.05/70.37	NA/31.92/30.58	-0.015	0.465
LP15245	rs248	19810826	GA/GG	52/706	0.034	69.34/70.5	32.94/30.52	-0.006	0.782
LP15266	rs116678290	19810847	TC/TT	9/728	0.006	70.61/70.13	26.93/30.64	0.01	0.823
LP15579	rs251	19811160	CC/TC/TT	24/235/478	0.192	74.57/68.88/70.6	32.32/29.01/31.42	0	0.987
LP15650_15651Ins1	rs252	19811234	DD/WD/WW	611/130/4	0.093	71.06/67.24/62.25	30.99/26.99/23.47	-0.013	0.281
LP16320	rs255	19811901	CC/TC/TT	50/253/426	0.244	71.66/70.42/70.19	31.07/30.86/30.64	0.001	0.941
LP16363	rs80143795	19811944	AA/AG/GG	585/142/15	0.115	69.67/71.77/75.85	30.53/30.65/39.67	0.011	0.314
LP16647	rs257	19812228	AA/CA/CC	697/44/4	0.034	69.98/72.55/86.31	30.21/36.58/35.53	0.011	0.558
LP16671	rs258	19812252	CC/CG/GG	695/50/1	0.035	70.28/68.74/60.79	30.77/28.48/NA	-0.004	0.841
LP16856	rs259	19812437	AA/AT	674/81	0.053	70.56/69.32	31.04/28.03	0.001	0.973
LP16928	rs260	19812509	CC/CG	629/110	0.076	70.38/69.26	30.32/32.41	-0.013	0.349
LP17039	rs261	19812620	AA/AG/GG	481/211/36	0.195	69.57/70.59/70.7	29.75/31.42/32.65	0	0.971
LP17231	rs263	19812812	CC/TC/TT	310/321/101	0.359	69.09/72.01/65.92	28.04/33.4/27.03	-0.006	0.408
LP1771	rs266	19813299	AA/AG/GG	512/202/23	0.17	70.63/68.11/70.6	31.03/28.92/31.3	-0.008	0.378
LP17993	rs144466625	19813574	GA/GG	1/746	0.001	57.76/70.15	NA/30.61	-0.044	0.749
rs59184895	rs59184895	19813610	CC/CT/TT	3/72/667	0.052	61.42/68.7/70.2	20.43/27.12/30.92	-0.005	0.772
LP18086	rs269	19813667	GG/GT/TT	174/366/208	0.479	70.42/69.86/71.69	30.73/31.3/29.94	-0.006	0.423
LP18095	rs270	19813676	AA/CA/CC	5/92/651	0.069	59.99/71.07/70.16	16.41/28.07/31.04	0.005	0.732
LP18395ins1	rs58935878	19813976	II/WI/WW	1/61/680	0.042	46.67/73/69.99	NA/35.58/30.2	0.002	0.901

Table A2.4. Continued

LPL variant	RefSNP ID[a]	Chr. Position (hg19)	Genotypes	GT Counts	MAF	Adjusted Mean of plasma TG	Standard Deviation	Beta	*P*
LP18708	rs276	19814289	CC/CT/TT	29/225/488	0.19	78.82/70.31/69.22	35.77/30.71/29.97	0.012	0.184
LP18822	rs277	19814403	CC/TC/TT	12/136/587	0.11	68.74/70.36/70.02	25.47/28.31/31.2	0.005	0.671
LP19115	rs279	19814696	CC/GC/GG	528/189/16	0.15	70.38/70.01/60.81	31.6/27.67/19.83	-0.002	0.825
LP19301	rs280	19814882	AA/GA/GG	3/82/659	0.058	55.54/69.89/70.35	31.09/30.28/30.72	-0.008	0.579
LP19407	rs17091775	19814988	AA/GA/GG	3/78/655	0.056	55.34/69.78/70.27	31.09/30.16/30.84	-0.008	0.587
LP19442	rs282	19815023	AA/AT/TT	214/344/178	0.477	70.12/69.17/72.11	29.31/29.99/32.6	0.001	0.853
LP20188	rs290	19815769	AA/GA/GG	18/157/493	0.145	69.03/70.77/70.5	36.12/27.25/32.06	0.004	0.728
LP20657	rs295	19816238	AA/CA/CC	287/330/126	0.39	72.17/69.04/70.19	32.41/29.62/29.94	-0.004	0.575
LP20670	rs145585712	19816251	GA/GG	24/723	0.016	76.17/70.07	39.16/30.31	0.02	0.496
LP21136	rs73601683	19816717	GA/GG	18/729	0.012	75.51/69.97	25.27/30.74	0.04	0.223
LP21299	rs299	19816880	CC/CT/TT	734/8/1	0.007	70.39/58.79/75.25	30.74/16.82/NA	-0.032	0.425
LP21306	rs300	19816887	AA/GA	722/16	0.011	70.17/68.37	30.47/35.18	-0.017	0.631
LP21353	rs301	19816934	CC/TC/TT	64/304/376	0.288	66.28/69.63/70.83	27.55/29.25/31.56	-0.006	0.466
LP22445	rs313	19818026	AA/AG/GG	528/183/18	0.15	70.55/70.05/61.04	31.89/26.91/27.14	-0.004	0.711
LP22461	rs314	19818042	AA/GA/GG	420/241/56	0.248	69.55/72.02/70.75	29.94/33.17/26.8	0.008	0.304
LP22774	rs77434393	19818355	CC/CT	723/37	0.024	70.06/73.63	30.65/30.19	0.02	0.394
LP22855	rs316	19818436	AA/CA/CC	41/255/445	0.225	62.49/71.18/69.84	18.17/31.44/30.66	-0.001	0.891
LP22970	rs5934	19818551	GA/GG	49/709	0.033	73.46/70.2	32.24/30.53	0.015	0.450
LP23388	rs318	19818969	CC/CG/GG	552/175/15	0.139	69.59/70.84/74.89	29.93/32.64/29.71	0.004	0.705
LP23395	rs319	19818976	AA/CA/CC	628/110/5	0.082	69.53/73.51/60.69	30.54/30.25/10.5	0.016	0.226
LP23605	rs321	19819186	GC/GG	13/733	0.009	65.97/70.3	16.08/30.84	0.001	0.988
LP23747	rs325	19819328	CC/CT/TT	3/60/681	0.043	57.03/67.25/70.38	25.42/29.17/30.73	-0.021	0.226
LP23858	rs326	19819439	AA/GA/GG	108/382/259	0.398	71.84/70.14/69.55	28.96/30.88/30.22	0.007	0.339
LP24064	rs149089920	19819645	AG/GG	2/747	0.001	69.33/70.2	31.11/30.61	-0.01	0.917
rs328	rs328	19819724	CC/GC/GG	690/59/3	0.042	70.59/68.58/57.29	30.72/29.67/25.42	-0.015	0.374
LP24505	rs329	19820086	AA/GA/GG	570/115/7	0.097	70.51/69.98/78.48	30.26/31.41/27.3	-0.003	0.813
LP24815	rs330	19820396	AA/AG/GG	3/122/620	0.085	52.9/69.5/70.56	13.65/30.26/30.78	-0.005	0.708
LP24829	rs138285812	19820410	GA/GG	38/704	0.025	73.79/69.98	31.4/30.71	0.022	0.339
LP24852	rs12679834	19820433	CC/TC/TT	5/77/666	0.058	80.47/70.56/70.06	44.56/32.11/30.39	0.004	0.812
LP24899	rs76423146	19820480	CC/TC/TT	537/180/27	0.157	70.08/71.29/68.21	29.82/33.67/26.56	-0.002	0.850
LP25380	rs28599962	19820961	GG/GT	721/31	0.021	70.18/71.19	30.55/33.67	-0.001	0.971
LP25579	Novel	19821160	AA/AG	738/8	0.005	70.38/46.88	30.65/19.05	-0.145	0.003
LP25886del1	rs28716400	19821467	DD/WD/WW	19/187/530	0.152	64.09/68.41/70.95	26.56/26.26/32.11	-0.008	0.400
LP26460	rs75946927	19822041	GG/TG/TT	7/113/626	0.087	62.24/73.22/69.93	34.45/32.37/30.38	0.008	0.548
LP27033del1	rs147900112	19822614	DD/WD/WW	22/190/524	0.157	65.32/69.25/70.94	28.83/27.83/31.81	-0.007	0.450
LP27050	rs114236375	19822631	GT/TT	17/726	0.012	86.18/70	43.42/30.21	0.069	0.044
LP27269	rs7818177	19822850	GA/GG	23/708	0.015	71.36/69.61	32.59/30.14	0.005	0.871
LP27629	Novel	19823210	CC/GC	744/2	0.001	70.14/67.41	30.66/4.95	0.021	0.832
LP27695	Novel	19823276	GG/GT	735/1	0.001	70.55/74.61	30.82/NA	0.047	0.733
LP27706	Novel	19823287	GG/GT	759/2	0.001	70.27/80.03	30.67/25.46	0.074	0.447
LP27928	rs187587525	19823509	GA/GG	5/740	0.003	58.68/70.25	19.57/30.69	-0.05	0.418
LP27969	Novel	19823550	AA/AG	743/2	0.001	70.24/67.45	30.69/4.95	0.02	0.834
LP28036	rs11570892	19823617	AA/AG/GG	419/267/44	0.24	69.89/69.97/74.84	29.15/32.6/31.21	0.006	0.509
LP28067	rs3208305	19823648	AA/TA/TT	230/370/144	0.443	70.79/69.52/71.91	31.13/30.79/30.24	0.002	0.820
LP28382	rs1059507	19823963	CC/CT/TT	594/145/5	0.103	70.23/70.66/60.07	30.3/32.11/20.74	0.001	0.905
LP28490	rs3200218	19824071	AA/GA/GG	611/125/5	0.093	69.77/73.41/62.4	30.57/31.01/11.39	0.015	0.228
LP28531	rs139240067	19824112	GA/GG	20/721	0.013	66.07/70.37	21.71/30.94	-0.007	0.827
LP28669	rs184363931	19824250	CC/TC	731/14	0.009	70.29/69.42	30.83/18.42	0.016	0.665
LP28911	rs13702	19824492	CC/CT/TT	216/379/155	0.459	69.89/70.23/71.21	30.37/31.45/29.24	0.004	0.623
LP29023	rs17091815	19824604	AA/AT/TT	608/121/2	0.084	70.32/69.95/38.85	30.34/29.84/4.95	-0.009	0.519
LP29047	rs78359368	19824628	GG/GT	736/10	0.007	70.35/54.47	30.67/24.91	-0.096	0.028
LP29098	rs187374932	19824679	TC/TT	8/749	0.005	49.24/70.74	21.15/30.84	-0.126	0.010
LP29126	rs147116359	19824707	AA/GA/GG	1/15/718	0.011	26.24/68.48/70.29	NA/31.43/30.59	-0.036	0.266
LP29168	rs79756214	19824749	TC/TT	24/720	0.016	72.52/69.97	37.07/30.34	0.009	0.752
LP29287	rs3916027	19824868	AA/AG/GG	134/344/258	0.413	69.65/69.2/71.49	28.55/31.23/30.35	-0.005	0.523
LP29487	rs4921683	19825068	AA/AT/TT	4/146/592	0.102	60.74/69.9/70.17	23.41/31.61/30.36	0	0.992
LP29543	rs76707496	19825124	AA/GA/GG	7/118/619	0.09	52.46/71.4/70.65	10.05/31.14/30.93	-0.007	0.562
LP29547	rs4921684	19825128	CC/TC/TT	639/120/1	0.079	70.86/67.19/39.5	31.22/26.9/NA	-0.012	0.354

W: Allele in the referecne sequence (NC_00008.10).; D: Deleted base/bases; I: Inserted base/bases

[a] db build 137

Table A2.5. Association results of HDL-C levels with 125 *LPL* SNPs in African blacks (n=788)

LPL variant	RefSNP ID[a]	Chr. Position (hg19)	Genotypes	GT Counts	MAF	Adjusted Mean of plasma HDL-C	Standard Deviation	Beta	*P*
rs147018794	rs147018794	19795467	GG/GT/TT	581/142/10	0.112	47.89/48.07/42.09	12.43/13.65/13.34	-0.213	0.481
LP208	rs1470186	19795581	CC/CT/TT	41/242/441	0.225	44.8/48.53/47.71	13/13.16/12.49	-0.107	0.637
LP428	rs73667465	19796009	AA/AG/GG	89/279/357	0.314	45.34/48.94/47.44	14.12/13.33/11.92	-0.130	0.512
LP1090	rs1800590	19796671	GG/GT/TT	166/343/215	0.468	47.31/48.25/47.4	13.8/12.77/11.87	-0.027	0.888
LP1107	rs75890454	19796688	TA/TT	28/710	0.020	47.46/47.84	15.11/12.63	-0.185	0.794
LP1155	Novel	19796736	AA/TA	739/1	0.001	47.86/29.63	12.72/NA	-5.631	0.125
LP1200_1201ins2	rs34513350	19796781	II/WI/WW	1/39/692	0.029	62.06/46.57/47.91	NA/14.37/12.64	-0.192	0.739
LP1264	Novel	19796845	GA/GG	11/740	0.008	52.15/47.75	11.86/12.65	1.330	0.231
LP1300	Novel	19796881	CC/CG	733/8	0.005	47.94/38.82	12.66/15.38	-2.981	0.022
LP1488	rs200412008	19797069	CC/CT	696/45	0.029	47.79/48.71	12.58/14.82	0.225	0.690
LP1498	rs141390463	19797079	AA/GA/GG	5/50/670	0.041	37.51/47.85/47.93	11.67/14.58/12.62	-0.533	0.244
LP2335	rs3779787	19797916	GG/GT	698/33	0.023	47.78/49.06	12.79/10.85	0.431	0.510
LP2758	rs146786419	19798339	CC/TC/TT	671/57/1	0.039	47.65/50.34/84.68	12.53/13.75/NA	1.075	0.028
LP2830	rs185670596	19798411	GC/GG	31/709	0.022	48.96/47.73	12.82/12.74	0.375	0.578
LP3725	rs115668974	19799306	CC/CT/TT	677/49/5	0.042	47.81/48.45/50.17	12.86/11.26/9.57	0.281	0.540
LP3964	rs17410577	19799545	CC/GC/GG	14/149/581	0.120	46.38/48.11/47.76	8.78/12.14/12.83	0.036	0.899
LP5531	rs1031045	19801112	AA/AG/GG	162/333/235	0.451	48.75/47.69/47.75	14.38/12.76/11.24	0.095	0.608
LP5949	rs112127208	19801530	GG/TG/TT	1/34/721	0.025	35.96/48.34/47.76	NA/11.97/12.72	-0.015	0.980
LP6554	rs56043715	19802135	AA/GA/GG	349/301/73	0.307	47.75/48.37/46.46	11.65/13.32/14.95	-0.105	0.611
LP6762	rs61274012	19802343	CC/CT/TT	1/42/694	0.030	48.54/48.07/47.85	NA/13.07/12.68	0.080	0.886
LP7130	rs28615996	19802711	CC/TC/TT	83/326/324	0.333	46.48/48.45/47.63	14.53/13.64/11.16	-0.087	0.666
LP7313	rs28645722	19802894	AA/GA/GG	66/279/381	0.281	47.53/47.99/47.78	15.34/13.19/11.96	-0.042	0.841
LP7503	rs6999612	19803084	AA/AG/GG	390/298/65	0.284	47.61/48.02/47.95	11.71/13.35/14.96	0.032	0.877
LP7556	rs59811201	19803137	CC/CT/TT	19/204/509	0.166	43.41/47.93/47.98	13.86/13.56/12.31	-0.266	0.304
LP7907	rs115064749	19803488	AA/AG/GG	689/42/1	0.030	47.73/47.7/62	12.63/14.47/NA	0.150	0.789
LP8441_8442del2	rs112943460	19804022	DD/WD/WW	1/40/689	0.029	61.95/46.49/47.91	NA/14/12.66	-0.213	0.709
LP8766	rs181367025	19804347	CT/TT	18/720	0.013	45.26/47.92	12.42/12.72	-0.814	0.352
LP9015	rs28445964	19804596	AA/GA/GG	418/260/51	0.247	47.87/47.62/47.43	11.78/13.87/14.43	-0.118	0.587
LP9232	rs145257746	19804813	AA/AC/CC	646/70/2	0.052	47.94/47.45/45.32	12.36/15.95/9.97	-0.265	0.545
LP9499	rs138110428	19805080	GA/GG	10/732	0.007	52.13/47.76	12.34/12.71	1.319	0.260
LP10100del1	Novel	19805681	WD/WW	33/706	0.022	50.84/47.67	13.71/12.69	0.926	0.156
LP10127	rs1801177	19805708	AA/AG/GG	3/70/675	0.050	55.62/46.96/47.83	10.9/14.1/12.57	-0.066	0.877
LP10170	rs148201569	19805751	CC/CG	737/4	0.003	47.88/38.47	12.7/15.57	-2.994	0.103
LP10234	rs11542065	19805815	GC/GG	25/713	0.018	49.38/47.68	14.42/12.66	0.472	0.528
LP10348	rs59054859	19805929	AA/AG/GG	567/150/9	0.118	47.53/49.17/45.69	12.6/13.35/10.66	0.327	0.281
LP10632	Novel	19806213	CC/CT	730/13	0.008	47.83/45.16	12.71/13.31	-0.839	0.413
LP10800	rs6991305	19806381	AA/AG/GG	1/67/670	0.045	84.63/49.23/47.61	NA/13.51/12.6	0.742	0.105
LP11050	rs7016529	19806631	CC/CT/TT	69/299/368	0.295	48.08/47.7/47.92	14.6/13.51/11.65	-0.057	0.785
LP11090	rs8176337	19806671	CC/CG/GG	80/302/357	0.313	47.18/47.79/48.08	9.24/12.88/13.31	-0.088	0.663
LP11895	rs189417962	19807476	TA/TT	10/746	0.007	52.07/47.68	12.34/12.68	1.325	0.256
LP12449	rs74304285	19808030	AA/GA/GG	2/77/645	0.056	41.96/48.51/47.43	12.73/12.12/12.88	0.232	0.586
LP13102	rs79760154	19808683	AA/CA/CC	608/123/5	0.091	48.05/47.25/45.44	12.12/15.25/5.93	-0.331	0.321
LP13443	rs115589061	19809024	CC/GC	709/32	0.023	47.92/45.96	12.68/13.08	-0.613	0.354
LP13691_13693del3	Novel	19809272	WD/WW	2/693	0.001	38.2/47.88	8.13/12.84	-2.807	0.282
LP13854	rs1121923	19809435	AA/GA/GG	13/137/590	0.111	46.85/48.07/47.84	19.02/12.62/12.58	-0.026	0.930
LP14114	rs73667472	19809695	AA/AG/GG	478/242/33	0.203	47.53/48.35/45.83	12.22/13.6/11.99	0.008	0.974
LP14241	rs75026342	19809822	CC/CT/TT	591/135/14	0.109	48.07/47.16/43.02	13/11.35/12.92	-0.404	0.170
LP15060del2	Novel	19810641	WD/WW	33/714	0.022	51.85/47.62	12.71/12.67	1.267	0.052
LP15206	rs343	19810787	AA/CA/CC	1/41/666	0.031	35.64/46.79/48.05	NA/11.73/12.86	-0.493	0.386
LP15245	rs248	19810826	GA/GG	53/699	0.034	50.56/47.56	16.24/12.35	0.816	0.120
LP15266	rs116678290	19810847	TC/TT	9/721	0.006	49.27/47.86	11.53/12.76	0.473	0.702
LP15579	rs251	19811160	CC/TC/TT	23/234/473	0.192	49.61/47.95/47.65	11.4/14.13/12.11	0.123	0.621
LP15650_15651Ins1	rs252	19811234	DD/WD/WW	607/128/4	0.093	47.75/48.27/41.96	12.68/12.95/9.17	0.030	0.929
LP16320	rs255	19811901	CC/TC/TT	49/252/423	0.244	49.13/47.64/47.79	13.19/12.97/12.7	0.079	0.721
LP16363	rs80143795	19811944	AA/AG/GG	579/142/15	0.115	48.03/46.96/46.22	13.07/11.6/10.53	-0.266	0.356
LP16647	rs257	19812228	AA/CA/CC	691/44/4	0.034	47.96/47.58/36.99	12.57/14.52/13.27	-0.583	0.232
LP16671	rs258	19812252	CC/CG/GG	690/49/1	0.035	47.78/48.78/35.87	12.7/13.01/NA	0.138	0.792
LP16856	rs259	19812437	AA/AT	671/79	0.053	47.59/49.43	12.73/11.81	0.581	0.180

Table A2.5. Continued

LPL variant	RefSNP ID[a]	Chr. Position (hg19)	Genotypes	GT Counts	MAF	Adjusted Mean of plasma HDL-C	Standard Deviation	Beta	*P*
LP16928	rs260	19812509	CC/CG	619/113	0.076	47.77/48.02	12.68/13.16	0.061	0.872
LP17039	rs261	19812620	AA/AG/GG	471/214/36	0.195	48.15/47.23/47.88	13.06/12.11/12.59	-0.149	0.527
LP17231	rs263	19812812	CC/TC/TT	309/314/103	0.359	47.12/48.82/47.68	12.28/12.91/13.22	0.178	0.358
LP1771	rs266	19813299	AA/AG/GG	506/200/24	0.170	47.92/47.77/47.6	12.14/14.17/13.02	-0.089	0.724
LP17993	rs144466625	19813574	GA/GG	2/739	0.001	38.79/47.83	9.83/12.72	-2.608	0.314
rs59184895	rs59184895	19813610	CC/CT/TT	3/69/663	0.052	53.67/48.62/47.77	12.38/12.59/12.74	0.360	0.399
LP18086	rs269	19813667	GG/GT/TT	173/360/209	0.479	48.5/48.05/46.84	12.63/12.49/13.09	0.258	0.170
LP18095	rs270	19813676	AA/CA/CC	5/94/643	0.069	49.88/48.36/47.71	10.84/12.27/12.82	0.241	0.512
LP18395ins1	rs58935878	19813976	II/WI/WW	1/58/677	0.042	35.77/48.58/47.78	NA/11.33/12.84	0.137	0.779
LP18708	rs276	19814289	CC/CT/TT	29/226/481	0.190	42.81/47.88/48.16	11.42/13.37/12.38	-0.391	0.103
LP18822	rs277	19814403	CC/TC/TT	12/137/581	0.110	45.89/47.3/47.74	13.61/13.03/12.68	-0.191	0.527
LP19115	rs279	19814696	CC/GC/GG	529/182/16	0.150	47.18/49.2/50.78	12.7/12.59/11.9	0.595	0.029
LP19301	rs280	19814882	AA/GA/GG	3/80/655	0.058	45.85/48.88/47.73	10.25/11.72/12.83	0.287	0.478
LP19407	rs17091775	19814988	AA/GA/GG	3/76/651	0.056	45.86/49.16/47.73	10.25/11.81/12.84	0.356	0.390
LP19442	rs282	19815023	AA/AT/TT	209/338/181	0.477	48.43/48.41/46.04	12.36/12.94/12.78	-0.359	0.055
LP20188	rs290	19815769	AA/GA/GG	18/153/494	0.145	47.21/49.31/47.74	11.79/13.69/12.61	0.264	0.354
LP20657	rs295	19816238	AA/CA/CC	289/325/122	0.390	46.44/48.77/48.4	12.8/12.73/12.14	0.384	0.043
LP20670	rs145585712	19816251	GA/GG	25/715	0.016	53.18/47.63	14.83/12.64	1.607	0.031
LP21136	rs73601683	19816717	GA/GG	17/724	0.012	42.28/47.96	10.4/12.74	-1.697	0.060
LP21299	rs299	19816880	CC/CT/TT	728/7/1	0.007	47.81/49.25/55.41	12.71/14.62/NA	0.679	0.541
LP21306	rs300	19816887	AA/GA	715/16	0.011	47.84/48.93	12.68/15.52	0.223	0.810
LP21353	rs301	19816934	CC/TC/TT	64/295/380	0.288	49.05/49.23/46.56	12.58/12.79/12.57	0.555	0.008
LP22445	rs313	19818026	AA/AG/GG	528/176/18	0.150	47.5/49.05/46.21	12.61/13.23/11.24	0.248	0.361
LP22461	rs314	19818042	AA/GA/GG	418/236/57	0.248	47.78/48.85/45.99	12.84/12.87/12.17	-0.021	0.922
LP22774	rs77434393	19818355	CC/CT	718/37	0.024	47.69/48.25	12.48/15.85	0.084	0.892
LP22855	rs316	19818436	AA/CA/CC	41/246/448	0.225	49.32/49.68/46.59	10.76/13.38/12.32	0.680	0.003
LP22970	rs5934	19818551	GA/GG	50/701	0.033	47.28/47.8	13.28/12.66	-0.171	0.751
LP23388	rs318	19818969	CC/CG/GG	547/173/16	0.139	47.89/47.87/44.85	12.46/13.47/14.15	-0.165	0.548
LP23395	rs319	19818976	AA/CA/CC	621/110/5	0.082	47.76/48.06/41.77	12.78/12.33/20.63	-0.083	0.812
LP23605	rs321	19819186	GC/GG	12/727	0.009	42.22/47.92	11.52/12.73	-1.754	0.102
LP23747	rs325	19819328	CC/CT/TT	3/59/676	0.043	44.58/48.38/47.76	8.54/12.35/12.78	0.085	0.852
LP23858	rs326	19819439	AA/GA/GG	110/377/257	0.398	46.55/47.94/48.07	14.25/11.62/13.42	-0.188	0.346
LP24064	rs149089920	19819645	AG/GG	2/741	0.001	47.2/47.8	25.24/12.71	-0.325	0.900
rs328	rs328	19819724	CC/GC/GG	684/58/3	0.042	47.75/47.61/44.4	12.69/12.3/8.54	-0.113	0.804
LP24505	rs329	19820086	AA/GA/GG	564/114/8	0.097	47.58/49.3/49.08	12.39/14.89/13.57	0.405	0.229
LP24815	rs330	19820396	AA/AG/GG	3/122/613	0.085	49.05/49.82/47.39	16.83/13.49/12.56	0.669	0.055
LP24829	rs138285812	19820410	GA/GG	38/698	0.025	45.01/47.94	12.39/12.75	-0.884	0.149
LP24852	rs12679834	19820433	CC/TC/TT	5/74/664	0.058	50.63/48.35/47.69	11.53/11.79/12.8	0.278	0.487
LP24899	rs76423146	19820480	CC/TC/TT	529/182/27	0.157	48.03/47.33/46.97	12.83/12.99/8.05	-0.175	0.486
LP25380	rs28599962	19820961	GG/GT	716/31	0.021	47.77/47.61	12.6/14.88	-0.116	0.863
LP25579	Novel	19821160	AA/AG	732/8	0.005	47.91/43.15	12.66/10.97	-1.392	0.282
LP25886del1	rs28716400	19821467	DD/WD/WW	19/181/530	0.152	47.55/49.1/47.44	12.02/13.28/12.6	0.331	0.215
LP26460	rs75946927	19822041	GG/TG/TT	7/112/621	0.087	48.2/47.68/47.83	7.83/11.58/12.97	0.022	0.948
LP27033del1	rs147900112	19822614	DD/WD/WW	22/186/525	0.157	47.41/48.78/47.28	11.23/13.06/12.63	0.295	0.256
LP27050	rs114236375	19822631	GT/TT	15/721	0.012	52.15/47.74	8.94/12.78	1.384	0.150
LP27269	rs7818177	19822850	GA/GG	23/703	0.015	47.78/47.85	15.74/12.72	-0.119	0.880
LP27629	Novel	19823210	CC/GC	738/2	0.001	47.88/39.66	12.69/21.99	-2.685	0.302
LP27695	Novel	19823276	GG/GT	730/1	0.001	47.76/63.98	12.74/NA	4.626	0.210
LP27706	Novel	19823287	GG/GT	754/2	0.001	47.79/42.85	12.66/16.12	-1.512	0.560
LP27928	rs187587525	19823509	GA/GG	5/734	0.003	45.58/47.85	17.96/12.69	-0.809	0.622
LP27969	Novel	19823550	AA/AG	737/2	0.001	47.86/39.72	12.72/21.99	-2.660	0.307
LP28036	rs11570892	19823617	AA/AG/GG	416/264/43	0.240	47.06/49.57/45.78	12.6/13.23/10.64	0.297	0.189
LP28067	rs3208305	19823648	AA/TA/TT	227/367/145	0.443	48.6/47.81/46.1	13.11/12.16/12.86	-0.358	0.061
LP28382	rs1059507	19823963	CC/CT/TT	588/145/5	0.103	47.4/49.65/51.27	12.74/12.58/7.85	0.689	0.031
LP28490	rs3200218	19824071	AA/GA/GG	603/126/5	0.093	47.94/47.74/42.39	12.8/12/21.05	-0.177	0.597
LP28531	rs139240067	19824112	GA/GG	19/715	0.013	46.4/47.83	11.16/12.76	-0.404	0.636
LP28669	rs184363931	19824250	CC/TC	725/13	0.009	47.86/46.22	12.69/15.23	-0.559	0.586
LP28911	rs13702	19824492	CC/CT/TT	214/373/156	0.459	49.17/47.86/45.81	13.41/12.13/12.87	-0.490	0.011
LP29023	rs17091815	19824604	AA/AT/TT	604/119/2	0.084	47.78/48.21/50.21	12.93/12.26/10.25	0.164	0.648
LP29047	rs78359368	19824628	GG/GT	730/10	0.007	47.97/39.89	12.66/14.17	-2.598	0.026
LP29098	rs187374932	19824679	TC/TT	8/744	0.005	37.15/47.91	12.66/12.62	-3.432	0.008
LP29126	rs147116359	19824707	AA/GA/GG	1/15/711	0.011	56.74/54.7/47.75	NA/14.69/12.68	1.877	0.027

Table A2.5. Continued

***LPL* variant**	**RefSNP ID[a]**	**Chr. Position (hg19)**	**Genotypes**	**GT Counts**	**MAF**	**Adjusted Mean of plasma HDL-C**	**Standard Deviation**	**Beta**	***P***
LP29168	rs79756214	19824749	TC/TT	24/714	0.016	46.19/47.92	12.48/12.74	-0.506	0.508
LP29287	rs3916027	19824868	AA/AG/GG	132/338/259	0.413	49.23/48.38/46.6	12.72/12.63/12.89	0.421	0.028
LP29487	rs4921683	19825068	AA/AT/TT	4/146/586	0.102	52.74/49.82/47.39	8.75/12.72/12.69	0.757	0.019
LP29543	rs76707496	19825124	AA/GA/GG	7/115/616	0.090	51.4/48.67/47.54	9.25/12.71/12.74	0.401	0.234
LP29547	rs4921684	19825128	CC/TC/TT	634/119/1	0.079	47.34/50.18/52.83	12.76/12.04/NA	0.869	0.016

W: Allele in the referecne sequence (NC_00008.10).; D: Deleted base/bases; I: Inserted base/bases

[a] db build 137

Table A2.6. Association results of LDL-C levels with 125 *LPL* SNPs in African blacks (n=788)

LPL variant	RefSNP ID[a]	Chr. Position (hg19)	Genotypes	GT Counts	MAF	Adjusted Mean of plasma LDL-C	Standard Deviation	Beta	*P*
rs147018794	rs147018794	19795467	GG/GT/TT	585/145/10	0.112	109.53/109.04/108.68	34.43/36/33.06	-0.082	0.789
LP208	rs1470186	19795581	CC/CT/TT	42/247/443	0.225	112.92/111.7/107.53	37.29/36.49/32.98	0.351	0.121
LP428	rs73667465	19796009	AA/AG/GG	91/283/359	0.314	105.92/113.07/107.04	33.03/37.5/32.4	0.128	0.518
LP1090	rs1800590	19796671	GG/GT/TT	172/346/213	0.468	109.26/110.01/107.33	34.07/35.42/34.16	0.128	0.503
LP1107	rs75890454	19796688	TA/TT	29/717	0.020	105.25/109.34	31.26/34.87	-0.436	0.536
LP1155	Novel	19796736	AA/TA	747/1	0.001	109.19/85.18	34.74/NA	-2.648	0.478
LP1200_1201ins2	rs34513350	19796781	II/WI/WW	1/39/700	0.029	120.97/103.72/109.42	NA/33.59/34.87	-0.538	0.358
LP1264	Novel	19796845	GA/GG	12/747	0.008	100.38/109.35	38.56/34.41	-1.100	0.307
LP1300	Novel	19796881	CC/CG	741/8	0.005	109.43/81.58	34.74/20.72	-3.213	0.015
LP1488	rs200412008	19797069	CC/CT	704/45	0.029	108.72/115.72	34.25/40.89	0.705	0.220
LP1498	rs141390463	19797079	AA/GA/GG	5/51/677	0.041	95.13/112.03/109.31	12.68/42.25/34.24	-0.068	0.883
LP2335	rs3779787	19797916	GG/GT	705/34	0.023	108.46/119.9	34.4/38.24	1.258	0.054
LP2758	rs146786419	19798339	CC/TC/TT	680/56/1	0.039	109.55/107.08/111.48	34.97/33.45/NA	-0.238	0.637
LP2830	rs185670596	19798411	GC/GG	33/715	0.022	107.78/109.34	33.75/34.73	-0.156	0.813
LP3725	rs115668974	19799306	CC/CT/TT	682/52/5	0.042	109.47/105.38/114.27	34.32/32.77/57.47	-0.298	0.509
LP3964	rs17410577	19799545	CC/GC/GG	13/154/585	0.120	105.49/109.34/109.47	52.17/34.85/34.14	-0.127	0.663
LP5531	rs1031045	19801112	AA/AG/GG	164/340/233	0.451	110.86/108.52/109.14	31.95/36.57/34.28	0.104	0.584
LP5949	rs112127208	19801530	GG/TG/TT	1/35/728	0.025	121.88/119.65/108.78	NA/37.93/34.31	1.155	0.057
LP6554	rs56043715	19802135	AA/GA/GG	354/303/74	0.307	108.67/110.19/105.54	32.99/36.77/31.02	-0.074	0.721
LP6762	rs61274012	19802343	CC/CT/TT	1/42/702	0.030	137.28/113.87/108.71	NA/34.76/34.55	0.723	0.199
LP7130	rs28615996	19802711	CC/TC/TT	84/325/331	0.333	108.68/109.18/109.62	31.26/36.27/34.01	-0.054	0.792
LP7313	rs28645722	19802894	AA/GA/GG	67/281/386	0.281	104.72/111.4/108.59	29.85/37.45/32.86	-0.034	0.870
LP7503	rs6999612	19803084	AA/AG/GG	394/300/66	0.284	109/110.78/104.28	32.86/37.4/29.4	-0.097	0.641
LP7556	rs59811201	19803137	CC/CT/TT	19/208/513	0.166	112.26/111.31/108.57	34.91/37.34/33.61	0.238	0.363
LP7907	rs115064749	19803488	AA/AG/GG	698/42/1	0.030	109.15/105.32/120.98	34.81/32.55/NA	-0.325	0.564
LP8441_8442del2	rs112943460	19804022	DD/WD/WW	1/40/697	0.029	120.81/105.96/109.38	NA/31.98/34.57	-0.271	0.635
LP8766	rs181367025	19804347	CT/TT	19/726	0.013	114.24/109.06	37.65/34.66	0.591	0.495
LP9015	rs28445964	19804596	AA/GA/GG	422/263/51	0.247	108.66/111.1/108.51	32.98/38.37/29.49	0.097	0.661
LP9232	rs145257746	19804813	AA/AC/CC	651/73/2	0.052	109.28/110.31/108.39	34.26/37.29/14.21	0.056	0.898
LP9499	rs138110428	19805080	GA/GG	11/738	0.007	100.69/109.42	40.38/34.27	-1.090	0.332
LP10100del1	Novel	19805681	WD/WW	33/714	0.022	105.58/109.14	32.81/34.59	-0.385	0.560
LP10127	rs1801177	19805708	AA/AG/GG	3/70/683	0.050	124.12/115.08/108.68	65.79/38.28/34.04	0.686	0.112
LP10170	rs148201569	19805751	CC/CG	744/4	0.003	109.5/62.28	34.53/33.62	-6.510	4.66E-04
LP10234	rs11542065	19805815	GC/GG	26/720	0.018	106.62/109.12	31.23/34.61	-0.244	0.741
LP10348	rs59054859	19805929	AA/AG/GG	568/157/9	0.118	108.68/111.43/103.19	35.01/33.41/18.35	0.238	0.429
LP10632	Novel	19806213	CC/CT	738/13	0.008	109.1/114.09	34.7/36.18	0.575	0.582
LP10800	rs6991305	19806381	AA/AG/GG	1/66/679	0.045	110.68/105.53/109.41	NA/30.15/34.93	-0.360	0.440
LP11050	rs7016529	19806631	CC/CT/TT	70/301/373	0.295	106.65/110.43/108.75	29.2/37.52/32.73	-0.018	0.931
LP11090	rs8176337	19806671	CC/CG/GG	80/310/357	0.313	107.86/107.49/111.53	32.7/37.09/33.04	-0.332	0.103
LP11895	rs189417962	19807476	TA/TT	11/752	0.007	100.69/109.52	40.38/34.43	-1.102	0.327
LP12449	rs74304285	19808030	AA/GA/GG	2/78/653	0.056	147.31/115.65/108.09	32.67/35.99/34.28	0.995	0.019
LP13102	rs79760154	19808683	AA/CA/CC	613/126/5	0.091	109.14/110.21/96.81	34.84/34.99/30.84	-0.015	0.965
LP13443	rs115589061	19809024	CC/GC	714/35	0.023	109.42/105.72	34.84/31.76	-0.413	0.521
LP13691_13693del3	Novel	19809272	WD/WW	2/698	0.001	79.89/109.46	29.49/34.96	-3.566	0.178
LP13854	rs1121923	19809435	AA/GA/GG	13/142/593	0.111	104.3/109.51/109.56	50.82/31.81/34.74	-0.105	0.722
LP14114	rs73667472	19809695	AA/AG/GG	480/249/32	0.203	108.72/111.28/104.81	33.76/36.19/32.4	0.060	0.798
LP14241	rs75026342	19809822	CC/CT/TT	602/133/13	0.109	108.78/111.84/103.2	35.02/33.79/29.44	0.172	0.571
LP15060del2	Novel	19810641	WD/WW	33/721	0.022	106.06/109.41	33.76/34.53	-0.373	0.572
LP15206	rs343	19810787	AA/CA/CC	1/41/674	0.031	98.04/114.03/109.19	NA/36.81/34.56	0.445	0.441
LP15245	rs248	19810826	GA/GG	50/710	0.034	108.39/109.25	36.37/34.46	-0.104	0.848
LP15266	rs116678290	19810847	TC/TT	9/729	0.006	113.04/109.02	32.41/34.46	0.528	0.670
LP15579	rs251	19811160	CC/TC/TT	24/236/478	0.192	106.63/107.46/110.01	30.18/33.25/35.53	-0.226	0.363
LP15650_15651Ins1	rs252	19811234	DD/WD/WW	611/130/4	0.093	110.92/101.67/103.27	34.32/33.89/41.83	-1.037	2.00E-03
LP16320	rs255	19811901	CC/TC/TT	50/258/423	0.244	112.78/109.41/108.91	28.12/36.12/34.83	0.173	0.437
LP16363	rs80143795	19811944	AA/AG/GG	590/140/14	0.115	108.79/112.33/98.28	34.98/34.27/29.41	0.110	0.712
LP16647	rs257	19812228	AA/CA/CC	699/44/4	0.034	108.78/116.11/95.75	34.36/39.76/13.86	0.388	0.433
LP16671	rs258	19812252	CC/CG/GG	697/50/1	0.035	109.99/97.55/119.98	34.74/33.32/NA	-1.339	0.011
LP16856	rs259	19812437	AA/AT	678/79	0.053	109.51/108.3	34.72/33.72	-0.118	0.790
LP16928	rs260	19812509	CC/CG	627/113	0.076	109.54/106.39	35.05/31.62	-0.300	0.429
LP17039	rs261	19812620	AA/AG/GG	482/212/35	0.195	109.49/109.52/107.07	35.5/33.92/26.29	-0.015	0.950
LP17231	rs263	19812812	CC/TC/TT	307/323/104	0.359	109.74/108.72/109.74	36.16/34.8/30.87	0.019	0.923
LP1771	rs266	19813299	AA/AG/GG	510/204/24	0.170	110.05/107.22/104.95	35.54/33.09/31.76	-0.285	0.264
LP17993	rs144466625	19813574	GA/GG	2/746	0.001	79.32/109.28	31.04/34.69	-3.504	0.184
rs59184895	rs59184895	19813610	CC/CT/TT	3/70/669	0.052	123.77/108.28/109.18	20.49/34.29/34.64	0.065	0.880
LP18086	rs269	19813667	GG/GT/TT	177/368/205	0.479	110.28/108.25/110.8	32.58/34.4/36.31	-0.003	0.988
LP18095	rs270	19813676	AA/CA/CC	5/94/651	0.069	105.89/110.36/109.02	56.58/36.95/34.27	0.018	0.961
LP18395ins1	rs58935878	19813976	II/WI/WW	1/61/682	0.042	97.95/113.04/108.78	NA/39.22/34.41	0.373	0.443
LP18708	rs276	19814289	CC/CT/TT	28/227/488	0.190	112.86/110.68/108.21	40.04/36.51/33.53	0.244	0.319

Table A2.6. Continued

LPL variant	RefSNP ID[a]	Chr. Position (hg19)	Genotypes	GT Counts	MAF	Adjusted Mean of plasma LDL-C	Standard Deviation	Beta	*P*
LP18822	rs277	19814403	CC/TC/TT	12/140/587	0.110	104.34/107.32/109.15	38.9/38.27/33.37	-0.313	0.298
LP19115	rs279	19814696	CC/GC/GG	531/187/16	0.150	109.27/109.02/112.26	35.69/32.59/32.94	0.078	0.776
LP19301	rs280	19814882	AA/GA/GG	3/81/662	0.058	96.78/116.84/108.22	30.03/34.01/34.59	0.770	0.059
LP19407	rs17091775	19814988	AA/GA/GG	3/77/658	0.056	96.58/116.52/108.38	30.03/34.04/34.66	0.711	0.089
LP19442	rs282	19815023	AA/AT/TT	213/341/182	0.477	110.22/109.23/108.12	35.33/33.53/36.17	-0.128	0.495
LP20188	rs290	19815769	AA/GA/GG	18/157/495	0.145	110.42/109.14/108.75	30.98/33.13/35.44	0.102	0.721
LP20657	rs295	19816238	AA/CA/CC	289/330/125	0.390	106.83/110.99/111.36	34.17/35.46/32.69	0.320	0.092
LP20670	rs145585712	19816251	GA/GG	25/723	0.016	109.86/109.02	37.95/34.42	0.055	0.942
LP21136	rs73601683	19816717	GA/GG	17/732	0.012	116.18/109.01	39.07/34.67	0.790	0.389
LP21299	rs299	19816880	CC/CT/TT	736/7/1	0.007	109.18/104.94/109.54	34.61/30.82/NA	-0.241	0.831
LP21306	rs300	19816887	AA/GA	723/16	0.011	109.17/108.45	34.61/27.02	0.062	0.947
LP21353	rs301	19816934	CC/TC/TT	63/303/380	0.288	110.35/110.93/107.52	33.81/34.53/34.28	0.285	0.176
LP22445	rs313	19818026	AA/AG/GG	530/182/18	0.150	109.16/109.49/109.58	35.59/32.86/32.76	0.078	0.775
LP22461	rs314	19818042	AA/GA/GG	423/242/54	0.248	109.67/112.02/101.75	33.09/37.52/32.77	-0.184	0.403
LP22774	rs77434393	19818355	CC/CT	725/37	0.024	109.1/112.62	34.06/43.48	0.252	0.689
LP22855	rs316	19818436	AA/CA/CC	40/254/449	0.225	106.97/111.42/108.58	29.86/35.66/34.7	0.160	0.490
LP22970	rs5934	19818551	GA/GG	50/709	0.033	110.65/109.03	37.2/34.2	0.144	0.791
LP23388	rs318	19818969	CC/CG/GG	551/175/17	0.139	109.73/106.79/112.4	35.13/32.8/38.55	-0.171	0.534
LP23395	rs319	19818976	AA/CA/CC	627/111/5	0.082	108.74/112.74/83.58	34.03/37.75/21.39	0.078	0.824
LP23605	rs321	19819186	GC/GG	12/735	0.009	113.37/109.21	24.85/34.79	0.636	0.556
LP23747	rs325	19819328	CC/CT/TT	3/59/684	0.043	102.27/117.27/108.46	2.39/39.8/34.31	0.726	0.116
LP23858	rs326	19819439	AA/GA/GG	107/381/263	0.398	105.29/110.93/108.01	34.71/35.84/32.39	-0.071	0.725
LP24064	rs149089920	19819645	AG/GG	2/749	0.001	133.75/109.09	2.47/34.72	2.937	0.266
rs328	rs328	19819724	CC/GC/GG	691/58/3	0.042	108.71/117.75/102.35	33.94/39.26/2.39	0.751	0.102
LP24505	rs329	19820086	AA/GA/GG	569/116/10	0.097	110.42/105.16/103.12	35.14/33.71/32.8	-0.558	0.092
LP24815	rs330	19820396	AA/AG/GG	3/120/623	0.085	157.51/109.13/108.8	48.97/32.39/34.84	0.354	0.317
LP24829	rs138285812	19820410	GA/GG	38/706	0.025	109.07/109.15	30.71/34.98	0.082	0.895
LP24852	rs12679834	19820433	CC/TC/TT	5/77/669	0.058	120.87/112.26/108.59	44.34/38.57/33.92	0.424	0.289
LP24899	rs76423146	19820480	CC/TC/TT	536/183/27	0.157	109.94/105.71/113.83	34.88/33.9/36.35	-0.188	0.459
LP25380	rs28599962	19820961	GG/GT	723/31	0.021	109.27/104.44	34.73/28.27	-0.463	0.496
LP25579	Novel	19821160	AA/AG	740/8	0.005	109.38/88.94	34.72/34.43	-2.403	0.070
LP25886del1	rs28716400	19821467	DD/WD/WW	19/185/534	0.152	109.25/110.02/109.13	32.94/31.95/35.88	0.125	0.641
LP26460	rs75946927	19822041	GG/TG/TT	6/112/629	0.087	109.96/113.16/108.77	28.86/37.83/34.03	0.382	0.270
LP27033del1	rs147900112	19822614	DD/WD/WW	22/187/530	0.157	109.79/108.52/109.19	30.84/31.98/35.71	0.017	0.949
LP27050	rs114236375	19822631	GT/TT	18/726	0.012	107.51/109.11	44.87/34.26	-0.330	0.710
LP27269	rs7818177	19822850	GA/GG	23/711	0.015	105.15/109.2	29.4/34.66	-0.385	0.623
LP27629	Novel	19823210	CC/GC	746/2	0.001	109.15/96.58	34.77/14.35	-1.230	0.642
LP27695	Novel	19823276	GG/GT	738/1	0.001	109.32/114.71	34.56/NA	0.862	0.816
LP27706	Novel	19823287	GG/GT	761/2	0.001	109.35/93.42	34.52/3.54	-1.686	0.521
LP27928	rs187587525	19823509	GA/GG	5/742	0.003	108.27/109.24	48.75/34.62	-0.295	0.860
LP27969	Novel	19823550	AA/AG	745/2	0.001	109.23/96.78	34.77/14.35	-1.220	0.645
LP28036	rs11570892	19823617	AA/AG/GG	422/266/43	0.240	107.98/110.28/111.44	34.33/33.83/37.88	0.241	0.286
LP28067	rs3208305	19823648	AA/TA/TT	232/371/143	0.443	110.35/110.33/105.42	33.84/35.23/34.41	-0.267	0.171
LP28382	rs1059507	19823963	CC/CT/TT	598/143/5	0.103	108.74/109.74/137.1	35.16/31.87/62.42	0.362	0.267
LP28490	rs3200218	19824071	AA/GA/GG	610/127/5	0.093	108.64/112.35/89.97	33.88/37.71/22.47	0.159	0.637
LP28531	rs139240067	19824112	GA/GG	19/723	0.013	105.34/109.2	26.78/34.94	-0.361	0.677
LP28669	rs184363931	19824250	CC/TC	732/14	0.009	108.98/109.36	34.46/39.5	0.005	0.996
LP28911	rs13702	19824492	CC/CT/TT	219/378/154	0.459	109.88/110.63/105.83	34.17/35.13/33.14	-0.209	0.279
LP29023	rs17091815	19824604	AA/AT/TT	611/120/2	0.084	108.79/110.73/105.97	34.31/36.06/40.23	0.166	0.643
LP29047	rs78359368	19824628	GG/GT	738/10	0.007	109.41/87.32	34.75/30.74	-2.561	0.031
LP29098	rs187374932	19824679	TC/TT	8/751	0.005	85.74/109.38	34.06/34.44	-2.801	0.034
LP29126	rs147116359	19824707	AA/GA/GG	1/15/719	0.011	115.09/117.88/108.68	NA/40.65/34.16	0.916	0.283
LP29168	rs79756214	19824749	TC/TT	24/722	0.016	103.61/109.27	33.37/34.83	-0.631	0.415
LP29287	rs3916027	19824868	AA/AG/GG	134/344/259	0.413	111.14/110.61/106.7	33.54/35.62/34.16	0.298	0.123
LP29487	rs4921683	19825068	AA/AT/TT	4/144/596	0.102	146.7/110.14/108.66	67.36/31.86/35.17	0.438	0.184
LP29543	rs76707496	19825124	AA/GA/GG	7/119/619	0.090	121.83/108.47/109.16	32.37/31.88/34.74	0.138	0.679
LP29547	rs4921684	19825128	CC/TC/TT	642/119/1	0.079	108.51/113.26/80.17	34.74/33.22/NA	0.518	0.154

W: Allele in the referecne sequence (NC_00008.10).; D: Deleted base/bases; I: Inserted base/bases

[a] db build 137

Table A2.7. Association results of TC levels with 125 *LPL* SNPs in Blacks (n=788)

LPL variant	RefSNP ID	Position	Genotype	GT Count	MAF	Adjusted Mean of plasma TC	Standard Deviation	Beta	P
rs147018794	rs147018794	19795467	GG/GT/TT	581/141/10	0.112	172.19/172.74/167.03	38.22/41.66/45.29	-0.043	0.792
LP208	rs1470186	19795581	CC/CT/TT	41/242/441	0.225	173.03/175.86/170.05	43.85/40.67/36.96	0.173	0.152
LP428	rs73667465	19796009	AA/AG/GG	89/279/357	0.314	165.87/177.58/169.31	39.57/42.43/35.37	0.036	0.730
LP1090	rs1800590	19796671	GG/GT/TT	168/341/215	0.468	171.62/173.51/169.87	39.77/40.26/36.38	0.042	0.675
LP1107	rs75890454	19796688	TA/TT	27/711	0.020	167.07/172.22	33.2/39.14	-0.240	0.531
LP1155		19796736	AA/TA	739/1	0.001	172.15/126.31	38.93/NA	-2.537	0.195
LP1200_1201ins2	rs34513350	19796781	II/WI/WW	1/40/691	0.029	195.93/167.16/172.36	NA/36.47/39.1	-0.180	0.553
LP1264		19796845	GA/GG	11/741	0.008	167.48/172.18	48.03/38.49	-0.279	0.637
LP1300		19796881	CC/CG	733/8	0.005	172.53/130.87	38.8/29.45	-2.390	6.00E-04
LP1488	rs200412008	19797069	CC/CT	696/45	0.029	171.66/178.51	38.52/44.14	0.335	0.268
LP1498	rs141390463	19797079	AA/GA/GG	5/50/670	0.041	150.91/175.81/172.25	19.88/51.27/37.99	-0.097	0.690
LP2335	rs3779787	19797916	GG/GT	698/33	0.023	171.32/183.13	38.67/43.05	0.596	0.089
LP2758	rs146786419	19798339	CC/TC/TT	672/56/1	0.039	172.27/173.21/209.71	38.96/39.52/NA	0.115	0.664
LP2830	rs185670596	19798411	GC/GG	31/709	0.022	168.97/172.3	39.28/38.86	-0.173	0.631
LP3725	rs115668974	19799306	CC/CT/TT	676/50/5	0.042	172.3/169.77/174.97	38.62/37.2/54.26	-0.071	0.769
LP3964	rs17410577	19799545	CC/GC/GG	14/150/580	0.120	166.14/172.62/172.27	46.13/38.87/38.63	-0.040	0.793
LP5531	rs1031045	19801112	AA/AG/GG	162/333/234	0.451	174.71/171.24/171.81	37.94/41.2/36.75	0.065	0.518
LP5949	rs112127208	19801530	GG/TG/TT	1/34/721	0.025	169.82/182.6/171.69	NA/43.7/38.41	0.484	0.135
LP6554	rs56043715	19802135	AA/GA/GG	348/303/72	0.307	170.94/173.92/167.74	36.28/41.7/36.8	-0.014	0.900
LP6762	rs61274012	19802343	CC/CT/TT	1/43/693	0.030	200.92/176.85/171.6	NA/41.15/38.74	0.325	0.269
LP7130	rs28615996	19802711	CC/TC/TT	82/327/323	0.333	170.73/172.98/171.84	36.64/41.41/37.18	-0.010	0.924
LP7313	rs28645722	19802894	AA/GA/GG	65/280/381	0.281	168.07/174.67/170.98	35.52/42.84/36.09	0.010	0.925
LP7503	rs6999612	19803084	AA/AG/GG	390/299/64	0.284	171.38/174.1/168.01	35.84/42.52/35.67	-0.014	0.899
LP7556	rs59811201	19803137	CC/CT/TT	19/204/509	0.166	171.73/175.13/171.3	43.61/41.96/37.52	0.114	0.411
LP7907	rs115064749	19803488	AA/AG/GG	690/43/1	0.030	171.89/169.66/195.96	39.08/35.93/NA	-0.035	0.905
LP8441_8442del2	rs112943460	19804022	DD/WD/WW	1/41/688	0.029	195.7/167.98/172.26	NA/35.92/38.89	-0.136	0.649
LP8766	rs181367025	19804347	CT/TT	18/720	0.013	175.49/171.98	44.98/38.73	0.144	0.758
LP9015	rs28445964	19804596	AA/GA/GG	418/260/50	0.247	171.11/174.26/172.54	36.03/44.1/35.57	0.071	0.545
LP9232	rs145257746	19804813	AA/AC/CC	648/69/2	0.052	172.06/174.93/165.72	38.09/45.03/31.82	0.077	0.743
LP9499	rs138110428	19805080	GA/GG	10/732	0.007	168.08/172.21	50.51/38.33	-0.263	0.671
LP10100del1		19805681	WD/WW	33/706	0.022	170.76/171.89	33.68/39	-0.021	0.952
LP10127	rs1801177	19805708	AA/AG/GG	3/70/675	0.050	198.34/176.71/171.64	73.08/41.96/38.23	0.310	0.171
LP10170	rs148201569	19805751	CC/CG	736/4	0.003	172.39/116.39	38.68/46	-3.556	2.76E-04
LP10234	rs11542065	19805815	GC/GG	24/715	0.018	169.24/171.9	33.28/38.84	-0.106	0.793
LP10348	rs59054859	19805929	AA/AG/GG	565/152/9	0.118	171.21/175.97/162.83	39.13/37.97/15.38	0.179	0.265
LP10632		19806213	CC/CT	730/13	0.008	172.05/172.48	38.8/45.05	-0.029	0.958
LP10800	rs6991305	19806381	AA/AG/GG	1/66/671	0.045	209.04/169.64/172.1	NA/35.49/39.15	-0.049	0.841
LP11050	rs7016529	19806631	CC/CT/TT	68/301/367	0.295	169.71/173.88/171.18	35/43.03/35.64	0.010	0.925
LP11090	rs8176337	19806671	CC/CG/GG	80/302/357	0.313	169.51/170.7/174.54	33.57/41.13/38.06	-0.162	0.130
LP11895	rs189417962	19807476	TA/TT	10/746	0.007	168.13/172.29	50.51/38.52	-0.263	0.672
LP12449	rs74304285	19808030	AA/GA/GG	2/78/646	0.056	203.33/179.17/170.71	21.92/42.21/38.31	0.475	0.034
LP13102	rs79760154	19808683	AA/CA/CC	608/123/5	0.091	171.99/173.91/154.89	38.47/41.79/33.76	-0.005	0.979
LP13443	rs115589061	19809024	CC/GC	709/32	0.023	172.15/170.86	39.2/32.68	-0.048	0.891
LP13691_13693del3		19809272	WD/WW	2/692	0.001	126.92/172.49	36.06/39.15	-2.620	0.059
LP13854	rs1121923	19809435	AA/GA/GG	13/138/589	0.111	165.26/173.11/172.39	62.58/36.38/38.6	-0.050	0.752
LP14114	rs73667472	19809695	AA/AG/GG	479/242/32	0.203	171.12/175.51/163.91	38.02/39.77/39.29	0.046	0.713
LP14241	rs75026342	19809822	CC/CT/TT	593/134/13	0.109	171.99/173.71/161.67	39.7/35.49/32.34	0.007	0.966
LP15060del2		19810641	WD/WW	33/714	0.022	172.35/172.16	34.2/38.82	0.045	0.896
LP15206	rs343	19810787	AA/CA/CC	1/41/667	0.031	143.8/176.35/172.33	NA/42.8/38.63	0.100	0.742
LP15245	rs248	19810826	GA/GG	52/700	0.034	174.15/171.94	41.26/38.58	0.110	0.697
LP15266	rs116678290	19810847	TC/TT	9/721	0.006	175.94/171.95	38.29/38.7	0.248	0.704
LP15579	rs251	19811160	CC/TC/TT	23/232/475	0.192	170.72/170.91/172.5	38.24/38.55/39.17	-0.073	0.581
LP15650_15651Ins1	rs252	19811234	DD/WD/WW	607/128/4	0.093	173.72/164.81/156.87	38.5/37.43/50.56	-0.494	0.005
LP16320	rs255	19811901	CC/TC/TT	49/253/422	0.244	176.05/173.24/171.31	36.86/40.68/38.47	0.115	0.332
LP16363	rs80143795	19811944	AA/AG/GG	581/141/14	0.115	171.99/174.14/158.64	39.7/36.17/31.43	-0.008	0.959
LP16647	rs257	19812228	AA/CA/CC	691/44/4	0.034	171.85/178.24/151.72	38.31/46.71/21.76	0.068	0.792
LP16671	rs258	19812252	CC/CG/GG	690/49/1	0.035	172.83/161.65/167.8	38.86/38.59/NA	-0.581	0.037
LP16856	rs259	19812437	AA/AT	671/79	0.053	172.37/171.38	39.16/34.88	-0.019	0.935
LP16928	rs260	19812509	CC/CG	620/112	0.076	172.35/169.5	38.87/38.65	-0.155	0.440
LP17039	rs261	19812620	AA/AG/GG	474/212/35	0.195	172.71/171.79/168.93	39.85/38.01/30.7	-0.054	0.667
LP17231	rs263	19812812	CC/TC/TT	308/315/103	0.359	171.65/173.27/171.26	39.57/38.88/37.65	0.023	0.824
LP1771	rs266	19813299	AA/AG/GG	508/198/24	0.170	172.77/170.38/167.87	38.9/39.4/37.66	-0.135	0.317
LP17993	rs144466625	19813574	GA/GG	2/738	0.001	165/172.04	9.19/38.99	-0.251	0.857
rs59184895	rs5918489518029	19813610	CC/CT/TT	3/69/662	0.052	188.76/170.34/172.05	22.52/36.34/39.21	0.017	0.940
LP18086	rs269	19813667	GG/GT/TT	174/361/207	0.479	173.9/171.58/172.58	38.39/38.01/40.13	0.038	0.702
LP18095	rs270	19813676	AA/CA/CC	5/94/643	0.069	166.63/174.15/171.81	53.78/39.22/38.79	0.074	0.705
LP18395ins1	rs58935878	19813976	II/WI/WW	1/59/676	0.042	143.64/178.63/171.51	NA/43.97/38.53	0.277	0.285
LP18708	rs276	19814289	CC/CT/TT	29/226/480	0.190	170.71/173.96/171.12	45.88/39.5/38.23	0.076	0.556

Table A2.7. Continued

***LPL* variant**	**RefSNP ID**	**Position**	**Genotype**	**GT Count**	**MAF**	**Adjusted Mean of plasma TC**	**Standard Deviation**	**Beta**	**P**
LP18822	rs277	19814403	CC/TC/TT	12/137/583	0.110	171.37/169.18/171.95	42.05/43.07/37.48	-0.144	0.365
LP19115	rs279	19814696	CC/GC/GG	527/183/16	0.150	171.79/172.59/174.78	39.87/36.84/34.88	0.080	0.581
LP19301	rs280	19814882	AA/GA/GG	3/80/655	0.058	153.05/180.68/171.11	23.12/39/38.68	0.375	0.082
LP19407	rs17091775	19814988	AA/GA/GG	3/76/651	0.056	152.82/180.68/171.25	23.12/39.46/38.65	0.357	0.106
LP19442	rs282	19815023	AA/AT/TT	210/337/181	0.477	173.92/172.11/169.74	39.65/36.94/41.86	-0.123	0.216
LP20188	rs290	19815769	AA/GA/GG	18/156/492	0.145	170.86/173.82/171.77	36.45/37.71/39.49	0.080	0.597
LP20657	rs295	19816238	AA/CA/CC	286/328/122	0.390	168.63/174.75/174.56	38.37/39.28/37.5	0.199	0.049
LP20670	rs145585712	19816251	GA/GG	25/715	0.016	179.48/171.65	47.02/38.5	0.377	0.343
LP21136	rs73601683	19816717	GA/GG	18/723	0.012	178.11/171.93	46.35/38.76	0.283	0.546
LP21299	rs299	19816880	CC/CT/TT	727/8/1	0.007	172.06/167.97/179.44	38.87/34.46/NA	-0.051	0.929
LP21306	rs300	19816887	AA/GA	715/16	0.011	172.1/170.83	38.76/35.94	-0.042	0.932
LP21353	rs301	19816934	CC/TC/TT	64/297/378	0.288	172.16/174.9/169.53	36.44/39.18/38.07	0.173	0.119
LP22445	rs313	19818026	AA/AG/GG	526/178/18	0.150	171.78/173.8/167.27	39.66/37.05/37.02	0.053	0.710
LP22461	rs314	19818042	AA/GA/GG	420/236/55	0.248	172.56/175.67/163.9	37.77/41.91/32.43	-0.066	0.569
LP22774	rs77434393	19818355	CC/CT	718/37	0.024	171.87/175.5	38.28/46.07	0.142	0.667
LP22855	rs316	19818436	AA/CA/CC	41/248/446	0.225	168.46/176.4/170.36	31.79/39.91/38.9	0.164	0.179
LP22970	rs5934	19818551	GA/GG	50/701	0.033	174.5/171.78	38.17/38.7	0.161	0.573
LP23388	rs318	19818969	CC/CG/GG	546/173/16	0.139	172.49/169.72/175.54	38.74/38.71/47.78	-0.089	0.545
LP23395	rs319	19818976	AA/CA/CC	621/109/5	0.082	171.37/175.45/155.26	38.46/41.78/38.1	0.094	0.617
LP23605	rs321	19819186	GC/GG	13/726	0.009	176.31/172.07	34.79/39.02	0.251	0.649
LP23747	rs325	19819328	CC/CT/TT	3/59/676	0.043	159.71/180.3/171.33	6.24/47.39/38.14	0.287	0.240
LP23858	rs326	19819439	AA/GA/GG	108/378/258	0.398	167.39/173.5/171.57	37.19/39.71/37.92	-0.063	0.553
LP24064	rs149089920	19819645	AG/GG	2/741	0.001	194.66/171.99	33.94/38.89	1.257	0.365
rs328	rs328	19819724	CC/GC/GG	683/58/3	0.042	171.51/180.14/159.41	37.88/46.62/6.24	0.276	0.256
LP24505	rs329	19820086	AA/GA/GG	565/113/9	0.097	173.16/169.09/179.45	38.95/40.3/31.96	-0.123	0.488
LP24815	rs330	19820396	AA/AG/GG	3/122/613	0.085	214.69/173.37/171.41	53.48/35.24/39.39	0.243	0.191
LP24829	rs138285812	19820410	GA/GG	38/698	0.025	168.99/172.2	33.86/39.15	-0.135	0.679
LP24852	rs12679834	19820433	CC/TC/TT	5/75/664	0.058	187.96/176.67/171.23	59.06/43.99/37.87	0.276	0.194
LP24899	rs76423146	19820480	CC/TC/TT	529/182/27	0.157	173.03/168.53/174.73	39.55/36.78/40.83	-0.119	0.378
LP25380	rs28599962	19820961	GG/GT	716/31	0.021	172.17/165.72	38.82/36.31	-0.337	0.346
LP25579		19821160	AA/AG	732/8	0.005	172.43/141.95	38.78/41.67	-1.747	0.012
LP25886del1	rs28716400	19821467	DD/WD/WW	19/183/528	0.152	169.25/173.84/171.89	38.7/36.26/39.98	0.070	0.623
LP26460	rs75946927	19822041	GG/TG/TT	6/111/623	0.087	167.06/176.56/171.58	31.58/39.23/38.79	0.205	0.263
LP27033del1	rs147900112	19822614	DD/WD/WW	22/188/524	0.157	169.94/172.21/171.84	36.19/36.28/39.88	0.018	0.898
LP27050	rs114236375	19822631	GT/TT	16/720	0.012	181.08/171.77	46.33/38.6	0.462	0.351
LP27269	rs7818177	19822850	GA/GG	23/704	0.015	166.87/172.08	40.07/38.73	-0.301	0.466
LP27629		19823210	CC/GC	738/2	0.001	172.11/149.58	38.94/35.36	-1.229	0.377
LP27695		19823276	GG/GT	731/1	0.001	172.24/193.03	38.71/NA	1.231	0.527
LP27706		19823287	GG/GT	754/2	0.001	172.2/151.71	38.7/24.75	-1.081	0.434
LP27928	rs187587525	19823509	GA/GG	5/734	0.003	165.43/172.21	68.81/38.63	-0.605	0.489
LP27969		19823550	AA/AG	737/2	0.001	172.2/149.97	38.95/35.36	-1.215	0.382
LP28036	rs11570892	19823617	AA/AG/GG	415/265/43	0.240	170.26/174.74/171.95	38.29/38.61/41.28	0.144	0.229
LP28067	rs3208305	19823648	AA/TA/TT	228/369/142	0.443	174.43/172.89/166.93	39.46/39.05/37.53	-0.187	0.071
LP28382	rs1059507	19823963	CC/CT/TT	588/145/5	0.103	171.42/173.93/198.36	39.93/33.66/64.4	0.253	0.140
LP28490	rs3200218	19824071	AA/GA/GG	604/125/5	0.093	171.51/175.23/163.58	38.46/40.92/30.2	0.134	0.453
LP28531	rs139240067	19824112	GA/GG	20/714	0.013	169.48/172.02	34.22/39.19	-0.117	0.793
LP28669	rs184363931	19824250	CC/TC	725/13	0.009	171.86/172.31	38.62/51.04	-0.069	0.899
LP28911	rs13702	19824492	CC/CT/TT	214/376/153	0.459	174.16/173.44/166.85	39.36/39.08/36.1	-0.178	0.083
LP29023	rs17091815	19824604	AA/AT/TT	605/119/2	0.084	171.71/173.53/162.63	38.35/41.69/28.99	0.046	0.807
LP29047	rs78359368	19824628	GG/GT	730/10	0.007	172.51/138.72	38.82/38.68	-1.941	1.84E-03
LP29098	rs187374932	19824679	TC/TT	8/744	0.005	133.11/172.46	41.11/38.49	-2.286	9.37E-04
LP29126	rs147116359	19824707	AA/GA/GG	1/15/711	0.011	177.36/186.15/171.54	NA/43.97/38.47	0.661	0.142
LP29168	rs79756214	19824749	TC/TT	24/714	0.016	163.68/172.3	37.99/39.02	-0.465	0.254
LP29287	rs3916027	19824868	AA/AG/GG	132/340/257	0.413	175.15/173.63/168.95	37.74/40.16/38.03	0.182	0.076
LP29487	rs4921683	19825068	AA/AT/TT	4/146/586	0.102	209.72/174.35/171.31	68.45/34.01/39.82	0.297	0.086
LP29543	rs76707496	19825124	AA/GA/GG	7/116/615	0.090	183.57/172.11/171.88	35.02/37.09/38.94	0.096	0.588
LP29547	rs4921684	19825128	CC/TC/TT	634/119/1	0.079	171.24/176.86/141.07	39.26/35.57/NA	0.298	0.120

Table A2.8. Association results of ApoB levels with 125 *LPL* SNPs in African blacks (n=788)

LPL variant	RefSNP ID^{a}	Chr. Position (hg19)	Genotypes	GT Counts	MAF	Adjusted Mean of plasma ApoB	Standard Deviation	Beta	*P*
rs147018794	rs147018794	19795467	GG/GT/TT	583/145/10	0.112	66.83/66.71/53.56	21.06/23.65/34	-0.967	0.254
LP208	rs1470186	19795581	CC/CT/TT	42/244/444	0.225	66.79/67.26/66.56	26.35/21.57/21.25	0.143	0.820
LP428	rs73667465	19796009	AA/AG/GG	89/282/360	0.314	65.81/66.64/66.66	22.3/22.59/21.3	-0.180	0.746
LP1090	rs1800590	19796671	GG/GT/TT	171/344/215	0.468	66.83/66.29/66.78	21.43/21.96/21.79	-0.008	0.988
LP1107	rs75890454	19796688	TA/TT	29/715	0.020	62.18/66.74	22/21.83	-2.239	0.252
LP1155	Novel	19796736	AA/TA	745/1	0.001	66.55/59.57	21.86/NA	-3.055	0.768
LP1200_1201ins2	rs34513350	19796781	II/WI/WW	1/40/697	0.029	75.62/66.24/66.62	NA/20.58/21.91	0.081	0.960
LP1264	Novel	19796845	GA/GG	12/750	0.008	69.14/66.59	20.57/21.86	1.325	0.659
LP1300	Novel	19796881	CC/CG	740/7	0.005	66.52/65.41	21.88/20.36	-0.426	0.914
LP1488	rs200412008	19797069	CC/CT	703/44	0.029	66.2/71.39	21.73/23.5	2.472	0.125
LP1498	rs141390463	19797079	AA/GA/GG	5/51/675	0.041	71.4/69.89/66.69	13.19/21.78/21.78	1.488	0.239
LP2335	rs3779787	19797916	GG/GT	703/34	0.023	66.07/73.67	21.65/23.53	3.626	0.045
LP2758	rs146786419	19798339	CC/TC/TT	678/56/1	0.039	66.81/65.63/59.05	21.83/21.47/NA	-0.668	0.630
LP2830	rs185670596	19798411	GC/GG	34/712	0.022	69.99/66.4	20.74/21.9	1.827	0.315
LP3725	rs115668974	19799306	CC/CT/TT	679/53/5	0.042	66.68/67.01/63.69	21.53/22.93/33.69	-0.159	0.899
LP3964	rs17410577	19799545	CC/GC/GG	14/155/586	0.120	67.57/66.37/66.85	22.95/22.56/21.72	-0.130	0.872
LP5531	rs1031045	19801112	AA/AG/GG	162/340/233	0.451	67.86/66.59/65.79	18.87/23.82/20.8	0.500	0.341
LP5949	rs112127208	19801530	GG/TG/TT	1/35/731	0.025	68.68/74.59/66.36	NA/22.66/21.75	3.611	0.033
LP6554	rs56043715	19802135	AA/GA/GG	353/304/72	0.307	66.32/67.16/65.61	20.97/23.13/18.86	0.020	0.972
LP6762	rs61274012	19802343	CC/CT/TT	1/43/699	0.030	82.2/69.37/66.25	NA/23.47/21.63	1.670	0.280
LP7130	rs28615996	19802711	CC/TC/TT	82/326/330	0.333	66.26/66.68/66.59	18.97/23.52/20.77	-0.067	0.906
LP7313	rs28645722	19802894	AA/GA/GG	65/281/386	0.281	64.61/67.52/66.41	20.27/23.07/21	-0.085	0.884
LP7503	rs6999612	19803084	AA/AG/GG	396/303/64	0.284	67.12/66.66/63.99	21/23.35/19.94	-0.574	0.324
LP7556	rs59811201	19803137	CC/CT/TT	18/206/514	0.166	58.41/69.13/66.22	24.49/22.97/20.98	0.325	0.655
LP7907	rs115064749	19803488	AA/AG/GG	700/43/1	0.030	66.38/66.53/75.72	22.09/19.61/NA	0.340	0.828
LP8441_8442del2	rs112943460	19804022	DD/WD/WW	1/41/694	0.029	75.66/66.2/66.67	NA/20.15/21.84	0.044	0.978
LP8766	rs181367025	19804347	CT/TT	19/724	0.013	75.03/66.37	21.18/21.71	4.236	0.076
LP9015	rs28445964	19804596	AA/GA/GG	423/261/50	0.247	66.19/68.64/63.53	20.89/23.39/18.3	0.184	0.762
LP9232	rs145257746	19804813	AA/AC/CC	654/73/2	0.052	66.95/66.25/49.83	21.59/23.61/21.4	-0.776	0.521
LP9499	rs138110428	19805080	GA/GG	11/741	0.007	71.18/66.66	19.68/21.97	2.303	0.464
LP10100del1	Novel	19805681	WD/WW	34/711	0.022	63.85/66.55	15.34/21.94	-1.154	0.522
LP10127	rs1801177	19805708	AA/AG/GG	2/69/688	0.050	76.56/71.93/66.32	31.63/20.7/21.77	2.715	0.027
LP10170	rs148201569	19805751	CC/CG	743/3	0.003	66.57/59.5	21.83/28.29	-3.528	0.555
LP10234	rs11542065	19805815	GC/GG	26/723	0.018	63.29/66.66	20.27/21.88	-1.578	0.443
LP10348	rs59054859	19805929	AA/AG/GG	568/156/8	0.118	66.38/67.87/68.89	22.05/20.91/12.82	0.749	0.375
LP10632	Novel	19806213	CC/CT	736/13	0.008	66.41/74.51	21.78/22.93	3.930	0.174
LP10800	rs6991305	19806381	AA/AG/GG	1/66/678	0.045	59.08/65.53/66.56	NA/18.51/22.01	-0.507	0.694
LP11050	rs7016529	19806631	CC/CT/TT	68/305/374	0.295	65.26/67.43/66.7	19.24/22.85/20.97	-0.096	0.868
LP11090	rs8176337	19806671	CC/CG/GG	81/310/358	0.313	62.36/66.24/68.37	18.33/22.75/21.61	-1.298	0.021
LP11895	rs189417962	19807476	TA/TT	11/755	0.007	71.16/66.68	19.68/21.8	2.277	0.467
LP12449	rs74304285	19808030	AA/GA/GG	2/79/653	0.056	95.9/71.29/65.87	28.43/23.23/21.66	3.014	0.010
LP13102	rs79760154	19808683	AA/CA/CC	611/126/5	0.091	66.49/68.96/47.21	21.63/21.81/16.94	0.315	0.735
LP13443	rs115589061	19809024	CC/GC	712/35	0.023	66.62/63.93	21.96/19.78	-1.233	0.491
LP13691_13693del3	Novel	19809272	WD/WW	2/697	0.001	54.76/66.68	13.27/22.08	-5.668	0.443
LP13854	rs1121923	19809435	AA/GA/GG	12/143/596	0.111	65.35/68.04/66.62	28.63/20.74/21.93	0.429	0.606
LP14114	rs73667472	19809695	AA/AG/GG	485/248/31	0.203	66.28/68.63/61.6	21.33/22.76/20.25	0.198	0.763
LP14241	rs75026342	19809822	CC/CT/TT	599/135/12	0.109	66.66/67.11/56.71	22.15/20.73/16.31	-0.494	0.560
LP15060del2	Novel	19810641	WD/WW	34/723	0.022	64.37/66.75	16.36/22.11	-1.014	0.577
LP15206	rs343	19810787	AA/CA/CC	1/42/676	0.031	69.78/70.11/66.3	NA/21.32/21.75	1.785	0.256
LP15245	rs248	19810826	GA/GG	50/713	0.034	72.26/66.3	22.58/21.78	2.907	0.055
LP15266	rs116678290	19810847	TC/TT	9/727	0.006	66.43/66.68	18.05/21.71	-0.016	0.996
LP15579	rs251	19811160	CC/TC/TT	24/235/477	0.192	65.53/66.28/66.99	22.31/20.83/22.15	-0.326	0.635
LP15650_15651Ins1	rs252	19811234	DD/WD/WW	612/132/4	0.093	67.72/61.95/69.93	22.13/20.62/10.2	-2.364	0.012
LP16320	rs255	19811901	CC/TC/TT	49/259/422	0.244	65.87/66.99/66.74	20.76/22.38/21.6	-0.057	0.926
LP16363	rs80143795	19811944	AA/AG/GG	587/142/13	0.115	66.72/67.59/56.9	21.94/21.16/14.36	-0.364	0.657
LP16647	rs257	19812228	AA/CA/CC	698/43/4	0.034	66.37/69.5/58.9	21.79/22.8/22.83	0.581	0.676
LP16671	rs258	19812252	CC/CG/GG	695/50/1	0.035	66.87/61.8/73.33	22.05/17.47/NA	-2.022	0.164
LP16856	rs259	19812437	AA/AT	679/81	0.053	66.47/68.56	22.15/20.14	1.092	0.370
LP16928	rs260	19812509	CC/CG	628/111	0.076	66.7/65.3	21.65/22.01	-0.701	0.507
LP17039	rs261	19812620	AA/AG/GG	481/213/33	0.195	66.94/67.17/62.18	21.93/22.28/16	-0.435	0.515
LP17231	rs263	19812812	CC/TC/TT	306/325/101	0.359	67.12/66.73/66.69	21.34/22.56/19.16	-0.112	0.837
LP1771	rs266	19813299	AA/AG/GG	510/202/24	0.170	67/66.59/59.65	21.86/20.98/26.59	-0.819	0.246
LP17993	rs144466625	19813574	GA/GG	2/744	0.001	59.93/66.56	1.73/21.81	-2.986	0.683
rs59184895	rs59184895	19813610	CC/CT/TT	3/72/665	0.052	71.79/66.91/66.35	7.26/20.82/21.91	0.501	0.672
LP18086	rs269	19813667	GG/GT/TT	176/372/205	0.479	66.06/66.36/68.8	21.04/22.01/21.97	-0.677	0.200

Table A2.8. Continued

LPL variant	RefSNP ID[a]	Chr. Position (hg19)	Genotypes	GT Counts	MAF	Adjusted Mean of plasma ApoB	Standard Deviation	Beta	*P*
LP18095	rs270	19813676	AA/CA/CC	5/95/648	0.069	69.95/68.79/66.15	29.01/21.32/21.88	1.231	0.233
LP18395ins1	rs58935878	19813976	II/WI/WW	1/62/679	0.042	69.81/70.89/66.12	NA/26.11/21.44	2.105	0.115
LP18708	rs276	19814289	CC/CT/TT	28/224/489	0.190	70.87/67.9/65.78	28.25/23.18/20.6	1.020	0.131
LP18822	rs277	19814403	CC/TC/TT	12/140/588	0.110	59.17/69.14/65.83	22.94/23.19/21.57	0.666	0.429
LP19115	rs279	19814696	CC/GC/GG	527/190/15	0.150	67/66.16/61.55	22.32/20.96/16.91	-0.618	0.418
LP19301	rs280	19814882	AA/GA/GG	3/81/660	0.058	57.56/68.91/66.38	24.74/19.1/22.07	0.816	0.470
LP19407	rs17091775	19814988	AA/GA/GG	3/77/656	0.056	57.47/69.05/66.58	24.74/18.52/21.97	0.778	0.497
LP19442	rs282	19815023	AA/AT/TT	213/342/179	0.477	66.36/67.62/65.39	20.7/22.17/22.48	-0.239	0.646
LP20188	rs290	19815769	AA/GA/GG	17/163/495	0.145	63.6/66.89/67.21	16.79/20.23/21.34	-0.365	0.627
LP20657	rs295	19816238	AA/CA/CC	286/336/125	0.390	65.4/68.14/66.84	21.38/22.23/21.59	0.534	0.314
LP20670	rs145585712	19816251	GA/GG	24/722	0.016	62.87/66.59	21.28/21.71	-1.806	0.397
LP21136	rs73601683	19816717	GA/GG	18/729	0.012	74.03/66.34	25.78/21.72	3.612	0.143
LP21299	rs299	19816880	CC/CT/TT	733/8/1	0.007	66.6/67.42/12.37	21.48/31.71/NA	-4.948	0.097
LP21306	rs300	19816887	AA/GA	721/16	0.011	66.67/66.15	21.82/16.61	-0.114	0.965
LP21353	rs301	19816934	CC/TC/TT	62/308/378	0.288	67.15/68.05/65.23	24.13/22.18/20.9	0.817	0.164
LP22445	rs313	19818026	AA/AG/GG	526/185/17	0.150	66.74/67.27/62.21	22.18/21.25/16.21	-0.115	0.879
LP22461	rs314	19818042	AA/GA/GG	421/243/56	0.248	66.41/68.32/66.6	22.04/22.49/16.01	0.479	0.428
LP22774	rs77434393	19818355	CC/CT	729/36	0.024	66.48/71.17	21.74/24.61	2.216	0.212
LP22855	rs316	19818436	AA/CA/CC	39/260/447	0.225	64.87/68.02/66.55	24.12/21.7/21.77	0.192	0.764
LP22970	rs5934	19818551	GA/GG	50/712	0.033	70.5/66.38	19.97/21.86	2.083	0.167
LP23388	rs318	19818969	CC/CG/GG	551/174/16	0.139	66.88/65.13/67.24	21.36/23.28/21.59	-0.613	0.425
LP23395	rs319	19818976	AA/CA/CC	624/112/5	0.082	66/69.66/61.97	21.66/22.96/21.07	1.315	0.179
LP23605	rs321	19819186	GC/GG	13/732	0.009	68.6/66.5	15.02/21.96	1.183	0.683
LP23747	rs325	19819328	CC/CT/TT	3/59/682	0.043	74.97/73.67/65.85	3.87/25.18/21.44	3.433	0.007
LP23858	rs326	19819439	AA/GA/GG	107/382/265	0.398	67.88/66.54/65.91	19.87/22.51/21.05	0.440	0.429
LP24064	rs149089920	19819645	AG/GG	2/747	0.001	88.24/66.46	4.39/21.83	10.606	0.147
rs328	rs328	19819724	CC/GC/GG	694/58/3	0.042	66.08/74.75/74.93	21.52/24.11/3.87	3.792	0.003
LP24505	rs329	19820086	AA/GA/GG	570/115/9	0.097	67.79/63.27/65.51	21.43/22.69/17.94	-1.806	0.048
LP24815	rs330	19820396	AA/AG/GG	3/121/620	0.085	91.71/66.87/66.26	19.07/21.71/21.71	0.886	0.364
LP24829	rs138285812	19820410	GA/GG	36/706	0.025	68.52/66.54	20.5/21.83	1.042	0.555
LP24852	rs12679834	19820433	CC/TC/TT	5/77/672	0.058	80.26/71.26/65.81	21.92/26.01/21.27	2.711	0.015
LP24899	rs76423146	19820480	CC/TC/TT	537/181/26	0.157	67.22/64.41/64.8	21.73/22.22/21.99	-1.068	0.133
LP25380	rs28599962	19820961	GG/GT	726/31	0.021	66.44/68.69	21.88/22.4	1.052	0.580
LP25579	Novel	19821160	AA/AG	739/7	0.005	66.51/66.87	21.79/22.3	0.230	0.953
LP25886del1	rs28716400	19821467	DD/WD/WW	18/188/530	0.152	62.32/66.54/66.72	16.81/21.5/22.3	-0.370	0.622
LP26460	rs75946927	19822041	GG/TG/TT	5/115/630	0.087	57.04/68.97/66.49	10.54/21.61/22.05	0.679	0.484
LP27033del1	rs147900112	19822614	DD/WD/WW	21/193/528	0.157	64.07/66.34/66.67	16.63/21.64/22.35	-0.290	0.692
LP27050	rs114236375	19822631	GT/TT	18/725	0.012	68.62/66.4	33.3/21.39	0.689	0.779
LP27269	rs7818177	19822850	GA/GG	23/714	0.015	67.16/66.5	24.09/21.92	0.236	0.914
LP27629	Novel	19823210	CC/GC	744/2	0.001	66.45/86.79	21.79/39.32	9.585	0.190
LP27695	Novel	19823276	GG/GT	741/1	0.001	66.62/84.81	21.92/NA	8.985	0.387
LP27706	Novel	19823287	GG/GT	764/2	0.001	66.74/51.7	21.87/12.8	-7.185	0.327
LP27928	rs187587525	19823509	GA/GG	5/740	0.003	80.05/66.56	25.85/21.63	6.413	0.162
LP27969	Novel	19823550	AA/AG	743/2	0.001	66.44/86.79	21.83/39.32	9.590	0.191
LP28036	rs11570892	19823617	AA/AG/GG	420/266/43	0.240	66.29/67.25/68.54	21.45/21.97/22.37	0.500	0.423
LP28067	rs3208305	19823648	AA/TA/TT	232/375/142	0.443	66.9/66.61/66.57	22.17/22.04/20.97	-0.072	0.895
LP28382	rs1059507	19823963	CC/CT/TT	595/144/5	0.103	66.17/68.22/69.74	21.92/20.95/32.57	0.995	0.267
LP28490	rs3200218	19824071	AA/GA/GG	607/128/5	0.093	65.86/69.58/66.47	21.55/22.54/18.24	1.570	0.092
LP28531	rs139240067	19824112	GA/GG	19/721	0.013	62.85/66.6	17.71/21.95	-1.764	0.463
LP28669	rs184363931	19824250	CC/TC	730/14	0.009	66.3/74.08	21.72/21.19	3.812	0.169
LP28911	rs13702	19824492	CC/CT/TT	219/382/153	0.459	66.96/66.83/66.59	21.85/22.12/20.93	-0.080	0.881
LP29023	rs17091815	19824604	AA/AT/TT	613/121/2	0.084	67.03/64.29/55.89	22.18/20.39/34.4	-1.388	0.165
LP29047	rs78359368	19824628	GG/GT	737/9	0.007	66.51/66.19	21.87/19.97	-0.048	0.989
LP29098	rs187374932	19824679	TC/TT	7/755	0.005	67.52/66.75	22.4/21.84	0.424	0.914
LP29126	rs147116359	19824707	AA/GA/GG	1/15/717	0.011	31.31/74.06/66.45	NA/23.6/21.55	1.001	0.673
LP29168	rs79756214	19824749	TC/TT	23/721	0.016	67.89/66.44	22.65/21.85	0.725	0.741
LP29287	rs3916027	19824868	AA/AG/GG	134/345/256	0.413	67.61/66.58/66.25	21.2/22.13/21.96	0.318	0.554
LP29487	rs4921683	19825068	AA/AT/TT	4/145/593	0.102	71.16/67.87/66.23	37.25/21.03/21.89	0.856	0.345
LP29543	rs76707496	19825124	AA/GA/GG	6/123/619	0.090	55.44/65.19/66.92	20.28/21.75/21.85	-1.191	0.202
LP29547	rs4921684	19825128	CC/TC/TT	644/120/1	0.079	66.67/66.81/79.39	22.19/19.82/NA	0.246	0.807

W: Allele in the referecne sequence (NC_00008.10).; D: Deleted base/bases; I: Inserted base/bases

[a] db build 137

Table A2.9. Association results of ApoA1 levels with 125 *LPL* SNPs in African blacks (n=788)

***LPL* variant**	**RefSNP ID^a**	**Chr. Position (hg19)**	**Genotypes**	**GT Counts**	**MAF**	**Adjusted Mean of plasma ApoA1**	**Standard Deviation**	**Beta**	***P***
rs147018794	rs147018794	19795467	GG/GT/TT	581/147/10	0.112	136.34/137.76/140.71	26.35/31.78/28.92	0.466	0.529
LP208	rs1470186	19795581	CC/CT/TT	42/246/442	0.225	136.34/138.06/135.87	29.14/30.25/25.88	0.365	0.513
LP428	rs73667465	19796009	AA/AG/GG	90/284/357	0.314	135.22/138.61/135.59	30.19/29.72/25.53	0.213	0.664
LP1090	rs1800590	19796671	GG/GT/TT	171/344/215	0.468	135.92/137.57/136.53	30.73/27.91/25.16	-0.120	0.798
LP1107	rs75890454	19796688	TA/TT	30/714	0.020	129.67/137.12	30.47/27.6	-2.536	0.135
LP1155	Novel	19796736	AA/TA	745/1	0.001	136.92/84.1	27.65/NA	-18.030	0.048
LP1200_1201ins2	rs34513350	19796781	II/WI/WW	1/40/697	0.029	154.95/137.73/136.83	NA/31.24/27.57	0.514	0.716
LP1264	Novel	19796845	GA/GG	12/749	0.008	137.54/136.79	30.21/27.66	0.227	0.932
LP1300	Novel	19796881	CC/CG	739/8	0.005	136.97/124.61	27.62/31.56	-4.177	0.197
LP1488	rs200412008	19797069	CC/CT	702/45	0.029	136.42/143.36	27.63/27.83	2.293	0.101
LP1498	rs141390463	19797079	AA/GA/GG	5/51/675	0.041	120.98/136.84/137.14	25.2/29.27/27.72	-0.871	0.439
LP2335	rs3779787	19797916	GG/GT	703/34	0.023	136.65/139.06	27.86/25.48	0.844	0.599
LP2758	rs146786419	19798339	CC/TC/TT	678/56/1	0.039	136.66/140.58/195.88	27.39/28.52/NA	1.846	0.128
LP2830	rs185670596	19798411	GC/GG	33/713	0.022	143.18/136.54	26.44/27.73	2.225	0.171
LP3725	rs115668974	19799306	CC/CT/TT	680/52/5	0.042	136.36/142.08/132.65	27.71/25.36/26.17	1.204	0.278
LP3964	rs17410577	19799545	CC/GC/GG	14/153/588	0.120	135.87/139.16/136.15	20.23/26.03/28.28	0.728	0.304
LP5531	rs1031045	19801112	AA/AG/GG	163/339/233	0.451	138.32/136.64/136.95	31.41/27.26/24.79	0.151	0.741
LP5949	rs112127208	19801530	GG/TG/TT	1/35/731	0.025	89.08/139.4/136.62	NA/25.9/27.79	0.016	0.991
LP6554	rs56043715	19802135	AA/GA/GG	350/305/74	0.307	136.02/137.8/136.37	25.37/29.29/30.62	0.207	0.683
LP6762	rs61274012	19802343	CC/CT/TT	1/43/699	0.030	169.86/141.14/136.47	NA/24.28/27.89	1.933	0.158
LP7130	rs28615996	19802711	CC/TC/TT	84/326/328	0.333	137.27/137.78/135.83	30.28/29.4/25.09	0.329	0.510
LP7313	rs28645722	19802894	AA/GA/GG	67/282/383	0.281	138.18/137.06/135.92	30.41/29.52/25.47	0.330	0.518
LP7503	rs6999612	19803084	AA/AG/GG	393/304/66	0.284	135.83/137.31/138.72	25.35/30.02/30.78	0.433	0.397
LP7556	rs59811201	19803137	CC/CT/TT	19/209/510	0.166	140.22/138.18/136.47	34.97/31.08/25.89	0.512	0.423
LP7907	rs115064749	19803488	AA/AG/GG	698/43/1	0.030	136.73/139.94/154.86	27.55/31.91/NA	1.181	0.390
LP8441_8442del2	rs112943460	19804022	DD/WD/WW	1/41/694	0.029	155.08/135.56/136.69	NA/29.02/27.46	-0.068	0.961
LP8766	rs181367025	19804347	CT/TT	19/725	0.013	130.98/136.96	34.77/27.42	-2.129	0.313
LP9015	rs28445964	19804596	AA/GA/GG	420/262/52	0.247	136.34/137.22/138.59	25.57/30.21/31.87	0.281	0.601
LP9232	rs145257746	19804813	AA/AC/CC	653/73/2	0.052	137.12/133.77/147.34	27.09/34.06/40.73	-0.931	0.386
LP9499	rs138110428	19805080	GA/GG	11/741	0.007	140.54/136.63	29.88/27.84	1.278	0.646
LP10100del1	Novel	19805681	WD/WW	34/711	0.022	142.37/136.41	25.21/27.84	1.999	0.212
LP10127	rs1801177	19805708	AA/AG/GG	3/70/686	0.050	181.91/135.18/136.8	53.75/26.6/27.69	0.657	0.536
LP10170	rs148201569	19805751	CC/CG	743/3	0.003	136.87/102.65	27.56/25.18	-11.619	0.027
LP10234	rs11542065	19805815	GC/GG	27/721	0.018	133.24/136.86	32.11/27.71	-1.285	0.475
LP10348	rs59054859	19805929	AA/AG/GG	571/153/8	0.118	136.95/136.53/120.88	27.33/28.56/28.09	-0.654	0.384
LP10632	Novel	19806213	CC/CT	736/13	0.008	136.85/132.77	27.55/36.21	-1.502	0.556
LP10800	rs6991305	19806381	AA/AG/GG	1/66/678	0.045	196.03/137.12/136.65	NA/29.33/27.46	0.688	0.545
LP11050	rs7016529	19806631	CC/CT/TT	70/306/371	0.295	138.71/137.64/135.79	30.54/30.22/24.88	0.481	0.345
LP11090	rs8176337	19806671	CC/CG/GG	81/307/361	0.313	132.84/137.36/137.47	24/26.81/29.36	-0.482	0.333
LP11895	rs189417962	19807476	TA/TT	11/755	0.007	140.58/136.59	29.88/27.74	1.304	0.639
LP12449	rs74304285	19808030	AA/GA/GG	2/79/652	0.056	144.94/141.2/136.04	33.3/25.68/28.22	1.724	0.099
LP13102	rs79760154	19808683	AA/CA/CC	611/126/5	0.091	137.41/135.41/134.07	26.74/31.56/26.62	-0.710	0.389
LP13443	rs115589061	19809024	CC/GC	713/34	0.023	136.83/136.05	27.81/22.8	-0.192	0.904
LP13691_13693del3	Novel	19809272	WD/WW	2/697	0.001	116.14/136.88	8.7/27.53	-6.743	0.292
LP13854	rs1121923	19809435	AA/GA/GG	12/140/599	0.111	132.07/137.23/136.8	27.62/29.87/27.03	-0.153	0.835
LP14114	rs73667472	19809695	AA/AG/GG	483/248/33	0.203	136.34/137.94/132.91	26.01/30.15/33.3	0.017	0.977
LP14241	rs75026342	19809822	CC/CT/TT	597/136/13	0.109	137.21/135.79/127.23	28.47/23.85/30.62	-0.788	0.285
LP15060del2	Novel	19810641	WD/WW	34/723	0.022	143.62/136.48	22.29/27.93	2.426	0.129
LP15206	rs343	19810787	AA/CA/CC	1/42/675	0.031	112.48/134.41/137.13	NA/22.87/28.05	-1.113	0.423
LP15245	rs248	19810826	GA/GG	50/713	0.034	141.46/136.52	30.13/27.41	1.601	0.229
LP15266	rs116678290	19810847	TC/TT	9/727	0.006	144.45/136.64	27.75/27.58	2.592	0.394
LP15579	rs251	19811160	CC/TC/TT	24/237/475	0.192	145.95/136.64/136.46	31.68/29.07/26.99	0.547	0.372
LP15650_15651Ins1	rs252	19811234	DD/WD/WW	612/133/4	0.093	137.27/134.2/139.49	28.15/25.53/34.44	-0.832	0.313
LP16320	rs255	19811901	CC/TC/TT	49/257/424	0.244	140.97/136.82/136.82	29.54/28.58/26.99	0.344	0.527
LP16363	rs80143795	19811944	AA/AG/GG	586/142/14	0.115	137.21/135.32/135.61	28.64/24.4/24.17	-0.460	0.526
LP16647	rs257	19812228	AA/CA/CC	697/44/4	0.034	136.87/139.47/121.5	27.8/24.74/29.58	-0.048	0.968
LP16671	rs258	19812252	CC/CG/GG	694/51/1	0.035	137.13/132.01/115.08	27.78/25.71/NA	-1.827	0.151
LP16856	rs259	19812437	AA/AT	679/81	0.053	136.18/140.82	27.92/24.63	1.571	0.141
LP16928	rs260	19812509	CC/CG	627/112	0.076	136.39/137.8	27.3/29	0.445	0.632
LP17039	rs261	19812620	AA/AG/GG	479/214/34	0.195	136.65/137.72/135.42	28.24/27.58/24.52	0.122	0.837
LP17231	rs263	19812812	CC/TC/TT	309/322/101	0.359	136.72/137.99/135.1	26.98/28.3/28.86	-0.109	0.823
LP1771	rs266	19813299	AA/AG/GG	508/204/24	0.170	137.02/135.93/142.65	26.71/29.59/33.47	0.072	0.908
LP17993	rs144466625	19813574	GA/GG	2/744	0.001	158.41/136.59	31.18/27.53	7.145	0.265
rs59184895	rs5918489518029	19813610	CC/CT/TT	3/72/665	0.052	166.03/138.92/136.27	23.33/25.09/27.91	1.500	0.151
LP18086	rs269	19813667	GG/GT/TT	175/370/208	0.479	137.46/136.04/138	28.23/28.1/26.1	-0.131	0.777

Table A2.9. Continued

LPL variant	RefSNP ID[a]	Chr. Position (hg19)	Genotypes	GT Counts	MAF	Adjusted Mean of plasma ApoA1	Standard Deviation	Beta	*P*
LP18095	rs270	19813676	AA/CA/CC	5/93/650	0.069	136.19/141.34/136.18	25.46/24.47/28.08	1.442	0.115
LP18395ins1	rs58935878	19813976	II/WI/WW	1/62/679	0.042	112.57/141.65/136.44	NA/28.75/27.67	1.360	0.247
LP18708	rs276	19814289	CC/CT/TT	29/225/487	0.190	135.47/137.81/136.27	30.27/29.67/26.42	0.215	0.718
LP18822	rs277	19814403	CC/TC/TT	12/138/588	0.110	140.81/139.75/135.96	29.02/28.25/27.65	1.125	0.131
LP19115	rs279	19814696	CC/GC/GG	530/187/15	0.150	136.18/137.92/141.47	28/26.81/29.96	0.670	0.322
LP19301	rs280	19814882	AA/GA/GG	3/80/661	0.058	141.57/135.97/137.02	22.03/26.66/27.77	-0.177	0.860
LP19407	rs17091775	19814988	AA/GA/GG	3/76/657	0.056	141.58/136.6/137.03	22.03/27.11/27.9	0.001	0.999
LP19442	rs282	19815023	AA/AT/TT	212/343/179	0.477	136.63/138.05/135.01	26.35/27.53/29.84	-0.266	0.566
LP20188	rs290	19815769	AA/GA/GG	17/159/497	0.145	128.53/138.28/136.84	27.14/27.82/27.52	-0.153	0.826
LP20657	rs295	19816238	AA/CA/CC	289/335/123	0.390	133.86/138.53/138.4	28.32/27.18/26.93	0.922	0.050
LP20670	rs145585712	19816251	GA/GG	24/722	0.016	134.9/136.76	39.62/27.27	-0.860	0.649
LP21136	rs73601683	19816717	GA/GG	18/729	0.012	143.16/136.66	28.51/27.71	2.152	0.323
LP21299	rs299	19816880	CC/CT/TT	733/8/1	0.007	136.39/162.29/167.51	27.53/37.72/NA	7.236	0.006
LP21306	rs300	19816887	AA/GA	721/16	0.011	136.7/137.69	27.61/26.29	0.361	0.875
LP21353	rs301	19816934	CC/TC/TT	62/306/381	0.288	139.71/139/134.65	26.7/28.04/27.74	1.103	0.035
LP22445	rs313	19818026	AA/AG/GG	529/182/17	0.150	136.64/138.45/128.62	27.82/27.8/26.49	0.001	0.999
LP22461	rs314	19818042	AA/GA/GG	420/242/58	0.248	137.1/137.33/136.08	28.39/26.39/27.44	-0.051	0.923
LP22774	rs77434393	19818355	CC/CT	728/37	0.024	136.2/144.55	27.53/30.23	2.717	0.076
LP22855	rs316	19818436	AA/CA/CC	39/258/449	0.225	141.98/139.18/135	27.32/27.19/28.01	1.292	0.022
LP22970	rs5934	19818551	GA/GG	49/713	0.033	141.43/136.28	22.21/28.06	1.792	0.184
LP23388	rs318	19818969	CC/CG/GG	553/173/15	0.139	137.62/134.79/125	26.84/29.38/31.41	-1.324	0.052
LP23395	rs319	19818976	AA/CA/CC	625/111/5	0.082	135.82/140.61/149.71	27.57/27.56/37.97	1.692	0.050
LP23605	rs321	19819186	GC/GG	13/732	0.009	132.74/136.84	30.17/27.61	-1.412	0.581
LP23747	rs325	19819328	CC/CT/TT	3/60/681	0.043	118.91/143.66/136.19	9.34/28.74/27.53	1.557	0.165
LP23858	rs326	19819439	AA/GA/GG	111/381/262	0.398	137.65/136.17/136.31	28.35/26.88/28.53	0.172	0.725
LP24064	rs149089920	19819645	AG/GG	2/747	0.001	139.75/136.81	27.86/27.66	1.045	0.871
rs328	rs328	19819724	CC/GC/GG	693/59/3	0.042	135.97/142.28/118.47	27.32/28.11/9.34	1.227	0.273
LP24505	rs329	19820086	AA/GA/GG	571/114/8	0.097	137.74/133.97/150.27	26.87/32.13/28.41	-0.537	0.518
LP24815	rs330	19820396	AA/AG/GG	3/121/620	0.085	140.67/142.1/135.61	43.04/26.25/27.88	2.031	0.019
LP24829	rs138285812	19820410	GA/GG	37/705	0.025	128.47/137.23	27.19/27.76	-2.894	0.060
LP24852	rs12679834	19820433	CC/TC/TT	5/78/670	0.058	136.61/144.29/135.81	30.32/30.04/27.45	2.207	0.024
LP24899	rs76423146	19820480	CC/TC/TT	535/182/27	0.157	136.99/136.6/133.9	27.56/28.23/27.68	-0.292	0.639
LP25380	rs28599962	19820961	GG/GT	726/31	0.021	136.67/138.92	27.55/33.28	0.671	0.690
LP25579	Novel	19821160	AA/AG	738/8	0.005	136.87/131.78	27.59/27.62	-1.656	0.607
LP25886del1	rs28716400	19821467	DD/WD/WW	18/186/532	0.152	132.7/138.76/136.52	24.91/27.38/27.93	0.318	0.630
LP26460	rs75946927	19822041	GG/TG/TT	6/115/629	0.087	141.15/134.47/136.94	24.26/26.04/28.09	-0.510	0.544
LP27033del1	rs147900112	19822614	DD/WD/WW	21/192/528	0.157	131.36/137.7/136.24	25.81/27.29/27.8	0.043	0.946
LP27050	rs114236375	19822631	GT/TT	18/725	0.012	153.31/136.35	33.5/27.44	5.479	0.012
LP27269	rs7818177	19822850	GA/GG	23/713	0.015	141.72/136.47	33.09/27.71	1.683	0.388
LP27629	Novel	19823210	CC/GC	744/2	0.001	136.84/147.38	27.71/25.67	3.559	0.581
LP27695	Novel	19823276	GG/GT	740/1	0.001	136.86/110.66	27.89/NA	-8.610	0.349
LP27706	Novel	19823287	GG/GT	764/2	0.001	136.74/105.44	27.69/26.23	-10.509	0.103
LP27928	rs187587525	19823509	GA/GG	5/740	0.003	144.66/136.7	34.38/27.56	2.587	0.525
LP27969	Novel	19823550	AA/AG	743/2	0.001	136.84/147.4	27.67/25.67	3.566	0.579
LP28036	rs11570892	19823617	AA/AG/GG	421/265/43	0.240	135.33/138.59/138.8	27.71/27.09/30.29	0.825	0.137
LP28067	rs3208305	19823648	AA/TA/TT	228/375/146	0.443	137.78/136.24/136.72	28.94/26.77/28.6	-0.204	0.669
LP28382	rs1059507	19823963	CC/CT/TT	596/143/5	0.103	135.91/139.84/162.97	28.08/24.74/32.41	1.770	0.025
LP28490	rs3200218	19824071	AA/GA/GG	608/127/5	0.093	136.16/139.22/152.57	27.6/28.02/35.82	1.252	0.130
LP28531	rs139240067	19824112	GA/GG	19/721	0.013	136.86/136.76	26.6/27.68	0.056	0.979
LP28669	rs184363931	19824250	CC/TC	730/14	0.009	136.75/135.86	27.53/37.36	-0.457	0.853
LP28911	rs13702	19824492	CC/CT/TT	216/381/157	0.459	138.25/136.51/135.93	28.72/27.23/27.3	-0.386	0.416
LP29023	rs17091815	19824604	AA/AT/TT	613/120/2	0.084	137.29/134.83/150.77	27.94/27.77/18.38	-0.605	0.496
LP29047	rs78359368	19824628	GG/GT	736/10	0.007	137.05/123.79	27.63/30.43	-4.465	0.123
LP29098	rs187374932	19824679	TC/TT	8/754	0.005	125.07/136.86	32.47/27.68	-3.984	0.220
LP29126	rs147116359	19824707	AA/GA/GG	1/15/717	0.011	179.04/147.22/136.51	NA/18.82/27.7	4.319	0.040
LP29168	rs79756214	19824749	TC/TT	23/721	0.016	128.17/137.24	27.99/27.6	-3.037	0.115
LP29287	rs3916027	19824868	AA/AG/GG	132/345/258	0.413	140.33/136.79/135.15	28.55/26.35/28.84	0.814	0.085
LP29487	rs4921683	19825068	AA/AT/TT	4/144/594	0.102	171.12/140.09/135.9	30.96/24.74/28.12	1.911	0.017
LP29543	rs76707496	19825124	AA/GA/GG	6/120/622	0.090	131.9/135.96/136.8	32.97/26.41/27.98	-0.358	0.667
LP29547	rs4921684	19825128	CC/TC/TT	644/120/1	0.079	135.94/140.6/216.67	28.14/24.08/NA	1.983	0.026

W: Allele in the referecne sequence (NC_00008.10); D: Deleted base/bases; I: Inserted base/bases

[a] db build 137

Table A2.10. ***LPL*** **4-SNP sliding window haplotype association results for HDL-C, TG in African blacks (n=788)**

				HDL-C			TG				
Win.	**Window SNP**	**Location**	**MAF**	**β**	***P****	**hap_*P*****	**β**	***P****	**hap_*P*****	**β**	***P****
1	rs1470187	5' flanking	0.112	-0.213	0.481	0.977	-0.043	0.792	0.308	0.005	0.628
1	rs1470186	5' flanking	0.225	-0.107	0.637	NA	0.173	0.152	NA	0.004	0.601
1	rs73667465	5' flanking	0.314	-0.13	0.512	NA	0.036	0.73	NA	0.001	0.848
1	rs1800590	Exon 1	0.468	-0.027	0.888	NA	0.042	0.675	NA	0.002	0.753
2	rs1470186	5' flanking	0.225	-0.107	0.637	0.985	0.173	0.152	0.45	0.004	0.601
2	rs73667465	5' flanking	0.314	-0.13	0.512	NA	0.036	0.73	NA	0.001	0.848
2	rs1800590	Exon 1-UTR	0.468	-0.027	0.888	NA	0.042	0.675	NA	0.002	0.753
2	rs75890454	Exon 1-UTR	0.02	-0.185	0.794	NA	-0.24	0.531	NA	-0.039	0.139
3	rs73667465	5' flanking	0.314	-0.13	0.512	0.86	0.036	0.73	0.898	0.001	0.848
3	rs1800590	Exon 1	0.468	-0.027	0.888	NA	0.042	0.675	NA	0.002	0.753
3	rs75890454	Exon 1-UTR	0.02	-0.185	0.794	NA	-0.24	0.531	NA	-0.039	0.139
3	LP1155	Exon 1-UTR	0.001	-5.631	0.125	NA	-2.537	0.195	NA	0.002	0.991
4	rs1800590	Exon 1	0.468	-0.027	0.888	0.646	0.042	0.675	0.475	0.002	0.753
4	rs75890454	Exon 1-UTR	0.02	-0.185	0.794	NA	-0.24	0.531	NA	-0.039	0.139
4	LP1155	Exon 1-UTR	0.001	-5.631	0.125	NA	-2.537	0.195	NA	0.002	0.991
4	rs34513350	Exon 1-UTR	0.029	-0.192	0.739	NA	-0.18	0.553	NA	0.006	0.778
5	rs75890454	Exon 1-UTR	0.02	-0.185	0.794	0.686	-0.24	0.531	0.65	-0.039	0.139
5	LP1155	Exon 1-UTR	0.001	-5.631	0.125	NA	-2.537	0.195	NA	0.002	0.991
5	rs34513350	Exon 1-UTR	0.029	-0.192	0.739	NA	-0.18	0.553	NA	0.006	0.778
5	LP1264	Exon 1-UTR	0.008	1.33	0.231	NA	-0.279	0.637	NA	0.032	0.431
6	LP1155	Exon 1-UTR	0.001	-5.631	0.125	0.62	-2.537	0.195	0.014	0.002	0.991
6	rs34513350	Exon 1-UTR	0.029	-0.192	0.739	NA	-0.18	0.553	NA	0.006	0.778
6	LP1264	Exon 1-UTR	0.008	1.33	0.231	NA	-0.279	0.637	NA	0.032	0.431
6	LP1300	Exon 1-UTR	0.005	-2.981	0.022	NA	-2.39	0.001	NA	-0.135	0.006
7	rs34513350	Exon 1-UTR	0.029	-0.192	0.739	0.877	-0.18	0.553	0.032	0.006	0.778
7	LP1264	Exon 1-UTR	0.008	1.33	0.231	NA	-0.279	0.637	NA	0.032	0.431
7	LP1300	Exon 1-UTR	0.005	-2.981	0.022	NA	-2.39	0.001	NA	-0.135	0.006
7	rs200412008	Exon 1-UTR	0.029	0.225	0.69	NA	0.335	0.268	NA	0.008	0.692
8	LP1264	Exon 1-UTR	0.008	1.33	0.231	0.413	-0.279	0.637	0.043	0.032	0.431
8	LP1300	Exon 1-UTR	0.005	-2.981	0.022	NA	-2.39	0.001	NA	-0.135	0.006
8	rs200412008	Exon 1-UTR	0.029	0.225	0.69	NA	0.335	0.268	NA	0.008	0.692
8	rs141390463	Intron 1	0.041	-0.533	0.244	NA	-0.097	0.69	NA	0.034	0.046
9	LP1300	Exon 1-UTR	0.005	-2.981	0.022	0.224	-2.39	0.001	0.001	-0.135	0.006
9	rs200412008	Exon 1-UTR	0.029	0.225	0.69	NA	0.335	0.268	NA	0.008	0.692
9	rs141390463	Intron 1	0.041	-0.533	0.244	NA	-0.097	0.69	NA	0.034	0.046
9	rs3779787	Intron 1	0.023	0.431	0.51	NA	0.596	0.089	NA	-0.022	0.372
10	rs200412008	Exon 1-UTR	0.029	0.225	0.69	0.106	0.335	0.268	0.32	0.008	0.692
10	rs141390463	Intron 1	0.041	-0.533	0.244	NA	-0.097	0.69	NA	0.034	0.046
10	rs3779787	Intron 1	0.023	0.431	0.51	NA	0.596	0.089	NA	-0.022	0.372
10	rs146786419	Intron 1	0.039	1.075	0.028	NA	0.115	0.664	NA	-0.049	0.009
11	rs141390463	Intron 1	0.041	-0.533	0.244	0.102	-0.097	0.69	0.445	0.034	0.046
11	rs3779787	Intron 1	0.023	0.431	0.51	NA	0.596	0.089	NA	-0.022	0.372
11	rs146786419	Intron 1	0.039	1.075	0.028	NA	0.115	0.664	NA	-0.049	0.009
11	rs185670596	Intron 1	0.022	0.375	0.578	NA	-0.173	0.631	NA	-0.013	0.599
12	rs3779787	Intron 1	0.023	0.431	0.51	0.196	0.596	0.089	0.645	-0.022	0.372
12	rs146786419	Intron 1	0.039	1.075	0.028	NA	0.115	0.664	NA	-0.049	0.009
12	rs185670596	Intron 1	0.022	0.375	0.578	NA	-0.173	0.631	NA	-0.013	0.599
12	rs115668974	Intron 1	0.042	0.281	0.54	NA	-0.071	0.769	NA	0.003	0.858
13	rs146786419	Intron 1	0.039	1.075	0.028	0.241	0.115	0.664	0.984	-0.049	0.009
13	rs185670596	Intron 1	0.022	0.375	0.578	NA	-0.173	0.631	NA	-0.013	0.599
13	rs115668974	Intron 1	0.042	0.281	0.54	NA	-0.071	0.769	NA	0.003	0.858
13	rs17410577	Intron 1	0.12	0.036	0.899	NA	-0.04	0.793	NA	-0.004	0.707
14	rs185670596	Intron 1	0.022	0.375	0.578	0.907	-0.173	0.631	0.583	-0.013	0.599
14	rs115668974	Intron 1	0.042	0.281	0.54	NA	-0.071	0.769	NA	0.003	0.858
14	rs17410577	Intron 1	0.12	0.036	0.899	NA	-0.04	0.793	NA	-0.004	0.707
14	rs1031045	Intron 1	0.451	0.095	0.608	NA	0.065	0.518	NA	0.006	0.373
15	rs115668974	Intron 1	0.042	0.281	0.54	0.778	-0.071	0.769	0.305	0.003	0.858
15	rs17410577	Intron 1	0.12	0.036	0.899	NA	-0.04	0.793	NA	-0.004	0.707
15	rs1031045	Intron 1	0.451	0.095	0.608	NA	0.065	0.518	NA	0.006	0.373
15	rs112127208	Intron 1	0.025	-0.015	0.98	NA	0.484	0.135	NA	-0.01	0.672

Table A2.10. Continued

				HDL-C			TG				
Win.	**Window SNP**	**Location**	**MAF**	**β**	***P****	**hap_*P*****	**β**	***P****	**hap_*P*****	**β**	***P****
16	rs17410577	Intron 1	0.12	0.036	0.899	0.674	-0.04	0.793	0.572	-0.004	0.707
16	rs1031045	Intron 1	0.451	0.095	0.608	NA	0.065	0.518	NA	0.006	0.373
16	rs112127208	Intron 1	0.025	-0.015	0.98	NA	0.484	0.135	NA	-0.01	0.672
16	rs56043715	Intron 1	0.307	-0.105	0.611	NA	-0.014	0.9	NA	0.007	0.388
17	rs1031045	Intron 1	0.451	0.095	0.608	0.727	0.065	0.518	0.423	0.006	0.373
17	rs112127208	Intron 1	0.025	-0.015	0.98	NA	0.484	0.135	NA	-0.01	0.672
17	rs56043715	Intron 1	0.307	-0.105	0.611	NA	-0.014	0.9	NA	0.007	0.388
17	rs61274012	Intron 1	0.03	0.08	0.886	NA	0.325	0.269	NA	-0.013	0.517
18	rs112127208	Intron 1	0.025	-0.015	0.98	0.99	0.484	0.135	0.46	-0.01	0.672
18	rs56043715	Intron 1	0.307	-0.105	0.611	NA	-0.014	0.9	NA	0.007	0.388
18	rs61274012	Intron 1	0.03	0.08	0.886	NA	0.325	0.269	NA	-0.013	0.517
18	rs28615996	Intron 1	0.333	-0.087	0.666	NA	-0.01	0.924	NA	0.01	0.2
19	rs56043715	Intron 1	0.307	-0.105	0.611	0.41	-0.014	0.9	0.379	0.007	0.388
19	rs61274012	Intron 1	0.03	0.08	0.886	NA	0.325	0.269	NA	-0.013	0.517
19	rs28615996	Intron 1	0.333	-0.087	0.666	NA	-0.01	0.924	NA	0.01	0.2
19	rs28645722	Intron 1	0.281	-0.042	0.841	NA	0.01	0.925	NA	0.008	0.318
20	rs61274012	Intron 1	0.03	0.08	0.886	0.928	0.325	0.269	0.57	-0.013	0.517
20	rs28615996	Intron 1	0.333	-0.087	0.666	NA	-0.01	0.924	NA	0.01	0.2
20	rs28645722	Intron 1	0.281	-0.042	0.841	NA	0.01	0.925	NA	0.008	0.318
20	rs6999612	Intron 1	0.284	0.032	0.877	NA	-0.014	0.899	NA	0.004	0.609
21	rs28615996	Intron 1	0.333	-0.087	0.666	0.642	-0.01	0.924	0.665	0.01	0.2
21	rs28645722	Intron 1	0.281	-0.042	0.841	NA	0.01	0.925	NA	0.008	0.318
21	rs6999612	Intron 1	0.284	0.032	0.877	NA	-0.014	0.899	NA	0.004	0.609
21	rs59811201	Intron 1	0.166	-0.266	0.304	NA	0.114	0.411	NA	0.015	0.132
22	rs28645722	Intron 1	0.281	-0.042	0.841	0.657	0.01	0.925	0.757	0.008	0.318
22	rs6999612	Intron 1	0.284	0.032	0.877	NA	-0.014	0.899	NA	0.004	0.609
22	rs59811201	Intron 1	0.166	-0.266	0.304	NA	0.114	0.411	NA	0.015	0.132
22	rs115064749	Intron 1	0.03	0.15	0.789	NA	-0.035	0.905	NA	0.005	0.818
23	rs6999612	Intron 1	0.284	0.032	0.877	0.279	-0.014	0.899	0.92	0.004	0.609
23	rs59811201	Intron 1	0.166	-0.266	0.304	NA	0.114	0.411	NA	0.015	0.132
23	rs115064749	Intron 1	0.03	0.15	0.789	NA	-0.035	0.905	NA	0.005	0.818
23	rs112943460	Intron 1	0.029	-0.213	0.709	NA	-0.136	0.649	NA	0.005	0.805
24	rs59811201	Intron 1	0.166	-0.266	0.304	0.376	0.114	0.411	0.836	0.015	0.132
24	rs115064749	Intron 1	0.03	0.15	0.789	NA	-0.035	0.905	NA	0.005	0.818
24	rs112943460	Intron 1	0.029	-0.213	0.709	NA	-0.136	0.649	NA	0.005	0.805
24	rs181367025	Intron 1	0.013	-0.814	0.352	NA	0.144	0.758	NA	0.007	0.831
25	rs115064749	Intron 1	0.03	0.15	0.789	0.766	-0.035	0.905	0.906	0.005	0.818
25	rs112943460	Intron 1	0.029	-0.213	0.709	NA	-0.136	0.649	NA	0.005	0.805
25	rs181367025	Intron 1	0.013	-0.814	0.352	NA	0.144	0.758	NA	0.007	0.831
25	rs28445964	Intron 1	0.247	-0.118	0.587	NA	0.071	0.545	NA	0.008	0.34
26	rs112943460	Intron 1	0.029	-0.213	0.709	0.921	-0.136	0.649	0.966	0.005	0.805
26	rs181367025	Intron 1	0.013	-0.814	0.352	NA	0.144	0.758	NA	0.007	0.831
26	rs28445964	Intron 1	0.247	-0.118	0.587	NA	0.071	0.545	NA	0.008	0.34
26	rs145257746	Intron 1	0.052	-0.265	0.545	NA	0.077	0.743	NA	0.005	0.737
27	rs181367025	Intron 1	0.013	-0.814	0.352	0.678	0.144	0.758	0.971	0.007	0.831
27	rs28445964	Intron 1	0.247	-0.118	0.587	NA	0.071	0.545	NA	0.008	0.34
27	rs145257746	Intron 1	0.052	-0.265	0.545	NA	0.077	0.743	NA	0.005	0.737
27	rs138110428	Intron 1	0.007	1.319	0.26	NA	-0.263	0.671	NA	0.048	0.252
28	rs28445964	Intron 1	0.247	-0.118	0.587	0.514	0.071	0.545	0.983	0.008	0.34
28	rs145257746	Intron 1	0.052	-0.265	0.545	NA	0.077	0.743	NA	0.005	0.737
28	rs138110428	Intron 1	0.007	1.319	0.26	NA	-0.263	0.671	NA	0.048	0.252
28	LP10100delT	Intron 1	0.022	0.926	0.156	NA	-0.021	0.952	NA	0.02	0.413
29	rs145257746	Intron 1	0.052	-0.265	0.545	0.442	0.077	0.743	0.648	0.005	0.737
29	rs138110428	Intron 1	0.007	1.319	0.26	NA	-0.263	0.671	NA	0.048	0.252
29	LP10100delT	Intron 1	0.022	0.926	0.156	NA	-0.021	0.952	NA	0.02	0.413
29	rs1801177	Exon 2	0.05	-0.066	0.877	NA	0.31	0.171	NA	0.023	0.153
30	rs138110428	Intron 1	0.007	1.319	0.26	0.608	-0.263	0.671	0.079	0.048	0.252
30	LP10100delT	Intron 1	0.022	0.926	0.156	NA	-0.021	0.952	NA	0.02	0.413
30	rs1801177	Exon 2	0.05	-0.066	0.877	NA	0.31	0.171	NA	0.023	0.153
30	rs148201569	Exon 2	0.003	-2.994	0.103	NA	-3.556	0	NA	-0.028	0.69
31	LP10100delT	Intron 1	0.022	0.926	0.156	0.142	-0.021	0.952	0.01	0.02	0.413
31	rs1801177	Exon 2	0.05	-0.066	0.877	NA	0.31	0.171	NA	0.023	0.153
31	rs148201569	Exon 2	0.003	-2.994	0.103	NA	-3.556	0	NA	-0.028	0.69
31	rs11542065	Exon 2	0.018	0.472	0.528	NA	-0.106	0.793	NA	-0.049	0.071

Table A2.10. Continued

				HDL-C			TG				
Win.	**Window SNP**	**Location**	**MAF**	**β**	***P****	**hap_*P*****	**β**	***P****	**hap_*P*****	**β**	***P****
32	rs1801177	Exon 2	0.05	-0.066	0.877	0.28	0.31	0.171	0.002	0.023	0.153
32	rs148201569	Exon 2	0.003	-2.994	0.103	NA	-3.556	0	NA	-0.028	0.69
32	rs11542065	Exon 2	0.018	0.472	0.528	NA	-0.106	0.793	NA	-0.049	0.071
32	rs59054859	Intron 2	0.118	0.327	0.281	NA	0.179	0.265	NA	0.006	0.62
33	rs148201569	Exon 2	0.003	-2.994	0.103	0.108	-3.556	0	0.209	-0.028	0.69
33	rs11542065	Exon 2	0.018	0.472	0.528	NA	-0.106	0.793	NA	-0.049	0.071
33	rs59054859	Intron 2	0.118	0.327	0.281	NA	0.179	0.265	NA	0.006	0.62
33	LP10632	Intron 2	0.008	-0.839	0.413	NA	-0.029	0.958	NA	-0.012	0.747
34	rs11542065	Exon 2	0.018	0.472	0.528	0.102	-0.106	0.793	0.843	-0.049	0.071
34	rs59054859	Intron 2	0.118	0.327	0.281	NA	0.179	0.265	NA	0.006	0.62
34	LP10632	Intron 2	0.008	-0.839	0.413	NA	-0.029	0.958	NA	-0.012	0.747
34	rs6991305	Intron 2	0.045	0.742	0.105	NA	-0.049	0.841	NA	-0.041	0.018
35	rs59054859	Intron 2	0.118	0.327	0.281	0.197	0.179	0.265	0.864	0.006	0.62
35	LP10632	Intron 2	0.008	-0.839	0.413	NA	-0.029	0.958	NA	-0.012	0.747
35	rs6991305	Intron 2	0.045	0.742	0.105	NA	-0.049	0.841	NA	-0.041	0.018
35	rs7016529	Intron 2	0.295	-0.057	0.785	NA	0.01	0.925	NA	0.007	0.392
36	LP10632	Intron 2	0.008	-0.839	0.413	0.237	-0.029	0.958	0.638	-0.012	0.747
36	rs6991305	Intron 2	0.045	0.742	0.105	NA	-0.049	0.841	NA	-0.041	0.018
36	rs7016529	Intron 2	0.295	-0.057	0.785	NA	0.01	0.925	NA	0.007	0.392
36	rs8176337	Intron 2	0.313	-0.088	0.663	NA	-0.162	0.13	NA	-0.01	0.177
37	rs6991305	Intron 2	0.045	0.742	0.105	0.355	-0.049	0.841	0.599	-0.041	0.018
37	rs7016529	Intron 2	0.295	-0.057	0.785	NA	0.01	0.925	NA	0.007	0.392
37	rs8176337	Intron 2	0.313	-0.088	0.663	NA	-0.162	0.13	NA	-0.01	0.177
37	rs189417962	Intron 2	0.007	1.325	0.256	NA	-0.263	0.672	NA	0.047	0.261
38	rs7016529	Intron 2	0.295	-0.057	0.785	0.889	0.01	0.925	0.259	0.007	0.392
38	rs8176337	Intron 2	0.313	-0.088	0.663	NA	-0.162	0.13	NA	-0.01	0.177
38	rs189417962	Intron 2	0.007	1.325	0.256	NA	-0.263	0.672	NA	0.047	0.261
38	rs74304285	Intron 2	0.056	0.232	0.586	NA	0.475	0.034	NA	-0.004	0.788
39	rs8176337	Intron 2	0.313	-0.088	0.663	0.53	-0.162	0.13	0.181	-0.01	0.177
39	rs189417962	Intron 2	0.007	1.325	0.256	NA	-0.263	0.672	NA	0.047	0.261
39	rs74304285	Intron 2	0.056	0.232	0.586	NA	0.475	0.034	NA	-0.004	0.788
39	rs79760154	Intron 2	0.091	-0.331	0.321	NA	-0.005	0.979	NA	0.009	0.482
40	rs189417962	Intron 2	0.007	1.325	0.256	0.134	-0.263	0.672	0.409	0.047	0.261
40	rs74304285	Intron 2	0.056	0.232	0.586	NA	0.475	0.034	NA	-0.004	0.788
40	rs79760154	Intron 2	0.091	-0.331	0.321	NA	-0.005	0.979	NA	0.009	0.482
40	rs115589061	Intron 2	0.023	-0.613	0.354	NA	-0.048	0.891	NA	-0.012	0.627
41	rs74304285	Intron 2	0.056	0.232	0.586	0.505	0.475	0.034	0.064	-0.004	0.788
41	rs79760154	Intron 2	0.091	-0.331	0.321	NA	-0.005	0.979	NA	0.009	0.482
41	rs115589061	Intron 2	0.023	-0.613	0.354	NA	-0.048	0.891	NA	-0.012	0.627
41	LP13691_13693delATC	Intron 2	0.001	-2.807	0.282	NA	-2.62	0.059	NA	-0.129	0.185
42	rs79760154	Intron 2	0.091	-0.331	0.321	0.532	-0.005	0.979	0.283	0.009	0.482
42	rs115589061	Intron 2	0.023	-0.613	0.354	NA	-0.048	0.891	NA	-0.012	0.627
42	LP13691_13693delATC	Intron 2	0.001	-2.807	0.282	NA	-2.62	0.059	NA	-0.129	0.185
42	rs1121923	Exon 3	0.111	-0.026	0.93	NA	-0.05	0.752	NA	0.006	0.562
43	rs115589061	Intron 2	0.023	-0.613	0.354	0.692	-0.048	0.891	0.065	-0.012	0.627
43	LP13691_13693delATC	Intron 2	0.001	-2.807	0.282	NA	-2.62	0.059	NA	-0.129	0.185
43	rs1121923	Intron 2	0.111	-0.026	0.93	NA	-0.05	0.752	NA	0.006	0.562
43	rs73667472	Intron 3	0.203	0.008	0.974	NA	0.046	0.713	NA	0.005	0.599
44	LP13691_13693delATC	Intron 2	0.001	-2.807	0.282	0.132	-2.62	0.059	0.364	-0.129	0.185
44	rs1121923	Intron 2	0.111	-0.026	0.93	NA	-0.05	0.752	NA	0.006	0.562
44	rs73667472	Intron 3	0.203	0.008	0.974	NA	0.046	0.713	NA	0.005	0.599
44	rs75026342	Intron 3	0.109	-0.404	0.17	NA	0.007	0.966	NA	0.014	0.213
45	rs1121923	Intron 2	0.111	-0.026	0.93	0.054	-0.05	0.752	0.966	0.006	0.562
45	rs73667472	Intron 3	0.203	0.008	0.974	NA	0.046	0.713	NA	0.005	0.599
45	rs75026342	Intron 3	0.109	-0.404	0.17	NA	0.007	0.966	NA	0.014	0.213
45	LP15060del	Intron 3	0.022	1.267	0.052	NA	0.045	0.896	NA	0.022	0.375
46	rs73667472	Intron 3	0.203	0.008	0.974	0.039	0.046	0.713	0.966	0.005	0.599
46	rs75026342	Intron 3	0.109	-0.404	0.17	NA	0.007	0.966	NA	0.014	0.213
46	LP15060del	Intron 3	0.022	1.267	0.052	NA	0.045	0.896	NA	0.022	0.375
46	rs343	Intron 3	0.031	-0.493	0.386	NA	0.1	0.742	NA	-0.015	0.465
47	rs75026342	Intron 3	0.109	-0.404	0.17	0.051	0.007	0.966	0.989	0.014	0.213
47	LP15060del	Intron 3	0.022	1.267	0.052	NA	0.045	0.896	NA	0.022	0.375
47	rs343	Intron 3	0.031	-0.493	0.386	NA	0.1	0.742	NA	-0.015	0.465
47	rs248	Exon 4	0.034	0.816	0.12	NA	0.11	0.697	NA	-0.006	0.782

Table A2.10. Continued

				HDL-C			TG				
Win.	**Window SNP**	**Location**	**MAF**	**β**	***P****	**hap_*P*****	**β**	***P****	**hap_*P*****	**β**	***P****
48	LP15060del	Intron 3	0.022	1.267	0.052	0.093	0.045	0.896	0.978	0.022	0.375
48	rs343	Intron 3	0.031	-0.493	0.386	NA	0.1	0.742	NA	-0.015	0.465
48	rs248	Exon 4	0.034	0.816	0.12	NA	0.11	0.697	NA	-0.006	0.782
48	rs116678290	Exon 4	0.006	0.473	0.702	NA	0.248	0.704	NA	0.01	0.823
49	rs343	Intron 3	0.031	-0.493	0.386	0.373	0.1	0.742	0.963	-0.015	0.465
49	rs248	Exon 4	0.034	0.816	0.12	NA	0.11	0.697	NA	-0.006	0.782
49	rs116678290	Exon 4	0.006	0.473	0.702	NA	0.248	0.704	NA	0.01	0.823
49	rs251	Intron 4	0.192	0.123	0.621	NA	-0.073	0.581	NA	0	0.987
50	rs248	Exon 4	0.034	0.816	0.12	0.441	0.11	0.697	0.045	-0.006	0.782
50	rs116678290	Exon 4	0.006	0.473	0.702	NA	0.248	0.704	NA	0.01	0.823
50	rs251	Intron 4	0.192	0.123	0.621	NA	-0.073	0.581	NA	0	0.987
50	rs252	Intron 4	0.093	0.03	0.929	NA	-0.494	0.005	NA	-0.013	0.281
51	rs116678290	Exon 4	0.006	0.473	0.702	0.821	0.248	0.704	0.046	0.01	0.823
51	rs251	Intron 4	0.192	0.123	0.621	NA	-0.073	0.581	NA	0	0.987
51	rs252	Intron 4	0.093	0.03	0.929	NA	-0.494	0.005	NA	-0.013	0.281
51	rs255	Intron 4	0.244	0.079	0.721	NA	0.115	0.332	NA	0.001	0.941
52	rs251	Intron 4	0.192	0.123	0.621	0.732	-0.073	0.581	0.067	0	0.987
52	rs252	Intron 4	0.093	0.03	0.929	NA	-0.494	0.005	NA	-0.013	0.281
52	rs255	Intron 4	0.244	0.079	0.721	NA	0.115	0.332	NA	0.001	0.941
52	rs80143795	Intron 4	0.115	-0.266	0.356	NA	-0.008	0.959	NA	0.011	0.314
53	rs252	Intron 4	0.093	0.03	0.929	0.565	-0.494	0.005	0.092	-0.013	0.281
53	rs255	Intron 4	0.244	0.079	0.721	NA	0.115	0.332	NA	0.001	0.941
53	rs80143795	Intron 4	0.115	-0.266	0.356	NA	-0.008	0.959	NA	0.011	0.314
53	rs257	Intron 4	0.034	-0.583	0.232	NA	0.068	0.792	NA	0.011	0.558
54	rs255	Intron 4	0.244	0.079	0.721	0.558	0.115	0.332	0.314	0.001	0.941
54	rs80143795	Intron 4	0.115	-0.266	0.356	NA	-0.008	0.959	NA	0.011	0.314
54	rs257	Intron 4	0.034	-0.583	0.232	NA	0.068	0.792	NA	0.011	0.558
54	rs258	Intron 4	0.035	0.138	0.792	NA	-0.581	0.037	NA	-0.004	0.841
55	rs80143795	Intron 4	0.115	-0.266	0.356	0.264	-0.008	0.959	0.488	0.011	0.314
55	rs257	Intron 4	0.034	-0.583	0.232	NA	0.068	0.792	NA	0.011	0.558
55	rs258	Intron 4	0.035	0.138	0.792	NA	-0.581	0.037	NA	-0.004	0.841
55	rs259	Intron 4	0.053	0.581	0.18	NA	-0.019	0.935	NA	0.001	0.973
56	rs257	Intron 4	0.034	-0.583	0.232	0.343	0.068	0.792	0.381	0.011	0.558
56	rs258	Intron 4	0.035	0.138	0.792	NA	-0.581	0.037	NA	-0.004	0.841
56	rs259	Intron 4	0.053	0.581	0.18	NA	-0.019	0.935	NA	0.001	0.973
56	rs260	Intron 4	0.076	0.061	0.872	NA	-0.155	0.44	NA	-0.013	0.349
57	rs258	Intron 4	0.035	0.138	0.792	0.734	-0.581	0.037	0.38	-0.004	0.841
57	rs259	Intron 4	0.053	0.581	0.18	NA	-0.019	0.935	NA	0.001	0.973
57	rs260	Intron 4	0.076	0.061	0.872	NA	-0.155	0.44	NA	-0.013	0.349
57	rs261	Intron 4	0.195	-0.149	0.527	NA	-0.054	0.667	NA	0	0.971
58	rs259	Intron 4	0.053	0.581	0.18	0.71	-0.019	0.935	0.981	0.001	0.973
58	rs260	Intron 4	0.076	0.061	0.872	NA	-0.155	0.44	NA	-0.013	0.349
58	rs261	Intron 4	0.195	-0.149	0.527	NA	-0.054	0.667	NA	0	0.971
58	rs263	Intron 4	0.359	0.178	0.358	NA	0.023	0.824	NA	-0.006	0.408
59	rs260	Intron 4	0.076	0.061	0.872	0.6	-0.155	0.44	0.851	-0.013	0.349
59	rs261	Intron 4	0.195	-0.149	0.527	NA	-0.054	0.667	NA	0	0.971
59	rs263	Intron 4	0.359	0.178	0.358	NA	0.023	0.824	NA	-0.006	0.408
59	rs266	Intron 4	0.17	-0.089	0.724	NA	-0.135	0.317	NA	-0.008	0.378
60	rs261	Intron 4	0.195	-0.149	0.527	0.702	-0.054	0.667	0.955	0	0.971
60	rs263	Intron 4	0.359	0.178	0.358	NA	0.023	0.824	NA	-0.006	0.408
60	rs266	Intron 4	0.17	-0.089	0.724	NA	-0.135	0.317	NA	-0.008	0.378
60	rs144466625	Exon 6	0.001	-2.608	0.314	NA	-0.251	0.857	NA	-0.044	0.749
61	rs263	Intron 4	0.359	0.178	0.358	0.617	0.023	0.824	0.889	-0.006	0.408
61	rs266	Intron 4	0.17	-0.089	0.724	NA	-0.135	0.317	NA	-0.008	0.378
61	rs144466625	Exon 6	0.001	-2.608	0.314	NA	-0.251	0.857	NA	-0.044	0.749
61	rs59184895	Intron 6	0.052	0.36	0.399	NA	0.017	0.94	NA	-0.005	0.772
62	rs266	Intron 4	0.17	-0.089	0.724	0.382	-0.135	0.317	0.821	-0.008	0.378
62	rs144466625	Exon 6	0.001	-2.608	0.314	NA	-0.251	0.857	NA	-0.044	0.749
62	rs59184895	Intron 6	0.052	0.36	0.399	NA	0.017	0.94	NA	-0.005	0.772
62	rs269	Intron 6	0.479	0.258	0.17	NA	0.038	0.702	NA	-0.006	0.423
63	rs144466625	Exon 6	0.001	-2.608	0.314	0.329	-0.251	0.857	0.979	-0.044	0.749
63	rs59184895	Intron 6	0.052	0.36	0.399	NA	0.017	0.94	NA	-0.005	0.772
63	rs269	Intron 6	0.479	0.258	0.17	NA	0.038	0.702	NA	-0.006	0.423
63	rs270	Intron 6	0.069	0.241	0.512	NA	0.074	0.705	NA	0.005	0.732

Table A2.10. Continued

				HDL-C			TG				
Win.	**Window SNP**	**Location**	**MAF**	**β**	***P****	**hap_*P*****	**β**	***P****	**hap_*P*****	**β**	***P****
64	rs59184895	Intron 6	0.052	0.36	0.399	0.465	0.017	0.94	0.846	-0.005	0.772
64	rs269	Intron 6	0.479	0.258	0.17	NA	0.038	0.702	NA	-0.006	0.423
64	rs270	Intron 6	0.069	0.241	0.512	NA	0.074	0.705	NA	0.005	0.732
64	rs58935878	Intron 6	0.042	0.137	0.779	NA	0.277	0.285	NA	0.002	0.901
65	rs269	Intron 6	0.479	0.258	0.17	0.461	0.038	0.702	0.779	-0.006	0.423
65	rs270	Intron 6	0.069	0.241	0.512	NA	0.074	0.705	NA	0.005	0.732
65	rs58935878	Intron 6	0.042	0.137	0.779	NA	0.277	0.285	NA	0.002	0.901
65	rs276	Intron 6	0.19	-0.391	0.103	NA	0.076	0.556	NA	0.012	0.184
66	rs270	Intron 6	0.069	0.241	0.512	0.736	0.074	0.705	0.25	0.005	0.732
66	rs58935878	Intron 6	0.042	0.137	0.779	NA	0.277	0.285	NA	0.002	0.901
66	rs276	Intron 6	0.19	-0.391	0.103	NA	0.076	0.556	NA	0.012	0.184
66	rs277	Intron 6	0.11	-0.191	0.527	NA	-0.144	0.365	NA	0.005	0.671
67	rs58935878	Intron 6	0.042	0.137	0.779	0.204	0.277	0.285	0.424	0.002	0.901
67	rs276	Intron 6	0.19	-0.391	0.103	NA	0.076	0.556	NA	0.012	0.184
67	rs277	Intron 6	0.11	-0.191	0.527	NA	-0.144	0.365	NA	0.005	0.671
67	rs279	Intron 6	0.15	0.595	0.029	NA	0.08	0.581	NA	-0.002	0.825
68	rs276	Intron 6	0.19	-0.391	0.103	0.222	0.076	0.556	0.13	0.012	0.184
68	rs277	Intron 6	0.11	-0.191	0.527	NA	-0.144	0.365	NA	0.005	0.671
68	rs279	Intron 6	0.15	0.595	0.029	NA	0.08	0.581	NA	-0.002	0.825
68	rs280	Intron 6	0.058	0.287	0.478	NA	0.375	0.082	NA	-0.008	0.579
69	rs277	Intron 6	0.11	-0.191	0.527	0.102	-0.144	0.365	0.295	0.005	0.671
69	rs279	Intron 6	0.15	0.595	0.029	NA	0.08	0.581	NA	-0.002	0.825
69	rs280	Intron 6	0.058	0.287	0.478	NA	0.375	0.082	NA	-0.008	0.579
69	rs17091775	Intron 6	0.056	0.356	0.39	NA	0.357	0.106	NA	-0.008	0.587
70	rs279	Intron 6	0.15	0.595	0.029	0.083	0.08	0.581	0.115	-0.002	0.825
70	rs280	Intron 6	0.058	0.287	0.478	NA	0.375	0.082	NA	-0.008	0.579
70	rs17091775	Intron 6	0.056	0.356	0.39	NA	0.357	0.106	NA	-0.008	0.587
70	rs282	Intron 6	0.477	-0.359	0.055	NA	-0.123	0.216	NA	0.001	0.853
71	rs280	Intron 6	0.058	0.287	0.478	0.418	0.375	0.082	0.357	-0.008	0.579
71	rs17091775	Intron 6	0.056	0.356	0.39	NA	0.357	0.106	NA	-0.008	0.587
71	rs282	Intron 6	0.477	-0.359	0.055	NA	-0.123	0.216	NA	0.001	0.853
71	rs290	Intron 6	0.145	0.264	0.354	NA	0.08	0.597	NA	0.004	0.728
72	rs17091775	Intron 6	0.056	0.356	0.39	0.276	0.357	0.106	0.293	-0.008	0.587
72	rs282	Intron 6	0.477	-0.359	0.055	NA	-0.123	0.216	NA	0.001	0.853
72	rs290	Intron 6	0.145	0.264	0.354	NA	0.08	0.597	NA	0.004	0.728
72	rs295	Intron 6	0.39	0.384	0.043	NA	0.199	0.049	NA	-0.004	0.575
73	rs282	Intron 6	0.477	-0.359	0.055	0.026	-0.123	0.216	0.22	0.001	0.853
73	rs290	Intron 6	0.145	0.264	0.354	NA	0.08	0.597	NA	0.004	0.728
73	rs295	Intron 6	0.39	0.384	0.043	NA	0.199	0.049	NA	-0.004	0.575
73	rs145585712	Intron 6	0.016	1.607	0.031	NA	0.377	0.343	NA	0.02	0.496
74	rs290	Intron 6	0.145	0.264	0.354	0.015	0.08	0.597	0.157	0.004	0.728
74	rs295	Intron 6	0.39	0.384	0.043	NA	0.199	0.049	NA	-0.004	0.575
74	rs145585712	Intron 6	0.016	1.607	0.031	NA	0.377	0.343	NA	0.02	0.496
74	rs73601683	Intron 6	0.012	-1.697	0.06	NA	0.283	0.546	NA	0.04	0.223
75	rs295	Intron 6	0.39	0.384	0.043	0.009	0.199	0.049	0.189	-0.004	0.575
75	rs145585712	Intron 6	0.016	1.607	0.031	NA	0.377	0.343	NA	0.02	0.496
75	rs73601683	Intron 6	0.012	-1.697	0.06	NA	0.283	0.546	NA	0.04	0.223
75	rs299	Intron 6	0.007	0.679	0.541	NA	-0.051	0.929	NA	-0.032	0.425
76	rs145585712	Intron 6	0.016	1.607	0.031	0.072	0.377	0.343	0.869	0.02	0.496
76	rs73601683	Intron 6	0.012	-1.697	0.06	NA	0.283	0.546	NA	0.04	0.223
76	rs299	Intron 6	0.007	0.679	0.541	NA	-0.051	0.929	NA	-0.032	0.425
76	rs300	Intron 6	0.011	0.223	0.81	NA	-0.042	0.932	NA	-0.017	0.631
77	rs73601683	Intron 6	0.012	-1.697	0.06	0.013	0.283	0.546	0.399	0.04	0.223
77	rs299	Intron 6	0.007	0.679	0.541	NA	-0.051	0.929	NA	-0.032	0.425
77	rs300	Intron 7	0.011	0.223	0.81	NA	-0.042	0.932	NA	-0.017	0.631
77	rs301	Intron 7	0.288	0.555	0.008	NA	0.173	0.119	NA	-0.006	0.466
78	rs299	Intron 6	0.007	0.679	0.541	0.011	-0.051	0.929	0.597	-0.032	0.425
78	rs300	Intron 7	0.011	0.223	0.81	NA	-0.042	0.932	NA	-0.017	0.631
78	rs301	Intron 7	0.288	0.555	0.008	NA	0.173	0.119	NA	-0.006	0.466
78	rs313	Intron 7	0.15	0.248	0.361	NA	0.053	0.71	NA	-0.004	0.711
79	rs300	Intron 7	0.011	0.223	0.81	0.041	-0.042	0.932	0.809	-0.017	0.631
79	rs301	Intron 7	0.288	0.555	0.008	NA	0.173	0.119	NA	-0.006	0.466
79	rs313	Intron 7	0.15	0.248	0.361	NA	0.053	0.71	NA	-0.004	0.711
79	rs314	Intron 7	0.248	-0.021	0.922	NA	-0.066	0.569	NA	0.008	0.304

Table A2.10. Continued

				HDL-C			TG				
Win.	**Window SNP**	**Location**	**MAF**	**β**	**P***	**hap_P****	**β**	**P***	**hap_P****	**β**	**P***
80	rs301	Intron 7	0.288	0.555	0.008	0.043	0.173	0.119	0.778	-0.006	0.466
80	rs313	Intron 7	0.15	0.248	0.361	NA	0.053	0.71	NA	-0.004	0.711
80	rs314	Intron 7	0.248	-0.021	0.922	NA	-0.066	0.569	NA	0.008	0.304
80	rs77434393	Intron 7	0.024	0.084	0.892	NA	0.142	0.667	NA	0.02	0.394
81	rs313	Intron 7	0.15	0.248	0.361	0.0002	0.053	0.71	0.816	-0.004	0.711
81	rs314	Intron 7	0.248	-0.021	0.922	NA	-0.066	0.569	NA	0.008	0.304
81	rs77434393	Intron 7	0.024	0.084	0.892	NA	0.142	0.667	NA	0.02	0.394
81	rs316	Exon 8	0.225	0.68	0.003	NA	0.164	0.179	NA	-0.001	0.891
82	rs314	Intron 7	0.248	-0.021	0.922	0.001	-0.066	0.569	0.385	0.008	0.304
82	rs77434393	Intron 7	0.024	0.084	0.892	NA	0.142	0.667	NA	0.02	0.394
82	rs316	Exon 8	0.225	0.68	0.003	NA	0.164	0.179	NA	-0.001	0.891
82	rs5934	Exon 8	0.033	-0.171	0.751	NA	0.161	0.573	NA	0.015	0.45
83	rs77434393	Intron 7	0.024	0.084	0.892	0.042	0.142	0.667	0.618	0.02	0.394
83	rs316	Exon 8	0.225	0.68	0.003	NA	0.164	0.179	NA	-0.001	0.891
83	rs5934	Exon 8	0.033	-0.171	0.751	NA	0.161	0.573	NA	0.015	0.45
83	rs318	Intron 8	0.139	-0.165	0.548	NA	-0.089	0.545	NA	0.004	0.705
84	rs316	Exon 8	0.225	0.68	0.003	0.044	0.164	0.179	0.665	-0.001	0.891
84	rs5934	Exon 8	0.033	-0.171	0.751	NA	0.161	0.573	NA	0.015	0.45
84	rs318	Intron 8	0.139	-0.165	0.548	NA	-0.089	0.545	NA	0.004	0.705
84	rs319	Intron 8	0.082	-0.083	0.812	NA	0.094	0.617	NA	0.016	0.226
85	rs5934	Exon 8	0.033	-0.171	0.751	0.533	0.161	0.573	0.914	0.015	0.45
85	rs318	Intron 8	0.139	-0.165	0.548	NA	-0.089	0.545	NA	0.004	0.705
85	rs319	Intron 8	0.082	-0.083	0.812	NA	0.094	0.617	NA	0.016	0.226
85	rs321	Intron 8	0.009	-1.754	0.102	NA	0.251	0.649	NA	0.001	0.988
86	rs318	Intron 8	0.139	-0.165	0.548	0.534	-0.089	0.545	0.696	0.004	0.705
86	rs319	Intron 8	0.082	-0.083	0.812	NA	0.094	0.617	NA	0.016	0.226
86	rs321	Intron 8	0.009	-1.754	0.102	NA	0.251	0.649	NA	0.001	0.988
86	rs325	Intron 8	0.043	0.085	0.852	NA	0.287	0.24	NA	-0.021	0.226
87	rs319	Intron 8	0.082	-0.083	0.812	0.335	0.094	0.617	0.587	0.016	0.226
87	rs321	Intron 8	0.009	-1.754	0.102	NA	0.251	0.649	NA	0.001	0.988
87	rs325	Intron 8	0.043	0.085	0.852	NA	0.287	0.24	NA	-0.021	0.226
87	rs326	Intron 8	0.398	-0.188	0.346	NA	-0.063	0.553	NA	0.007	0.339
88	rs321	Intron 8	0.009	-1.754	0.102	0.25	0.251	0.649	0.552	0.001	0.988
88	rs325	Intron 8	0.043	0.085	0.852	NA	0.287	0.24	NA	-0.021	0.226
88	rs326	Intron 8	0.398	-0.188	0.346	NA	-0.063	0.553	NA	0.007	0.339
88	rs149089920	Exon 9	0.001	-0.325	0.9	NA	1.257	0.365	NA	-0.01	0.917
89	rs325	Intron 8	0.043	0.085	0.852	0.308	0.287	0.24	0.673	-0.021	0.226
89	rs326	Intron 8	0.398	-0.188	0.346	NA	-0.063	0.553	NA	0.007	0.339
89	rs149089920	Exon 9	0.001	-0.325	0.9	NA	1.257	0.365	NA	-0.01	0.917
89	rs328	Exon 9	0.042	-0.113	0.804	NA	0.276	0.256	NA	-0.015	0.374
90	rs326	Intron 8	0.398	-0.188	0.346	0.107	-0.063	0.553	0.619	0.007	0.339
90	rs149089920	Exon 9	0.001	-0.325	0.9	NA	1.257	0.365	NA	-0.01	0.917
90	rs328	Exon 9	0.042	-0.113	0.804	NA	0.276	0.256	NA	-0.015	0.374
90	rs329	Intron 9	0.097	0.405	0.229	NA	-0.123	0.488	NA	-0.003	0.813
91	rs149089920	Exon 9	0.001	-0.325	0.9	0.203	1.257	0.365	0.342	-0.01	0.917
91	rs328	Exon 9	0.042	-0.113	0.804	NA	0.276	0.256	NA	-0.015	0.374
91	rs329	Intron 9	0.097	0.405	0.229	NA	-0.123	0.488	NA	-0.003	0.813
91	rs330	Intron 9	0.085	0.669	0.055	NA	0.243	0.191	NA	-0.005	0.708
92	rs328	Exon 9	0.042	-0.113	0.804	0.111	0.276	0.256	0.454	-0.015	0.374
92	rs329	Intron 9	0.097	0.405	0.229	NA	-0.123	0.488	NA	-0.003	0.813
92	rs330	Intron 9	0.085	0.669	0.055	NA	0.243	0.191	NA	-0.005	0.708
92	rs138285812	Intron 9	0.025	-0.884	0.149	NA	-0.135	0.679	NA	0.022	0.339
93	rs329	Intron 9	0.097	0.405	0.229	0.083	-0.123	0.488	0.467	-0.003	0.813
93	rs330	Intron 9	0.085	0.669	0.055	NA	0.243	0.191	NA	-0.005	0.708
93	rs138285812	Intron 9	0.025	-0.884	0.149	NA	-0.135	0.679	NA	0.022	0.339
93	rs12679834	Intron 9	0.058	0.278	0.487	NA	0.276	0.194	NA	0.004	0.812
94	rs330	Intron 9	0.085	0.669	0.055	0.215	0.243	0.191	0.376	-0.005	0.708
94	rs138285812	Intron 9	0.025	-0.884	0.149	NA	-0.135	0.679	NA	0.022	0.339
94	rs12679834	Intron 9	0.058	0.278	0.487	NA	0.276	0.194	NA	0.004	0.812
94	rs76423146	Intron 9	0.157	-0.175	0.486	NA	-0.119	0.378	NA	-0.002	0.85
95	rs138285812	Intron 9	0.025	-0.884	0.149	0.779	-0.135	0.679	0.41	0.022	0.339
95	rs12679834	Intron 9	0.058	0.278	0.487	NA	0.276	0.194	NA	0.004	0.812
95	rs76423146	Intron 9	0.157	-0.175	0.486	NA	-0.119	0.378	NA	-0.002	0.85
95	rs28599962	Intron 9	0.021	-0.116	0.863	NA	-0.337	0.346	NA	-0.001	0.971

Table A2.10. Continued

				HDL-C				TG			
Win.	**Window SNP**	**Location**	**MAF**	**β**	***P****	**hap_*P*****	**β**	***P****	**hap_*P*****	**β**	***P****
96	rs12679834	Intron 9	0.058	0.278	0.487	0.726	0.276	0.194	0.046	0.004	0.812
96	rs76423146	Intron 9	0.157	-0.175	0.486	NA	-0.119	0.378	NA	-0.002	0.85
96	rs28599962	Intron 9	0.021	-0.116	0.863	NA	-0.337	0.346	NA	-0.001	0.971
96	LP25579	Intron 9	0.005	-1.392	0.282	NA	-1.747	0.012	NA	-0.145	0.003
97	rs76423146	Intron 9	0.157	-0.175	0.486	0.722	-0.119	0.378	0.383	-0.002	0.85
97	rs28599962	Intron 9	0.021	-0.116	0.863	NA	-0.337	0.346	NA	-0.001	0.971
97	LP25579	Intron 9	0.005	-1.392	0.282	NA	-1.747	0.012	NA	-0.145	0.003
97	rs28716400	Intron 9	0.152	0.331	0.215	NA	0.07	0.623	NA	-0.008	0.4
98	rs28599962	Intron 9	0.021	-0.116	0.863	0.6	-0.337	0.346	0.092	-0.001	0.971
98	LP25579	Intron 9	0.005	-1.392	0.282	NA	-1.747	0.012	NA	-0.145	0.003
98	rs28716400	Intron 9	0.152	0.331	0.215	NA	0.07	0.623	NA	-0.008	0.4
98	rs75946927	Intron 9	0.087	0.022	0.948	NA	0.205	0.263	NA	0.008	0.548
99	LP25579	Intron 9	0.005	-1.392	0.282	0.476	-1.747	0.012	0.242	-0.145	0.003
99	rs28716400	Intron 9	0.152	0.331	0.215	NA	0.07	0.623	NA	-0.008	0.4
99	rs75946927	Intron 9	0.087	0.022	0.948	NA	0.205	0.263	NA	0.008	0.548
99	rs147900112	Intron 9	0.157	0.295	0.256	NA	0.018	0.898	NA	-0.007	0.45
100	rs28716400	Intron 9	0.152	0.331	0.215	0.284	0.07	0.623	0.629	-0.008	0.4
100	rs75946927	Intron 9	0.087	0.022	0.948	NA	0.205	0.263	NA	0.008	0.548
100	rs147900112	Intron 9	0.157	0.295	0.256	NA	0.018	0.898	NA	-0.007	0.45
100	rs114236375	Intron 9	0.012	1.384	0.15	NA	0.462	0.351	NA	0.069	0.044
101	rs75946927	Intron 9	0.087	0.022	0.948	0.345	0.205	0.263	0.573	0.008	0.548
101	rs147900112	Intron 9	0.157	0.295	0.256	NA	0.018	0.898	NA	-0.007	0.45
101	rs114236375	Intron 9	0.012	1.384	0.15	NA	0.462	0.351	NA	0.069	0.044
101	rs7818177	Exon 10 UTR	0.015	-0.119	0.88	NA	-0.301	0.466	NA	0.005	0.871
102	rs147900112	Intron 9	0.157	0.295	0.256	0.448	0.018	0.898	0.806	-0.007	0.45
102	rs114236375	Intron 9	0.012	1.384	0.15	NA	0.462	0.351	NA	0.069	0.044
102	rs7818177	Exon 10 UTR	0.015	-0.119	0.88	NA	-0.301	0.466	NA	0.005	0.871
102	LP27629	Exon 10 UTR	0.001	-2.685	0.302	NA	-1.229	0.377	NA	0.021	0.832
103	rs114236375	Intron 9	0.012	1.384	0.15	0.508	0.462	0.351	0.661	0.069	0.044
103	rs7818177	Exon 10 UTR	0.015	-0.119	0.88	NA	-0.301	0.466	NA	0.005	0.871
103	LP27629	Exon 10 UTR	0.001	-2.685	0.302	NA	-1.229	0.377	NA	0.021	0.832
103	LP27695	Exon 10 UTR	0.001	4.626	0.21	NA	1.231	0.527	NA	0.047	0.733
104	rs7818177	Exon 10 UTR	0.015	-0.119	0.88	0.89	-0.301	0.466	0.542	0.005	0.871
104	LP27629	Exon 10 UTR	0.001	-2.685	0.302	NA	-1.229	0.377	NA	0.021	0.832
104	LP27695	Exon 10 UTR	0.001	4.626	0.21	NA	1.231	0.527	NA	0.047	0.733
104	LP27706	Exon 10 UTR	0.001	-1.512	0.56	NA	-1.081	0.434	NA	0.074	0.447
105	LP27629	Exon 10 UTR	0.001	-2.685	0.302	0.5	-1.229	0.377	0.296	0.021	0.832
105	LP27695	Exon 10 UTR	0.001	4.626	0.21	NA	1.231	0.527	NA	0.047	0.733
105	LP27706	Exon 10 UTR	0.001	-1.512	0.56	NA	-1.081	0.434	NA	0.074	0.447
105	rs187587525	Exon 10 UTR	0.003	-0.809	0.622	NA	-0.605	0.489	NA	-0.05	0.418
106	LP27695	Exon 10 UTR	0.001	4.626	0.21	0.5	1.231	0.527	0.296	0.047	0.733
106	LP27706	Exon 10 UTR	0.001	-1.512	0.56	NA	-1.081	0.434	NA	0.074	0.447
106	rs187587525	Exon 10 UTR	0.003	-0.809	0.622	NA	-0.605	0.489	NA	-0.05	0.418
106	LP27969	Exon 10 UTR	0.001	-2.66	0.307	NA	-1.215	0.382	NA	0.02	0.834
107	LP27706	Exon 10 UTR	0.001	-1.512	0.56	0.204	-1.081	0.434	0.174	0.074	0.447
107	rs187587525	Exon 10 UTR	0.003	-0.809	0.622	NA	-0.605	0.489	NA	-0.05	0.418
107	LP27969	Exon 10 UTR	0.001	-2.66	0.307	NA	-1.215	0.382	NA	0.02	0.834
107	rs11570892	Exon 10 UTR	0.24	0.297	0.189	NA	0.144	0.229	NA	0.006	0.509
108	rs187587525	Exon 10 UTR	0.003	-0.809	0.622	0.072	-0.605	0.489	0.222	-0.05	0.418
108	LP27969	Exon 10 UTR	0.001	-2.66	0.307	NA	-1.215	0.382	NA	0.02	0.834
108	rs11570892	Exon 10 UTR	0.24	0.297	0.189	NA	0.144	0.229	NA	0.006	0.509
108	rs3208305	Exon 10 UTR	0.443	-0.358	0.061	NA	-0.187	0.071	NA	0.002	0.82
109	LP27969	Exon 10 UTR	0.001	-2.66	0.307	0.064	-1.215	0.382	0.315	0.02	0.834
109	rs11570892	Exon 10 UTR	0.24	0.297	0.189	NA	0.144	0.229	NA	0.006	0.509
109	rs3208305	Exon 10 UTR	0.443	-0.358	0.061	NA	-0.187	0.071	NA	0.002	0.82
109	rs1059507	Exon 10 UTR	0.103	0.689	0.031	NA	0.253	0.14	NA	0.001	0.905
110	rs11570892	Exon 10 UTR	0.24	0.297	0.189	0.143	0.144	0.229	0.206	0.006	0.509
110	rs3208305	Exon 10 UTR	0.443	-0.358	0.061	NA	-0.187	0.071	NA	0.002	0.82
110	rs1059507	Exon 10 UTR	0.103	0.689	0.031	NA	0.253	0.14	NA	0.001	0.905
110	rs3200218	Exon 10 UTR	0.093	-0.177	0.597	NA	0.134	0.453	NA	0.015	0.228
111	rs3208305	Exon 10 UTR	0.443	-0.358	0.061	0.117	-0.187	0.071	0.281	0.002	0.82
111	rs1059507	Exon 10 UTR	0.103	0.689	0.031	NA	0.253	0.14	NA	0.001	0.905
111	rs3200218	Exon 10 UTR	0.093	-0.177	0.597	NA	0.134	0.453	NA	0.015	0.228
111	rs139240067	Exon 10 UTR	0.013	-0.404	0.636	NA	-0.117	0.793	NA	-0.007	0.827

Table A2.10. Continued

				HDL-C			TG				
Win.	**Window SNP**	**Location**	**MAF**	**β**	***P****	**hap_*P*****	**β**	***P****	**hap_*P*****	**β**	***P****
112	rs1059507	Exon 10 UTR	0.103	0.689	0.031	0.299	0.253	0.14	0.539	0.001	0.905
112	rs3200218	Exon 10 UTR	0.093	-0.177	0.597	NA	0.134	0.453	NA	0.015	0.228
112	rs139240067	Exon 10 UTR	0.013	-0.404	0.636	NA	-0.117	0.793	NA	-0.007	0.827
112	rs184363931	Exon 10 UTR	0.009	-0.559	0.586	NA	-0.069	0.899	NA	0.016	0.665
113	rs3200218	Exon 10 UTR	0.093	-0.177	0.597	0.071	0.134	0.453	0.263	0.015	0.228
113	rs139240067	Exon 10 UTR	0.013	-0.404	0.636	NA	-0.117	0.793	NA	-0.007	0.827
113	rs184363931	Exon 10 UTR	0.009	-0.559	0.586	NA	-0.069	0.899	NA	0.016	0.665
113	rs13702	Exon 10 UTR	0.459	-0.49	0.011	NA	-0.178	0.083	NA	0.004	0.623
114	rs139240067	Exon 10 UTR	0.013	-0.404	0.636	0.072	-0.117	0.793	0.53	-0.007	0.827
114	rs184363931	Exon 10 UTR	0.009	-0.559	0.586	NA	-0.069	0.899	NA	0.016	0.665
114	rs13702	Exon 10 UTR	0.459	-0.49	0.011	NA	-0.178	0.083	NA	0.004	0.623
114	rs17091815	Exon 10 UTR	0.084	0.164	0.648	NA	0.046	0.807	NA	-0.009	0.519
115	rs184363931	Exon 10 UTR	0.009	-0.559	0.586	0.014	-0.069	0.899	0.078	0.016	0.665
115	rs13702	Exon 10 UTR	0.459	-0.49	0.011	NA	-0.178	0.083	NA	0.004	0.623
115	rs17091815	Exon 10 UTR	0.084	0.164	0.648	NA	0.046	0.807	NA	-0.009	0.519
115	rs78359368	Exon 10 UTR	0.007	-2.598	0.026	NA	-1.941	0.002	NA	-0.096	0.028
116	rs13702	Exon 10 UTR	0.459	-0.49	0.011	0.01	-0.178	0.083	0.008	0.004	0.623
116	rs17091815	Exon 10 UTR	0.084	0.164	0.648	NA	0.046	0.807	NA	-0.009	0.519
116	rs78359368	Exon 10 UTR	0.007	-2.598	0.026	NA	-1.941	0.002	NA	-0.096	0.028
116	rs187374932	Exon 10 UTR	0.005	-3.432	0.008	NA	-2.286	0.001	NA	-0.126	0.01
117	rs17091815	Exon 10 UTR	0.084	0.164	0.648	0.022	0.046	0.807	0.008	-0.009	0.519
117	rs78359368	Exon 10 UTR	0.007	-2.598	0.026	NA	-1.941	0.002	NA	-0.096	0.028
117	rs187374932	Exon 10 UTR	0.005	-3.432	0.008	NA	-2.286	0.001	NA	-0.126	0.01
117	rs147116359	Exon 10 UTR	0.011	1.877	0.027	NA	0.661	0.142	NA	-0.036	0.266
118	rs78359368	Exon 10 UTR	0.007	-2.598	0.026	0.019	-1.941	0.002	0.004	-0.096	0.028
118	rs187374932	Exon 10 UTR	0.005	-3.432	0.008	NA	-2.286	0.001	NA	-0.126	0.01
118	rs147116359	Exon 10 UTR	0.011	1.877	0.027	NA	0.661	0.142	NA	-0.036	0.266
118	rs79756214	Exon 10 UTR	0.016	-0.506	0.508	NA	-0.465	0.254	NA	0.009	0.752
119	rs187374932	Exon 10 UTR	0.005	-3.432	0.008	0.005	-2.286	0.001	0.003	-0.126	0.01
119	rs147116359	Exon 10 UTR	0.011	1.877	0.027	NA	0.661	0.142	NA	-0.036	0.266
119	rs79756214	Exon 10 UTR	0.016	-0.506	0.508	NA	-0.465	0.254	NA	0.009	0.752
119	rs3916027	Exon 10 UTR	0.413	0.421	0.028	NA	0.182	0.076	NA	-0.005	0.523
120	rs147116359	Exon 10 UTR	0.011	1.877	0.027	0.063	0.661	0.142	0.265	-0.036	0.266
120	rs79756214	Exon 10 UTR	0.016	-0.506	0.508	NA	-0.465	0.254	NA	0.009	0.752
120	rs3916027	Exon 10 UTR	0.413	0.421	0.028	NA	0.182	0.076	NA	-0.005	0.523
120	rs4921683	Exon 10 UTR	0.102	0.757	0.019	NA	0.297	0.086	NA	0	0.992
121	rs79756214	Exon 10 UTR	0.016	-0.506	0.508	0.099	-0.465	0.254	0.361	0.009	0.752
121	rs3916027	Exon 10 UTR	0.413	0.421	0.028	NA	0.182	0.076	NA	-0.005	0.523
121	rs4921683	Exon 10 UTR	0.102	0.757	0.019	NA	0.297	0.086	NA	0	0.992
121	rs76707496	Exon 10 UTR	0.09	0.401	0.234	NA	0.096	0.588	NA	-0.007	0.562
122	rs3916027	Exon 10 UTR	0.413	0.421	0.028	0.069	0.182	0.076	0.361	-0.005	0.523
122	rs4921683	Exon 10 UTR	0.102	0.757	0.019	NA	0.297	0.086	NA	0	0.992
122	rs76707496	Exon 10 UTR	0.09	0.401	0.234	NA	0.096	0.588	NA	-0.007	0.562
122	rs4921684	Exon 10 UTR	0.079	0.869	0.016	NA	0.298	0.12	NA	-0.012	0.354

Table A2.11. ***LPL*** **4-SNP sliding window haplotype association results for TC, ApoA1 and ApoB in African blacks (n=788)**

				TC			ApoA1			ApoB		
Win.	**Window SNP**	**Location**	**MAF**	**hap_P****	**β**	**P***	**hap_P****	**β**	**P***	**hap_P****	**β**	**P***
1	rs1470187	5' flanking	0.112	0.935	-0.082	0.789	0.185	0.466	0.529	0.806	-0.97	0.254
1	rs1470186	5' flanking	0.225	NA	0.351	0.121	NA	0.365	0.513	NA	0.143	0.82
1	rs73667465	5' flanking	0.314	NA	0.128	0.518	NA	0.213	0.664	NA	-0.18	0.746
1	rs1800590	Exon 1	0.468	NA	0.128	0.503	NA	-0.12	0.798	NA	-0.01	0.988
2	rs1470186	5' flanking	0.225	0.626	0.351	0.121	0.422	0.365	0.513	0.402	0.143	0.82
2	rs73667465	5' flanking	0.314	NA	0.128	0.518	NA	0.213	0.664	NA	-0.18	0.746
2	rs1800590	Exon 1-UTR	0.468	NA	0.128	0.503	NA	-0.12	0.798	NA	-0.01	0.988
2	rs75890454	Exon 1-UTR	0.02	NA	-0.436	0.536	NA	-2.536	0.135	NA	-2.24	0.252
3	rs73667465	5' flanking	0.314	0.47	0.128	0.518	0.814	0.213	0.664	0.28	-0.18	0.746
3	rs1800590	Exon 1	0.468	NA	0.128	0.503	NA	-0.12	0.798	NA	-0.01	0.988
3	rs75890454	Exon 1-UTR	0.02	NA	-0.436	0.536	NA	-2.536	0.135	NA	-2.24	0.252
3	LP1155	Exon 1-UTR	0.001	NA	-2.648	0.478	NA	-18.03	0.048	NA	-3.06	0.768
4	rs1800590	Exon 1	0.468	0.439	0.128	0.503	0.663	-0.12	0.798	0.497	-0.01	0.988
4	rs75890454	Exon 1-UTR	0.02	NA	-0.436	0.536	NA	-2.536	0.135	NA	-2.24	0.252
4	LP1155	Exon 1-UTR	0.001	NA	-2.648	0.478	NA	-18.03	0.048	NA	-3.06	0.768
4	rs34513350	Exon 1-UTR	0.029	NA	-0.538	0.358	NA	0.514	0.716	NA	0.081	0.96
5	rs75890454	Exon 1-UTR	0.02	0.343	-0.436	0.536	0.366	-2.536	0.135	0.584	-2.24	0.252
5	LP1155	Exon 1-UTR	0.001	NA	-2.648	0.478	NA	-18.03	0.048	NA	-3.06	0.768
5	rs34513350	Exon 1-UTR	0.029	NA	-0.538	0.358	NA	0.514	0.716	NA	0.081	0.96
5	LP1264	Exon 1-UTR	0.008	NA	-1.1	0.307	NA	0.227	0.932	NA	1.325	0.659
6	LP1155	Exon 1-UTR	0.001	0.534	-2.648	0.478	0.03	-18.03	0.048	0.49	-3.06	0.768
6	rs34513350	Exon 1-UTR	0.029	NA	-0.538	0.358	NA	0.514	0.716	NA	0.081	0.96
6	LP1264	Exon 1-UTR	0.008	NA	-1.1	0.307	NA	0.227	0.932	NA	1.325	0.659
6	LP1300	Exon 1-UTR	0.005	NA	-3.213	0.015	NA	-4.177	0.197	NA	-0.43	0.914
7	rs34513350	Exon 1-UTR	0.029	0.681	-0.538	0.358	0.042	0.514	0.716	0.419	0.081	0.96
7	LP1264	Exon 1-UTR	0.008	NA	-1.1	0.307	NA	0.227	0.932	NA	1.325	0.659
7	LP1300	Exon 1-UTR	0.005	NA	-3.213	0.015	NA	-4.177	0.197	NA	-0.43	0.914
7	rs200412008	Exon 1-UTR	0.029	NA	0.705	0.22	NA	2.293	0.101	NA	2.472	0.125
8	LP1264	Exon 1-UTR	0.008	0.15	-1.1	0.307	0.079	0.227	0.932	0.338	1.325	0.659
8	LP1300	Exon 1-UTR	0.005	NA	-3.213	0.015	NA	-4.177	0.197	NA	-0.43	0.914
8	rs200412008	Exon 1-UTR	0.029	NA	0.705	0.22	NA	2.293	0.101	NA	2.472	0.125
8	rs141390463	Intron 1	0.041	NA	-0.068	0.883	NA	-0.871	0.439	NA	1.488	0.239
9	LP1300	Exon 1-UTR	0.005	0.006	-3.213	0.015	0.011	-4.177	0.197	0.369	-0.43	0.914
9	rs200412008	Exon 1-UTR	0.029	NA	0.705	0.22	NA	2.293	0.101	NA	2.472	0.125
9	rs141390463	Intron 1	0.041	NA	-0.068	0.883	NA	-0.871	0.439	NA	1.488	0.239
9	rs3779787	Intron 1	0.023	NA	1.258	0.054	NA	0.844	0.599	NA	3.626	0.045
10	rs200412008	Exon 1-UTR	0.029	0.022	0.705	0.22	0.278	2.293	0.101	0.285	2.472	0.125
10	rs141390463	Intron 1	0.041	NA	-0.068	0.883	NA	-0.871	0.439	NA	1.488	0.239
10	rs3779787	Intron 1	0.023	NA	1.258	0.054	NA	0.844	0.599	NA	3.626	0.045
10	rs146786419	Intron 1	0.039	NA	-0.238	0.637	NA	1.846	0.128	NA	-0.67	0.63
11	rs141390463	Intron 1	0.041	0.023	-0.068	0.883	0.356	-0.871	0.439	0.26	1.488	0.239
11	rs3779787	Intron 1	0.023	NA	1.258	0.054	NA	0.844	0.599	NA	3.626	0.045
11	rs146786419	Intron 1	0.039	NA	-0.238	0.637	NA	1.846	0.128	NA	-0.67	0.63
11	rs185670596	Intron 1	0.022	NA	-0.156	0.813	NA	2.225	0.171	NA	1.827	0.315
12	rs3779787	Intron 1	0.023	0.008	1.258	0.054	0.451	0.844	0.599	0.17	3.626	0.045
12	rs146786419	Intron 1	0.039	NA	-0.238	0.637	NA	1.846	0.128	NA	-0.67	0.63
12	rs185670596	Intron 1	0.022	NA	-0.156	0.813	NA	2.225	0.171	NA	1.827	0.315
12	rs115668974	Intron 1	0.042	NA	-0.298	0.509	NA	1.204	0.278	NA	-0.16	0.899
13	rs146786419	Intron 1	0.039	0.02	-0.238	0.637	0.914	1.846	0.128	0.189	-0.67	0.63
13	rs185670596	Intron 1	0.022	NA	-0.156	0.813	NA	2.225	0.171	NA	1.827	0.315
13	rs115668974	Intron 1	0.042	NA	-0.298	0.509	NA	1.204	0.278	NA	-0.16	0.899
13	rs17410577	Intron 1	0.12	NA	-0.127	0.663	NA	0.728	0.304	NA	-0.13	0.872
14	rs185670596	Intron 1	0.022	0.377	-0.156	0.813	0.355	2.225	0.171	0.481	1.827	0.315
14	rs115668974	Intron 1	0.042	NA	-0.298	0.509	NA	1.204	0.278	NA	-0.16	0.899
14	rs17410577	Intron 1	0.12	NA	-0.127	0.663	NA	0.728	0.304	NA	-0.13	0.872
14	rs1031045	Intron 1	0.451	NA	0.104	0.584	NA	0.151	0.741	NA	0.5	0.341
15	rs115668974	Intron 1	0.042	0.901	-0.298	0.509	0.179	1.204	0.278	0.769	-0.16	0.899
15	rs17410577	Intron 1	0.12	NA	-0.127	0.663	NA	0.728	0.304	NA	-0.13	0.872
15	rs1031045	Intron 1	0.451	NA	0.104	0.584	NA	0.151	0.741	NA	0.5	0.341
15	rs112127208	Intron 1	0.025	NA	1.155	0.057	NA	0.016	0.991	NA	3.611	0.033
16	rs17410577	Intron 1	0.12	0.802	-0.127	0.663	0.341	0.728	0.304	0.864	-0.13	0.872
16	rs1031045	Intron 1	0.451	NA	0.104	0.584	NA	0.151	0.741	NA	0.5	0.341
16	rs112127208	Intron 1	0.025	NA	1.155	0.057	NA	0.016	0.991	NA	3.611	0.033
16	rs56043715	Intron 1	0.307	NA	-0.074	0.721	NA	0.207	0.683	NA	0.02	0.972
17	rs1031045	Intron 1	0.451	0.866	0.104	0.584	0.166	0.151	0.741	0.712	0.5	0.341
17	rs112127208	Intron 1	0.025	NA	1.155	0.057	NA	0.016	0.991	NA	3.611	0.033
17	rs56043715	Intron 1	0.307	NA	-0.074	0.721	NA	0.207	0.683	NA	0.02	0.972
17	rs61274012	Intron 1	0.03	NA	0.723	0.199	NA	1.933	0.158	NA	1.67	0.28
18	rs112127208	Intron 1	0.025	0.661	1.155	0.057	0.208	0.016	0.991	0.722	3.611	0.033

Table A2.11. Continued

				TC			ApoA1			ApoB		
Win.	**Window SNP**	**Location**	**MAF**	**hap_*P*****	**β**	***P****	**hap_*P*****	**β**	***P****	**hap_*P*****	**β**	***P****
18	rs56043715	Intron 1	0.307	NA	-0.074	0.721	NA	0.207	0.683	NA	0.02	0.972
18	rs61274012	Intron 1	0.03	NA	0.723	0.199	NA	1.933	0.158	NA	1.67	0.28
18	rs28615996	Intron 1	0.333	NA	-0.054	0.792	NA	0.329	0.51	NA	-0.07	0.906
19	rs56043715	Intron 1	0.307	0.677	-0.074	0.721	0.492	0.207	0.683	0.552	0.02	0.972
19	rs61274012	Intron 1	0.03	NA	0.723	0.199	NA	1.933	0.158	NA	1.67	0.28
19	rs28615996	Intron 1	0.333	NA	-0.054	0.792	NA	0.329	0.51	NA	-0.07	0.906
19	rs28645722	Intron 1	0.281	NA	-0.034	0.87	NA	0.33	0.518	NA	-0.09	0.884
20	rs61274012	Intron 1	0.03	0.766	0.723	0.199	0.568	1.933	0.158	0.647	1.67	0.28
20	rs28615996	Intron 1	0.333	NA	-0.054	0.792	NA	0.329	0.51	NA	-0.07	0.906
20	rs28645722	Intron 1	0.281	NA	-0.034	0.87	NA	0.33	0.518	NA	-0.09	0.884
20	rs6999612	Intron 1	0.284	NA	-0.097	0.641	NA	0.433	0.397	NA	-0.57	0.324
21	rs28615996	Intron 1	0.333	0.556	-0.054	0.792	0.436	0.329	0.51	0.936	-0.07	0.906
21	rs28645722	Intron 1	0.281	NA	-0.034	0.87	NA	0.33	0.518	NA	-0.09	0.884
21	rs6999612	Intron 1	0.284	NA	-0.097	0.641	NA	0.433	0.397	NA	-0.57	0.324
21	rs59811201	Intron 1	0.166	NA	0.238	0.363	NA	0.512	0.423	NA	0.325	0.655
22	rs28645722	Intron 1	0.281	0.641	-0.034	0.87	0.464	0.33	0.518	0.852	-0.09	0.884
22	rs6999612	Intron 1	0.284	NA	-0.097	0.641	NA	0.433	0.397	NA	-0.57	0.324
22	rs59811201	Intron 1	0.166	NA	0.238	0.363	NA	0.512	0.423	NA	0.325	0.655
22	rs115064749	Intron 1	0.03	NA	-0.325	0.564	NA	1.181	0.39	NA	0.34	0.828
23	rs6999612	Intron 1	0.284	0.658	-0.097	0.641	0.555	0.433	0.397	0.202	-0.57	0.324
23	rs59811201	Intron 1	0.166	NA	0.238	0.363	NA	0.512	0.423	NA	0.325	0.655
23	rs115064749	Intron 1	0.03	NA	-0.325	0.564	NA	1.181	0.39	NA	0.34	0.828
23	rs112943460	Intron 1	0.029	NA	-0.271	0.635	NA	-0.068	0.961	NA	0.044	0.978
24	rs59811201	Intron 1	0.166	0.456	0.238	0.363	0.783	0.512	0.423	0.123	0.325	0.655
24	rs115064749	Intron 1	0.03	NA	-0.325	0.564	NA	1.181	0.39	NA	0.34	0.828
24	rs112943460	Intron 1	0.029	NA	-0.271	0.635	NA	-0.068	0.961	NA	0.044	0.978
24	rs181367025	Intron 1	0.013	NA	0.591	0.495	NA	-2.129	0.313	NA	4.236	0.076
25	rs115064749	Intron 1	0.03	0.743	-0.325	0.564	0.794	1.181	0.39	0.687	0.34	0.828
25	rs112943460	Intron 1	0.029	NA	-0.271	0.635	NA	-0.068	0.961	NA	0.044	0.978
25	rs181367025	Intron 1	0.013	NA	0.591	0.495	NA	-2.129	0.313	NA	4.236	0.076
25	rs28445964	Intron 1	0.247	NA	0.097	0.661	NA	0.281	0.601	NA	0.184	0.762
26	rs112943460	Intron 1	0.029	0.925	-0.271	0.635	0.932	-0.068	0.961	0.449	0.044	0.978
26	rs181367025	Intron 1	0.013	NA	0.591	0.495	NA	-2.129	0.313	NA	4.236	0.076
26	rs28445964	Intron 1	0.247	NA	0.097	0.661	NA	0.281	0.601	NA	0.184	0.762
26	rs145257746	Intron 1	0.052	NA	0.056	0.898	NA	-0.931	0.386	NA	-0.78	0.521
27	rs181367025	Intron 1	0.013	0.675	0.591	0.495	0.876	-2.129	0.313	0.688	4.236	0.076
27	rs28445964	Intron 1	0.247	NA	0.097	0.661	NA	0.281	0.601	NA	0.184	0.762
27	rs145257746	Intron 1	0.052	NA	0.056	0.898	NA	-0.931	0.386	NA	-0.78	0.521
27	rs138110428	Intron 1	0.007	NA	-1.09	0.332	NA	1.278	0.646	NA	2.303	0.464
28	rs28445964	Intron 1	0.247	0.537	0.097	0.661	0.916	0.281	0.601	0.571	0.184	0.762
28	rs145257746	Intron 1	0.052	NA	0.056	0.898	NA	-0.931	0.386	NA	-0.78	0.521
28	rs138110428	Intron 1	0.007	NA	-1.09	0.332	NA	1.278	0.646	NA	2.303	0.464
28	LP10100delT	Intron 1	0.022	NA	-0.385	0.56	NA	1.999	0.212	NA	-1.15	0.522
29	rs145257746	Intron 1	0.052	0.348	0.056	0.898	0.326	-0.931	0.386	0.624	-0.78	0.521
29	rs138110428	Intron 1	0.007	NA	-1.09	0.332	NA	1.278	0.646	NA	2.303	0.464
29	LP10100delT	Intron 1	0.022	NA	-0.385	0.56	NA	1.999	0.212	NA	-1.15	0.522
29	rs1801177	Exon 2	0.05	NA	0.686	0.112	NA	0.657	0.536	NA	2.715	0.027
30	rs138110428	Intron 1	0.007	0.327	-1.09	0.332	0.014	1.278	0.646	0.509	2.303	0.464
30	LP10100delT	Intron 1	0.022	NA	-0.385	0.56	NA	1.999	0.212	NA	-1.15	0.522
30	rs1801177	Exon 2	0.05	NA	0.686	0.112	NA	0.657	0.536	NA	2.715	0.027
30	rs148201569	Exon 2	0.003	NA	-6.51	0	NA	-11.62	0.027	NA	-3.53	0.555
31	LP10100delT	Intron 1	0.022	0.234	-0.385	0.56	0.005	1.999	0.212	0.075	-1.15	0.522
31	rs1801177	Exon 2	0.05	NA	0.686	0.112	NA	0.657	0.536	NA	2.715	0.027
31	rs148201569	Exon 2	0.003	NA	-6.51	0	NA	-11.62	0.027	NA	-3.53	0.555
31	rs11542065	Exon 2	0.018	NA	-0.244	0.741	NA	-1.285	0.475	NA	-1.58	0.443
32	rs1801177	Exon 2	0.05	0.24	0.686	0.112	0.004	0.657	0.536	0.153	2.715	0.027
32	rs148201569	Exon 2	0.003	NA	-6.51	0	NA	-11.62	0.027	NA	-3.53	0.555
32	rs11542065	Exon 2	0.018	NA	-0.244	0.741	NA	-1.285	0.475	NA	-1.58	0.443
32	rs59054859	Intron 2	0.118	NA	0.238	0.429	NA	-0.654	0.384	NA	0.749	0.375
33	rs148201569	Exon 2	0.003	0.333	-6.51	0	0.521	-11.62	0.027	0.354	-3.53	0.555
33	rs11542065	Exon 2	0.018	NA	-0.244	0.741	NA	-1.285	0.475	NA	-1.58	0.443
33	rs59054859	Intron 2	0.118	NA	0.238	0.429	NA	-0.654	0.384	NA	0.749	0.375
33	LP10632	Intron 2	0.008	NA	0.575	0.582	NA	-1.502	0.556	NA	3.93	0.174
34	rs11542065	Exon 2	0.018	0.05	-0.244	0.741	0.795	-1.285	0.475	0.814	-1.58	0.443
34	rs59054859	Intron 2	0.118	NA	0.238	0.429	NA	-0.654	0.384	NA	0.749	0.375
34	LP10632	Intron 2	0.008	NA	0.575	0.582	NA	-1.502	0.556	NA	3.93	0.174
34	rs6991305	Intron 2	0.045	NA	-0.36	0.44	NA	0.688	0.545	NA	-0.51	0.694
35	rs59054859	Intron 2	0.118	0.073	0.238	0.429	0.781	-0.654	0.384	0.756	0.749	0.375
35	LP10632	Intron 2	0.008	NA	0.575	0.582	NA	-1.502	0.556	NA	3.93	0.174
35	rs6991305	Intron 2	0.045	NA	-0.36	0.44	NA	0.688	0.545	NA	-0.51	0.694
35	rs7016529	Intron 2	0.295	NA	-0.018	0.931	NA	0.481	0.345	NA	-0.1	0.868
36	LP10632	Intron 2	0.008	0.047	0.575	0.582	0.406	-1.502	0.556	0.592	3.93	0.174

Table A2.11. Continued

				TC			ApoA1			ApoB		
Win.	Window SNP	Location	MAF	hap_P**	β	P*	hap_P**	β	P*	hap_P**	β	P*
36	rs6991305	Intron 2	0.045	NA	-0.36	0.44	NA	0.688	0.545	NA	-0.51	0.694
36	rs7016529	Intron 2	0.295	NA	-0.018	0.931	NA	0.481	0.345	NA	-0.1	0.868
36	rs8176337	Intron 2	0.313	NA	-0.332	0.103	NA	-0.482	0.333	NA	-1.3	0.021
37	rs6991305	Intron 2	0.045	0.024	-0.36	0.44	0.304	0.688	0.545	0.842	-0.51	0.694
37	rs7016529	Intron 2	0.295	NA	-0.018	0.931	NA	0.481	0.345	NA	-0.1	0.868
37	rs8176337	Intron 2	0.313	NA	-0.332	0.103	NA	-0.482	0.333	NA	-1.3	0.021
37	rs189417962	Intron 2	0.007	NA	-1.102	0.327	NA	1.304	0.639	NA	2.277	0.467
38	rs7016529	Intron 2	0.295	0.391	-0.018	0.931	0.119	0.481	0.345	0.538	-0.1	0.868
38	rs8176337	Intron 2	0.313	NA	-0.332	0.103	NA	-0.482	0.333	NA	-1.3	0.021
38	rs189417962	Intron 2	0.007	NA	-1.102	0.327	NA	1.304	0.639	NA	2.277	0.467
38	rs74304285	Intron 2	0.056	NA	0.995	0.019	NA	1.724	0.099	NA	3.014	0.01
39	rs8176337	Intron 2	0.313	0.398	-0.332	0.103	0.076	-0.482	0.333	0.412	-1.3	0.021
39	rs189417962	Intron 2	0.007	NA	-1.102	0.327	NA	1.304	0.639	NA	2.277	0.467
39	rs74304285	Intron 2	0.056	NA	0.995	0.019	NA	1.724	0.099	NA	3.014	0.01
39	rs79760154	Intron 2	0.091	NA	-0.015	0.965	NA	-0.71	0.389	NA	0.315	0.735
40	rs189417962	Intron 2	0.007	0.576	-1.102	0.327	0.138	1.304	0.639	0.433	2.277	0.467
40	rs74304285	Intron 2	0.056	NA	0.995	0.019	NA	1.724	0.099	NA	3.014	0.01
40	rs79760154	Intron 2	0.091	NA	-0.015	0.965	NA	-0.71	0.389	NA	0.315	0.735
40	rs115589061	Intron 2	0.023	NA	-0.413	0.521	NA	-0.192	0.904	NA	-1.23	0.491
41	rs74304285	Intron 2	0.056	0.809	0.995	0.019	0.074	1.724	0.099	0.551	3.014	0.01
41	rs79760154	Intron 2	0.091	NA	-0.015	0.965	NA	-0.71	0.389	NA	0.315	0.735
41	rs115589061	Intron 2	0.023	NA	-0.413	0.521	NA	-0.192	0.904	NA	-1.23	0.491
41	LP13691_13693delATC	Intron 2	0.001	NA	-3.566	0.178	NA	-6.743	0.292	NA	-5.67	0.443
42	rs79760154	Intron 2	0.091	0.38	-0.015	0.965	0.445	-0.71	0.389	0.714	0.315	0.735
42	rs115589061	Intron 2	0.023	NA	-0.413	0.521	NA	-0.192	0.904	NA	-1.23	0.491
42	LP13691_13693delATC	Intron 2	0.001	NA	-3.566	0.178	NA	-6.743	0.292	NA	-5.67	0.443
42	rs1121923	Exon 3	0.111	NA	-0.105	0.722	NA	-0.153	0.835	NA	0.429	0.606
43	rs115589061	Intron 2	0.023	0.48	-0.413	0.521	0.218	-0.192	0.904	0.876	-1.23	0.491
43	LP13691_13693delATC	Intron 2	0.001	NA	-3.566	0.178	NA	-6.743	0.292	NA	-5.67	0.443
43	rs1121923	Intron 2	0.111	NA	-0.105	0.722	NA	-0.153	0.835	NA	0.429	0.606
43	rs73667472	Intron 3	0.203	NA	0.06	0.798	NA	0.017	0.977	NA	0.198	0.763
44	LP13691_13693delATC	Intron 2	0.001	0.627	-3.566	0.178	0.673	-6.743	0.292	0.372	-5.67	0.443
44	rs1121923	Intron 2	0.111	NA	-0.105	0.722	NA	-0.153	0.835	NA	0.429	0.606
44	rs73667472	Intron 3	0.203	NA	0.06	0.798	NA	0.017	0.977	NA	0.198	0.763
44	rs75026342	Intron 3	0.109	NA	0.172	0.571	NA	-0.788	0.285	NA	-0.49	0.56
45	rs1121923	Intron 2	0.111	0.423	-0.105	0.722	0.972	-0.153	0.835	0.323	0.429	0.606
45	rs73667472	Intron 3	0.203	NA	0.06	0.798	NA	0.017	0.977	NA	0.198	0.763
45	rs75026342	Intron 3	0.109	NA	0.172	0.571	NA	-0.788	0.285	NA	-0.49	0.56
45	LP15060del	Intron 3	0.022	NA	-0.373	0.572	NA	2.426	0.129	NA	-1.01	0.577
46	rs73667472	Intron 3	0.203	0.487	0.06	0.798	0.915	0.017	0.977	0.311	0.198	0.763
46	rs75026342	Intron 3	0.109	NA	0.172	0.571	NA	-0.788	0.285	NA	-0.49	0.56
46	LP15060del	Intron 3	0.022	NA	-0.373	0.572	NA	2.426	0.129	NA	-1.01	0.577
46	rs343	Intron 3	0.031	NA	0.445	0.441	NA	-1.113	0.423	NA	1.785	0.256
47	rs75026342	Intron 3	0.109	0.572	0.172	0.571	0.87	-0.788	0.285	0.256	-0.49	0.56
47	LP15060del	Intron 3	0.022	NA	-0.373	0.572	NA	2.426	0.129	NA	-1.01	0.577
47	rs343	Intron 3	0.031	NA	0.445	0.441	NA	-1.113	0.423	NA	1.785	0.256
47	rs248	Exon 4	0.034	NA	-0.104	0.848	NA	1.601	0.229	NA	2.907	0.055
48	LP15060del	Intron 3	0.022	0.849	-0.373	0.572	0.892	2.426	0.129	0.255	-1.01	0.577
48	rs343	Intron 3	0.031	NA	0.445	0.441	NA	-1.113	0.423	NA	1.785	0.256
48	rs248	Exon 4	0.034	NA	-0.104	0.848	NA	1.601	0.229	NA	2.907	0.055
48	rs116678290	Exon 4	0.006	NA	0.528	0.67	NA	2.592	0.394	NA	-0.02	0.996
49	rs343	Intron 3	0.031	0.951	0.445	0.441	0.826	-1.113	0.423	0.436	1.785	0.256
49	rs248	Exon 4	0.034	NA	-0.104	0.848	NA	1.601	0.229	NA	2.907	0.055
49	rs116678290	Exon 4	0.006	NA	0.528	0.67	NA	2.592	0.394	NA	-0.02	0.996
49	rs251	Intron 4	0.192	NA	-0.226	0.363	NA	0.547	0.372	NA	-0.33	0.635
50	rs248	Exon 4	0.034	0.83	-0.104	0.848	0.012	1.601	0.229	0.378	2.907	0.055
50	rs116678290	Exon 4	0.006	NA	0.528	0.67	NA	2.592	0.394	NA	-0.02	0.996
50	rs251	Intron 4	0.192	NA	-0.226	0.363	NA	0.547	0.372	NA	-0.33	0.635
50	rs252	Intron 4	0.093	NA	-1.037	0.002	NA	-0.832	0.313	NA	-2.36	0.012
51	rs116678290	Exon 4	0.006	0.924	0.528	0.67	0.013	2.592	0.394	0.675	-0.02	0.996
51	rs251	Intron 4	0.192	NA	-0.226	0.363	NA	0.547	0.372	NA	-0.33	0.635
51	rs252	Intron 4	0.093	NA	-1.037	0.002	NA	-0.832	0.313	NA	-2.36	0.012
51	rs255	Intron 4	0.244	NA	0.173	0.437	NA	0.344	0.527	NA	-0.06	0.926
52	rs251	Intron 4	0.192	0.852	-0.226	0.363	0.021	0.547	0.372	0.815	-0.33	0.635
52	rs252	Intron 4	0.093	NA	-1.037	0.002	NA	-0.832	0.313	NA	-2.36	0.012
52	rs255	Intron 4	0.244	NA	0.173	0.437	NA	0.344	0.527	NA	-0.06	0.926
52	rs80143795	Intron 4	0.115	NA	0.11	0.712	NA	-0.46	0.526	NA	-0.36	0.657
53	rs252	Intron 4	0.093	0.669	-1.037	0.002	0.043	-0.832	0.313	0.799	-2.36	0.012
53	rs255	Intron 4	0.244	NA	0.173	0.437	NA	0.344	0.527	NA	-0.06	0.926
53	rs80143795	Intron 4	0.115	NA	0.11	0.712	NA	-0.46	0.526	NA	-0.36	0.657
53	rs257	Intron 4	0.034	NA	0.388	0.433	NA	-0.048	0.968	NA	0.581	0.676
54	rs255	Intron 4	0.244	0.808	0.173	0.437	0.122	0.344	0.527	0.616	-0.06	0.926

Table A2.11. Continued

				TC			ApoA1			ApoB		
Win.	**Window SNP**	**Location**	**MAF**	**hap_P****	**β**	**P***	**hap_P****	**β**	**P***	**hap_P****	**β**	**P***
54	rs80143795	Intron 4	0.115	NA	0.11	0.712	NA	-0.46	0.526	NA	-0.36	0.657
54	rs257	Intron 4	0.034	NA	0.388	0.433	NA	-0.048	0.968	NA	0.581	0.676
54	rs258	Intron 4	0.035	NA	-1.339	0.011	NA	-1.827	0.151	NA	-2.02	0.164
55	rs80143795	Intron 4	0.115	0.873	0.11	0.712	0.06	-0.46	0.526	0.447	-0.36	0.657
55	rs257	Intron 4	0.034	NA	0.388	0.433	NA	-0.048	0.968	NA	0.581	0.676
55	rs258	Intron 4	0.035	NA	-1.339	0.011	NA	-1.827	0.151	NA	-2.02	0.164
55	rs259	Intron 4	0.053	NA	-0.118	0.79	NA	1.571	0.141	NA	1.092	0.37
56	rs257	Intron 4	0.034	0.917	0.388	0.433	0.152	-0.048	0.968	0.48	0.581	0.676
56	rs258	Intron 4	0.035	NA	-1.339	0.011	NA	-1.827	0.151	NA	-2.02	0.164
56	rs259	Intron 4	0.053	NA	-0.118	0.79	NA	1.571	0.141	NA	1.092	0.37
56	rs260	Intron 4	0.076	NA	-0.3	0.429	NA	0.445	0.632	NA	-0.7	0.507
57	rs258	Intron 4	0.035	0.761	-1.339	0.011	0.163	-1.827	0.151	0.433	-2.02	0.164
57	rs259	Intron 4	0.053	NA	-0.118	0.79	NA	1.571	0.141	NA	1.092	0.37
57	rs260	Intron 4	0.076	NA	-0.3	0.429	NA	0.445	0.632	NA	-0.7	0.507
57	rs261	Intron 4	0.195	NA	-0.015	0.95	NA	0.122	0.837	NA	-0.44	0.515
58	rs259	Intron 4	0.053	0.936	-0.118	0.79	0.977	1.571	0.141	0.595	1.092	0.37
58	rs260	Intron 4	0.076	NA	-0.3	0.429	NA	0.445	0.632	NA	-0.7	0.507
58	rs261	Intron 4	0.195	NA	-0.015	0.95	NA	0.122	0.837	NA	-0.44	0.515
58	rs263	Intron 4	0.359	NA	0.019	0.923	NA	-0.109	0.823	NA	-0.11	0.837
59	rs260	Intron 4	0.076	0.873	-0.3	0.429	0.895	0.445	0.632	0.748	-0.7	0.507
59	rs261	Intron 4	0.195	NA	-0.015	0.95	NA	0.122	0.837	NA	-0.44	0.515
59	rs263	Intron 4	0.359	NA	0.019	0.923	NA	-0.109	0.823	NA	-0.11	0.837
59	rs266	Intron 4	0.17	NA	-0.285	0.264	NA	0.072	0.908	NA	-0.82	0.246
60	rs261	Intron 4	0.195	0.881	-0.015	0.95	0.914	0.122	0.837	0.508	-0.44	0.515
60	rs263	Intron 4	0.359	NA	0.019	0.923	NA	-0.109	0.823	NA	-0.11	0.837
60	rs266	Intron 4	0.17	NA	-0.285	0.264	NA	0.072	0.908	NA	-0.82	0.246
60	rs144466625	Exon 6	0.001	NA	-3.504	0.184	NA	7.145	0.265	NA	-2.99	0.683
61	rs263	Intron 4	0.359	0.878	0.019	0.923	0.919	-0.109	0.823	0.364	-0.11	0.837
61	rs266	Intron 4	0.17	NA	-0.285	0.264	NA	0.072	0.908	NA	-0.82	0.246
61	rs144466625	Exon 6	0.001	NA	-3.504	0.184	NA	7.145	0.265	NA	-2.99	0.683
61	rs59184895	Intron 6	0.052	NA	0.065	0.88	NA	1.5	0.151	NA	0.501	0.672
62	rs266	Intron 4	0.17	0.744	-0.285	0.264	0.454	0.072	0.908	0.389	-0.82	0.246
62	rs144466625	Exon 6	0.001	NA	-3.504	0.184	NA	7.145	0.265	NA	-2.99	0.683
62	rs59184895	Intron 6	0.052	NA	0.065	0.88	NA	1.5	0.151	NA	0.501	0.672
62	rs269	Intron 6	0.479	NA	-0.003	0.988	NA	-0.131	0.777	NA	-0.68	0.2
63	rs144466625	Exon 6	0.001	0.886	-3.504	0.184	0.776	7.145	0.265	0.174	-2.99	0.683
63	rs59184895	Intron 6	0.052	NA	0.065	0.88	NA	1.5	0.151	NA	0.501	0.672
63	rs269	Intron 6	0.479	NA	-0.003	0.988	NA	-0.131	0.777	NA	-0.68	0.2
63	rs270	Intron 6	0.069	NA	0.018	0.961	NA	1.442	0.115	NA	1.231	0.233
64	rs59184895	Intron 6	0.052	0.94	0.065	0.88	0.952	1.5	0.151	0.142	0.501	0.672
64	rs269	Intron 6	0.479	NA	-0.003	0.988	NA	-0.131	0.777	NA	-0.68	0.2
64	rs270	Intron 6	0.069	NA	0.018	0.961	NA	1.442	0.115	NA	1.231	0.233
64	rs58935878	Intron 6	0.042	NA	0.373	0.443	NA	1.36	0.247	NA	2.105	0.115
65	rs269	Intron 6	0.479	0.457	-0.003	0.988	0.812	-0.131	0.777	0.447	-0.68	0.2
65	rs270	Intron 6	0.069	NA	0.018	0.961	NA	1.442	0.115	NA	1.231	0.233
65	rs58935878	Intron 6	0.042	NA	0.373	0.443	NA	1.36	0.247	NA	2.105	0.115
65	rs276	Intron 6	0.19	NA	0.244	0.319	NA	0.215	0.718	NA	1.02	0.131
66	rs270	Intron 6	0.069	0.698	0.018	0.961	0.38	1.442	0.115	0.519	1.231	0.233
66	rs58935878	Intron 6	0.042	NA	0.373	0.443	NA	1.36	0.247	NA	2.105	0.115
66	rs276	Intron 6	0.19	NA	0.244	0.319	NA	0.215	0.718	NA	1.02	0.131
66	rs277	Intron 6	0.11	NA	-0.313	0.298	NA	1.125	0.131	NA	0.666	0.429
67	rs58935878	Intron 6	0.042	0.806	0.373	0.443	0.489	1.36	0.247	0.247	2.105	0.115
67	rs276	Intron 6	0.19	NA	0.244	0.319	NA	0.215	0.718	NA	1.02	0.131
67	rs277	Intron 6	0.11	NA	-0.313	0.298	NA	1.125	0.131	NA	0.666	0.429
67	rs279	Intron 6	0.15	NA	0.078	0.776	NA	0.67	0.322	NA	-0.62	0.418
68	rs276	Intron 6	0.19	0.488	0.244	0.319	0.09	0.215	0.718	0.584	1.02	0.131
68	rs277	Intron 6	0.11	NA	-0.313	0.298	NA	1.125	0.131	NA	0.666	0.429
68	rs279	Intron 6	0.15	NA	0.078	0.776	NA	0.67	0.322	NA	-0.62	0.418
68	rs280	Intron 6	0.058	NA	0.77	0.059	NA	-0.177	0.86	NA	0.816	0.47
69	rs277	Intron 6	0.11	0.904	-0.313	0.298	0.208	1.125	0.131	0.267	0.666	0.429
69	rs279	Intron 6	0.15	NA	0.078	0.776	NA	0.67	0.322	NA	-0.62	0.418
69	rs280	Intron 6	0.058	NA	0.77	0.059	NA	-0.177	0.86	NA	0.816	0.47
69	rs17091775	Intron 6	0.056	NA	0.711	0.089	NA	0.001	0.999	NA	0.778	0.497
70	rs279	Intron 6	0.15	0.346	0.078	0.776	0.092	0.67	0.322	0.727	-0.62	0.418
70	rs280	Intron 6	0.058	NA	0.77	0.059	NA	-0.177	0.86	NA	0.816	0.47
70	rs17091775	Intron 6	0.056	NA	0.711	0.089	NA	0.001	0.999	NA	0.778	0.497
70	rs282	Intron 6	0.477	NA	-0.128	0.495	NA	-0.266	0.566	NA	-0.24	0.646
71	rs280	Intron 6	0.058	0.986	0.77	0.059	0.366	-0.177	0.86	0.744	0.816	0.47
71	rs17091775	Intron 6	0.056	NA	0.711	0.089	NA	0.001	0.999	NA	0.778	0.497
71	rs282	Intron 6	0.477	NA	-0.128	0.495	NA	-0.266	0.566	NA	-0.24	0.646
71	rs290	Intron 6	0.145	NA	0.102	0.721	NA	-0.153	0.826	NA	-0.37	0.627
72	rs17091775	Intron 6	0.056	0.931	0.711	0.089	0.244	0.001	0.999	0.119	0.778	0.497

Table A2.11. Continued

				TC			ApoA1			ApoB		
Win.	**Window SNP**	**Location**	**MAF**	**hap_P****	**β**	**P***	**hap_P****	**β**	**P***	**hap_P****	**β**	**P***
72	rs282	Intron 6	0.477	NA	-0.128	0.495	NA	-0.266	0.566	NA	-0.24	0.646
72	rs290	Intron 6	0.145	NA	0.102	0.721	NA	-0.153	0.826	NA	-0.37	0.627
72	rs295	Intron 6	0.39	NA	0.32	0.092	NA	0.922	0.05	NA	0.534	0.314
73	rs282	Intron 6	0.477	0.854	-0.128	0.495	0.334	-0.266	0.566	0.215	-0.24	0.646
73	rs290	Intron 6	0.145	NA	0.102	0.721	NA	-0.153	0.826	NA	-0.37	0.627
73	rs295	Intron 6	0.39	NA	0.32	0.092	NA	0.922	0.05	NA	0.534	0.314
73	rs145585712	Intron 6	0.016	NA	0.055	0.942	NA	-0.86	0.649	NA	-1.81	0.397
74	rs290	Intron 6	0.145	0.45	0.102	0.721	0.26	-0.153	0.826	0.225	-0.37	0.627
74	rs295	Intron 6	0.39	NA	0.32	0.092	NA	0.922	0.05	NA	0.534	0.314
74	rs145585712	Intron 6	0.016	NA	0.055	0.942	NA	-0.86	0.649	NA	-1.81	0.397
74	rs73601683	Intron 6	0.012	NA	0.79	0.389	NA	2.152	0.323	NA	3.612	0.143
75	rs295	Intron 6	0.39	0.601	0.32	0.092	0.391	0.922	0.05	0.009	0.534	0.314
75	rs145585712	Intron 6	0.016	NA	0.055	0.942	NA	-0.86	0.649	NA	-1.81	0.397
75	rs73601683	Intron 6	0.012	NA	0.79	0.389	NA	2.152	0.323	NA	3.612	0.143
75	rs299	Intron 6	0.007	NA	-0.241	0.831	NA	7.236	0.006	NA	-4.95	0.097
76	rs145585712	Intron 6	0.016	0.587	0.055	0.942	0.939	-0.86	0.649	0.068	-1.81	0.397
76	rs73601683	Intron 6	0.012	NA	0.79	0.389	NA	2.152	0.323	NA	3.612	0.143
76	rs299	Intron 6	0.007	NA	-0.241	0.831	NA	7.236	0.006	NA	-4.95	0.097
76	rs300	Intron 6	0.011	NA	0.062	0.947	NA	0.361	0.875	NA	-0.11	0.965
77	rs73601683	Intron 6	0.012	0.439	0.79	0.389	0.446	2.152	0.323	0.015	3.612	0.143
77	rs299	Intron 6	0.007	NA	-0.241	0.831	NA	7.236	0.006	NA	-4.95	0.097
77	rs300	Intron 7	0.011	NA	0.062	0.947	NA	0.361	0.875	NA	-0.11	0.965
77	rs301	Intron 7	0.288	NA	0.285	0.176	NA	1.103	0.035	NA	0.817	0.164
78	rs299	Intron 6	0.007	0.774	-0.241	0.831	0.735	7.236	0.006	0.015	-4.95	0.097
78	rs300	Intron 7	0.011	NA	0.062	0.947	NA	0.361	0.875	NA	-0.11	0.965
78	rs301	Intron 7	0.288	NA	0.285	0.176	NA	1.103	0.035	NA	0.817	0.164
78	rs313	Intron 7	0.15	NA	0.078	0.775	NA	0.001	0.999	NA	-0.12	0.879
79	rs300	Intron 7	0.011	0.796	0.062	0.947	0.859	0.361	0.875	0.198	-0.11	0.965
79	rs301	Intron 7	0.288	NA	0.285	0.176	NA	1.103	0.035	NA	0.817	0.164
79	rs313	Intron 7	0.15	NA	0.078	0.775	NA	0.001	0.999	NA	-0.12	0.879
79	rs314	Intron 7	0.248	NA	-0.184	0.403	NA	-0.051	0.923	NA	0.479	0.428
80	rs301	Intron 7	0.288	0.777	0.285	0.176	0.84	1.103	0.035	0.048	0.817	0.164
80	rs313	Intron 7	0.15	NA	0.078	0.775	NA	0.001	0.999	NA	-0.12	0.879
80	rs314	Intron 7	0.248	NA	-0.184	0.403	NA	-0.051	0.923	NA	0.479	0.428
80	rs77434393	Intron 7	0.024	NA	0.252	0.689	NA	2.717	0.076	NA	2.216	0.212
81	rs313	Intron 7	0.15	0.436	0.078	0.775	0.864	0.001	0.999	0.021	-0.12	0.879
81	rs314	Intron 7	0.248	NA	-0.184	0.403	NA	-0.051	0.923	NA	0.479	0.428
81	rs77434393	Intron 7	0.024	NA	0.252	0.689	NA	2.717	0.076	NA	2.216	0.212
81	rs316	Exon 8	0.225	NA	0.16	0.49	NA	1.292	0.022	NA	0.192	0.764
82	rs314	Intron 7	0.248	0.715	-0.184	0.403	0.878	-0.051	0.923	0.024	0.479	0.428
82	rs77434393	Intron 7	0.024	NA	0.252	0.689	NA	2.717	0.076	NA	2.216	0.212
82	rs316	Exon 8	0.225	NA	0.16	0.49	NA	1.292	0.022	NA	0.192	0.764
82	rs5934	Exon 8	0.033	NA	0.144	0.791	NA	1.792	0.184	NA	2.083	0.167
83	rs77434393	Intron 7	0.024	0.815	0.252	0.689	0.918	2.717	0.076	0.011	2.216	0.212
83	rs316	Exon 8	0.225	NA	0.16	0.49	NA	1.292	0.022	NA	0.192	0.764
83	rs5934	Exon 8	0.033	NA	0.144	0.791	NA	1.792	0.184	NA	2.083	0.167
83	rs318	Intron 8	0.139	NA	-0.171	0.534	NA	-1.324	0.052	NA	-0.61	0.425
84	rs316	Exon 8	0.225	0.845	0.16	0.49	0.945	1.292	0.022	0.019	0.192	0.764
84	rs5934	Exon 8	0.033	NA	0.144	0.791	NA	1.792	0.184	NA	2.083	0.167
84	rs318	Intron 8	0.139	NA	-0.171	0.534	NA	-1.324	0.052	NA	-0.61	0.425
84	rs319	Intron 8	0.082	NA	0.078	0.824	NA	1.692	0.05	NA	1.315	0.179
85	rs5934	Exon 8	0.033	0.854	0.144	0.791	0.935	1.792	0.184	0.128	2.083	0.167
85	rs318	Intron 8	0.139	NA	-0.171	0.534	NA	-1.324	0.052	NA	-0.61	0.425
85	rs319	Intron 8	0.082	NA	0.078	0.824	NA	1.692	0.05	NA	1.315	0.179
85	rs321	Intron 8	0.009	NA	0.636	0.556	NA	-1.412	0.581	NA	1.183	0.683
86	rs318	Intron 8	0.139	0.575	-0.171	0.534	0.519	-1.324	0.052	0.062	-0.61	0.425
86	rs319	Intron 8	0.082	NA	0.078	0.824	NA	1.692	0.05	NA	1.315	0.179
86	rs321	Intron 8	0.009	NA	0.636	0.556	NA	-1.412	0.581	NA	1.183	0.683
86	rs325	Intron 8	0.043	NA	0.726	0.116	NA	1.557	0.165	NA	3.433	0.007
87	rs319	Intron 8	0.082	0.513	0.078	0.824	0.565	1.692	0.05	0.197	1.315	0.179
87	rs321	Intron 8	0.009	NA	0.636	0.556	NA	-1.412	0.581	NA	1.183	0.683
87	rs325	Intron 8	0.043	NA	0.726	0.116	NA	1.557	0.165	NA	3.433	0.007
87	rs326	Intron 8	0.398	NA	-0.071	0.725	NA	0.172	0.725	NA	0.44	0.429
88	rs321	Intron 8	0.009	0.586	0.636	0.556	0.31	-1.412	0.581	0.527	1.183	0.683
88	rs325	Intron 8	0.043	NA	0.726	0.116	NA	1.557	0.165	NA	3.433	0.007
88	rs326	Intron 8	0.398	NA	-0.071	0.725	NA	0.172	0.725	NA	0.44	0.429
88	rs149089920	Exon 9	0.001	NA	2.937	0.266	NA	1.045	0.871	NA	10.61	0.147
89	rs325	Intron 8	0.043	0.467	0.726	0.116	0.358	1.557	0.165	0.551	3.433	0.007
89	rs326	Intron 8	0.398	NA	-0.071	0.725	NA	0.172	0.725	NA	0.44	0.429
89	rs149089920	Exon 9	0.001	NA	2.937	0.266	NA	1.045	0.871	NA	10.61	0.147
89	rs328	Exon 9	0.042	NA	0.751	0.102	NA	1.227	0.273	NA	3.792	0.003
90	rs326	Intron 8	0.398	0.722	-0.071	0.725	0.294	0.172	0.725	0.511	0.44	0.429

Table A2.11. Continued

				TC			ApoA1			ApoB		
Win.	Window SNP	Location	MAF	hap_P**	β	P*	hap_P**	β	P*	hap_P**	β	P*
90	rs149089920	Exon 9	0.001	NA	2.937	0.266	NA	1.045	0.871	NA	10.61	0.147
90	rs328	Exon 9	0.042	NA	0.751	0.102	NA	1.227	0.273	NA	3.792	0.003
90	rs329	Intron 9	0.097	NA	-0.558	0.092	NA	-0.537	0.518	NA	-1.81	0.048
91	rs149089920	Exon 9	0.001	0.898	2.937	0.266	0.106	1.045	0.871	0.119	10.61	0.147
91	rs328	Exon 9	0.042	NA	0.751	0.102	NA	1.227	0.273	NA	3.792	0.003
91	rs329	Intron 9	0.097	NA	-0.558	0.092	NA	-0.537	0.518	NA	-1.81	0.048
91	rs330	Intron 9	0.085	NA	0.354	0.317	NA	2.031	0.019	NA	0.886	0.364
92	rs328	Exon 9	0.042	0.774	0.751	0.102	0.171	1.227	0.273	0.037	3.792	0.003
92	rs329	Intron 9	0.097	NA	-0.558	0.092	NA	-0.537	0.518	NA	-1.81	0.048
92	rs330	Intron 9	0.085	NA	0.354	0.317	NA	2.031	0.019	NA	0.886	0.364
92	rs138285812	Intron 9	0.025	NA	0.082	0.895	NA	-2.894	0.06	NA	1.042	0.555
93	rs329	Intron 9	0.097	0.887	-0.558	0.092	0.188	-0.537	0.518	0.004	-1.81	0.048
93	rs330	Intron 9	0.085	NA	0.354	0.317	NA	2.031	0.019	NA	0.886	0.364
93	rs138285812	Intron 9	0.025	NA	0.082	0.895	NA	-2.894	0.06	NA	1.042	0.555
93	rs12679834	Intron 9	0.058	NA	0.424	0.289	NA	2.207	0.024	NA	2.711	0.015
94	rs330	Intron 9	0.085	0.835	0.354	0.317	0.556	2.031	0.019	0.005	0.886	0.364
94	rs138285812	Intron 9	0.025	NA	0.082	0.895	NA	-2.894	0.06	NA	1.042	0.555
94	rs12679834	Intron 9	0.058	NA	0.424	0.289	NA	2.207	0.024	NA	2.711	0.015
94	rs76423146	Intron 9	0.157	NA	-0.188	0.459	NA	-0.292	0.639	NA	-1.07	0.133
95	rs138285812	Intron 9	0.025	0.737	0.082	0.895	0.677	-2.894	0.06	0.116	1.042	0.555
95	rs12679834	Intron 9	0.058	NA	0.424	0.289	NA	2.207	0.024	NA	2.711	0.015
95	rs76423146	Intron 9	0.157	NA	-0.188	0.459	NA	-0.292	0.639	NA	-1.07	0.133
95	rs28599962	Intron 9	0.021	NA	-0.463	0.496	NA	0.671	0.69	NA	1.052	0.58
96	rs12679834	Intron 9	0.058	0.105	0.424	0.289	0.302	2.207	0.024	0.246	2.711	0.015
96	rs76423146	Intron 9	0.157	NA	-0.188	0.459	NA	-0.292	0.639	NA	-1.07	0.133
96	rs28599962	Intron 9	0.021	NA	-0.463	0.496	NA	0.671	0.69	NA	1.052	0.58
96	LP25579	Intron 9	0.005	NA	-2.403	0.07	NA	-1.656	0.607	NA	0.23	0.953
97	rs76423146	Intron 9	0.157	0.133	-0.188	0.459	0.687	-0.292	0.639	0.968	-1.07	0.133
97	rs28599962	Intron 9	0.021	NA	-0.463	0.496	NA	0.671	0.69	NA	1.052	0.58
97	LP25579	Intron 9	0.005	NA	-2.403	0.07	NA	-1.656	0.607	NA	0.23	0.953
97	rs28716400	Intron 9	0.152	NA	0.125	0.641	NA	0.318	0.63	NA	-0.37	0.622
98	rs28599962	Intron 9	0.021	0.043	-0.463	0.496	0.336	0.671	0.69	0.921	1.052	0.58
98	LP25579	Intron 9	0.005	NA	-2.403	0.07	NA	-1.656	0.607	NA	0.23	0.953
98	rs28716400	Intron 9	0.152	NA	0.125	0.641	NA	0.318	0.63	NA	-0.37	0.622
98	rs75946927	Intron 9	0.087	NA	0.382	0.27	NA	-0.51	0.544	NA	0.679	0.484
99	LP25579	Intron 9	0.005	0.203	-2.403	0.07	0.385	-1.656	0.607	0.855	0.23	0.953
99	rs28716400	Intron 9	0.152	NA	0.125	0.641	NA	0.318	0.63	NA	-0.37	0.622
99	rs75946927	Intron 9	0.087	NA	0.382	0.27	NA	-0.51	0.544	NA	0.679	0.484
99	rs147900112	Intron 9	0.157	NA	0.017	0.949	NA	0.043	0.946	NA	-0.29	0.692
100	rs28716400	Intron 9	0.152	0.231	0.125	0.641	0.845	0.318	0.63	0.14	-0.37	0.622
100	rs75946927	Intron 9	0.087	NA	0.382	0.27	NA	-0.51	0.544	NA	0.679	0.484
100	rs147900112	Intron 9	0.157	NA	0.017	0.949	NA	0.043	0.946	NA	-0.29	0.692
100	rs114236375	Intron 9	0.012	NA	-0.33	0.71	NA	5.479	0.012	NA	0.689	0.779
101	rs75946927	Intron 9	0.087	0.265	0.382	0.27	0.807	-0.51	0.544	0.11	0.679	0.484
101	rs147900112	Intron 9	0.157	NA	0.017	0.949	NA	0.043	0.946	NA	-0.29	0.692
101	rs114236375	Intron 9	0.012	NA	-0.33	0.71	NA	5.479	0.012	NA	0.689	0.779
101	rs7818177	Exon 10 UTR	0.015	NA	-0.385	0.623	NA	1.683	0.388	NA	0.236	0.914
102	rs147900112	Intron 9	0.157	0.298	0.017	0.949	0.962	0.043	0.946	0.087	-0.29	0.692
102	rs114236375	Intron 9	0.012	NA	-0.33	0.71	NA	5.479	0.012	NA	0.689	0.779
102	rs7818177	Exon 10 UTR	0.015	NA	-0.385	0.623	NA	1.683	0.388	NA	0.236	0.914
102	LP27629	Exon 10 UTR	0.001	NA	-1.23	0.642	NA	3.559	0.581	NA	9.585	0.19
103	rs114236375	Intron 9	0.012	0.238	-0.33	0.71	0.92	5.479	0.012	0.06	0.689	0.779
103	rs7818177	Exon 10 UTR	0.015	NA	-0.385	0.623	NA	1.683	0.388	NA	0.236	0.914
103	LP27629	Exon 10 UTR	0.001	NA	-1.23	0.642	NA	3.559	0.581	NA	9.585	0.19
103	LP27695	Exon 10 UTR	0.001	NA	0.862	0.816	NA	-8.61	0.349	NA	8.985	0.387
104	rs7818177	Exon 10 UTR	0.015	0.735	-0.385	0.623	0.717	1.683	0.388	0.385	0.236	0.914
104	LP27629	Exon 10 UTR	0.001	NA	-1.23	0.642	NA	3.559	0.581	NA	9.585	0.19
104	LP27695	Exon 10 UTR	0.001	NA	0.862	0.816	NA	-8.61	0.349	NA	8.985	0.387
104	LP27706	Exon 10 UTR	0.001	NA	-1.686	0.521	NA	-10.51	0.103	NA	-7.19	0.327
105	LP27629	Exon 10 UTR	0.001	0.977	-1.23	0.642	0.579	3.559	0.581	0.733	9.585	0.19
105	LP27695	Exon 10 UTR	0.001	NA	0.862	0.816	NA	-8.61	0.349	NA	8.985	0.387
105	LP27706	Exon 10 UTR	0.001	NA	-1.686	0.521	NA	-10.51	0.103	NA	-7.19	0.327
105	rs187587525	Exon 10 UTR	0.003	NA	-0.295	0.86	NA	2.587	0.525	NA	6.413	0.162
106	LP27695	Exon 10 UTR	0.001	0.977	0.862	0.816	0.578	-8.61	0.349	0.733	8.985	0.387
106	LP27706	Exon 10 UTR	0.001	NA	-1.686	0.521	NA	-10.51	0.103	NA	-7.19	0.327
106	rs187587525	Exon 10 UTR	0.003	NA	-0.295	0.86	NA	2.587	0.525	NA	6.413	0.162
106	LP27969	Exon 10 UTR	0.001	NA	-1.22	0.645	NA	3.566	0.579	NA	9.59	0.191
107	LP27706	Exon 10 UTR	0.001	0.775	-1.686	0.521	0.424	-10.51	0.103	0.294	-7.19	0.327
107	rs187587525	Exon 10 UTR	0.003	NA	-0.295	0.86	NA	2.587	0.525	NA	6.413	0.162
107	LP27969	Exon 10 UTR	0.001	NA	-1.22	0.645	NA	3.566	0.579	NA	9.59	0.191
107	rs11570892	Exon 10 UTR	0.24	NA	0.241	0.286	NA	0.825	0.137	NA	0.5	0.423
108	rs187587525	Exon 10 UTR	0.003	0.838	-0.295	0.86	0.618	2.587	0.525	0.295	6.413	0.162

Table A2.11. Continued

				TC			ApoA1			ApoB		
Win.	**Window SNP**	**Location**	**MAF**	**hap_*P*****	**β**	***P****	**hap_*P*****	**β**	***P****	**hap_*P*****	**β**	***P****
108	LP27969	Exon 10 UTR	0.001	NA	-1.22	0.645	NA	3.566	0.579	NA	9.59	0.191
108	rs11570892	Exon 10 UTR	0.24	NA	0.241	0.286	NA	0.825	0.137	NA	0.5	0.423
108	rs3208305	Exon 10 UTR	0.443	NA	-0.267	0.171	NA	-0.204	0.669	NA	-0.07	0.895
109	LP27969	Exon 10 UTR	0.001	0.963	-1.22	0.645	0.707	3.566	0.579	0.171	9.59	0.191
109	rs11570892	Exon 10 UTR	0.24	NA	0.241	0.286	NA	0.825	0.137	NA	0.5	0.423
109	rs3208305	Exon 10 UTR	0.443	NA	-0.267	0.171	NA	-0.204	0.669	NA	-0.07	0.895
109	rs1059507	Exon 10 UTR	0.103	NA	0.362	0.267	NA	1.77	0.025	NA	0.995	0.267
110	rs11570892	Exon 10 UTR	0.24	0.594	0.241	0.286	0.445	0.825	0.137	0.105	0.5	0.423
110	rs3208305	Exon 10 UTR	0.443	NA	-0.267	0.171	NA	-0.204	0.669	NA	-0.07	0.895
110	rs1059507	Exon 10 UTR	0.103	NA	0.362	0.267	NA	1.77	0.025	NA	0.995	0.267
110	rs3200218	Exon 10 UTR	0.093	NA	0.159	0.637	NA	1.252	0.13	NA	1.57	0.092
111	rs3208305	Exon 10 UTR	0.443	0.901	-0.267	0.171	0.654	-0.204	0.669	0.078	-0.07	0.895
111	rs1059507	Exon 10 UTR	0.103	NA	0.362	0.267	NA	1.77	0.025	NA	0.995	0.267
111	rs3200218	Exon 10 UTR	0.093	NA	0.159	0.637	NA	1.252	0.13	NA	1.57	0.092
111	rs139240067	Exon 10 UTR	0.013	NA	-0.361	0.677	NA	0.056	0.979	NA	-1.76	0.463
112	rs1059507	Exon 10 UTR	0.103	0.792	0.362	0.267	0.763	1.77	0.025	0.096	0.995	0.267
112	rs3200218	Exon 10 UTR	0.093	NA	0.159	0.637	NA	1.252	0.13	NA	1.57	0.092
112	rs139240067	Exon 10 UTR	0.013	NA	-0.361	0.677	NA	0.056	0.979	NA	-1.76	0.463
112	rs184363931	Exon 10 UTR	0.009	NA	0.005	0.996	NA	-0.457	0.853	NA	3.812	0.169
113	rs3200218	Exon 10 UTR	0.093	0.815	0.159	0.637	0.694	1.252	0.13	0.392	1.57	0.092
113	rs139240067	Exon 10 UTR	0.013	NA	-0.361	0.677	NA	0.056	0.979	NA	-1.76	0.463
113	rs184363931	Exon 10 UTR	0.009	NA	0.005	0.996	NA	-0.457	0.853	NA	3.812	0.169
113	rs13702	Exon 10 UTR	0.459	NA	-0.209	0.279	NA	-0.386	0.416	NA	-0.08	0.881
114	rs139240067	Exon 10 UTR	0.013	0.954	-0.361	0.677	0.849	0.056	0.979	0.828	-1.76	0.463
114	rs184363931	Exon 10 UTR	0.009	NA	0.005	0.996	NA	-0.457	0.853	NA	3.812	0.169
114	rs13702	Exon 10 UTR	0.459	NA	-0.209	0.279	NA	-0.386	0.416	NA	-0.08	0.881
114	rs17091815	Exon 10 UTR	0.084	NA	0.166	0.643	NA	-0.605	0.496	NA	-1.39	0.165
115	rs184363931	Exon 10 UTR	0.009	0.592	0.005	0.996	0.429	-0.457	0.853	0.454	3.812	0.169
115	rs13702	Exon 10 UTR	0.459	NA	-0.209	0.279	NA	-0.386	0.416	NA	-0.08	0.881
115	rs17091815	Exon 10 UTR	0.084	NA	0.166	0.643	NA	-0.605	0.496	NA	-1.39	0.165
115	rs78359368	Exon 10 UTR	0.007	NA	-2.561	0.031	NA	-4.465	0.123	NA	-0.05	0.989
116	rs13702	Exon 10 UTR	0.459	0.13	-0.209	0.279	0.139	-0.386	0.416	0.323	-0.08	0.881
116	rs17091815	Exon 10 UTR	0.084	NA	0.166	0.643	NA	-0.605	0.496	NA	-1.39	0.165
116	rs78359368	Exon 10 UTR	0.007	NA	-2.561	0.031	NA	-4.465	0.123	NA	-0.05	0.989
116	rs187374932	Exon 10 UTR	0.005	NA	-2.801	0.034	NA	-3.984	0.22	NA	0.424	0.914
117	rs17091815	Exon 10 UTR	0.084	0.086	0.166	0.643	0.112	-0.605	0.496	0.075	-1.39	0.165
117	rs78359368	Exon 10 UTR	0.007	NA	-2.561	0.031	NA	-4.465	0.123	NA	-0.05	0.989
117	rs187374932	Exon 10 UTR	0.005	NA	-2.801	0.034	NA	-3.984	0.22	NA	0.424	0.914
117	rs147116359	Exon 10 UTR	0.011	NA	0.916	0.283	NA	4.319	0.04	NA	1.001	0.673
118	rs78359368	Exon 10 UTR	0.007	0.098	-2.561	0.031	0.089	-4.465	0.123	0.03	-0.05	0.989
118	rs187374932	Exon 10 UTR	0.005	NA	-2.801	0.034	NA	-3.984	0.22	NA	0.424	0.914
118	rs147116359	Exon 10 UTR	0.011	NA	0.916	0.283	NA	4.319	0.04	NA	1.001	0.673
118	rs79756214	Exon 10 UTR	0.016	NA	-0.631	0.415	NA	-3.037	0.115	NA	0.725	0.741
119	rs187374932	Exon 10 UTR	0.005	0.068	-2.801	0.034	0.105	-3.984	0.22	0.052	0.424	0.914
119	rs147116359	Exon 10 UTR	0.011	NA	0.916	0.283	NA	4.319	0.04	NA	1.001	0.673
119	rs79756214	Exon 10 UTR	0.016	NA	-0.631	0.415	NA	-3.037	0.115	NA	0.725	0.741
119	rs3916027	Exon 10 UTR	0.413	NA	0.298	0.123	NA	0.814	0.085	NA	0.318	0.554
120	rs147116359	Exon 10 UTR	0.011	0.849	0.916	0.283	0.485	4.319	0.04	0.055	1.001	0.673
120	rs79756214	Exon 10 UTR	0.016	NA	-0.631	0.415	NA	-3.037	0.115	NA	0.725	0.741
120	rs3916027	Exon 10 UTR	0.413	NA	0.298	0.123	NA	0.814	0.085	NA	0.318	0.554
120	rs4921683	Exon 10 UTR	0.102	NA	0.438	0.184	NA	1.911	0.017	NA	0.856	0.345
121	rs79756214	Exon 10 UTR	0.016	0.973	-0.631	0.415	0.608	-3.037	0.115	0.121	0.725	0.741
121	rs3916027	Exon 10 UTR	0.413	NA	0.298	0.123	NA	0.814	0.085	NA	0.318	0.554
121	rs4921683	Exon 10 UTR	0.102	NA	0.438	0.184	NA	1.911	0.017	NA	0.856	0.345
121	rs76707496	Exon 10 UTR	0.09	NA	0.138	0.679	NA	-0.358	0.667	NA	-1.19	0.202
122	rs3916027	Exon 10 UTR	0.413	0.673	0.298	0.123	0.581	0.814	0.085	0.172	0.318	0.554
122	rs4921683	Exon 10 UTR	0.102	NA	0.438	0.184	NA	1.911	0.017	NA	0.856	0.345
122	rs76707496	Exon 10 UTR	0.09	NA	0.138	0.679	NA	-0.358	0.667	NA	-1.19	0.202
122	rs4921684	Exon 10 UTR	0.079	NA	0.518	0.154	NA	1.983	0.026	NA	0.246	0.807

W: Allele in the referecne sequence (NC_00008.10).; D: Deleted base/bases; I: Inserted base/bases

Table A2.12. Summary of *LPL* 4-SNP sliding haplotype association with TG in African blacks (n=788)

	Window	loc.1	loc.2	loc.3	loc.4	Hap.freq.	Coef.	S.E.	Test statistic	*P*-value
	1	G	C	A	G	0.111	-0.001	0.012	-0.044	0.965
Geno.1	1	G	T	A	G	0.094	-0.001	0.012	-0.052	0.958
Geno.3	1	G	T	G	G	0.146	0.003	0.011	0.317	0.751
Geno.4	1	T	C	A	G	0.111	0.007	0.012	0.578	0.563
Geno.6	1	*	*	*	*	0.006	0.041	0.045	0.895	0.371
Geno.rare	1	G	T	G	T	0.532	NA	NA	NA	NA
haplo.base	2	C	A	G	A	0.019	-0.035	0.026	-1.350	0.177
Geno.11	2	C	A	G	T	0.202	0.006	0.009	0.690	0.490
Geno.2	2	T	A	G	T	0.096	0.000	0.012	0.037	0.971
Geno.61	2	T	G	G	T	0.146	0.004	0.011	0.337	0.736
Geno.7	2	*	*	*	*	0.005	0.043	0.046	0.938	0.348
Geno.rare1	2	T	G	T	T	0.532	NA	NA	NA	NA
haplo.base1	3	A	G	A	A	0.019	-0.036	0.026	-1.382	0.167
Geno.12	3	A	G	T	A	0.297	0.005	0.008	0.594	0.552
Geno.21	3	G	G	T	A	0.151	0.004	0.011	0.334	0.739
Geno.41	3	G	T	T	A	0.532	NA	NA	NA	NA
haplo.base2	4	G	A	A	W	0.019	-0.038	0.026	-1.436	0.151
Geno.22	4	G	T	A	W	0.449	0.004	0.007	0.585	0.558
Geno.31	4	T	T	A	I	0.028	0.007	0.022	0.329	0.742
Geno.5	4	T	T	A	W	0.503	NA	NA	NA	NA
haplo.base3	5	A	A	W	G	0.018	-0.043	0.027	-1.606	0.109
Geno.32	5	T	A	I	G	0.027	0.003	0.022	0.160	0.873
Geno.51	5	*	*	*	*	0.010	0.030	0.043	0.704	0.482
Geno.rare2	5	T	A	W	G	0.945	NA	NA	NA	NA
haplo.base4	6	A	I	G	C	0.028	0.005	0.021	0.223	0.824
Geno.23	6	*	*	*	*	0.014	-0.033	0.032	-1.044	0.297
Geno.rare3	6	A	W	G	C	0.958	NA	NA	NA	NA
haplo.base5	7	I	G	C	C	0.028	0.005	0.021	0.240	0.810
Geno.24	7	W	G	C	T	0.030	0.009	0.021	0.438	0.661
Geno.62	7	*	*	*	*	0.013	-0.034	0.032	-1.057	0.291
Geno.rare4	7	W	G	C	C	0.929	NA	NA	NA	NA
haplo.base6	8	G	C	C	A	0.033	0.036	0.019	1.899	0.058
Geno.42	8	G	C	T	G	0.028	0.013	0.022	0.584	0.559
Geno.71	8	*	*	*	*	0.015	-0.035	0.032	-1.115	0.265
Geno.rare5	8	G	C	C	G	0.924	NA	NA	NA	NA
haplo.base7	9	C	C	A	G	0.039	0.041	0.017	2.343	0.019
Geno.13	9	C	C	G	T	0.022	-0.015	0.025	-0.598	0.550
Geno.43	9	C	T	G	G	0.028	0.014	0.022	0.638	0.523
Geno.63	9	*	*	*	*	0.008	-0.117	0.056	-2.090	0.037
Geno.rare6	9	C	C	G	G	0.903	NA	NA	NA	NA
haplo.base8	10	C	A	G	C	0.040	0.035	0.017	2.061	0.040
Geno.14	10	C	G	G	T	0.037	-0.044	0.019	-2.323	0.020
Geno.52	10	C	G	T	C	0.021	-0.008	0.026	-0.300	0.764
Geno.64	10	T	G	G	C	0.029	0.011	0.022	0.511	0.609
Geno.9	10	*	*	*	*	0.003	-0.126	NA	NA	NA
Geno.rare7	10	C	G	G	C	0.871	NA	NA	NA	NA
haplo.base9	11	A	G	C	G	0.041	0.032	0.017	1.857	0.064
Geno.25	11	G	G	C	C	0.022	-0.016	0.024	-0.664	0.507
Geno.53	11	G	G	T	G	0.037	-0.049	0.019	-2.586	0.010
Geno.72	11	G	T	C	G	0.023	-0.020	0.024	-0.818	0.413
Geno.8	11	G	G	C	G	0.876	NA	NA	NA	NA
haplo.base10	12	G	C	C	C	0.022	-0.017	0.024	-0.717	0.474
Geno.15	12	G	C	G	T	0.038	0.020	0.018	1.112	0.267
Geno.44	12	G	T	G	C	0.033	-0.031	0.020	-1.557	0.120
Geno.54	12	T	C	G	C	0.022	-0.015	0.025	-0.592	0.554

Table A2.12. Continued

	Window	loc.1	loc.2	loc.3	loc.4	Hap.freq.	Coef.	S.E.	Test statistic	*P*-value
Geno.73	12	*	*	*	*	0.004	-0.202	0.064	-3.154	0.002
Geno.rare8	12	G	C	G	C	0.880	NA	NA	NA	NA
haplo.base11	13	C	C	C	G	0.021	-0.012	0.025	-0.469	0.639
Geno.26	13	C	G	C	C	0.077	-0.007	0.013	-0.551	0.582
Geno.45	13	C	G	T	C	0.039	0.018	0.018	0.973	0.331
Geno.65	13	T	G	C	G	0.034	-0.037	0.020	-1.870	0.062
Geno.81	13	*	*	*	*	0.004	-0.187	0.064	-2.907	0.004
Geno.rare9	13	C	G	C	G	0.825	NA	NA	NA	NA
haplo.base12	14	C	C	G	A	0.022	-0.009	0.025	-0.366	0.714
Geno.33	14	G	C	C	G	0.077	0.002	0.014	0.128	0.899
Geno.74	14	G	C	G	A	0.426	0.008	0.007	1.127	0.260
Geno.82	14	G	T	C	G	0.041	0.013	0.018	0.726	0.468
Geno.111	14	*	*	*	*	0.002	-0.173	0.089	-1.947	0.052
Geno.rare10	14	G	C	G	G	0.432	NA	NA	NA	NA
haplo.base13	15	C	C	G	T	0.076	-0.007	0.014	-0.503	0.615
Geno.34	15	C	G	G	G	0.023	-0.019	0.024	-0.801	0.424
Geno.66	15	C	G	G	T	0.409	-0.006	0.008	-0.799	0.425
Geno.75	15	T	C	G	T	0.041	0.002	0.018	0.088	0.930
Geno.91	15	*	*	*	*	0.003	-0.045	0.078	-0.575	0.565
Geno.rare11	15	C	G	A	T	0.447	NA	NA	NA	NA
haplo.base14	16	C	G	T	A	0.117	0.002	0.012	0.135	0.893
Geno.35	16	G	A	T	A	0.142	0.001	0.011	0.098	0.922
Geno.76	16	G	A	T	G	0.305	0.008	0.008	0.994	0.320
Geno.83	16	G	G	G	A	0.023	-0.012	0.025	-0.484	0.628
Geno.92	16	*	*	*	*	0.005	-0.051	0.060	-0.847	0.397
Geno.rare12	16	G	G	T	A	0.409	NA	NA	NA	NA
haplo.base15	17	A	T	A	T	0.143	-0.001	0.011	-0.085	0.932
Geno.36	17	A	T	G	T	0.306	0.007	0.008	0.895	0.371
Geno.55	17	G	G	A	T	0.023	-0.015	0.024	-0.617	0.538
Geno.77	17	G	T	A	C	0.030	-0.012	0.021	-0.578	0.564
Geno.93	17	*	*	*	*	0.003	0.022	0.080	0.273	0.785
Geno.rare13	17	G	T	A	T	0.495	NA	NA	NA	NA
haplo.base16	18	G	A	T	T	0.023	-0.005	0.024	-0.201	0.841
Geno.27	18	T	A	C	T	0.030	-0.011	0.021	-0.506	0.613
Geno.46	18	T	A	T	C	0.024	0.031	0.023	1.330	0.184
Geno.56	18	T	G	T	C	0.309	0.009	0.008	1.099	0.272
Geno.78	18	*	*	*	*	0.001	-0.033	0.106	-0.316	0.752
Geno.rare14	18	T	A	T	T	0.612	NA	NA	NA	NA
haplo.base17	19	A	C	T	G	0.029	-0.010	0.021	-0.477	0.633
Geno.28	19	A	T	C	G	0.024	0.030	0.023	1.285	0.199
Geno.47	19	G	T	C	A	0.282	0.009	0.008	1.201	0.230
Geno.84	19	G	T	C	G	0.026	0.000	0.023	0.004	0.997
Geno.94	19	*	*	*	*	0.004	0.002	0.061	0.033	0.973
Geno.rare15	19	A	T	T	G	0.636	NA	NA	NA	NA
haplo.base18	20	C	T	G	A	0.028	-0.010	0.021	-0.463	0.643
Geno.48	20	T	C	A	G	0.278	0.006	0.008	0.736	0.462
Geno.79	20	T	C	G	A	0.046	0.013	0.017	0.756	0.450
Geno.85	20	*	*	*	*	0.012	0.027	0.036	0.745	0.456
Geno.rare16	20	T	T	G	A	0.635	NA	NA	NA	NA
haplo.base19	21	C	A	G	C	0.166	0.013	0.010	1.312	0.190
Geno.37	21	C	A	G	T	0.111	-0.003	0.011	-0.287	0.774
Geno.49	21	C	G	A	T	0.047	0.013	0.017	0.754	0.451
Geno.57	21	*	*	*	*	0.011	0.032	0.039	0.810	0.418
Geno.rare17	21	T	G	A	T	0.664	NA	NA	NA	NA
haplo.base20	22	A	G	C	A	0.166	0.012	0.010	1.237	0.216
Geno.38	22	A	G	T	A	0.111	-0.004	0.011	-0.352	0.725
Geno.58	22	G	A	T	G	0.030	0.006	0.021	0.293	0.770
Geno.710	22	*	*	*	*	0.011	0.031	0.038	0.803	0.422
Geno.rare18	22	G	A	T	A	0.681	NA	NA	NA	NA

Table A2.12. Continued

	Window	loc.1	loc.2	loc.3	loc.4	Hap.freq.	Coef.	S.E.	Test statistic	*P*-value
haplo.base21	23	A	T	G	D	0.030	0.009	0.021	0.452	0.651
Geno.39	23	G	C	A	W	0.168	0.012	0.010	1.206	0.228
Geno.410	23	G	T	A	W	0.113	-0.005	0.011	-0.475	0.635
Geno.67	23	*	*	*	*	0.001	0.064	0.000	1.45E+16	0.000
Geno.rare19	23	A	T	A	W	0.688	NA	NA	NA	NA
haplo.base22	24	C	A	W	T	0.166	0.015	0.010	1.545	0.123
Geno.16	24	T	A	W	C	0.013	0.010	0.032	0.318	0.751
Geno.310	24	T	G	D	T	0.030	0.010	0.021	0.504	0.614
Geno.59	24	T	A	W	T	0.791	NA	NA	NA	NA
haplo.base23	25	A	W	C	A	0.013	0.010	0.032	0.310	0.757
Geno.17	25	A	W	T	G	0.246	0.008	0.008	1.014	0.311
Geno.411	25	G	D	T	A	0.030	0.010	0.021	0.499	0.618
Geno.510	25	A	W	T	A	0.711	NA	NA	NA	NA
haplo.base24	26	D	T	A	A	0.030	0.007	0.021	0.348	0.728
Geno.18	26	W	C	A	A	0.013	0.010	0.032	0.310	0.757
Geno.412	26	W	T	G	A	0.196	0.008	0.009	0.935	0.350
Geno.86	26	W	T	G	C	0.050	0.008	0.017	0.468	0.640
Geno.95	26	*	*	*	*	0.003	0.042	0.079	0.532	0.595
Geno.rare20	26	W	T	A	A	0.708	NA	NA	NA	NA
haplo.base25	27	C	A	A	G	0.013	0.010	0.032	0.298	0.766
Geno.19	27	T	G	A	G	0.189	0.007	0.009	0.720	0.472
Geno.68	27	T	G	C	G	0.050	0.007	0.017	0.424	0.672
Geno.87	27	*	*	*	*	0.010	0.048	0.038	1.291	0.197
Geno.rare21	27	T	A	A	G	0.738	NA	NA	NA	NA
haplo.base26	28	A	A	G	D	0.023	0.023	0.024	0.934	0.351
Geno.110	28	G	A	G	W	0.189	0.007	0.009	0.777	0.437
Geno.69	28	G	C	G	W	0.050	0.008	0.017	0.448	0.654
Geno.96	28	*	*	*	*	0.010	0.050	0.038	1.320	0.187
Geno.rare22	28	A	A	G	W	0.728	NA	NA	NA	NA
haplo.base27	29	A	G	D	G	0.021	0.019	0.026	0.744	0.457
Geno.311	29	A	G	W	A	0.049	0.023	0.016	1.423	0.155
Geno.413	29	C	G	W	G	0.052	0.007	0.016	0.442	0.659
Geno.97	29	*	*	*	*	0.009	0.054	0.041	1.330	0.184
Geno.rare23	29	A	G	W	G	0.869	NA	NA	NA	NA
haplo.base28	30	G	D	G	C	0.021	0.020	0.026	0.765	0.444
Geno.312	30	G	W	A	C	0.049	0.023	0.016	1.418	0.157
Geno.414	30	*	*	*	*	0.012	0.034	0.035	0.967	0.334
Geno.rare24	30	G	W	G	C	0.918	NA	NA	NA	NA
haplo.base29	31	D	G	C	G	0.021	0.019	0.026	0.744	0.457
Geno.29	31	W	A	C	G	0.049	0.022	0.016	1.355	0.176
Geno.415	31	W	G	C	C	0.018	-0.047	0.027	-1.735	0.083
Geno.511	31	*	*	*	*	0.004	-0.012	0.068	-0.182	0.855
Geno.rare25	31	W	G	C	G	0.907	NA	NA	NA	NA
haplo.base30	32	A	C	G	A	0.050	0.022	0.016	1.373	0.170
Geno.112	32	G	C	C	A	0.018	-0.047	0.027	-1.745	0.081
Geno.313	32	G	C	G	G	0.117	0.004	0.011	0.396	0.692
Geno.512	32	*	*	*	*	0.003	-0.026	0.093	-0.281	0.779
Geno.rare26	32	G	C	G	A	0.812	NA	NA	NA	NA
haplo.base31	33	C	C	A	C	0.018	-0.048	0.027	-1.736	0.083
Geno.113	33	C	G	G	C	0.116	0.003	0.011	0.287	0.774
Geno.610	33	*	*	*	*	0.011	-0.017	0.037	-0.447	0.655
Geno.rare27	33	C	G	A	C	0.855	NA	NA	NA	NA
haplo.base32	34	C	A	C	G	0.017	-0.053	0.028	-1.898	0.058
Geno.210	34	G	A	C	A	0.044	-0.043	0.018	-2.452	0.014
Geno.513	34	G	G	C	G	0.117	0.002	0.011	0.137	0.891
Geno.98	34	*	*	*	*	0.009	-0.013	0.040	-0.318	0.751
Geno.rare28	34	G	A	C	G	0.814	NA	NA	NA	NA
haplo.base33	35	A	C	A	C	0.044	-0.039	0.017	-2.208	0.028

Table A2.12. Continued

	Window	loc.1	loc.2	loc.3	loc.4	Hap.freq.	Coef.	S.E.	Test statistic	*P*-value
Geno.114	35	A	C	G	C	0.251	0.013	0.008	1.615	0.107
Geno.211	35	G	C	G	T	0.114	0.005	0.012	0.444	0.657
Geno.611	35	*	*	*	*	0.011	0.007	0.036	0.191	0.848
Geno.rare29	35	A	C	G	T	0.579	NA	NA	NA	NA
haplo.base34	36	C	A	C	G	0.044	-0.043	0.018	-2.408	0.016
Geno.212	36	C	G	C	G	0.250	0.009	0.009	1.002	0.317
Geno.416	36	C	G	T	C	0.309	-0.009	0.008	-1.070	0.285
Geno.514	36	*	*	*	*	0.012	0.000	0.035	0.006	0.995
Geno.rare30	36	C	G	T	G	0.385	NA	NA	NA	NA
haplo.base35	37	A	C	G	T	0.044	-0.043	0.018	-2.415	0.016
Geno.314	37	G	C	G	T	0.242	0.008	0.009	0.874	0.382
Geno.612	37	G	T	C	T	0.309	-0.009	0.008	-1.093	0.275
Geno.711	37	*	*	*	*	0.010	0.051	0.037	1.379	0.168
Geno.rare31	37	G	T	G	T	0.394	NA	NA	NA	NA
haplo.base36	38	C	G	T	G	0.282	-0.001	0.009	-0.135	0.893
Geno.515	38	T	C	T	G	0.310	-0.011	0.009	-1.214	0.225
Geno.712	38	T	G	T	A	0.053	-0.011	0.017	-0.674	0.500
Geno.88	38	*	*	*	*	0.014	0.047	0.034	1.398	0.163
Geno.rare32	38	T	G	T	G	0.341	NA	NA	NA	NA
haplo.base37	39	C	T	G	A	0.308	-0.011	0.008	-1.379	0.168
Geno.115	39	G	T	A	A	0.057	-0.007	0.016	-0.450	0.653
Geno.613	39	G	T	G	C	0.086	0.001	0.013	0.108	0.914
Geno.99	39	*	*	*	*	0.012	0.046	0.037	1.230	0.219
Geno.rare33	39	G	T	G	A	0.537	NA	NA	NA	NA
haplo.base38	40	T	A	A	C	0.052	-0.009	0.017	-0.544	0.586
Geno.417	40	T	G	A	G	0.019	-0.021	0.027	-0.768	0.443
Geno.89	40	T	G	C	C	0.087	0.007	0.013	0.570	0.569
Geno.910	40	*	*	*	*	0.012	0.054	0.037	1.444	0.149
Geno.rare34	40	T	G	A	C	0.830	NA	NA	NA	NA
haplo.base39	41	A	A	C	W	0.054	-0.004	0.016	-0.225	0.822
Geno.116	41	G	A	G	W	0.019	-0.003	0.028	-0.120	0.904
Geno.614	41	G	C	C	W	0.088	0.012	0.013	0.918	0.359
Geno.810	41	*	*	*	*	0.005	-0.078	0.177	-0.441	0.659
Geno.rare35	41	G	A	C	W	0.834	NA	NA	NA	NA
haplo.base40	42	A	C	W	A	0.110	0.006	0.011	0.547	0.585
Geno.213	42	A	G	W	G	0.020	-0.002	0.027	-0.062	0.951
Geno.418	42	C	C	W	G	0.090	0.012	0.013	0.965	0.335
Geno.713	42	*	*	*	*	0.003	-0.149	0.132	-1.124	0.261
Geno.rare36	42	A	C	W	G	0.778	NA	NA	NA	NA
haplo.base41	43	C	W	A	A	0.110	0.006	0.011	0.579	0.563
Geno.214	43	C	W	G	G	0.203	0.006	0.009	0.649	0.516
Geno.516	43	G	W	G	A	0.019	0.002	0.030	0.059	0.953
Geno.615	43	*	*	*	*	0.003	-0.162	0.082	-1.964	0.050
Geno.rare37	43	C	W	G	A	0.664	NA	NA	NA	NA
haplo.base42	44	W	A	A	C	0.110	0.009	0.011	0.765	0.445
Geno.215	44	W	G	A	T	0.108	0.016	0.011	1.383	0.167
Geno.517	44	W	G	G	C	0.204	0.008	0.009	0.838	0.402
Geno.616	44	*	*	*	*	0.003	-0.024	0.077	-0.313	0.754
Geno.rare38	44	W	G	A	C	0.575	NA	NA	NA	NA
haplo.base43	45	A	A	C	W	0.110	0.010	0.011	0.849	0.396
Geno.216	45	G	A	C	D	0.023	0.026	0.024	1.078	0.281
Geno.419	45	G	A	T	W	0.109	0.016	0.012	1.355	0.176
Geno.617	45	G	G	C	W	0.204	0.008	0.009	0.935	0.350
Geno.811	45	*	*	*	*	0.001	0.151	0.131	1.152	0.250
Geno.rare39	45	G	A	C	W	0.554	NA	NA	NA	NA
haplo.base44	46	A	C	D	C	0.023	0.025	0.024	1.018	0.309
Geno.217	46	A	C	W	A	0.031	-0.011	0.021	-0.521	0.603
Geno.315	46	A	T	W	C	0.108	0.014	0.012	1.203	0.230
Geno.618	46	G	C	W	C	0.204	0.006	0.009	0.713	0.476

Table A2.12. Continued

	Window	loc.1	loc.2	loc.3	loc.4	Hap.freq.	Coef.	S.E.	Test statistic	*P*-value
Geno.911	46	*	*	*	*	0.001	0.144	0.130	1.108	0.268
Geno.rare40	46	A	C	W	C	0.633	NA	NA	NA	NA
haplo.base45	47	C	D	C	G	0.023	0.023	0.024	0.953	0.341
Geno.218	47	C	W	A	G	0.031	-0.013	0.021	-0.617	0.537
Geno.316	47	C	W	C	A	0.034	-0.003	0.020	-0.135	0.893
Geno.420	47	T	W	C	G	0.109	0.014	0.011	1.246	0.213
Geno.714	47	C	W	C	G	0.803	NA	NA	NA	NA
haplo.base46	48	D	C	G	T	0.023	0.020	0.024	0.848	0.397
Geno.219	48	W	A	G	T	0.031	-0.015	0.021	-0.697	0.486
Geno.317	48	W	C	A	T	0.034	-0.005	0.020	-0.271	0.787
Geno.421	48	*	*	*	*	0.006	0.010	0.046	0.206	0.837
Geno.rare41	48	W	C	G	T	0.906	NA	NA	NA	NA
haplo.base47	49	A	G	T	T	0.031	-0.016	0.021	-0.776	0.438
Geno.220	49	C	A	T	T	0.034	-0.007	0.020	-0.335	0.738
Geno.422	49	C	G	T	C	0.192	-0.001	0.009	-0.096	0.924
Geno.619	49	*	*	*	*	0.006	0.008	0.046	0.172	0.864
Geno.rare42	49	C	G	T	T	0.737	NA	NA	NA	NA
haplo.base48	50	A	T	T	D	0.034	-0.007	0.020	-0.365	0.715
Geno.221	50	G	T	C	D	0.192	-0.002	0.009	-0.237	0.813
Geno.518	50	G	T	T	W	0.087	-0.015	0.013	-1.171	0.242
Geno.812	50	*	*	*	*	0.006	0.003	0.046	0.071	0.943
Geno.rare43	50	G	T	T	D	0.680	NA	NA	NA	NA
haplo.base49	51	T	C	D	C	0.139	-0.002	0.011	-0.198	0.843
Geno.222	51	T	C	D	T	0.053	0.001	0.017	0.044	0.965
Geno.318	51	T	T	D	C	0.102	0.001	0.013	0.055	0.956
Geno.519	51	T	T	W	T	0.087	-0.015	0.013	-1.148	0.251
Geno.715	51	*	*	*	*	0.006	0.004	0.046	0.092	0.927
Geno.rare44	51	T	T	D	T	0.612	NA	NA	NA	NA
haplo.base50	52	C	D	C	A	0.139	0.000	0.011	-0.009	0.993
Geno.117	52	C	D	T	A	0.053	0.003	0.018	0.185	0.853
Geno.223	52	T	D	C	A	0.102	0.003	0.013	0.200	0.842
Geno.423	52	T	D	T	G	0.116	0.010	0.011	0.907	0.364
Geno.620	52	T	W	T	A	0.093	-0.011	0.013	-0.848	0.397
Geno.813	52	T	D	T	A	0.496	NA	NA	NA	NA
haplo.base51	53	D	C	A	A	0.243	0.001	0.009	0.137	0.891
Geno.118	53	D	T	A	C	0.035	0.011	0.019	0.612	0.541
Geno.520	53	D	T	G	A	0.116	0.011	0.011	0.953	0.341
Geno.621	53	W	T	A	A	0.093	-0.011	0.013	-0.855	0.393
Geno.814	53	D	T	A	A	0.513	NA	NA	NA	NA
haplo.base52	54	C	A	A	C	0.242	0.003	0.009	0.357	0.721
Geno.119	54	T	A	A	G	0.035	-0.001	0.020	-0.029	0.977
Geno.622	54	T	A	C	C	0.035	0.013	0.019	0.696	0.487
Geno.716	54	T	G	A	C	0.116	0.012	0.011	1.111	0.267
Geno.815	54	T	A	A	C	0.572	NA	NA	NA	NA
haplo.base53	55	A	A	C	T	0.052	0.005	0.017	0.282	0.778
Geno.224	55	A	A	G	A	0.034	0.000	0.020	0.018	0.985
Geno.319	55	A	C	C	A	0.034	0.013	0.019	0.718	0.473
Geno.521	55	G	A	C	A	0.116	0.012	0.011	1.095	0.274
Geno.717	55	*	*	*	*	0.002	-0.065	0.129	-0.502	0.616
Geno.rare45	55	A	A	C	A	0.762	NA	NA	NA	NA
haplo.base54	56	A	C	A	G	0.074	-0.013	0.014	-0.886	0.376
Geno.225	56	A	C	T	C	0.052	0.001	0.017	0.075	0.940
Geno.320	56	A	G	A	C	0.034	-0.002	0.020	-0.121	0.904
Geno.424	56	C	C	A	C	0.034	0.010	0.019	0.550	0.583
Geno.718	56	*	*	*	*	0.002	-0.061	0.120	-0.512	0.609
Geno.rare46	56	A	C	A	C	0.804	NA	NA	NA	NA
haplo.base55	57	C	A	C	G	0.121	0.007	0.011	0.596	0.551
Geno.226	57	C	A	G	G	0.074	-0.011	0.015	-0.787	0.431
Geno.425	57	C	T	C	A	0.052	0.002	0.017	0.131	0.896

Table A2.12. Continued

	Window	loc.1	loc.2	loc.3	loc.4	Hap.freq.	Coef.	S.E.	Test statistic	*P*-value
Geno.522	57	G	A	C	A	0.034	-0.002	0.020	-0.120	0.904
Geno.719	57	*	*	*	*	0.003	-0.106	0.099	-1.074	0.283
Geno.rare47	57	C	A	C	A	0.715	NA	NA	NA	NA
haplo.base56	58	A	C	A	T	0.221	-0.003	0.009	-0.329	0.742
Geno.227	58	A	C	G	C	0.112	0.006	0.012	0.495	0.621
Geno.321	58	A	G	G	T	0.073	-0.012	0.015	-0.811	0.418
Geno.720	58	T	C	A	T	0.053	0.000	0.017	-0.030	0.976
Geno.912	58	*	*	*	*	0.014	-0.010	0.042	-0.231	0.817
Geno.rare48	58	A	C	A	C	0.527	NA	NA	NA	NA
haplo.base57	59	C	A	C	G	0.069	0.006	0.015	0.368	0.713
Geno.228	59	C	A	T	A	0.263	0.001	0.009	0.119	0.906
Geno.322	59	C	A	T	G	0.014	-0.042	0.037	-1.148	0.251
Geno.426	59	C	G	C	A	0.111	0.006	0.012	0.500	0.617
Geno.523	59	G	G	T	G	0.073	-0.010	0.015	-0.677	0.498
Geno.131	59	*	*	*	*	0.015	-0.011	0.036	-0.299	0.765
Geno.rare49	59	C	A	C	A	0.456	NA	NA	NA	NA
haplo.base58	60	A	C	G	G	0.069	0.006	0.016	0.362	0.718
Geno.229	60	A	T	A	G	0.263	0.001	0.009	0.070	0.945
Geno.323	60	A	T	G	G	0.018	-0.037	0.037	-1.019	0.309
Geno.427	60	G	C	A	G	0.113	0.007	0.012	0.593	0.554
Geno.524	60	G	T	G	G	0.075	-0.011	0.014	-0.754	0.451
Geno.913	60	*	*	*	*	0.007	-0.001	0.063	-0.017	0.986
Geno.rare50	60	A	C	A	G	0.455	NA	NA	NA	NA
haplo.base59	61	C	G	G	T	0.075	-0.003	0.016	-0.196	0.845
Geno.428	61	T	A	G	C	0.046	-0.004	0.017	-0.255	0.799
Geno.525	61	T	A	G	T	0.219	-0.003	0.010	-0.358	0.720
Geno.623	61	T	G	G	T	0.092	-0.016	0.014	-1.166	0.244
Geno.914	61	*	*	*	*	0.008	-0.025	0.049	-0.517	0.606
Geno.rare51	61	C	A	G	T	0.561	NA	NA	NA	NA
haplo.base60	62	A	G	C	G	0.052	-0.005	0.016	-0.278	0.781
Geno.120	62	A	G	T	G	0.292	0.001	0.009	0.128	0.898
Geno.230	62	G	G	T	G	0.131	-0.015	0.011	-1.356	0.175
Geno.624	62	G	G	T	T	0.036	0.016	0.021	0.774	0.439
Geno.721	62	*	*	*	*	0.001	-0.048	NA	NA	NA
Geno.rare52	62	A	G	T	T	0.487	NA	NA	NA	NA
haplo.base61	63	G	C	G	C	0.053	-0.006	0.016	-0.363	0.716
Geno.324	63	G	T	G	C	0.424	-0.005	0.008	-0.690	0.490
Geno.722	63	G	T	T	A	0.069	0.002	0.014	0.135	0.893
Geno.816	63	G	T	T	C	0.454	NA	NA	NA	NA
haplo.base62	64	C	G	C	W	0.053	-0.006	0.016	-0.384	0.701
Geno.325	64	T	G	C	I	0.042	0.001	0.018	0.031	0.975
Geno.723	64	T	G	C	W	0.382	-0.006	0.008	-0.771	0.441
Geno.817	64	T	T	A	W	0.069	0.002	0.014	0.129	0.897
Geno.915	64	T	T	C	W	0.454	NA	NA	NA	NA
haplo.base63	65	G	C	I	T	0.042	0.011	0.019	0.576	0.565
Geno.121	65	G	C	W	C	0.017	0.062	0.035	1.789	0.074
Geno.231	65	T	A	W	T	0.069	0.011	0.014	0.738	0.461
Geno.526	65	T	C	W	C	0.175	0.012	0.010	1.200	0.230
Geno.625	65	T	C	W	T	0.278	0.006	0.009	0.701	0.483
Geno.724	65	G	C	W	T	0.418	NA	NA	NA	NA
haplo.base64	66	A	W	T	C	0.064	0.011	0.014	0.754	0.451
Geno.326	66	C	I	T	T	0.041	0.009	0.018	0.469	0.639
Geno.725	66	C	W	C	C	0.033	0.019	0.021	0.912	0.362
Geno.818	66	C	W	C	T	0.158	0.012	0.010	1.173	0.241
Geno.916	66	C	W	T	C	0.012	-0.041	0.041	-0.986	0.324
Geno.10	66	*	*	*	*	0.007	-0.010	0.050	-0.192	0.847
Geno.rare53	66	C	W	T	T	0.685	NA	NA	NA	NA
haplo.base65	67	I	T	T	C	0.042	0.006	0.018	0.316	0.752
Geno.232	67	W	C	C	C	0.034	0.024	0.023	1.022	0.307

Table A2.12. Continued

	Window	loc.1	loc.2	loc.3	loc.4	Hap.freq.	Coef.	S.E.	Test statistic	*P*-value
Geno.327	67	W	C	T	C	0.157	0.011	0.011	0.977	0.329
Geno.429	67	W	T	C	C	0.074	0.000	0.015	0.007	0.994
Geno.626	67	W	T	T	G	0.151	0.001	0.011	0.134	0.893
Geno.917	67	W	T	T	C	0.541	NA	NA	NA	NA
haplo.base66	68	C	C	C	G	0.034	0.025	0.023	1.094	0.274
Geno.122	68	C	T	C	G	0.157	0.008	0.011	0.721	0.471
Geno.233	68	T	C	C	G	0.074	-0.003	0.015	-0.200	0.841
Geno.430	68	T	T	C	A	0.056	-0.014	0.016	-0.860	0.390
Geno.527	68	T	T	G	G	0.148	-0.003	0.011	-0.255	0.799
Geno.819	68	*	*	*	*	0.003	0.139	0.080	1.746	0.081
Geno.rare54	68	T	T	C	G	0.527	NA	NA	NA	NA
haplo.base67	69	C	C	G	G	0.108	0.003	0.012	0.283	0.777
Geno.234	69	T	C	A	A	0.057	-0.010	0.015	-0.634	0.526
Geno.328	69	T	G	G	G	0.150	-0.003	0.010	-0.262	0.793
Geno.627	69	T	C	G	G	0.684	NA	NA	NA	NA
haplo.base68	70	C	A	A	A	0.057	-0.012	0.016	-0.745	0.456
Geno.123	70	C	G	G	A	0.317	0.003	0.008	0.381	0.703
Geno.528	70	G	G	G	A	0.149	-0.004	0.011	-0.345	0.730
Geno.820	70	*	*	*	*	0.003	0.137	0.080	1.712	0.087
Geno.rare55	70	C	G	G	T	0.475	NA	NA	NA	NA
haplo.base69	71	A	A	A	G	0.058	-0.008	0.015	-0.524	0.601
Geno.235	71	G	G	A	A	0.143	0.001	0.011	0.137	0.891
Geno.529	71	G	G	A	G	0.325	0.001	0.008	0.102	0.919
Geno.628	71	*	*	*	*	0.003	0.002	0.097	0.021	0.983
Geno.rare56	71	G	G	T	G	0.471	NA	NA	NA	NA
haplo.base70	72	A	A	G	C	0.058	-0.005	0.016	-0.336	0.737
Geno.124	72	G	A	A	C	0.142	-0.002	0.011	-0.226	0.821
Geno.329	72	G	A	G	A	0.137	0.005	0.011	0.455	0.649
Geno.431	72	G	A	G	C	0.188	-0.001	0.010	-0.116	0.908
Geno.530	72	*	*	*	*	0.004	0.057	0.071	0.797	0.426
Geno.rare57	72	G	T	G	A	0.471	NA	NA	NA	NA
haplo.base71	73	A	A	C	G	0.140	-0.001	0.011	-0.065	0.948
Geno.236	73	A	G	A	G	0.137	0.006	0.011	0.597	0.551
Geno.330	73	A	G	C	G	0.247	-0.003	0.009	-0.281	0.779
Geno.432	73	T	G	A	A	0.016	0.020	0.029	0.688	0.492
Geno.726	73	*	*	*	*	0.005	0.058	0.071	0.823	0.411
Geno.rare58	73	T	G	A	G	0.454	NA	NA	NA	NA
haplo.base72	74	A	C	G	G	0.143	-0.003	0.011	-0.247	0.805
Geno.629	74	G	A	A	G	0.016	0.020	0.029	0.692	0.489
Geno.727	74	G	A	G	A	0.012	0.041	0.033	1.223	0.222
Geno.821	74	G	C	G	G	0.250	-0.002	0.009	-0.255	0.799
Geno.1110	74	*	*	*	*	0.003	0.124	0.077	1.611	0.108
Geno.rare59	74	G	A	G	G	0.577	NA	NA	NA	NA
haplo.base73	75	A	A	G	C	0.016	0.019	0.029	0.651	0.515
Geno.125	75	A	G	A	C	0.012	0.039	0.033	1.186	0.236
Geno.237	75	C	G	G	C	0.392	-0.002	0.007	-0.347	0.728
Geno.531	75	*	*	*	*	0.007	-0.031	0.040	-0.771	0.441
Geno.rare60	75	A	G	G	C	0.573	NA	NA	NA	NA
haplo.base74	76	A	G	C	A	0.016	0.020	0.029	0.697	0.486
Geno.331	76	G	A	C	A	0.012	0.040	0.033	1.226	0.221
Geno.433	76	G	G	C	G	0.011	-0.016	0.035	-0.456	0.648
Geno.728	76	*	*	*	*	0.007	-0.030	0.040	-0.759	0.448
Geno.rare61	76	G	G	C	A	0.954	NA	NA	NA	NA
haplo.base75	77	A	C	A	T	0.012	0.038	0.033	1.148	0.252
Geno.126	77	G	C	A	C	0.289	-0.005	0.008	-0.650	0.516
Geno.238	77	*	*	*	*	0.018	-0.023	0.026	-0.887	0.375
Geno.rare62	77	G	C	A	T	0.682	NA	NA	NA	NA
haplo.base76	78	C	A	C	A	0.147	-0.005	0.011	-0.493	0.622
Geno.127	78	C	A	C	G	0.141	-0.008	0.010	-0.801	0.423

Table A2.12. Continued

	Window	loc.1	loc.2	loc.3	loc.4	Hap.freq.	Coef.	S.E.	Test statistic	*P*-value
Geno.239	78	C	A	T	G	0.011	0.014	0.035	0.399	0.690
Geno.434	78	*	*	*	*	0.018	-0.025	0.027	-0.926	0.355
Geno.rare63	78	C	A	T	A	0.683	NA	NA	NA	NA
haplo.base77	79	A	C	A	A	0.143	-0.004	0.011	-0.370	0.712
Geno.128	79	A	C	G	A	0.143	-0.006	0.011	-0.598	0.550
Geno.332	79	A	T	A	G	0.245	0.006	0.009	0.651	0.515
Geno.532	79	A	T	G	A	0.011	0.016	0.035	0.471	0.638
Geno.630	79	G	T	A	A	0.009	-0.038	0.046	-0.835	0.404
Geno.822	79	*	*	*	*	0.005	0.086	0.063	1.361	0.174
Geno.rare64	79	A	T	A	A	0.443	NA	NA	NA	NA
haplo.base78	80	C	A	A	C	0.144	-0.001	0.011	-0.118	0.906
Geno.129	80	C	G	A	C	0.143	-0.004	0.011	-0.398	0.690
Geno.435	80	T	A	A	T	0.024	0.022	0.024	0.936	0.350
Geno.729	80	T	A	G	C	0.245	0.008	0.009	0.877	0.381
Geno.823	80	T	G	A	C	0.011	0.019	0.035	0.545	0.586
Geno.918	80	*	*	*	*	0.004	0.060	0.066	0.909	0.363
Geno.rare65	80	T	A	A	C	0.428	NA	NA	NA	NA
haplo.base79	81	A	A	C	A	0.095	0.017	0.013	1.291	0.197
Geno.130	81	A	A	T	C	0.023	0.038	0.025	1.501	0.134
Geno.436	81	A	G	C	C	0.249	0.012	0.009	1.437	0.151
Geno.631	81	G	A	C	A	0.132	-0.001	0.011	-0.066	0.948
Geno.919	81	G	A	C	C	0.021	0.008	0.028	0.278	0.781
Geno.101	81	*	*	*	*	0.003	-0.122	0.078	-1.572	0.116
Geno.rare66	81	A	A	C	C	0.477	NA	NA	NA	NA
haplo.base80	82	A	C	A	G	0.225	0.004	0.009	0.422	0.673
Geno.132	82	A	T	C	G	0.023	0.033	0.025	1.313	0.189
Geno.632	82	G	C	C	A	0.031	0.019	0.021	0.886	0.376
Geno.824	82	G	C	C	G	0.217	0.009	0.009	0.981	0.327
Geno.920	82	*	*	*	*	0.004	-0.032	0.133	-0.243	0.808
Geno.rare67	82	A	C	C	G	0.501	NA	NA	NA	NA
haplo.base81	83	C	A	G	C	0.228	0.002	0.009	0.193	0.847
Geno.240	83	C	C	A	C	0.032	0.017	0.021	0.816	0.415
Geno.333	83	C	C	G	G	0.138	0.005	0.011	0.470	0.639
Geno.633	83	T	C	G	C	0.024	0.022	0.023	0.920	0.358
Geno.825	83	C	C	G	C	0.577	NA	NA	NA	NA
haplo.base82	84	A	G	C	A	0.228	0.002	0.009	0.205	0.838
Geno.241	84	C	A	C	C	0.032	0.017	0.021	0.849	0.396
Geno.437	84	C	G	C	C	0.050	0.013	0.017	0.777	0.438
Geno.730	84	C	G	G	A	0.138	0.006	0.011	0.514	0.607
Geno.826	84	C	G	C	A	0.551	NA	NA	NA	NA
haplo.base83	85	A	C	C	G	0.032	0.017	0.020	0.832	0.405
Geno.133	85	G	C	C	G	0.050	0.012	0.017	0.747	0.456
Geno.533	85	G	G	A	G	0.137	0.005	0.010	0.477	0.633
Geno.731	85	*	*	*	*	0.009	0.004	0.039	0.094	0.925
Geno.rare68	85	G	C	A	G	0.772	NA	NA	NA	NA
haplo.base84	86	C	A	G	C	0.044	-0.018	0.017	-1.065	0.287
Geno.242	86	C	C	G	T	0.081	0.016	0.013	1.184	0.237
Geno.438	86	G	A	G	T	0.137	0.004	0.010	0.383	0.702
Geno.634	86	*	*	*	*	0.009	0.002	0.039	0.052	0.959
Geno.rare69	86	C	A	G	T	0.729	NA	NA	NA	NA
haplo.base85	87	A	G	C	G	0.044	-0.018	0.017	-1.052	0.293
Geno.334	87	A	G	T	A	0.320	0.002	0.008	0.182	0.856
Geno.439	87	C	G	T	A	0.079	0.018	0.014	1.304	0.193
Geno.732	87	*	*	*	*	0.011	-0.013	0.036	-0.353	0.724
Geno.rare70	87	A	G	T	G	0.546	NA	NA	NA	NA
haplo.base86	88	G	C	G	G	0.044	-0.017	0.017	-1.005	0.315
Geno.335	88	G	T	A	G	0.399	0.006	0.008	0.732	0.464
Geno.534	88	*	*	*	*	0.010	0.001	0.036	0.024	0.981
Geno.rare71	88	G	T	G	G	0.547	NA	NA	NA	NA

Table A2.12. Continued

	Window	loc.1	loc.2	loc.3	loc.4	Hap.freq.	Coef.	S.E.	Test statistic	*P*-value
haplo.base87	89	C	G	G	G	0.044	-0.018	0.017	-1.024	0.306
Geno.243	89	T	A	G	C	0.399	0.006	0.008	0.769	0.442
Geno.440	89	*	*	*	*	0.002	0.058	0.097	0.593	0.554
Geno.rare72	89	T	G	G	C	0.555	NA	NA	NA	NA
haplo.base88	90	A	G	C	A	0.397	0.007	0.008	0.898	0.370
Geno.244	90	G	G	C	G	0.091	0.003	0.013	0.221	0.825
Geno.635	90	G	G	G	A	0.043	-0.012	0.017	-0.690	0.490
Geno.733	90	*	*	*	*	0.004	-0.046	0.068	-0.679	0.497
Geno.rare73	90	G	G	C	A	0.465	NA	NA	NA	NA
haplo.base89	91	G	C	A	A	0.086	-0.006	0.013	-0.495	0.621
Geno.245	91	G	C	G	G	0.093	-0.004	0.013	-0.294	0.769
Geno.441	91	G	G	A	G	0.043	-0.016	0.017	-0.922	0.357
Geno.535	91	*	*	*	*	0.001	-0.014	0.098	-0.143	0.886
Geno.rare74	91	G	C	A	G	0.776	NA	NA	NA	NA
haplo.base90	92	C	A	A	G	0.086	-0.006	0.013	-0.424	0.672
Geno.134	92	C	A	G	A	0.025	0.020	0.023	0.860	0.390
Geno.246	92	C	G	G	G	0.093	-0.003	0.013	-0.253	0.800
Geno.536	92	G	A	G	G	0.043	-0.015	0.017	-0.850	0.396
Geno.636	92	C	A	G	G	0.752	NA	NA	NA	NA
haplo.base91	93	A	A	G	T	0.086	-0.004	0.013	-0.333	0.739
Geno.247	93	A	G	A	T	0.025	0.022	0.023	0.939	0.348
Geno.336	93	A	G	G	C	0.058	0.004	0.015	0.264	0.792
Geno.442	93	G	G	G	T	0.093	-0.003	0.013	-0.205	0.837
Geno.921	93	A	G	G	T	0.737	NA	NA	NA	NA
haplo.base92	94	A	G	T	C	0.086	-0.005	0.013	-0.368	0.713
Geno.135	94	G	A	T	T	0.025	0.021	0.023	0.926	0.355
Geno.248	94	G	G	C	C	0.058	0.003	0.015	0.221	0.825
Geno.337	94	G	G	T	T	0.132	-0.006	0.010	-0.621	0.535
Geno.637	94	G	G	T	C	0.699	NA	NA	NA	NA
haplo.base93	95	A	T	T	G	0.025	0.022	0.023	0.941	0.347
Geno.136	95	G	C	C	G	0.054	-0.002	0.016	-0.145	0.885
Geno.249	95	G	T	C	T	0.019	-0.008	0.027	-0.285	0.776
Geno.638	95	G	T	T	G	0.130	-0.008	0.010	-0.742	0.458
Geno.734	95	*	*	*	*	0.004	0.103	0.083	1.239	0.216
Geno.rare75	95	G	T	C	G	0.768	NA	NA	NA	NA
haplo.base94	96	C	C	G	A	0.058	0.003	0.015	0.192	0.848
Geno.137	96	T	C	T	A	0.020	-0.004	0.026	-0.150	0.881
Geno.735	96	T	T	G	A	0.157	-0.002	0.009	-0.229	0.819
Geno.922	96	*	*	*	*	0.005	-0.144	0.064	-2.260	0.024
Geno.rare76	96	T	C	G	A	0.760	NA	NA	NA	NA
haplo.base95	97	C	G	A	D	0.149	-0.009	0.010	-0.904	0.366
Geno.138	97	C	T	A	W	0.020	-0.006	0.026	-0.218	0.828
Geno.537	97	T	G	A	W	0.153	-0.003	0.010	-0.320	0.749
Geno.827	97	*	*	*	*	0.010	-0.097	0.042	-2.298	0.022
Geno.rare77	97	C	G	A	W	0.669	NA	NA	NA	NA
haplo.base96	98	G	A	D	T	0.153	-0.009	0.010	-0.953	0.341
Geno.250	98	G	A	W	G	0.085	0.005	0.013	0.391	0.696
Geno.338	98	T	A	W	T	0.020	-0.003	0.026	-0.119	0.906
Geno.828	98	*	*	*	*	0.006	-0.142	0.053	-2.664	0.008
Geno.rare78	98	G	A	W	T	0.736	NA	NA	NA	NA
haplo.base97	99	A	D	T	D	0.156	-0.009	0.010	-0.890	0.374
Geno.251	99	A	W	G	W	0.085	0.005	0.013	0.407	0.684
Geno.443	99	*	*	*	*	0.009	-0.074	0.040	-1.844	0.066
Geno.rare79	99	A	W	T	W	0.749	NA	NA	NA	NA
haplo.base98	100	D	T	D	T	0.156	-0.006	0.010	-0.626	0.531
Geno.339	100	W	G	W	T	0.085	0.008	0.013	0.667	0.505
Geno.538	100	W	T	W	G	0.011	0.071	0.035	2.022	0.044
Geno.736	100	*	*	*	*	0.004	0.041	0.070	0.596	0.551

Table A2.12. Continued

	Window	loc.1	loc.2	loc.3	loc.4	Hap.freq.	Coef.	S.E.	Test statistic	*P*-value
Geno.rare80	100	W	T	W	T	0.744	NA	NA	NA	NA
haplo.base99	101	G	W	T	G	0.085	0.008	0.013	0.652	0.515
Geno.340	101	T	D	T	G	0.158	-0.005	0.010	-0.566	0.572
Geno.639	101	T	W	G	G	0.010	0.075	0.038	2.011	0.045
Geno.737	101	T	W	T	A	0.016	0.007	0.030	0.233	0.816
Geno.829	101	T	W	T	G	0.729	NA	NA	NA	NA
haplo.base100	102	D	T	G	C	0.157	-0.006	0.010	-0.652	0.515
Geno.341	102	W	G	G	C	0.010	0.076	0.039	1.963	0.050
Geno.539	102	W	T	A	C	0.016	0.005	0.029	0.184	0.854
Geno.640	102	*	*	*	*	0.003	0.008	0.131	0.063	0.950
Geno.rare81	102	W	T	G	C	0.814	NA	NA	NA	NA
haplo.base101	103	G	G	C	G	0.011	0.068	0.034	2.012	0.045
Geno.139	103	T	A	C	G	0.016	0.006	0.029	0.216	0.829
Geno.252	103	*	*	*	*	0.002	0.031	0.097	0.316	0.752
Geno.rare82	103	T	G	C	G	0.971	NA	NA	NA	NA
haplo.base102	104	A	C	G	G	0.016	0.005	0.029	0.165	0.869
Geno.140	104	*	*	*	*	0.003	0.047	0.069	0.687	0.492
Geno.rare83	104	G	C	G	G	0.981	NA	NA	NA	NA
haplo.base103	105	*	*	*	*	0.007	-0.001	0.046	-0.027	0.978
Geno.rare84	105	C	G	G	G	0.993	NA	NA	NA	NA
haplo.base104	106	*	*	*	*	0.007	-0.001	0.046	-0.027	0.978
Geno.rare85	106	G	G	G	A	0.993	NA	NA	NA	NA
haplo.base105	107	G	G	A	G	0.238	0.006	0.008	0.699	0.484
Geno.444	107	*	*	*	*	0.006	-0.005	0.046	-0.102	0.918
Geno.rare86	107	G	G	A	A	0.756	NA	NA	NA	NA
haplo.base106	108	G	A	A	A	0.336	-0.003	0.009	-0.374	0.709
Geno.342	108	G	A	G	A	0.218	0.004	0.010	0.376	0.707
Geno.540	108	G	A	G	T	0.022	0.021	0.033	0.634	0.526
Geno.641	108	*	*	*	*	0.005	-0.028	0.052	-0.537	0.591
Geno.rare87	108	G	A	A	T	0.420	NA	NA	NA	NA
haplo.base107	109	A	A	A	C	0.336	-0.002	0.009	-0.223	0.824
Geno.141	109	A	G	A	C	0.116	0.004	0.013	0.288	0.774
Geno.343	109	A	G	A	T	0.104	0.000	0.012	-0.016	0.987
Geno.445	109	A	G	T	C	0.023	0.024	0.034	0.704	0.482
Geno.541	109	*	*	*	*	0.001	0.021	0.097	0.218	0.827
Geno.rare88	109	A	A	T	C	0.419	NA	NA	NA	NA
haplo.base108	110	A	T	C	A	0.332	0.000	0.009	-0.012	0.991
Geno.344	110	A	T	C	G	0.086	0.011	0.014	0.794	0.428
Geno.446	110	G	A	C	A	0.113	0.003	0.014	0.200	0.841
Geno.542	110	G	A	T	A	0.104	0.002	0.013	0.122	0.903
Geno.738	110	G	T	C	A	0.022	0.022	0.034	0.652	0.515
Geno.923	110	*	*	*	*	0.005	0.112	0.062	1.804	0.072
Geno.rare89	110	A	A	C	A	0.338	NA	NA	NA	NA
haplo.base109	111	A	T	A	G	0.104	0.002	0.013	0.192	0.848
Geno.543	111	T	C	A	G	0.349	0.000	0.008	0.053	0.958
Geno.830	111	T	C	G	G	0.088	0.012	0.013	0.897	0.370
Geno.924	111	*	*	*	*	0.017	0.015	0.030	0.495	0.621
Geno.rare90	111	A	C	A	G	0.442	NA	NA	NA	NA
haplo.base110	112	C	A	A	C	0.013	-0.004	0.031	-0.126	0.900
Geno.142	112	C	G	G	C	0.091	0.015	0.013	1.206	0.228
Geno.447	112	T	A	G	C	0.102	0.001	0.012	0.090	0.928
Geno.544	112	*	*	*	*	0.009	0.019	0.037	0.510	0.610
Geno.rare91	112	C	A	G	C	0.784	NA	NA	NA	NA
haplo.base111	113	A	A	C	T	0.014	-0.004	0.031	-0.134	0.894
Geno.143	113	A	G	C	T	0.353	0.001	0.008	0.108	0.914
Geno.345	113	G	G	C	T	0.091	0.015	0.013	1.141	0.254
Geno.642	113	*	*	*	*	0.009	0.019	0.037	0.516	0.606
Geno.rare92	113	A	G	C	C	0.532	NA	NA	NA	NA

Table A2.12. Continued

	Window	loc.1	loc.2	loc.3	loc.4	Hap.freq.	Coef.	S.E.	Test statistic	*P*-value
haplo.base112	114	A	C	T	A	0.014	-0.005	0.031	-0.164	0.869
Geno.346	114	G	C	C	T	0.085	-0.005	0.014	-0.364	0.716
Geno.643	114	G	C	T	A	0.446	0.003	0.008	0.414	0.679
Geno.739	114	*	*	*	*	0.009	0.017	0.037	0.444	0.657
Geno.rare93	114	G	C	C	A	0.446	NA	NA	NA	NA
haplo.base113	115	C	C	A	G	0.446	-0.005	0.008	-0.608	0.543
Geno.144	115	C	C	T	G	0.085	-0.010	0.014	-0.733	0.464
Geno.253	115	*	*	*	*	0.016	-0.035	0.029	-1.198	0.231
Geno.rare94	115	C	T	A	G	0.453	NA	NA	NA	NA
haplo.base114	116	C	T	G	T	0.085	-0.005	0.014	-0.368	0.713
Geno.347	116	T	A	G	T	0.453	0.005	0.008	0.634	0.526
Geno.448	116	*	*	*	*	0.007	-0.096	0.046	-2.072	0.039
Geno.rare95	116	C	A	G	T	0.456	NA	NA	NA	NA
haplo.base115	117	A	G	T	A	0.012	-0.037	0.032	-1.169	0.243
Geno.145	117	T	G	T	G	0.085	-0.009	0.013	-0.654	0.514
Geno.644	117	*	*	*	*	0.007	-0.098	0.048	-2.062	0.040
Geno.rare96	117	A	G	T	G	0.897	NA	NA	NA	NA
haplo.base116	118	G	T	A	T	0.012	-0.036	0.032	-1.148	0.251
Geno.254	118	G	T	G	C	0.016	0.006	0.028	0.224	0.823
Geno.348	118	*	*	*	*	0.007	-0.097	0.046	-2.102	0.036
Geno.rare97	118	G	T	G	T	0.966	NA	NA	NA	NA
haplo.base117	119	T	A	T	A	0.012	-0.038	0.032	-1.204	0.229
Geno.349	119	T	G	C	G	0.016	0.003	0.029	0.088	0.930
Geno.545	119	T	G	T	A	0.405	-0.006	0.007	-0.799	0.425
Geno.645	119	*	*	*	*	0.005	-0.130	0.049	-2.662	0.008
Geno.rare98	119	T	G	T	G	0.562	NA	NA	NA	NA
haplo.base118	120	A	T	A	A	0.012	-0.037	0.032	-1.162	0.246
Geno.146	120	G	C	G	T	0.016	0.004	0.029	0.149	0.882
Geno.449	120	G	T	A	A	0.088	0.000	0.014	-0.007	0.994
Geno.546	120	G	T	A	T	0.316	-0.006	0.008	-0.742	0.458
Geno.646	120	*	*	*	*	0.005	-0.024	0.062	-0.391	0.696
Geno.rare99	120	G	T	G	T	0.562	NA	NA	NA	NA
haplo.base119	121	C	G	T	G	0.016	0.006	0.029	0.220	0.826
Geno.147	121	T	A	A	G	0.099	-0.004	0.013	-0.279	0.780
Geno.350	121	T	A	T	A	0.089	-0.008	0.013	-0.601	0.548
Geno.450	121	T	A	T	G	0.227	-0.003	0.009	-0.362	0.717
Geno.547	121	*	*	*	*	0.005	0.030	0.061	0.488	0.626
Geno.rare100	121	T	G	T	G	0.564	NA	NA	NA	NA
haplo.base120	122	A	A	G	C	0.018	0.030	0.029	1.041	0.298
Geno.255	122	A	A	G	T	0.081	-0.013	0.014	-0.939	0.348
Geno.351	122	A	T	A	C	0.089	-0.008	0.013	-0.628	0.530
Geno.451	122	A	T	G	C	0.226	-0.003	0.009	-0.330	0.741
Geno.548	122	*	*	*	*	0.006	0.035	0.062	0.564	0.573
Geno.rare101	122	G	T	G	C	0.580	NA	NA	NA	NA

Hap.freq: Haplotyle frequency, **Coef.** : Coefficient, **S.E.:** Standart Error

Table A2.13. Summary of *LPL* 4-SNP sliding haplotype association with HDL-C in African blacks (n=788)

	Window	loc.1	loc.2	loc.3	loc.4	Hap.freq.	Coef.	S.E.	Test statistic	P-value
Geno.1	1	G	C	A	G	0.112	0.038	0.311	0.124	0.902
Geno.3	1	G	T	A	G	0.096	-0.124	0.328	-0.379	0.705
Geno.4	1	G	T	G	G	0.144	0.136	0.292	0.467	0.641
Geno.6	1	T	C	A	G	0.109	-0.161	0.310	-0.520	0.603
Geno.rare	1	*	*	*	*	0.006	0.184	1.210	0.152	0.879
haplo.base	1	G	T	G	T	0.532	NA	NA	NA	NA
Geno.11	2	C	A	G	A	0.018	0.082	0.720	0.114	0.909
Geno.2	2	C	A	G	T	0.201	-0.068	0.243	-0.278	0.781
Geno.61	2	T	A	G	T	0.098	-0.127	0.327	-0.389	0.697
Geno.7	2	T	G	G	T	0.145	0.143	0.291	0.493	0.622
Geno.rare1	2	*	*	*	*	0.006	-0.265	1.204	-0.220	0.826
haplo.base1	2	T	G	T	T	0.532	NA	NA	NA	NA
Geno.12	3	A	G	A	A	0.018	0.080	0.719	0.111	0.911
Geno.21	3	A	G	T	A	0.299	-0.092	0.208	-0.445	0.656
Geno.41	3	G	G	T	A	0.149	0.169	0.289	0.584	0.560
haplo.base2	3	G	T	T	A	0.533	NA	NA	NA	NA
Geno.22	4	G	A	A	W	0.018	0.041	0.718	0.056	0.955
Geno.31	4	G	T	A	W	0.449	-0.043	0.191	-0.224	0.823
Geno.5	4	T	T	A	I	0.028	-0.228	0.577	-0.395	0.693
Geno.rare2	4	*	*	*	*	0.001	-5.726	0.000	-3.14E+16	0.000
haplo.base3	4	T	T	A	W	0.504	NA	NA	NA	NA
Geno.23	5	A	A	W	G	0.017	-0.154	0.738	-0.209	0.835
Geno.42	5	T	A	I	G	0.027	-0.358	0.586	-0.610	0.542
Geno.rare3	5	*	*	*	*	0.009	1.064	1.083	0.982	0.326
haplo.base4	5	T	A	W	G	0.947	NA	NA	NA	NA
Geno.24	6	A	I	G	C	0.028	-0.234	0.571	-0.409	0.682
Geno.rare4	6	*	*	*	*	0.013	-0.737	0.859	-0.858	0.391
haplo.base5	6	A	W	G	C	0.959	NA	NA	NA	NA
Geno.25	7	I	G	C	C	0.028	-0.217	0.572	-0.380	0.704
Geno.62	7	W	G	C	T	0.030	0.266	0.562	0.474	0.636
Geno.rare5	7	*	*	*	*	0.013	-0.455	0.880	-0.516	0.606
haplo.base6	7	W	G	C	C	0.930	NA	NA	NA	NA
Geno.43	8	G	C	C	A	0.034	-0.750	0.496	-1.513	0.131
Geno.71	8	G	C	T	G	0.029	0.262	0.574	0.457	0.648
Geno.rare6	8	*	*	*	*	0.014	-0.434	0.872	-0.498	0.619
haplo.base7	8	G	C	C	G	0.923	NA	NA	NA	NA
Geno.13	9	C	C	A	G	0.041	-0.444	0.454	-0.976	0.329
Geno.44	9	C	C	G	T	0.023	0.409	0.651	0.627	0.531
Geno.63	9	C	T	G	G	0.029	0.282	0.571	0.494	0.622
Geno.rare7	9	*	*	*	*	0.006	-2.733	1.448	-1.887	0.060
haplo.base8	9	C	C	G	G	0.901	NA	NA	NA	NA
Geno.14	10	C	A	G	C	0.041	-0.585	0.454	-1.288	0.198
Geno.51	10	C	G	G	T	0.039	1.058	0.497	2.129	0.034
Geno.64	10	C	G	T	C	0.022	0.255	0.661	0.386	0.699
Geno.9	10	T	G	G	C	0.030	0.184	0.566	0.325	0.745
Geno.rare8	10	*	*	*	*	0.001	6.623	NA	NA	NA
haplo.base9	10	C	G	G	C	0.867	NA	NA	NA	NA
Geno.26	11	A	G	C	G	0.041	-0.470	0.453	-1.036	0.301
Geno.52	11	G	G	C	C	0.021	0.439	0.667	0.659	0.510
Geno.72	11	G	G	T	G	0.040	1.176	0.493	2.384	0.017
Geno.8	11	G	T	C	G	0.022	0.457	0.670	0.682	0.495
haplo.base10	11	G	G	C	G	0.875	NA	NA	NA	NA
Geno.15	12	G	C	C	C	0.021	0.487	0.668	0.730	0.466
Geno.45	12	G	C	G	T	0.037	0.345	0.491	0.703	0.482
Geno.53	12	G	T	G	C	0.036	1.256	0.519	2.419	0.016
Geno.73	12	T	C	G	C	0.022	0.537	0.659	0.815	0.415
Geno.rare9	12	*	*	*	*	0.004	0.820	2.053	0.399	0.690
haplo.base11	12	G	C	G	C	0.879	NA	NA	NA	NA
Geno.27	13	C	C	C	G	0.021	0.429	0.671	0.640	0.522
Geno.32	13	C	G	C	C	0.078	0.017	0.360	0.048	0.962
Geno.54	13	C	G	T	C	0.038	0.344	0.483	0.713	0.476
Geno.65	13	T	G	C	G	0.037	1.224	0.516	2.374	0.018
Geno.rare10	13	*	*	*	*	0.003	1.011	2.107	0.480	0.632
haplo.base12	13	C	G	C	G	0.822	NA	NA	NA	NA
Geno.33	14	C	C	G	A	0.021	0.431	0.676	0.637	0.524
Geno.66	14	G	C	C	G	0.077	-0.018	0.381	-0.047	0.962
Geno.74	14	G	C	G	A	0.426	0.126	0.199	0.634	0.527
Geno.10	14	G	T	C	G	0.041	0.362	0.478	0.758	0.448
Geno.rare11	14	*	*	*	*	0.002	1.546	2.510	0.616	0.538

Table A2.13. Continued

	Window	loc.1	loc.2	loc.3	loc.4	Hap.freq.	Coef.	S.E.	Test statistic	P-value
haplo.base13	14	G	C	G	G	0.432	NA	NA	NA	NA
Geno.34	15	C	C	G	T	0.077	-0.157	0.378	-0.415	0.678
Geno.67	15	C	G	G	G	0.023	-0.228	0.636	-0.358	0.720
Geno.75	15	C	G	G	T	0.410	-0.139	0.200	-0.695	0.487
Geno.91	15	T	C	G	T	0.041	0.209	0.470	0.444	0.657
Geno.rare12	15	*	*	*	*	0.003	2.322	2.402	0.967	0.334
haplo.base14	15	C	G	A	T	0.446	NA	NA	NA	NA
Geno.35	16	C	G	T	A	0.117	0.083	0.314	0.264	0.792
Geno.76	16	G	A	T	A	0.140	0.385	0.300	1.283	0.200
Geno.81	16	G	A	T	G	0.305	-0.005	0.221	-0.024	0.981
Geno.92	16	G	G	G	A	0.022	-0.098	0.657	-0.150	0.881
Geno.rare13	16	*	*	*	*	0.005	1.854	1.568	1.183	0.237
haplo.base15	16	G	G	T	A	0.410	NA	NA	NA	NA
Geno.36	17	A	T	A	T	0.142	0.386	0.292	1.321	0.187
Geno.55	17	A	T	G	T	0.306	-0.008	0.212	-0.037	0.971
Geno.77	17	G	G	A	T	0.022	-0.159	0.668	-0.238	0.812
Geno.93	17	G	T	A	C	0.030	0.156	0.560	0.279	0.781
Geno.rare14	17	*	*	*	*	0.004	1.902	1.923	0.990	0.323
haplo.base16	17	G	T	A	T	0.497	NA	NA	NA	NA
Geno.28	18	G	A	T	T	0.022	-0.139	0.631	-0.221	0.825
Geno.46	18	T	A	C	T	0.030	0.048	0.558	0.086	0.931
Geno.56	18	T	A	T	C	0.025	-0.231	0.613	-0.378	0.706
Geno.78	18	T	G	T	C	0.310	-0.063	0.208	-0.303	0.762
Geno.rare15	18	*	*	*	*	0.001	1.536	2.662	0.577	0.564
haplo.base17	18	T	A	T	T	0.611	NA	NA	NA	NA
Geno.29	19	A	C	T	G	0.028	-0.361	0.582	-0.620	0.535
Geno.47	19	A	T	C	G	0.025	-0.280	0.619	-0.452	0.651
Geno.82	19	G	T	C	A	0.283	-0.048	0.211	-0.226	0.821
Geno.94	19	G	T	C	G	0.025	-0.656	0.635	-1.034	0.302
Geno.rare16	19	*	*	*	*	0.004	3.368	1.588	2.121	0.034
haplo.base18	19	A	T	T	G	0.634	NA	NA	NA	NA
Geno.48	20	C	T	G	A	0.028	-0.293	0.630	-0.465	0.642
Geno.79	20	T	C	A	G	0.279	-0.018	0.211	-0.084	0.933
Geno.83	20	T	C	G	A	0.045	-0.346	0.491	-0.705	0.481
Geno.rare17	20	*	*	*	*	0.014	0.719	1.001	0.718	0.473
haplo.base19	20	T	T	G	A	0.634	NA	NA	NA	NA
Geno.37	21	C	A	G	C	0.165	-0.238	0.258	-0.922	0.357
Geno.49	21	C	A	G	T	0.113	0.333	0.301	1.108	0.268
Geno.57	21	C	G	A	T	0.047	-0.137	0.456	-0.300	0.764
Geno.rare18	21	*	*	*	*	0.012	0.073	0.990	0.074	0.941
haplo.base20	21	T	G	A	T	0.662	NA	NA	NA	NA
Geno.38	22	A	G	C	A	0.165	-0.225	0.256	-0.876	0.381
Geno.58	22	A	G	T	A	0.113	0.347	0.300	1.159	0.247
Geno.710	22	G	A	T	G	0.029	0.092	0.564	0.164	0.870
Geno.rare19	22	*	*	*	*	0.012	0.058	0.979	0.059	0.953
haplo.base21	22	G	A	T	A	0.680	NA	NA	NA	NA
Geno.39	23	A	T	G	D	0.030	-0.003	0.554	-0.005	0.996
Geno.410	23	G	C	A	W	0.167	-0.227	0.256	-0.887	0.375
Geno.68	23	G	T	A	W	0.115	0.442	0.300	1.475	0.141
Geno.rare20	23	*	*	*	*	0.001	3.410	0.000	2.00E+16	0.000
haplo.base22	23	A	T	A	W	0.686	NA	NA	NA	NA
Geno.210	24	C	A	W	T	0.165	-0.268	0.258	-1.038	0.300
Geno.411	24	T	A	W	C	0.012	-0.842	0.865	-0.974	0.331
Geno.69	24	T	G	D	T	0.029	-0.143	0.558	-0.256	0.798
Geno.rare21	24	*	*	*	*	0.001	5.319	0.000	3.04E+16	0.000
haplo.base23	24	T	A	W	T	0.793	NA	NA	NA	NA
Geno.16	25	A	W	C	A	0.012	-0.842	0.869	-0.969	0.333
Geno.310	25	A	W	T	G	0.248	-0.109	0.218	-0.503	0.615
Geno.412	25	G	D	T	A	0.030	-0.114	0.556	-0.205	0.838
haplo.base24	25	A	W	T	A	0.710	NA	NA	NA	NA
Geno.17	26	D	T	A	A	0.029	-0.271	0.567	-0.477	0.633
Geno.413	26	W	C	A	A	0.012	-0.851	0.873	-0.974	0.330
Geno.84	26	W	T	G	A	0.200	-0.063	0.239	-0.263	0.793
Geno.95	26	W	T	G	C	0.049	-0.255	0.452	-0.564	0.573
Geno.rare22	26	*	*	*	*	0.003	0.039	2.210	0.018	0.986
haplo.base25	26	W	T	A	A	0.707	NA	NA	NA	NA
Geno.18	27	C	A	A	G	0.012	-0.822	0.872	-0.943	0.346
Geno.610	27	T	G	A	G	0.193	-0.088	0.242	-0.364	0.716
Geno.711	27	T	G	C	G	0.049	-0.269	0.452	-0.596	0.551
Geno.rare23	27	*	*	*	*	0.010	1.010	1.032	0.979	0.328
haplo.base26	27	T	A	A	G	0.736	NA	NA	NA	NA
Geno.19	28	A	A	G	D	0.022	0.885	0.651	1.360	0.174
Geno.611	28	G	A	G	W	0.193	-0.043	0.242	-0.180	0.857
Geno.85	28	G	C	G	W	0.049	-0.227	0.452	-0.501	0.616
Geno.rare24	28	*	*	*	*	0.010	1.086	1.033	1.051	0.294

Table A2.13. Continued

	Window	loc.1	loc.2	loc.3	loc.4	Hap.freq.	Coef.	S.E.	Test statistic	P-value
haplo.base27	28	A	A	G	W	0.726	NA	NA	NA	NA
Geno.311	29	A	G	D	G	0.021	0.701	0.730	0.959	0.338
Geno.414	29	A	G	W	A	0.050	-0.128	0.443	-0.290	0.772
Geno.86	29	C	G	W	G	0.051	-0.190	0.440	-0.432	0.666
Geno.rare25	29	*	*	*	*	0.008	1.713	1.325	1.293	0.196
haplo.base28	29	A	G	W	G	0.870	NA	NA	NA	NA
Geno.312	30	G	D	G	C	0.021	0.943	0.732	1.288	0.198
Geno.415	30	G	W	A	C	0.050	-0.040	0.443	-0.089	0.929
Geno.rare26	30	*	*	*	*	0.011	0.113	1.077	0.105	0.916
haplo.base29	30	G	W	G	C	0.918	NA	NA	NA	NA
Geno.211	31	D	G	C	G	0.022	1.182	0.662	1.784	0.075
Geno.416	31	W	A	C	G	0.050	0.050	0.424	0.117	0.907
Geno.59	31	W	G	C	C	0.016	0.781	0.749	1.043	0.297
Geno.rare27	31	*	*	*	*	0.004	-3.729	1.815	-2.055	0.040
haplo.base30	31	W	G	C	G	0.908	NA	NA	NA	NA
Geno.110	32	A	C	G	A	0.051	-0.024	0.422	-0.056	0.955
Geno.313	32	G	C	C	A	0.016	0.789	0.754	1.047	0.295
Geno.510	32	G	C	G	G	0.116	0.347	0.301	1.154	0.249
Geno.rare28	32	*	*	*	*	0.003	-2.953	1.946	-1.517	0.130
haplo.base31	32	G	C	G	A	0.814	NA	NA	NA	NA
Geno.111	33	C	C	A	C	0.015	1.338	0.817	1.638	0.102
Geno.612	33	C	G	G	C	0.115	0.412	0.304	1.356	0.175
Geno.rare29	33	*	*	*	*	0.012	-1.512	0.984	-1.536	0.125
haplo.base32	33	C	G	A	C	0.858	NA	NA	NA	NA
Geno.212	34	C	A	C	G	0.015	1.352	0.820	1.648	0.100
Geno.511	34	G	A	C	A	0.046	0.877	0.457	1.921	0.055
Geno.96	34	G	G	C	G	0.115	0.458	0.305	1.503	0.133
Geno.rare30	34	*	*	*	*	0.009	-0.942	1.135	-0.830	0.407
haplo.base33	34	G	A	C	G	0.814	NA	NA	NA	NA
Geno.112	35	A	C	A	C	0.046	0.805	0.460	1.753	0.080
Geno.213	35	A	C	G	C	0.249	-0.133	0.224	-0.592	0.554
Geno.613	35	G	C	G	T	0.114	0.381	0.311	1.226	0.221
Geno.rare31	35	*	*	*	*	0.011	-0.890	0.989	-0.899	0.369
haplo.base34	35	A	C	G	T	0.579	NA	NA	NA	NA
Geno.214	36	C	A	C	G	0.046	0.695	0.466	1.491	0.136
Geno.417	36	C	G	C	G	0.248	-0.223	0.245	-0.910	0.363
Geno.512	36	C	G	T	C	0.310	-0.114	0.226	-0.505	0.614
Geno.rare32	36	*	*	*	*	0.012	-1.222	0.944	-1.295	0.196
haplo.base35	36	C	G	T	G	0.384	NA	NA	NA	NA
Geno.314	37	A	C	G	T	0.046	0.720	0.465	1.550	0.122
Geno.614	37	G	C	G	T	0.241	-0.252	0.245	-1.027	0.305
Geno.712	37	G	T	C	T	0.310	-0.112	0.224	-0.501	0.616
Geno.rare33	37	*	*	*	*	0.010	0.346	1.037	0.334	0.739
haplo.base36	37	G	T	G	T	0.393	NA	NA	NA	NA
Geno.513	38	C	G	T	G	0.283	-0.118	0.242	-0.490	0.625
Geno.713	38	T	C	T	G	0.311	-0.103	0.232	-0.443	0.658
Geno.97	38	T	G	T	A	0.052	0.045	0.454	0.099	0.921
Geno.rare34	38	*	*	*	*	0.014	0.740	0.892	0.830	0.407
haplo.base37	38	T	G	T	G	0.341	NA	NA	NA	NA
Geno.113	39	C	T	G	A	0.307	-0.183	0.218	-0.841	0.401
Geno.615	39	G	T	A	A	0.054	0.006	0.461	0.012	0.990
Geno.98	39	G	T	G	C	0.081	-0.617	0.434	-1.424	0.155
Geno.rare35	39	*	*	*	*	0.015	1.919	1.170	1.640	0.102
haplo.base38	39	G	T	G	A	0.542	NA	NA	NA	NA
Geno.418	40	T	A	A	C	0.052	-0.061	0.441	-0.138	0.890
Geno.87	40	T	G	A	G	0.021	-0.867	0.691	-1.253	0.210
Geno.99	40	T	G	C	C	0.085	-0.539	0.354	-1.522	0.128
Geno.rare36	40	*	*	*	*	0.011	2.304	1.098	2.098	0.036
haplo.base39	40	T	G	A	C	0.831	NA	NA	NA	NA
Geno.114	41	A	A	C	W	0.052	-0.066	0.446	-0.147	0.883
Geno.616	41	G	A	G	W	0.021	-0.888	0.699	-1.270	0.204
Geno.88	41	G	C	C	W	0.085	-0.502	0.359	-1.398	0.163
Geno.rare37	41	*	*	*	*	0.006	2.199	2.177	1.010	0.313
haplo.base40	41	G	A	C	W	0.836	NA	NA	NA	NA
Geno.215	42	A	C	W	A	0.111	-0.083	0.296	-0.280	0.779
Geno.419	42	A	G	W	G	0.021	-0.409	0.711	-0.575	0.566
Geno.714	42	C	C	W	G	0.089	-0.263	0.341	-0.772	0.440
Geno.rare38	42	*	*	*	*	0.002	-4.282	NA	NA	NA
haplo.base41	42	A	C	W	G	0.777	NA	NA	NA	NA
Geno.216	43	C	W	A	A	0.111	-0.050	0.298	-0.168	0.867
Geno.420	43	C	W	G	G	0.203	0.027	0.237	0.113	0.910
Geno.514	43	G	W	G	A	0.021	-0.494	0.696	-0.709	0.479
Geno.rare39	43	*	*	*	*	0.002	-3.907	2.589	-1.509	0.132
haplo.base42	43	C	W	G	A	0.663	NA	NA	NA	NA
Geno.217	44	W	A	A	C	0.111	-0.085	0.298	-0.286	0.775

Table A2.13. Continued

	Window	loc.1	loc.2	loc.3	loc.4	Hap.freq.	Coef.	S.E.	Test statistic	P-value
Geno.515	44	W	G	A	T	0.108	-0.401	0.309	-1.296	0.195
Geno.617	44	W	G	G	C	0.202	-0.022	0.243	-0.090	0.928
Geno.rare40	44	*	*	*	*	0.003	-4.859	2.180	-2.228	0.026
haplo.base43	44	W	G	A	C	0.576	NA	NA	NA	NA
Geno.218	45	A	A	C	W	0.111	-0.041	0.297	-0.139	0.890
Geno.421	45	G	A	C	D	0.022	1.173	0.649	1.808	0.071
Geno.618	45	G	A	T	W	0.108	-0.303	0.310	-0.976	0.329
Geno.715	45	G	G	C	W	0.203	0.048	0.243	0.199	0.842
Geno.rare41	45	*	*	*	*	0.001	-8.585	3.186	-2.695	0.007
haplo.base44	45	G	A	C	W	0.556	NA	NA	NA	NA
Geno.219	46	A	C	D	C	0.022	1.160	0.647	1.792	0.073
Geno.315	46	A	C	W	A	0.031	-0.521	0.557	-0.935	0.350
Geno.619	46	A	T	W	C	0.108	-0.316	0.309	-1.022	0.307
Geno.910	46	G	C	W	C	0.203	0.029	0.240	0.123	0.903
Geno.rare42	46	*	*	*	*	0.001	-8.593	3.169	-2.711	0.007
haplo.base45	46	A	C	W	C	0.636	NA	NA	NA	NA
Geno.220	47	C	D	C	G	0.022	1.228	0.648	1.896	0.058
Geno.316	47	C	W	A	G	0.031	-0.449	0.558	-0.804	0.422
Geno.422	47	C	W	C	A	0.035	0.886	0.527	1.681	0.093
Geno.716	47	T	W	C	G	0.109	-0.381	0.298	-1.281	0.201
haplo.base46	47	C	W	C	G	0.804	NA	NA	NA	NA
Geno.221	48	D	C	G	T	0.022	1.303	0.647	2.015	0.044
Geno.317	48	W	A	G	T	0.031	-0.388	0.557	-0.697	0.486
Geno.423	48	W	C	A	T	0.035	0.973	0.525	1.854	0.064
Geno.rare43	48	*	*	*	*	0.006	0.523	1.215	0.431	0.667
haplo.base47	48	W	C	G	T	0.906	NA	NA	NA	NA
Geno.222	49	A	G	T	T	0.030	-0.408	0.564	-0.723	0.470
Geno.424	49	C	A	T	T	0.035	0.937	0.526	1.780	0.075
Geno.620	49	C	G	T	C	0.190	0.151	0.248	0.612	0.541
Geno.rare44	49	*	*	*	*	0.007	0.463	1.217	0.380	0.704
haplo.base48	49	C	G	T	T	0.738	NA	NA	NA	NA
Geno.223	50	A	T	T	D	0.035	0.971	0.527	1.842	0.066
Geno.516	50	G	T	C	D	0.191	0.169	0.250	0.675	0.500
Geno.89	50	G	T	T	W	0.086	0.054	0.348	0.155	0.877
Geno.rare45	50	*	*	*	*	0.006	0.529	1.218	0.434	0.665
haplo.base49	50	G	T	T	D	0.682	NA	NA	NA	NA
Geno.224	51	T	C	D	C	0.141	-0.001	0.285	-0.005	0.996
Geno.318	51	T	C	D	T	0.050	0.616	0.474	1.300	0.194
Geno.517	51	T	T	D	C	0.100	0.288	0.334	0.862	0.389
Geno.717	51	T	T	W	T	0.086	0.036	0.350	0.102	0.919
Geno.rare46	51	*	*	*	*	0.006	0.476	1.215	0.392	0.695
haplo.base50	51	T	T	D	T	0.616	NA	NA	NA	NA
Geno.115	52	C	D	C	A	0.141	-0.055	0.292	-0.188	0.851
Geno.225	52	C	D	T	A	0.051	0.546	0.481	1.134	0.257
Geno.425	52	T	D	C	A	0.100	0.243	0.339	0.715	0.475
Geno.621	52	T	D	T	G	0.115	-0.252	0.302	-0.836	0.403
Geno.718	52	T	W	T	A	0.092	0.035	0.348	0.101	0.920
haplo.base51	52	T	D	T	A	0.501	NA	NA	NA	NA
Geno.116	53	D	C	A	A	0.242	-0.031	0.230	-0.134	0.894
Geno.518	53	D	T	A	C	0.035	-0.646	0.491	-1.315	0.189
Geno.622	53	D	T	G	A	0.116	-0.362	0.300	-1.204	0.229
Geno.810	53	W	T	A	A	0.092	-0.052	0.347	-0.151	0.880
haplo.base52	53	D	T	A	A	0.514	NA	NA	NA	NA
Geno.117	54	C	A	A	C	0.242	-0.022	0.228	-0.098	0.922
Geno.519	54	T	A	A	G	0.034	0.026	0.533	0.049	0.961
Geno.623	54	T	A	C	C	0.035	-0.644	0.494	-1.303	0.193
Geno.719	54	T	G	A	C	0.116	-0.363	0.300	-1.211	0.226
haplo.base53	54	T	A	A	C	0.573	NA	NA	NA	NA
Geno.226	55	A	A	C	T	0.051	0.326	0.450	0.726	0.468
Geno.319	55	A	A	G	A	0.033	-0.056	0.531	-0.105	0.917
Geno.520	55	A	C	C	A	0.034	-0.780	0.501	-1.558	0.120
Geno.720	55	G	A	C	A	0.116	-0.325	0.289	-1.124	0.262
Geno.rare47	55	*	*	*	*	0.002	5.362	3.427	1.565	0.118
haplo.base54	55	A	A	C	A	0.764	NA	NA	NA	NA
Geno.227	56	A	C	A	G	0.077	0.045	0.374	0.119	0.905
Geno.320	56	A	C	T	C	0.051	0.354	0.452	0.783	0.434
Geno.426	56	A	G	A	C	0.033	-0.086	0.539	-0.159	0.874
Geno.721	56	C	C	A	C	0.034	-0.792	0.506	-1.564	0.118
Geno.rare48	56	*	*	*	*	0.002	5.342	3.364	1.588	0.113
haplo.base55	56	A	C	A	C	0.803	NA	NA	NA	NA
Geno.228	57	C	A	C	G	0.122	-0.253	0.289	-0.875	0.382
Geno.427	57	C	A	G	G	0.077	0.076	0.378	0.202	0.840
Geno.521	57	C	T	C	A	0.052	0.567	0.447	1.268	0.205
Geno.722	57	G	A	C	A	0.033	0.100	0.541	0.185	0.853
Geno.rare49	57	*	*	*	*	0.003	0.751	2.600	0.289	0.773

Table A2.13. Continued

	Window	loc.1	loc.2	loc.3	loc.4	Hap.freq.	Coef.	S.E.	Test statistic	P-value
haplo.base56	57	C	A	C	A	0.714	NA	NA	NA	NA
Geno.229	58	A	C	A	T	0.221	0.091	0.238	0.383	0.702
Geno.321	58	A	C	G	C	0.112	-0.261	0.309	-0.843	0.400
Geno.723	58	A	G	G	T	0.075	0.082	0.391	0.210	0.834
Geno.911	58	T	C	A	T	0.052	0.591	0.448	1.320	0.187
Geno.rare50	58	*	*	*	*	0.014	-0.034	1.058	-0.032	0.974
haplo.base57	58	A	C	A	C	0.525	NA	NA	NA	NA
Geno.230	59	C	A	C	G	0.066	0.031	0.420	0.073	0.942
Geno.322	59	C	A	T	A	0.261	0.272	0.236	1.153	0.249
Geno.428	59	C	A	T	G	0.015	-1.362	1.012	-1.345	0.179
Geno.522	59	C	G	C	A	0.111	-0.290	0.314	-0.926	0.355
Geno.131	59	G	G	T	G	0.076	-0.011	0.399	-0.026	0.979
Geno.rare51	59	*	*	*	*	0.014	0.412	0.940	0.439	0.661
haplo.base58	59	C	A	C	A	0.457	NA	NA	NA	NA
Geno.231	60	A	C	G	G	0.067	0.040	0.433	0.092	0.927
Geno.323	60	A	T	A	G	0.262	0.258	0.237	1.089	0.277
Geno.429	60	A	T	G	G	0.019	-1.092	1.012	-1.079	0.281
Geno.523	60	G	C	A	G	0.113	-0.299	0.318	-0.938	0.349
Geno.912	60	G	T	G	G	0.076	0.125	0.381	0.328	0.743
Geno.rare52	60	*	*	*	*	0.008	-0.427	1.479	-0.289	0.773
haplo.base59	60	A	C	A	G	0.455	NA	NA	NA	NA
Geno.430	61	C	G	G	T	0.072	-0.390	0.433	-0.901	0.368
Geno.524	61	T	A	G	C	0.044	0.539	0.473	1.139	0.255
Geno.624	61	T	A	G	T	0.218	0.059	0.252	0.234	0.815
Geno.913	61	T	G	G	T	0.094	0.256	0.361	0.711	0.477
Geno.rare53	61	*	*	*	*	0.008	-1.127	1.225	-0.920	0.358
haplo.base60	61	C	A	G	T	0.563	NA	NA	NA	NA
Geno.118	62	A	G	C	G	0.051	0.417	0.435	0.958	0.339
Geno.232	62	A	G	T	G	0.290	0.196	0.231	0.847	0.398
Geno.625	62	G	G	T	G	0.134	0.225	0.296	0.759	0.448
Geno.724	62	G	G	T	T	0.034	-0.813	0.614	-1.323	0.186
Geno.rare54	62	*	*	*	*	0.001	-2.522	2.581	-0.977	0.329
haplo.base61	62	A	G	T	T	0.490	NA	NA	NA	NA
Geno.431	63	G	C	G	C	0.051	0.511	0.438	1.168	0.243
Geno.811	63	G	T	G	C	0.424	0.320	0.201	1.597	0.111
Geno.914	63	G	T	T	A	0.071	0.415	0.380	1.092	0.275
Geno.rare55	63	*	*	*	*	0.001	-2.371	2.580	-0.919	0.358
haplo.base62	63	G	T	T	C	0.452	NA	NA	NA	NA
Geno.324	64	C	G	C	W	0.051	0.527	0.437	1.205	0.229
Geno.725	64	T	G	C	I	0.041	0.284	0.486	0.584	0.559
Geno.812	64	T	G	C	W	0.384	0.317	0.210	1.513	0.131
Geno.915	64	T	T	A	W	0.071	0.419	0.380	1.103	0.271
haplo.base63	64	T	T	C	W	0.453	NA	NA	NA	NA
Geno.119	65	G	C	I	T	0.041	-0.107	0.503	-0.213	0.832
Geno.233	65	G	C	W	C	0.017	-0.587	0.923	-0.636	0.525
Geno.525	65	T	A	W	T	0.071	0.039	0.378	0.104	0.917
Geno.626	65	T	C	W	C	0.178	-0.509	0.274	-1.856	0.064
Geno.726	65	T	C	W	T	0.274	-0.295	0.235	-1.257	0.209
haplo.base64	65	G	C	W	T	0.420	NA	NA	NA	NA
Geno.325	66	A	W	T	C	0.066	0.120	0.381	0.315	0.753
Geno.727	66	C	I	T	T	0.040	0.069	0.496	0.138	0.890
Geno.813	66	C	W	C	C	0.033	-0.618	0.541	-1.142	0.254
Geno.916	66	C	W	C	T	0.161	-0.336	0.269	-1.250	0.212
Geno.101	66	C	W	T	C	0.012	-0.566	0.980	-0.578	0.563
Geno.rare56	66	*	*	*	*	0.007	-0.028	1.258	-0.022	0.982
haplo.base65	66	C	W	T	T	0.682	NA	NA	NA	NA
Geno.234	67	I	T	T	C	0.041	0.126	0.490	0.258	0.797
Geno.326	67	W	C	C	C	0.034	-0.242	0.589	-0.410	0.682
Geno.432	67	W	C	T	C	0.160	-0.329	0.285	-1.157	0.248
Geno.627	67	W	T	C	C	0.076	-0.097	0.393	-0.248	0.804
Geno.917	67	W	T	T	G	0.147	0.557	0.280	1.990	0.047
haplo.base66	67	W	T	T	C	0.541	NA	NA	NA	NA
Geno.120	68	C	C	C	G	0.034	-0.282	0.590	-0.478	0.633
Geno.235	68	C	T	C	G	0.160	-0.287	0.284	-1.010	0.313
Geno.433	68	T	C	C	G	0.076	-0.043	0.394	-0.109	0.913
Geno.526	68	T	T	C	A	0.056	0.382	0.433	0.882	0.378
Geno.814	68	T	T	G	G	0.145	0.620	0.285	2.175	0.030
Geno.rare57	68	*	*	*	*	0.002	-2.227	3.241	-0.687	0.492
haplo.base67	68	T	T	C	G	0.526	NA	NA	NA	NA
Geno.236	69	C	C	G	G	0.109	-0.039	0.302	-0.130	0.897
Geno.327	69	T	C	A	A	0.057	0.364	0.410	0.889	0.374
Geno.628	69	T	G	G	G	0.147	0.636	0.274	2.320	0.021
haplo.base68	69	T	C	G	G	0.686	NA	NA	NA	NA
Geno.121	70	C	A	A	A	0.057	0.466	0.423	1.103	0.271
Geno.527	70	C	G	G	A	0.314	0.161	0.215	0.750	0.453

Table A2.13. Continued

	Window	loc.1	loc.2	loc.3	loc.4	Hap.freq.	Coef.	S.E.	Test statistic	P-value
Geno.815	70	G	G	G	A	0.146	0.735	0.280	2.622	0.009
Geno.rare58	70	*	*	*	*	0.003	-1.803	2.713	-0.665	0.507
haplo.base69	70	C	G	G	T	0.481	NA	NA	NA	NA
Geno.237	71	A	A	A	G	0.058	0.452	0.413	1.094	0.274
Geno.528	71	G	G	A	A	0.141	0.378	0.282	1.341	0.180
Geno.629	71	G	G	A	G	0.322	0.324	0.217	1.493	0.136
Geno.rare59	71	*	*	*	*	0.003	0.469	2.559	0.183	0.855
haplo.base70	71	G	G	T	G	0.477	NA	NA	NA	NA
Geno.122	72	A	A	G	C	0.057	0.412	0.418	0.986	0.324
Geno.328	72	G	A	A	C	0.140	0.504	0.283	1.778	0.076
Geno.434	72	G	A	G	A	0.135	0.129	0.286	0.451	0.652
Geno.529	72	G	A	G	C	0.187	0.421	0.262	1.604	0.109
Geno.rare60	72	*	*	*	*	0.004	-1.519	1.930	-0.787	0.431
haplo.base71	72	G	T	G	A	0.477	NA	NA	NA	NA
Geno.238	73	A	A	C	G	0.138	0.588	0.285	2.064	0.039
Geno.329	73	A	G	A	G	0.135	0.189	0.286	0.661	0.509
Geno.435	73	A	G	C	G	0.246	0.496	0.237	2.093	0.037
Geno.728	73	T	G	A	A	0.017	1.866	0.745	2.506	0.012
Geno.rare61	73	*	*	*	*	0.005	-1.399	1.924	-0.727	0.467
haplo.base72	73	T	G	A	G	0.460	NA	NA	NA	NA
Geno.630	74	A	C	G	G	0.140	0.526	0.281	1.867	0.062
Geno.729	74	G	A	A	G	0.016	1.967	0.774	2.541	0.011
Geno.816	74	G	A	G	A	0.012	-1.403	0.895	-1.568	0.117
Geno.1110	74	G	C	G	G	0.248	0.387	0.229	1.688	0.092
Geno.rare62	74	*	*	*	*	0.003	-2.324	2.137	-1.087	0.277
haplo.base73	74	G	A	G	G	0.581	NA	NA	NA	NA
Geno.123	75	A	A	G	C	0.017	1.784	0.741	2.406	0.016
Geno.239	75	A	G	A	C	0.012	-1.388	0.896	-1.549	0.122
Geno.530	75	C	G	G	C	0.388	0.428	0.191	2.245	0.025
Geno.rare63	75	*	*	*	*	0.006	0.839	1.099	0.763	0.445
haplo.base74	75	A	G	G	C	0.577	NA	NA	NA	NA
Geno.330	76	A	G	C	A	0.017	1.563	0.739	2.114	0.035
Geno.436	76	G	A	C	A	0.012	-1.645	0.890	-1.848	0.065
Geno.730	76	G	G	C	G	0.011	0.227	0.917	0.248	0.805
Geno.rare64	76	*	*	*	*	0.006	0.721	1.102	0.655	0.513
haplo.base75	76	G	G	C	A	0.954	NA	NA	NA	NA
Geno.124	77	A	C	A	T	0.012	-1.481	0.894	-1.656	0.098
Geno.240	77	G	C	A	C	0.285	0.540	0.208	2.600	0.010
Geno.rare65	77	*	*	*	*	0.017	0.503	0.713	0.705	0.481
haplo.base76	77	G	C	A	T	0.686	NA	NA	NA	NA
Geno.125	78	C	A	C	A	0.147	0.509	0.275	1.848	0.065
Geno.241	78	C	A	C	G	0.138	0.604	0.279	2.168	0.030
Geno.437	78	C	A	T	G	0.011	-1.966	0.911	-2.158	0.031
Geno.rare66	78	*	*	*	*	0.017	0.532	0.728	0.731	0.465
haplo.base77	78	C	A	T	A	0.687	NA	NA	NA	NA
Geno.126	79	A	C	A	A	0.144	0.574	0.297	1.930	0.054
Geno.331	79	A	C	G	A	0.140	0.638	0.287	2.221	0.027
Geno.531	79	A	T	A	G	0.242	0.166	0.234	0.711	0.477
Geno.631	79	A	T	G	A	0.011	-1.974	0.920	-2.147	0.032
Geno.817	79	G	T	A	A	0.011	0.250	0.918	0.272	0.786
Geno.rare67	79	*	*	*	*	0.004	-0.352	1.816	-0.194	0.846
haplo.base78	79	A	T	A	A	0.448	NA	NA	NA	NA
Geno.127	80	C	A	A	C	0.144	0.583	0.298	1.956	0.051
Geno.438	80	C	G	A	C	0.140	0.645	0.289	2.232	0.026
Geno.731	80	T	A	A	T	0.025	0.238	0.621	0.383	0.702
Geno.818	80	T	A	G	C	0.243	0.172	0.235	0.733	0.464
Geno.918	80	T	G	A	C	0.012	-1.931	0.919	-2.101	0.036
Geno.rare68	80	*	*	*	*	0.004	-0.374	1.809	-0.207	0.836
haplo.base79	80	T	A	A	C	0.433	NA	NA	NA	NA
Geno.128	81	A	A	C	A	0.094	0.431	0.364	1.185	0.236
Geno.439	81	A	A	T	C	0.023	-0.280	0.655	-0.428	0.669
Geno.632	81	A	G	C	C	0.244	-0.038	0.227	-0.167	0.868
Geno.919	81	G	A	C	A	0.129	0.631	0.287	2.201	0.028
Geno.102	81	G	A	C	C	0.022	-0.780	0.710	-1.098	0.273
Geno.rare69	81	*	*	*	*	0.005	8.106	1.722	4.707	0.000
haplo.base80	81	A	A	C	C	0.484	NA	NA	NA	NA
Geno.129	82	A	C	A	G	0.220	0.670	0.239	2.799	0.005
Geno.633	82	A	T	C	G	0.023	-0.306	0.670	-0.456	0.648
Geno.819	82	G	C	C	A	0.032	-0.130	0.545	-0.239	0.811
Geno.920	82	G	C	C	G	0.213	0.113	0.241	0.470	0.638
Geno.rare70	82	*	*	*	*	0.005	5.909	2.188	2.700	0.007
haplo.base81	82	A	C	C	G	0.508	NA	NA	NA	NA
Geno.242	83	C	A	G	C	0.224	0.723	0.235	3.081	0.002
Geno.332	83	C	C	A	C	0.033	0.009	0.535	0.017	0.986
Geno.634	83	C	C	G	G	0.139	0.099	0.283	0.349	0.727

Table A2.13. Continued

	Window	loc.1	loc.2	loc.3	loc.4	Hap.freq.	Coef.	S.E.	Test statistic	P-value
Geno.820	83	T	C	G	C	0.025	0.238	0.615	0.387	0.699
haplo.base82	83	C	C	G	C	0.578	NA	NA	NA	NA
Geno.243	84	A	G	C	A	0.224	0.724	0.237	3.062	0.002
Geno.440	84	C	A	C	C	0.033	0.006	0.535	0.011	0.991
Geno.732	84	C	G	C	C	0.049	0.135	0.443	0.306	0.760
Geno.821	84	C	G	G	A	0.140	0.106	0.284	0.372	0.710
haplo.base83	84	C	G	C	A	0.554	NA	NA	NA	NA
Geno.130	85	A	C	C	G	0.033	-0.220	0.534	-0.412	0.680
Geno.532	85	G	C	C	G	0.049	-0.119	0.439	-0.270	0.787
Geno.733	85	G	G	A	G	0.139	-0.154	0.274	-0.564	0.573
Geno.rare71	85	*	*	*	*	0.008	-1.764	1.133	-1.558	0.120
haplo.base84	85	G	C	A	G	0.771	NA	NA	NA	NA
Geno.244	86	C	A	G	C	0.044	0.016	0.455	0.036	0.971
Geno.533	86	C	C	G	T	0.081	-0.168	0.350	-0.480	0.631
Geno.734	86	G	A	G	T	0.139	-0.152	0.275	-0.553	0.581
Geno.rare72	86	*	*	*	*	0.008	-1.761	1.125	-1.566	0.118
haplo.base85	86	C	A	G	T	0.727	NA	NA	NA	NA
Geno.441	87	A	G	C	G	0.044	-0.069	0.459	-0.151	0.880
Geno.534	87	A	G	T	A	0.320	-0.289	0.221	-1.311	0.190
Geno.822	87	C	G	T	A	0.080	-0.207	0.362	-0.572	0.567
Geno.rare73	87	*	*	*	*	0.010	-1.760	0.981	-1.794	0.073
haplo.base86	87	A	G	T	G	0.546	NA	NA	NA	NA
Geno.333	88	G	C	G	G	0.044	-0.065	0.459	-0.142	0.887
Geno.535	88	G	T	A	G	0.400	-0.269	0.204	-1.319	0.187
Geno.rare74	88	*	*	*	*	0.010	-1.650	0.988	-1.670	0.095
haplo.base87	88	G	T	G	G	0.546	NA	NA	NA	NA
Geno.245	89	C	G	G	G	0.044	-0.062	0.456	-0.135	0.892
Geno.442	89	T	A	G	C	0.400	-0.246	0.202	-1.216	0.224
Geno.rare75	89	*	*	*	*	0.002	-3.154	2.570	-1.227	0.220
haplo.base88	89	T	G	G	C	0.554	NA	NA	NA	NA
Geno.246	90	A	G	C	A	0.397	-0.276	0.211	-1.310	0.191
Geno.635	90	G	G	C	G	0.092	0.140	0.349	0.401	0.689
Geno.735	90	G	G	G	A	0.043	-0.174	0.465	-0.373	0.709
Geno.rare76	90	*	*	*	*	0.004	3.902	1.680	2.323	0.020
haplo.base89	90	G	G	C	A	0.464	NA	NA	NA	NA
Geno.247	91	G	C	A	A	0.087	0.698	0.345	2.021	0.044
Geno.443	91	G	C	G	G	0.095	0.513	0.328	1.566	0.118
Geno.536	91	G	G	A	G	0.043	0.024	0.455	0.053	0.958
Geno.rare77	91	*	*	*	*	0.001	-0.024	2.566	-0.009	0.993
haplo.base90	91	G	C	A	G	0.774	NA	NA	NA	NA
Geno.132	92	C	A	A	G	0.087	0.669	0.346	1.934	0.054
Geno.248	92	C	A	G	A	0.026	-0.754	0.610	-1.237	0.217
Geno.537	92	C	G	G	G	0.094	0.498	0.328	1.521	0.129
Geno.636	92	G	A	G	G	0.043	-0.022	0.455	-0.049	0.961
haplo.base91	92	C	A	G	G	0.749	NA	NA	NA	NA
Geno.249	93	A	A	G	T	0.087	0.706	0.347	2.035	0.042
Geno.334	93	A	G	A	T	0.026	-0.699	0.611	-1.144	0.253
Geno.444	93	A	G	G	C	0.057	0.370	0.399	0.927	0.354
Geno.921	93	G	G	G	T	0.094	0.517	0.329	1.570	0.117
haplo.base92	93	A	G	G	T	0.736	NA	NA	NA	NA
Geno.133	94	A	G	T	C	0.087	0.642	0.348	1.845	0.065
Geno.250	94	G	A	T	T	0.026	-0.746	0.609	-1.226	0.221
Geno.335	94	G	G	C	C	0.056	0.316	0.401	0.787	0.432
Geno.637	94	G	G	T	T	0.134	0.019	0.274	0.068	0.946
haplo.base93	94	G	G	T	C	0.697	NA	NA	NA	NA
Geno.134	95	A	T	T	G	0.026	-0.831	0.609	-1.365	0.173
Geno.251	95	G	C	C	G	0.054	0.240	0.422	0.568	0.570
Geno.638	95	G	T	C	T	0.020	-0.213	0.712	-0.300	0.764
Geno.736	95	G	T	T	G	0.133	-0.061	0.275	-0.220	0.826
Geno.rare78	95	*	*	*	*	0.003	0.051	2.636	0.019	0.985
haplo.base94	95	G	T	C	G	0.765	NA	NA	NA	NA
Geno.135	96	C	C	G	A	0.055	0.265	0.405	0.654	0.513
Geno.737	96	T	C	T	A	0.019	-0.038	0.732	-0.053	0.958
Geno.922	96	T	T	G	A	0.160	-0.180	0.251	-0.719	0.472
Geno.rare79	96	*	*	*	*	0.007	-1.379	1.697	-0.813	0.416
haplo.base95	96	T	C	G	A	0.760	NA	NA	NA	NA
Geno.136	97	C	G	A	D	0.146	0.289	0.276	1.047	0.295
Geno.538	97	C	T	A	W	0.020	-0.080	0.681	-0.117	0.907
Geno.823	97	T	G	A	W	0.156	-0.178	0.260	-0.686	0.493
Geno.rare80	97	*	*	*	*	0.010	-0.237	1.219	-0.194	0.846
haplo.base96	97	C	G	A	W	0.668	NA	NA	NA	NA
Geno.252	98	G	A	D	T	0.150	0.334	0.264	1.268	0.205
Geno.336	98	G	A	W	G	0.084	-0.016	0.340	-0.046	0.963
Geno.824	98	T	A	W	T	0.020	-0.011	0.689	-0.016	0.987
Geno.rare81	98	*	*	*	*	0.006	-1.395	1.423	-0.980	0.327

Table A2.13. Continued

	Window	loc.1	loc.2	loc.3	loc.4	Hap.freq.	Coef.	S.E.	Test statistic	P-value
haplo.base97	98	G	A	W	T	0.740	NA	NA	NA	NA
Geno.253	99	A	D	T	D	0.154	0.342	0.257	1.331	0.184
Geno.445	99	A	W	G	W	0.084	-0.015	0.340	-0.045	0.964
Geno.rare82	99	*	*	*	*	0.009	-0.733	1.063	-0.689	0.491
haplo.base98	99	A	W	T	W	0.753	NA	NA	NA	NA
Geno.337	100	D	T	D	T	0.153	0.370	0.256	1.442	0.150
Geno.539	100	W	G	W	T	0.084	0.026	0.339	0.078	0.938
Geno.rare83	100	*	*	*	*	0.014	1.128	0.865	1.304	0.193
haplo.base99	100	W	T	W	T	0.749	NA	NA	NA	NA
Geno.338	101	G	W	T	G	0.083	-0.026	0.343	-0.076	0.940
Geno.639	101	T	D	T	G	0.156	0.321	0.257	1.249	0.212
Geno.825	101	T	W	T	A	0.015	-0.290	0.804	-0.361	0.718
Geno.rare84	101	*	*	*	*	0.011	1.644	0.994	1.654	0.099
haplo.base100	101	T	W	T	G	0.735	NA	NA	NA	NA
Geno.339	102	D	T	G	C	0.155	0.309	0.256	1.207	0.228
Geno.640	102	W	T	A	C	0.016	-0.076	0.763	-0.099	0.921
Geno.rare85	102	*	*	*	*	0.012	1.003	0.947	1.059	0.290
haplo.base101	102	W	T	G	C	0.817	NA	NA	NA	NA
Geno.137	103	G	G	C	G	0.010	1.431	0.948	1.509	0.132
Geno.254	103	T	A	C	G	0.016	-0.111	0.764	-0.145	0.885
Geno.rare86	103	*	*	*	*	0.002	-0.134	2.576	-0.052	0.958
haplo.base102	103	T	G	C	G	0.972	NA	NA	NA	NA
Geno.138	104	A	C	G	G	0.016	-0.145	0.762	-0.191	0.849
Geno.rare87	104	*	*	*	*	0.003	-0.727	1.822	-0.399	0.690
haplo.base103	104	G	C	G	G	0.981	NA	NA	NA	NA
Geno.rare88	105	*	*	*	*	0.007	-0.778	1.218	-0.639	0.523
haplo.base104	105	C	G	G	G	0.993	NA	NA	NA	NA
Geno.rare89	106	*	*	*	*	0.007	-0.778	1.218	-0.639	0.523
haplo.base105	106	G	G	G	A	0.993	NA	NA	NA	NA
Geno.446	107	G	G	A	G	0.238	0.307	0.223	1.374	0.170
Geno.rare90	107	*	*	*	*	0.006	-1.301	1.218	-1.068	0.286
haplo.base106	107	G	G	A	A	0.755	NA	NA	NA	NA
Geno.340	108	G	A	A	A	0.336	0.200	0.223	0.897	0.370
Geno.540	108	G	A	G	A	0.217	0.594	0.256	2.320	0.021
Geno.641	108	G	A	G	T	0.023	-1.274	0.785	-1.622	0.105
Geno.rare91	108	*	*	*	*	0.005	-1.029	1.381	-0.745	0.456
haplo.base107	108	G	A	A	T	0.420	NA	NA	NA	NA
Geno.139	109	A	A	A	C	0.337	0.201	0.223	0.900	0.369
Geno.341	109	A	G	A	C	0.114	0.360	0.336	1.073	0.284
Geno.447	109	A	G	A	T	0.106	0.810	0.327	2.475	0.014
Geno.541	109	A	G	T	C	0.024	-1.285	0.765	-1.678	0.094
Geno.rare92	109	*	*	*	*	0.001	-2.323	2.553	-0.910	0.363
haplo.base108	109	A	A	T	C	0.419	NA	NA	NA	NA
Geno.342	110	A	T	C	A	0.331	-0.205	0.239	-0.859	0.391
Geno.448	110	A	T	C	G	0.088	-0.183	0.365	-0.503	0.615
Geno.542	110	G	A	C	A	0.111	0.173	0.362	0.478	0.633
Geno.738	110	G	A	T	A	0.106	0.620	0.344	1.800	0.072
Geno.923	110	G	T	C	A	0.023	-1.490	0.775	-1.924	0.055
Geno.rare93	110	*	*	*	*	0.005	-0.600	1.637	-0.367	0.714
haplo.base109	110	A	A	C	A	0.338	NA	NA	NA	NA
Geno.543	111	A	T	A	G	0.105	0.464	0.335	1.386	0.166
Geno.826	111	T	C	A	G	0.348	-0.365	0.222	-1.645	0.100
Geno.924	111	T	C	G	G	0.090	-0.260	0.351	-0.742	0.458
Geno.rare94	111	*	*	*	*	0.016	-0.582	0.796	-0.731	0.465
haplo.base110	111	A	C	A	G	0.441	NA	NA	NA	NA
Geno.140	112	C	A	A	C	0.013	-0.418	0.846	-0.494	0.622
Geno.449	112	C	G	G	C	0.093	-0.139	0.335	-0.415	0.678
Geno.642	112	T	A	G	C	0.103	0.631	0.323	1.955	0.051
Geno.rare95	112	*	*	*	*	0.009	-0.568	1.021	-0.556	0.578
haplo.base111	112	C	A	G	C	0.783	NA	NA	NA	NA
Geno.141	113	A	A	C	T	0.013	-0.749	0.847	-0.885	0.376
Geno.343	113	A	G	C	T	0.353	-0.569	0.208	-2.739	0.006
Geno.643	113	G	G	C	T	0.093	-0.417	0.338	-1.232	0.218
Geno.rare96	113	*	*	*	*	0.009	-0.809	1.013	-0.799	0.425
haplo.base112	113	A	G	C	C	0.532	NA	NA	NA	NA
Geno.344	114	A	C	T	A	0.013	-0.767	0.847	-0.905	0.366
Geno.644	114	G	C	C	T	0.085	-0.145	0.364	-0.399	0.690
Geno.739	114	G	C	T	A	0.446	-0.559	0.201	-2.781	0.006
Geno.rare97	114	*	*	*	*	0.009	-0.862	1.016	-0.849	0.396
haplo.base113	114	G	C	C	A	0.447	NA	NA	NA	NA
Geno.142	115	C	C	A	G	0.447	0.525	0.201	2.614	0.009
Geno.255	115	C	C	T	G	0.085	0.376	0.359	1.047	0.295
Geno.rare98	115	*	*	*	*	0.016	-1.142	0.774	-1.475	0.141
haplo.base114	115	C	T	A	G	0.453	NA	NA	NA	NA
Geno.345	116	C	T	G	T	0.085	-0.106	0.361	-0.295	0.768

Table A2.13. Continued

	Window	loc.1	loc.2	loc.3	loc.4	Hap.freq.	Coef.	S.E.	Test statistic	P-value
Geno.450	116	T	A	G	T	0.453	-0.497	0.199	-2.491	0.013
Geno.rare99	116	*	*	*	*	0.007	-2.661	1.242	-2.142	0.033
haplo.base115	116	C	A	G	T	0.456	NA	NA	NA	NA
Geno.143	117	A	G	T	A	0.012	1.804	0.836	2.159	0.031
Geno.645	117	T	G	T	G	0.085	0.159	0.348	0.455	0.649
Geno.rare100	117	*	*	*	*	0.007	-2.490	1.298	-1.919	0.055
haplo.base116	117	A	G	T	G	0.897	NA	NA	NA	NA
Geno.256	118	G	T	A	T	0.012	1.783	0.836	2.133	0.033
Geno.346	118	G	T	G	C	0.016	-0.472	0.747	-0.631	0.528
Geno.rare101	118	*	*	*	*	0.007	-2.521	1.242	-2.030	0.043
haplo.base117	118	G	T	G	T	0.965	NA	NA	NA	NA
Geno.347	119	T	A	T	A	0.012	1.897	0.839	2.262	0.024
Geno.544	119	T	G	C	G	0.016	-0.244	0.756	-0.322	0.747
Geno.646	119	T	G	T	A	0.404	0.339	0.193	1.763	0.078
Geno.rare102	119	*	*	*	*	0.005	-3.109	1.288	-2.414	0.016
haplo.base118	119	T	G	T	G	0.563	NA	NA	NA	NA
Geno.144	120	A	T	A	A	0.012	1.908	0.845	2.258	0.024
Geno.451	120	G	C	G	T	0.016	-0.171	0.762	-0.225	0.822
Geno.545	120	G	T	A	A	0.089	0.687	0.361	1.906	0.057
Geno.647	120	G	T	A	T	0.314	0.326	0.209	1.559	0.119
Geno.rare103	120	*	*	*	*	0.005	1.078	1.763	0.611	0.541
haplo.base119	120	G	T	G	T	0.564	NA	NA	NA	NA
Geno.145	121	C	G	T	G	0.016	-0.194	0.761	-0.255	0.799
Geno.348	121	T	A	A	G	0.100	0.830	0.336	2.468	0.014
Geno.452	121	T	A	T	A	0.088	0.595	0.337	1.766	0.078
Geno.546	121	T	A	T	G	0.226	0.212	0.236	0.898	0.369
Geno.rare104	121	*	*	*	*	0.005	1.087	1.544	0.704	0.482
haplo.base120	121	T	G	T	G	0.565	NA	NA	NA	NA
Geno.257	122	A	A	G	C	0.019	0.386	0.841	0.459	0.646
Geno.349	122	A	A	G	T	0.081	0.962	0.361	2.668	0.008
Geno.453	122	A	T	A	C	0.088	0.604	0.335	1.805	0.072
Geno.547	122	A	T	G	C	0.225	0.228	0.235	0.970	0.333
Geno.rare105	122	*	*	*	*	0.006	1.442	2.004	0.720	0.472
haplo.base121	122	G	T	G	C	0.581	NA	NA	NA	NA

Hap.freq: Haplotyle frequency, **Coef.** : Coefficient, **S.E.:** Standart Error

Table A2.14. Summary of *LPL* 4-SNP sliding haplotypes for association with LDL-C in African blacks (n=788)

	Window	loc.1	loc.2	loc.3	loc.4	Hap.freq.	Coef.	S.E.	Test statistic	*P*-value
Geno.1	1	G	C	A	G	0.112	0.731	0.316	2.311	0.021
Geno.3	1	G	T	A	G	0.095	-0.372	0.331	-1.124	0.261
Geno.4	1	G	T	G	G	0.147	0.083	0.294	0.282	0.778
Geno.6	1	T	C	A	G	0.111	-0.065	0.310	-0.209	0.835
Geno.rare	1	*	*	*	*	0.006	-0.327	1.290	-0.253	0.800
haplo.base	1	G	T	G	T	0.528	NA	NA	NA	NA
Geno.11	2	C	A	G	A	0.019	-0.332	0.704	-0.472	0.637
Geno.2	2	C	A	G	T	0.203	0.392	0.244	1.610	0.108
Geno.61	2	T	A	G	T	0.097	-0.380	0.329	-1.154	0.249
Geno.7	2	T	G	G	T	0.147	0.046	0.293	0.159	0.874
Geno.rare1	2	*	*	*	*	0.005	-0.098	1.258	-0.078	0.938
haplo.base1	2	T	G	T	T	0.528	NA	NA	NA	NA
Geno.12	3	A	G	A	A	0.019	-0.391	0.708	-0.553	0.580
Geno.21	3	A	G	T	A	0.299	0.154	0.210	0.736	0.462
Geno.41	3	G	G	T	A	0.152	0.068	0.293	0.232	0.817
haplo.base2	3	G	T	T	A	0.529	NA	NA	NA	NA
Geno.22	4	G	A	A	W	0.019	-0.378	0.707	-0.535	0.593
Geno.31	4	G	T	A	W	0.453	0.127	0.193	0.658	0.510
Geno.5	4	T	T	A	I	0.028	-0.478	0.583	-0.820	0.413
haplo.base3	4	T	T	A	W	0.499	NA	NA	NA	NA
Geno.32	5	A	A	W	G	0.018	-0.235	0.736	-0.319	0.750
Geno.51	5	T	A	I	G	0.026	-0.416	0.594	-0.700	0.484
Geno.rare2	5	*	*	*	*	0.010	-1.613	1.155	-1.396	0.163
haplo.base4	5	T	A	W	G	0.946	NA	NA	NA	NA
Geno.23	6	A	I	G	C	0.027	-0.592	0.577	-1.026	0.305
Geno.rare3	6	*	*	*	*	0.014	-2.003	0.847	-2.365	0.018
haplo.base5	6	A	W	G	C	0.959	NA	NA	NA	NA
Geno.24	7	I	G	C	C	0.027	-0.561	0.577	-0.973	0.331
Geno.62	7	W	G	C	T	0.029	0.739	0.569	1.298	0.195
Geno.rare4	7	*	*	*	*	0.013	-1.926	0.869	-2.215	0.027
haplo.base6	7	W	G	C	C	0.930	NA	NA	NA	NA
Geno.42	8	G	C	C	A	0.034	0.253	0.501	0.505	0.614
Geno.71	8	G	C	T	G	0.029	0.778	0.577	1.348	0.178
Geno.rare5	8	*	*	*	*	0.014	-1.850	0.878	-2.108	0.035
haplo.base7	8	G	C	C	G	0.923	NA	NA	NA	NA
Geno.13	9	C	C	A	G	0.040	0.162	0.459	0.353	0.724
Geno.43	9	C	C	G	T	0.022	1.539	0.669	2.300	0.022
Geno.63	9	C	T	G	G	0.029	0.805	0.572	1.407	0.160
Geno.rare6	9	*	*	*	*	0.006	-3.502	1.486	-2.357	0.019
haplo.base8	9	C	C	G	G	0.902	NA	NA	NA	NA
Geno.14	10	C	A	G	C	0.041	-0.142	0.462	-0.307	0.759
Geno.52	10	C	G	G	T	0.039	-0.193	0.494	-0.390	0.696
Geno.64	10	C	G	T	C	0.022	1.147	0.671	1.710	0.088
Geno.9	10	T	G	G	C	0.029	0.502	0.589	0.853	0.394
Geno.rare7	10	*	*	*	*	0.002	5.150	0.000	1.48E+16	0.000
haplo.base9	10	C	G	G	C	0.868	NA	NA	NA	NA
Geno.25	11	A	G	C	G	0.041	0.021	0.465	0.046	0.964
Geno.53	11	G	G	C	C	0.022	-0.106	0.662	-0.160	0.873
Geno.72	11	G	G	T	G	0.039	-0.216	0.498	-0.434	0.664
Geno.8	11	G	T	C	G	0.022	1.401	0.689	2.033	0.042
haplo.base10	11	G	G	C	G	0.875	NA	NA	NA	NA
Geno.15	12	G	C	C	C	0.021	-0.105	0.680	-0.154	0.878
Geno.44	12	G	C	G	T	0.038	-0.355	0.488	-0.728	0.467
Geno.54	12	G	T	G	C	0.036	-0.318	0.516	-0.616	0.538
Geno.73	12	T	C	G	C	0.023	1.225	0.661	1.852	0.064
Geno.rare8	12	*	*	*	*	0.004	0.584	1.642	0.356	0.722
haplo.base11	12	G	C	G	C	0.878	NA	NA	NA	NA
Geno.26	13	C	C	C	G	0.020	-0.156	0.695	-0.225	0.822
Geno.45	13	C	G	C	C	0.076	0.044	0.371	0.120	0.905
Geno.65	13	C	G	T	C	0.039	-0.496	0.484	-1.025	0.306
Geno.81	13	T	G	C	G	0.037	-0.326	0.510	-0.640	0.522
Geno.rare9	13	*	*	*	*	0.005	0.355	1.661	0.214	0.831
haplo.base12	13	C	G	C	G	0.823	NA	NA	NA	NA
Geno.16	14	C	C	G	A	0.022	-0.125	0.662	-0.189	0.850
Geno.55	14	G	C	C	G	0.075	-0.138	0.418	-0.331	0.741
Geno.66	14	G	C	G	A	0.428	0.018	0.198	0.091	0.927
Geno.91	14	G	T	C	G	0.042	-0.570	0.482	-1.183	0.237
Geno.rare10	14	*	*	*	*	0.003	5.681	3.095	1.835	0.067
haplo.base13	14	G	C	G	G	0.430	NA	NA	NA	NA
Geno.33	15	C	C	G	T	0.076	-0.061	0.397	-0.154	0.878
Geno.67	15	C	G	G	G	0.023	1.061	0.627	1.692	0.091
Geno.74	15	C	G	G	T	0.407	-0.083	0.200	-0.415	0.678

Table A2.14. Continued

	Window	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**Hap.freq.**	**Coef.**	**S.E.**	**Test statistic**	***P*-value**
Geno.92	15	T	C	G	T	0.042	-0.530	0.477	-1.110	0.267
Geno.rare11	15	*	*	*	*	0.004	3.608	2.735	1.319	0.188
haplo.base14	15	C	G	A	T	0.449	NA	NA	NA	NA
Geno.34	16	C	G	T	A	0.117	-0.107	0.319	-0.335	0.738
Geno.75	16	G	A	T	A	0.144	0.311	0.299	1.039	0.299
Geno.82	16	G	A	T	G	0.305	0.006	0.222	0.026	0.979
Geno.93	16	G	G	G	A	0.023	1.218	0.648	1.880	0.061
Geno.rare12	16	*	*	*	*	0.005	1.452	1.702	0.853	0.394
haplo.base15	16	G	G	T	A	0.406	NA	NA	NA	NA
Geno.35	17	A	T	A	T	0.145	0.423	0.291	1.454	0.146
Geno.56	17	A	T	G	T	0.306	0.101	0.213	0.476	0.634
Geno.76	17	G	G	A	T	0.023	1.433	0.665	2.156	0.031
Geno.94	17	G	T	A	C	0.030	0.857	0.567	1.512	0.131
Geno.rare13	17	*	*	*	*	0.003	-1.224	2.329	-0.525	0.600
haplo.base16	17	G	T	A	T	0.493	NA	NA	NA	NA
Geno.27	18	G	A	T	T	0.023	1.283	0.626	2.050	0.041
Geno.46	18	T	A	C	T	0.030	0.754	0.566	1.332	0.183
Geno.57	18	T	A	T	C	0.023	-0.590	0.635	-0.930	0.353
Geno.77	18	T	G	T	C	0.310	0.022	0.206	0.107	0.915
Geno.rare14	18	*	*	*	*	0.001	-0.897	2.467	-0.364	0.716
haplo.base17	18	T	A	T	T	0.613	NA	NA	NA	NA
Geno.28	19	A	C	T	G	0.029	0.753	0.579	1.301	0.194
Geno.47	19	A	T	C	G	0.023	-0.872	0.650	-1.343	0.180
Geno.83	19	G	T	C	A	0.284	-0.016	0.212	-0.076	0.939
Geno.95	19	G	T	C	G	0.026	-0.305	0.633	-0.483	0.630
Geno.rare15	19	*	*	*	*	0.003	1.308	2.150	0.608	0.543
haplo.base18	19	A	T	T	G	0.636	NA	NA	NA	NA
Geno.48	20	C	T	G	A	0.028	0.805	0.579	1.391	0.165
Geno.78	20	T	C	A	G	0.279	-0.062	0.210	-0.296	0.768
Geno.84	20	T	C	G	A	0.044	-0.318	0.472	-0.673	0.501
Geno.rare16	20	*	*	*	*	0.013	0.523	0.981	0.533	0.594
haplo.base19	20	T	T	G	A	0.636	NA	NA	NA	NA
Geno.36	21	C	A	G	C	0.167	0.158	0.259	0.608	0.543
Geno.49	21	C	A	G	T	0.112	-0.463	0.303	-1.529	0.127
Geno.58	21	C	G	A	T	0.045	-0.340	0.467	-0.728	0.467
Geno.rare17	21	*	*	*	*	0.012	0.534	0.959	0.557	0.578
haplo.base20	21	T	G	A	T	0.664	NA	NA	NA	NA
Geno.37	22	A	G	C	A	0.167	0.173	0.258	0.670	0.503
Geno.59	22	A	G	T	A	0.112	-0.453	0.302	-1.501	0.134
Geno.79	22	G	A	T	G	0.029	-0.367	0.563	-0.653	0.514
Geno.rare18	22	*	*	*	*	0.012	0.450	0.927	0.485	0.628
haplo.base21	22	G	A	T	A	0.680	NA	NA	NA	NA
Geno.38	23	A	T	G	D	0.029	-0.324	0.574	-0.565	0.572
Geno.410	23	G	C	A	W	0.168	0.137	0.258	0.532	0.595
Geno.68	23	G	T	A	W	0.115	-0.420	0.301	-1.395	0.163
Geno.rare19	23	*	*	*	*	0.002	-1.807	NA	NA	NA
haplo.base22	23	A	T	A	W	0.687	NA	NA	NA	NA
Geno.29	24	C	A	W	T	0.165	0.239	0.260	0.918	0.359
Geno.411	24	T	A	W	C	0.013	0.619	0.855	0.725	0.469
Geno.69	24	T	G	D	T	0.028	-0.317	0.575	-0.551	0.582
Geno.rare20	24	*	*	*	*	0.001	0.978	0.000	1.77E+15	0.000
haplo.base23	24	T	A	W	T	0.792	NA	NA	NA	NA
Geno.17	25	A	W	C	A	0.013	0.609	0.857	0.710	0.478
Geno.39	25	A	W	T	G	0.248	0.104	0.218	0.477	0.634
Geno.412	25	G	D	T	A	0.029	-0.291	0.564	-0.516	0.606
haplo.base24	25	A	W	T	A	0.710	NA	NA	NA	NA
Geno.18	26	D	T	A	A	0.028	-0.229	0.583	-0.392	0.695
Geno.413	26	W	C	A	A	0.013	0.621	0.861	0.721	0.471
Geno.85	26	W	T	G	A	0.198	0.106	0.240	0.443	0.658
Geno.96	26	W	T	G	C	0.051	0.018	0.448	0.041	0.968
Geno.rare21	26	*	*	*	*	0.003	1.557	2.230	0.698	0.485
haplo.base25	26	W	T	A	A	0.707	NA	NA	NA	NA
Geno.19	27	C	A	A	G	0.013	0.622	0.856	0.727	0.468
Geno.610	27	T	G	A	G	0.191	0.143	0.242	0.589	0.556
Geno.86	27	T	G	C	G	0.051	0.068	0.447	0.153	0.878
Geno.rare22	27	*	*	*	*	0.010	-0.579	1.017	-0.569	0.570
haplo.base26	27	T	A	A	G	0.736	NA	NA	NA	NA
Geno.110	28	A	A	G	D	0.022	-0.351	0.660	-0.532	0.595
Geno.611	28	G	A	G	W	0.191	0.120	0.243	0.493	0.622
Geno.97	28	G	C	G	W	0.051	0.050	0.447	0.112	0.911
Geno.rare23	28	*	*	*	*	0.010	-0.609	1.015	-0.600	0.549
haplo.base27	28	A	A	G	W	0.726	NA	NA	NA	NA
Geno.310	29	A	G	D	G	0.020	-0.132	0.714	-0.185	0.853
Geno.414	29	A	G	W	A	0.048	0.747	0.437	1.710	0.088
Geno.98	29	C	G	W	G	0.051	0.099	0.442	0.224	0.823

Table A2.14. Continued

	Window	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**Hap.freq.**	**Coef.**	**S.E.**	**Test statistic**	***P*-value**
Geno.rare24	29	*	*	*	*	0.010	-1.323	1.034	-1.279	0.201
haplo.base28	29	A	G	W	G	0.871	NA	NA	NA	NA
Geno.311	30	G	D	G	C	0.020	-0.243	0.687	-0.353	0.724
Geno.415	30	G	W	A	C	0.049	0.708	0.433	1.635	0.103
Geno.rare25	30	*	*	*	*	0.012	-2.471	0.906	-2.728	0.007
haplo.base29	30	G	W	G	C	0.919	NA	NA	NA	NA
Geno.210	31	D	G	C	G	0.021	-0.244	0.679	-0.360	0.719
Geno.416	31	W	A	C	G	0.049	0.714	0.430	1.661	0.097
Geno.510	31	W	G	C	C	0.017	-0.246	0.731	-0.336	0.737
Geno.rare26	31	*	*	*	*	0.004	-5.532	1.789	-3.093	0.002
haplo.base30	31	W	G	C	G	0.909	NA	NA	NA	NA
Geno.111	32	A	C	G	A	0.050	0.661	0.424	1.558	0.120
Geno.312	32	G	C	C	A	0.017	-0.195	0.731	-0.267	0.790
Geno.511	32	G	C	G	G	0.119	0.252	0.300	0.839	0.402
Geno.rare27	32	*	*	*	*	0.003	-6.396	2.191	-2.919	0.004
haplo.base31	32	G	C	G	A	0.810	NA	NA	NA	NA
Geno.112	33	C	C	A	C	0.017	-0.282	0.747	-0.378	0.706
Geno.612	33	C	G	G	C	0.119	0.233	0.301	0.773	0.440
Geno.rare28	33	*	*	*	*	0.011	-1.068	0.970	-1.101	0.271
haplo.base32	33	C	G	A	C	0.853	NA	NA	NA	NA
Geno.211	34	C	A	C	G	0.017	-0.279	0.747	-0.373	0.709
Geno.512	34	G	A	C	A	0.046	-0.327	0.462	-0.707	0.480
Geno.99	34	G	G	C	G	0.119	0.231	0.303	0.761	0.447
Geno.rare29	34	*	*	*	*	0.009	0.577	1.121	0.514	0.607
haplo.base33	34	G	A	C	G	0.810	NA	NA	NA	NA
Geno.113	35	A	C	A	C	0.046	-0.319	0.465	-0.686	0.493
Geno.212	35	A	C	G	C	0.250	0.066	0.224	0.293	0.769
Geno.613	35	G	C	G	T	0.117	0.216	0.316	0.683	0.495
Geno.rare30	35	*	*	*	*	0.011	0.738	1.000	0.738	0.461
haplo.base34	35	A	C	G	T	0.577	NA	NA	NA	NA
Geno.213	36	C	A	C	G	0.045	-0.523	0.472	-1.107	0.268
Geno.417	36	C	G	C	G	0.249	-0.129	0.246	-0.524	0.601
Geno.513	36	C	G	T	C	0.312	-0.399	0.228	-1.749	0.081
Geno.rare31	36	*	*	*	*	0.012	0.272	0.949	0.287	0.774
haplo.base35	36	C	G	T	G	0.382	NA	NA	NA	NA
Geno.214	37	A	C	G	T	0.045	-0.524	0.469	-1.116	0.265
Geno.514	37	G	C	G	T	0.241	-0.090	0.247	-0.364	0.716
Geno.614	37	G	T	C	T	0.312	-0.390	0.226	-1.724	0.085
Geno.rare32	37	*	*	*	*	0.010	-1.073	1.012	-1.060	0.289
haplo.base36	37	G	T	G	T	0.391	NA	NA	NA	NA
Geno.515	38	C	G	T	G	0.282	-0.063	0.244	-0.259	0.796
Geno.710	38	T	C	T	G	0.312	-0.294	0.233	-1.261	0.208
Geno.87	38	T	G	T	A	0.052	0.898	0.460	1.951	0.051
Geno.rare33	38	*	*	*	*	0.015	-0.589	0.907	-0.650	0.516
haplo.base37	38	T	G	T	G	0.339	NA	NA	NA	NA
Geno.114	39	C	T	G	A	0.310	-0.261	0.213	-1.227	0.220
Geno.615	39	G	T	A	A	0.056	0.879	0.423	2.078	0.038
Geno.910	39	G	T	G	C	0.085	-0.055	0.359	-0.153	0.879
Geno.rare34	39	*	*	*	*	0.012	-1.159	1.035	-1.120	0.263
haplo.base38	39	G	T	G	A	0.536	NA	NA	NA	NA
Geno.418	40	T	A	A	C	0.053	1.080	0.439	2.460	0.014
Geno.88	40	T	G	A	G	0.022	-0.167	0.709	-0.236	0.814
Geno.911	40	T	G	C	C	0.087	0.065	0.350	0.187	0.852
Geno.rare35	40	*	*	*	*	0.011	-1.306	1.211	-1.079	0.281
haplo.base39	40	T	G	A	C	0.827	NA	NA	NA	NA
Geno.115	41	A	A	C	W	0.055	1.074	0.431	2.495	0.013
Geno.616	41	G	A	G	W	0.022	-0.059	0.692	-0.085	0.933
Geno.89	41	G	C	C	W	0.088	0.135	0.343	0.392	0.695
Geno.rare36	41	*	*	*	*	0.004	-3.732	2.805	-1.331	0.184
haplo.base40	41	G	A	C	W	0.831	NA	NA	NA	NA
Geno.215	42	A	C	W	A	0.112	-0.145	0.298	-0.488	0.626
Geno.419	42	A	G	W	G	0.022	-0.175	0.686	-0.255	0.798
Geno.711	42	C	C	W	G	0.090	0.039	0.341	0.115	0.908
Geno.rare37	42	*	*	*	*	0.003	-4.190	3.028	-1.384	0.167
haplo.base41	42	A	C	W	G	0.774	NA	NA	NA	NA
Geno.216	43	C	W	A	A	0.112	-0.135	0.300	-0.449	0.653
Geno.516	43	C	W	G	G	0.204	0.081	0.238	0.340	0.734
Geno.617	43	G	W	G	A	0.022	0.179	0.704	0.254	0.799
Geno.rare38	43	*	*	*	*	0.003	-5.800	1.836	-3.159	0.002
haplo.base42	43	C	W	G	A	0.659	NA	NA	NA	NA
Geno.217	44	W	A	A	C	0.112	-0.093	0.302	-0.307	0.759
Geno.618	44	W	G	A	T	0.105	0.220	0.315	0.699	0.485
Geno.712	44	W	G	G	C	0.204	0.080	0.245	0.326	0.744
Geno.rare39	44	*	*	*	*	0.003	-3.188	2.445	-1.304	0.193
haplo.base43	44	W	G	A	C	0.575	NA	NA	NA	NA

Table A2.14. Continued

	Window	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**Hap.freq.**	**Coef.**	**S.E.**	**Test statistic**	***P*-value**
Geno.218	45	A	A	C	W	0.112	-0.087	0.303	-0.287	0.774
Geno.420	45	G	A	C	D	0.022	-0.331	0.663	-0.500	0.617
Geno.619	45	G	A	T	W	0.105	0.185	0.320	0.578	0.563
Geno.810	45	G	G	C	W	0.204	0.072	0.247	0.292	0.770
Geno.rare40	45	*	*	*	*	0.001	-1.498	5.019	-0.298	0.765
haplo.base44	45	G	A	C	W	0.555	NA	NA	NA	NA
Geno.219	46	A	C	D	C	0.022	-0.299	0.663	-0.452	0.652
Geno.313	46	A	C	W	A	0.030	0.472	0.567	0.832	0.406
Geno.620	46	A	T	W	C	0.105	0.221	0.325	0.681	0.496
Geno.912	46	G	C	W	C	0.204	0.114	0.246	0.464	0.643
Geno.rare41	46	*	*	*	*	0.001	-1.583	5.715	-0.277	0.782
haplo.base45	46	A	C	W	C	0.637	NA	NA	NA	NA
Geno.220	47	C	D	C	G	0.022	-0.328	0.661	-0.497	0.620
Geno.314	47	C	W	A	G	0.030	0.448	0.566	0.791	0.429
Geno.421	47	C	W	C	A	0.033	-0.052	0.545	-0.096	0.923
Geno.713	47	T	W	C	G	0.106	0.169	0.302	0.561	0.575
haplo.base46	47	C	W	C	G	0.809	NA	NA	NA	NA
Geno.221	48	D	C	G	T	0.022	-0.359	0.659	-0.545	0.586
Geno.315	48	W	A	G	T	0.030	0.429	0.565	0.759	0.448
Geno.422	48	W	C	A	T	0.033	-0.084	0.542	-0.156	0.876
Geno.rare42	48	*	*	*	*	0.006	0.531	1.241	0.428	0.669
haplo.base47	48	W	C	G	T	0.909	NA	NA	NA	NA
Geno.222	49	A	G	T	T	0.029	0.387	0.576	0.673	0.501
Geno.423	49	C	A	T	T	0.033	-0.111	0.543	-0.205	0.838
Geno.621	49	C	G	T	C	0.192	-0.213	0.249	-0.856	0.392
Geno.rare43	49	*	*	*	*	0.007	0.445	1.247	0.357	0.721
haplo.base48	49	C	G	T	T	0.739	NA	NA	NA	NA
Geno.223	50	A	T	T	D	0.033	-0.263	0.539	-0.489	0.625
Geno.517	50	G	T	C	D	0.192	-0.371	0.250	-1.483	0.138
Geno.811	50	G	T	T	W	0.087	-1.205	0.351	-3.437	0.001
Geno.rare44	50	*	*	*	*	0.006	0.225	1.240	0.181	0.856
haplo.base49	50	G	T	T	D	0.681	NA	NA	NA	NA
Geno.224	51	T	C	D	C	0.141	-0.194	0.286	-0.677	0.498
Geno.316	51	T	C	D	T	0.051	-0.776	0.472	-1.644	0.101
Geno.518	51	T	T	D	C	0.102	0.181	0.333	0.544	0.586
Geno.812	51	T	T	W	T	0.087	-1.174	0.353	-3.323	0.001
Geno.rare45	51	*	*	*	*	0.006	0.276	1.240	0.223	0.824
haplo.base50	51	T	T	D	T	0.611	NA	NA	NA	NA
Geno.116	52	C	D	C	A	0.141	-0.222	0.294	-0.755	0.450
Geno.225	52	C	D	T	A	0.052	-0.791	0.477	-1.660	0.097
Geno.519	52	T	D	C	A	0.103	0.168	0.338	0.497	0.619
Geno.813	52	T	D	T	G	0.113	-0.063	0.305	-0.206	0.837
Geno.10	52	T	W	T	A	0.093	-1.104	0.351	-3.150	0.002
haplo.base51	52	T	D	T	A	0.498	NA	NA	NA	NA
Geno.117	53	D	C	A	A	0.246	0.044	0.232	0.189	0.850
Geno.520	53	D	T	A	C	0.035	0.321	0.498	0.646	0.519
Geno.622	53	D	T	G	A	0.113	0.042	0.304	0.138	0.890
Geno.814	53	W	T	A	A	0.093	-1.002	0.350	-2.862	0.004
haplo.base52	53	D	T	A	A	0.514	NA	NA	NA	NA
Geno.118	54	C	A	A	C	0.245	0.133	0.230	0.579	0.563
Geno.623	54	T	A	A	G	0.035	-1.243	0.528	-2.356	0.019
Geno.714	54	T	A	C	C	0.035	0.381	0.501	0.761	0.447
Geno.815	54	T	G	A	C	0.113	0.120	0.304	0.395	0.693
haplo.base53	54	T	A	A	C	0.572	NA	NA	NA	NA
Geno.226	55	A	A	C	T	0.052	-0.125	0.435	-0.286	0.775
Geno.317	55	A	A	G	A	0.034	-1.060	0.522	-2.033	0.042
Geno.521	55	A	C	C	A	0.035	0.341	0.488	0.697	0.486
Geno.715	55	G	A	C	A	0.112	0.135	0.292	0.460	0.645
Geno.rare46	55	*	*	*	*	0.001	-11.969	NA	NA	NA
haplo.base54	55	A	A	C	A	0.766	NA	NA	NA	NA
Geno.227	56	A	C	A	G	0.076	-0.379	0.379	-1.001	0.317
Geno.318	56	A	C	T	C	0.051	-0.125	0.449	-0.279	0.780
Geno.424	56	A	G	A	C	0.033	-1.284	0.532	-2.415	0.016
Geno.716	56	C	C	A	C	0.034	0.300	0.494	0.607	0.544
Geno.rare47	56	*	*	*	*	0.002	-2.498	3.067	-0.815	0.416
haplo.base55	56	A	C	A	C	0.803	NA	NA	NA	NA
Geno.228	57	C	A	C	G	0.119	0.030	0.292	0.101	0.920
Geno.425	57	C	A	G	G	0.076	-0.451	0.379	-1.191	0.234
Geno.522	57	C	T	C	A	0.052	-0.195	0.442	-0.441	0.659
Geno.717	57	G	A	C	A	0.035	-1.341	0.518	-2.591	0.010
Geno.rare48	57	*	*	*	*	0.002	1.694	2.684	0.631	0.528
haplo.base56	57	C	A	C	A	0.717	NA	NA	NA	NA
Geno.229	58	A	C	A	T	0.225	0.084	0.238	0.352	0.725
Geno.319	58	A	C	G	C	0.109	0.078	0.315	0.248	0.804
Geno.718	58	A	G	G	T	0.075	-0.272	0.394	-0.691	0.490

Table A2.14. Continued

	Window	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**Hap.freq.**	**Coef.**	**S.E.**	**Test statistic**	***P*-value**
Geno.913	58	T	C	A	T	0.051	-0.117	0.452	-0.259	0.796
Geno.rare49	58	*	*	*	*	0.014	0.080	1.074	0.074	0.941
haplo.base57	58	A	C	A	C	0.525	NA	NA	NA	NA
Geno.230	59	C	A	C	G	0.067	-0.007	0.419	-0.016	0.988
Geno.320	59	C	A	T	A	0.262	0.136	0.235	0.577	0.564
Geno.426	59	C	A	T	G	0.017	-0.768	0.867	-0.886	0.376
Geno.523	59	C	G	C	A	0.108	0.094	0.321	0.294	0.769
Geno.131	59	G	G	T	G	0.075	-0.366	0.406	-0.900	0.368
Geno.rare50	59	*	*	*	*	0.014	0.358	1.013	0.353	0.724
haplo.base58	59	C	A	C	A	0.457	NA	NA	NA	NA
Geno.231	60	A	C	G	G	0.067	-0.043	0.440	-0.098	0.922
Geno.321	60	A	T	A	G	0.263	0.123	0.237	0.519	0.604
Geno.427	60	A	T	G	G	0.021	-0.520	0.819	-0.635	0.526
Geno.524	60	G	C	A	G	0.110	0.133	0.326	0.407	0.684
Geno.914	60	G	T	G	G	0.076	-0.097	0.384	-0.252	0.801
Geno.rare51	60	*	*	*	*	0.008	-1.379	1.459	-0.945	0.345
haplo.base59	60	A	C	A	G	0.455	NA	NA	NA	NA
Geno.428	61	C	G	G	T	0.073	-0.350	0.415	-0.844	0.399
Geno.525	61	T	A	G	C	0.044	-0.106	0.481	-0.220	0.826
Geno.624	61	T	A	G	T	0.220	0.092	0.250	0.368	0.713
Geno.915	61	T	G	G	T	0.095	-0.166	0.354	-0.468	0.640
Geno.rare52	61	*	*	*	*	0.008	0.126	1.241	0.102	0.919
haplo.base60	61	C	A	G	T	0.558	NA	NA	NA	NA
Geno.119	62	A	G	C	G	0.050	0.112	0.450	0.248	0.804
Geno.232	62	A	G	T	G	0.294	0.161	0.227	0.710	0.478
Geno.625	62	G	G	T	G	0.134	-0.287	0.292	-0.984	0.326
Geno.719	62	G	G	T	T	0.034	0.264	0.575	0.459	0.647
Geno.rare53	62	*	*	*	*	0.002	-4.261	2.297	-1.855	0.064
haplo.base61	62	A	G	T	T	0.485	NA	NA	NA	NA
Geno.429	63	G	C	G	C	0.051	0.017	0.440	0.038	0.970
Geno.816	63	G	T	G	C	0.429	0.006	0.202	0.032	0.975
Geno.916	63	G	T	T	A	0.070	0.008	0.384	0.022	0.983
Geno.rare54	63	*	*	*	*	0.001	-3.471	2.613	-1.328	0.184
haplo.base62	63	G	T	T	C	0.449	NA	NA	NA	NA
Geno.322	64	C	G	C	W	0.051	0.014	0.441	0.031	0.975
Geno.720	64	T	G	C	I	0.042	0.357	0.480	0.745	0.457
Geno.817	64	T	G	C	W	0.388	-0.054	0.211	-0.257	0.797
Geno.917	64	T	T	A	W	0.070	0.011	0.384	0.030	0.976
haplo.base63	64	T	T	C	W	0.449	NA	NA	NA	NA
Geno.120	65	G	C	I	T	0.042	0.452	0.497	0.910	0.363
Geno.233	65	G	C	W	C	0.017	0.743	0.920	0.808	0.419
Geno.526	65	T	A	W	T	0.070	0.091	0.383	0.237	0.813
Geno.626	65	T	C	W	C	0.175	0.225	0.277	0.815	0.416
Geno.721	65	T	C	W	T	0.273	-0.025	0.236	-0.106	0.916
haplo.base64	65	G	C	W	T	0.423	NA	NA	NA	NA
Geno.323	66	A	W	T	C	0.065	-0.106	0.384	-0.276	0.782
Geno.627	66	C	I	T	T	0.041	0.383	0.487	0.786	0.432
Geno.722	66	C	W	C	C	0.034	0.267	0.573	0.467	0.641
Geno.818	66	C	W	C	T	0.157	0.229	0.274	0.834	0.405
Geno.918	66	C	W	T	C	0.013	-1.962	1.058	-1.854	0.064
Geno.rare55	66	*	*	*	*	0.007	1.650	1.362	1.211	0.226
haplo.base65	66	C	W	T	T	0.684	NA	NA	NA	NA
Geno.234	67	I	T	T	C	0.042	0.391	0.485	0.806	0.420
Geno.324	67	W	C	C	C	0.035	0.510	0.648	0.788	0.431
Geno.430	67	W	C	T	C	0.156	0.167	0.299	0.559	0.576
Geno.628	67	W	T	C	C	0.075	-0.618	0.422	-1.466	0.143
Geno.919	67	W	T	T	G	0.149	0.089	0.280	0.318	0.751
haplo.base66	67	W	T	T	C	0.542	NA	NA	NA	NA
Geno.121	68	C	C	C	G	0.035	0.507	0.639	0.793	0.428
Geno.235	68	C	T	C	G	0.155	0.155	0.297	0.522	0.602
Geno.431	68	T	C	C	G	0.075	-0.579	0.420	-1.380	0.168
Geno.527	68	T	T	C	A	0.058	0.683	0.412	1.659	0.097
Geno.819	68	T	T	G	G	0.149	0.063	0.278	0.225	0.822
Geno.rare56	68	*	*	*	*	0.001	8.128	NA	NA	NA
haplo.base67	68	T	T	C	G	0.528	NA	NA	NA	NA
Geno.236	69	C	C	G	G	0.110	-0.291	0.305	-0.953	0.341
Geno.325	69	T	C	A	A	0.056	0.605	0.434	1.395	0.164
Geno.629	69	T	G	G	G	0.148	0.033	0.278	0.120	0.904
Geno.rare57	69	*	*	*	*	0.002	4.661	6.921	0.674	0.501
haplo.base68	69	T	C	G	G	0.684	NA	NA	NA	NA
Geno.122	70	C	A	A	A	0.057	0.660	0.423	1.561	0.119
Geno.528	70	C	G	G	A	0.314	0.092	0.219	0.420	0.675
Geno.820	70	G	G	G	A	0.148	0.082	0.281	0.292	0.771
Geno.rare58	70	*	*	*	*	0.003	4.878	3.928	1.242	0.215
haplo.base69	70	C	G	G	T	0.478	NA	NA	NA	NA

Table A2.14. Continued

	Window	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**Hap.freq.**	**Coef.**	**S.E.**	**Test statistic**	***P*-value**
Geno.237	71	A	A	A	G	0.057	0.747	0.417	1.790	0.074
Geno.529	71	G	G	A	A	0.142	0.129	0.284	0.453	0.651
Geno.630	71	G	G	A	G	0.323	0.036	0.220	0.165	0.869
Geno.rare59	71	*	*	*	*	0.003	2.112	2.447	0.863	0.388
haplo.base70	71	G	G	T	G	0.474	NA	NA	NA	NA
Geno.123	72	A	A	G	C	0.057	0.745	0.417	1.788	0.074
Geno.326	72	G	A	A	C	0.142	0.095	0.285	0.335	0.738
Geno.432	72	G	A	G	A	0.135	-0.235	0.289	-0.810	0.418
Geno.530	72	G	A	G	C	0.188	0.263	0.263	1.001	0.317
Geno.rare60	72	*	*	*	*	0.004	1.807	1.906	0.948	0.344
haplo.base71	72	G	T	G	A	0.474	NA	NA	NA	NA
Geno.238	73	A	A	C	G	0.140	0.110	0.288	0.383	0.702
Geno.327	73	A	G	A	G	0.136	-0.230	0.291	-0.790	0.430
Geno.433	73	A	G	C	G	0.246	0.395	0.240	1.650	0.099
Geno.723	73	T	G	A	A	0.017	0.167	0.758	0.220	0.826
Geno.rare61	73	*	*	*	*	0.005	1.810	1.889	0.958	0.338
haplo.base72	73	T	G	A	G	0.457	NA	NA	NA	NA
Geno.631	74	A	C	G	G	0.142	0.157	0.283	0.553	0.581
Geno.724	74	G	A	A	G	0.017	0.257	0.754	0.341	0.733
Geno.821	74	G	A	G	A	0.011	1.021	0.904	1.129	0.259
Geno.1110	74	G	C	G	G	0.248	0.482	0.234	2.065	0.039
Geno.rare62	74	*	*	*	*	0.003	2.706	2.082	1.300	0.194
haplo.base73	74	G	A	G	G	0.579	NA	NA	NA	NA
Geno.124	75	A	A	G	C	0.017	0.236	0.755	0.313	0.754
Geno.239	75	A	G	A	C	0.011	0.989	0.905	1.093	0.275
Geno.531	75	C	G	G	C	0.390	0.352	0.193	1.820	0.069
Geno.rare63	75	*	*	*	*	0.006	-0.148	1.113	-0.133	0.894
haplo.base74	75	A	G	G	C	0.576	NA	NA	NA	NA
Geno.328	76	A	G	C	A	0.017	0.056	0.758	0.073	0.942
Geno.434	76	G	A	C	A	0.011	0.776	0.909	0.854	0.394
Geno.725	76	G	G	C	G	0.011	0.069	0.946	0.073	0.942
Geno.rare64	76	*	*	*	*	0.006	-0.250	1.125	-0.222	0.825
haplo.base75	76	G	G	C	A	0.955	NA	NA	NA	NA
Geno.125	77	A	C	A	T	0.011	0.896	0.906	0.988	0.323
Geno.240	77	G	C	A	C	0.286	0.294	0.213	1.381	0.168
Geno.rare65	77	*	*	*	*	0.017	-0.008	0.726	-0.011	0.991
haplo.base76	77	G	C	A	T	0.685	NA	NA	NA	NA
Geno.126	78	C	A	C	A	0.146	0.374	0.282	1.325	0.186
Geno.241	78	C	A	C	G	0.141	0.133	0.280	0.474	0.636
Geno.435	78	C	A	T	G	0.011	-0.225	0.942	-0.239	0.811
Geno.rare66	78	*	*	*	*	0.017	-0.018	0.759	-0.024	0.981
haplo.base77	78	C	A	T	A	0.685	NA	NA	NA	NA
Geno.127	79	A	C	A	A	0.142	0.276	0.305	0.905	0.366
Geno.329	79	A	C	G	A	0.142	0.077	0.290	0.265	0.791
Geno.532	79	A	T	A	G	0.242	-0.157	0.240	-0.655	0.513
Geno.632	79	A	T	G	A	0.011	-0.255	0.934	-0.273	0.785
Geno.822	79	G	T	A	A	0.011	0.013	0.938	0.014	0.989
Geno.rare67	79	*	*	*	*	0.005	1.244	1.866	0.666	0.505
haplo.base78	79	A	T	A	A	0.448	NA	NA	NA	NA
Geno.128	80	C	A	A	C	0.142	0.285	0.305	0.934	0.351
Geno.436	80	C	G	A	C	0.142	0.090	0.291	0.309	0.757
Geno.726	80	T	A	A	T	0.024	0.245	0.632	0.387	0.699
Geno.823	80	T	A	G	C	0.242	-0.147	0.241	-0.609	0.543
Geno.920	80	T	G	A	C	0.011	-0.243	0.931	-0.261	0.794
Geno.rare68	80	*	*	*	*	0.004	1.233	1.868	0.660	0.509
haplo.base79	80	T	A	A	C	0.433	NA	NA	NA	NA
Geno.129	81	A	A	C	A	0.095	0.067	0.355	0.190	0.850
Geno.437	81	A	A	T	C	0.023	0.372	0.652	0.571	0.568
Geno.633	81	A	G	C	C	0.246	-0.170	0.233	-0.730	0.466
Geno.921	81	G	A	C	A	0.130	0.116	0.294	0.394	0.694
Geno.101	81	G	A	C	C	0.022	-0.637	0.696	-0.915	0.360
Geno.rare69	81	*	*	*	*	0.002	-1.406	2.410	-0.583	0.560
haplo.base80	81	A	A	C	C	0.481	NA	NA	NA	NA
Geno.130	82	A	C	A	G	0.223	0.139	0.244	0.569	0.569
Geno.634	82	A	T	C	G	0.023	0.388	0.649	0.597	0.550
Geno.824	82	G	C	C	A	0.031	-0.025	0.560	-0.045	0.964
Geno.922	82	G	C	C	G	0.213	-0.147	0.251	-0.585	0.559
Geno.rare70	82	*	*	*	*	0.004	1.264	6.870	0.184	0.854
haplo.base81	82	A	C	C	G	0.506	NA	NA	NA	NA
Geno.242	83	C	A	G	C	0.225	0.147	0.236	0.622	0.534
Geno.330	83	C	C	A	C	0.033	0.175	0.547	0.319	0.750
Geno.635	83	C	C	G	G	0.141	-0.103	0.283	-0.363	0.717
Geno.825	83	T	C	G	C	0.024	0.269	0.626	0.430	0.667
haplo.base82	83	C	C	G	C	0.577	NA	NA	NA	NA
Geno.243	84	A	G	C	A	0.225	0.139	0.238	0.585	0.559

Table A2.14. Continued

	Window	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**Hap.freq.**	**Coef.**	**S.E.**	**Test statistic**	***P*-value**
Geno.438	84	C	A	C	C	0.033	0.161	0.546	0.296	0.768
Geno.727	84	C	G	C	C	0.050	0.053	0.446	0.119	0.905
Geno.826	84	C	G	G	A	0.141	-0.107	0.285	-0.374	0.708
haplo.base83	84	C	G	C	A	0.551	NA	NA	NA	NA
Geno.132	85	A	C	C	G	0.033	0.133	0.542	0.246	0.806
Geno.533	85	G	C	C	G	0.050	0.019	0.441	0.043	0.965
Geno.728	85	G	G	A	G	0.140	-0.168	0.273	-0.614	0.539
Geno.rare71	85	*	*	*	*	0.008	0.626	1.141	0.549	0.583
haplo.base84	85	G	C	A	G	0.769	NA	NA	NA	NA
Geno.244	86	C	A	G	C	0.044	0.720	0.461	1.562	0.119
Geno.534	86	C	C	G	T	0.082	0.106	0.355	0.299	0.765
Geno.729	86	G	A	G	T	0.140	-0.124	0.276	-0.448	0.654
Geno.rare72	86	*	*	*	*	0.008	0.708	1.139	0.622	0.534
haplo.base85	86	C	A	G	T	0.727	NA	NA	NA	NA
Geno.439	87	A	G	C	G	0.044	0.702	0.463	1.516	0.130
Geno.535	87	A	G	T	A	0.316	-0.079	0.221	-0.359	0.720
Geno.827	87	C	G	T	A	0.080	0.180	0.364	0.494	0.622
Geno.rare73	87	*	*	*	*	0.010	-0.038	1.007	-0.038	0.970
haplo.base86	87	A	G	T	G	0.550	NA	NA	NA	NA
Geno.331	88	G	C	G	G	0.044	0.734	0.463	1.587	0.113
Geno.536	88	G	T	A	G	0.396	0.003	0.205	0.012	0.990
Geno.rare74	88	*	*	*	*	0.009	1.040	1.000	1.040	0.299
haplo.base87	88	G	T	G	G	0.551	NA	NA	NA	NA
Geno.245	89	C	G	G	G	0.043	0.672	0.461	1.459	0.145
Geno.440	89	T	A	G	C	0.396	-0.016	0.203	-0.079	0.937
Geno.rare75	89	*	*	*	*	0.002	2.121	2.591	0.818	0.413
haplo.base88	89	T	G	G	C	0.559	NA	NA	NA	NA
Geno.246	90	A	G	C	A	0.394	-0.087	0.212	-0.410	0.682
Geno.636	90	G	G	C	G	0.095	-0.497	0.338	-1.471	0.142
Geno.730	90	G	G	G	A	0.042	0.686	0.469	1.464	0.144
Geno.rare76	90	*	*	*	*	0.004	0.197	1.777	0.111	0.912
haplo.base89	90	G	G	C	A	0.465	NA	NA	NA	NA
Geno.247	91	G	C	A	A	0.085	0.358	0.352	1.017	0.310
Geno.441	91	G	C	G	G	0.098	-0.478	0.321	-1.490	0.137
Geno.537	91	G	G	A	G	0.042	0.757	0.460	1.643	0.101
Geno.rare77	91	*	*	*	*	0.001	2.933	2.592	1.132	0.258
haplo.base90	91	G	C	A	G	0.774	NA	NA	NA	NA
Geno.133	92	C	A	A	G	0.085	0.355	0.353	1.004	0.316
Geno.248	92	C	A	G	A	0.025	0.145	0.614	0.236	0.814
Geno.538	92	C	G	G	G	0.098	-0.484	0.321	-1.505	0.133
Geno.637	92	G	A	G	G	0.042	0.756	0.462	1.635	0.102
haplo.base91	92	C	A	G	G	0.749	NA	NA	NA	NA
Geno.249	93	A	A	G	T	0.085	0.347	0.354	0.980	0.327
Geno.332	93	A	G	A	T	0.026	0.140	0.611	0.229	0.819
Geno.442	93	A	G	G	C	0.056	0.566	0.407	1.390	0.165
Geno.923	93	G	G	G	T	0.096	-0.370	0.329	-1.125	0.261
Geno.rare78	93	*	*	*	*	0.002	-5.129	3.034	-1.690	0.091
haplo.base92	93	A	G	G	T	0.735	NA	NA	NA	NA
Geno.134	94	A	G	T	C	0.084	0.377	0.356	1.060	0.290
Geno.250	94	G	A	T	T	0.025	0.167	0.614	0.273	0.785
Geno.333	94	G	G	C	C	0.058	0.451	0.399	1.131	0.259
Geno.638	94	G	G	T	T	0.133	-0.191	0.275	-0.695	0.488
haplo.base93	94	G	G	T	C	0.699	NA	NA	NA	NA
Geno.135	95	A	T	T	G	0.025	0.109	0.611	0.178	0.859
Geno.251	95	G	C	C	G	0.055	0.585	0.420	1.393	0.164
Geno.639	95	G	T	C	T	0.019	-0.246	0.722	-0.341	0.733
Geno.731	95	G	T	T	G	0.131	-0.153	0.279	-0.551	0.582
Geno.rare79	95	*	*	*	*	0.003	-3.959	3.803	-1.041	0.298
haplo.base94	95	G	T	C	G	0.766	NA	NA	NA	NA
Geno.136	96	C	C	G	A	0.055	0.460	0.434	1.059	0.290
Geno.732	96	T	C	T	A	0.019	-0.297	0.716	-0.414	0.679
Geno.924	96	T	T	G	A	0.157	-0.143	0.258	-0.555	0.579
Geno.rare80	96	*	*	*	*	0.007	-2.411	1.825	-1.321	0.187
haplo.base95	96	T	C	G	A	0.761	NA	NA	NA	NA
Geno.137	97	C	G	A	D	0.147	0.033	0.276	0.119	0.905
Geno.539	97	C	T	A	W	0.020	-0.379	0.691	-0.549	0.583
Geno.828	97	T	G	A	W	0.155	-0.208	0.260	-0.799	0.424
Geno.rare81	97	*	*	*	*	0.009	-1.205	1.156	-1.042	0.298
haplo.base96	97	C	G	A	W	0.669	NA	NA	NA	NA
Geno.252	98	G	A	D	T	0.152	0.107	0.265	0.404	0.686
Geno.334	98	G	A	W	G	0.083	0.361	0.344	1.049	0.294
Geno.829	98	T	A	W	T	0.020	-0.310	0.688	-0.451	0.652
Geno.rare82	98	*	*	*	*	0.005	-2.258	1.400	-1.613	0.107
haplo.base97	98	G	A	W	T	0.740	NA	NA	NA	NA
Geno.253	99	A	D	T	D	0.154	0.052	0.259	0.202	0.840

Table A2.14. Continued

	Window	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**Hap.freq.**	**Coef.**	**S.E.**	**Test statistic**	***P*-value**
Geno.443	99	A	W	G	W	0.083	0.355	0.344	1.034	0.302
Geno.rare83	99	*	*	*	*	0.010	-1.298	0.989	-1.312	0.190
haplo.base98	99	A	W	T	W	0.753	NA	NA	NA	NA
Geno.335	100	D	T	D	T	0.154	0.079	0.259	0.304	0.761
Geno.540	100	W	G	W	T	0.083	0.382	0.344	1.109	0.268
Geno.733	100	W	T	W	G	0.012	-0.259	0.888	-0.291	0.771
Geno.rare84	100	*	*	*	*	0.005	0.002	1.485	0.001	0.999
haplo.base99	100	W	T	W	T	0.747	NA	NA	NA	NA
Geno.336	101	G	W	T	G	0.083	0.369	0.345	1.070	0.285
Geno.640	101	T	D	T	G	0.156	0.044	0.260	0.170	0.865
Geno.734	101	T	W	G	G	0.012	-0.273	0.901	-0.303	0.762
Geno.830	101	T	W	T	A	0.016	-0.428	0.794	-0.539	0.590
haplo.base100	101	T	W	T	G	0.733	NA	NA	NA	NA
Geno.337	102	D	T	G	C	0.155	0.003	0.258	0.010	0.992
Geno.541	102	W	G	G	C	0.011	-0.318	0.913	-0.349	0.727
Geno.641	102	W	T	A	C	0.016	-0.422	0.782	-0.540	0.589
Geno.rare85	102	*	*	*	*	0.002	-0.919	NA	NA	NA
haplo.base101	102	W	T	G	C	0.816	NA	NA	NA	NA
Geno.138	103	G	G	C	G	0.012	-0.326	0.875	-0.372	0.710
Geno.254	103	T	A	C	G	0.016	-0.425	0.782	-0.544	0.587
Geno.rare86	103	*	*	*	*	0.002	-0.576	2.589	-0.223	0.824
haplo.base102	103	T	G	C	G	0.970	NA	NA	NA	NA
Geno.139	104	A	C	G	G	0.016	-0.422	0.783	-0.540	0.590
Geno.rare87	104	*	*	*	*	0.003	-1.019	1.841	-0.554	0.580
haplo.base103	104	G	C	G	G	0.981	NA	NA	NA	NA
Geno.rare88	105	*	*	*	*	0.007	-0.647	1.231	-0.526	0.599
haplo.base104	105	C	G	G	G	0.993	NA	NA	NA	NA
Geno.rare89	106	*	*	*	*	0.007	-0.649	1.231	-0.528	0.598
haplo.base105	106	G	G	G	A	0.993	NA	NA	NA	NA
Geno.444	107	G	G	A	G	0.236	0.257	0.227	1.134	0.257
Geno.rare90	107	*	*	*	*	0.006	-0.736	1.229	-0.599	0.550
haplo.base106	107	G	G	A	A	0.758	NA	NA	NA	NA
Geno.338	108	G	A	A	A	0.340	0.143	0.227	0.632	0.528
Geno.542	108	G	A	G	A	0.216	0.398	0.258	1.545	0.123
Geno.642	108	G	A	G	T	0.021	-0.251	0.872	-0.288	0.774
Geno.rare91	108	*	*	*	*	0.005	-0.332	1.403	-0.237	0.813
haplo.base107	108	G	A	A	T	0.419	NA	NA	NA	NA
Geno.140	109	A	A	A	C	0.340	0.136	0.227	0.597	0.551
Geno.339	109	A	G	A	C	0.116	0.386	0.339	1.139	0.255
Geno.445	109	A	G	A	T	0.102	0.450	0.333	1.349	0.178
Geno.543	109	A	G	T	C	0.022	-0.181	0.895	-0.202	0.840
Geno.rare92	109	*	*	*	*	0.001	-1.041	2.597	-0.401	0.689
haplo.base108	109	A	A	T	C	0.418	NA	NA	NA	NA
Geno.340	110	A	T	C	A	0.330	-0.131	0.244	-0.535	0.593
Geno.446	110	A	T	C	G	0.088	0.037	0.363	0.101	0.920
Geno.544	110	G	A	C	A	0.113	0.230	0.377	0.610	0.542
Geno.735	110	G	A	T	A	0.102	0.340	0.350	0.969	0.333
Geno.925	110	G	T	C	A	0.020	-0.763	1.050	-0.727	0.468
Geno.rare93	110	*	*	*	*	0.005	2.904	1.626	1.786	0.075
haplo.base109	110	A	A	C	A	0.341	NA	NA	NA	NA
Geno.545	111	A	T	A	G	0.102	0.257	0.338	0.762	0.447
Geno.831	111	T	C	A	G	0.346	-0.224	0.221	-1.017	0.309
Geno.926	111	T	C	G	G	0.089	0.013	0.352	0.036	0.971
Geno.rare94	111	*	*	*	*	0.016	0.173	0.816	0.212	0.832
haplo.base110	111	A	C	A	G	0.447	NA	NA	NA	NA
Geno.141	112	C	A	A	C	0.013	-0.306	0.860	-0.356	0.722
Geno.447	112	C	G	G	C	0.092	0.179	0.338	0.530	0.596
Geno.643	112	T	A	G	C	0.100	0.398	0.327	1.218	0.224
Geno.rare95	112	*	*	*	*	0.009	0.086	1.008	0.085	0.932
haplo.base111	112	C	A	G	C	0.785	NA	NA	NA	NA
Geno.142	113	A	A	C	T	0.013	-0.450	0.853	-0.528	0.598
Geno.341	113	A	G	C	T	0.351	-0.285	0.210	-1.356	0.175
Geno.644	113	G	G	C	T	0.093	0.049	0.342	0.142	0.887
Geno.rare96	113	*	*	*	*	0.009	-0.058	0.999	-0.058	0.954
haplo.base112	113	A	G	C	C	0.534	NA	NA	NA	NA
Geno.342	114	A	C	T	A	0.013	-0.447	0.856	-0.522	0.602
Geno.645	114	G	C	C	T	0.084	0.098	0.375	0.263	0.793
Geno.736	114	G	C	T	A	0.444	-0.189	0.204	-0.928	0.354
Geno.rare97	114	*	*	*	*	0.009	-0.062	1.004	-0.062	0.951
haplo.base113	114	G	C	C	A	0.450	NA	NA	NA	NA
Geno.143	115	C	C	A	G	0.450	0.154	0.203	0.758	0.449
Geno.255	115	C	C	T	G	0.084	0.245	0.369	0.664	0.507
Geno.rare98	115	*	*	*	*	0.016	-0.945	0.772	-1.224	0.221
haplo.base114	115	C	T	A	G	0.450	NA	NA	NA	NA
Geno.343	116	C	T	G	T	0.084	0.113	0.372	0.303	0.762

Table A2.14. Continued

	Window	loc.1	loc.2	loc.3	loc.4	Hap.freq.	Coef.	S.E.	Test statistic	*P*-value
Geno.448	116	T	A	G	T	0.450	-0.140	0.202	-0.695	0.487
Geno.rare99	116	*	*	*	*	0.007	-2.559	1.245	-2.056	0.040
haplo.base115	116	C	A	G	T	0.459	NA	NA	NA	NA
Geno.144	117	A	G	T	A	0.012	0.903	0.853	1.059	0.290
Geno.646	117	T	G	T	G	0.084	0.174	0.356	0.488	0.626
Geno.rare100	117	*	*	*	*	0.007	-2.503	1.305	-1.917	0.056
haplo.base116	117	A	G	T	G	0.897	NA	NA	NA	NA
Geno.256	118	G	T	A	T	0.012	0.872	0.853	1.022	0.307
Geno.344	118	G	T	G	C	0.016	-0.632	0.756	-0.835	0.404
Geno.rare101	118	*	*	*	*	0.007	-2.540	1.243	-2.043	0.041
haplo.base117	118	G	T	G	T	0.966	NA	NA	NA	NA
Geno.345	119	T	A	T	A	0.012	0.961	0.853	1.126	0.260
Geno.546	119	T	G	C	G	0.016	-0.478	0.767	-0.624	0.533
Geno.647	119	T	G	T	A	0.404	0.218	0.195	1.120	0.263
Geno.rare102	119	*	*	*	*	0.005	-2.652	1.310	-2.025	0.043
haplo.base118	119	T	G	T	G	0.563	NA	NA	NA	NA
Geno.145	120	A	T	A	A	0.012	1.125	0.867	1.298	0.195
Geno.449	120	G	C	G	T	0.016	-0.415	0.777	-0.534	0.594
Geno.547	120	G	T	A	A	0.086	0.368	0.369	0.998	0.318
Geno.648	120	G	T	A	T	0.317	0.237	0.211	1.120	0.263
Geno.rare103	120	*	*	*	*	0.005	1.115	1.628	0.685	0.494
haplo.base119	120	G	T	G	T	0.563	NA	NA	NA	NA
Geno.146	121	C	G	T	G	0.016	-0.428	0.771	-0.554	0.579
Geno.346	121	T	A	A	G	0.097	0.516	0.342	1.509	0.132
Geno.450	121	T	A	T	A	0.090	0.263	0.339	0.776	0.438
Geno.548	121	T	A	T	G	0.227	0.208	0.238	0.875	0.382
Geno.rare104	121	*	*	*	*	0.005	0.305	1.517	0.201	0.841
haplo.base120	121	T	G	T	G	0.565	NA	NA	NA	NA
Geno.257	122	A	A	G	C	0.017	0.502	0.767	0.654	0.513
Geno.347	122	A	A	G	T	0.080	0.595	0.366	1.626	0.104
Geno.451	122	A	T	A	C	0.090	0.286	0.337	0.848	0.396
Geno.549	122	A	T	G	C	0.227	0.228	0.234	0.972	0.331
Geno.rare105	122	*	*	*	*	0.006	0.299	1.513	0.197	0.844
haplo.base121	122	G	T	G	C	0.581	NA	NA	NA	NA

Hap.freq: Haplotyle frequency, **Coef.** : Coefficient, **S.E.:** Standart Error

Table A2.15. Summary of *LPL* 4-SNP sliding haplotypes for association with ApoA1 in African blacks (n=788)

	Window	loc.1	loc.2	loc.3	loc.4	Hap.freq.	Coef.	S.E.	Test statistic	*P*-value
Geno.1	1	G	C	A	G	0.111	0.023	0.782	0.030	0.976
Geno.3	1	G	T	A	G	0.095	-0.320	0.820	-0.390	0.696
Geno.4	1	G	T	G	G	0.146	-0.779	0.722	-1.079	0.281
Geno.6	1	T	C	A	G	0.113	0.595	0.766	0.777	0.437
Geno.rare	1	*	*	*	*	0.005	-0.994	3.282	-0.303	0.762
haplo.base	1	G	T	G	T	0.530	NA	NA	NA	NA
Geno.11	2	C	A	G	A	0.020	-2.456	1.704	-1.442	0.150
Geno.2	2	C	A	G	T	0.203	0.575	0.599	0.960	0.337
Geno.61	2	T	A	G	T	0.096	-0.322	0.815	-0.395	0.693
Geno.7	2	T	G	G	T	0.146	-0.763	0.717	-1.064	0.288
Geno.rare1	2	*	*	*	*	0.005	-1.557	3.250	-0.479	0.632
haplo.base1	2	T	G	T	T	0.530	NA	NA	NA	NA
Geno.12	3	A	G	A	A	0.020	-2.544	1.703	-1.494	0.136
Geno.21	3	A	G	T	A	0.299	0.249	0.513	0.486	0.627
Geno.41	3	G	G	T	A	0.150	-0.724	0.714	-1.014	0.311
haplo.base2	3	G	T	T	A	0.530	NA	NA	NA	NA
Geno.22	4	G	A	A	W	0.020	-2.592	1.723	-1.504	0.133
Geno.31	4	G	T	A	W	0.450	-0.002	0.473	-0.004	0.996
Geno.5	4	T	T	A	I	0.028	0.411	1.432	0.287	0.774
haplo.base3	4	T	T	A	W	0.501	NA	NA	NA	NA
Geno.32	5	A	A	W	G	0.019	-2.396	1.770	-1.354	0.176
Geno.51	5	T	A	I	G	0.027	0.180	1.446	0.124	0.901
Geno.rare2	5	*	*	*	*	0.009	-0.780	2.937	-0.265	0.791
haplo.base4	5	T	A	W	G	0.945	NA	NA	NA	NA
Geno.23	6	A	I	G	C	0.028	0.294	1.424	0.207	0.836
Geno.rare3	6	*	*	*	*	0.014	-2.348	2.116	-1.109	0.268
haplo.base5	6	A	W	G	C	0.958	NA	NA	NA	NA
Geno.24	7	I	G	C	C	0.028	0.445	1.430	0.311	0.756
Geno.62	7	W	G	C	T	0.030	2.143	1.425	1.504	0.133
Geno.rare4	7	*	*	*	*	0.013	-1.524	2.182	-0.698	0.485
haplo.base6	7	W	G	C	C	0.929	NA	NA	NA	NA
Geno.42	8	G	C	C	A	0.033	-1.164	1.244	-0.936	0.350
Geno.71	8	G	C	T	G	0.029	2.028	1.450	1.399	0.162
Geno.rare5	8	*	*	*	*	0.014	-1.292	2.178	-0.593	0.553
haplo.base7	8	G	C	C	G	0.924	NA	NA	NA	NA
Geno.13	9	C	C	A	G	0.041	-0.732	1.133	-0.645	0.519
Geno.43	9	C	C	G	T	0.022	0.906	1.636	0.554	0.580
Geno.63	9	C	T	G	G	0.029	2.216	1.457	1.521	0.129
Geno.rare6	9	*	*	*	*	0.007	-3.638	3.800	-0.958	0.339
haplo.base8	9	C	C	G	G	0.902	NA	NA	NA	NA
Geno.14	10	C	A	G	C	0.041	-0.900	1.141	-0.789	0.430
Geno.52	10	C	G	G	T	0.039	1.918	1.233	1.556	0.120
Geno.64	10	C	G	T	C	0.022	0.815	1.681	0.485	0.628
Geno.9	10	T	G	G	C	0.029	2.369	1.445	1.639	0.102
Geno.rare7	10	*	*	*	*	0.002	2.846	NA	NA	NA
haplo.base9	10	C	G	G	C	0.868	NA	NA	NA	NA
Geno.25	11	A	G	C	G	0.041	-0.763	1.125	-0.678	0.498
Geno.53	11	G	G	C	C	0.022	2.341	1.623	1.443	0.150
Geno.72	11	G	G	T	G	0.039	1.992	1.240	1.606	0.109
Geno.8	11	G	T	C	G	0.022	0.947	1.639	0.578	0.564
haplo.base10	11	G	G	C	G	0.874	NA	NA	NA	NA
Geno.15	12	G	C	C	C	0.022	2.438	1.620	1.505	0.133
Geno.44	12	G	C	G	T	0.039	1.774	1.180	1.503	0.133
Geno.54	12	G	T	G	C	0.036	2.491	1.289	1.932	0.054
Geno.73	12	T	C	G	C	0.023	1.163	1.615	0.720	0.472
Geno.rare8	12	*	*	*	*	0.003	-2.481	5.005	-0.496	0.620
haplo.base11	12	G	C	G	C	0.877	NA	NA	NA	NA
Geno.26	13	C	C	C	G	0.022	2.388	1.626	1.469	0.142
Geno.45	13	C	G	C	C	0.078	0.598	0.899	0.665	0.506
Geno.65	13	C	G	T	C	0.040	1.779	1.171	1.520	0.129
Geno.81	13	T	G	C	G	0.037	2.472	1.286	1.922	0.055
Geno.rare9	13	*	*	*	*	0.003	-3.013	5.357	-0.563	0.574
haplo.base12	13	C	G	C	G	0.821	NA	NA	NA	NA
Geno.33	14	C	C	G	A	0.022	2.367	1.649	1.435	0.152
Geno.82	14	G	C	C	G	0.076	0.699	0.959	0.728	0.467
Geno.91	14	G	C	G	A	0.428	0.295	0.501	0.588	0.557
Geno.121	14	G	T	C	G	0.042	1.746	1.193	1.464	0.144
Geno.rare10	14	*	*	*	*	0.002	-4.005	6.413	-0.624	0.533
haplo.base13	14	G	C	G	G	0.430	NA	NA	NA	NA
Geno.34	15	C	C	G	T	0.076	0.263	0.948	0.278	0.781
Geno.66	15	C	G	G	G	0.023	-0.311	1.570	-0.198	0.843
Geno.74	15	C	G	G	T	0.407	-0.396	0.505	-0.784	0.433
Geno.92	15	T	C	G	T	0.042	1.274	1.167	1.092	0.275

Table A2.15. Continued

	Window	loc.1	loc.2	loc.3	loc.4	Hap.freq.	Coef.	S.E.	Test statistic	*P*-value
Geno.rare11	15	*	*	*	*	0.003	0.899	5.335	0.169	0.866
haplo.base14	15	C	G	A	T	0.449	NA	NA	NA	NA
Geno.35	16	C	G	T	A	0.117	0.970	0.782	1.240	0.215
Geno.75	16	G	A	T	A	0.141	0.113	0.765	0.148	0.883
Geno.83	16	G	A	T	G	0.308	0.465	0.554	0.839	0.402
Geno.93	16	G	G	G	A	0.023	-0.007	1.617	-0.004	0.997
Geno.rare12	16	*	*	*	*	0.005	0.253	4.220	0.060	0.952
haplo.base15	16	G	G	T	A	0.406	NA	NA	NA	NA
Geno.36	17	A	T	A	T	0.142	0.070	0.743	0.094	0.926
Geno.55	17	A	T	G	T	0.308	0.349	0.530	0.658	0.511
Geno.76	17	G	G	A	T	0.022	-0.413	1.713	-0.241	0.810
Geno.94	17	G	T	A	C	0.030	2.079	1.389	1.497	0.135
Geno.rare13	17	*	*	*	*	0.004	3.528	5.618	0.628	0.530
haplo.base16	17	G	T	A	T	0.494	NA	NA	NA	NA
Geno.27	18	G	A	T	T	0.023	0.107	1.559	0.069	0.945
Geno.46	18	T	A	C	T	0.030	2.085	1.379	1.512	0.131
Geno.56	18	T	A	T	C	0.023	0.464	1.606	0.289	0.773
Geno.84	18	T	G	T	C	0.312	0.432	0.512	0.844	0.399
Geno.rare14	18	*	*	*	*	0.001	1.883	6.916	0.272	0.786
haplo.base17	18	T	A	T	T	0.611	NA	NA	NA	NA
Geno.28	19	A	C	T	G	0.028	1.689	1.435	1.177	0.240
Geno.47	19	A	T	C	G	0.022	0.395	1.623	0.243	0.808
Geno.85	19	G	T	C	A	0.285	0.508	0.522	0.974	0.330
Geno.95	19	G	T	C	G	0.025	-1.243	1.586	-0.784	0.433
Geno.rare15	19	*	*	*	*	0.004	4.168	3.945	1.057	0.291
haplo.base18	19	A	T	T	G	0.635	NA	NA	NA	NA
Geno.48	20	C	T	G	A	0.029	1.905	1.459	1.306	0.192
Geno.77	20	T	C	A	G	0.281	0.513	0.521	0.986	0.325
Geno.86	20	T	C	G	A	0.044	-0.049	1.195	-0.041	0.967
Geno.rare16	20	*	*	*	*	0.013	0.216	2.548	0.085	0.932
haplo.base19	20	T	T	G	A	0.634	NA	NA	NA	NA
Geno.37	21	C	A	G	C	0.168	0.429	0.645	0.665	0.506
Geno.49	21	C	A	G	T	0.113	0.439	0.756	0.580	0.562
Geno.57	21	C	G	A	T	0.045	0.099	1.157	0.085	0.932
Geno.rare17	21	*	*	*	*	0.012	-0.618	2.347	-0.263	0.792
haplo.base20	21	T	G	A	T	0.663	NA	NA	NA	NA
Geno.38	22	A	G	C	A	0.167	0.461	0.641	0.719	0.472
Geno.58	22	A	G	T	A	0.113	0.471	0.753	0.625	0.532
Geno.78	22	G	A	T	G	0.029	1.053	1.426	0.739	0.460
Geno.rare18	22	*	*	*	*	0.012	-0.812	2.373	-0.342	0.732
haplo.base21	22	G	A	T	A	0.678	NA	NA	NA	NA
Geno.39	23	A	T	G	D	0.029	0.714	1.383	0.516	0.606
Geno.410	23	G	C	A	W	0.169	0.403	0.638	0.632	0.528
Geno.67	23	G	T	A	W	0.115	0.507	0.748	0.678	0.498
Geno.rare19	23	*	*	*	*	0.002	14.880	NA	NA	NA
haplo.base22	23	A	T	A	W	0.685	NA	NA	NA	NA
Geno.29	24	C	A	W	T	0.167	0.447	0.644	0.695	0.487
Geno.411	24	T	A	W	C	0.012	-2.507	2.199	-1.140	0.255
Geno.68	24	T	G	D	T	0.029	0.458	1.388	0.330	0.741
Geno.rare20	24	*	*	*	*	0.001	17.075	0.000	3.78E+16	0.000
haplo.base23	24	T	A	W	T	0.790	NA	NA	NA	NA
Geno.16	25	A	W	C	A	0.013	-2.097	2.124	-0.987	0.324
Geno.310	25	A	W	T	G	0.249	0.257	0.541	0.475	0.635
Geno.412	25	G	D	T	A	0.030	0.598	1.377	0.434	0.664
haplo.base24	25	A	W	T	A	0.708	NA	NA	NA	NA
Geno.17	26	D	T	A	A	0.028	0.393	1.535	0.256	0.798
Geno.413	26	W	C	A	A	0.012	-0.977	2.225	-0.439	0.661
Geno.87	26	W	T	G	A	0.198	0.553	0.602	0.918	0.359
Geno.96	26	W	T	G	C	0.050	-0.208	1.123	-0.185	0.853
Geno.rare21	26	*	*	*	*	0.005	-10.836	4.707	-2.302	0.022
haplo.base25	26	W	T	A	A	0.707	NA	NA	NA	NA
Geno.18	27	C	A	A	G	0.013	-2.131	2.130	-1.000	0.317
Geno.69	27	T	G	A	G	0.192	0.503	0.605	0.831	0.406
Geno.88	27	T	G	C	G	0.051	-0.673	1.106	-0.609	0.543
Geno.rare22	27	*	*	*	*	0.010	0.194	2.511	0.077	0.938
haplo.base26	27	T	A	A	G	0.735	NA	NA	NA	NA
Geno.19	28	A	A	G	D	0.023	2.081	1.613	1.290	0.197
Geno.610	28	G	A	G	W	0.192	0.615	0.606	1.015	0.310
Geno.97	28	G	C	G	W	0.051	-0.593	1.106	-0.536	0.592
Geno.rare23	28	*	*	*	*	0.010	0.381	2.520	0.151	0.880
haplo.base27	28	A	A	G	W	0.725	NA	NA	NA	NA
Geno.311	29	A	G	D	G	0.021	2.114	1.728	1.223	0.222
Geno.414	29	A	G	W	A	0.049	0.679	1.088	0.624	0.533
Geno.98	29	C	G	W	G	0.052	-0.685	1.085	-0.632	0.528
Geno.rare24	29	*	*	*	*	0.009	1.219	2.759	0.442	0.659

Table A2.15. Continued

	Window	loc.1	loc.2	loc.3	loc.4	Hap.freq.	Coef.	S.E.	Test statistic	*P*-value
haplo.base28	29	A	G	W	G	0.869	NA	NA	NA	NA
Geno.312	30	G	D	G	C	0.021	2.240	1.696	1.320	0.187
Geno.415	30	G	W	A	C	0.049	0.736	1.078	0.683	0.495
Geno.rare25	30	*	*	*	*	0.011	-1.436	2.464	-0.583	0.560
haplo.base29	30	G	W	G	C	0.919	NA	NA	NA	NA
Geno.210	31	D	G	C	G	0.022	2.519	1.628	1.547	0.122
Geno.416	31	W	A	C	G	0.049	0.829	1.059	0.783	0.434
Geno.59	31	W	G	C	C	0.018	-1.190	1.772	-0.671	0.502
Geno.rare26	31	*	*	*	*	0.003	-13.262	5.188	-2.556	0.011
haplo.base30	31	W	G	C	G	0.908	NA	NA	NA	NA
Geno.110	32	A	C	G	A	0.050	0.506	1.056	0.479	0.632
Geno.313	32	G	C	C	A	0.018	-1.426	1.785	-0.799	0.425
Geno.510	32	G	C	G	G	0.115	-0.698	0.762	-0.916	0.360
Geno.rare27	32	*	*	*	*	0.002	-11.780	6.446	-1.827	0.068
haplo.base31	32	G	C	G	A	0.815	NA	NA	NA	NA
Geno.111	33	C	C	A	C	0.018	-0.761	1.867	-0.407	0.684
Geno.611	33	C	G	G	C	0.115	-0.703	0.764	-0.920	0.358
Geno.rare28	33	*	*	*	*	0.011	-3.590	2.578	-1.393	0.164
haplo.base32	33	C	G	A	C	0.857	NA	NA	NA	NA
Geno.211	34	C	A	C	G	0.017	-0.627	1.930	-0.325	0.745
Geno.511	34	G	A	C	A	0.045	0.608	1.167	0.521	0.603
Geno.99	34	G	G	C	G	0.116	-0.648	0.768	-0.844	0.399
Geno.rare29	34	*	*	*	*	0.009	-1.655	2.869	-0.577	0.564
haplo.base33	34	G	A	C	G	0.813	NA	NA	NA	NA
Geno.112	35	A	C	A	C	0.046	0.653	1.159	0.563	0.574
Geno.212	35	A	C	G	C	0.252	0.382	0.559	0.683	0.495
Geno.612	35	G	C	G	T	0.113	-0.525	0.790	-0.664	0.507
Geno.rare30	35	*	*	*	*	0.011	-1.453	2.520	-0.576	0.565
haplo.base34	35	A	C	G	T	0.578	NA	NA	NA	NA
Geno.213	36	C	A	C	G	0.046	0.598	1.178	0.508	0.612
Geno.417	36	C	G	C	G	0.251	0.347	0.614	0.566	0.572
Geno.512	36	C	G	T	C	0.310	-0.274	0.564	-0.486	0.627
Geno.rare31	36	*	*	*	*	0.012	-2.693	2.316	-1.163	0.245
haplo.base35	36	C	G	T	G	0.381	NA	NA	NA	NA
Geno.314	37	A	C	G	T	0.046	0.672	1.177	0.571	0.568
Geno.613	37	G	C	G	T	0.243	0.364	0.619	0.587	0.557
Geno.79	37	G	T	C	T	0.310	-0.253	0.562	-0.451	0.652
Geno.rare32	37	*	*	*	*	0.010	-0.683	2.476	-0.276	0.783
haplo.base36	37	G	T	G	T	0.391	NA	NA	NA	NA
Geno.513	38	C	G	T	G	0.284	0.500	0.607	0.824	0.410
Geno.710	38	T	C	T	G	0.311	-0.092	0.580	-0.158	0.874
Geno.89	38	T	G	T	A	0.053	1.562	1.123	1.391	0.165
Geno.rare33	38	*	*	*	*	0.014	0.979	2.195	0.446	0.656
haplo.base37	38	T	G	T	G	0.338	NA	NA	NA	NA
Geno.113	39	C	T	G	A	0.309	-0.449	0.530	-0.847	0.397
Geno.614	39	G	T	A	A	0.057	1.541	1.037	1.486	0.138
Geno.910	39	G	T	G	C	0.086	-0.791	0.907	-0.871	0.384
Geno.rare34	39	*	*	*	*	0.012	-0.202	2.736	-0.074	0.941
haplo.base38	39	G	T	G	A	0.536	NA	NA	NA	NA
Geno.418	40	T	A	A	C	0.052	1.399	1.118	1.252	0.211
Geno.810	40	T	G	A	G	0.022	-0.190	1.667	-0.114	0.909
Geno.911	40	T	G	C	C	0.086	-0.839	0.888	-0.945	0.345
Geno.rare35	40	*	*	*	*	0.012	2.325	2.714	0.857	0.392
haplo.base39	40	T	G	A	C	0.828	NA	NA	NA	NA
Geno.114	41	A	A	C	W	0.053	1.564	0.908	1.723	0.085
Geno.615	41	G	A	G	W	0.021	-0.181	1.678	-0.108	0.914
Geno.811	41	G	C	C	W	0.087	-0.730	0.779	-0.937	0.349
Geno.rare36	41	*	*	*	*	0.006	-0.207	NA	NA	NA
haplo.base40	41	G	A	C	W	0.832	NA	NA	NA	NA
Geno.214	42	A	C	W	A	0.109	-0.294	0.747	-0.394	0.694
Geno.419	42	A	G	W	G	0.022	-0.247	1.638	-0.151	0.880
Geno.711	42	C	C	W	G	0.091	-0.750	0.843	-0.890	0.374
Geno.rare37	42	*	*	*	*	0.002	-7.087	0.000	-6.63E+15	0.000
haplo.base41	42	A	C	W	G	0.776	NA	NA	NA	NA
Geno.215	43	C	W	A	A	0.109	-0.203	0.752	-0.270	0.787
Geno.514	43	C	W	G	G	0.205	-0.029	0.583	-0.050	0.960
Geno.616	43	G	W	G	A	0.023	-0.300	1.613	-0.186	0.853
Geno.rare38	43	*	*	*	*	0.001	-6.779	6.374	-1.064	0.288
haplo.base42	43	C	W	G	A	0.661	NA	NA	NA	NA
Geno.216	44	W	A	A	C	0.109	-0.329	0.754	-0.436	0.663
Geno.515	44	W	G	A	T	0.108	-0.784	0.766	-1.023	0.307
Geno.617	44	W	G	G	C	0.204	-0.125	0.597	-0.209	0.835
Geno.rare39	44	*	*	*	*	0.002	-8.856	6.346	-1.395	0.163
haplo.base43	44	W	G	A	C	0.576	NA	NA	NA	NA
Geno.217	45	A	A	C	W	0.109	-0.122	0.758	-0.161	0.872

Table A2.15. Continued

	Window	loc.1	loc.2	loc.3	loc.4	Hap.freq.	Coef.	S.E.	Test statistic	*P*-value
Geno.420	45	G	A	C	D	0.022	2.292	1.601	1.432	0.153
Geno.618	45	G	A	T	W	0.108	-0.492	0.773	-0.636	0.525
Geno.812	45	G	G	C	W	0.205	-0.006	0.597	-0.010	0.992
Geno.rare40	45	*	*	*	*	0.001	-18.172	0.000	-1.85E+16	0.000
haplo.base44	45	G	A	C	W	0.555	NA	NA	NA	NA
Geno.218	46	A	C	D	C	0.022	2.257	1.603	1.408	0.160
Geno.315	46	A	C	W	A	0.031	-1.263	1.392	-0.907	0.365
Geno.619	46	A	T	W	C	0.108	-0.637	0.767	-0.830	0.407
Geno.912	46	G	C	W	C	0.205	-0.046	0.594	-0.078	0.938
Geno.rare41	46	*	*	*	*	0.001	-12.406	NA	NA	NA
haplo.base45	46	A	C	W	C	0.633	NA	NA	NA	NA
Geno.219	47	C	D	C	G	0.022	2.383	1.602	1.488	0.137
Geno.316	47	C	W	A	G	0.031	-1.079	1.391	-0.776	0.438
Geno.421	47	C	W	C	A	0.033	1.531	1.348	1.135	0.257
Geno.712	47	T	W	C	G	0.109	-0.667	0.744	-0.897	0.370
haplo.base46	47	C	W	C	G	0.805	NA	NA	NA	NA
Geno.220	48	D	C	G	T	0.022	2.535	1.597	1.587	0.113
Geno.317	48	W	A	G	T	0.031	-0.957	1.386	-0.690	0.490
Geno.422	48	W	C	A	T	0.033	1.710	1.340	1.276	0.202
Geno.rare42	48	*	*	*	*	0.006	2.788	3.075	0.907	0.365
haplo.base47	48	W	C	G	T	0.908	NA	NA	NA	NA
Geno.221	49	A	G	T	T	0.031	-0.965	1.380	-0.699	0.484
Geno.423	49	C	A	T	T	0.033	1.682	1.338	1.257	0.209
Geno.620	49	C	G	T	C	0.194	0.608	0.610	0.996	0.320
Geno.rare43	49	*	*	*	*	0.006	2.798	3.059	0.915	0.361
haplo.base48	49	C	G	T	T	0.737	NA	NA	NA	NA
Geno.222	50	A	T	T	D	0.033	1.649	1.339	1.231	0.219
Geno.516	50	G	T	C	D	0.194	0.518	0.617	0.839	0.401
Geno.713	50	G	T	T	W	0.089	-0.876	0.852	-1.027	0.305
Geno.rare44	50	*	*	*	*	0.006	2.589	3.098	0.836	0.404
haplo.base49	50	G	T	T	D	0.679	NA	NA	NA	NA
Geno.223	51	T	C	D	C	0.141	0.649	0.710	0.914	0.361
Geno.318	51	T	C	D	T	0.053	-0.207	1.161	-0.178	0.858
Geno.517	51	T	T	D	C	0.101	-0.229	0.848	-0.271	0.787
Geno.714	51	T	T	W	T	0.089	-0.977	0.858	-1.138	0.255
Geno.rare45	51	*	*	*	*	0.006	2.395	3.094	0.774	0.439
haplo.base50	51	T	T	D	T	0.610	NA	NA	NA	NA
Geno.115	52	C	D	C	A	0.141	0.520	0.729	0.713	0.476
Geno.224	52	C	D	T	A	0.053	-0.307	1.178	-0.261	0.794
Geno.424	52	T	D	C	A	0.101	-0.290	0.861	-0.336	0.737
Geno.715	52	T	D	T	G	0.115	-0.488	0.755	-0.646	0.518
Geno.913	52	T	W	T	A	0.095	-0.806	0.854	-0.944	0.345
haplo.base51	52	T	D	T	A	0.495	NA	NA	NA	NA
Geno.116	53	D	C	A	A	0.244	0.145	0.578	0.252	0.801
Geno.518	53	D	T	A	C	0.035	-0.178	1.232	-0.144	0.885
Geno.621	53	D	T	G	A	0.115	-0.514	0.751	-0.684	0.494
Geno.813	53	W	T	A	A	0.095	-0.831	0.851	-0.976	0.329
haplo.base52	53	D	T	A	A	0.512	NA	NA	NA	NA
Geno.117	54	C	A	A	C	0.243	0.177	0.569	0.310	0.756
Geno.622	54	T	A	A	G	0.036	-1.794	1.293	-1.388	0.166
Geno.716	54	T	A	C	C	0.035	-0.184	1.234	-0.149	0.881
Geno.814	54	T	G	A	C	0.115	-0.502	0.747	-0.672	0.502
haplo.base53	54	T	A	A	C	0.571	NA	NA	NA	NA
Geno.225	55	A	A	C	T	0.052	1.612	1.102	1.463	0.144
Geno.319	55	A	A	G	A	0.035	-1.701	1.320	-1.289	0.198
Geno.519	55	A	C	C	A	0.035	-0.206	1.222	-0.168	0.866
Geno.717	55	G	A	C	A	0.115	-0.499	0.726	-0.688	0.492
Geno.rare46	55	*	*	*	*	0.001	-5.171	11.215	-0.461	0.645
haplo.base54	55	A	A	C	A	0.763	NA	NA	NA	NA
Geno.226	56	A	C	A	G	0.076	0.512	0.952	0.538	0.590
Geno.320	56	A	C	T	C	0.052	1.725	1.114	1.549	0.122
Geno.425	56	A	G	A	C	0.034	-1.606	1.328	-1.209	0.227
Geno.718	56	C	C	A	C	0.035	-0.055	1.227	-0.045	0.964
Geno.rare47	56	*	*	*	*	0.001	-3.046	10.242	-0.297	0.766
haplo.base55	56	A	C	A	C	0.802	NA	NA	NA	NA
Geno.227	57	C	A	C	G	0.120	-0.206	0.727	-0.284	0.777
Geno.426	57	C	A	G	G	0.075	0.654	0.960	0.681	0.496
Geno.520	57	C	T	C	A	0.052	1.687	1.098	1.536	0.125
Geno.719	57	G	A	C	A	0.035	-1.661	1.305	-1.272	0.204
Geno.rare48	57	*	*	*	*	0.003	-2.508	6.488	-0.387	0.699
haplo.base56	57	C	A	C	A	0.715	NA	NA	NA	NA
Geno.228	58	A	C	A	T	0.221	-0.608	0.599	-1.014	0.311
Geno.321	58	A	C	G	C	0.111	-0.420	0.782	-0.537	0.592
Geno.720	58	A	G	G	T	0.075	0.555	0.990	0.560	0.575
Geno.914	58	T	C	A	T	0.052	1.461	1.110	1.316	0.189

Table A2.15. Continued

	Window	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**Hap.freq.**	**Coef.**	**S.E.**	**Test statistic**	***P*-value**
Geno.rare49	58	*	*	*	*	0.013	0.490	2.908	0.168	0.866
haplo.base57	58	A	C	A	C	0.528	NA	NA	NA	NA
Geno.229	59	C	A	C	G	0.068	-0.226	1.058	-0.214	0.831
Geno.322	59	C	A	T	A	0.259	-0.172	0.593	-0.290	0.772
Geno.427	59	C	A	T	G	0.016	-3.407	2.415	-1.411	0.159
Geno.521	59	C	G	C	A	0.110	-0.600	0.785	-0.764	0.445
Geno.131	59	G	G	T	G	0.075	0.500	1.005	0.498	0.619
Geno.rare50	59	*	*	*	*	0.014	0.561	2.518	0.223	0.824
haplo.base58	59	C	A	C	A	0.458	NA	NA	NA	NA
Geno.230	60	A	C	G	G	0.069	-0.356	1.087	-0.327	0.744
Geno.323	60	A	T	A	G	0.260	-0.191	0.595	-0.322	0.748
Geno.428	60	A	T	G	G	0.020	-3.090	2.355	-1.312	0.190
Geno.522	60	G	C	A	G	0.112	-0.625	0.788	-0.794	0.428
Geno.915	60	G	T	G	G	0.076	0.288	0.949	0.304	0.761
Geno.rare51	60	*	*	*	*	0.006	5.819	4.129	1.409	0.159
haplo.base59	60	A	C	A	G	0.456	NA	NA	NA	NA
Geno.429	61	C	G	G	T	0.074	-0.904	1.047	-0.863	0.388
Geno.523	61	T	A	G	C	0.046	1.734	1.168	1.484	0.138
Geno.623	61	T	A	G	T	0.215	-0.918	0.628	-1.462	0.144
Geno.916	61	T	G	G	T	0.095	0.522	0.890	0.587	0.557
Geno.rare52	61	*	*	*	*	0.008	-0.025	3.124	-0.008	0.994
haplo.base60	61	C	A	G	T	0.561	NA	NA	NA	NA
Geno.118	62	A	G	C	G	0.053	1.367	1.074	1.272	0.204
Geno.231	62	A	G	T	G	0.290	-0.673	0.578	-1.164	0.245
Geno.624	62	G	G	T	G	0.133	0.160	0.734	0.218	0.827
Geno.721	62	G	G	T	T	0.037	-1.202	1.442	-0.834	0.405
Geno.rare53	62	*	*	*	*	0.001	7.231	6.441	1.123	0.262
haplo.base61	62	A	G	T	T	0.486	NA	NA	NA	NA
Geno.430	63	G	C	G	C	0.053	1.586	1.080	1.468	0.142
Geno.815	63	G	T	G	C	0.424	-0.107	0.502	-0.214	0.830
Geno.917	63	G	T	T	A	0.069	1.487	0.955	1.557	0.120
Geno.rare54	63	*	*	*	*	0.001	7.737	6.515	1.188	0.235
haplo.base62	63	G	T	T	C	0.453	NA	NA	NA	NA
Geno.324	64	C	G	C	W	0.053	1.500	1.077	1.394	0.164
Geno.722	64	T	G	C	I	0.043	1.456	1.179	1.234	0.218
Geno.816	64	T	G	C	W	0.382	-0.301	0.526	-0.572	0.568
Geno.918	64	T	T	A	W	0.069	1.466	0.954	1.536	0.125
haplo.base63	64	T	T	C	W	0.453	NA	NA	NA	NA
Geno.119	65	G	C	I	T	0.043	1.561	1.232	1.268	0.205
Geno.232	65	G	C	W	C	0.017	0.713	2.470	0.289	0.773
Geno.524	65	T	A	W	T	0.069	1.597	0.952	1.678	0.094
Geno.625	65	T	C	W	C	0.175	0.414	0.688	0.601	0.548
Geno.723	65	T	C	W	T	0.277	-0.122	0.595	-0.206	0.837
haplo.base64	65	G	C	W	T	0.419	NA	NA	NA	NA
Geno.325	66	A	W	T	C	0.064	1.761	0.955	1.844	0.066
Geno.724	66	C	I	T	T	0.042	1.623	1.209	1.342	0.180
Geno.817	66	C	W	C	C	0.034	0.917	1.341	0.684	0.494
Geno.919	66	C	W	C	T	0.157	0.347	0.681	0.509	0.611
Geno.10	66	C	W	T	C	0.011	-0.819	2.700	-0.303	0.762
Geno.rare55	66	*	*	*	*	0.007	-0.602	3.319	-0.181	0.856
haplo.base65	66	C	W	T	T	0.684	NA	NA	NA	NA
Geno.233	67	I	T	T	C	0.043	1.873	1.202	1.558	0.120
Geno.326	67	W	C	C	C	0.035	0.923	1.540	0.599	0.549
Geno.431	67	W	C	T	C	0.157	0.637	0.737	0.864	0.388
Geno.626	67	W	T	C	C	0.075	1.815	1.036	1.752	0.080
Geno.920	67	W	T	T	G	0.148	1.092	0.702	1.555	0.120
haplo.base66	67	W	T	T	C	0.542	NA	NA	NA	NA
Geno.120	68	C	C	C	G	0.035	0.626	1.575	0.398	0.691
Geno.327	68	C	T	C	G	0.157	0.559	0.744	0.752	0.452
Geno.525	68	T	C	C	G	0.074	1.790	1.056	1.695	0.090
Geno.627	68	T	T	C	A	0.055	0.329	1.096	0.300	0.764
Geno.921	68	T	T	G	G	0.146	1.048	0.721	1.454	0.146
Geno.rare56	68	*	*	*	*	0.002	-1.914	8.326	-0.230	0.818
haplo.base67	68	T	T	C	G	0.530	NA	NA	NA	NA
Geno.234	69	C	C	G	G	0.108	1.282	0.758	1.692	0.091
Geno.328	69	T	C	A	A	0.056	0.124	1.025	0.121	0.904
Geno.628	69	T	G	G	G	0.148	0.908	0.688	1.320	0.187
haplo.base68	69	T	C	G	G	0.686	NA	NA	NA	NA
Geno.122	70	C	A	A	A	0.056	-0.048	1.052	-0.046	0.963
Geno.526	70	C	G	G	A	0.318	0.059	0.539	0.109	0.913
Geno.818	70	G	G	G	A	0.147	0.833	0.703	1.185	0.236
Geno.rare57	70	*	*	*	*	0.003	-3.917	6.712	-0.584	0.560
haplo.base69	70	C	G	G	T	0.477	NA	NA	NA	NA
Geno.235	71	A	A	A	G	0.057	0.070	1.035	0.067	0.946
Geno.527	71	G	G	A	A	0.142	-0.149	0.717	-0.207	0.836

Table A2.15. Continued

	Window	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**Hap.freq.**	**Coef.**	**S.E.**	**Test statistic**	***P*-value**
Geno.629	71	G	G	A	G	0.326	0.515	0.546	0.944	0.346
Geno.rare58	71	*	*	*	*	0.003	5.635	6.676	0.844	0.399
haplo.base70	71	G	G	T	G	0.472	NA	NA	NA	NA
Geno.123	72	A	A	G	C	0.056	0.026	1.041	0.025	0.980
Geno.329	72	G	A	A	C	0.141	0.122	0.718	0.170	0.865
Geno.432	72	G	A	G	A	0.138	-0.909	0.712	-1.278	0.202
Geno.528	72	G	A	G	C	0.188	1.435	0.657	2.184	0.029
Geno.rare59	72	*	*	*	*	0.004	-2.616	4.086	-0.640	0.522
haplo.base71	72	G	T	G	A	0.473	NA	NA	NA	NA
Geno.236	73	A	A	C	G	0.140	0.169	0.729	0.231	0.817
Geno.330	73	A	G	A	G	0.138	-0.936	0.715	-1.310	0.191
Geno.433	73	A	G	C	G	0.245	1.016	0.596	1.704	0.089
Geno.725	73	T	G	A	A	0.016	-0.654	1.912	-0.342	0.732
Geno.rare60	73	*	*	*	*	0.005	-2.498	4.844	-0.516	0.606
haplo.base72	73	T	G	A	G	0.457	NA	NA	NA	NA
Geno.630	74	A	C	G	G	0.142	0.420	0.716	0.586	0.558
Geno.726	74	G	A	A	G	0.016	-0.318	1.902	-0.167	0.867
Geno.819	74	G	A	G	A	0.012	2.700	2.194	1.231	0.219
Geno.1110	74	G	C	G	G	0.248	1.317	0.581	2.267	0.024
Geno.rare61	74	*	*	*	*	0.003	-3.380	5.185	-0.652	0.515
haplo.base73	74	G	A	G	G	0.580	NA	NA	NA	NA
Geno.124	75	A	A	G	C	0.016	-0.171	1.896	-0.090	0.928
Geno.237	75	A	G	A	C	0.012	2.798	2.187	1.279	0.201
Geno.529	75	C	G	G	C	0.389	1.055	0.477	2.214	0.027
Geno.rare62	75	*	*	*	*	0.007	7.542	2.629	2.869	0.004
haplo.base74	75	A	G	G	C	0.576	NA	NA	NA	NA
Geno.331	76	A	G	C	A	0.016	-0.734	1.879	-0.391	0.696
Geno.434	76	G	A	C	A	0.012	2.162	2.163	0.999	0.318
Geno.727	76	G	G	C	G	0.011	0.472	2.303	0.205	0.838
Geno.rare63	76	*	*	*	*	0.007	7.228	2.626	2.753	0.006
haplo.base75	76	G	G	C	A	0.954	NA	NA	NA	NA
Geno.125	77	A	C	A	T	0.012	2.770	2.181	1.270	0.205
Geno.238	77	G	C	A	C	0.285	1.225	0.520	2.354	0.019
Geno.rare64	77	*	*	*	*	0.018	3.740	1.757	2.128	0.034
haplo.base76	77	G	C	A	T	0.685	NA	NA	NA	NA
Geno.126	78	C	A	C	A	0.146	1.844	0.692	2.664	0.008
Geno.239	78	C	A	C	G	0.138	0.347	0.699	0.496	0.620
Geno.435	78	C	A	T	G	0.012	-2.035	2.222	-0.916	0.360
Geno.rare65	78	*	*	*	*	0.018	3.756	1.787	2.101	0.036
haplo.base77	78	C	A	T	A	0.686	NA	NA	NA	NA
Geno.127	79	A	C	A	A	0.143	1.927	0.753	2.559	0.011
Geno.332	79	A	C	G	A	0.141	0.573	0.720	0.796	0.426
Geno.530	79	A	T	A	G	0.247	0.491	0.587	0.837	0.403
Geno.631	79	A	T	G	A	0.012	-1.937	2.256	-0.859	0.391
Geno.820	79	G	T	A	A	0.011	0.578	2.317	0.249	0.803
Geno.rare66	79	*	*	*	*	0.004	2.230	4.567	0.488	0.625
haplo.base78	79	A	T	A	A	0.442	NA	NA	NA	NA
Geno.128	80	C	A	A	C	0.143	2.074	0.753	2.755	0.006
Geno.436	80	C	G	A	C	0.141	0.749	0.723	1.036	0.300
Geno.728	80	T	A	A	T	0.024	3.172	1.551	2.046	0.041
Geno.821	80	T	A	G	C	0.248	0.666	0.589	1.131	0.259
Geno.922	80	T	G	A	C	0.012	-1.626	2.253	-0.722	0.471
Geno.rare67	80	*	*	*	*	0.004	2.372	4.549	0.521	0.602
haplo.base79	80	T	A	A	C	0.428	NA	NA	NA	NA
Geno.129	81	A	A	C	A	0.096	2.401	0.889	2.701	0.007
Geno.437	81	A	A	T	C	0.022	2.412	1.671	1.444	0.149
Geno.632	81	A	G	C	C	0.251	0.427	0.570	0.749	0.454
Geno.923	81	G	A	C	A	0.130	0.716	0.729	0.982	0.326
Geno.101	81	G	A	C	C	0.022	-0.759	1.769	-0.429	0.668
Geno.rare68	81	*	*	*	*	0.003	10.738	4.768	2.252	0.025
haplo.base80	81	A	A	C	C	0.476	NA	NA	NA	NA
Geno.130	82	A	C	A	G	0.223	1.539	0.593	2.594	0.010
Geno.633	82	A	T	C	G	0.023	2.901	1.583	1.832	0.067
Geno.822	82	G	C	C	A	0.030	2.135	1.383	1.544	0.123
Geno.924	82	G	C	C	G	0.219	0.235	0.592	0.396	0.692
Geno.rare69	82	*	*	*	*	0.003	7.105	7.960	0.893	0.372
haplo.base81	82	A	C	C	G	0.501	NA	NA	NA	NA
Geno.240	83	C	A	G	C	0.226	1.266	0.585	2.163	0.031
Geno.333	83	C	C	A	C	0.032	2.069	1.346	1.537	0.125
Geno.634	83	C	C	G	G	0.137	-0.814	0.710	-1.148	0.252
Geno.823	83	T	C	G	C	0.024	2.960	1.533	1.931	0.054
haplo.base82	83	C	C	G	C	0.581	NA	NA	NA	NA
Geno.241	84	A	G	C	A	0.226	1.313	0.591	2.221	0.027
Geno.438	84	C	A	C	C	0.032	2.042	1.349	1.514	0.131
Geno.729	84	C	G	C	C	0.051	1.744	1.095	1.593	0.112

Table A2.16. Summary of *LPL* 4-SNP sliding haplotypes for association with ApoB in African blacks (n=788)

	Win	loc.1	loc.2	loc.3	loc.4	Hap.freq	Coef.	S.E.	Test Statistic	*P*-value
Geno.1	1	G	C	A	G	0.110	1.151	0.886	1.299	0.194
Geno.3	1	G	T	A	G	0.094	-0.875	0.933	-0.938	0.348
Geno.4	1	G	T	G	G	0.148	0.432	0.822	0.526	0.599
Geno.6	1	T	C	A	G	0.112	-0.826	0.862	-0.958	0.338
Geno.rare	1	*	*	*	*	0.006	-4.717	3.454	-1.365	0.173
haplo.base	1	G	T	G	T	0.530	NA	NA	NA	NA
Geno.11	2	C	A	G	A	0.020	-2.187	1.970	-1.110	0.267
Geno.2	2	C	A	G	T	0.201	0.321	0.681	0.472	0.637
Geno.61	2	T	A	G	T	0.096	-0.813	0.927	-0.877	0.381
Geno.7	2	T	G	G	T	0.148	0.339	0.818	0.414	0.679
Geno.rare1	2	*	*	*	*	0.005	-5.148	3.453	-1.491	0.136
haplo.base1	2	T	G	T	T	0.530	NA	NA	NA	NA
Geno.12	3	A	G	A	A	0.020	-2.244	1.972	-1.138	0.256
Geno.21	3	A	G	T	A	0.297	-0.055	0.584	-0.094	0.925
Geno.41	3	G	G	T	A	0.153	0.200	0.814	0.246	0.806
haplo.base2	3	G	T	T	A	0.530	NA	NA	NA	NA
Geno.22	4	G	A	A	W	0.019	-2.201	1.971	-1.117	0.265
Geno.31	4	G	T	A	W	0.450	0.092	0.540	0.170	0.865
Geno.5	4	T	T	A	I	0.029	0.151	1.613	0.094	0.925
haplo.base3	4	T	T	A	W	0.501	NA	NA	NA	NA
Geno.32	5	A	A	W	G	0.018	-1.956	2.040	-0.959	0.338
Geno.51	5	T	A	I	G	0.027	0.437	1.643	0.266	0.790
Geno.rare2	5	*	*	*	*	0.009	0.128	3.218	0.040	0.968
haplo.base4	5	T	A	W	G	0.945	NA	NA	NA	NA
Geno.23	6	A	I	G	C	0.028	0.198	1.612	0.123	0.902
Geno.rare3	6	*	*	*	*	0.013	0.516	2.442	0.211	0.833
haplo.base5	6	A	W	G	C	0.959	NA	NA	NA	NA
Geno.24	7	I	G	C	C	0.028	0.289	1.611	0.179	0.858
Geno.62	7	W	G	C	T	0.029	2.458	1.600	1.537	0.125
Geno.rare4	7	*	*	*	*	0.013	0.854	2.442	0.350	0.727
haplo.base6	7	W	G	C	C	0.930	NA	NA	NA	NA
Geno.42	8	G	C	C	A	0.033	1.698	1.434	1.185	0.237
Geno.71	8	G	C	T	G	0.028	2.740	1.655	1.656	0.098
Geno.rare5	8	*	*	*	*	0.014	0.498	2.410	0.207	0.836
haplo.base7	8	G	C	C	G	0.925	NA	NA	NA	NA
Geno.13	9	C	C	A	G	0.039	2.105	1.315	1.601	0.110
Geno.43	9	C	C	G	T	0.022	4.750	1.904	2.495	0.013
Geno.63	9	C	T	G	G	0.028	3.426	1.691	2.026	0.043
Geno.rare6	9	*	*	*	*	0.007	-2.609	3.931	-0.664	0.507
haplo.base8	9	C	C	G	G	0.904	NA	NA	NA	NA
Geno.14	10	C	A	G	C	0.040	1.932	1.293	1.495	0.135
Geno.52	10	C	G	G	T	0.039	-0.424	1.386	-0.306	0.760
Geno.64	10	C	G	T	C	0.022	4.832	1.875	2.577	0.010
Geno.9	10	T	G	G	C	0.027	3.699	1.685	2.196	0.028
Geno.rare7	10	*	*	*	*	0.002	-11.670	NA	NA	NA
haplo.base9	10	C	G	G	C	0.869	NA	NA	NA	NA
Geno.25	11	A	G	C	G	0.041	1.703	1.287	1.324	0.186
Geno.53	11	G	G	C	C	0.023	2.081	1.810	1.150	0.251
Geno.72	11	G	G	T	G	0.039	-0.393	1.397	-0.282	0.778
Geno.8	11	G	T	C	G	0.022	4.065	1.874	2.169	0.030
haplo.base10	11	G	G	C	G	0.874	NA	NA	NA	NA
Geno.15	12	G	C	C	C	0.022	2.094	1.858	1.127	0.260
Geno.44	12	G	C	G	T	0.039	0.515	1.383	0.373	0.709
Geno.54	12	G	T	G	C	0.036	-0.047	1.472	-0.032	0.975
Geno.73	12	T	C	G	C	0.023	3.839	1.842	2.084	0.038
Geno.rare8	12	*	*	*	*	0.005	-3.941	5.336	-0.739	0.460
haplo.base11	12	G	C	G	C	0.876	NA	NA	NA	NA
Geno.26	13	C	C	C	G	0.021	2.123	1.904	1.115	0.265
Geno.45	13	C	G	C	C	0.078	0.128	1.013	0.127	0.899
Geno.65	13	C	G	T	C	0.039	0.157	1.351	0.116	0.908
Geno.81	13	T	G	C	G	0.037	-0.156	1.462	-0.106	0.915
Geno.rare9	13	*	*	*	*	0.005	-4.611	5.436	-0.848	0.397
haplo.base12	13	C	G	C	G	0.821	NA	NA	NA	NA
Geno.16	14	C	C	G	A	0.023	2.119	1.831	1.157	0.247
Geno.55	14	G	C	C	G	0.077	0.186	1.065	0.174	0.862
Geno.66	14	G	C	G	A	0.427	0.473	0.557	0.850	0.396
Geno.91	14	G	T	C	G	0.042	-0.275	1.322	-0.208	0.835
Geno.rare10	14	*	*	*	*	0.002	6.659	0.021	322.901	0.000
haplo.base13	14	G	C	G	G	0.429	NA	NA	NA	NA
Geno.33	15	C	C	G	T	0.077	-0.274	1.061	-0.258	0.797
Geno.67	15	C	G	G	G	0.023	3.406	1.773	1.921	0.055
Geno.74	15	C	G	G	T	0.406	-0.798	0.564	-1.416	0.157

Table A2.16. Continued

	Win	loc.1	loc.2	loc.3	loc.4	Hap.freq	Coef.	S.E.	Test Statistic	*P*-value
Geno.92	15	T	C	G	T	0.042	-0.616	1.306	-0.472	0.637
Geno.rare11	15	*	*	*	*	0.003	2.941	7.728	0.381	0.704
haplo.base14	15	C	G	A	T	0.448	NA	NA	NA	NA
Geno.34	16	C	G	T	A	0.118	0.442	0.875	0.505	0.614
Geno.75	16	G	A	T	A	0.144	1.474	0.845	1.743	0.082
Geno.82	16	G	A	T	G	0.304	0.460	0.627	0.734	0.463
Geno.93	16	G	G	G	A	0.023	4.583	1.875	2.444	0.015
Geno.rare12	16	*	*	*	*	0.005	-2.305	4.737	-0.487	0.627
haplo.base15	16	G	G	T	A	0.405	NA	NA	NA	NA
Geno.35	17	A	T	A	T	0.145	1.500	0.825	1.819	0.069
Geno.56	17	A	T	G	T	0.305	0.489	0.595	0.821	0.412
Geno.76	17	G	G	A	T	0.022	4.897	1.876	2.611	0.009
Geno.94	17	G	T	A	C	0.030	2.189	1.561	1.402	0.161
Geno.rare13	17	*	*	*	*	0.003	-7.644	5.640	-1.355	0.176
haplo.base16	17	G	T	A	T	0.494	NA	NA	NA	NA
Geno.27	18	G	A	T	T	0.023	4.569	1.754	2.605	0.009
Geno.46	18	T	A	C	T	0.030	1.851	1.560	1.187	0.236
Geno.57	18	T	A	T	C	0.024	0.900	1.782	0.505	0.614
Geno.83	18	T	G	T	C	0.308	0.045	0.578	0.078	0.938
Geno.rare14	18	*	*	*	*	0.001	-10.030	7.200	-1.393	0.164
haplo.base17	18	T	A	T	T	0.614	NA	NA	NA	NA
Geno.28	19	A	C	T	G	0.029	1.440	1.651	0.872	0.383
Geno.47	19	A	T	C	G	0.023	0.063	1.824	0.034	0.972
Geno.84	19	G	T	C	A	0.282	-0.193	0.597	-0.323	0.747
Geno.95	19	G	T	C	G	0.026	-0.597	1.826	-0.327	0.744
Geno.rare15	19	*	*	*	*	0.004	2.549	5.129	0.497	0.619
haplo.base18	19	A	T	T	G	0.637	NA	NA	NA	NA
Geno.48	20	C	T	G	A	0.029	1.692	1.640	1.032	0.303
Geno.77	20	T	C	A	G	0.277	-0.365	0.593	-0.615	0.539
Geno.85	20	T	C	G	A	0.044	0.185	1.331	0.139	0.890
Geno.rare16	20	*	*	*	*	0.013	-0.189	2.765	-0.068	0.945
haplo.base19	20	T	T	G	A	0.637	NA	NA	NA	NA
Geno.36	21	C	A	G	C	0.164	-0.039	0.740	-0.053	0.958
Geno.49	21	C	A	G	T	0.113	-0.984	0.858	-1.147	0.252
Geno.58	21	C	G	A	T	0.046	0.237	1.298	0.183	0.855
Geno.rare17	21	*	*	*	*	0.012	-0.767	2.957	-0.259	0.795
haplo.base20	21	T	G	A	T	0.665	NA	NA	NA	NA
Geno.37	22	A	G	C	A	0.164	-0.054	0.734	-0.073	0.942
Geno.59	22	A	G	T	A	0.113	-0.998	0.855	-1.168	0.243
Geno.78	22	G	A	T	G	0.030	0.102	1.560	0.065	0.948
Geno.rare18	22	*	*	*	*	0.012	-0.778	2.614	-0.298	0.766
haplo.base21	22	G	A	T	A	0.681	NA	NA	NA	NA
Geno.38	23	A	T	G	D	0.030	0.166	1.552	0.107	0.915
Geno.410	23	G	C	A	W	0.166	-0.151	0.735	-0.206	0.837
Geno.68	23	G	T	A	W	0.115	-1.114	0.852	-1.306	0.192
Geno.rare19	23	*	*	*	*	0.001	1.151	0.000	3.85E+15	0.000
haplo.base22	23	A	T	A	W	0.688	NA	NA	NA	NA
Geno.29	24	C	A	W	T	0.163	0.421	0.740	0.569	0.569
Geno.411	24	T	A	W	C	0.013	4.349	2.403	1.810	0.071
Geno.69	24	T	G	D	T	0.029	0.432	1.572	0.275	0.783
Geno.rare20	24	*	*	*	*	0.001	4.032	NA	NA	NA
haplo.base23	24	T	A	W	T	0.794	NA	NA	NA	NA
Geno.17	25	A	W	C	A	0.013	4.351	2.404	1.810	0.071
Geno.39	25	A	W	T	G	0.246	0.301	0.621	0.485	0.628
Geno.412	25	G	D	T	A	0.030	0.487	1.554	0.314	0.754
haplo.base24	25	A	W	T	A	0.711	NA	NA	NA	NA
Geno.18	26	D	T	A	A	0.029	0.168	1.613	0.104	0.917
Geno.413	26	W	C	A	A	0.013	4.478	2.454	1.825	0.068
Geno.86	26	W	T	G	A	0.196	0.325	0.686	0.473	0.636
Geno.96	26	W	T	G	C	0.050	-0.534	1.277	-0.418	0.676
Geno.rare21	26	*	*	*	*	0.003	-2.259	6.665	-0.339	0.735
haplo.base25	26	W	T	A	A	0.709	NA	NA	NA	NA
Geno.19	27	C	A	A	G	0.013	4.356	2.413	1.805	0.071
Geno.610	27	T	G	A	G	0.189	0.231	0.691	0.335	0.738
Geno.87	27	T	G	C	G	0.050	-0.633	1.262	-0.501	0.616
Geno.rare22	27	*	*	*	*	0.010	1.612	2.833	0.569	0.570
haplo.base26	27	T	A	A	G	0.738	NA	NA	NA	NA
Geno.110	28	A	A	G	D	0.023	-1.096	1.830	-0.599	0.550
Geno.611	28	G	A	G	W	0.189	0.102	0.693	0.148	0.882
Geno.97	28	G	C	G	W	0.051	-0.733	1.263	-0.580	0.562
Geno.rare23	28	*	*	*	*	0.010	1.467	2.838	0.517	0.606
haplo.base27	28	A	A	G	W	0.728	NA	NA	NA	NA
Geno.310	29	A	G	D	G	0.021	-1.159	1.923	-0.603	0.547
Geno.414	29	A	G	W	A	0.046	2.798	1.262	2.217	0.027
Geno.98	29	C	G	W	G	0.052	-0.686	1.225	-0.560	0.576

	Win	loc.1	loc.2	loc.3	loc.4	Hap.freq	Coef.	S.E.	Test Statistic	*P*-value
Geno.rare24	29	*	*	*	*	0.009	2.086	2.933	0.711	0.477
haplo.base28	29	A	G	W	G	0.872	NA	NA	NA	NA
Geno.311	30	G	D	G	C	0.021	-1.034	1.904	-0.543	0.587
Geno.415	30	G	W	A	C	0.046	2.831	1.259	2.250	0.025
Geno.rare25	30	*	*	*	*	0.011	1.011	2.615	0.387	0.699
haplo.base29	30	G	W	G	C	0.921	NA	NA	NA	NA
Geno.210	31	D	G	C	G	0.021	-1.058	1.907	-0.555	0.579
Geno.416	31	W	A	C	G	0.046	2.796	1.260	2.218	0.027
Geno.510	31	W	G	C	C	0.017	-1.494	2.062	-0.724	0.469
Geno.rare26	31	*	*	*	*	0.004	-2.590	4.857	-0.533	0.594
haplo.base30	31	W	G	C	G	0.911	NA	NA	NA	NA
Geno.111	32	A	C	G	A	0.048	2.749	1.238	2.221	0.027
Geno.312	32	G	C	C	A	0.017	-1.332	2.065	-0.645	0.519
Geno.511	32	G	C	G	G	0.117	0.784	0.858	0.914	0.361
Geno.rare27	32	*	*	*	*	0.002	-3.237	7.466	-0.434	0.665
haplo.base31	32	G	C	G	A	0.815	NA	NA	NA	NA
Geno.112	33	C	C	A	C	0.017	-1.329	2.104	-0.631	0.528
Geno.612	33	C	G	G	C	0.117	0.703	0.861	0.816	0.415
Geno.rare28	33	*	*	*	*	0.011	2.585	2.851	0.907	0.365
haplo.base32	33	C	G	A	C	0.856	NA	NA	NA	NA
Geno.211	34	C	A	C	G	0.017	-1.362	2.106	-0.647	0.518
Geno.512	34	G	A	C	A	0.046	-0.375	1.305	-0.287	0.774
Geno.99	34	G	G	C	G	0.117	0.727	0.863	0.842	0.400
Geno.rare29	34	*	*	*	*	0.009	3.951	3.087	1.280	0.201
haplo.base33	34	G	A	C	G	0.811	NA	NA	NA	NA
Geno.113	35	A	C	A	C	0.046	-0.404	1.311	-0.308	0.758
Geno.212	35	A	C	G	C	0.248	0.139	0.638	0.217	0.828
Geno.613	35	G	C	G	T	0.115	0.736	0.893	0.824	0.410
Geno.rare30	35	*	*	*	*	0.011	4.334	2.740	1.582	0.114
haplo.base34	35	A	C	G	T	0.580	NA	NA	NA	NA
Geno.213	36	C	A	C	G	0.046	-1.158	1.328	-0.872	0.384
Geno.417	36	C	G	C	G	0.247	-0.558	0.700	-0.797	0.426
Geno.513	36	C	G	T	C	0.313	-1.531	0.644	-2.378	0.018
Geno.rare31	36	*	*	*	*	0.012	1.451	2.665	0.545	0.586
haplo.base35	36	C	G	T	G	0.383	NA	NA	NA	NA
Geno.214	37	A	C	G	T	0.046	-1.238	1.320	-0.937	0.349
Geno.514	37	G	C	G	T	0.240	-0.690	0.703	-0.981	0.327
Geno.614	37	G	T	C	T	0.312	-1.584	0.638	-2.483	0.013
Geno.rare32	37	*	*	*	*	0.010	-0.154	2.826	-0.054	0.957
haplo.base36	37	G	T	G	T	0.392	NA	NA	NA	NA
Geno.515	38	C	G	T	G	0.281	-0.581	0.694	-0.837	0.403
Geno.79	38	T	C	T	G	0.313	-1.321	0.659	-2.004	0.045
Geno.88	38	T	G	T	A	0.052	2.381	1.292	1.843	0.066
Geno.rare33	38	*	*	*	*	0.015	0.633	2.570	0.246	0.806
haplo.base37	38	T	G	T	G	0.339	NA	NA	NA	NA
Geno.114	39	C	T	G	A	0.311	-1.056	0.600	-1.759	0.079
Geno.615	39	G	T	A	A	0.057	2.643	1.173	2.254	0.024
Geno.910	39	G	T	G	C	0.086	0.080	1.021	0.078	0.938
Geno.rare34	39	*	*	*	*	0.012	0.609	2.893	0.211	0.833
haplo.base38	39	G	T	G	A	0.534	NA	NA	NA	NA
Geno.418	40	T	A	A	C	0.052	3.130	1.300	2.407	0.016
Geno.89	40	T	G	A	G	0.022	-0.747	1.880	-0.397	0.691
Geno.911	40	T	G	C	C	0.087	0.425	1.008	0.421	0.674
Geno.rare35	40	*	*	*	*	0.011	2.155	3.572	0.603	0.546
haplo.base39	40	T	G	A	C	0.827	NA	NA	NA	NA
Geno.115	41	A	A	C	W	0.054	3.683	1.201	3.066	0.002
Geno.616	41	G	A	G	W	0.022	-0.027	1.870	-0.014	0.988
Geno.810	41	G	C	C	W	0.089	0.623	0.957	0.651	0.515
Geno.rare36	41	*	*	*	*	0.004	-10.028	0.008	-1.32E+03	0.000
haplo.base40	41	G	A	C	W	0.831	NA	NA	NA	NA
Geno.215	42	A	C	W	A	0.111	0.442	0.837	0.528	0.598
Geno.419	42	A	G	W	G	0.023	-1.124	1.800	-0.624	0.533
Geno.710	42	C	C	W	G	0.091	0.359	0.955	0.376	0.707
Geno.rare37	42	*	*	*	*	0.002	-5.604	0.000	-4.89E+15	0.000
haplo.base41	42	A	C	W	G	0.773	NA	NA	NA	NA
Geno.216	43	C	W	A	A	0.111	0.440	0.845	0.521	0.603
Geno.516	43	C	W	G	G	0.203	0.218	0.667	0.327	0.744
Geno.617	43	G	W	G	A	0.023	-1.136	1.793	-0.633	0.527
Geno.rare38	43	*	*	*	*	0.001	-5.503	7.314	-0.752	0.452
haplo.base42	43	C	W	G	A	0.661	NA	NA	NA	NA
Geno.217	44	W	A	A	C	0.111	0.420	0.847	0.496	0.620
Geno.618	44	W	G	A	T	0.106	-0.248	0.893	-0.278	0.781
Geno.711	44	W	G	G	C	0.202	0.247	0.688	0.359	0.720
Geno.rare39	44	*	*	*	*	0.003	-7.715	6.749	-1.143	0.253
haplo.base43	44	W	G	A	C	0.579	NA	NA	NA	NA

Table A2.16. Continued

	Win	loc.1	loc.2	loc.3	loc.4	Hap.freq	Coef.	S.E.	Test Statistic	*P*-value
Geno.218	45	A	A	C	W	0.111	0.412	0.848	0.486	0.627
Geno.517	45	G	A	C	D	0.022	-1.012	1.815	-0.557	0.577
Geno.712	45	G	A	T	W	0.105	-0.156	0.913	-0.171	0.864
Geno.912	45	G	G	C	W	0.201	0.287	0.695	0.414	0.679
Geno.rare40	45	*	*	*	*	0.001	-14.655	10.012	-1.464	0.144
haplo.base44	45	G	A	C	W	0.558	NA	NA	NA	NA
Geno.219	46	A	C	D	C	0.022	-0.969	1.810	-0.535	0.593
Geno.313	46	A	C	W	A	0.031	1.749	1.577	1.109	0.268
Geno.619	46	A	T	W	C	0.105	-0.079	0.906	-0.087	0.931
Geno.913	46	G	C	W	C	0.201	0.324	0.689	0.471	0.638
Geno.rare41	46	*	*	*	*	0.002	-15.230	9.055	-1.682	0.093
haplo.base45	46	A	C	W	C	0.639	NA	NA	NA	NA
Geno.220	47	C	D	C	G	0.022	-0.783	1.808	-0.433	0.665
Geno.314	47	C	W	A	G	0.031	1.950	1.577	1.236	0.217
Geno.420	47	C	W	C	A	0.033	2.932	1.513	1.938	0.053
Geno.713	47	T	W	C	G	0.107	-0.280	0.850	-0.329	0.742
haplo.base46	47	C	W	C	G	0.807	NA	NA	NA	NA
Geno.221	48	D	C	G	T	0.022	-0.732	1.803	-0.406	0.685
Geno.315	48	W	A	G	T	0.031	1.989	1.572	1.265	0.206
Geno.421	48	W	C	A	T	0.033	2.989	1.505	1.986	0.047
Geno.rare42	48	*	*	*	*	0.006	0.298	3.475	0.086	0.932
haplo.base47	48	W	C	G	T	0.908	NA	NA	NA	NA
Geno.222	49	A	G	T	T	0.031	1.927	1.580	1.220	0.223
Geno.422	49	C	A	T	T	0.033	2.996	1.512	1.981	0.048
Geno.620	49	C	G	T	C	0.192	-0.160	0.702	-0.228	0.820
Geno.rare43	49	*	*	*	*	0.006	0.361	3.480	0.104	0.917
haplo.base48	49	C	G	T	T	0.738	NA	NA	NA	NA
Geno.223	50	A	T	T	D	0.033	2.593	1.504	1.725	0.085
Geno.518	50	G	T	C	D	0.193	-0.492	0.706	-0.696	0.486
Geno.811	50	G	T	T	W	0.088	-2.442	0.967	-2.526	0.012
Geno.rare44	50	*	*	*	*	0.006	-0.655	3.507	-0.187	0.852
haplo.base49	50	G	T	T	D	0.680	NA	NA	NA	NA
Geno.224	51	T	C	D	C	0.141	-0.303	0.803	-0.377	0.706
Geno.316	51	T	C	D	T	0.052	-1.867	1.329	-1.405	0.161
Geno.519	51	T	T	D	C	0.103	-0.764	0.948	-0.806	0.420
Geno.714	51	T	T	W	T	0.088	-2.636	0.973	-2.709	0.007
Geno.rare45	51	*	*	*	*	0.006	-1.028	3.505	-0.293	0.769
haplo.base50	51	T	T	D	T	0.610	NA	NA	NA	NA
Geno.116	52	C	D	C	A	0.141	-0.515	0.826	-0.624	0.533
Geno.225	52	C	D	T	A	0.052	-2.126	1.348	-1.577	0.115
Geno.423	52	T	D	C	A	0.103	-0.917	0.962	-0.954	0.341
Geno.715	52	T	D	T	G	0.113	-0.896	0.865	-1.036	0.301
Geno.914	52	T	W	T	A	0.094	-2.737	0.965	-2.836	0.005
haplo.base51	52	T	D	T	A	0.497	NA	NA	NA	NA
Geno.117	53	D	C	A	A	0.245	-0.509	0.658	-0.774	0.439
Geno.520	53	D	T	A	C	0.034	0.138	1.399	0.099	0.921
Geno.621	53	D	T	G	A	0.113	-0.734	0.866	-0.848	0.397
Geno.812	53	W	T	A	A	0.094	-2.565	0.964	-2.661	0.008
haplo.base52	53	D	T	A	A	0.513	NA	NA	NA	NA
Geno.118	54	C	A	A	C	0.245	-0.234	0.650	-0.360	0.719
Geno.622	54	T	A	A	G	0.035	-2.119	1.482	-1.430	0.153
Geno.716	54	T	A	C	C	0.034	0.339	1.407	0.241	0.810
Geno.813	54	T	G	A	C	0.113	-0.530	0.867	-0.611	0.541
haplo.base53	54	T	A	A	C	0.572	NA	NA	NA	NA
Geno.226	55	A	A	C	T	0.051	1.156	1.237	0.934	0.351
Geno.317	55	A	A	G	A	0.034	-1.930	1.488	-1.297	0.195
Geno.521	55	A	C	C	A	0.034	0.567	1.404	0.404	0.686
Geno.717	55	G	A	C	A	0.113	-0.394	0.838	-0.470	0.638
Geno.rare46	55	*	*	*	*	0.002	-3.693	8.265	-0.447	0.655
haplo.base54	55	A	A	C	A	0.766	NA	NA	NA	NA
Geno.227	56	A	C	A	G	0.075	-0.716	1.078	-0.664	0.507
Geno.318	56	A	C	T	C	0.051	1.132	1.243	0.911	0.363
Geno.424	56	A	G	A	C	0.034	-1.954	1.491	-1.310	0.190
Geno.718	56	C	C	A	C	0.033	0.547	1.408	0.389	0.698
Geno.rare47	56	*	*	*	*	0.002	-3.695	7.851	-0.471	0.638
haplo.base55	56	A	C	A	C	0.805	NA	NA	NA	NA
Geno.228	57	C	A	C	G	0.119	-0.525	0.831	-0.632	0.528
Geno.425	57	C	A	G	G	0.075	-0.878	1.080	-0.813	0.417
Geno.522	57	C	T	C	A	0.053	0.923	1.225	0.753	0.451
Geno.719	57	G	A	C	A	0.034	-2.103	1.480	-1.421	0.156
Geno.rare48	57	*	*	*	*	0.002	0.425	7.528	0.056	0.955
haplo.base56	57	C	A	C	A	0.717	NA	NA	NA	NA
Geno.229	58	A	C	A	T	0.224	-0.287	0.691	-0.415	0.678
Geno.319	58	A	C	G	C	0.110	-0.604	0.909	-0.664	0.507
Geno.720	58	A	G	G	T	0.074	-0.973	1.123	-0.867	0.386

Table A2.16. Continued

	Win	loc.1	loc.2	loc.3	loc.4	Hap.freq	Coef.	S.E.	Test Statistic	*P*-value
Geno.915	58	T	C	A	T	0.052	0.760	1.244	0.610	0.542
Geno.rare49	58	*	*	*	*	0.013	1.621	3.625	0.447	0.655
haplo.base57	58	A	C	A	C	0.527	NA	NA	NA	NA
Geno.230	59	C	A	C	G	0.067	-0.570	1.207	-0.473	0.637
Geno.320	59	C	A	T	A	0.261	-0.021	0.671	-0.031	0.975
Geno.426	59	C	A	T	G	0.017	-2.346	2.595	-0.904	0.366
Geno.523	59	C	G	C	A	0.108	-0.581	0.899	-0.646	0.518
Geno.131	59	G	G	T	G	0.074	-1.064	1.151	-0.924	0.356
Geno.rare50	59	*	*	*	*	0.013	-0.344	3.035	-0.113	0.910
haplo.base58	59	C	A	C	A	0.458	NA	NA	NA	NA
Geno.231	60	A	C	G	G	0.069	-0.949	1.263	-0.752	0.453
Geno.321	60	A	T	A	G	0.262	-0.106	0.676	-0.157	0.876
Geno.427	60	A	T	G	G	0.021	-1.358	2.494	-0.545	0.586
Geno.524	60	G	C	A	G	0.111	-0.590	0.907	-0.650	0.516
Geno.916	60	G	T	G	G	0.075	-0.639	1.080	-0.592	0.554
Geno.rare51	60	*	*	*	*	0.006	-1.694	5.690	-0.298	0.766
haplo.base59	60	A	C	A	G	0.456	NA	NA	NA	NA
Geno.428	61	C	G	G	T	0.073	-0.993	1.192	-0.833	0.405
Geno.525	61	T	A	G	C	0.046	0.199	1.306	0.152	0.879
Geno.623	61	T	A	G	T	0.218	-0.052	0.719	-0.072	0.943
Geno.917	61	T	G	G	T	0.094	-0.716	1.021	-0.701	0.483
Geno.rare52	61	*	*	*	*	0.008	0.684	3.281	0.209	0.835
haplo.base60	61	C	A	G	T	0.560	NA	NA	NA	NA
Geno.119	62	A	G	C	G	0.053	0.111	1.212	0.091	0.927
Geno.232	62	A	G	T	G	0.293	-0.665	0.644	-1.032	0.303
Geno.624	62	G	G	T	G	0.133	-1.088	0.831	-1.310	0.191
Geno.721	62	G	G	T	T	0.036	-0.662	1.584	-0.418	0.676
Geno.rare53	62	*	*	*	*	0.002	-3.207	7.358	-0.436	0.663
haplo.base61	62	A	G	T	T	0.484	NA	NA	NA	NA
Geno.429	63	G	C	G	C	0.053	0.260	1.220	0.213	0.832
Geno.814	63	G	T	G	C	0.427	-0.637	0.569	-1.120	0.263
Geno.918	63	G	T	T	A	0.071	0.845	1.073	0.787	0.431
Geno.rare54	63	*	*	*	*	0.001	-3.178	7.346	-0.433	0.665
haplo.base62	63	G	T	T	C	0.448	NA	NA	NA	NA
Geno.322	64	C	G	C	W	0.053	0.169	1.218	0.139	0.889
Geno.722	64	T	G	C	I	0.043	1.975	1.333	1.482	0.139
Geno.815	64	T	G	C	W	0.385	-1.019	0.594	-1.716	0.087
Geno.919	64	T	T	A	W	0.071	0.837	1.070	0.782	0.434
haplo.base63	64	T	T	C	W	0.449	NA	NA	NA	NA
Geno.120	65	G	C	I	T	0.043	2.957	1.386	2.133	0.033
Geno.233	65	G	C	W	C	0.016	0.863	2.760	0.313	0.755
Geno.526	65	T	A	W	T	0.071	1.828	1.065	1.716	0.086
Geno.625	65	T	C	W	C	0.174	1.600	0.780	2.051	0.041
Geno.723	65	T	C	W	T	0.274	0.577	0.667	0.865	0.387
haplo.base64	65	G	C	W	T	0.422	NA	NA	NA	NA
Geno.430	66	A	W	T	C	0.066	1.599	1.060	1.508	0.132
Geno.816	66	C	I	T	T	0.042	2.388	1.364	1.751	0.080
Geno.920	66	C	W	C	C	0.034	2.120	1.585	1.338	0.181
Geno.10	66	C	W	C	T	0.156	1.039	0.761	1.365	0.173
Geno.1110	66	C	W	T	C	0.011	-5.218	2.843	-1.835	0.067
Geno.rare55	66	*	*	*	*	0.007	2.107	3.512	0.600	0.549
haplo.base65	66	C	W	T	T	0.685	NA	NA	NA	NA
Geno.234	67	I	T	T	C	0.043	2.367	1.349	1.755	0.080
Geno.323	67	W	C	C	C	0.035	2.485	1.753	1.418	0.157
Geno.431	67	W	C	T	C	0.155	0.877	0.824	1.065	0.287
Geno.626	67	W	T	C	C	0.076	0.190	1.142	0.166	0.868
Geno.921	67	W	T	T	G	0.150	-0.209	0.789	-0.265	0.791
haplo.base66	67	W	T	T	C	0.541	NA	NA	NA	NA
Geno.121	68	C	C	C	G	0.035	2.173	1.755	1.238	0.216
Geno.235	68	C	T	C	G	0.154	0.623	0.823	0.757	0.449
Geno.432	68	T	C	C	G	0.075	0.128	1.152	0.111	0.912
Geno.527	68	T	T	C	A	0.058	0.684	1.159	0.590	0.555
Geno.817	68	T	T	G	G	0.150	-0.473	0.785	-0.602	0.547
Geno.rare56	68	*	*	*	*	0.001	25.846	NA	NA	NA
haplo.base67	68	T	T	C	G	0.528	NA	NA	NA	NA
Geno.236	69	C	C	G	G	0.110	0.595	0.849	0.701	0.484
Geno.324	69	T	C	A	A	0.055	0.510	1.241	0.411	0.681
Geno.627	69	T	G	G	G	0.148	-0.596	0.790	-0.754	0.451
Geno.rare57	69	*	*	*	*	0.003	7.579	10.327	0.734	0.463
haplo.base68	69	T	C	G	G	0.684	NA	NA	NA	NA
Geno.122	70	C	A	A	A	0.057	0.592	1.184	0.500	0.617
Geno.528	70	C	G	G	A	0.315	0.632	0.614	1.029	0.304
Geno.818	70	G	G	G	A	0.149	-0.448	0.788	-0.569	0.569
Geno.rare58	70	*	*	*	*	0.003	9.696	6.840	1.418	0.157
haplo.base69	70	C	G	G	T	0.476	NA	NA	NA	NA

Table A2.16. Continued

	Win	loc.1	loc.2	loc.3	loc.4	Hap.freq	Coef.	S.E.	Test Statistic	*P*-value
Geno.237	71	A	A	A	G	0.058	0.861	1.167	0.738	0.461
Geno.529	71	G	G	A	A	0.145	-0.200	0.818	-0.244	0.807
Geno.628	71	G	G	A	G	0.323	0.497	0.626	0.793	0.428
Geno.rare59	71	*	*	*	*	0.003	3.959	7.444	0.532	0.595
haplo.base70	71	G	G	T	G	0.472	NA	NA	NA	NA
Geno.123	72	A	A	G	C	0.057	0.864	1.181	0.732	0.464
Geno.325	72	G	A	A	C	0.144	-0.207	0.826	-0.251	0.802
Geno.433	72	G	A	G	A	0.135	-0.280	0.822	-0.341	0.733
Geno.530	72	G	A	G	C	0.188	1.134	0.756	1.500	0.134
Geno.rare60	72	*	*	*	*	0.004	1.268	4.816	0.263	0.792
haplo.base71	72	G	T	G	A	0.472	NA	NA	NA	NA
Geno.238	73	A	A	C	G	0.142	-0.237	0.832	-0.285	0.776
Geno.326	73	A	G	A	G	0.135	-0.321	0.825	-0.389	0.697
Geno.434	73	A	G	C	G	0.246	0.991	0.681	1.455	0.146
Geno.724	73	T	G	A	A	0.016	-1.621	2.175	-0.746	0.456
Geno.rare61	73	*	*	*	*	0.005	1.246	5.656	0.220	0.826
haplo.base72	73	T	G	A	G	0.456	NA	NA	NA	NA
Geno.629	74	A	C	G	G	0.145	-0.120	0.822	-0.146	0.884
Geno.725	74	G	A	A	G	0.016	-1.441	2.165	-0.665	0.506
Geno.819	74	G	A	G	A	0.012	3.967	2.470	1.606	0.109
Geno.1111	74	G	C	G	G	0.248	1.070	0.666	1.607	0.108
Geno.rare62	74	*	*	*	*	0.003	-0.356	6.263	-0.057	0.955
haplo.base73	74	G	A	G	G	0.576	NA	NA	NA	NA
Geno.124	75	A	A	G	C	0.016	-1.540	2.162	-0.712	0.477
Geno.239	75	A	G	A	C	0.012	3.789	2.465	1.537	0.125
Geno.531	75	C	G	G	C	0.393	0.548	0.541	1.014	0.311
Geno.rare63	75	*	*	*	*	0.007	-4.828	3.004	-1.607	0.108
haplo.base74	75	A	G	G	C	0.573	NA	NA	NA	NA
Geno.327	76	A	G	C	A	0.016	-1.809	2.148	-0.842	0.400
Geno.435	76	G	A	C	A	0.012	3.471	2.457	1.413	0.158
Geno.726	76	G	G	C	G	0.011	-0.205	2.623	-0.078	0.938
Geno.rare64	76	*	*	*	*	0.007	-4.928	2.999	-1.643	0.101
haplo.base75	76	G	G	C	A	0.954	NA	NA	NA	NA
Geno.125	77	A	C	A	T	0.012	3.916	2.467	1.587	0.113
Geno.240	77	G	C	A	C	0.288	0.880	0.598	1.471	0.142
Geno.rare65	77	*	*	*	*	0.018	-2.020	2.000	-1.010	0.313
haplo.base76	77	G	C	A	T	0.683	NA	NA	NA	NA
Geno.126	78	C	A	C	A	0.147	1.745	0.801	2.178	0.030
Geno.241	78	C	A	C	G	0.140	-0.190	0.793	-0.239	0.811
Geno.436	78	C	A	T	G	0.012	0.652	2.533	0.257	0.797
Geno.rare66	78	*	*	*	*	0.018	-2.014	2.104	-0.957	0.339
haplo.base77	78	C	A	T	A	0.683	NA	NA	NA	NA
Geno.127	79	A	C	A	A	0.143	2.649	0.857	3.093	0.002
Geno.328	79	A	C	G	A	0.143	0.292	0.813	0.359	0.719
Geno.532	79	A	T	A	G	0.245	1.227	0.662	1.852	0.064
Geno.630	79	A	T	G	A	0.012	1.331	2.533	0.526	0.599
Geno.820	79	G	T	A	A	0.011	0.183	2.628	0.070	0.944
Geno.rare67	79	*	*	*	*	0.004	-7.450	4.981	-1.496	0.135
haplo.base78	79	A	T	A	A	0.442	NA	NA	NA	NA
Geno.128	80	C	A	A	C	0.142	3.021	0.867	3.486	0.001
Geno.437	80	C	G	A	C	0.143	0.482	0.812	0.594	0.553
Geno.727	80	T	A	A	T	0.022	4.114	1.959	2.100	0.036
Geno.821	80	T	A	G	C	0.246	1.422	0.662	2.148	0.032
Geno.922	80	T	G	A	C	0.012	1.611	2.525	0.638	0.524
Geno.rare68	80	*	*	*	*	0.005	-9.442	4.277	-2.207	0.028
haplo.base79	80	T	A	A	C	0.430	NA	NA	NA	NA
Geno.129	81	A	A	C	A	0.095	1.343	1.045	1.285	0.199
Geno.438	81	A	A	T	C	0.022	3.605	1.920	1.877	0.061
Geno.631	81	A	G	C	C	0.249	0.753	0.653	1.152	0.250
Geno.923	81	G	A	C	A	0.131	-0.016	0.835	-0.019	0.985
Geno.101	81	G	A	C	C	0.023	0.339	1.990	0.170	0.865
Geno.rare69	81	*	*	*	*	0.003	-7.272	6.251	-1.163	0.245
haplo.base80	81	A	A	C	C	0.477	NA	NA	NA	NA
Geno.130	82	A	C	A	G	0.224	0.532	0.678	0.785	0.433
Geno.632	82	A	T	C	G	0.022	2.986	1.833	1.629	0.104
Geno.822	82	G	C	C	A	0.031	2.126	1.566	1.358	0.175
Geno.924	82	G	C	C	G	0.216	0.522	0.677	0.770	0.441
Geno.rare70	82	*	*	*	*	0.004	2.441	0.008	305.100	0.000
haplo.base81	82	A	C	C	G	0.502	NA	NA	NA	NA
Geno.242	83	C	A	G	C	0.227	0.229	0.669	0.343	0.732
Geno.329	83	C	C	A	C	0.033	2.153	1.530	1.407	0.160
Geno.633	83	C	C	G	G	0.139	-0.425	0.802	-0.531	0.596
Geno.823	83	T	C	G	C	0.023	2.265	1.770	1.280	0.201
haplo.base82	83	C	C	G	C	0.577	NA	NA	NA	NA
Geno.243	84	A	G	C	A	0.227	0.201	0.676	0.297	0.767

Table A2.16. Continued

	Win	loc.1	loc.2	loc.3	loc.4	Hap.freq	Coef.	S.E.	Test Statistic	*P*-value
Geno.439	84	C	A	C	C	0.033	2.074	1.526	1.359	0.174
Geno.728	84	C	G	C	C	0.051	0.692	1.241	0.558	0.577
Geno.824	84	C	G	G	A	0.139	-0.435	0.808	-0.538	0.590
haplo.base83	84	C	G	C	A	0.550	NA	NA	NA	NA
Geno.132	85	A	C	C	G	0.033	2.038	1.514	1.347	0.178
Geno.533	85	G	C	C	G	0.051	0.658	1.224	0.538	0.591
Geno.729	85	G	G	A	G	0.138	-0.534	0.775	-0.689	0.491
Geno.rare71	85	*	*	*	*	0.009	1.320	2.889	0.457	0.648
haplo.base84	85	G	C	A	G	0.770	NA	NA	NA	NA
Geno.244	86	C	A	G	C	0.044	3.526	1.279	2.757	0.006
Geno.534	86	C	C	G	T	0.082	1.464	0.977	1.499	0.134
Geno.730	86	G	A	G	T	0.138	-0.314	0.774	-0.406	0.685
Geno.rare72	86	*	*	*	*	0.009	1.702	2.878	0.592	0.554
haplo.base85	86	C	A	G	T	0.727	NA	NA	NA	NA
Geno.330	87	A	G	C	G	0.044	3.813	1.294	2.946	0.003
Geno.440	87	A	G	T	A	0.314	0.526	0.628	0.838	0.402
Geno.731	87	C	G	T	A	0.081	1.721	1.008	1.707	0.088
Geno.rare73	87	*	*	*	*	0.011	1.428	2.721	0.525	0.600
haplo.base86	87	A	G	T	G	0.550	NA	NA	NA	NA
Geno.331	88	G	C	G	G	0.044	3.889	1.294	3.006	0.003
Geno.535	88	G	T	A	G	0.395	0.835	0.578	1.446	0.149
Geno.rare74	88	*	*	*	*	0.010	3.317	2.692	1.232	0.218
haplo.base87	88	G	T	G	G	0.551	NA	NA	NA	NA
Geno.245	89	C	G	G	G	0.043	3.664	1.281	2.860	0.004
Geno.441	89	T	A	G	C	0.395	0.770	0.571	1.349	0.178
Geno.rare75	89	*	*	*	*	0.002	9.593	7.185	1.335	0.182
haplo.base88	89	T	G	G	C	0.560	NA	NA	NA	NA
Geno.246	90	A	G	C	A	0.393	0.600	0.601	0.999	0.318
Geno.634	90	G	G	C	G	0.093	-1.270	0.982	-1.293	0.196
Geno.732	90	G	G	G	A	0.042	3.997	1.305	3.064	0.002
Geno.rare76	90	*	*	*	*	0.004	3.171	5.469	0.580	0.562
haplo.base89	90	G	G	C	A	0.468	NA	NA	NA	NA
Geno.247	91	G	C	A	A	0.086	0.999	0.981	1.018	0.309
Geno.442	91	G	C	G	G	0.096	-1.634	0.928	-1.761	0.079
Geno.536	91	G	G	A	G	0.042	3.781	1.276	2.964	0.003
Geno.rare77	91	*	*	*	*	0.001	10.758	7.192	1.496	0.135
haplo.base90	91	G	C	A	G	0.774	NA	NA	NA	NA
Geno.133	92	C	A	A	G	0.086	1.004	0.984	1.020	0.308
Geno.248	92	C	A	G	A	0.024	1.429	1.783	0.802	0.423
Geno.537	92	C	G	G	G	0.096	-1.633	0.933	-1.751	0.080
Geno.635	92	G	A	G	G	0.042	3.822	1.280	2.986	0.003
haplo.base91	92	C	A	G	G	0.752	NA	NA	NA	NA
Geno.332	93	A	A	G	T	0.086	0.985	0.990	0.995	0.320
Geno.443	93	A	G	A	T	0.024	1.439	1.793	0.803	0.422
Geno.538	93	A	G	G	C	0.056	2.762	1.133	2.439	0.015
Geno.102	93	G	G	G	T	0.094	-1.618	0.964	-1.678	0.094
Geno.rare78	93	*	*	*	*	0.002	-0.054	7.510	-0.007	0.994
haplo.base92	93	A	G	G	T	0.738	NA	NA	NA	NA
Geno.134	94	A	G	T	C	0.085	0.988	0.991	0.997	0.319
Geno.249	94	G	A	T	T	0.024	1.471	1.761	0.835	0.404
Geno.333	94	G	G	C	C	0.058	2.737	1.107	2.473	0.014
Geno.636	94	G	G	T	T	0.132	-1.273	0.770	-1.655	0.098
haplo.base93	94	G	G	T	C	0.701	NA	NA	NA	NA
Geno.135	95	A	T	T	G	0.024	1.419	1.751	0.811	0.418
Geno.250	95	G	C	C	G	0.057	2.910	1.105	2.634	0.009
Geno.637	95	G	T	C	T	0.020	1.766	1.910	0.924	0.356
Geno.733	95	G	T	T	G	0.132	-1.338	0.762	-1.756	0.079
Geno.rare79	95	*	*	*	*	0.001	-21.240	NA	NA	NA
haplo.base94	95	G	T	C	G	0.766	NA	NA	NA	NA
Geno.136	96	C	C	G	A	0.056	2.675	1.129	2.370	0.018
Geno.734	96	T	C	T	A	0.018	0.867	2.085	0.416	0.678
Geno.925	96	T	T	G	A	0.157	-0.934	0.708	-1.320	0.187
Geno.rare80	96	*	*	*	*	0.006	-1.051	4.586	-0.229	0.819
haplo.base95	96	T	C	G	A	0.763	NA	NA	NA	NA
Geno.137	97	C	G	A	D	0.148	-0.622	0.778	-0.800	0.424
Geno.539	97	C	T	A	W	0.020	0.218	1.947	0.112	0.911
Geno.825	97	T	G	A	W	0.152	-1.203	0.738	-1.629	0.104
Geno.rare81	97	*	*	*	*	0.009	-0.713	3.337	-0.214	0.831
haplo.base96	97	C	G	A	W	0.671	NA	NA	NA	NA
Geno.251	98	G	A	D	T	0.152	-0.306	0.747	-0.409	0.683
Geno.334	98	G	A	W	G	0.083	0.633	0.968	0.654	0.514
Geno.826	98	T	A	W	T	0.020	0.506	1.940	0.261	0.794
Geno.rare82	98	*	*	*	*	0.005	0.205	4.410	0.046	0.963
haplo.base97	98	G	A	W	T	0.740	NA	NA	NA	NA
Geno.252	99	A	D	T	D	0.156	-0.249	0.725	-0.343	0.732

Table A2.16. Continued

	Win	loc.1	loc.2	loc.3	loc.4	Hap.freq	Coef.	S.E.	Test Statistic	*P*-value
Geno.444	99	A	W	G	W	0.084	0.604	0.967	0.624	0.533
Geno.rare83	99	*	*	*	*	0.009	-1.876	2.878	-0.652	0.515
haplo.base98	99	A	W	T	W	0.751	NA	NA	NA	NA
Geno.335	100	D	T	D	T	0.155	-0.093	0.727	-0.128	0.898
Geno.540	100	W	G	W	T	0.084	0.622	0.965	0.644	0.520
Geno.735	100	W	T	W	G	0.011	2.818	2.813	1.002	0.317
Geno.rare84	100	*	*	*	*	0.005	-7.228	3.928	-1.840	0.066
haplo.base99	100	W	T	W	T	0.745	NA	NA	NA	NA
Geno.336	101	G	W	T	G	0.083	0.687	0.970	0.708	0.479
Geno.638	101	T	D	T	G	0.158	-0.165	0.730	-0.226	0.821
Geno.736	101	T	W	G	G	0.011	1.273	2.839	0.448	0.654
Geno.827	101	T	W	T	A	0.015	0.324	2.205	0.147	0.883
haplo.base100	101	T	W	T	G	0.731	NA	NA	NA	NA
Geno.337	102	D	T	G	C	0.157	-0.327	0.722	-0.453	0.651
Geno.541	102	W	G	G	C	0.012	-0.230	2.628	-0.088	0.930
Geno.639	102	W	T	A	C	0.016	0.226	2.170	0.104	0.917
Geno.rare85	102	*	*	*	*	0.002	12.026	0.000	1.05E+16	0.000
haplo.base101	102	W	T	G	C	0.814	NA	NA	NA	NA
Geno.138	103	G	G	C	G	0.012	0.729	2.475	0.295	0.768
Geno.253	103	T	A	C	G	0.016	0.282	2.177	0.130	0.897
Geno.rare86	103	*	*	*	*	0.002	9.389	7.270	1.292	0.197
haplo.base102	103	T	G	C	G	0.970	NA	NA	NA	NA
Geno.139	104	A	C	G	G	0.016	0.242	2.173	0.111	0.911
Geno.rare87	104	*	*	*	*	0.003	2.778	5.162	0.538	0.591
haplo.base103	104	G	C	G	G	0.981	NA	NA	NA	NA
Geno.rare88	105	*	*	*	*	0.007	4.641	3.452	1.345	0.179
haplo.base104	105	C	G	G	G	0.993	NA	NA	NA	NA
Geno.rare89	106	*	*	*	*	0.007	4.640	3.451	1.345	0.179
haplo.base105	106	G	G	G	A	0.993	NA	NA	NA	NA
Geno.445	107	G	G	A	G	0.237	0.489	0.640	0.764	0.445
Geno.rare90	107	*	*	*	*	0.006	4.286	3.455	1.241	0.215
haplo.base106	107	G	G	A	A	0.757	NA	NA	NA	NA
Geno.338	108	G	A	A	A	0.341	-0.044	0.641	-0.069	0.945
Geno.542	108	G	A	G	A	0.215	0.278	0.733	0.380	0.704
Geno.640	108	G	A	G	T	0.022	2.144	2.447	0.876	0.381
Geno.rare91	108	*	*	*	*	0.005	7.658	3.930	1.949	0.052
haplo.base107	108	G	A	A	T	0.417	NA	NA	NA	NA
Geno.140	109	A	A	A	C	0.341	0.029	0.641	0.045	0.964
Geno.339	109	A	G	A	C	0.115	-0.436	0.966	-0.452	0.652
Geno.446	109	A	G	A	T	0.103	0.928	0.941	0.986	0.324
Geno.543	109	A	G	T	C	0.023	2.154	2.443	0.882	0.378
Geno.rare92	109	*	*	*	*	0.001	9.799	7.270	1.348	0.178
haplo.base108	109	A	A	T	C	0.417	NA	NA	NA	NA
Geno.340	110	A	T	C	A	0.327	-0.464	0.690	-0.671	0.502
Geno.447	110	A	T	C	G	0.089	1.343	1.017	1.321	0.187
Geno.544	110	G	A	C	A	0.113	-0.629	1.067	-0.590	0.556
Geno.737	110	G	A	T	A	0.103	0.827	0.993	0.832	0.405
Geno.828	110	G	T	C	A	0.022	2.425	2.603	0.932	0.352
Geno.rare93	110	*	*	*	*	0.004	4.649	4.954	0.938	0.348
haplo.base109	110	A	A	C	A	0.343	NA	NA	NA	NA
Geno.545	111	A	T	A	G	0.104	1.108	0.951	1.166	0.244
Geno.738	111	T	C	A	G	0.343	-0.152	0.627	-0.243	0.808
Geno.829	111	T	C	G	G	0.092	1.502	0.981	1.530	0.126
Geno.rare94	111	*	*	*	*	0.015	-0.468	2.331	-0.201	0.841
haplo.base110	111	A	C	A	G	0.447	NA	NA	NA	NA
Geno.141	112	C	A	A	C	0.013	-1.331	2.396	-0.555	0.579
Geno.448	112	C	G	G	C	0.093	1.739	0.940	1.850	0.065
Geno.641	112	T	A	G	C	0.101	1.225	0.914	1.340	0.181
Geno.rare95	112	*	*	*	*	0.009	4.345	2.820	1.541	0.124
haplo.base111	112	C	A	G	C	0.784	NA	NA	NA	NA
Geno.142	113	A	A	C	T	0.013	-1.596	2.387	-0.669	0.504
Geno.341	113	A	G	C	T	0.349	-0.372	0.593	-0.628	0.530
Geno.642	113	G	G	C	T	0.094	1.449	0.951	1.523	0.128
Geno.rare96	113	*	*	*	*	0.009	4.032	2.798	1.441	0.150
haplo.base112	113	A	G	C	C	0.535	NA	NA	NA	NA
Geno.254	114	A	C	T	A	0.013	-1.928	2.396	-0.805	0.421
Geno.449	114	G	C	C	T	0.085	-1.343	1.034	-1.299	0.194
Geno.546	114	G	C	T	A	0.443	-0.200	0.572	-0.350	0.726
Geno.rare97	114	*	*	*	*	0.009	3.508	2.813	1.247	0.213
haplo.base113	114	G	C	C	A	0.450	NA	NA	NA	NA
Geno.143	115	C	C	A	G	0.450	0.266	0.572	0.465	0.642
Geno.255	115	C	C	T	G	0.085	-1.094	1.018	-1.075	0.283
Geno.rare98	115	*	*	*	*	0.015	2.331	2.211	1.054	0.292
haplo.base114	115	C	T	A	G	0.450	NA	NA	NA	NA
Geno.342	116	C	T	G	T	0.085	-1.449	1.030	-1.407	0.160

Table A2.16. Continued

	Win	loc.1	loc.2	loc.3	loc.4	Hap.freq	Coef.	S.E.	Test Statistic	*P*-value
Geno.547	116	T	A	G	T	0.450	-0.324	0.569	-0.569	0.570
Geno.rare99	116	*	*	*	*	0.006	-0.290	3.689	-0.079	0.937
haplo.base115	116	C	A	G	T	0.459	NA	NA	NA	NA
Geno.144	117	A	G	T	A	0.011	0.761	2.443	0.312	0.756
Geno.643	117	T	G	T	G	0.084	-1.365	0.990	-1.378	0.168
Geno.rare100	117	*	*	*	*	0.006	0.102	3.820	0.027	0.979
haplo.base116	117	A	G	T	G	0.898	NA	NA	NA	NA
Geno.145	118	G	T	A	T	0.012	1.027	2.402	0.428	0.669
Geno.256	118	G	T	G	C	0.015	0.757	2.175	0.348	0.728
Geno.rare101	118	*	*	*	*	0.006	-0.076	3.692	-0.021	0.984
haplo.base117	118	G	T	G	T	0.967	NA	NA	NA	NA
Geno.343	119	T	A	T	A	0.012	1.190	2.407	0.494	0.621
Geno.548	119	T	G	C	G	0.016	0.952	2.205	0.432	0.666
Geno.644	119	T	G	T	A	0.406	0.276	0.548	0.503	0.615
Geno.rare102	119	*	*	*	*	0.005	0.703	3.919	0.179	0.858
haplo.base118	119	T	G	T	G	0.562	NA	NA	NA	NA
Geno.146	120	A	T	A	A	0.012	1.191	2.436	0.489	0.625
Geno.450	120	G	C	G	T	0.015	0.878	2.219	0.396	0.693
Geno.549	120	G	T	A	A	0.087	0.814	1.028	0.791	0.429
Geno.645	120	G	T	A	T	0.318	0.114	0.589	0.193	0.847
Geno.rare103	120	*	*	*	*	0.005	-2.777	4.477	-0.620	0.535
haplo.base119	120	G	T	G	T	0.562	NA	NA	NA	NA
Geno.147	121	C	G	T	G	0.015	0.941	2.202	0.427	0.669
Geno.344	121	T	A	A	G	0.098	1.143	0.957	1.194	0.233
Geno.451	121	T	A	T	A	0.091	-0.921	0.948	-0.972	0.331
Geno.550	121	T	A	T	G	0.228	0.566	0.662	0.855	0.393
Geno.rare104	121	*	*	*	*	0.005	-2.370	4.150	-0.571	0.568
haplo.base120	121	T	G	T	G	0.563	NA	NA	NA	NA
Geno.257	122	A	A	G	C	0.017	4.658	2.238	2.081	0.038
Geno.345	122	A	A	G	T	0.080	0.219	1.021	0.214	0.830
Geno.452	122	A	T	A	C	0.091	-0.976	0.943	-1.035	0.301
Geno.551	122	A	T	G	C	0.228	0.560	0.654	0.857	0.392
Geno.rare105	122	*	*	*	*	0.006	-2.839	4.188	-0.678	0.498
haplo.base121	122	G	T	G	C	0.578	NA	NA	NA	NA

Hap.freq: Haplotyle frequency, **Coef.** : Coefficient, **S.E.:** Standart Error

APPENDIX A3. Supplementary Figure-*LPL* Annotated FASTA Sequence.

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                    ataaat atagtagatt ggaggttctg atttgatgag
37   ccagtttctc agccataaac tgagaggggg ttggggatac acttcattgt
87   ccttcctggc taatgtaaat cccttatatt taaaaagata tttaaaagta rs1470187[G/T]
137  ttccaagcat tttggcagaa aagcatagta tctaatgtta tttttttctt
187  attttatgtg catgcctctt aTccatttaa aaatagcttt actgacctat p.208[T/C]/rs1470186
237  aatttacaca ctatataatt ctcccattga aagtgcataa ttctgttgct
287  tttagtatat ttacagagtt gTgcagcatc agcataatgt aatctagaac p.308[T/C]/ rs114637785
337  attgtcatca actaccccca aatctctatt cttcccttcc cctattaatt
387  acccagcccc aggcaagcac tgatctactt ttggtctcta tGgatttgtc p.428[G/A]/rs73667465
437  tatttgtgga cactttaaat ggaatcatac aatatgtgtc ttttgcgact
487  atcttctttc acttatcata actcaatacg gctttagatt atttgacctc
537  gatgttctgc ctCtgaacat aaaatattat ccttgcattc cttgatgagt p.549[C/T]/rs17091742
587  ttgaggattg agaataattt gcatgagaca aaaattagaa actagttaga
637  gcaagtaggc ttttctccat cacataagct gatccatctt gccaatgtta
687  aaacaccaga ttgtacaagc acaagctggg acgcaatgtg tgtccctcta
737  tccctacatt gactttgcgg gggtggggat ggggtgcggg gtgagtgagg
787  gaggactgca agtgacaaac aggattcgtc aaaagagagg tgtattaaag
837  tgccgatcaa Atgtaattta acagctaaac tttccctcct tggaaaacag p.847[A/T]
887  gtgattgttg agtatttaac gtgaatcgat gtaaacctgt gtttggtgct
937  tagacagggg gcccccgggt Aaagtggaac cccttaagct aagcgaacag p.957[A/T]
987  gagcctaaca aagc
1001 aaatttttcc gtctgccctt tccccctctt ctcgttggca gggttgatcc Exon 1
1051 tcattactgt ttgctcaaac gtttagaagt gaatttaggt ccctcccccc p.1090[T/G]/rs1800590
1101 aacttaTgat tttatagcca ataggtgatg aggtttattt gcatatttcc p.1107[T/A]/rs75890454
1151 agtcAcataa gcagccttgg cgtgaaaaca gtgtcagact cgattccccC p.1155[A/T]
1201 Tcttcctcct cctcaaggga aagctgccca cttctagctg ccctgccatc p.1200_1201InsCC/rs34513350
1251 ccctttaaag ggcGacttgc tcagcgccaa accgcggctc cagccctctC p.1264[G/A];p.1300[C/G]
1301 cagcctccgg ctcagccggc tcatcagtcg gtccgcgcct tgcagctcct
1351 ccagagggac gcgccccgag ATGGAGAGCA AAGCCCTGCT CGTGCTGACT
1401 CTGGCCGTGT GGCTCCAGAG TCTGACCGCC TCCCGCGGAG GGGTGGCCGC
1451 CGCCGACCGT AAGTTTTGCG CGCAAACTCC CCTCCACCTG CAGACCCTGC p.1488[C/T]/rs200412008; p.1498[G/A]/rs141390463 Intron 1
1501 GGGTGGCCAC TGCCACCCGA ACTGAGGATG AGAAGAAGGA AGTTGGAAGG
1551 GGCGGTGGAT GCGCCCAGGG ACTCTCCCAG CCTGGGCTCT AGCCCCGAAA
1601 CGGTCCCCGG AGTGGGATCC AGGAGGGGCC GGGAGGGAAT CTCCTCCCGA
1651 TCGTGAAGCG GCGGCGCCCA GTTCCCGCTT TTTCTCTCTG CCGGGTTCCC
1701 GCGCTATCCC TTCCACTCTG GCTGGGACCG CGTTCCCGGG CTCGCAGGCT p.1729[C/A]/ rs185205408; p.1737[C/T]
1751 CCGCCGGGGA GGTTCCGGGG TGTGGGGGCC GGGACGGCGG AGGCGGGGAG
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1851 CTGGAATGAA AGGCGCGCGG GCCAAGGTGA CCTCGCCTTG GTTGGCACTG
1901 CGGCTCAGCC CCCGCCCGGG GACTCGCGGG CCGACTGTGG CCCCTTCTGG
1951 GGAAGCCGGG GCGCGGGGAG GCGTTCCGGG CATCTCAGCC GCACGGGGTA p.1977delC
2001 CGCTCGCCCT CGGCGGGGCC CCTCGCTCCG CTGTGGGAGT GGCAGTGGGT p.2005[C/T]
2051 GTCGGGGTGG AGAAAGTACG CGTGGCGCGG AGTCCTGGGG ACGCGGCGTC p.2053[C/G]/rs7839976
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2151 CCCCTCTTTT CTTAGTGCCC TGAGAACCCA GCGAGGGGCT GACCCTCCCG
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2401 CCGCTCGCTG GGGTCCAGGC GTTCGGGGCC AAATGAGAAT GTCTCAGACC
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2701 TTGTGAAACA TTTTTGTTAG GTTAAAAAAC AAAAAGTTGG CAGGGAGCAG
2751 TGGCTCACCC ATGTAGTCCC AGCACTTCGG GAGGCCGAGG CCGGAAGACA p.2758[C/T]
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3251 CATAGAATAA CGTCATTTTC ATTGCAAAAC AAGCACCGAA ATATGTCATC p.3253[T/C]
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3401 GTTTGGATGA GGCCAATGTT CTCTGAGCCT GGTGTAACTC TTGCCTCTTT p.3434[G/A]
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3501 TGCTTTTCCT AGCTGTAAAT ATATTAAGGA AGGATTATTT CCAAGTAGAC p.3505[T/G]
3551 TGGAAACGAT GCCCTCCCAT CCCCTCCACT TTCACTCTAC TCACCCAATA p.3558[G/A]/rs34309063
3601 TATCATGCCT CTCCCATCAC AGCAACTTTC TCCCTCTTTC TCCTCCAGAT
3651 GCATTCATCT AGGAAGGTAA GAATTTCAGG GAGAGAAAGA TGTCACCGTG
3701 GTAGAAAGAC AGGGATCACC TCCTCTGGGC TCTTGAGTTT ACTTATTCAT p.3725[C/T]
3751 TCTGGATTCT TTCTAACAAG AATATGAGGA CATGAGGCAC TGTCCTCAGG p.3783[A/T]
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3851 CGTGAAGAGC TAGGAGAGGG AGAGTATGGT CAGTGCTTAG CAGCTGAAGT
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3901 TCCACTTGCC TGGCCATCGT GAATTTCCAG GCTGTCTTCT GAGTTGAACA
3951 TGATGGCAAA GGA**G**AGCAAA ATAGCAGATG TCACTGAAGG AGAGCTCAGC **p.3964[G/C]/rs17410577**
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4051 GGGAAGAGC**T** GCGATGGAAA ATTTTCGCTT TCTTTCAGCA GCTTATTTTT **p.4060[T/G]/rs1534649**
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4151 AGTTTACTGC CTTATGCCAG ATTGTTCAAG AAAATGCCTT GCAACTTACA
4201 ATATTTTGCA GCTAGTTTCT TCCGTGACCA CCACAAAGAC TGCATTGACT
4251 TAAATATGAA GATGTTCCAG CCATCAAAAT GATGGTTGGT GATGATTTTG
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4351 AAGGTCTGGA TGAAGAGACC ATTTGGATTT ACTAATAAGG TAAATTCCAA
4401 CTTTTATGGC AATAAAAACA ACA**A**AAACAC TTATCAGTGT AAAGCTTTGG **p.4424[A/G]/rs13266204**
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4701 CTTGTGGCCA TTTTAA**G**ATT GTCTGTGTGC ACTGACACCA TTTGCGTACT **p.4717[G/T]**
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4851 TCATTCCTTT TGCTCTTCCC AGTCTGTGCT CTCAGAATGA TCAAATGCTA
4901 TCTAAGTAGT GTGGTGATTT TGACTGTTTG AATGAATAAA CGAAAAC**G**TC **p.4948[G/C]/rs6997330;**
4951 TCCCACCATT ATTTGACAGT AGAATAGAAC AAAGATGACC CAGTTGGC**G**T **p.4999[G/A]**
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5351 TTAGCACTTA CATTTTAACT AAAAAGAATA GCGTCCCCAT GTT**T**ATTCAG **p.5394[T/C]**
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5451 GTGTTA**G**TTT GAGACAACTG GATGTTTCCA TTTGCCA**T**CC TCAGCAACAA **p.5457[G/C]; p.5488[T/A]**
5501 GAAGAAAGTA GTCTCAGATT AACCAGGTAA **G**TATTTTGTA TTTCACTTAA **p.5531[G/A]/rs1031045**
5551 AAAATCTTGA CTGAAATATG CCTATGTGAT GACACTCAAC CAAATTATTT
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5701 TTTTAACCCC TCTTTTTCAG TA**A**TGTGGAA GGTTAGCCCT AATATTGGAG **p.5723[A/G]**

5751 AAAATTCAGG GTAAAATTCA G**G**TGATTCAT ACAGGATTTA TT**T**TTCCTAT **p.5772[G/A]/rs60633545; p.5793[T/C]/** rs144495763
5801 TCCATTAATA AAACAACTTT TATAAAAATA AAAAGTAGGC TGGCACAGTG
5851 GCTCACTCCT GTAATCCCAG **C**ATTTTGGGA GGCCGAGGC**G** GGTGGATCAT **p.5871[C/G]; p.5890[G/A]**
5901 GAGGTCGGGA GTTCAAGACC AGCGTGGCCA GGATGGTGAA ACCCCATC**T**C **p.5949[T/G]/rs112127208**
5951 TACTAAAAAT ACAAAAATTA GCCAGGCGTG GTGGCAGGCA CCTGTAATCC
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6451 GAGTTCTTGT ACCTCATGTC ATTGCATAAA TGTTCATCTT ACTCACGTGA
6501 TGACTTTGAT CTGCCTTTAA AGCACCATCT GCTGCTTTCC TGGGATGCTC
6551 AA**CA**CTTCCC TCTTTCTAGC AACAAGAATT ACCACTCTT**C** CCCTCTATAC **p.6553[C/T]/rs59254395; p.6554[A/G]/rs56043715; p.6590[C/T]**
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6651 GAGTTATTAT CTATGTTAGA ATAAATTCTT TGTCTTTGTT TACACACTCA
6701 GATTTGTAGT TATTTATTTA GGAATTTAGG AATAAAGATT CCATAGTCAG
6751 GAAAGGCACA A**T**TTATAACT TGCGTGTTAC CCAAAACTCT CCCCTAAGGG **p.6762[T/C]/rs61274012**
6801 CTTAATATGG ACATTTCTGA **T**GAGGCCTGA TGGG**C**AG**G**TG GTACGGTGAT **p.6821[T/C]/rs10104051; p.6835[C/A]; p.6838[G/A]/rs73667467**
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7101 CTGCTGCCCA ATAGCAATCA CAGGATGCA**T** TGGGACAAAT AAATATACTG **p.7130[T/C]/rs28615996**
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7201 GTTTGGGAAG CATATTCATC TTACGACACT GAGACATCCT CGGG**G**GGTTG **p.7245[G/A]/ rs114636902**
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7351 ACCATCACAG AGCACATAGA GTGGTATATT TTCCTGT**C**AA ATGAAAATCA **p.7388[C/G]/rs28575919**
7401 TTTTCT**T**TAA AAGTGAAATG AAAGTCTCTA AATACAAATT TACTAGAGGA **p.7407[T/G]/ rs114437971**

7451 TGTGTAAATT TCCTACTTTT CATTACATAC TCTGGACCCA ACAGAGGGAA
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7601 CAAAGAAAAT **T**TGTGGTCAT TTCAAAACCA CCAGCAATTC CAGGGACACC **p.7611[T/G]**
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12951  GATTTTCTTG CCTTATCTGA AATAAGCTGC CTGGGGACTC ACAGGCACAG
13001  ACGAAGGGAA ATGAGGAGGC TCTCCAGCTG TGTCATGAGA CACCCAAAGG p.13003[G/T]/rs80181352
13051  AATGCTTAGC ATGTAGCATG CATGTGATAC ATCCCAGCAG GTTGCTTAGA
13101  CACAGCTATC TTGGAGCTTT GCCACTTGCT TGGATGTCAC TGGCTTTAAG p.13102[A/C]/rs79760154; p.13106[C/T]/rs80341714
13151  TACAGGGTTC CCATTGTGAA GTAGGGGATC CTGGCTGAAA CAGGGAGACA p.13156[G/T/A]/rs7002728
13201  TTAACATTAC ATTCTGAAGA AATGACATCA ACCTCTCCTG ATCTTGAAAG
13251  CCAACTACAA AGGGTGCCCA ACACCCCAAC CTTGAAGGGA GGCGAAGGTG
13301  AGTGGGACTG GACCAATTCA ACAGGGTTCT GCTCCTAGCC AGGTGCTCCT p.13311[G/A]/rs114236319; p.13321[A/G]
13351  GCTAGTTTCC TCAAAGACCC ACTTTGCATT CAGACCAATC TTTCCTTTTA
13401  ATAGTATAAA TGATCAAAAT TTTATTGAAT GTCTAAAATA TACTTTTTAA p.13443[C/G]/rs115589061
13451  ATGGGAAGCA TGGTGAACCC CAATCTGCCG TTCCTCAACT CAACTCAATG
13501  CCTTCCTGGC TTACTTAGAT CTGCCTTGGA AGGGACAGAC CTGTCTCTGA
13551  ACACTGTTCT GTTATTTGAT TTTTCTATCT GTGCCAATGG GTTTCCAATC
13601  AAGTTTGTTT TTTCCATTTC ATGCAGGTGT ATTGGGCTGA TGTATCTATG
13651  ACAAGTGGTA GGTGGGTATT TTAAGAAAGC TTGTGTCATC ATCTTCAGGT p.13691_13693delATC Exon 3
13701  AACAGGAATG TATGAGAGTT GGGTGCCAAA ACTTGTGGCC GCCCTGTACA
13751  AGAGAGAACC AGACTCCAAT GTCATTGTGG TGGACTGGCT GTCACGGGCT
13801  CAGGAGCATT ACCCAGTGTC CGCGGGCTAC ACCAAACTGG TGGGACAGGA
13851  TGTGGCCCGG TTTATCAACT GGATGGAGGT AAGACTGGGA GAAGGAGACT  p.13854[G/A]/rs1121923 Intron 3
13901  TATGTGTCCA AAACAGTGTT TTTGACTGGA GCCAGAAAAC CGGCTGTTCT
13951  TTCTTCCTTT TCTCTTAGAT TTAAATATTT TCTGGGGGCA TTCAAATCTT
14001  CAGAATCAGC GTGGATATTA TTTTATATCC AAAAGCAACA TTTTGATAAG
14051  AATAGACTAT AAGGCCAATA AATAGTCCTG CCCTGCTCTA TCGTTTGATA
14101  TTTTCACAGT GAATAGATCT GCTGAGACCA ATAACTAAGT GGGCCCAACA  p.14114[T/C]/rs73667472
14151  GAAAAAAGCT TGTGATTTTC GGACAGAGGA AAGATGGCAT GTTCAGCCAG
14201  ACCCTTCCCT ACCAGTTGGC TGGCCTGTGG ACATCTTATC CTCACCTTGA  p.14213[C/A]/rs58670071; p.14241[C/T]/rs75026342
14251  CATACCAATC TCTTTCATGA AAATATTAAT AGTACTTATT CTTTAGTGTG
14301  AAATAGGATG AACGTTTTTG TTGAGCATTG GGAGAGTGAT GGAATTGAGC  p.14314[G/A]
14351  TAGGAAGATG TTGGAAGGGA AGGTGCATAG GATAGAAGGG AACTGAGGTC
14401  TGGAGTTCTG ACTTAGCTGC AAGAGACCCA CTTTTTCACA CGATCCCTTG
14451  AGAAGTACCT CTGAAAAGTA TCTTGGGGTT GGAAAGAAGC TGATACTCTG
14501  ACCAAGGCAA ATTATTTTAA CCAGGTAATT GGAAGTAAAA AATAAGCTGT  p.14530[T/G]
14551  GTTTATTAGA CTGATCATAA AAGACAAAAG TTCTTTTCTT GTCTTTTTTG
14601  CTGACCAGGC AAATGAACAT GGGCAAACGG GATCACCTCC CTGGGGCTCA
14651  GGCTTCTCAC CTGTTAAATG AGGGGCTGGA CCATGTACCT CTGGTCCCTT
14701  CCACTGAATG TTTCCTGAGT CTGTCATTGC TTGGCTAACC TTCAATGATA
14751  AAGTGATACA GATATTTAGA GTAAGGAATA ATGGGAAAAT ATATACCCAT p.14790[T/C]/rs113443162
14801  ATACTATACA TTCAAACATA CACACATATA CATATATGCA TGCATATAAA p.14829[T/G]
14851  TGTATACGCA TATGTATATG TGTATATGTT TGTACGTATA GTATATGGTT p.14886[G/A];p.14898[G/T]/rs193260945
14901  ATATATGCAA ATACATATAC ATATACAAAC ATATGCATAT ATTATATACA
14951  TAAATAATAC TATTTCAGAT GCATGGAAAA ACTTTGTAAT TTAAATCTGC p.14997[C/A]
15001  TATTAAAGAA AGAGAAAATC AATTCTGGAT TTGTTTACGG AAAAGTGAAA
15051  CAAAAGAAAA AGACAATTTT AACACTAGAG AATATTTTCT CTCTCTTACC p.15060_15061delAA
15101  TGTAACACAA AATTAAAATA AGTAGAATTA GTTTTCAGTA TTTCCTATAT p.15115[A/C]/rs57345602
15151  TTGGAAAACA ATATTTATAT TCATTTTGTT TCTTTTAGTT TTATTTTTGG
15201  CAGAACTGTC AGCACCTTCA TTTTCTTTTT CTTCCAAAGG AGGAGTTTAA Exon 4 p.15206[C/A]/rs343;p.15210[C/A]/rs247;p.15245[G/A]/rs248
15251  CTACCCTCTG GACAATGTCC ATCTCTTGGG ATACAGCCTT GGAGCCCATG p.15266[T/C]/ rs116678290
15301  CTGCTGGCAT TGCAGGAAGT CTGACCAATA AGAAAGTCAA CAGAATTACT
15351  GGTAAGAAAG CAATTTCGTT GGTCTTATCA TAAGAGGTGA AAAGACTGTC  Intron 4
15401  ATTCTGAGAG AGAATCAGAA CAAATTTTGT TAAATACCCA CATGTGTGGT p.15425[T/C]/rs249; p.15448_15449insTG; rs74959097[MAF:0.008];
rs78191607[MAF:0.008]
15451  GTTCTTCCCG GAGACATGAC CAGCACTTGA TTATCTCATT GTAGGGCTCT
15501  TTATTAGGGA TAAGAAAAAA CACAGACGCT CTCACTGGCT TACTATCCAC p.15540_15554del15
15551  TGGCAATAGC ACAGAAATAA AGCATAATTA CACACAATGC CTGCAGATTT p.15579[T/C]/rs251
15601  CTCTGGGAAG CCTGTTTCCT CCCACTCTCA GCTCTGTGTT TTAGTAGTGT p.15650_15651InsA
15651  AAATGCACAT CAGTACTAGG AGAAAAGAAG AAGGACCAAT TCCAGAGGCC
15701  ACTTCGAAAG AAGACCGTCA TCTAGGCAAA GGTGTGGCAT ACACACAGAG
15751  AGAAAGAACC CACCACTGTT TATACATCTT CTCGACATAT TCAGAAATAA
15801  TCTACAAAAG GAAATCCAGC CATCCTGAGT GGAAATTGCT GCATAAGGCT p.15836[T/C]/rs253
15851  AGTTTAAGAG ACTCAAATTC ATTTTAGAAG GAGCCAAGCC TCCTTTTATG p.15884[C/T]
15901  TCTCTCTAAG TAAAGATACC ATGACTGTAG AATAGGAGCT AATAAGAATC p.15920[C/A]
15951  TAAATAGCTG CCAGTGCATT CAAATGATGA GCAGTGACAT GCGAATGTCA
16001  TACGAATGGA AATTTACAAA TCTGTGTTCC TGCTTTTTTC CCTTTTAAGG Exon 5
16051  CCTCGATCCA GCTGGACCTA ACTTTGAGTA TGCAGAAGCC CCGAGTCGTC
16101  TTTCTCCTGA TGATGCAGAT TTTGTAGACG TCTTACACAC ATTCACCAGA
16151  GGGTCCCCTG GTCGAAGCAT TGGAATCCAG AAACCAGTTG GGCATGTTGA
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16201  CATTTACCCG AATGGAGGTA CTTTTCAGCC AGGATGTAAC ATTGGAGAAG
16251  CTATCCGCGT GATTGCAGAG AGAGGACTTG GAGGTAAATA TTATTTAGAA Intron 5
16301  GCGAATTAAA TGTGACTCTT ATCCTTAACC CTTATTGACC CAATGTCCTA p.16316[C/G]/rs254; p.16320[T/C]/rs255
16351  CTCAGTAGCT TCAAAGTATG TAGTTTTCAT ATACACATTT GGCCAAATTA p.16363[A/G]/rs80143795; p.16386[C/T]/rs256; p.16392[G/A]
16401  TGTTTCTGAA GAATTCTGCA ATGTTCAGCA TGACCACCTT ACAGCCAGGC p.16421[A/G]
16451  AGACAGCCAT TTTATCTTTT ATTTACTATA CTGTAGGCTA CACTGAGCAG
16501  TGCACTTACA GTAGCAAGAG AAAAAGGTGG GATTTTAGAC AGGAAGACTC
16551  CACTGACCTC AAAAATGGCA TCATAAAATG CTATCTGGCC ACATGTTGTC
16601  ATACCTTGAA TGTAGCTGCA AAGCCAATGG AAAGATTTTA GATGTTACTG p.16647[A/C]/rs257
16651  GAACAGAAGA TGTTAATTAG CATAAATCTT CCAAAATGTT CAGAACATAA p.16671[C/G]/rs258
16701  TGTTAGCTTA ATGTTTTACT TTAATAATGT TAGCTTGTGT TAAATTTATG
16751  ATTTTTGTTT GTTTGTTTTT TGAGATAGAG TCTTATTCTA TTGCCCAAGC
16801  TGGGGTGCAG TCACACAATC ACAGGGACTT GCAATGTTGC CCAGGCTGGT
16851  CTCAAACTCC TGGCCTCAAG TGATCCTCCT GCCTCAGCCT CCCAAAGTTC p.16856[A/T]/rs259
16901  TGGGATTGCA GCTGTGAGCC ACCACGCCCA GTTTACGATT TATTTTTAAG p.16928[C/G]/rs260
16951  AGCCCCTTGC ATACTTTATA GACATTGGGA CCTACCTAGG ATATTCTCGT
17001  TATTTTTGTG CACGTAATAG AACTTAGAGC ATATTGTTAC TATTTTCGAT p.17039[A/G]/rs261
17051  TGTCCTAAAA ACTTACAAGG AATTCATTCT TATGGCATTG CTGATTATTT p.17061[A/T]/rs262
17101  CTATGTTCAT TTGATATAAA AGAGTGTTAG TAGGGGCAGA ACCCTCAATT
17151  GTACATAATA TCAATGATAA AATACAATTC ATTTAACAAT TACCCTCTTA
17201  AGATGTGGTT TCTAGAAATA CAAATTGTCC CTAACTTACA GTTTTCCAAC p.17229[C/G]; p.17231[C/T]/rs263
17251  TTTACAATTG GGCTGTAACA CCATTTTAAG TTGAGAAGCA CGTGATGGTT
17301  TGACTTAAAA CTTTTTGACA TTATGATGGG TTTTGGGGGT ATTAAGTGCA
17351  TTTTGACTTA CAGTATTTTT GACTTATGAA GAATTTATTG TAAGGCAAGG
17401 GGCAGGTATA TGTTTCTAGA AGCACCTAGA AGTGTTAGAC ACTTTCAATG
17451  TAAGAGAAGG ATGAGATAAA CAAGGAAATC AACCTCCACC TTGGAGGCTT
17501  ATTACAGCTT CATAAACATA CTCATAAATA TAAGAAGCAC AAAAGTCAAA
17551  AATTCCCTGT GAACTTGCAA CTTTCACTCT CTTGAAGGTG GGTGGGCCGC  p.17599[G/A]/rs264
17601  TACCACCAAG AATATCTCCT GAAATAGGGC CTACAATCAT AAATGCACAG
17651  GACTATATCC TTGGGTGATT CTACTCTAAC ACCACATCTC ACCTATTTTA
17701  GACATGCCAA ATGAAACACT CTTTGTGAAT TTCTGCCGAG ATACAATCTT  p.17718[A/G]/rs266
17751  GGTGTCTCTT TTTTACCCAG ATGTGGACCA GCTAGTGAAG TGCTCCCACG  Exon 6
17801  AGCGCTCCAT TCATCTCTTC ATCGACTCTC TGTTGAATGA AGAAAATCCA
17851  AGTAAGGCCT ACAGGTGCAG TTCCAAGGAA GCCTTTGAGA AAGGGCTCTG
17901  CTTGAGTTGT AGAAAGAACC GCTGCAACAA TCTGGGCTAT GAGATCAATA
17951  AAGTCAGAGC CAAAAGAAGC AGCAAAATGT ACCTGAAGAC TCGTTCTCAG  p.17993[G/A]
18001  ATGCCCTACA AAGGTAGGCT GGAGACTGTT GTAAATAAGG AAACCAAGGA  Intron 6 rs59184895[MAF:0.04]
18051  GTCCTATTTC ATCATGCTCA CTGCATCACA TGTACTGATT CTGTCCATTG  p.18086[T/G]/rs269 p.18095[C/A]/rs270
18101  GAACAGAGAT GATGACTGGT GTTACTAAAC CCTGAGCCCT GGTGTTTCTG  p.18121[G/A]/rs271
18151  TTGATAGGGG GTTGCATTGA TCCATTTGTC TGAGGCTTCT AATTCCCATT
18201  GTCAGCAAGG TCCCAGTGCT CAGTGTGGGA TTTGCAGCCT TGCTCGCTGC
18251  CCTCCCCTGT AAATGTGGCC ATTAGCATGG GCTAGGCTAT CAGCACAGAG
18301  CTCAGAGCTC ATTTGGAACC ATCCACCTCG GGTCAACAAA CTATAACCCT  p.18347[C/A]/rs272
18351  TGTGCCAAAT CCAGCCTACT TCCTGCTTTT GTAAATAGTT TTTTTTAAAA  p.18395_18396insT; p.18399_18400insA
18401  TTTTAAGTTC AGGGGTACGT ATGTAGGTTT GCTAAAAAGG TAAACTTGTG
18451  ACATGGGAGT TTGTTGTCCA GAATATTCCA TCACCCAGGT ATTAAGCTTA
18501  GTACCCATTA GTTACTTTTC CTGAAGCTCT CCCTCCTCCC ACCCTCTGGG
18551  AGGCCCCAGT GTCTGTTGTT CCCCTCTATG TGCTCATGCA AAGTTTTATT  p.18600[T/G]
18601  AGGACACAGC CACACACATT CATTACCATA TTGTCAAAGG CTGGTTTCAT
18651  GCCACCATAA CAGAGTTGAT AGCCCACAGA GCCTAAAATA TTTACTCCCT  p.18652[C/T]/rs275
18701  GGCCCTTTAC AGAATGTTCA CAACTTACAT AAAGGCAAGG ACCATCTGTC  p.18708[T/C]/rs276
18751  TTATTTATTT ATTTATTTAA TTTGAGATGA AGTCTAGCTT TCTCCTAGGC
18801  TGGAGGAGAG GGGCATGATC TTGGCTCACC ACAACCTCTG CCTCCCGGGT  p.18822[T/C]/rs277
18851  TCAAATGATT CCCCTGCCTC AGCCTCCGGA GTAGCTGGGA TAACAGGCAT
18901  GCACCATCAT GCCCAGCTAA TTTTTGTATT TTTAGTAGAG AGGGGGTTTC  p.18942[G/A]/rs278
18951  ACCGTGTTGA CCAGGCTGGT CTCGAACTGC TGACCTCAGG TGATCTGCCC  p.18992[G/A]
19001  TCCTTGGCCT CATCTGTCTT TTTAAATGCA ACTATTCCTG GAAGGCAAGA
19051  ATATCTCACA CCTTCTAAGA TACTGCCATT TTGCCAGGAG TTTGTTTCAC
19101  ACTTGAATTT CAAGCTTGGC CTCTTGTTTA GAGGCAGACC TAAAGGAATG  p.19115[C/G]/rs279
19151  GTCGGAAAAT GAGAGAGGAG GTCTTCGGAT AAATCCGGTG AGAGGGACCA
19201  ACTTCAGGAA GGGTGGCTTT TGTGGAATCC AGATGGAAAC CTGAGGGAAG
19251  GGATGATATT AAAGAACAGT GGCCCCAGGT AAAACATATG GCACCCATGT
19301  GTAAGGTGAT TCTTAGAATC TGTAGAGGTG TCTTTCGTGG TATAGAGGTT  p.19301[G/A]/rs280
19351  GAGGCACCTG TGCTTCAAGG AAACCTTAAC TCTTCAAAAT CAGGCAATGC
19401  GTATGAGGTA AAGAGAGGAC TGTGGGACCA TAATCTTGAA GACACAGACA  p.19407[G/A]/rs17091775; p.19442[A/T]/rs281; p.19445[C/G]/rs282
19451  GGCTTCACTC ATCCCTGCCT CCTGCACCAG TGGGTTCAAG GCTCTGTCAG
19501  TGTCCCCTAG GGGCACTTCA CCACTCCCAG CTTCTTCAGC TCTGGCCTGT  p.19517[T/C]/rs283;p.19525[T/C]/rs284
19551  CCTGCTGCCT GCAAGGGTTT TGCTTAATTC TCAATTCAAT GTCTCTTCAT
19601  CTTTTAGTAG CTGTGGGGTT TTGTTGTTGT TCTTCTGTTT TTGCTTAGTA  p.19608[T/C]/rs285
19651  TCTGACTACT TTTTAATTAT AAAAAGAGAT GTATCTAAAC AAAATAGAGA
19701  TTGTTATCAG AAGTTCACAA CATTTATTAA AAATTTTTTC ACCTGGACAA
19751  GAGTCTAAAG CAGCATAAAA ATATGGTCTG CTATATTCTA AACCATCAGT
19801  CTTAAGAGAT CTGTGTCTCA GCTTAAGAGA AAATACATTT AATAGACAGT
19851  AACACAAATA AGAAAAAAAT CTGACCAAGG ATAGTGGGAT ATAGAAGAAA
19901  AAACATTCCA AGAATTATTT TATTTATTTA TTTATTTATT TATTTATTTA
19951  TTTATTTATT TATTTTTGAG ACACAGTCTC GCTCAGTTAC CCAGGCTGGA  p.19975[A/G]/rs287
20001  GTGCAGCGGC GCAATCTTAG CTCACTGCAA CCTCTGCYTT CYGGTTCAAG p.20038[T/C]/rs289; p.20042[C/T]
20051  CGATTCTCCT GCCTCAGCCT CCTGAGTAAC TGGGATTACA GGCACCCGCC
20101  ACCACGCCCA ACTAATTTCT GTATTTTTCT TAGTAGAAAC AGGGTTTCAC  p.20109[C/G]
20151  CATGTTGGCC AAGCTAGTCT CAAACTCCTG ACCTCAGGTG ATTCACCCAC  p.20188[G/A]/rs290
20201  CAAGGCCTCC CAAAGTGCTG GGATTACAGG CATGAGCCAC CATGCCTGGC
20251  CTCCAAGAAC TCTTTTTTCC TCCATCATCA TGGTTCTATT TTAGTCCTGC  p.20271[T/C]/rs291
20301  TGCCTTTCCT TTTAACCTCT CCCCAGGCCC ATTTGCTCAG GGTTTTTGGT
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20351  AGAGACCAGA GGAGGGGCAG GGAGGAGATA TAGAAGTTCA ACTACCTGCT
20401  TCCAGAGGCT GTCCCTAGTA TAGAATACTT TAGGGGCTGG CTTTACAAGG
20451  CAGTCCTTGT GGCCTCACTG ATGGCTCAAT GAAATAAGTT CTTTTTTAAA  p.20474[G/A]/rs292
20501  AAAAATTTTA TTTATTTCCA TAGGTTATTG GGGGAACAGG TGGTGTTTGG  p.20505_20506insA; p.20544[T/C]/rs294
20551  TTACATGAGT AAGTTCTTTA GTAGTGATTT GTGAGATTTT GGTGTGCCCA
20601  TTACGGAATG GAAAAATCAA CGAAATAAGT TCTATGATGC ACCTACTAGA
20651  CACCTAATCT GCGCTAGATG GTGGGGGAAT TAAGAGCATG GGCATGATCC  p.20657[A/C]/rs295;p.20670[G/A]
20701  TGTGACCGGA AGCCCGCTTA CAGTCAGGGT GGAGGACAGA CCTACTCATG
20751  AAACAAACAC AGTGACATAT AGTGACACAG AAGCAAATGT CAAATATGCT  p.20790[T/C]/rs297
20801  TGCTCCAGAT GCTAAGGCAC AAGATGGCCA AGGATGGCGG AGTTCATGGA
20851  GAAAGCATCA TGAGTGTTTT GGCCTTCTGA TTTGATCTCC CTAGCACCCC  p.20884[G/A]
20901  TCAAAGATGG CTACTTCCTA ATGCTGCTTG GCAATTCAGA CACATTTGGG
20951  TTTTTCCTAT GCATATAACC ACACTTTTCT GAAAGGGAGT AGAATTCAAG
21001  GTCTGCATTT TCTAGGTATG AACACTGTGC ATGATGAAGT CTTTCCAAGC
21051  CACACCAGTG GTTCCATGTG TGTGCACTTC CGGTTTGAGT GCTAGTGAGA
21101  TACTTCTGTG GTTCTGAATT GCCTGACTAT TTGGGGTTGT GATATTTTCA  p.21136[G/A]/rs73601683
21151  TAAAGATTGA TCAACATGTT CGAATTTCCT CCCCAACAGT CTTCCATTAC  Exon 7
21201  CAAGTAAAGA TTCATTTTTC TGGGACTGAG AGTGAAACCC ATACCAATCA
21251  GGCCTTTGAG ATTTCTCTGT ATGGCACCGT GGCCGAGAGT GAGAACATCC  rs298; p.21299[C/T]/rs299
21301  CATTCACTCT GTGAGTAGCA CAGGGGGGCG GTCATCATGG CACCAGTCCC  Intron 7 p.21306[A/G]/rs300
21351  TCTCCTGCCA TAACCCTTGG TCTGAGCAGC AGAAGCAGAG AGCGATGCCT  p.21353[T/C]/rs301
21401  AGAAAACAAG TCTTTAGTTA AAAAAATCAG AATTTCAAAA TTGAGGTCTT
21451  TCCTCTATTT GATATTGAGA AAAAAATGCT TCAAATTGGC CATTTTATTT
21501  TCACTTACTA GTTATATTTT TTTATTTATC ATCTTATATC TGTTTATTTC  p.21548[T/G]
21551  TTTTATAAAG CTGCTGTTAA ACAATATAAT TAAACTATCT CAAAAGGTTT  p.21596[G/T]
21601  GACATTAAAG AAAATGAGCA ATGGTAACAG GAAACCACTC TATAGATGTA
21651  CATATAATAT GTACAGAAAA TATAAGTAGT AAGAAGTCCA TGACAAAGTG  rs303[MAF:0.42]
21701  TTAGCTCTTT TTTTTTTTTT TTTTTTTTTT TTTTTTGAGA TGGAGTCTCT
21751  CTCTATTGCC CAGGCTGGAG TGCAGTGATT CGATCTCAGC TCACTGCAAC  p.21780[T/G]/rs304
21801  CTCTACCTCC CGAGTTCAAA CAATTCTTCT GTCTCAGCCT CCCGAGTAGC  p.21820[A/G]/rs305
21851  TGGGGCTGCA GGTGCCCACC ACCATGCCCA GCTAATTTTT GTATGTTTAG  p.21862[G/A]/rs306
21901  TAGCGACAGG GTCTCACCAT GTTGGCCAAG CTGGTCTTGA ATTCCTGATC
21951  TCAGGTGATC CACCCGCCTC GGCCTCCCAA AGTGCTGGGA TTACAGGTGT
22001  GAGCCACCAT GCCCAGCCTA CCCTTTACTA CTAATCAAAG AAATAAAAGT
22051  AAGGCAACTT GATACTTTTA CAATTACTAG ATGAACAAAT CTTTAAAAAT
22101  AGCCAGTGCA GACAAGGTGG TGAAGCAGAA CATGCGAACC TACCATGCAT
22151  CATTCACGGC TAGAACCCTC CAGGTGCGGA AGGTAGTATT TTAATAACTT
22201  TCCATAGCTA CAAAATATTA TTACATAGAA GGGAGTGATT TTTTTCTAAT
22251  ATTTATCCTA AAGAAATAGT CAACAAACAT TTTTAAAAAC ATCAATTACA
22301  GTCGTACCTA TACTAGCATA AATTAGAAAC CCAGTATCCA ACATTGAGGC
22351  AGTGGGTAAA TGAATCGTGG TTTATCAAGT CATTAAAATC AATCTAGCCT
22401  TTAAAAACTA TAATTGTAGG AAACCCAGGA AAACATAGTA AAAAATGGAA  p.22416[G/C]/rs312; p.22445[A/G]/rs313
22451  TATAAAATCT AAAGAGAATA AAGAATAGAG AATCGTATGT GTGCTATGAT  p.22461[A/G]/rs314
22501  TGTAGCTAAA TAACGTTCAA GTATCAACAC AAATTGAAAA GGAATACATG
22551  AAAATGAAAA TTATATTTCT GAATGATTGA CTTCAGGATT TTCTTTTAGA
22601  ATTGTATTAA ATAGTTCATG TCATTAGGAT AAATGCTGGA ATGTGGATAT
22651  AATTTAAAAT ATACTAAATG CCATCGACCT TCATTTTGAG TTCTTTGTTG
22701  GACATTTTTG TGCATTTTTA AAATATCCCC TAAATAATAA AGCTATTTAT
22751  ATTTGGAGAG GAGAAAAAAA AGTGGGGGGC AGGGAGAGCT GATCTCTATA  p.22774[G/A]/rs77434393
22801  ACTAACCAAA TTTATTGCTT TTTTGTTTAG GCCTGAAGTT TCCACAAATA  Exon 8
22851  AGACCTACTC CTTCCTAATT TACACAGAGG TAGATATTGG AGAACTACTC  p.22855[C/A]/rs316
22901  ATGTTGAAGC TCAAATGGAA GAGTGATTCA TACTTTAGCT GGTCAGACTG
22951  GTGGAGCAGT CCCGGCTTCG CCATTCAGAA GATCAGAGTA AAAGCAGGAG  p.22970[G/A]/rs5934
23001  AGACTCAGAA AAAGTAATTA AATGTATTTT TCTTCCTTCA CTTTAGACCC  Intron 8
23051  CCACCTGATG TCAGGACCTA GGGGCTGTAT TTCAGGGGCC TTCACAATTC
23101  AGGGAGAGCT TTAGGAAACC TTGTATTTAT TACTGTATGA TGTAGATTTT
23151  CTTTAGGAGT CTTCTTTTAT TTTCTTATTT TTGGGGGGCA GGGGGGGGGA  p.23190_23191InsAG; p.23192[G/T]/ rs74304287
23201  AGTGACAGTA TTTTTGTATT TCATGTAAGG AAAACATAAG CCCTGAATCG
23251  CTCACAGTTA TTCAGTGAGA GCTGGGATTA GAAGTCAGGA ATCTCAGCTT
23301  CTCATTTGGC ACTGTTTCTT GTAAGTACAA AATAGTTAGG GAACAAACCT
23351  CCGAGATGCT ACCTGGATAA TCAAAGATTC AAACCAACCT CTTCAAGAAG  p.23388[C/G]/rs318; p.23395[A/C]/rs319
23401  GGTGAGATTC CAAGATAATC TCAACCTGTC TCCGCAGCCC CACCCATGTG
23451  TACCCATAAA ATGAATTACA CAGAGATCGC TATAGGATTT AAAGCTTTTA  p.23496[T/G]/rs320
23501  TACTAAATGT GCTGGGATTT TGCAAACTAT AGTGTGCTGT TATTGTTAAT
23551  TTAAAAAAAC TCTAAGTTAG GATTGACAAA TTATTTCTCT TTAGTCATTT  p.23573[T/C]/rs77243948; p.23593[A/G]
23601  GCTTGTATCA CCAAAGAAGC AAACAAACAA ACAAAAAAAA AAAGAAAAAG  p.23605[G/C]/rs321; p.23632[C/A]; p.23636[A/C]/rs322
23651  ATCTTGGGGA TGGAAATGTT ATAAAGAATC TTTTTTACAC TAGCAATGTC
23701  TAGCTGAAGG CAGATGCCCT AATTCCTTAA TGCAGATGCT AAGAGATGGC  p.23747[T/C]/rs325
23751  AGAGTTGATC TTTTATCATC TCTTGGTGAA AGCCCAGTAA CATAAGACTG
23801 CTCTAGGCTG TCTGCATGCC TGTCTATCTA AATTAACTAG CTTGGTTGCT
23851  GAACACCGGG TTAGGCTCTC AAATTACCCT CTGATTCTGA TGTGGCCTGA  p.23858[G/A]/rs326; p.23866[C/G]/rs7005541
23901  GTGTGACAGT TAATTATTGG GAATATCAAA ACAATTACCC AGCATGATCA  p.23919[G/A]
23951  TGTATTATTT AAACAGTCCT GACAGAACTG TACCTTTGTG AACAGTGCTT  p.23955[T/G]/rs327
24001  TTGATTGTTC TACATGGCAT ATTCACATCC ATTTTCTTCC ACAGGGTGAT  Exon 9
24051  CTTCTGTTCT AGGGAGAAAG TGTCTCATTT GCAGAAAGGA AAGGCACCTG  p.24064[G/A]
24101  CGGTATTTGT GAAATGCCAT GACAAGTCTC TGAATAAGAA GTCAGGCTGG  rs328[MAF:0.4]Intron 9
24151  TGAGCATTCT GGGCTAAAGC TGACTGGGCA TCCTGAGCTT GCACCCTAAG
24201  GGAGGCAGCT TCATGCATTC CTCTTCACCC CATCACCAGC AGCTTGCCCT
24251  GACTCATGTG ATCAAAGCAT TCAATCAGTC TTTCTTAGTC CTTCTGCATA
24301  TGTATCAAAT GGGTCTGTTG CTTTATGCAA TACTTCCTCT TTTTTTCTTT
24351  CTCCTCTTGT TTCTCCCAGC CCGGACCTTC AACCCAGGCA CACATTTTAG  p.24373[G/A]
24401  GTTTTATTTT ACTCCTTGAA CTACCCCTGA ATCTTCACTT CTCCTTTTTT
24451  CTCTACTGCG TCTCTGCTGA CTTTGCAGAT GCCATCTGCA GAGCATGTAA
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 24501  CACAAGTTTA GTAGTTGCCG TTCTGGCTGT GGGTGCAGCT CTTCCCAGGA  p.24505[A/G]/rs329
 24551  TGTATTCAGG GAAGTAAAAA GATCTCACTG CATCACCTGC AGCCACATAG
 24601  TTCTTGATTC TCCAAGTGCC AGCATACTCC GGGACACACA GCCAACAGGG
 24651  CTGCCCCAAG CACCCATCTC AAAACCCTCA AAGCTGCCAA GCAAACAGAA
 24701  TGAGAGTTAT AGGAAACTGT TCTCTCTTCT ATCTCCAAAC AACTCTGTGC
 24751  CTCTTTCCTA CCTGACCTTT AGGGCTAATC CATGTGGCAG CTGTTAGCTG
 24801  CATCTTTCCA GAGCGTCAGT ACTGAGAGGA CACTAAGCAT GTGACCTTCA  p.24815[G/A]/rs330; p.24824[G/A]/rs331; p.24829[G/A]
 24851  CTACTCCTGT TCCGAATTCC AGGAATATGC CCTTTTCAAC CCTCCACACA  p.24852[T/C]/rs12679834; p.24863[T/C]; p.24899[C/T]/rs76423146
 24901  TCCCCTGCCA GACAGCAAGT GCTAATGGGT TACAGGAACA AAGGGGAGAA
 24951  ATATTAGATC ATGTCATACA AGCCAGTGAC ACAAGAAATG AAGGGAAAGG  p.24957[G/A]
 25001  CTAGACACAG TGTCATCTGG AAACAGGAAA AGCAATTGCT TTTGGTTTAT
 25051  TCTTTTCCTA GTTTGCATTT GGGACAAATG TATAGAATAA GAATTGCCTT  p.25080[G/A]/rs28681081
 25101  CATGCCTGCA ATCCCAGCAC TTTGGGAGGC TGAGGCAGGT GGATCACCTG
 25151  AGGTCAGGAG TTTGAGACCA GCCTGGCCAA CGTGGCGAAA CCACCTCTCT
 25201  ACTAAAAATA TAAAAATTAG CTGGGTGTGG CGGCACATGC CTGTAATCCC
 25251  AGCTACTCGG CAGGCTGAGG CGGGAGAATT GCTTGAACCG GGGAGGCAGA  p.25272[G/A]
 25301  GGTTGCAGTG AGATGAGATC GCGCCATTAT ATTCCAGCCT GGGCAACAGA  p.25335[C/T]
 25351  GAAAGACTCC ATCTCAAAAA AAAAAAAAAC ATGCCTATTA GGAAAAGTAT  p.25352[A/C]/ rs145391587; p.25380[C/A]
 25401  ATTAAAGACC CTATGTGTAA CATCTTTAAT GTTTTTAAAT TCTACTTTAT  p.25414[T/C/G]/rs28599962
 25451  AATAGATTTT ATACATGTTT ACTATAAATA GATTAGGAAA AATAAGCAAA   p.25460[T/C]
 25501  AATAAAATAA AATCACTGTG ACCATATCAC TCAGAGACAA CCCCAATTAA
 25551  CGTTTTTATT TATATTCTTT CGGACTTTAT ATATACATAA TATTTATATG  p.25579[A/G]
 25601  TTTTTCGTCC TTTACAAAAA TAGAATTATG GTGTATATAC TCTGAATGAC
 25651  TAGATGAGAA CATCTGGATC AAAAGCATTA ATGTAAGAGC ATTCAGGATA  p.25652[A/G]/rs17116619; p.25666[G/A]/rs28439839
 25701 AACTCAAAAT GGAGAATAGT TAGTGGTATT GAGCCAGGCA AAATAACGCA
 25751  ATTCTTATCT AACTGGAGAC TTTTCTTCTA AGAGGTTATT ACGTTGTTTT
 25801  TCCTCATCAC AAATCTGAGG CAATATCATA CTTTCTTCAG TTCTTAGAAA  p.25805[C/T]/rs28424158; p.25844[T/G]/rs75278536
 25851  GAGACTTTTA GATGAAGTYT TTTTTGTTTG TTTTGGTTTT TTTTTTCTTG  p.25869[T/C]; p.25886delG
 25901  AGATGGAGTT TTGCTCTTGC TGCCCAGGCT GGAGTGTAGT GGCTCGATCT
 25951  CAGCTCACTG CAACCTCCAC CTCCTGGGTT CAAGCAATTC TCCTGCCTCA
 26001  GCCTCCCAAG TAGCTGGGAT TACACGTGTC CGCCACCACA CCTGGCTAAT
 26051  TTCGTATTTT TAGTAGAGAA AGGGTTTCAC CATGTTGGTC AGGCTGGTCT  p.26054[G/A]; p.26057[T/C]
 26101  TGAACTCCTA ACCTCAGGTT ATCCACCTGC CTCGGCCTCC CAAAGTGCTG
 26151  GGATTATAGG TGTGAGTCAC CACACCCGGC CCTAGATGCA GTTTTATACA  p.26183[T/C]
 26201  TGCATTTGTA TTACACATAA ATAGCATGCA TATTCTGCCA GAGCATCTAC  p.26201[T/G]/rs77069344; p.26220[A/T]/rs80307903;
p.26234[T/G]/rs10099160
 26251  AACTTTAAAT CTACATGTGA ATGTGAAAAT AAAACCTCAT TAAATTAGTA
 26301  AATAACTCTA GCTGCTTGTA AAGCACGTCC AGTCGTATTT TTTATATGTT
 26351  ACAAGACTTT ATCTGAGAAA GCCTAATGAA GCATTCCTTG TCTGATTATA  p.26377[T/C]
 26401  GGATTACTGA CAGAACAGTT ATTTAGACAG AGAATGTTCA GATGCGTTTT
 26451  ATTTTTATTT TTTACTTTTA TTTATTTTTG AGACAGTCTC GTTCTGTTGC  p.26460[T/G]/rs75946927
 26501  CCAGGCTAGA ATGTGGTGGC GTGATCTCGG CTCAATGCAA CTCTGCCTCC
 26551  CGGGTTCAAG TGATTCTTGT GCCTCAGCCT GACAAGTAGC TGGGATTATA
 26601  GGTGCCCGTT ACCATGCCCA GCTAATTTTT CTGTTTTTAG TAGAGACGGA
 26651  GTTTCACCAT ATTGGCCAGG CTGGTCATTG AACTCCTAAC CTCAGGTGAT
 26701  GTGCCTGTCT CAGCCTCCCA ATGTGCTGGG ATTACAGGCA TGAGCCACAG
 26751  CACCCAGCCA GATGCATTTT TAAAAACGTA CCTGAACTTT ATCTAGGAGG
 26801  TAATTATAAA TTAGACTAAT AATCTTCTAC AGTTTCTTTC TTCTGTGATT
 26851  AAAATCAATC AAATCAAAGA TTCTCTTTCT CACACCTTCT GCTAACTCCT
 26901  CAGAAACCTC ATATCACAAG AAATGAAATG GAACAGGCCT TTCGTTTGAT
 26951  ACATTTTAGA ATAAGAAATC CTCTAAATTT AGAAGTCATT TGGCCCAGTC
 27001  CTCCAAAAAT GATGCACCTT ATTGGGACGG GGCTAAATAG TTGCTCCAGT  p.27033delC;p.27050[T/G]
 27051  GTCTTCCATT CCTACAAACC TGCCATTCTC TGATCCATTA TACACATCTC  p.27075[A/G];p.27076[T/C]/rs114991789
 27101  CCCTGGGTTT ATTCTCACAA CCTTTGTTCT GAAATTCCAT TTGAAGGCTT  p.27113[T/C]/rs10283151
 27151  TTTCCATCCT AAAACCAGTG GGGGACAGGC GGGAATTGTA AAACACTCAG
 27201  AAGATAATAA ATTGCCCTTT TTCCTGTGCT TTTTCTCAGA aactgggGa   Exon 10-5’UTR p.27229[C/T]/rs11570891; p.27249[G/A]/rs4922115
 27251  atctacagaa caaagaaCGg catgtgaatt ctgtgaagaa tgaagtggag  p.27268[C/T]; p.27269[G/A]/rs7818177
 27301  gaagtaactt ttacaaaaca tacccagtgt ttggggtgtt tcaaaagtgg
 27351  attttcctga atattaatcc cagccctacc cttgttagtt attttaggag
 27401  acagtctcaa gcactaaaaa gtggctaatt caatttatgg ggtatagtgg
 27451  ccaaatagca catcctccaa cgttaaaaga cagtggatca tgaaaagtgc
 27501  tgttttgtcc tttgagaaag aaataattgt ttgagcgcag agtaaaataa
 27551  ggctccttca tgtggcgtat tgggccatag cctataattg gttagaacct
 27601  cctattttaa Ttggaattct ggatctttCg gactgaggcc ttctcaaact  p.27611[T/C]/rs3289; p.27629[C/G]
 27651  ttactctaag tctccaagaa tacagaaaat gcttttcCgc ggcaCgaatc  p.27695[C/A]
 27701  agactCatct acacagcagt atgaatgatg ttttagaatg attccctctt  p.27706[C/A]
 27751  gctattggaa tgtggtccag acgtcaacca ggAacatgta acttggagag
 27801  ggacgaagaa agggtctgat aaacacagag gttttaaaca gtccctacca
 27851  ttggcctgca tcatgacaaa gttacaaatt caaggagata taaaatctag
 27901  atcaattaat tcttaatagg ctttatcGtt tattgcttaa tccctctctc  p.27928[G/A]
 27951  ccccttcttt tttgtctcAa gattatatta taataatgtt ctctgggtag  p.27969[A/G]
 28001  gtgttgaaaa tgagcctgta atcctcagct gacacAtaat ttgaatggtg  p.28036[A/G]/rs11570892
 28051  cagaaaaaaa aAaagaAacc gtaattttat tattagattc tcCaaatgat  rs77671382[A/C][MAF]; p.28062[A/G]; p.28067[A/T]/rs3208305;
p.28093[C/T]/rs1803924
 28101  tttcatcaat ttaaaatcat tcaatatctg acagttactc ttcagtttta
 28151  ggcttacctt ggtcatgctt cagttgtact tccagtgcgt ctcttttgtt
 28201  cctggctttg acatgaaaag ataggtttga gttcaaattt tgcattgtgt
 28251  gagcttctac agattttaga caaggaccgt ttttactaag taaaagggtg
 28301  gagaggttcc tggggtggat tcctaagcag tgcttgtaaa ccatcgcgtg
 28351  caatgagcca gatggagtac catgagggtt gCtatttgtt gtttttaaca  p.28382[C/T]/rs1059507
 28401  actaatCaag agtgaatgaa caactattta taaactagat ctcctatttt
 28451  tcagaatgct cttCtacgta taaatatgaa atgataaagA tgtcaaatat  p.28464[C/A]/rs3735964; p.28490[A/G]/rs3200218
 28501  ctcagaggct atagctggga acccgactgt Gaaagtatgt gatatctgaa  p.28531[G/A]
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 28551  cacatactag aaagctctgc atgtgtgttg tccttcagca taattcggaa
 28601  gggaaaacag tcgatcaagg gatgtattgg aacatgtcgg agtagaaatt
 28651  gttccTgatg tgccagaaCt tcgacccttt ctctgagaga gatgatcgtg  p.28656[T/C]/rs58998793; p.28669[C/T]
 28701  cctataaata gtaggaccaa tgttgtgatt aacatcatca ggcttggaat
 28751  gaattctctc taaaaataaa atgatgtatg atttgttgtt ggcatcccct
 28801  ttattaattc attaaatttc tggatttggg ttgtgaccca gggtgcatta
 28851  acttaaaaga ttcactaaag cagcacatag cactgggaac tctggctccg
 28901  aaaaactttg Ctatatatat caaggatgtt ctggctttac attttattta  p.28911[C/T]/rs13702
 28951  ttagctgtaa atacatgtgt ggatgtgtaa aTggagcttg tacatattgg  p.28982[T/C]/rs1059611
 29001  aaaggtcatt gtggctatct gcAtttataa atgtgtggtg ctaacTGtat  p.29023[A/T]/rs17091815; p.29046_29047insTT;
p.29047[G/T]/rs78359368
 29051  gtgtctttat cagtgatggt ctcacagagc caactCaCtc ttatgaaAtg  p.29086[C/T]/rs15285; p.29088[C/A]/rs3866471; p.29098[A/G]
 29101  ggctttaacA aaacaagaaa gaaacGtact taactgtgtg aagaaatgga  p.29110[A/C]; p.29126[G/A]
 29151  atcagctttt aataaaaTtg acaacatttt attaccaca p.29168[T/C]/rs79756214
 29190  ctaagtcatt attttgtatc attttttaaag taaatttatt cttaggtcag  rs71510671
 29240  attcactcag catattttga ctaagtaacc actgtactta gtaaaccGaa  p.29287[G/A]/rs3916027
 29290  gagcttctga gaattatagt gtaccTtata gatattttta acatttatat  p.29315[T/G]/rs9644636
 29340  ttgtataaag ctaaagaaag ccttacatat cctttaaact gactatagaa
 29390  gaaaatgata cagaattttg cctgcataaa gtacacagga ctattcttgc
 29440  ctacaatatg ctttttcaca agcaaaatgt tagactaata taaggcaTct  p.29487[T/A]/rs4921683
 29490  ttggccattt tatagtgtac atcatctcta tttctgaggc ctcattgtta
 29540  gctGtaaCgc aagtagcatt tgtgcaataa aatgaactat ttgggatggg  p.29543[G/A]/rs76707496; p.29547[C/T]/rs4921684;
 29590  agggtacatt ttttagaact ttgctttggg ttgccttgat aattaatagc
 29640  atatagtcca tttatgcagc taagtaggga ttgcttctta gtacagtcag
 29690  gaagaattta gcccagaaaa caattaTttc aatggccact gacccaaact
 29740  tccaggctga agagcaatgg cgtgatcatg gctcactgca cctccacctc
 29790  ccaggctcaa gtgattctcc tgcctcagcc tcccaaGtag atggtactac  p.29826[G/A]
 29840  aagcacaCgc cactgcaccc agctaatttt tgtatttttt gtagagatgg  p.29847[C/T]
 29890  gggtttcacc atgttgccca ggctggtctt aaattcctgg cctcaagtgt
 29940  ctgcccccct tggcctccca aagtgctgga attacaggca tgagccacca
 29990  tgtccagcct tgacccaaac ttttattgtc agttagctat tggggcttct
 30040  ggagtttggg Tctcccctga caggaggggg ctccccagtt cacacttggc  p.30050[T/A]/rs77004748
 30090  cactgcccat caattcctgt tgatatgatc aacaagatag acaattgcaa
 30140  atgttgctga ggatgtggag aagtgtgaac ctgtgtaagt ggctgatggg
 30190  aatgtaaaat ggcacagcca ctatggagaa caatttggta gtatttccaa
 30240  agttaagcat agagtttaac ccatatgacc cagcaattcc actcctagat
 30290  atatacccaa gaga
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Appendix Figure A3.1- *LPL* Annotated FASTA Sequence. The color FASTA representation of the *LPL* annotated reference sequence was adapted and modified from the CHIP Bioinformatics database (http://snpper.chip.org). The color code for the reference sequence is as follows: green for 5' and 3' flanking regions, grey for introns, black for exons. Capital letters are used to show introns and coding exons whereas small letters show the the UTRs and flanking regions. The variants identified in this study also listed in dbSNP build 137 are shown with refSNP ID; novel variants are shown in red. The small deletions and insertion locations identified in our study are shown by highlighting the region in yellow. We identified a large deletion in intron 2 which was not reported before in any public databases and it is highlighted in *italics.*

APPENDIX B. SUPPLEMENTARY TABLES AND FIGURES FOR CETP GENE RESEQUENCING AND ASSOCIATION ANALYSES

APPENDIX B1. Supplementary Tables for CETP gene resequencing and association analyses

TABLE B1.1. Variants identified in the sequencing sample of 95 NHW individuals

CETP Variant	**Position**	**RefSNPID**	**Amino Acid change**	**Alleles**	**Location**	**HWE (p-value)**	**Call rate**	**MAF**	**[c]RegulomeDB Score**
CTP220	220	rs12447924		T>C	5' flanking	1.000	98.9	0.17	No data
CTP240	240	rs12720918		T>C	5' flanking	0.879	98.9	0.309	6
CTP273del1	273	rs36229491		W>D	5' flanking	0.843	97.9	0.360	6
CTP557	557	rs17231506		C>T	5' flanking	1.000	100	0.363	6
CTP848	848	rs12708968		T>C	5' flanking	0.912	100	0.089	5
CTP923	923	rs4783961		A>G	5' flanking	0.977	100	0.432	4
CTP1019	1019	rs17245715		C>T	5' flanking	0.912	100	0.089	2b
CTP1067	1067	rs4783962		C>T	5' flanking	1.000	100	0.168	4
CTP1263	1263	rs1800776		C>A	5' flanking	0.624	98.9	0.064	3a
CTP1265	1265	rs1800775		A>C	5' flanking	0.834	98.9	0.463	3a
CTP2133	2133	rs17231534		C>A	Intron 1	1.000	100	0.042	5
CTP2187	2187	rs3816117		T>C	Intron 1	1.000	96.8	0.435	5
CTP2240	2240	rs711752		G>A	Intron 1	0.834	98.9	0.463	5
CTP2308	2308	rs5030708		C>T	Intron 1	1.000	98.9	0.016	5
CTP2317	2317	rs708272	Taq1B	G>A	Intron 1	0.843	96.8	0.467	5
CTP2676del2	2676	rs34145065		W>D	Intron 1	0.985	98.9	0.457	No data
CTP2678	2678	rs34620476		C>A	Intron 1	0.985	98.9	0.457	No data
CTP3262	3262	rs1864163		G>A	Intron 2	1.000	100	0.289	5
CTP3381del1	3381	rs5817083		W>D	Intron 2	0.968	100	0.3	6
CTP3399	3399	rs4587963		T>A	Intron 2	1.000	98.9	0.17	No data
CTP3412	**3412**	**Novel**		**A>G**	**Intron 2**	**1.000**	**98.9**	**0.005**	No data
CTP3581	3581	rs4369653		T>C	Intron 2	0.096	92.6	0.136	No data
CTP3686	3686	rs7194225		G>C	Intron 2	0.858	92.6	0.08	No data
CTP3854	**3854**	**Novel**		**G>T**	**Intron 2**	**1.000**	**92.6**	**0.006**	No data
CTP4559	**4559**	**Novel**		**C>T**	**Intron 2**	**1.000**	**97.9**	**0.005**	No data
CTP4602	4602	rs9929488		G>C	Intron 2	0.491	97.9	0.312	4
CTP4948	4948	rs12720926		A>G	Intron 2	0.183	86.3	0.463	2b
CTP5288	5288	rs7203984		A>C	Intron 2	0.834	86.3	0.293	5
CTP5358	5358	rs11508026		C>T	Intron 2	0.975	86.3	0.451	5
CTP5810del1	5810	rs17231569		W>D	Intron 2	1.000	91.6	0.241	5
CTP5979	5979	rs708273		G>A	Intron 2	0.850	91.6	0.213	5
CTP6314	6314	rs820299		A>G	Intron 2	0.045	95.8	0.352	5
CTP6725	6725	rs8045855		T>A	Intron 2	0.006	88.4	0.101	6
CTP6914	6914	rs12720922		G>A	Intron 2	0.002	81.1	0.097	5
CTP8695	8695	rs9926440		G>C	Intron 2	0.086	98.9	0.33	5
CTP8764	8764	rs9939224		G>T	Intron 2	0.574	98.9	0.245	5
CTP9178	9178	rs11076174		T>C	Intron 2	0.788	95.8	0.099	No data
CTP10459	10459	rs139040281		A>C	Intron 5	1.000	98.9	0.005	No data
CTP10921	10921	rs7205804		G>A	Intron 5	0.507	98.9	0.452	5
CTP10924	10924	rs12708972		C>T	Intron 5	1.000	100	0.005	4
CTP11194	11194	rs34523084		C>T	Intron 6	1.000	100	0.016	1f
CTP11332	11332	rs1532625		C>T	Intron 7	0.592	100	0.458	4
CTP11510	11510	rs1532624		C>A	Intron 7	0.739	97.9	0.457	5
CTP11581	11581	rs12708974		C>T	Intron 7	1.000	95.8	0.093	5
CTP11793	11793	rs117040820		C>T	Intron 7	1.000	98.9	0.005	5
CTP12103	12103	rs12720873		G>A	Intron 8	1.000	100	0.026	5
CTP12123	**12123**	**Novel**		**T>A**	**Intron 8**	**1.000**	**100**	**0.005**	**No data**
CTP12178	12178	rs148654654		C>T	Intron 8	1.000	100	0.005	No data
CTP12331del1	12331	rs67114203		W>D	Intron 8	1.000	100	0.232	6
CTP12336	12336	rs289712		C>T	Intron 8	1.000	100	0.232	No data
CTP12409	12409	rs11076175		A>G	Intron 8	1.000	98.9	0.234	5
CTP12621	12621	rs7499892		C>T	Intron 8	1.000	100	0.237	4
CTP12746	12746	rs187766748		A>G	Intron 8	1.000	100	0.011	No data
CTP12860	12860	rs289713		A>T	Intron 8	1.000	100	0.237	5
CTP13071	13071	rs187468344		C>T	Intron 8	1.000	100	0.011	No data
CTP13223	13223	rs9930761		T>C	Intron 8	0.995	100	0.084	4
CTP13327	13327	rs28381707		G>T	Exon 9	1.000	100	0.005	3a
CTP13384	13384	rs5883	Phe287Phe	C>T	Exon 9	0.712	100	0.068	4
CTP13477	13477	rs11076176		T>G	Intron 9	0.876	100	0.189	5
CTP13482	13482	rs289714		A>G	Intron 9	0.876	100	0.189	5
CTP13641	13641	rs158477		G>A	Intron 9	1.000	100	0.495	5
CTP13683	13683	rs11644475		A>G	Intron 9	1.000	100	0.026	No data
CTP13765	13765	rs158478		A>C	Intron 9	1.000	100	0.489	No data

Table B1.1. Continued

CETP Variant	Position	RefSNPID	Amino Acid change	Alleles	Location	HWE (p-value)	Call rate	MAF	[c]RegulomeDB Score
CTP13868	**13868**	**Novel**		**C>T**	**Intron 9**	**1.000**	**100**	**0.005**	**No data**
CTP14079	14079	rs158479		A>G	Intron 9	1.000	100	0.489	2b
CTP14123	14123	rs181381869		G>A	Intron 9	1.000	98.9	0.016	No data
CTP14232del2	**14232**	**Novel**		**W>D**	**Intron 9**	**1.000**	**100**	**0.011**	**No data**
CTP14258	14258	rs158480		A>G	Intron 9	0.655	100	0.105	No data
CTP14318	14318	rs158617		G>A	Intron 9	0.655	100	0.105	No data
CTP14539	14539	rs289715		T>A	Intron 9	0.655	100	0.105	No data
CTP15277	**15277**	**Novel**		**A>G**	**Intron 10**	**1.000**	**100**	**0.005**	**No data**
CTP15407	15407	rs289716		A>T	Intron 10	0.015	100	0.3	No data
CTP15419	15419	rs289717		G>A	Intron 10	0.309	100	0.316	No data
CTP15688del1	15688	rs35874588		W>D	Intron 10	0.049	100	0.3	5
CTP15800	15800	rs736274		T>A	Intron 10	0.646	98.9	0.106	5
CTP15963	15963	rs289718		T>C	Intron 10	0.028	97.9	0.28	5
CTP15972	15972	rs289719		C>T	Intron 10	0.009	95.8	0.269	5
CTP16016	16016	rs2033254		T>C	Intron 10	0.101	100	0.395	4
CTP16059	16059	rs183439140		C>T	Intron 10	1.000	100	0.005	No data
CTP16148	16148	rs72771489		G>A	Intron 10	1.000	100	0.005	5
CTP16263	16263	rs56208677		C>T	Intron 10	1.000	100	0.105	5
CTP16413	16413	rs71387147		T>G	Intron 10	0.619	100	0.063	5
CTP16508	**16508**	**Novel**		**G>C**	**Intron 10**	**1.000**	**100**	**0.005**	**No data**
CTP16517	16517	rs117427818		C>T	Intron 10	1.000	100	0.026	No data
CTP16550	16550	rs142980129		G>T	Intron 10	1.000	100	0.005	No data
CTP16598	**16598**	**Novel**		**C>T**	**Intron 10**	**1.000**	**100**	**0.016**	**No data**
CTP16859	16859	rs11860407		A>G	Intron 10	0.014	66.3	0.468	6
CTP16979	16979	rs1968905		G>T	Intron 10	0.327	90.5	0.134	6
CTP17025	17025	rs12720897		T>G	Intron 10	1.000	90.5	0.035	No data
CTP17216	17216	rs4784744		G>A	Intron 10	0.179	89.5	0.324	5
CTP17274	17274	rs12720898		C>T	Intron 10	1.000	90.5	0.035	5
CTP18256	18256	rs28381709		C>A	Intron 11	1.000	100	0.005	5
CTP18413	18413	rs12708980		T>G	Intron 11	0.069	100	0.389	6
CTP18597	18597	rs12720889		A>T	Intron 11	0.072	100	0.289	6
CTP18663	**18663**	**Novel**		**C>T**	**Intron 11**	**1.000**	**100**	**0.005**	**6**
CTP18678	**18678**	**Novel**		**T>G**	**Intron 11**	**1.000**	**100**	**0.005**	**No data**
CTP18717	18717	rs143024882		C>A	Intron 11	1.000	100	0.016	No data
CTP18733	18733	rs291043		A>G	Intron 11	0.143	100	0.332	6
CTP18921	18921	rs17239354		G>A	Intron 11	1.000	100	0.042	No data
CTP20354	20354	rs12447620		G>A	Intron 11	1.000	30.5	0.086	No data
CTP20446	20446	rs12708983		T>C	Intron 11	1.000	100	0.021	6
CTP20593	**20593**	**Novel**		**G>A**	**Intron 11**	**1.000**	**100**	**0.005**	**No data**
CTP20645	20645	rs12708985		C>T	Intron 11	0.705	100	0.116	No data
CTP20675	**20675**	**Novel**		**C>T**	**Intron 11**	**1.000**	**100**	**0.005**	**No data**
CTP20804	**20804**	**Novel**		**G>A**	**Intron 11**	**1.000**	**100**	**0.005**	**No data**
CTP20910	20910	rs4784745		A>G	Intron 11	0.193	100	0.337	5
CTP21126	21126	rs5880	Ala373Pro	G>C	Exon 12	1.000	100	0.026	5
CTP21371del12	21371	rs11276066		D>W	Intron 12	0.655	100	0.105	4
CTP21580	21580	rs1800774		C>T	Intron 12	0.299	100	0.4	4
CTP22127	22127	rs5882	I405V	A>G	Exon 14	0.437	100	0.274	5
CTP22327	22327	rs111379440		C>T	Intron 14	1.000	100	0.005	6
CTP22349	22349	rs12720882		A>G	Intron 14	1.000	100	0.011	No data
CTP22888del1	**22888**	**Novel**		**W>D**	**Intron 14**	**1.000**	**100**	**0.005**	No data
CTP22997	22997	rs12720887		C>T	Intron 14	1.000	100	0.021	4
CTP23037	23037	rs9923854		T>G	Intron 14	1.000	100	0.121	3a
CTP23353	23353	rs1800777	R451Q	G>A	Exon 15	1.000	100	0.021	4
CTP23508	23508	rs289741		A>G	Intron 15	0.355	100	0.268	4
CTP23696	23696	rs1801706		G>A	3' UTR-Exon 16	0.487	100	0.163	4
CTP23796	23796	rs289742		G>C	3' flanking	0.655	100	0.105	4
CTP23830	23830	rs289743		A>G	3' flanking	0.355	100	0.268	2b
CTP24136	24136	rs289744		T>G	3' flanking	0.355	100	0.268	5
CTP24669	24669	rs66495554		C>T	3' flanking	0.198	100	0.405	3a
CTP24889	24889	rs112039804		T>A	3' flanking	0.655	100	0.105	2b
CTP25425	25425	rs12720917		T>C	3' flanking	1.000	100	0.174	4
CTP25565	25565	rs289745		A>C	3' flanking	1.000	100	0.463	4

MAF: minor allele frequency; Bold: novel variants

[a]Positions in the reference sequence NC_000016

[b]Variants are reported based on the allele in the reference sequence.

[c]RegulomeDB scores were generated by using http://regulome.stanford.edu/. Scores represents;
1a- eQTL + TF binding + matched TF motif + matched DNase Footprint + DNase peak;
1b- eQTL + TF binding + any motif +
DNase Footprint + DNase peak; 1c- eQTL + TF binding + matched TF motif + DNase peak; 1d- eQTL + TF binding + any motif + DNase peak; 1e- eQTL + TF binding + matched TF motif;
1f- eQTL + TF binding /
DNase peak; 2a- TF binding + matched TF motif + matched DNase Footprint + DNase peak; 2b- TF binding + any motif + DNase Footprint + DNase peak; 2c- TF binding + matched TF motif + DNase peak;
3a- TF binding + any motif + DNase peak; 3b- TF binding + matched TF motif; 4- TF binding + DNase peak; 5-TF binding or DNase peak; 6-other

TABLE B1.2. Variants identified in the sequencing sample of 95 African blacks

CETP Variant	[a]Position	RefSNP ID	AminoAcid change	[b]Alleles	Location	HWE (p-value)	Call rate	MAF	[c]RegulomeDB Score
CTP109	109	Novel		T>G	5' flanking	1.000	100	0.005	No data
CTP163	163	rs13332526		A>G	5' flanking	1.000	100	0.058	5
CTP187	187	rs148562851		A>G	5' flanking	0.216	100	0.037	No data
CTP220	220	rs12447924		T>C	5' flanking	0.978	100	0.195	No data
CTP240	240	rs12720918		T>C	5' flanking	0.484	100	0.258	6
CTP266	266	rs13332571		A>G	5' flanking	1.000	100	0.058	6
CTP273del1	273	rs36229491		D>W	5' flanking	1.000	98.9	0.096	No data
CTP296	296	Novel		G>A	5' flanking	1.000	98.9	0.005	No data
CTP452	452	Novel		C>A	5' flanking	1.000	100	0.011	No data
CTP546	546	Novel		A>C	5' flanking	1.000	100	0.005	No data
CTP557	557	rs17231506		C>T	5' flanking	1.000	100	0.095	6
CTP848	848	rs12708968		T>C	5' flanking	1.000	85.3	0.062	5
CTP870	870	rs13338602		C>G	5' flanking	1.000	85.3	0.062	5
CTP923	923	rs4783961		A>G	5' flanking	0.975	86.3	0.451	4
CTP950	950	rs146122874		C>T	5' flanking	0.181	86.3	0.037	No data
CTP1067	1067	rs4783962		C>T	5' flanking	0.821	97.9	0.075	3a
CTP1153	1153	rs17237883		G>A	5' flanking	1.000	97.9	0.043	4
CTP1189	1189	rs114856405		C>A	5' flanking	1.000	87.4	0.036	4
CTP1263	1263	rs1800776		C>A	5' flanking	1.000	100	0.032	3a
CTP1265	1265	rs1800775	Taq1B	A>C	5' flanking	0.817	96.8	0.348	3a
CTP1856	1856	rs17231520		G>A	5' flanking	1.000	100	0.142	5
CTP1937	1937	rs34119551	D6V	T>A	Exon 1	1.000	98.9	0.021	5
CTP1964	1964	rs34065661	A15G	C>G	Exon 1	1.000	98.9	0.144	5
CTP1986	1986	rs5884	*Synonymous*	C>A	Exon 1	1.000	98.9	0.059	5
CTP2089	2089	rs34680782		C>A	Intron 1	1.000	97.9	0.022	5
CTP2133	2133	rs17231534		C>A	Intron 1	1.000	97.9	0.231	5
CTP2187	2187	rs3816117		C>T	Intron 1	0.725	88.4	0.351	5
CTP2240	2240	rs711752		G>A	Intron 1	1.000	95.8	0.269	5
CTP2317	2317	rs708272		G>A	Intron 1	1.000	96.8	0.272	5
CTP2676del2	2676	rs34145065		W>D	Intron 1	1.000	94.7	0.117	No data
CTP2678	2678	rs34620476		C>A	Intron 1	1.000	94.7	0.117	No data
CTP2692	2692	rs60195610		G>A	Intron 1	0.110	95.8	0.027	No data
CTP2736	2736	rs59008849		G>T	Intron 1	1.000	94.7	0.006	No data
CTP3101	3101	rs9935228		A>G	Intron 2	1.000	75.8	0.076	5
CTP3153	3153	Novel		G>A	Intron 2	1.000	98.9	0.005	No data
CTP3262	3262	rs1864163		G>A	Intron 2	0.788	98.9	0.255	5
CTP3347	3347	rs75313088		G>A	Intron 2	1.000	98.9	0.037	5
CTP3381del1	3381	rs5817083		W>D	Intron 2	0.058	98.9	0.415	6
CTP3399	3399	rs4587963		T>A	Intron 2	0.000	61.1	0.129	No data
CTP3581	3581	rs4369653		T>C	Intron 2	0.003	66.3	0.111	No data
CTP3686	3686	rs7194225		G>C	Intron 2	0.003	66.3	0.111	No data
CTP3803_3804Ins1	3803	Novel		W>I	Intron 2	1.000	65.3	0.016	No data
CTP3918	3918	Novel		T>A	Intron 2	0.455	61.1	0.069	No data
CTP4299	4299	rs114908369		C>A	Intron 2	1.000	96.8	0.027	5
CTP4602	4602	rs9929488		G>C	Intron 2	0.781	97.9	0.478	4
CTP4791	4791	rs12720906		T>G	Intron 2	1.000	97.9	0.022	4
CTP4948	4948	rs12720926		A>G	Intron 2	1.000	100	0.032	2b
CTP4957	4957	rs17237939		G>A	Intron 2	1.000	100	0.042	2b
CTP5130	5130	rs116604371		T>A	Intron 2	1.000	100	0.005	3a
CTP5209	5209	Novel		C>T	Intron 2	1.000	98.9	0.005	No data
CTP5215del1	5215	**rs35585922**		W>D	Intron 2	0.690	100	0.205	5
CTP5288	5288	rs7203984		C>A	Intron 2	0.008	70.5	0.396	5
CTP5358	5358	rs11508026		C>T	Intron 2	1.000	70.5	0.045	5
CTP5375	5375	rs80296794		T>C	Intron 2	1.000	70.5	0.03	5
CTP5383del1	5383	rs71383212		W>D	Intron 2	0.675	98.9	0.229	5
CTP5593	5593	rs112236143		C>A	Intron 2	1.000	87.4	0.024	4
CTP5808	5808	rs17237946		C>T	Intron 2	1.000	98.9	0.021	5
CTP5810del1	5810	rs17231569		W>D	Intron 2	0.592	98.9	0.378	5
CTP5979	5979	rs708273		G>A	Intron 2	0.097	96.8	0.103	5
CTP5990	5990	rs17231583		G>C	Intron 2	1.000	86.3	0.018	5
CTP6022_6023Ins1	6022	rs142058276		W>I	Intron 2	0.737	96.8	0.12	No data
CTP6221	6221	rs17231590		A>G	Intron 2	0.364	98.9	0.048	5
CTP6239	6239	rs17237953		C>A	Intron 2	1.000	98.9	0.032	5
CTP6251	6251	rs35619327		C>T	Intron 2	1.000	95.8	0.022	5
CTP6314	6314	rs820299		G>A	Intron 2	0.038	94.7	0.444	5
CTP6361	6361	Novel		G>C	Intron 2	1.000	94.7	0.006	No data
CTP6427	6427	rs17237967		G>A	Intron 2	1.000	94.7	0.039	No data
CTP6725	6725	rs8045855		T>A	Intron 2	0.081	87.4	0.422	6
CTP6914	6914	rs12720922		G>A	Intron 2	0.642	91.6	0.333	5
CTP8695	8695	rs9926440		C>G	Intron 2	0.653	100	0.226	5

Table B1.2. Continued

CETP Variant	[a]Position	RefSNP ID	AminoAcid change	[b]Alleles	Location	HWE (p-value)	Call rate	MAF	[c]RegulomeDB Score
CTP8698	8698	rs192306644		G>A	Intron 2	1.000	96.8	0.005	
CTP8742	8742	rs12720863		A>G	Intron 2	1.000	100	0.021	
CTP8764	8764	rs9939224		G>T	Intron 2	1.000	98.9	0.372	5
CTP9075	9075	rs60531466		C>T	Intron 2	1.000	100	0.121	No data
CTP9178	9178	rs11076174		T>C	Intron 2	1.000	100	0.111	No data
CTP9282	9282	rs13306230		C>A	Intron 2	1.000	100	0.005	No data
CTP9493	9493	rs12708971		T>C	Intron 3	1.000	100	0.016	4
CTP9670	9670	rs60896367		G>C	Intron 4	1.000	100	0.005	No data
CTP9693	9693	rs35752722		G>A	Intron 4	1.000	100	0.011	No data
CTP9755	9755	rs891141		T>G	Intron 4	0.487	100	0.163	6
CTP9841	9841	Novel		G>A	Intron 4	1.000	97.9	0.005	No data
CTP9878	9878	rs34716057	R137W	C>T	Exon 5	1.000	100	0.021	No data
CTP10009	10009	s891142		C>T	Intron 5	0.914	100	0.137	No data
CTP10012	10012	rs891143		C>T	Intron 5	0.324	100	0.132	No data
CTP10491	10491	rs12720861		G>A	Intron 5	1.000	96.8	0.13	4
CTP10694	10694	rs12720860		C>T	Intron 5	1.000	96.8	0.13	5
CTP10775	10775	Novel		G>A	Intron 5	1.000	96.8	0.011	
CTP10779	10779	rs12720862		A>G	Intron 5	1.000	96.8	0.13	6
CTP10921	10921	rs7205804		G>A	Intron 5	1.000	100	0.1	5
CTP10934	10934	rs12708973		A>G	Intron 5	1.000	100	0.016	5
CTP10943	10943	rs148134355		G>A	Intron 5	1.000	100	0.016	No data
CTP10983	10983	rs34611098	*Synonymous*	G>A	Exon 6	1.000	100	0.005	5
CTP11332	11332	rs1532625		C>T	Intron 7	1.000	100	0.095	1f
CTP11433	11433	Novel		G>A	Intron 7	1.000	97.9	0.005	No data
CTP11456	11456	rs12720925		T>C	Intron 7	1.000	97.9	0.022	4
CTP11510	11510	rs1532624		C>A	Intron 7	1.000	97.9	0.097	4
CTP11651	11651	rs12597250		T>C	Intron 7	0.487	100	0.163	5
CTP11795	11795	rs12720871		C>G	Intron 7	1.000	97.9	0.038	5
CTP11913	11913	rs12720872		C>T	Intron 7	0.703	97.9	0.151	5
CTP12281	12281	Novel		C>T	Intron 8	1.000	95.8	0.005	No data
CTP12331del1	12331	rs67114203		D>W	Intron 8	0.922	95.8	0.253	No data
CTP12336C>T	12336	rs289712		C>T	Intron 8	1.000	95.8	0.104	6
CTP12336C>A	12336	rs289712		C>A	Intron 8	1.000	95.8	0.027	6
CTP12409	12409	rs11076175		A>G	Intron 8	1.000	95.8	0.231	4
CTP12621	12621	rs7499892		C>T	Intron 8	0.968	100	0.3	5
CTP12627	12627	rs146562593		G>A	Intron 8	1.000	100	0.005	No data
CTP12860	12860	rs289713		T>A	Intron 8	0.419	100	0.432	5
CTP12913	12913	rs191754368		C>T	Intron 8	1.000	100	0.021	No data
CTP12970	12970	rs182480194		T>A	Intron 8	1.000	100	0.005	No data
CTP12981	12981	rs146782017		G>A	Intron 8	1.000	100	0.005	No data
CTP13223	13223	rs9930761		T>C	Intron 8	0.812	98.9	0.213	4
CTP13279	13279	rs35878799	*Synonymous*	T>C	Exon 9	1.000	98.9	0.005	4
CTP13384	13384	rs5883	FL287	C>T	Exon 9	0.878	97.9	0.204	4
CTP13477	13477	rs11076176		T>G	Intron 9	0.714	100	0.353	5
CTP13482	13482	rs289714		G>A	Intron 9	0.885	100	0.484	5
CTP13641	13641	rs158477		G>A	Intron 9	0.731	100	0.479	5
CTP13765	13765	rs158478		A>C	Intron 9	1.000	100	0.389	No data
CTP13849	13849	Novel		C>T	Intron 9	1.000	100	0.016	No data
CTP14079	14079	rs158479		G>A	Intron 9	0.677	97.9	0.355	2b
CTP14192	14192	rs12720892		G>A	Intron 9	1.000	100	0.032	No data
CTP14258	14258	rs158480		A>G	Intron 9	1.000	100	0.426	No data
CTP14318	14318	rs158617		G>A	Intron 9	1.000	100	0.384	No data
CTP144488_14451 del4	14448	rs147606537		W>D	Intron 9	1.000	100	0.011	No data
CTP14539	14539	rs289715		T>A	Intron 9	1.000	100	0.216	No data
CTP14715	14715	rs186780244		C>G	Intron 9	1.000	100	0.005	No data
CTP15196	15196	rs116351574		A>G	Intron 10	1.000	92.6	0.011	No data
CTP15226	15226	rs2303789		T>G	Intron 10	1.000	90.5	0.035	No data
CTP15231	15231	rs12720877		C>T	Intron 10	1.000	90.5	0.076	No data
CTP15232	15232	rs13306232		G>C	Intron 10	1.000	90.5	0.006	No data
CTP15407	15407	rs289716		T>A	Intron 10	0.830	86.3	0.415	No data
CTP15419	15419	rs289717		G>A	Intron 10	1.000	92.6	0.125	No data
CTP15542	15542	rs12708976		C>T	Intron 10	1.000	94.7	0.022	No data
CTP15597	15597	rs116578082		G>A	Intron 10	1.000	94.7	0.006	No data
CTP15639	15639	rs12720942		A>G	Intron 10	1.000	100	0.037	5
CTP15688del1	15688	rs35874588		W>D	Intron 10	0.874	100	0.374	No data
CTP15800	15800	rs736274		T>A	Intron 10	1.000	98.9	0.021	5
CTP15830	15830	rs12720939		C>A	Intron 10	1.000	100	0.037	5
CTP15913	15913	rs12720937		C>G	Intron 10	1.000	100	0.037	No data
CTP15963	15963	rs289718		C>T	Intron 10	1.000	100	0.384	5
CTP15972	15972	rs289719		T>C	Intron 10	1.000	100	0.463	5
CTP16016	16016	rs2033254		T>C	Intron 10	0.498	100	0.295	4
CTP16146	16146	rs112205272		G>A	Intron 10	1.000	98.9	0.043	5
CTP16363	16363	rs112409939		A>G	Intron 10	1.000	97.9	0.043	5
CTP16413	16413	rs71387147		T>G	Intron 10	1.000	97.9	0.032	5

Table B1.2. Continued

CETP Variant	[a]Position	RefSNP ID	AminoAcid change	[b]Alleles	Location	HWE (p-value)	Call rate	MAF	[c]RegulomeDB Score
CTP16508	16508	Novel		G>A	Intron 10	1.000	94.7	0.006	5
CTP16709	16709	rs151104194		G>C	Intron 10	1.000	94.7	0.006	No data
CTP16859	16859	rs11860407		A>G	Intron 10	0.005	60	0.368	6
CTP16935	16935	rs12720901		T>A	Intron 10	1.000	89.5	0.012	No data
CTP16979	16979	rs1968905		G>T	Intron 10	0.601	94.7	0.372	6
CTP17154	17154	rs12720903		G>A	Intron 10	1.000	94.7	0.067	6
CTP17216	17216	rs4784744		G>A	Intron 10	0.940	94.7	0.083	5
CTP17483	17483	rs291044		G>A	Intron 10	1.000	76.8	0.062	5
CTP17575	17575	rs114486472		G>A	Intron 10	1.000	98.9	0.021	5
CTP17740	17740	Novel		C>T	Intron 10	1.000	100	0.016	No data
CTP17860	17860	rs8053613		C>T	Intron 10	1.000	100	0.005	5
CTP17875	17875	rs34337891		T>C	Intron 10	1.000	100	0.005	5
CTP17918	17918	rs34426213		C>T	Intron 10	1.000	100	0.037	5
CTP17970	17970	rs891144		C>T	Intron 10	0.775	100	0.184	5
CTP18388	18388	rs12708979		C>T	Intron 11	1.000	100	0.032	6
CTP18413	18413	rs12708980		T>G	Intron 11	1.000	100	0.332	6
CTP18597	18597	rs12720889		A>T	Intron 11	0.576	98.9	0.245	6
CTP18689	18689	Novel		C>T	Intron 11	1.000	100	0.005	No data
CTP18733	18733	rs291043		A>G	Intron 11	0.901	100	0.079	6
CTP18746	18746	Novel		C>T	Intron 11	1.000	100	0.005	No data
CTP18970	18970	rs114203109		G>A	Intron 11	1.000	100	0.032	6
CTP19317	19317	Novel		C>T	Intron 11	1.000	100	0.005	No data
CTP19519	19519	rs146251160		G>A	Intron 11	1.000	74.7	0.014	No data
CTP19561	19561	rs12708981		G>A	Intron 11	1.000	69.5	0.091	6
CTP19606	19606	rs12720858		C>T	Intron 11	0.995	75.8	0.097	No data
CTP19607	19607	Novel		G>A	Intron 11	1.000	76.8	0.068	No data
CTP19700	19700	rs12720857		T>C	Intron 11	0.895	97.9	0.091	6
CTP19734	19734	rs145189439		A>G	Intron 11	1.000	100	0.032	No data
CTP19757	19757	Novel		A>G	Intron 11	1.000	100	0.005	No data
CTP19789	19789	rs74678905		G>A	Intron 11	1.000	100	0.079	No data
CTP19872	19872	rs148807012		C>T	Intron 11	1.000	100	0.005	No data
CTP19881	19881	rs17238225		G>T	Intron 11	1.000	100	0.084	5
CTP20072	20072	rs80180245		C>T	Intron 11	1.000	100	0.084	5
CTP20284	20284	rs17238232		T>C	Intron 11	1.000	97.9	0.081	No data
CTP20354	20354	rs12447620		G>A	Intron 11	0.492	96.8	0.348	No data
CTP20374	20374	rs17231869		C>T	Intron 11	1.000	74.7	0.085	No data
CTP20442	20442	rs12708982		T>G	Intron 11	1.000	100	0.005	No data
CTP20457	20457	rs12708984		C>T	Intron 11	1.000	98.9	0.08	6
CTP20551	20551	rs115390156		C>A	Intron 11	1.000	100	0.005	No data
CTP20593	20593	Novel		G>A	Intron 11	1.000	100	0.011	No data
CTP20624	20624	Novel		A>G	Intron 11	1.000	100	0.005	No data
CTP20641	20641	rs189327489		T>C	Intron 11	1.000	100	0.084	No data
CTP20645	20645	rs12708985		C>T	Intron 11	1.000	98.9	0.181	No data
CTP20725	20725	rs140776547		C>T	Intron 11	1.000	100	0.021	No data
CTP20844	20844	rs13331688		G>A	Intron 11	1.000	100	0.037	4
CTP20855	20855	rs111754336		T>C	Intron 11	1.000	100	0.084	4
CTP20910	20910	rs4784745		A>G	Intron 11	0.806	100	0.074	4
CTP21111	21111	rs34855278	V385M	G>A	Exon 12	1.000	100	0.021	5
CTP21119C>G	21119	rs7192120	*Synonymous*	C>G	Exon 12	1.000	100	0.084	5
CTP21119C>T	21119	rs7192120		C>T	Exon 12	1.000	100	0.016	5
CTP21280	21280	rs7198026		T>C	Intron 12	1.000	100	0.084	3a
CTP21324	21324	rs140421500		A>C	Intron 12	1.000	98.9	0.011	No data
CTP21340	21340	Novel		G>C	Intron 12	1.000	98.9	0.005	No data
CTP21371del12	21371	rs11276066		D>W	Intron 12	0.543	97.9	0.317	4
CTP21415	21415	rs7197854		A>G	Intron 12	0.997	98.9	0.085	4
CTP21454	21454	rs114948973		G>A	Intron 12	1.000	98.9	0.021	2b
CTP21482	21482	rs7197340		C>G	Intron 12	0.912	100	0.089	4
CTP21498	21498	rs7195984		A>G	Intron 12	0.978	100	0.195	4
CTP21579	21579	rs7196174		G>T	Intron 12	1.000	100	0.084	4
CTP21580	21580	rs1800774		C>T	Intron 12	0.653	100	0.226	4
CTP21760	21760	rs78603009		T>C	Intron 13	1.000	100	0.084	5
CTP21937	21937	rs14251794		C>T	Intron 13	1.000	100	0.005	No data
CTP22127	22127	rs5882	I405V	G>A	Exon 14	0.810	100	0.326	5
CTP22162	22162	rs5886	*Synonymous*	G>A	Exon 14	0.823	100	0.095	5
CTP22337	22337	rs8045701		T>C	Intron 14	0.814	98.9	0.096	6
CTP22480	22480	rs12598103		C>G	Intron 14	0.814	98.9	0.096	5
CTP22554	22554	rs12596364		T>C	Intron 14	0.997	98.9	0.085	5
CTP22562	22562	rs12720884		T>G	Intron 14	0.997	98.9	0.085	5
CTP22683	22683	rs11076177		G>A	Intron 14	0.988	97.9	0.086	No data
CTP22985	22985	rs289740		T>C	Intron 14	0.623	98.9	0.112	4
CTP23037	23037	rs9923854		T>G	Intron 14	0.895	98.9	0.191	3a
CTP23152	23152	rs150048432		G>A	Intron 14	1.000	98.9	0.005	No data
CTP23201	23201	rs36051594		C>T	Intron 14	1.000	100	0.037	2b
CTP23508	23508	rs289741		G>A	Intron 15	0.940	100	0.316	4
CTP23696	23696	rs1801706		G>A	3'UTR-Exon 16	0.246	100	0.221	4

Table B1.2. Continued

CETP Variant	[a]Position	RefSNP ID	AminoAcid change	[b]Alleles	Location	HWE (p-value)	Call rate	MAF	[c]RegulomeDB Score
CTP23796	23796	rs289742		G>C	3' flanking	1.000	100	0.368	4
CTP23830	23830	rs289743		G>A	3' flanking	1.000	100	0.321	2b
CTP23858	23858	Novel		G>A	3' flanking	1.000	100	0.005	No data
CTP24136	24136	rs289744		G>T	3' flanking	0.940	100	0.316	3a
CTP24258	24258	rs76732052		T>G	3' flanking	1.000	100	0.005	5
CTP24499	24499	rs12720875		C>T	3' flanking	1.000	94.7	0.033	6
CTP24586	24586	rs7192754		G>T	3' flanking	0.980	96.8	0.087	6
CTP24669	24669	rs66495554		C>T	3' flanking	1.000	96.8	0.179	No data
CTP24767	24767	Novel		T>C	3' flanking	1.000	96.8	0.005	No data
CTP24881	24881	rs114646974		A>G	3' flanking	1.000	96.8	0.011	2b
CTP24889	24889	rs112039804		T>A	3' flanking	1.000	96.8	0.136	No data
CTP24899	24899	rs138161274		C>G	3' flanking	1.000	95.8	0.027	No data
CTP25049	25049	Novel		G>T	3' flanking	1.000	100	0.005	No data
CTP25064	25064	rs12720874		T>C	3' flanking	0.894	100	0.126	6
CTP25217	25217	rs76500832		A>G	3' flanking	1.000	98.9	0.011	5
CTP25218	25218	rs12720916		A>G	3' flanking	1.000	98.9	0.032	5
CTP25565	25565	rs289745		A>C	3' flanking	0.046	98.9	0.213	4

MAF: minor allele frequency

[a]Positions in the reference sequence NC_000016

[b]Variants are reported based on the allele in the reference sequence.

[c]RegulomeDB scores were generated by using http://regulome.stanford.edu/. Scores represents; 1a- eQTL + TF binding + matched TF motif + matched DNase Footprint + DNase peak; 1b- eQTL + TF binding + any motif + DNase Footprint + DNase peak; 1c- eQTL + TF binding + matched TF motif + DNase peak; 1d- eQTL + TF binding + any motif + DNase peak; 1e- eQTL + TF binding + matched TF motif; 1f- eQTL + TF binding / DNase peak; 2a- TF binding + matched TF motif + matched DNase Footprint + DNase peak; 2b- TF binding + any motif + DNase Footprint + DNase peak; 2c- TF binding + matched TF motif + DNase peak; 3a- TF binding + any motif + DNase peak; 3b- TF binding + matched TF motif; 4- TF binding + DNase peak; 5-TF binding or DNase peak; 6-other

TABLE B1.3. Distrubition of *CETP* variants between extremely high (n=47) and low (n=48) HDL-C/TG groups in NHWs

***CETP* variant**	**Position**	**Minor allele**	**Ref SNP ID**	**Location**	**High HDL-C /Low TG group allele counts**	**Low HDL-C/High TG group allele counts**	**MAF in High HDL-C/Low TG group**	**MAF in Low HDL-C/High TG group**	**MAF in the total sample**
CTP220	220	C	rs12447924	5' flanking	82:10	74:22	0.109	0.229	0.174
CTP240	240	C	rs12720918	5' flanking	69:23	61:35	0.25	0.365	0.335
CTP273del1	273	D	rs36229491	5' flanking	44:46	23:73	0.489	0.240	0.360
CTP557	557	T	rs17231506	5' flanking	47:47	22:74	0.500	0.229	0.451
CTP848	848	C	rs12708968	5' flanking	87:7	86:10	0.074	0.104	0.097
CTP923	923	A	rs4783961	5' flanking	61:33	47:49	0.649	0.49	0.463
CTP1019	1019	T	rs17245715	5' flanking	87:7	86:10	0.074	0.104	0.093
CTP1067	1067	T	rs4783962	5' flanking	84:10	74:22	0.106	0.229	0.163
CTP1263	1263	A	rs1800776	5' flanking	88:4	88:8	0.043	0.083	0.064
CTP1265	1265	A	rs1800775	5' flanking	60:32	41:55	0.652	0.427	0.432
CTP2133	2133	A	rs17231534	Intron 1	93:1	89:7	0.011	0.073	0.026
CTP2187	2187	C	rs3816117	Intron 1	58:34	40:52	0.630	0.435	0.495
CTP2240	2240	A	rs711752	Intron 1	54:40	34:60	0.574	0.362	0.489
CTP2308	2308	T	rs5030708	Intron 1	93:1	92:2	0.011	0.021	0.011
CTP2317	2317	A	rs708272	Intron 1	53:39	33:59	0.576	0.359	0.489
CTP2676del2	2676	D	rs34145065	Intron 1	53:41	34:60	0.564	0.362	0.468
CTP2678	2678	A	rs34620476	Intron 1	53:41	34:60	0.564	0.362	0.463
CTP3262	3262	A	rs1864163	Intron 2	71:23	64:32	0.245	0.333	0.293
CTP3381del1	3381	D	rs5817083	Intron 2	69:25	64:32	0.266	0.333	0.319
CTP3399	3399	A	rs4587963	Intron 2	81:11	75:21	0.12	0.219	0.174
CTP3412	3412	G	Novel	Intron 2	92:0	95:1	0	0.01	0.005
CTP3581	3581	C	rs4369653	Intron 2	82:8	70:16	0.089	0.186	0.101
CTP3686	3686	C	rs7194225	Intron 2	84:6	78:8	0.067	0.093	0.099
CTP3854	3854	T	Novel	Intron 2	90:0	85:1	0	0.012	0.006
CTP4559	4559	T	Novel	Intron 2	94:0	91:1	0	0.011	0.005
CTP4602	4602	C	rs9929488	Intron 2	66:28	62:30	0.298	0.326	0.332
CTP4948	4948	G	rs12720926	Intron 2	45:35	31:53	0.562	0.369	0.463
CTP5288	5288	C	rs7203984	Intron 2	62:18	54:30	0.225	0.357	0.245
CTP5358	5358	T	rs11508026	Intron 2	45:35	29:55	0.562	0.345	0.467
CTP5810delG	5810	D	rs17231569	Intron 2	66:20	66:22	0.233	0.25	0.312
CTP5979	5979	A	rs708273	Intron 2	70:16	67:21	0.186	0.239	0.241
CTP6314	6314	G	rs820299	Intron 2	66:24	56:36	0.267	0.391	0.324
CTP6725	6725	A	rs8045855	Intron 2	73:3	78:14	0.039	0.152	0.042
CTP6914	6914	A	rs12720922	Intron 2	73:5	66:10	0.064	0.132	0.121
CTP8695	8695	C	rs9926440	Intron 2	66:26	59:37	0.283	0.385	0.337
CTP8764	8764	T	rs9939224	Intron 2	74:18	68:28	0.196	0.292	0.234
CTP9178	9178	C	rs11076174	Intron 2	80:6	84:12	0.07	0.125	0.086
CTP10459	10459	C	rs139040281	Intron 3	1:91	0:96	0.011	0	0.005
CTP10921	10921	A	rs7205804	Intron 5	51:41	34:62	0.554	0.354	0.458
CTP10924	10924	T	rs12708972	Intron 5	94:0	95:1	0	0.01	0.005
CTP11194	11194	T	rs34523084	Intron 6	93:1	94:2	0.011	0.021	0.011
CTP11332	11332	T	rs1532625	Intron 7	53:41	34:62	0.564	0.354	0.463
CTP11510	11510	A	rs1532624	Intron 7	51:39	34:62	0.567	0.354	0.463
CTP11581	11581	T	rs12708974	Intron 7	83:5	82:12	0.057	0.128	0.089
CTP11793	11793		rs117040820	Intron 7	1:93	0:94	0.011	0	0.005
CTP12103	12103	A	rs12720873	Intron 8	92:2	93:3	0.021	0.031	0.063
CTP12123	12123	A	Novel	Intron 8	94:0	95:1	0	0.01	0.005
CTP12178	12178	T	rs148654654	Intron 8	1:93	0:96	0.011	0	0.005
CTP12331del1	12331	D	rs67114203	Intron 8	78:16	79:17	0.17	0.177	0.17
CTP12336	12336	T	rs289712	Intron 8	78:16	69:27	0.17	0.281	0.213
CTP12409	12409	G	rs11076175	Intron 8	75:19	69:25	0.202	0.266	0.237
CTP12621	12621	T	rs7499892	Intron 8	75:19	70:26	0.202	0.271	0.226
CTP12746	12746	G	rs187766748	Intron 8	1:93	1:95	0.011	0.01	0.011
CTP12860	12860	T	rs289713	Intron 8	75:19	70:26	0.202	0.271	0.237
CTP13071	13071	T	rs187468344	Intron 8	94:0	94:2	0	0.021	0.016
CTP13223	13223	C	rs9930761	Intron 8	10:84	6:90	0.106	0.062	0.084
CTP13327	13327	T	rs28381707	Exon 9	1:93	0:96	0.011	0	0.005
CTP13384	13384	T	rs5883	Exon 9	8:86	5:91	0.085	0.052	0.068
CTP13477	13477	G	rs11076176	Intron 9	78:16	76:20	0.17	0.208	0.168
CTP13482	13482	G	rs289714	Intron 9	78:16	76:20	0.17	0.208	0.17
CTP13641	13641	G	rs158477	Intron 9	53:41	43:53	0.564	0.448	0.468
CTP13683	13683	G	rs11644475	Intron 9	92:2	93:3	0.021	0.031	0.021
CTP13765	13765	A	rs158478	Intron 9	54:40	43:53	0.574	0.448	0.467
CTP13868	13868	T	Novel	Intron 9	1:93	0:96	0.011	0	0.005
CTP14079	14079	G	rs158479	Intron 9	52:42	41:55	0.553	0.427	0.457
CTP14123	14123	A	rs181381869	Intron 9	2:92	1:93	0.021	0.011	0.021
CTP14232del2	14232	D	Novel	Intron 9	1:93	1:95	0.011	0.01	0.011
CTP14258	14258	G	rs158480	Intron 9	11:83	9:87	0.117	0.094	0.105
CTP14318	14318	A	rs158617	Intron 9	11:83	9:87	0.117	0.094	0.105
CTP14539	14539	A	rs289715	Intron 9	11:83	9:87	0.117	0.094	0.105

Table B1.3. Continued

CETP variant	Position	Minor allele	Ref SNP ID	Location	High HDL-C /Low TG group allele counts	Low HDL-C/High TG group allele counts	MAF in High HDL-C/Low TG group	MAF in Low HDL-C/High TG group	MAF in the total sample
CTP15277	15277	G	Novel	Intron 10	94:0	95:1	0	0.01	0.005
CTP15407	15407	T	rs289716	Intron 10	30:64	27:69	0.319	0.281	0.289
CTP15419	15419	A	rs289717	Intron 10	70:22	58:38	0.239	0.396	0.3
CTP15688del1	15688	D	rs35874588	Intron 10	27:67	26:70	0.287	0.271	0.28
CTP15800	15800	A	rs736274	Intron 10	11:83	9:85	0.117	0.096	0.105
CTP15963	15963	C	rs289718	Intron 10	28:66	24:68	0.298	0.261	0.274
CTP15972	15972	T	rs289719	Intron 10	27:67	22:66	0.287	0.25	0.268
CTP16016	16016	C	rs2033254	Intron 10	43:51	32:64	0.457	0.333	0.4
CTP16059	16059	T	rs183439140	Intron 10	1:93	0:96	0.011	0	0.005
CTP16148	16148	A	rs72771489	Intron 10	94:0	95:1	0	0.01	0.005
CTP16263	16263	T	rs56208677	Intron 10	12:82	8:88	0.128	0.083	0.106
CTP16413	16413	G	rs71387147	Intron 10	89:5	89:7	0.053	0.073	0.08
CTP16508	16508	C	Novel	Intron 10	94:0	95:1	0	0.01	0.005
CTP16517	16517	T	rs117427818	Intron 10	92:2	93:3	0.021	0.031	0.026
CTP16550	16550	T	rs142980129	Intron 10	1:93	0:96	0.011	0	0.005
CTP16598	16598	T	Novel	Intron 10	93:1	94:2	0.011	0.021	0.016
CTP16859	16859	G	rs11860407	Intron 10	32:30	27:37	0.516	0.422	0.452
CTP16979	16979	T	rs1968905	Intron 10	14:72	9:77	0.163	0.105	0.134
CTP17025	17025	-	rs12720897	Intron 10	3:83	3:83	0.035	0.035	0.035
CTP17216	17216	A	rs4784744	Intron 10	65:21	50:34	0.244	0.405	0.289
CTP17274	17274	-	rs12720898	Intron 10	3:83	3:83	0.035	0.035	0.035
CTP18256	18256	A	rs28381709	Intron 11	1:93	0:96	0.011	0	0.005
CTP18413	18413	G	rs12708980	Intron 11	42:52	32:64	0.447	0.333	0.3
CTP18597	18597	T	rs12720889	Intron 11	29:65	26:70	0.309	0.271	0.279
CTP18663	18663	T	Novel	Intron 11	94:0	95:1	0	0.01	0.005
CTP18678	18678	G	Novel	Intron 11	1:93	0:96	0.011	0	0.005
CTP18717	18717	A	rs143024882	Intron 11	93:1	94:2	0.011	0.021	0.016
CTP18733	18733	G	rs291043	Intron 11	71:23	56:40	0.245	0.417	0.309
CTP18921	18921	A	rs17239354	Intron 11	4:90	4:92	0.043	0.042	0.042
CTP20354	20354	A	rs12447620	Intron 11	32:2	21:3	0.059	0.125	0.089
CTP20446	20446	C	rs12708983	Intron 11	3:91	1:95	0.032	0.01	0.021
CTP20593	20593	A	Novel	Intron 11	1:93	0:96	0.011	0	0.005
CTP20645	20645	T	rs12708985	Intron 11	12:82	10:86	0.128	0.104	0.116
CTP20675	20675	T	Novel	Intron 11	1:93	0:96	0.011	0	0.005
CTP20804	20804	A	Novel	Intron 11	94:0	95:1	0	0.01	0.005
CTP20910	20910	G	rs4784745	Intron 11	70:24	56:40	0.255	0.417	0.33
CTP21126	21126	C	rs5880	Exon 12	92:2	93:3	0.021	0.031	0.026
CTP21371del12	21371	W	rs11276066	Intron 12	11:83	9:87	0.117	0.094	0.105
CTP21580	21580	T	rs1800774	Intron 12	45:49	31:65	0.479	0.323	0.405
CTP22127	22127	G	rs5882	Exon 14	26:68	26:70	0.277	0.271	0.268
CTP22327	22327	T	rs111379440	Intron 14	94:0	95:1	0	0.01	0.005
CTP22349	22349	G	rs12720882	Intron 14	94:0	94:2	0	0.021	0.016
CTP22888del1	22888	D	Novel	Intron 14	94:0	95:1	0	0.01	0.005
CTP22997	22997	T	rs12720887	Intron 14	3:91	1:95	0.032	0.01	0.016
CTP23037	23037	G	rs9923854	Intron 14	83:11	84:12	0.117	0.125	0.136
CTP23353	23353	A	rs1800777	Exon 15	93:1	93:3	0.011	0.031	0.026
CTP23508	23508	G	rs289741	Intron 15	26:68	25:71	0.277	0.26	0.363
CTP23696	23696	A	rs1801706	3' UTR	79:15	80:16	0.16	0.167	0.189
CTP23796	23796	C	rs289742	3' flanking	11:83	9:87	0.117	0.094	0.105
CTP23830	23830	G	rs289743	3' flanking	26:68	25:71	0.277	0.26	0.269
CTP24136	24136	G	rs289744	3' flanking	26:68	25:71	0.277	0.26	0.268
CTP24669	24669	T	rs66495554	3' flanking	44:50	33:63	0.468	0.344	0.389
CTP24889	24889	A	rs112039804	3' flanking	11:83	9:87	0.117	0.094	0.105
CTP25425	25425	C	rs12720917	3' flanking	79:15	78:18	0.16	0.188	0.189
CTP25565	25565	C	rs289745	3' flanking	44:50	44:52	0.468	0.458	0.395

W: Allele in the reference sequence; D/I: Deleted or inserted alleles

TABLE B1.4. Distrubition of *CETP* variants between extremely high (n=47) and low (n=48) HDL-C/TG groups in African blacks

***CETP* variant**	**[a]Position**	**Minor allele**	**RefSNP ID**	**Location**	**High HDL-C /Low TGgroup allele counts**	**Low HDL-C/High TG group allele counts**	**MAF in High HDL-C/Low TG group**	**MAF in Low HDL-C/High TG group**	**MAF in the total sample**
CTP109	109	G	Novel	5' flanking	93:1	96:0	0.011	0	0.005
CTP163	163	G	rs13332526	5' flanking	86:8	93:3	0.085	0.031	0.058
CTP187	187	G	rs148562851	5' flanking	1:93	6:90	0.011	0.062	0.037
CTP220	220	C	rs12447924	5' flanking	74:20	79:17	0.213	0.177	0.195
CTP240	240	C	rs12720918	5' flanking	67:27	74:22	0.287	0.229	0.258
CTP266	266	G	rs13332571	5' flanking	86:8	93:3	0.085	0.031	0.058
CTP272del1	272	W	rs36229491	5' flanking	81:11	89:7	0.12	0.073	0.096
CTP296	296	A	Novel	5' flanking	93:1	94:0	0.011	0	0.005
CTP452	452	A	Novel	5' flanking	92:2	96:0	0.021	0	0.011
CTP546	546	C	Novel	5' flanking	0:94	1:95	0	0.010	0.005
CTP557	557	T	rs17231506	5' flanking	83:11	89:7	0.117	0.073	0.095
CTP848	848	C	rs12708968	5' flanking	71:7	81:3	0.09	0.036	0.062
CTP870	870	G	rs13338602	5' flanking	71:7	81:3	0.09	0.036	0.062
CTP923	923	G	rs4783961	5' flanking	40:40	50:34	0.5	0.405	0.451
CTP950	950	T	rs146122874	5' flanking	0:80	6:78	0	0.071	0.037
CTP1067	1067	T	rs4783962	5' flanking	83:7	89:7	0.078	0.073	0.075
CTP1153	1153	A	rs17237883	5' flanking	87:5	91:3	0.054	0.032	0.043
CTP1189	1189	A	rs114856405	5' flanking	1:79	5:81	0.012	0.058	0.036
CTP1263	1263	A	rs1800776	5' flanking	90:4	94:2	0.043	0.021	0.032
CTP1265	1265	C	rs1800775	5' flanking	56:38	64:26	0.404	0.289	0.348
CTP1856	1856	A	rs17231520	5' flanking	2:92	25:71	0.021	0.260	0.142
CTP1937	1937	A	rs34119551	Exon 1	0:92	4:92	0	0.042	0.021
CTP1964	1964	G	rs34065661	Exon 1	2:90	25:71	0.022	0.260	0.144
CTP1986	1986	A	rs5884	Exon 1	84:8	93:3	0.087	0.031	0.059
CTP2089	2089	A	rs34680782	Intron 1	1:91	3:91	0.011	0.032	0.022
CTP2133	2133	A	rs17231534	Intron 1	69:23	74:20	0.25	0.213	0.231
CTP2187	2187	T	rs3816117	Intron 1	48:34	61:25	0.415	0.291	0.351
CTP2240	2240	A	rs711752	Intron 1	15:73	34:60	0.17	0.362	0.269
CTP2317	2317	A	rs708272	Intron 1	15:75	35:59	0.167	0.372	0.272
CTP2676del2	2676	D	rs34145065	Intron 1	75:11	84:10	0.128	0.106	0.117
CTP2678	2678	A	rs34620476	Intron 1	75:11	84:10	0.128	0.106	0.117
CTP2692	2692	A	rs60195610	Intron 1	0:88	5:89	0	0.053	0.027
CTP2736	2736	T	rs59008849	Intron 1	0:86	1:93	0	0.011	0.006
CTP3101	3101	G	rs9935228	Intron 2	60:8	73:3	0.118	0.039	0.076
CTP3153	3153	A	Novel	Intron 2	0:94	1:93	0	0.011	0.005
CTP3262	3262	A	rs1864163	Intron 2	65:29	75:19	0.309	0.202	0.255
CTP3347	3347	A	rs75313088	Intron 2	2:92	5:89	0.021	0.053	0.037
CTP3381del1	3381	W	rs5817083	Intron 2	49:45	61:33	0.479	0.351	0.415
CTP3399	3399	A	rs4587963	Intron 2	42:10	59:5	0.192	0.078	0.129
CTP3581	3581	C	rs4369653	Intron 2	6:56	8:56	0.097	0.125	0.111
CTP3686	3686	C	rs7194225	Intron 2	6:56	8:56	0.097	0.125	0.111
CTP3803_3804Ins1	3803	D	Novel	Intron 2	0:62	2:60	0	0.032	0.016
CTP3918	3918	A	Novel	Intron 2	55:5	53:3	0.083	0.054	0.069
CTP4299	4299	A	rs114908369	Intron 2	89:3	90:2	0.033	0.022	0.027
CTP4602	4602	C	rs9929488	Intron 2	45:47	52:42	0.489	0.553	0.478
CTP4791	4791	G	rs12720906	Intron 2	1:91	3:91	0.011	0.032	0.022
CTP4948	4948	G	rs12720926	Intron 2	90:4	94:2	0.043	0.021	0.032
CTP4957	4957	A	rs17237939	Intron 2	89:5	93:3	0.053	0.031	0.042
CTP5130	5130	A	rs116604371	Intron 2	93:1	96:0	0.011	0	0.005
CTP5209	5209	T	Novel	Intron 2	0:92	1:95	0	0.010	0.005
CTP5215del1	5215	D	rs35585922	Intron 2	17:77	22:74	0.181	0.229	0.205
CTP5288	5288	A	rs7203984	Intron 2	40:28	41:25	0.412	0.379	0.396
CTP5358	5358	T	rs11508026	Intron 2	64:4	64:2	0.059	0.03	0.045
CTP5375	5375	C	rs80296794	Intron 2	65:3	65:1	0.044	0.015	0.03
CTP5383del1	5383	D	rs71383212	Intron 2	18:74	25:71	0.196	0.260	0.229
CTP5593	5593	A	rs112236143	Intron 2	79:3	83:1	0.037	0.012	0.024
CTP5808	5808	-	rs17237946	Intron 2	2:92	2:92	0.021	0.021	0.021

Table B1.4. Continued

***CETP* variant**	**[a]Position**	**Minor allele**	**RefSNP ID**	**Location**	**High HDL-C /Low TGgroup allele counts**	**Low HDL-C/High TG group allele counts**	**MAF in High HDL-C/Low TG group**	**MAF in Low HDL-C/High TG group**	**MAF in the total sample**
CTP5810del1	5810	D	rs17231569	Intron 2	35:59	36:58	0.372	0.383	0.378
CTP5979	5979	A	rs708273	Intron 2	81:11	84:8	0.12	0.087	0.103
CTP5990	5990	C	rs17231583	Intron 2	0:90	3:71	0	0.041	0.018
CTP6022_6023Ins1	6022	I	rs142058276	Intron 2	8:82	14:80	0.089	0.149	0.12
CTP6221	6221	G	rs17231590	Intron 2	88:6	91:3	0.064	0.032	0.048
CTP6239	6239	A	rs17237953	Intron 2	90:4	92:2	0.043	0.021	0.032
CTP6251	6251	T	rs35619327	Intron 2	89:3	89:1	0.033	0.011	0.022
CTP6314	6314	A	rs820299	Intron 2	51:41	49:39	0.446	0.443	0.444
CTP6361	6361	C	Novel	Intron 2	91:1	88:0	0.011	0	0.006
CTP6427	6427	A	rs17237967	Intron 2	87:5	86:2	0.054	0.023	0.039
CTP6725	6725	A	rs8045855	Intron 2	34:50	36:46	0.405	0.439	0.422
CTP6914	6914	A	rs12720922	Intron 2	28:62	30:54	0.311	0.357	0.333
CTP8695	8695	G	rs9926440	Intron 2	67:27	80:16	0.287	0.167	0.226
CTP8698	8698	A	rs192306644	Intron 2	93:1	90:0	0.011	0	0.005
CTP8742	8742	G	rs12720863	Intron 2	91:3	95:1	0.032	0.01	0.021
CTP8764	8764	T	rs9939224	Intron 2	32:60	38:58	0.348	0.396	0.372
CTP9075	9075	T	rs60531466	Intron 2	9:85	14:82	0.096	0.146	0.121
CTP9178	9178	C	rs11076174	Intron 2	81:13	88:8	0.138	0.083	0.111
CTP9282	9282	A	rs13306230	Intron 2	0:94	1:95	0	0.010	0.005
CTP9493	9493	C	rs12708971	Intron 3	0:94	3:93	0	0.031	0.016
CTP9670	9670	C	rs60896367	Intron 4	0:94	1:95	0	0.010	0.005
CTP9693	9693	A	rs35752722	Intron 4	93:1	95:1	0.011	0.01	0.011
CTP9755	9755	G	rs891141	Intron 4	10:84	21:75	0.106	0.219	0.163
CTP9841	9841	A	Novel	Intron 4	93:1	92:0	0.011	0	0.005
CTP9878	9878	T	rs34716057	Exon 5	1:93	3:93	0.011	0.031	0.021
CTP10009	10009	T	rs891142	Intron 5	6:88	20:76	0.064	0.208	0.137
CTP10012	10012	T	rs891143	Intron 5	6:88	19:77	0.064	0.198	0.132
CTP10491	10491	A	rs12720861	Intron 5	10:80	14:80	0.111	0.149	0.13
CTP10694	10694	T	rs12720860	Intron 5	10:80	14:80	0.111	0.149	0.13
CTP10775	10775	A	Novel	Intron 5	89:1	93:1	0.011	0.011	0.011
CTP10779	10779	G	rs12720862	Intron 5	10:80	14:80	0.111	0.149	0.13
CTP10921	10921	A	rs7205804	Intron 5	79:15	92:4	0.16	0.042	0.1
CTP10934	10934	G	rs12708973	Intron 5	91:3	96:0	0.032	0	0.016
CTP10943	10943	A	rs148134355	Intron 5	92:2	95:1	0.021	0.01	0.016
CTP10983	10983	A	rs34611098	Exon 6	0:94	1:95	0	0.010	0.005
CTP11332	11332	T	rs1532625	Intron 7	79:15	93:3	0.16	0.031	0.095
CTP11433	11433	A	Novel	Intron 7	0:92	1:93	0	0.011	0.005
CTP11456	11456	C	rs12720925	Intron 7	90:2	92:2	0.022	0.021	0.022
CTP11510	11510	A	rs1532624	Intron 7	77:15	91:3	0.163	0.032	0.097
CTP11651	11651	C	rs12597250	Intron 7	14:80	17:79	0.149	0.177	0.163
CTP11795	11795	G	rs12720871	Intron 7	2:90	5:89	0.022	0.053	0.038
CTP11913	11913	T	rs12720872	Intron 7	78:14	80:14	0.152	0.149	0.151
CTP12281	12281	T	Novel	Intron 8	0:86	1:95	0	0.010	0.005
CTP12331del1	12331	W	rs67114203	Intron 8	16:70	30:66	0.186	0.312	0.253
CTP12336C>T	12336	T	rs289712	Intron 8	77:9	86:10	0.105	0.104	0.104
CTP12336C>A	12336	A	rs289712	Intron 8	82:4	95:1	0.047	0.01	0.027
CTP12409	12409	G	rs11076175	Intron 8	61:25	79:17	0.291	0.177	0.231
CTP12621	12621	T	rs7499892	Intron 8	63:31	70:26	0.33	0.271	0.3
CTP12627	12627	A	rs146562593	Intron 8	93:1	96:0	0.011	0	0.005
CTP12860	12860	A	rs289713	Intron 8	51:43	57:39	0.457	0.406	0.432
CTP12913	12913	T	rs191754368	Intron 8	1:93	3:93	0.011	0.031	0.021
CTP12970	12970	A	rs182480194	Intron 8	0:94	1:95	0	0.010	0.005
CTP12981	12981	A	rs146782017	Intron 8	0:94	1:95	0	0.010	0.005
CTP13223	13223	C	rs9930761	Intron 8	16:78	24:70	0.17	0.255	0.213
CTP13279	13279	C	rs35878799	Exon 9	93:1	94:0	0.011	0	0.005
CTP13384	13384	T	rs5883	Exon 9	15:79	23:69	0.16	0.250	0.204
CTP13477	13477	G	rs11076176	Intron 9	56:38	67:29	0.404	0.302	0.353
CTP13482	13482	A	rs289714	Intron 9	45:49	47:49	0.479	0.490	0.484
CTP13641	13641	A	rs158477	Intron 9	39:55	52:44	0.415	0.542	0.479
CTP13765	13765	C	rs158478	Intron 9	32:62	42:54	0.34	0.438	0.389
CTP13849	13849	T	Novel	Intron 9	92:2	95:1	0.021	0.01	0.016

Table B1.4. Continued

***CETP* variant**	**[a]Position**	**Minor allele**	**RefSNP ID**	**Location**	**High HDL-C /Low TGgroup allele counts**	**Low HDL-C/High TG group allele counts**	**MAF in High HDL-C/Low TG group**	**MAF in Low HDL-C/High TG group**	**MAF in the total sample**
CTP14079	14079	A	rs158479	Intron 9	30:64	36:56	0.319	0.391	0.355
CTP14192	14192	A	rs12720892	Intron 9	91:3	93:3	0.032	0.031	0.032
CTP14258	14258	G	rs158480	Intron 9	52:42	57:39	0.447	0.406	0.426
CTP14318	14318	A	rs158617	Intron 9	57:37	60:36	0.394	0.375	0.384
CTP14448del4	14448	D	rs147606537	Intron 9	0:94	2:94	0	0.021	0.011
CTP14539	14539	A	rs289715	Intron 9	73:21	76:20	0.223	0.208	0.216
CTP14715	14715	G	rs186780244	Intron 9	93:1	96:0	0.011	0	0.005
CTP15196	15196	G	rs116351574	Intron 10	85:1	89:1	0.012	0.011	0.011
CTP15226	15226	G	rs2303789	Intron 10	81:3	85:3	0.036	0.034	0.035
CTP15231	15231	T	rs12720877	Intron 10	77:7	82:6	0.083	0.068	0.076
CTP15232	15232	C	rs13306232	Intron 10	83:1	88:0	0.012	0	0.006
CTP15407	15407	A	rs289716	Intron 10	42:34	54:34	0.447	0.386	0.415
CTP15419	15419	A	rs289717	Intron 10	69:13	85:9	0.159	0.096	0.125
CTP15542	15542	T	rs12708976	Intron 10	86:2	90:2	0.023	0.022	0.022
CTP15597	15597	A	rs116578082	Intron 10	0:88	1:91	0	0.011	0.006
CTP15639	15639	G	rs12720942	Intron 10	90:4	93:3	0.043	0.031	0.037
CTP15688del1	15688	D	rs35874588	Intron 10	55:39	64:32	0.415	0.333	0.374
CTP15800	15800	A	rs736274	Intron 10	90:4	94:0	0.043	0	0.021
CTP15830	15830	A	rs12720939	Intron 10	90:4	93:3	0.043	0.031	0.037
CTP15913	15913	G	rs12720937	Intron 10	90:4	93:3	0.043	0.031	0.037
CTP15963	15963	T	rs289718	Intron 10	55:39	62:34	0.415	0.354	0.384
CTP15972	15972	C	rs289719	Intron 10	48:46	54:42	0.489	0.438	0.463
CTP16016	16016	C	rs2033254	Intron 10	65:29	69:27	0.309	0.281	0.295
CTP16146	16146	A	rs112205272	Intron 10	88:4	92:4	0.043	0.042	0.043
CTP16363	16363	G	rs112409939	Intron 10	86:4	92:4	0.044	0.042	0.043
CTP16413	16413	G	rs71387147	Intron 10	86:4	94:2	0.044	0.021	0.032
CTP16508	16508	A	Novel	Intron 10	87:1	92:0	0.011	0	0.006
CTP16709	16709	C	rs151104194	Intron 10	87:1	92:0	0.011	0	0.006
CTP16859	16859	G	rs11860407	Intron 10	20:40	22:32	0.333	0.407	0.368
CTP16935	16935	A	rs12720901	Intron 10	82:2	86:0	0.024	0	0.012
CTP16979	16979	T	rs1968905	Intron 10	31:59	36:54	0.344	0.400	0.372
CTP17154	17154	-	rs12720903	Intron 10	6:84	6:84	0.067	0.067	0.067
CTP17216	17216	A	rs4784744	Intron 10	81:9	84:6	0.1	0.067	0.083
CTP17483	17483	A	rs291044	Intron 10	67:7	70:2	0.095	0.028	0.062
CTP17575	17575	A	rs114486472	Intron 10	1:91	3:93	0.011	0.031	0.021
CTP17740	17740	T	Novel	Intron 10	92:2	95:1	0.021	0.01	0.016
CTP17860	17860	T	rs8053613	Intron 10	0:94	1:95	0	0.010	0.005
CTP17875	17875	C	rs34337891	Intron 10	93:1	96:0	0.011	0	0.005
CTP17918	17918	T	rs34426213	Intron 10	3:91	4:92	0.032	0.042	0.037
CTP17970	17970	T	rs891144	Intron 10	75:19	80:16	0.202	0.167	0.184
CTP18388	18388	T	rs12708979	Intron 11	2:92	4:92	0.021	0.042	0.032
CTP18413	18413	G	rs12708980	Intron 11	59:35	68:28	0.372	0.292	0.332
CTP18597	18597	T	rs12720889	Intron 11	20:72	26:70	0.217	0.271	0.245
CTP18689	18689	T	Novel	Intron 11	0:94	1:95	0	0.010	0.005
CTP18733	18733	G	rs291043	Intron 11	84:10	91:5	0.106	0.052	0.079
CTP18746	18746	T	Novel	Intron 11	93:1	96:0	0.011	0	0.005
CTP18970	18970	A	rs114203109	Intron 11	88:6	96:0	0.064	0	0.032
CTP19317	19317	T	Novel	Intron 11	93:1	96:0	0.011	0	0.005
CTP19519	19519	A	rs146251160	Intron 11	69:1	71:1	0.014	0.014	0.014
CTP19561	19561	-	rs12708981	Intron 11	6:60	6:60	0.091	0.091	0.091
CTP19606	19606	T	rs12720858	Intron 11	63:7	67:7	0.1	0.095	0.097
CTP19607	19607	A	Novel	Intron 11	67:5	69:5	0.069	0.068	0.068
CTP19700	19700	C	rs12720857	Intron 11	8:84	9:85	0.087	0.096	0.091
CTP19734	19734	G	rs145189439	Intron 11	91:3	93:3	0.032	0.031	0.032
CTP19757	19757	G	Novel	Intron 11	0:94	1:95	0	0.010	0.005
CTP19789	19789	A	rs74678905	Intron 11	7:87	8:88	0.074	0.083	0.079
CTP19872	19872	T	rs148807012	Intron 11	0:94	1:95	0	0.010	0.005
CTP19881	19881	T	rs17238225	Intron 11	86:8	88:8	0.085	0.083	0.084
CTP20072	20072	T	rs80180245	Intron 11	86:8	88:8	0.085	0.083	0.084
CTP20284	20284	C	rs17238232	Intron 11	82:8	89:7	0.089	0.073	0.081
CTP20354	20354	A	rs12447620	Intron 11	32:62	32:58	0.34	0.356	0.348

Table B1.4. Continued

***CETP* variant**	**^{a}Position**	**Minor allele**	**RefSNP ID**	**Location**	**High HDL-C /Low TGgroup allele counts**	**Low HDL-C/High TG group allele counts**	**MAF in High HDL-C/Low TG group**	**MAF in Low HDL-C/High TG group**	**MAF in the total sample**
CTP20374	20374	T	rs17231869	Intron 11	6:72	6:58	0.077	0.094	0.085
CTP20442	20442	G	rs12708982	Intron 11	93:1	96:0	0.011	0	0.005
CTP20457	20457	T	rs12708984	Intron 11	86:8	87:7	0.085	0.074	0.08
CTP20551	20551	A	rs115390156	Intron 11	93:1	96:0	0.011	0	0.005
CTP20593	20593	A	Novel	Intron 11	93:1	95:1	0.011	0.01	0.011
CTP20624	20624	G	Novel	Intron 11	93:1	96:0	0.011	0	0.005
CTP20641	20641	C	rs189327489	Intron 11	86:8	88:8	0.085	0.083	0.084
CTP20645	20645	T	rs12708985	Intron 11	16:76	18:78	0.174	0.188	0.181
CTP20725	20725	T	rs140776547	Intron 11	1:93	3:93	0.011	0.031	0.021
CTP20844	20844	A	rs13331688	Intron 11	88:6	95:1	0.064	0.01	0.037
CTP20855	20855	C	rs111754336	Intron 11	86:8	88:8	0.085	0.083	0.084
CTP20910	20910	G	rs4784745	Intron 11	85:9	91:5	0.096	0.052	0.074
CTP21111	21111	A	rs34855278	Exon 12	90:4	96:0	0.043	0	0.021
CTP21119C>G	21119	G	rs7192120	Exon 12	86:8	88:8	0.085	0.083	0.084
CTP21119C>T	21119	T	rs7192120	Exon 12	91:3	96:0	0.032	0	0.016
CTP21280	21280	C	rs7198026	Intron 12	86:8	88:8	0.085	0.083	0.084
CTP21324	21324	C	rs140421500	Intron 12	91:1	95:1	0.011	0.01	0.011
CTP21340	21340	C	Novel	Intron 12	0:92	1:95	0	0.010	0.005
CTP21371del12	21371	W	rs11276066	Intron 12	62:30	65:29	0.326	0.309	0.317
CTP21415	21415	-	rs7197854	Intron 12	8:86	8:86	0.085	0.085	0.085
CTP21454	21454	-	rs114948973	Intron 12	2:92	2:92	0.021	0.021	0.021
CTP21482	21482	G	rs7197340	Intron 12	8:86	9:87	0.085	0.094	0.089
CTP21498	21498	G	rs7195984	Intron 12	14:80	23:73	0.149	0.240	0.195
CTP21579	21579	T	rs7196174	Intron 12	86:8	88:8	0.085	0.083	0.084
CTP21580	21580	T	rs1800774	Intron 12	71:23	76:20	0.245	0.208	0.226
CTP21760	21760	C	rs78603009	Intron 13	86:8	88:8	0.085	0.083	0.084
CTP21937	21937	T	rs142517945 Novel	Intron 13	93:1	96:0	0.011	0	0.005
CTP22127	22127	A	rs5882	Exon 14	60:34	68:28	0.362	0.292	0.326
CTP22162	22162	A	rs5886	Exon 14	85:9	87:9	0.096	0.094	0.095
CTP22337	22337	-	rs8045701	Intron 14	9:85	9:85	0.096	0.096	0.096
CTP22480	22480	-	rs12598103	Intron 14	9:85	9:85	0.096	0.096	0.096
CTP22554	22554	-	rs12596364	Intron 14	8:86	8:86	0.085	0.085	0.085
CTP22562	22562	-	rs12720884	Intron 14	8:86	8:86	0.085	0.085	0.085
CTP22683	22683	A	rs11076177	Intron 14	8:86	8:84	0.085	0.087	0.086
CTP22985	22985	C	rs289740	Intron 14	6:86	15:81	0.065	0.156	0.112
CTP23037	23037	G	rs9923854	Intron 14	13:79	23:73	0.141	0.240	0.191
CTP23152	23152	A	rs150048432	Intron 14	0:92	1:95	0	0.010	0.005
CTP23201	23201	T	rs36051594	Intron 14	3:91	4:92	0.032	0.042	0.037
CTP23508	23508	A	rs289741	Intron 15	61:33	69:27	0.351	0.281	0.316
CTP23696	23696	A	rs1801706	3'UTR- Exon 16	16:78	26:70	0.17	0.271	0.221
CTP23796	23796	C	rs289742	3' flanking	58:36	62:34	0.383	0.354	0.368
CTP23830	23830	A	rs289743	3' flanking	61:33	68:28	0.351	0.292	0.321
CTP23858	23858	A	Novel	3' flanking	0:94	1:95	0	0.010	0.005
CTP24136	24136	T	rs289744	3' flanking	62:32	68:28	0.34	0.292	0.316
CTP24258	24258	G	rs76732052	3' flanking	93:1	96:0	0.011	0	0.005
CTP24499	24499	T	rs12720875	3' flanking	2:84	4:90	0.023	0.043	0.033
CTP24586	24586	T	rs7192754	3' flanking	80:8	88:8	0.091	0.083	0.087
CTP24669	24669	T	rs66495554	3' flanking	69:19	82:14	0.216	0.146	0.179
CTP24767	24767	C	Novel	3' flanking	0:88	1:95	0	0.010	0.005
CTP24881	24881	G	rs114646974	3' flanking	86:2	96:0	0.023	0	0.011
CTP24889	24889	A	rs112039804	3' flanking	72:16	87:9	0.182	0.094	0.136
CTP24899	24899	G	rs138161274	3' flanking	2:84	3:93	0.023	0.031	0.027
CTP25049	25049	T	Novel	3' flanking	93:1	96:0	0.011	0	0.005
CTP25064	25064	C	rs12720874	3' flanking	77:17	89:7	0.181	0.073	0.126
CTP25217	25217	G	rs76500832	3' flanking	91:1	95:1	0.011	0.01	0.011
CTP25218	25218	G	rs12720916	3' flanking	89:3	93:3	0.033	0.031	0.032
CTP25565	25565	C	rs289745	3' flanking	17:75	23:73	0.185	0.240	0.213

MAF: minor allele frequency; ^{a}Positions in the reference sequence (NC_000016.9); Bold: Variant results in amino acid change.

TABLE B1.5. The genotype call rates and features of the genotyped 111 *CETP* SNPs in NHWs

CETP variant	RefSNP ID	[a]Chr. Position	[b]Position	Locations	ObsHet	PredHet	HWpval	% Call rate	MAF	Alleles	Selection criteria
rs247615	rs247615		-9210	5' flanking	0.339	0.282	1.8851E-09	95.8	0.17	A:G	Reported association
rs9989419	rs9989419	56985139	-8834	5' flanking	0.463	0.48	0.4369	98.6	0.339	G:A	Reported association
rs247617	rs247617	56990716	-3257	5' flanking	0.428	0.454	0.1728	98.9	0.348	C:A	Reported association
rs183130	rs183130	56991363	-2610	5' flanking	0.426	0.454	0.1539	98.9	0.348	C:T	Reported association
rs6499863	rs6499863	56992017	-1956	5' flanking	0.297	0.284	0.3091	99.2	0.171	G:A	Reported association
rs12149545	rs12149545	56993161	-812	5' flanking	0.438	0.443	0.8307	99.8	0.331	G:A	Reported association
rs12708967	rs12708967	56993211	-762	5' flanking	0.336	0.326	0.5352	99.7	0.205	T:C	Reported association
rs3764261	rs3764261	56993325	-648	5' flanking	0.448	0.442	0.8156	97.3	0.329	G:T	Reported association
CTP240	rs12720918	56994211	240	5' flanking	0.282	0.369	1.40E-07	88.6	0.244	T:C	TagSNP
CTP557	rs17231506	56994528	557	5' flanking	0.434	0.451	0.3751	99.7	0.344	C:T	TagSNP
CTP848	rs12708968	56994819	848	5' flanking	0.154	0.15	0.7977	99	0.082	T:C	Reported association
CTP923	rs4783961	56994894	923	5' flanking	0.503	0.496	0.797	99.7	0.456	A:G	TagSNP
CTP1019	rs17245715	56994990	1019	5' flanking	0.154	0.151	0.7755	99.7	0.082	C:T	TagSNP
CTP1067	rs4783962	56995038	1067	5' flanking	0.316	0.312	0.8877	99.5	0.193	C:T	TagSNP
CTP1265	rs1800775	56995236	1265	5' flanking	0.505	0.5	0.8771	100	0.488	A:C	Reported association
CTP2133	rs17231534	56996104	2133	Intron 1	0.09	0.086	0.5495	100	0.045	C:A	Uncommon/rare
CTP2187	rs3816117	56996158	2187	Intron 1	0.501	0.5	1	99.5	0.487	C:T	TagSNP
CTP2240	rs711752	56996211	2240	Intron 1	0.494	0.494	1	99.4	0.444	G:A	Reported association
CTP2308	rs5030708	56996279	2308	Intron 1	0.063	0.061	1	99.7	0.031	C:T	Uncommon/rare
CTP2317	rs708272	56996288	2317	Intron 1	0.494	0.493	1	99.2	0.443	G:A	Reported association (Taq1B)
CTP3262	rs1864163	56997233	3262	Intron 2	0.39	0.389	1	99.4	0.265	G:A	TagSNP
CTP3412	Novel	56997383	3412	Intron 2	0.002	0.002	1	99	0.001	A:G	Uncommon/rare
CTP3581	rs4369653	56997551	3581	Intron 2	0.387	0.387	1	97.3	0.263	A:G	TagSNP
CTP3686	rs7194225	56997656	3686	Intron 2	0.165	0.162	0.8858	99.8	0.089	G:C	TagSNP
CTP4559	Novel	56998529	4559	Intron 2	0.003	0.003	1	99.5	0.002	C:T	Uncommon/rare
CTP4602	rs9929488	56998572	4602	Intron 2	0.407	0.411	0.8666	97.8	0.289	G:C	TagSNP
CTP5288	rs7203984	56999258	5288	Intron 2	0.309	0.326	0.2229	97.6	0.205	A:C	TagSNP
CTP5358	rs11508026	56999328	5358	Intron 2	0.431	0.499	0.0009	98.9	0.473	C:T	Reported association
CTP5810	rs17231569	56999780	5810	Intron 2	0.285	0.307	0.0969	99	0.189	G:A	TagSNP
CTP5979	rs708273	56999949	5979	Intron 2	0.395	0.387	0.6917	98.9	0.263	G:A	TagSNP
CTP6314	rs820299	57000284	6314	Intron 2	0.439	0.459	0.3219	98.6	0.356	A:G	TagSNP
CTP6914	rs12720922	57000884	6914	Intron 2	0.283	0.31	0.0446	99.2	0.191	G:A	TagSNP
rs4784741	rs4784741	57001216	7244	Intron 2	0	0	1	56.2	0	C:C	Variant in GAP
rs12708969	rs12708969	57001584	7616	Intron 2	0.513	0.493	0.3626	99.4	0.44	G:T	Variant in GAP
rs60545348	rs60545348	57001985	8017	Intron 2	0.398	0.392	0.8365	99.5	0.268	A:C	Variant in GAP
rs9924080	rs9924080	57002152	8184	Intron 2	0	0	1	98.9	0	C:C	Variant in GAP
rs9924087	rs9924087	57002242	8274	Intron 2	0.164	0.164	1	99.5	0.09	G:A	Variant in GAP
rs12597002	rs12597002	57002404	8436	Intron 2	0.398	0.391	0.7507	99.4	0.267	C:A	Variant in GAP
CTP8695	rs9926440	57002663	8695	Intron 2	0.419	0.421	0.9512	99.5	0.301	G:C	TagSNP
CTP8764	rs9939224	57002732	8764	Intron 2	0.309	0.325	0.2436	99.2	0.204	G:T	TagSNP
CTP9178	rs11076174	57003146	9178	Intron 2	0.137	0.138	0.9152	99.7	0.075	T:C	TagSNP
CTP10009	rs891142	57003977	10009	Intron 5	0.003	0.003	1	99.4	0.002	C:T	Reported association
CTP10459	rs139040281	57004427	10459	Intron 5	0.003	0.003	1	99.7	0.002	A:C	Uncommon/rare
CTP10921	rs7205804	57004889	10921	Intron 5	0.498	0.496	1	99.2	0.454	G:A	Reported association
CTP10924	rs12708972	57004892	10924	Intron 5	0.018	0.018	1	99.5	0.009	C:T	Uncommon/rare
CTP11194	rs34523084	57005163	11194	Intron 6	0.015	0.015	1	98.6	0.007	C:T	Uncommon/rare
CTP11510	rs1532624	57005479	11510	Intron 7	0.499	0.495	0.9321	99.5	0.452	C:A	Reported association
CTP11581	rs12708974	57005550	11581	Intron 7	0.18	0.192	0.1712	99.8	0.108	C:T	TagSNP
CTP11793	rs117040820	57005762	11793	Intron 7	0.032	0.032	1	99.2	0.016	C:T	Uncommon/rare
CTP12103	rs12720873	57006072	12103	Intron 8	0.074	0.074	1	99.5	0.039	G:A	Uncommon/rare
CTP12123	Novel	57006092	12123	Intron 8	0.002	0.002	1	99.4	0.001	T:A	Uncommon/rare
CTP12178	rs148654654	57006147	12178	Intron 8	0.015	0.014	1	99.4	0.007	C:T	Uncommon/rare
CTP12336	rs289712	57006305	12336	Intron 8	0.399	0.389	0.6136	98.9	0.264	C:T	TagSNP
CTP12409	rs11076175	57006378	12409	Intron 8	0.277	0.3	0.076	99	0.184	A:G	Reported association
CTP12621	rs7499892	57006590	12621	Intron 8	0.276	0.301	0.0522	99.4	0.185	C:T	Reported association
CTP12746	rs187766748	57006715	12746	Intron 8	0.013	0.013	1	98.9	0.006	A:G	Uncommon/rare
CTP13071	rs187468344	57007040	13071	Intron 8	0.011	0.011	1	98.7	0.006	C:T	Uncommon/rare
CTP13223	rs9930761	57007192	13223	Intron 8	0.152	0.149	0.8141	100	0.081	T:C	TagSNP
CTP13327	rs28381707	57007296	13327	Exon 9	0.01	0.01	1	99.5	0.005	G:T	Exon/Exon-Intron Junctions
CTP13384	rs5883	57007353	13384	Exon 9	0.134	0.13	0.8077	99.5	0.07	C:T	TagSNP
CTP13482	rs289714	57007451	13482	Intron 9	0.294	0.296	0.9364	99.7	0.181	T:C	TagSNP
CTP13683	rs11644475	57007652	13683	Intron 9	0.072	0.072	1	100	0.038	A:G	Uncommon/rare
CTP13765	rs158478	57007734	13765	Intron 9	0.483	0.5	0.4526	96.5	0.494	A:C	TagSNP (EcoN1)
CTP13868	Novel	57007837	13868	Intron 9	0.003	0.003	1	100	0.002	G:A	Uncommon/rare
CTP14079	rs158479	57008048	14079	Intron 9	0.494	0.5	0.825	99.2	0.499	A:G	Reported association
CTP14123	rs181381869	57008092	14123	Intron 9	0.022	0.022	1	100	0.011	C:T	Uncommon/rare
CTP15277	Novel	57009246	15277	Intron 10	0.002	0.002	1	100	0.001	A:G	Uncommon/rare
CTP15419	rs289717	57009388	15419	Intron 10	0.428	0.435	0.734	100	0.32	C:T	Reported association

Table B1.5. Continued

CETP variant	RefSNP ID	[a]Chr. Position	[b]Position	Locations	ObsHet	PredHet	HWpval	% Call rate	MAF	Alleles	Selection criteria
CTP15688del1	rs35874588	57009657	15688	Intron 10	0.41	0.421	0.5846	98.9	0.301	A:G	TagSNP
CTP15963	rs289718	57009932	15963	Intron 10	0.403	0.423	0.259	99.8	0.304	T:C	Reported association
CTP15972	rs289719	57009941	15972	Intron 10	0.405	0.421	0.3886	99.4	0.301	G:A	Reported association
CTP16016	rs2033254	57009985	16016	Intron 10	0.445	0.468	0.2504	99.7	0.374	T:C	TagSNP
CTP16059	rs183439140	57010028	16059	Intron 10	0.01	0.01	1	99.7	0.005	C:T	Uncommon/rare
CTP16148	rs72771489	57010117	16148	Intron 10	0.018	0.018	1	99.7	0.009	G:A	Uncommon/rare
CTP16263	rs56208677	57010232	16263	Intron 10	0.14	0.144	0.6333	99.7	0.078	C:T	TagSNP
CTP16413	rs71387147	57010382	16413	Intron 10	0.152	0.148	0.8368	99.4	0.081	T:G	TagSNP
CTP16508	Novel	57010477	16508	Intron 10	0.006	0.006	1	99.5	0.003	G:C	Uncommon/rare
CTP16517	rs117427818	57010486	16517	Intron 10	0.085	0.102	0.0022	99.7	0.054	G:A	Uncommon/rare
CTP16550	rs142980129	57010519	16550	Intron 10	0.01	0.01	1	100	0.005	G:T	Uncommon/rare
CTP16598	Novel	57010567	16598	Intron 10	0.005	0.005	1	98.7	0.002	C:T	Uncommon/rare
CTP16979	rs1968905	57010948	16979	Intron 10	0	0	1	99.5	0	G:G	TagSNP
CTP17216	rs4784744	57011185	17216	Intron 10	0.428	0.436	0.7319	99.5	0.32	G:A	TagSNP
CTP17274	rs12720898	57011243	17274	Intron 10	0.103	0.106	0.6109	99.8	0.056	C:T	Uncommon/rare
CTP17483	rs291044	57011452	17483	Intron 10	0.428	0.435	0.734	100	0.32	G:A	Reported association
CTP18256	rs28381709	57012222	18256	Intron 11	0.003	0.003	1	98.9	0.002	C:A	Uncommon/rare
CTP18413	rs12708980	57012379	18413	Intron 11	0.449	0.478	0.1592	98.1	0.395	T:G	Extra tagSNPs
CTP18597	rs12720889	57012563	18597	Intron 11	0.391	0.412	0.223	99.2	0.291	A:T	Reported association
CTP18663	Novel	57012629	18663	Intron 11	0.002	0.002	1	100	0.001	C:T	Uncommon/rare
CTP18678	Novel	57012644	18678	Intron 11	0	0	1	99.4	0	T:T	Uncommon/rare
CTP18717	rs143024882	57012683	18717	Intron 11	0.005	0.005	1	98.4	0.002	C:A	Uncommon/rare
CTP20354	rs12447620	57014319	20354	Intron 11	0.212	0.223	0.2998	95	0.128	G:A	TagSNP
CTP20446	rs12708983	57014411	20446	Intron 11	0.066	0.073	0.1025	99.5	0.038	T:C	Uncommon/rare
CTP20593	Novel	57014558	20593	Intron 11	0.002	0.002	1	100	0.001	G:A	Uncommon/rare
CTP20804	Novel	57014769	20804	Intron 11	0.01	0.01	1	100	0.005	C:T	Uncommon/rare
CTP20910	rs4784745	57014875	20910	Intron 11	0.428	0.43	0.9962	99.5	0.312	A:G	TagSNP
CTP21126	rs5880	57015091	21126	Exon 12	0.091	0.107	0.0045	100	0.057	G:C	Exon/Exon-Intron Junctions
CTP21580	rs1800774	57015545	21580	Intron 12	0.447	0.475	0.1676	98.6	0.388	C:T	TagSNP
CTP22127	rs5882	57016092	22127	Exon 14 (I405V)	0.422	0.433	0.5471	99.2	0.317	A:G	Exon/Exon-Intron Junctions
CTP22327	rs111379440	57016292	22327	Intron 14	0.003	0.003	1	99	0.002	C:T	Uncommon/rare
CTP22349	rs12720882	57016314	22349	Intron 14	0.018	0.018	1	99.5	0.009	A:G	Uncommon/rare
CTP22888	Novel	57016853	22888	Intron 14	0.002	0.002	1	99.7	0.001	G:A	Uncommon/rare
CTP22997	rs12720887	57016962	22997	Intron 14	0.026	0.026	1	99	0.013	C:T	Uncommon/rare
CTP23037	rs9923854	57017002	23037	Intron 14	0.215	0.202	0.1514	99.4	0.114	T:G	TagSNP
CTP23353	rs1800777	57017319	23353	Exon 15	0.058	0.068	0.0103	99.8	0.035	G:A	Exon/Exon-Intron Junctions
crs5887	rs5887	57017552	23586	Exon 16	0	0	1	99.5	0	G:G	Exon/Exon-Intron Junctions
CTP23696	rs1801706	57017662	23696	3'UTR - Exon 16	0.282	0.283	1	98.7	0.17	G:A	TagSNP
CTP23796	rs289742	57017762	23796	3' flanking	0.217	0.223	0.6021	99.5	0.128	C:G	Reported association
CTP23830	rs289743	57017796	23830	3' flanking	0.405	0.42	0.4264	98.9	0.3	A:G	Reported association
CTP24136	rs289744	57018102	24136	3' flanking	0.402	0.421	0.2931	99.4	0.301	A:C	TagSNP
CTP25425	rs12720917	57019391	25425	3' flanking	0.294	0.284	0.4651	99	0.172	T:C	TagSNP
CTP25565	rs289745	57019532	25565	3' flanking	0.494	0.484	0.6487	99.8	0.409	A:C	TagSNP

[a]The nucleotide position on chromosome 16 build 131. [b]Position in the baseline reference sequence (NC_000016)

References for reported associations: Bansal et al. 2003; Willer et al. 2008; Boes et al. 2009; Teslovich et al. 2010; Spirin et al. 2007; Ridker et al. 2009; Kim et al. 2011: Edmondson et al. 2011

[c]rs5887: Genotyped in the 623 NHWs since it was not identified in 95 sequencing samples, however it was also found non-polymorphic in the entire sample (MAF for HapMAP CEU=0.02)

TABLE B1.6. The genotype call rates and features of the 131 SNPs genotyped in the entire African blacks (n=788)

***CET*P Variant**	**RefSNP ID**	**Position**	**Location**	**ObsHET**	**PredHET**	**HWpval**	**%Call rate**	**MAF**	**Alleles**	**Selection criteria**
CTPrs247615	rs247615	-9210	5' flanking	0.353	0.354	0.9975	95.3	0.23	A:G	Reported association
CTPrs9989419	rs9989419	-8834	5' flanking	0.456	0.449	0.749	94.9	0.34	A:G	Reported association
CTPrs183130	rs183130	-2610	5' flanking	0.366	0.369	0.8848	95.7	0.244	C:T	Reported association
CTPrs3764261	rs3764261	-648	5' flanking-Promoter	0.423	0.437	0.3928	94.3	0.323	C:A	Reported association
CTPp187	rs148562851	187	5' flanking	0.04	0.044	0.5357	96.1	0.022	C:T	Uncommon/rare
CTPp220	rs12447924	220	5' flanking	0.038	0.04	0.1089	96.6	0.02	A:G	TagSNPs
CTPp557	rs17231506	557	5' flanking	0.325	0.348	0.9255	91.2	0.224	T:C	TagSNPs
CTPp848	rs12708968	848	5' flanking	0.187	0.188	0.8296	96.6	0.105	C:T	TagSNPs
CTPp923	rs4783961	923	5' flanking	0.121	0.118	0.167	95.3	0.063	T:C	TagSNPs
CTPp950	rs146122874	950	5' flanking	0.47	0.496	0.1004	93.8	0.454	G:A	Uncommon/rare
CTPp1067	rs4783962	1067	5' flanking	0.172	0.175	0.795	94.9	0.097	C:T	TagSNPs
CTPp1153	rs17237883	1153	5' flanking	0.058	0.059	1	95.6	0.031	G:A	Uncommon/rare
CTPp1189	rs114856405	1189	5' flanking	0.062	0.07	0.0274	96.2	0.036	C:A	Uncommon/rare
CTPp1265	rs1800775	1265	5' flanking	0.466	0.478	0.5331	95.6	0.395	A:C	TagSNPs
CTPp1856	rs17231520	1856	5'UTR-Exon1	0.162	0.164	0.8324	96.4	0.09	G:A	Exon/Exon-Intron Junctions
CTP1964	rs34065661	1964	Exon 1	0.164	0.161	0.8573	98.4	0.088	G:C	TagSNPs
CTPp1986	rs5884	1986	Exon 1	0.122	0.122	1	96.4	0.065	C:A	Exon/Exon-Intron Junctions
CTPp2089	rs34680782	2089	Intron 1	0.034	0.039	0.0627	95.7	0.02	C:A	Uncommon/rare
CTPp2133	rs17231534	2133	Intron 1	0.28	0.291	0.331	96.2	0.177	C:A	TagSNPs
CTPp2187	rs3816117	2187	Intron 1	0.46	0.477	0.3525	93.8	0.394	C:T	TagSNPs
CTPp2240	rs711752	2240	Intron 1	0.34	0.357	0.2278	95.6	0.232	G:A	TagSNPs
CTPp2317	rs708272	2317	Intron 1	0.343	0.361	0.1993	95.8	0.236	G:A	Reported association(Taq1B)
CTP2692	rs60195610	2692	Intron 1	0.044	0.045	0.6799	98.5	0.023	C:T	Uncommon/rare
CTPp3101	rs9935228	3101	Intron 2	0.154	0.166	0.0763	95.8	0.091	A:G	TagSNPs
CTPp3262	rs1864163	3262	Intron 2	0.39	0.401	0.5	93.7	0.278	G:A	TagSNPs
CTPp3347	rs75313088	3347	Intron 2	0.061	0.069	0.0241	96.1	0.036	G:A	Uncommon/rare
CTPp3381del1	rs5817083	3381	Intron 2	0.497	0.477	0.2821	95.2	0.393	G:A	TagSNPs
CTP3581	rs4369653	3581	Intron 2	0.346	0.334	0.3878	97.5	0.212	A:G	TagSNPs
CTPp3686	rs7194225	3686	Intron 2	0.289	0.301	0.3104	94.4	0.185	G:C	TagSNPs
CTPp4299	rs114908369	4299	Intron 2	0.05	0.049	1	96.8	0.025	C:A	Uncommon/rare
CTPp4602	rs9929488	4602	Intron 2	0.484	0.497	0.497	94.7	0.463	G:C	TagSNPs
CTPp4791	rs12720906	4791	Intron 2	0.057	0.066	0.0165	94.9	0.034	T:G	Uncommon/rare
CTP4948	rs12720926	4948	Intron 2	0.054	0.053	1	98.2	0.027	A:G	Uncommon/rare
CTP4957	rs17237939	4957	Intron 2	0.089	0.092	0.5176	96.7	0.049	C:T	Uncommon/rare
CTPp5215del1	rs35585922	5215	Intron 2	0.237	0.253	0.1183	92.6	0.149	G:A	TagSNPs
CTPp5288	rs7203984	5288	Intron 2	0.492	0.492	1	93.9	0.438	C:A	TagSNPs
CTP5358	rs11508026	5358	Intron 2	0.054	0.053	1	98.4	0.027	A:G	Uncommon/rare
CTP5375	rs80296794	5375	Intron 2	0.043	0.042	1	98	0.021	T:C	Uncommon/rare
CTPp5383del1	rs71383212	5383	Intron 2	0.315	0.265	6.21E-10	94.3	0.157	G:A	TagSNPs
CTPp5593	rs112236143	5593	Intron 2	0.039	0.039	1	93.3	0.02	C:A	Uncommon/rare
CTPp5979	rs708273	5979	Intron 2	0.179	0.18	0.9697	95.7	0.1	G:A	TagSNPs
CTPp5990	rs17231583	5990	Intron 2	0.032	0.039	0.0046	95.3	0.02	G:C	Uncommon/rare
CTPp6022ins1	rs142058276	6022	Intron 2	0.156	0.151	0.4792	95.1	0.082	G:C	TagSNPs
CTP6221	rs17231590	6221	Intron 2	0.106	0.11	0.5112	98.2	0.058	A:G	Uncommon/rare
CTP6239	rs17237953	6239	Intron 2	0.071	0.076	0.202	95.1	0.039	G:T	Uncommon/rare
CTPp6251	rs35619327	6251	Intron 2	0.047	0.046	1	95.2	0.023	C:T	Uncommon/rare
CTPp6314	rs820299	6314	Intron 2	0.508	0.5	0.7266	95.4	0.495	A:G	TagSNPs
CTPp6427	rs17237967	6427	Intron 2	0.058	0.067	0.016	91.8	0.035	G:A	Uncommon/rare
CTP6725	rs8045855	6725	Intron 2	0.476	0.488	0.5304	94.2	0.423	A:T	TagSNPs
CTPp6914	rs12720922	6914	Intron 2	0.461	0.456	0.8351	95.2	0.352	G:A	TagSNPs
CTPrs17231611	rs17231611	7278	Intron 2	0.093	0.117	1.42E-05	94.2	0.063	T:C	Variant in the gap
CTP rs12708969	rs12708969	7616	Intron 2	0.175	0.189	0.0852	91.4	0.106	C:A	Variant in the gap
CTP rs9936680	rs9936680	8184	Intron 2	0	0	1	96.7	0	C:C	Variant in the gap
CTP8274	rs9924087	8274	Intron 2	0.287	0.328	0.0014	94.5	0.207	G:A	Variant in the gap
rs12597002	rs12597002	8436	Intron 2	0.178	0.175	0.8239	96.7	0.097	C:A	Variant in the gap
CTPp8742	rs12720863	8742	Intron 2	0.043	0.045	0.6609	96.3	0.023	A:G	Uncommon/rare
CTPp8764	rs9939224	8764	Intron 2	0.464	0.459	0.8205	95.2	0.356	G:T	TagSNPs
CTPp9178	rs11076174	9178	Intron 2	0.238	0.229	0.4149	95.6	0.132	T:C	TagSNPs
CTPp9282	rs13306230	9282	Intron 2	0.003	0.003	1	96.2	0.001	C:A	Exon/Exon-Intron Junctions
CTPp9493	rs12708971	9493	Intron 3	0.029	0.037	0.003	95.2	0.019	T:C	Uncommon/rare
CTP9755	rs891141	9755	Intron 4	0.215	0.225	0.2611	98.5	0.13	A:C	TagSNPs
CTPp9841	Novel	9841	Intron 4	0.001	0.001	1	96.4	0.001	G:A	Exon/Exon-Intron Junctions
CTP9878	rs34716057	9878	Exon 5	0.062	0.065	0.4204	98.1	0.034	G:A	Exon/Exon-Intron Junctions
CTPp10012	rs891143	10012	Intron 5	0.167	0.164	0.8442	94.9	0.09	C:T	TagSNPs
CTPp10779	rs12720862	10779	Intron 5	0.198	0.199	0.9613	96.3	0.112	A:G	TagSNPs
CTP10921	rs7205804	10921	Intron 5	0.166	0.176	0.1826	97.2	0.097	G:A	TagSNPs
CTP10934	rs12708973	10934	Intron 5	0.018	0.018	1	99.4	0.009	A:G	Uncommon/rare
CTPp10943	rs148134355	10943	Intron 5	0.009	0.009	1	95.1	0.005	G:A	Exon/Exon-Intron Junctions
CTPp10983	rs34611098	10983	Exon 6	0.003	0.003	1	96.6	0.001	G:A	Exon/Exon-Intron Junctions
CTPp11456	rs12720925	11456	Intron 7	0.082	0.081	1	95.8	0.042	T:C	Uncommon/rare
CTPp11510	rs1532624	11510	Intron 7	0.169	0.176	0.3324	96.3	0.097	C:A	Reported association
CTPp11795	rs12720871	11795	Intron 7	0.115	0.123	0.1789	94.8	0.066	C:G	Uncommon/rare

Table B1.6. Continued

***CET*P Variant**	**RefSNP ID**	**Position**	**Location**	**ObsHET**	**PredHET**	**HWpval**	**%Call rate**	**MAF**	**Alleles**	**Selection criteria**
CTPp11913	rs12720872	11913	Intron 7	0.237	0.233	0.7485	95.7	0.135	C:T	TagSNPs
CTPp12336	rs79398303	12336	Intron 8	0.001	0.001	0.6384	95.1	0.001	T:A	TagSNPs
*CTPp12336	rs79398303	12336	Intron 8	0.02	0.02	1	95.1	0.01	C:A	TagSNPs
*CTPp12336	rs79398303	12336	Intron 8	0.176	0.172	1	95.1	0.095	C:T	TagSNPs
*CTPp12409	rs11076175	12409	Intron 8	0.358	0.368	0.5165	95.3	0.243	A:G	TagSNPs
CTPp12621	rs7499892	12621	Intron 8	0.465	0.47	0.8335	94.2	0.377	C:T	TagSNPs
CTPp12860	rs289713	12860	Intron 8	0.477	0.495	0.3385	92.4	0.451	T:A	TagSNPs
CTPp12913	rs191754368	12913	Intron 8	0.033	0.037	0.0536	97	0.019	C:T	Uncommon/rare
CTPp13223	rs9930761	13223	Intron 8	0.253	0.252	1	93.4	0.148	T:C	TagSNPs
CTPp13279	rs35878799	13279	Exon 9	0.023	0.022	1	95.7	0.011	T:C	Exon/Exon-Intron Junctions
CTPp13384	rs5883	13384	Exon 9	0.27	0.262	0.4684	96.2	0.155	C:T	Exon/Exon-Intron Junctions
CTPp13477	rs11076176	13477	Intron 9	0.477	0.481	0.848	95.1	0.403	T:G	TagSNPs
CTPp13482	rs289714	13482	Intron 9	0.493	0.494	0.9966	94.4	0.447	G:A	TagSNPs
CTP13641	rs158477	13641	Intron 9	0.477	0.491	0.5226	78.2	0.433	C:T	TagSNPs
CTP14079	rs158479	14079	Intron 9	0.447	0.439	0.6857	95.2	0.325	G:A	TagSNPs
CTP14192	rs12720892	14192	Intron 9	0.079	0.083	0.3475	99.4	0.043	G:A	Uncommon/rare
CTP14258	rs158480	14258	Intron 9	0.475	0.494	0.3343	91.9	0.445	G:A	TagSNPs
CTPp14448del4	rs147606537	14448	Intron 9	0.037	0.036	1	96.7	0.018	G:A	Uncommon/rare
CTPp14539	rs289715	14539	Intron 9	0.349	0.347	1	94.7	0.224	T:A	TagSNPs
CTPp15226	rs2303789	15226	Intron 10	0.117	0.122	0.4188	96.2	0.065	T:G	Uncommon/rare
CTPp15407	rs289716	15407	Intron 10	0.488	0.499	0.5871	94.2	0.476	T:A	TagSNPs
CTPp15419	rs289717	15419	Intron 10	0.261	0.25	0.2877	95.7	0.147	G:A	TagSNPs
CTPp15542	rs12708976	15542	Intron 10	0.087	0.09	0.4674	96.4	0.047	C:T	Uncommon/rare
CTPp15639	rs12720942	15639	Intron 10	0.12	0.124	0.4635	96.6	0.066	A:G	Uncommon/rare
CTP15800	rs736274	15800	Intron 10	0.03	0.032	0.3554	98.9	0.016	A:T	Uncommon/rare
CTPp15830	rs12720939	15830	Intron 10	0.001	0.014	2.64E-12	96.2	0.007	C:A	Uncommon/rare
CTPp15913	rs12720937	15913	Intron 10	0.119	0.124	0.4363	94.8	0.066	C:G	Uncommon/rare
CTPp15963	rs289718	15963	Intron 10	0.466	0.492	0.1667	94.2	0.438	C:T	TagSNPs
CTP15972	rs289719	15972	Intron 10	0.5	0.5	1	97.2	0.493	G:A	TagSNPs
CTPp16016	rs2033254	16016	Intron 10	0.406	0.433	0.1008	94.8	0.317	T:C	TagSNPs
CTPp16146	rs112205272	16146	Intron 10	0.113	0.118	0.3321	95.8	0.063	G:A	Uncommon/rare
CTPp16363	rs112409939	16363	Intron 10	0.115	0.12	0.3734	96.1	0.064	A:G	Uncommon/rare
CTPp16413	rs71387147	16413	Intron 10	0.05	0.049	1	88.7	0.025	T:G	Uncommon/rare
CTPp16859	rs11860407	16859	Intron 10	0.285	0.374	2.23E-05	45.4	0.249	A:G	TagSNPs
CTP16979	rs1968905	16979	Intron 10	0.482	0.461	0.2466	97	0.36	G:T	TagSNPs
CTP17154	rs12720903	17154	Intron 10	0.122	0.126	0.5425	98.5	0.068	G:A	TagSNPs
CTPp17216	rs4784744	17216	Intron 10	0.182	0.181	1	95.4	0.1	G:A	TagSNPs
CTPp17483	rs291044	17483	Intron 10	0.185	0.183	0.9523	95.2	0.102	G:A	TagSNPs
CTPp17575	rs114486472	17575	Intron 10	0.035	0.039	0.0634	95.2	0.02	G:A	Uncommon/rare
CTPp17918	rs34426213	17918	Intron 10	0.077	0.081	0.2792	94.2	0.042	C:T	Uncommon/rare
CTP17970	rs891144	17970	Intron 10	0.324	0.338	0.297	98	0.215	G:A	TagSNPs
CTP18388	rs12708979	18388	Intron 11	0.055	0.058	0.3001	99	0.03	G:A	Uncommon/rare
CTP18413	rs12708980	18413	Intron 11	0.411	0.45	0.0223	91.8	0.342	A:C	TagSNPs
CTP18597	rs12720889	18597	Intron 11	0.315	0.324	0.5078	97	0.204	A:T	TagSNPs
CTP18733	rs291043	18733	Intron 11	0.147	0.158	0.0922	97	0.086	A:G	TagSNPs
CTPp18970	rs114203109	18970	Intron 11	0.085	0.081	0.507	94.3	0.042	G:A	Uncommon/rare
CTP19734	rs145189439	19734	Intron 11	0.094	0.099	0.2897	97.2	0.052	T:C	Uncommon/rare
CTPp20645	rs12708985	20645	Intron 11	1	0.5	3.28E-224	95.1	0.5	C:C	TagSNPs
CTPp20910	rs4784745	20910	Intron 11	0.136	0.14	0.5052	95.2	0.076	A:G	TagSNPs
CTP21111	rs34855278	21111	Exon 12	0.03	0.029	1	98.4	0.015	G:A	Uncommon/rare
*CTPp21119	rs7192120	21119	Intron 12	0.001	0.001	1	95.7	0.001	G:T	TagSNPs
*CTPp21119	rs7192120	21119	Exon 12	0.021	0.021	1	95.7	0.011	C:T	TagSNPs
*CTPp21119	rs7192120	21119	Exon 12	0.123	0.123	1	95.7	0.066	C:G	TagSNPs
CTPp21454	rs114948973	21454	Intron 12	0.035	0.037	0.4566	94.3	0.019	G:A	Uncommon/rare
CTPp21498	rs7195984	21498	Intron 12	0.264	0.281	0.1315	92.4	0.169	A:G	TagSNPs
CTPp21579	rs7196174	21579	Intron 12	0.129	0.13	0.9998	95.6	0.07	G:T	Exon/Exon-Intron Junctions
CTPp21580	rs1800774	21580	Intron 12	0.321	0.339	0.1725	95.2	0.217	C:T	TagSNPs
CTPp22127	rs5882	22127	Exon 14	0.398	0.428	0.0666	94.7	0.31	G:A	Exon/Exon-Intron Junctions
CTPp22162	rs5886	22162	Exon 14	0.154	0.151	0.8264	95.6	0.082	G:A	TagSNPs
CTPp22985	rs289740	22985	Intron 14	0.204	0.206	0.8796	95.1	0.117	T:C	TagSNPs
CTP23201	rs36051594	23201	Intron 14	0.078	0.084	0.1151	99.1	0.044	G:A	Uncommon/rare
CTPp23696	rs1801706	23696	3'UTR-Exon16	0.278	0.29	0.2848	95.6	0.176	G:A	TagSNPs
CTPp23796	rs289742	23796	3' flanking	0.47	0.487	0.3711	94.4	0.421	G:C	TagSNPs
CTPp23830	rs289743	23830	3' flanking	0.401	0.431	0.0669	95.8	0.315	G:A	TagSNPs
CTPrs289744	rs289744	24136	3' flanking	0.404	0.425	0.2006	93.7	0.306	G:T	Reported association
CTP24499	rs12720875	24499	3' flanking	0.058	0.061	0.3458	98.6	0.032	G:A	Uncommon/rare
CTPp24669	rs66495554	24669	3' flanking	0.304	0.311	0.5724	96.6	0.193	C:T	TagSNPs
CTPp24881	rs114646974	24881	3' flanking	0.007	0.007	1	94.7	0.003	A:G	Uncommon/rare
CTPp24899	rs138161274	24899	3' flanking	0.052	0.053	0.8571	95.6	0.027	C:G	Uncommon/rare
CTP25064	rs12720874	25064	3' flanking	0.246	0.259	0.21	92.9	0.153	T:C	TagSNPs
CTPp25218	rs12720916	25218	3' flanking	0.045	0.049	0.1491	96.8	0.025	A:G	Uncommon/rare
CTPp25565	rs289745	25565	3' flanking	0.292	0.313	0.092	95.1	0.194	T:G	TagSNPs

*triallelic SNPs and highlighted SNPs are excluded from association analyses.

References for reported associations: Bansal et al. 2003; Willer et al. 2008; Boes et al. 2009; Teslovich et al. 2010; Spirin et al. 2007; Ridker et al. 2009; Edmondson et al. 2011

TABLE B1.7. LD groups ($r^2 \geq 0.80$, MAF ≥ 0.01) of 104 *CETP* SNPs successfully genotyped in the 623 NHWs

LD bins	Alleles Captured
1	rs289744, rs289719, CTP15688Ins1, rs289743, rs5882, rs12720889, rs289718
2	rs711752, rs1532624, rs708272, rs12708969, rs11508026, rs7205804
3	rs12720922, rs17231569, rs11076175, rs7203984, rs7499892, rs9939224
4	rs79398303, rs12597002, rs4369653, rs60545348, rs708273
5	rs183130, rs247617, rs17231506, rs3764261, rs12149545
6	rs4784744, rs291044, rs289717, rs4784745
7	rs1800774, rs2033254, rs12708980
8	rs9924087, rs7194225
9	rs9926440, rs9929488
10	rs12447620, rs289742
11	rs12720873, rs11644475
12	rs17245715, rs12708968
13	rs5880, rs117427818
14	rs5883, rs9930761
15	rs158479, rs158478
16	rs1800775, rs3816117
17	rs820299
18	rs9923854
19	rs56208677
20	rs17231534
21	rs1800777
22	rs1864163
23	rs6499863
24	rs12708967
25	rs12708983
26	rs289745
27	rs4783961
28	rs117040820
29	rs11076174
30	rs289714
31	CTP14123
32	rs1801706
33	rs12720887
34	rs4783962
35	rs12708974
36	rs71387147
37	rs12720898
38	rs5030708
39	rs9989419
40	rs12720917

TABLE B1.8. LD groups ($r^2 \geq 0.80$, MAF ≥ 0.01) of 131 *CETP* SNPs successfully genotyped in 788 African blacks

LD Bins	Variants
1	rs12720942, rs2303789, rs112409939, rs112205272, rs12720937
2	rs114486472, rs12708971, rs17231583
3	rs289743, rs289744, rs5882
4	rs5883, rs9930761, rs35585922
5	rs17231590, rs17237967, rs17237939
6	rs5886, rs12720903, rs7196174
7	rs146122874, rs60195610, rs148562851
8	rs289716, rs289718
9	rs34855278, rs736274
10	rs891143, rs142058276
11	rs114856405, rs75313088
12	rs9939224, rs12720922
13	rs17231520, rs34065661
14	rs291043, rs4784745
15	rs1532624, rs7205804
16	rs12720872, rs12720862
17	rs12720875, rs12708979
18	rs12597002, rs708273
19	rs112236143, rs35619327
20	rs3816117, rs1800775
21	rs711752, rs708272
22	rs11508026, rs12720926
23	rs34680782, rs191754368
24	rs7194225, rs17231534
25	rs5884, rs12708968
26	rs291044, rs4784744
27	rs1801706, rs12720889
28	rs12708976
29	rs289714
30	rs12720871
31	rs289742
32	rs12720925
33	rs247615
34	rs17237883
35	rs9929488
36	rs71387147
37	rs12708969
38	rs158479
39	rs289715
40	rs289713
41	rs145189439
42	rs8045855
43	rs12720916
44	rs12720892
45	rs1968905
46	rs158480
47	rs891141
48	rs9935228
49	rs2033254
50	rs289745
51	rs12720863
52	rs34426213
53	rs1864163
54	rs4783962
55	rs9924087
56	rs7499892
57	rs11076176
58	rs17231506
59	rs4369653
60	rs114908369
61	rs3764261
62	rs820299
63	CTPp14448del4
64	rs5817083
65	rs66495554
66	rs289717
67	rs12708980
68	rs12720906
69	rs7203984
70	rs11076174
71	rs34716057
72	rs9989419

Table B1.8. Continued

73	rs1800774
74	rs289740
75	rs11076175
76	rs289719
77	rs4783961
78	rs36051594
79	rs114203109
80	rs7195984
81	rs891144
82	rs12447924
83	rs183130
84	rs114948973
85	rs12720874
86	rs17237953
87	rs35878799
88	rs138161274
89	rs80296794

TABLE B1.9. Association results of HDL-C levels with 104 *CETP* SNPs in NHWs (n=623)

CETP Variant	RefSNP ID	Position in Ref (NM_000078)	Genotypes (GTs)	GT Count	Locations	MAF	Adjusted Mean of plasma HDL-C	Standard Deviation	Beta	*P*
rs9989419	rs9989419	-8834	AA/GA/GG	103/285/224	5' flanking	0.3998	49.35/49.74/51.97	14.55/13.73/13.95	-0.026	0.014
rs247617	rs247617	-3257	AA/CA/CC	81/263/270	5' flanking	0.3474	53.75/51.31/48.82	13.88/13.87/13.94	0.043	7.41E-05
rs183130	rs183130	-2610	CC/TC/TT	271/262/81	5' flanking	0.3466	48.99/51.13/53.74	14.07/13.8/13.88	0.040	1.91E-04
rs6499863	rs6499863	-1956	AA/GA/GG	14/184/418	5' flanking	0.1715	47.85/50.1/50.92	13.26/12.95/14.54	-0.014	3.50E-01
rs12149545	rs12149545	-812	AA/GA/GG	68/272/280	5' flanking	0.3304	54.13/51.27/49.02	14.26/13.87/13.92	0.042	1.66E-04
rs12708967	rs12708967	-762	CC/CT/TT	23/209/387	5' flanking	0.2053	50.14/48.75/51.51	17.07/13.38/13.93	-0.034	1.14E-02
rs3764261	rs3764261	-648	GG/GT/TT	271/271/62	5' flanking	0.3284	49.09/51.22/54.43	14.07/14.08/13.64	0.043	1.63E-04
rs17231506	rs17231506	557	CC/TC/TT	273/269/77	5' flanking	0.3430	48.99/51.23/54.01	14.05/13.85/14.08	0.042	1.25E-04
rs12708968	rs12708968	848	CC/CT/TT	3/94/518	5' flanking	0.0818	48.33/49.91/50.59	9.17/14.79/13.91	-0.016	0.432
rs4783961	rs4783961	923	AA/AG/GG	180/312/127	5' flanking	0.4565	51.17/50.49/49.89	13.61/14.35/13.93	-0.013	0.216
rs17245715	rs17245715	1019	CC/CT/TT	521/95/3	5' flanking	0.0821	50.69/50.05/48.4	13.94/14.74/9.17	-0.014	0.462
rs4783962	rs4783962	1067	CC/TC/TT	400/196/22	5' flanking	0.1935	50.62/50.68/50.15	13.8/14.21/17.64	-0.005	0.702
rs1800775	rs1800775	1265	AA/CA/CC	159/315/147	5' flanking	0.4888	51.64/50.96/48.62	13.55/14.47/13.5	-0.027	1.25E-02
rs17231534	rs17231534	2133	CA/CC	56/565	Intron 1	0.0449	47.4/50.9	12.31/14.14/0	-0.057	3.05E-02
rs3816117	rs3816117	2187	CC/CT/TT	160/311/147	Intron 1	0.4879	51.8/50.79/48.99	13.73/14.2/13.97	-0.025	1.84E-02
rs711752	rs711752	2240	AA/AG/GG	119/306/192	Intron 1	0.4426	52.65/50.9/48.93	13.85/14.15/13.88	0.033	2.19E-03
rs5030708	rs5030708	2308	CC/CT	580/39	Intron 1	0.0314	50.69/49	14.19/11.82/0	-0.024	4.46E-01
rs708272	rs708272	2317	AA/GA/GG	118/306/192	Intron 1	0.4417	52.63/50.72/48.9	13.9/14.08/13.88	0.033	2.42E-03
rs1864163	rs1864163	3262	AA/GA/GG	43/242/332	Intron 2	0.2649	45.38/50.26/51.57	10.76/14.05/14.28	-0.035	3.28E-03
CTP3412	Novel	3412	AA/GA	614/1	Intron 2	8.10E-04	50.64/36.34	14.06/NA	-0.369	4.96E-02
rs4369653	rs4369653	3581	AA/AG/GG	327/235/42	Intron 2	0.2632	50.81/50.71/48.87	13.68/13.89/15.04	-0.012	0.327
rs7194225	rs7194225	3686	CC/CG/GG	4/103/513	Intron 2	0.0892	54.8/49.91/50.6	8.29/13.1/14.14	-0.001	0.944
CTP4559	Novel	4559	CC/CT	616/2	Intron 2	1.61E-03	50.49/55.07	13.98/30.41/0	0.025	0.850
rs9929488	rs9929488	4602	CC/GC/GG	52/248/307	Intron 2	0.2890	49/50.03/51.26	12.58/13.94/13.98	-0.018	0.117
rs7203984	rs7203984	5288	AA/CA/CC	387/188/31	Intron 2	0.2056	51.3/50.52/44.86	13.89/14.22/10.61	-0.032	0.011
rs11508026	rs11508026	5358	CC/CT/TT	192/266/156	Intron 2	0.4724	49.02/50.74/51.88	13.92/14.13/13.93	0.025	0.012
rs17231569	rs17231569	5810	DD/WD/WW	29/176/410	Intron 2	0.1896	43.65/50.7/50.99	9.91/14.44/13.86	-0.031	0.019
rs708273	rs708273	5979	AA/AG/GG	40/244/330	Intron 2	0.2630	48.46/50.76/50.71	14.22/14.43/13.61	-0.012	0.344
rs820299	rs820299	6314	AA/AG/GG	258/270/84	Intron 2	0.3567	50.74/50.81/49.28	13.71/14.32/13.91	-0.010	0.337
rs12720922	rs12720922	6914	AA/AG/GG	31/175/410	Intron 2	0.1917	44.56/50.64/51.06	10.62/14.63/13.99	-0.030	0.022
rs12708969	Novel	7616	GG/TG/TT	188/318/111	Intron 2	0.4394	49.3/50.67/52.57	13.86/14.16/13.48	0.028	0.009
rs60545348	rs60545348	8017	AA/CA/CC	328/247/43	Intron 2	0.2685	50.86/50.48/49.06	13.68/14.45/14.86	-0.014	0.232
rs9924087	rs9924087	8274	AA/GA/GG	5/102/511	Intron 2	0.0903	53.2/50.48/50.62	7.3/14.04/14.1	0.003	0.875
rs12597002	rs12597002	8436	AA/AC/CC	42/247/328	Intron 2	0.2674	49.13/50.59/50.67	15.28/14.34/13.63	-0.011	0.367
rs9926440	rs9926440	8695	CC/CG/GG	57/260/301	Intron 2	0.3016	48.49/49.98/51.57	13.09/14.5/13.75	-0.027	0.019
rs9939224	rs9939224	8764	GG/GT/TT	394/191/31	Intron 2	0.2047	51.12/50.37/44.57	13.73/15.01/11.1	-0.034	0.008
rs11076174	rs11076174	9178	CC/TC/TT	4/85/530	Intron 2	0.0749	45.33/49.83/50.7	10.28/14.58/13.99	-0.023	0.254
rs891142	rs891142	10009	CC/CT	615/2	Intron 5	1.62E-03	50.61/43.21	14.06/10.61/0	-0.103	0.436
CTP10459		10459	AA/CA	617/2	Intron 5	1.61E-03	50.57/57.45	14.07/0/0	0.138	0.299
rs7205804	rs7205804	10921	AA/AG/GG	124/308/184	Intron 5	0.4531	52.45/50.79/48.96	13.77/14.16/14	0.031	0.004
rs12708972	rs12708972	10924	CC/TC	607/11	Intron 5	8.87E-03	50.57/48.73	14.09/11.35/0	-0.020	0.723
rs34523084	rs34523084	11194	CC/TC	603/9	Intron 6	7.33E-03	50.58/46.43	13.87/22.4/0	-0.119	0.058
rs1532624	rs1532624	11510	AA/CA/CC	123/310/185	Intron 7	0.451	52.63/50.79/48.97	13.65/14.17/13.98	0.032	0.003
rs12708974	rs12708974	11581	CC/TC/TT	498/111/11	Intron 7	0.107	50.88/48.87/55.57	14.16/12.86/17.66	-0.010	0.539
rs117040820	rs117040820	11793	CC/CT	596/20	Intron 7	0.016	50.61/48.71	14.11/11/0	-0.021	0.625
rs12720873	rs12720873	12103	AA/AG/GG	1/46/571	Intron 8	0.0387	52.17/51.83/50.43	NA/12.99/14.14	0.026	0.345
CTP12123	Novel	12123	AT/TT	1/616	Intron 8	8.08E-04	27.15/50.64	NA/14.02	-0.621	8.71E-04
rs148654654	rs148654654	12178	CC/TC	608/9	Intron 8	7.27E-03	50.47/58.54	14.05/14.88/0	0.129	0.039
rs289712	rs289712	12336	CC/CT/TT	328/246/40	Intron 8	0.264	50.73/50.38/49.96	13.79/14.3/15.37	-0.009	0.461
rs11076175	rs11076175	12409	AA/AG/GG	416/171/28	Intron 8	0.184	51.19/50.44/44.13	13.96/14.62/10.09	-0.034	0.010
rs7499892	rs7499892	12621	CC/CT/TT	417/171/29	Intron 8	0.1850	50.98/50.5/43.65	13.93/14.61/9.91	-0.033	0.011
rs187766748	rs187766748	12746	AA/AG	606/8	Intron 8	6.49E-03	50.57/46.98	14.04/13.54/0	-0.059	0.377
rs187468344	rs187468344	13071	CC/TC	606/7	Intron 8	5.69E-03	50.57/45.52	14.03/14.33/0	-0.111	0.120
rs9930761	rs9930761	13223	CC/CT/TT	3/95/523	Intron 8	0.081	55.08/51.01/50.48	12.1/14.25/14.03	0.013	0.523
rs28381707	rs28381707	13327	GG/GT	612/6	Exon 9	4.84E-03	50.49/60.06	14.01/15.69/0	0.145	0.059
rs5883	rs5883	13384	CC/CT/TT	533/83/2	Exon 9	0.07	50.42/51.43/58.32	14.06/14.22/3.54	0.022	0.304
rs289714	rs289714	13482	CC/CT/TT	21/183/415	Intron 9	0.1812	44.49/50.34/50.96	12.99/13.49/14.29	-0.025	0.064
rs11644475	rs11644475	13683	AA/GA/GG	575/45/1	Intron 9	0.037	50.49/51.71/52.2	14.13/13.04/NA	0.023	0.412
rs158478	rs158478	13765	AA/CA/CC	157/290/152	Intron 9	0.49	50.5/50.85/50.38	13.29/14.25/14.61	-0.003	0.754
CTP13868	Novel	13868	GA/GG	2/619	Intron 9	1.61E-03	67.5/50.53	41.01/13.93/0	0.179	0.176
rs158479	rs158479	14079	AA/GA/GG	157/305/154	Intron 9	0.4984	50.03/51.08/50.11	14.54/14.34/12.91	0.004	0.735
CTP14123	rs181381869	14123	CC/CT	607/14	Intron 9	0.0112	50.51/53.88	14.01/15.05/0	0.050	0.318
CTP15277	Novel	15277	AA/AG	620/1	Intron 10	8.03E-04	50.61/33.2	14.04/NA	-0.295	0.115
rs289717	rs289717	15419	CC/CT/TT	288/267/66	Intron 10	0.3202	51.05/50.4/49.25	13.92/13.77/15.77	-0.015	0.186
rs35874588	rs35874588	15688	DD/WD/WW	304/252/58	Intron 10	0.3003	49.74/51.33/52.31	14.13/13.87/14.57	0.022	0.055
rs289718	rs289718	15963	CC/CT/TT	63/250/307	Intron 10	0.303	52.06/51.45/49.64	14.44/13.8/14.1	0.023	0.043
rs289719	rs289719	15972	AA/GA/GG	60/250/307	Intron 10	0.300	52.35/51.28/49.66	14.53/13.83/14.1	0.023	0.043

Table B1.9. Continued

***CETP* Variant**	**RefSNP ID**	**Position in Ref (NM_000078)**	**Genotypes (GTs)**	**GT Count**	**Locations**	**MAF**	**Adjusted Mean of plasma HDL-C**	**Standard Deviation**	**Beta**	***P***
rs2033254	rs2033254	16016	CC/TC/TT	93/276/250	Intron 10	0.3736	48.81/51.22/50.59	13.1/14.12/14.31	-0.007	0.529
rs183439140	rs183439140	16059	CC/CT	613/6	Intron 10	4.83E-03	50.54/55.68	14.02/17.15/0	0.080	0.296
rs72771489	rs72771489	16148	GA/GG	11/608	Intron 10	8.86E-03	49.59/50.61	13.41/14.06/0	-0.018	0.759
rs56208677	rs56208677	16263	CC/TC/TT	528/86/5	Intron 10	0.077	50.31/51.64/62.27	13.86/14.68/17	0.033	0.096
rs71387147	rs71387147	16413	GG/GT/TT	3/94/520	Intron 10	0.08	50.02/49.07/50.87	16.62/12.54/14.34	-0.021	0.279
CTP16508	Novel	16508	CG/GG	4/614	Intron 10	3.23E-03	43.07/50.59	9.75/14.03/0	-0.142	0.129
rs117427818	rs117427818	16517	AA/GA/GG	7/53/559	Intron 10	0.053	43.34/50.08/50.72	8.47/12.81/14.19	-0.024	0.281
rs142980129	rs142980129	16550	GG/GT	615/6	Intron 10	4.82E-03	50.53/55.69	14.01/17.15/0	0.080	0.295
CTP16598	Novel	16598	CC/CT	610/3	Intron 10	2.44E-03	50.64/45.77	14.12/13.08/0	-0.077	0.477
rs4784744	rs4784744	17216	AA/GA/GG	66/266/286	Intron 10	0.321	49.24/50.43/51.09	15.77/13.78/13.93	-0.015	0.178
rs12720898	rs12720898	17274	CC/CT/TT	553/64/3	Intron 10	0.056	50.45/51.18/57.73	13.9/15.17/19.66	0.015	0.520
rs291044	rs291044	17483	AA/AG/GG	66/267/288	Intron 10	0.32	49.25/50.4/51.05	15.77/13.77/13.92	-0.015	0.186
rs28381709	rs28381709	18256	CA/CC	2/612	Intron 11	1.62E-03	74.78/50.5	18.38/14.01/0	0.368	0.006
rs12708980	rs12708980	18413	GG/GT/TT	103/274/232	Intron 11	0.3944	49.08/51.08/50.84	13.05/13.94/14.79	-0.007	0.484
rs12720889	rs12720889	18597	AA/AT/TT	317/241/58	Intron 11	0.2905	49.57/51.62/52.25	13.9/14.19/14.54	0.025	0.031
CTP18663	Novel	18663	CC/CT	620/1	Intron 11	8.03E-04	50.62/28.16	14.04/NA	-0.382	0.041
CTP18717	rs143024882	18717	CA/CC	3/608	Intron 11	2.45E-03	44.19/50.6	14.18/14.1/0	-0.114	0.295
rs12447620	rs12447620	20354	AA/GA/GG	13/124/453	Intron 11	0.127	53.23/51.43/50.36	13.01/13.86/14.23	0.021	0.193
rs12708983	rs12708983	20446	CC/TC/TT	3/40/575	Intron 11	0.037	55.57/50.63/50.51	17.04/11.69/14.2	0.019	0.488
CTP20593	Novel	20593	GA/GG	1/620	Intron 11	8.03E-04	87.8/50.52	NA/13.92	0.399	0.033
CTP20804	Novel	20804	CC/CT	615/6	Intron 11	4.82E-03	50.66/42.04	14.02/13.55/0	-0.161	0.036
rs4784745	rs4784745	20910	AA/AG/GG	291/266/61	Intron 11	0.312	50.71/50.68/49.05	13.65/13.82/16.47	-0.013	0.266
rs5880	rs5880	21126	CC/CG/GG	7/57/557	Exon 12	0.057	43.35/49.33/50.8	8.47/12.82/14.19	-0.032	0.133
rs1800774	rs1800774	21580	CC/TC/TT	238/274/100	Intron 12	0.387	50.4/51.29/48.99	14.46/14.27/12.66	-0.003	0.811
rs5882	rs5882	22127	AA/GA/GG	291/260/65	Exon 14	0.317	49.96/51.23/50.9	14.22/14.11/13.25	0.013	0.252
rs111379440	rs111379440	22327	CC/CT	613/2	Intron 14	1.62E-03	50.65/38.6	14.09/14.14/0	-0.206	0.121
rs12720882	rs12720882	22349	AA/GA	607/11	Intron 14	8.87E-03	50.58/48.27	14.05/13.53/0	-0.041	0.471
CTP22888delA	Novel	22888	WD/WW	1/618	Intron 14	8.05E-04	33.46/50.62	NA/14.05	-0.285	0.128
rs12720887	rs12720887	22997	CC/CT	599/16	Intron 14	0.013	50.51/54.69	14.07/15.14/0	0.065	0.172
rs9923854	rs9923854	23037	GG/GT/TT	4/132/481	Intron 14	0.113	52.37/50.76/50.56	13.23/13.81/14.17	0.005	0.760
rs1800777	rs1800777	23353	AA/AG/GG	4/36/580	Exon 15	0.0354	44.34/46.95/50.87	9.74/13.51/14.07	-0.061	0.023
rs1801706	rs1801706	23696	AA/GA/GG	18/173/422	Exon 16-UTR	0.1707	51.27/51.13/50.35	13.64/14.5/13.99	0.009	0.508
rs289742	rs289742	23796	CC/GC/GG	473/133/12	3' flanking	0.1274	50.3/51.52/53.3	14.13/13.96/13.3	0.022	0.165
rs289743	rs289743	23830	AA/GA/GG	306/249/59	3' flanking	0.299	49.73/51.39/51.76	14.09/14.17/13.72	0.020	0.077
rs289744	rs289744	24136	AA/CA/CC	308/248/61	3' flanking	0.30	49.74/51.43/51.35	14.04/14.16/13.62	0.018	0.113
rs12720917	rs12720917	25425	CC/TC/TT	15/182/418	3' flanking	0.17	46.18/51.15/50.42	11.68/13.69/14.24	0.001	0.919
rs289745	rs289745	25565	AA/CA/CC	212/307/101	3' flanking	0.409	51.09/50.68/49.34	14.19/13.79/14.42	-0.014	0.215

TABLE B1.10. Association results of TG levels with 103 *CETP* SNPs in NHWs (n=623)

CETP Variant	RefSNP ID	Position in Ref (NM_000078)	Genotypes (GTs)	GT Count	Locations	MAF	Adjusted Mean of plasma TG	Standard Deviation	Beta	*P*
rs9989419	rs9989419	-8834	AA/GA/GG	102/284/225	5' flanking	0.400	138.74/142.5/132.5	69.12/67.65/62.07	0.027	0.244
rs247617	rs247617	-3257	AA/CA/CC	82/263/268	5' flanking	0.347	134.76/136.66/141.4	65.58/62.88/68.64	-0.024	0.313
rs183130	rs183130	-2610	CC/TC/TT	269/262/82	5' flanking	0.347	140.73/135.87/134.72	68.59/62.44/65.58	-0.022	0.340
rs6499863	rs6499863	-1956	AA/GA/GG	14/182/419	5' flanking	0.172	126.16/138.5/137.81	46.67/59.79/68.14	0.010	0.748
rs12149545	rs12149545	-812	AA/GA/GG	69/271/278	5' flanking	0.330	133.1/136.96/140.35	65.75/62.53/68.72	-0.022	0.356
rs12708967	rs12708967	-762	CC/CT/TT	23/209/385	5' flanking	0.205	137.86/145.58/133.93	63.08/72.74/61.41	0.042	0.150
rs3764261	rs3764261	-648	GG/GT/TT	269/270/63	5' flanking	0.328	140.2/136.64/133.42	68.46/64.5/61.76	-0.021	0.405
rs17231506	rs17231506	557	CC/TC/TT	271/268/78	5' flanking	0.343	140.43/135.63/135.31	68.6/61.39/66.02	-0.019	0.420
rs12708968	rs12708968	848	CC/CT/TT	3/94/516	5' flanking	0.082	129.98/143.97/136.76	63.45/71.97/64.47	0.031	0.462
rs4783961	rs4783961	923	AA/AG/GG	181/311/125	5' flanking	0.457	136.77/139.94/133.48	65.3/66.51/62.13	-0.004	0.876
rs17245715	rs17245715	1019	CC/CT/TT	519/95/3	5' flanking	0.082	136.93/143.69/129.8	64.92/71.21/63.45	0.031	0.464
rs4783962	rs4783962	1067	CC/TC/TT	400/194/22	5' flanking	0.194	140.24/132.55/139.65	65.57/63.91/82.77	-0.037	0.213
rs1800775	rs1800775	1265	AA/CA/CC	161/312/146	5' flanking	0.489	136.82/139.71/135.37	62.38/68.58/63.62	-0.004	0.864
rs17231534	rs17231534	2133	CA/CC	56/563	Intron 1	0.045	146.97/137.03	70.78/65.16/0	0.071	0.211
rs3816117	rs3816117	2187	CC/CT/TT	162/309/146	Intron 1	0.488	136.9/138.64/135.63	62.06/67.49/64.21	-0.005	0.842
rs711752	rs711752	2240	AA/AG/GG	121/303/191	Intron 1	0.443	132.63/138.81/138.35	59.86/66.59/66.34	-0.016	0.499
rs5030708	rs5030708	2308	CC/CT	580/37	Intron 1	0.031	138.13/136.49	66.09/61.93/0	0.000	0.999
rs708272	rs708272	2317	AA/GA/GG	120/303/191	Intron 1	0.442	132.53/139.53/138.39	60.1/67.25/66.34	-0.016	0.493
rs1864163	rs1864163	3262	AA/GA/GG	43/240/333	Intron 2	0.265	141.34/140.33/135.43	71.44/64.23/65.33	0.025	0.336
CTP3412	Novel	3412	AA/GA	612/1	Intron 2	0.001	137.99/222.28	65.82/NA	0.562	0.166
rs4369653	rs4369653	3581	AA/AG/GG	329/232/41	Intron 2	0.263	138.31/136.42/129.13	65.14/64.03/59.86	-0.019	0.475
rs7194225	rs7194225	3686	CC/CG/GG	4/103/511	Intron 2	0.089	103.27/142.26/137.42	43.91/67.19/65.55	0.017	0.681
CTP4559	Novel	4559	CC/CT	614/2	Intron 2	0.002	138.01/118.26	65.89/48.79/0	-0.077	0.787
rs9929488	rs9929488	4602	CC/GC/GG	52/248/305	Intron 2	0.289	137.56/142.25/134.82	60.77/71.11/62.47	0.025	0.329
rs7203984	rs7203984	5288	AA/CA/CC	387/187/31	Intron 2	0.206	135.09/141.66/140.14	64.12/68.34/70.46	0.025	0.364
rs11508026	rs11508026	5358	CC/CT/TT	190/264/158	Intron 2	0.472	138.21/138.6/136.15	66.29/67.81/61.4	-0.004	0.859
rs17231569	rs17231569	5810	DD/WD/WW	29/175/409	Intron 2	0.190	140.42/141.86/135.66	72.44/67.54/64.35	0.023	0.418
rs708273	rs708273	5979	AA/AG/GG	39/243/331	Intron 2	0.263	124.07/140.58/137.34	52.2/68.03/64.9	-0.008	0.755
rs820299	rs820299	6314	AA/AG/GG	259/268/83	Intron 2	0.357	136.65/141.73/130.68	66.49/64.44/68.5	-0.003	0.910
rs12720922	rs12720922	6914	AA/AG/GG	31/174/409	Intron 2	0.192	136.86/142.65/136.11	71.53/67.67/64.73	0.017	0.541
rs12708969	Novel	7616	GG/TG/TT	187/315/113	Intron 2	0.439	137.54/140.16/131.93	66.18/67.72/59.11	-0.012	0.599
rs60545348	rs60545348	8017	AA/CA/CC	330/244/42	Intron 2	0.269	137.93/139.62/128.93	65.2/67.54/59.17	-0.007	0.787
rs9924087	Novel	8274	AA/GA/GG	5/102/509	Intron 2	0.090	99.6/142.07/137.14	39.61/67.14/65.5	0.010	0.802
rs12597002	rs12597002	8436	AA/AC/CC	41/245/329	Intron 2	0.267	127.56/140.1/137.9	58.93/67.72/65.14	-0.009	0.740
rs9926440	rs9926440	8695	CC/CG/GG	57/258/302	Intron 2	0.302	141.7/141.08/134.58	70.52/69.19/61.94	0.023	0.357
rs9939224	rs9939224	8764	GG/GT/TT	394/189/31	Intron 2	0.205	135.74/142.09/141.25	62.64/71.17/71.28	0.018	0.521
rs11076174	rs11076174	9178	CC/TC/TT	4/83/530	Intron 2	0.075	133/142.18/137.47	54.42/70.6/65.17	0.022	0.612
rs891142	rs891142	10009	CC/CT	613/2	Intron 5	0.002	137.94/157.75	65.86/31.11/0	0.197	0.490
rs139040281	rs139040281	10459	AA/CA	615/2	Intron 5	0.002	138.01/105.09	65.78/16.26/0	-0.153	0.591
rs7205804	rs7205804	10921	AA/AG/GG	125/306/183	Intron 5	0.453	132.71/140.17/138.4	59.83/68.31/65.57	-0.016	0.484
rs12708972	rs12708972	10924	CC/TC	605/11	Intron 5	0.009	137.95/148.97	66.22/35.07/0	0.131	0.287
rs34523084	rs34523084	11194	CC/TC	603/7	Intron 6	0.007	138.05/125.23	65.25/78.52/0	-0.124	0.418
rs1532624	rs1532624	11510	AA/CA/CC	125/308/184	Intron 7	0.452	131.64/140.42/137.99	59.36/68.19/65.77	-0.016	0.477
rs12708974	rs12708974	11581	CC/TC/TT	496/111/11	Intron 7	0.108	136.72/146/114.05	64.97/70.82/39.1	0.017	0.634
rs117040820	rs117040820	11793	CC/CT	594/20	Intron 7	0.016	138.31/125.3	66.02/60.47/0	-0.074	0.418
rs12720873	rs12720873	12103	AA/AG/GG	1/46/569	Intron 8	0.039	93.29/134.4/138.52	NA/64/66.02	-0.030	0.609
*CTP12123	Novel	12123	NA	NA	Intron 8	NA	NA	NA	NA	NA
rs148654654	rs148654654	12178	CC/TC	606/9	Intron 8	0.007	138.45/111.19	66.05/54.72/0	-0.188	0.167
rs289712	rs289712	12336	CC/CT/TT	328/245/39	Intron 8	0.265	137.94/139.44/123.68	65.07/66.85/56.92	-0.017	0.531
rs11076175	rs11076175	12409	AA/AG/GG	416/170/28	Intron 8	0.184	135.44/143.49/134.84	64.1/68.45/67.99	0.022	0.430
rs7499892	rs7499892	12621	CC/CT/TT	416/170/29	Intron 8	0.185	135.98/141.42/140.41	64.43/67.41/72.44	0.019	0.496
rs187766748	rs187766748	12746	AA/AG	605/8	Intron 8	0.006	138.51/120.85	66.01/37.52/0	-0.123	0.396
rs187468344	rs187468344	13071	CC/TC	605/6	Intron 8	0.006	137.55/184.91	65.72/71.28/0	0.298	0.071
rs9930761	rs9930761	13223	CC/CT/TT	3/95/521	Intron 8	0.081	118.3/140.53/137.57	28.54/62.76/66.45	0.021	0.622
rs28381707	rs28381707	13327	GG/GT	610/6	Exon 9	0.005	137.6/133.12	65.38/42.46/0	0.021	0.901
rs5883	rs5883	13384	CC/CT/TT	531/83/2	Exon 9	0.070	137.74/139.91/121.95	66.39/61.99/40.31	0.021	0.646
rs289714	rs289714	13482	CC/CT/TT	21/182/414	Intron 9	0.181	156.62/136.52/137.78	73.33/60.98/67.37	0.023	0.442
rs11644475	rs11644475	13683	AA/GA/GG	573/45/1	Intron 9	0.038	138.17/135.87/93.34	65.99/63.77/NA	-0.014	0.819
rs158478	rs158478	13765	AA/CA/CC	156/291/150	Intron 9	0.495	134.72/138.81/138.36	63.61/65.3/69.02	0.010	0.663
CTP13868	Novel	13868	GA/GG	2/617	Intron 9	0.002	219.76/137.67	69.3/65.67/0	0.537	0.060
rs158479	rs158479	14079	AA/GA/GG	155/306/154	Intron 9	0.498	138.2/138.51/135.96	68.45/64.61/63.69	-0.005	0.843
CTP14123	rs181381869	14123	CC/CT	605/14	Intron 9	0.011	138.15/128.42	65.92/59.07/0	-0.069	0.527
CTP15277	Novel	15277	AA/AG	618/1	Intron 10	0.001	138.02/87.44	65.80/NA	-0.273	0.499
rs289717	rs289717	15419	CC/CT/TT	289/266/64	Intron 10	0.320	136.85/138.89/138.85	63.32/68.01/68.1	0.007	0.785
rs35874588	rs35874588	15688	DD/WD/WW	302/251/59	Intron 10	0.300	137.19/138.66/138.55	65.86/66.04/68.19	0.008	0.761
rs289718	rs289718	15963	CC/CT/TT	64/250/305	Intron 10	0.304	136.67/138.81/137.48	65.88/66.28/65.51	0.002	0.923
rs289719	rs289719	15972	AA/GA/GG	61/249/305	Intron 10	0.300	135.49/138.88/137.43	63.54/66.41/65.51	0.002	0.932
rs2033254	rs2033254	16016	CC/TC/TT	93/276/248	Intron 10	0.374	136.42/137.57/138.63	70.69/59.32/70.84	-0.006	0.791
rs183439140	rs183439140	16059	CC/CT	611/6	Intron 10	0.005	137.98/130.47	65.92/41.24/0	0.001	0.994
rs72771489	rs72771489	16148	GA/GG	11/606	Intron 10	0.009	137.94/137.9	51.06/65.94/0	0.039	0.751

Table B1.10. Continued

***CETP* Variant**	**RefSNP ID**	**Position in Ref (NM_000078)**	**Genotypes (GTs)**	**GT Count**	**Locations**	**MAF**	**Adjusted Mean of plasma TG**	**Standard Deviation**	**Beta**	***P***
rs56208677	rs56208677	16263	CC/TC/TT	527/85/5	Intron 10	0.077	140.33/121.99/152.61	66.22/58.34/95.93	-0.102	0.016
rs71387147	rs71387147	16413	GG/GT/TT	3/92/520	Intron 10	0.081	164.36/134.17/138	75.44/58.22/66.39	0.003	0.949
CTP16508	Novel	16508	CG/GG	3/613	Intron 10	0.003	135.06/138.16	36.53/65.94/0	0.059	0.800
rs117427818	rs117427818	16517	AA/GA/GG	7/53/557	Intron 10	0.054	143.45/136.49/138.01	67.43/60.99/66.39	0.005	0.909
rs142980129	rs142980129	16550	GG/GT	613/6	Intron 10	0.005	138.01/130.38	65.97/41.24/0	0.000	0.998
CTP16598	Novel	16598	CC/CT	608/3	Intron 10	0.002	138.22/109.43	66.09/31.18/0	-0.117	0.617
rs4784744	rs4784744	17216	AA/GA/GG	64/265/287	Intron 10	0.321	138.87/139.03/136.89	68.1/67.99/63.52	0.007	0.765
rs12720898	rs12720898	17274	CC/CT/TT	551/64/3	Intron 10	0.056	137.73/141.08/112.55	65.32/71.4/24.17	-0.003	0.944
rs291044	rs291044	17483	AA/AG/GG	64/266/289	Intron 10	0.320	138.85/138.89/136.85	68.1/68.01/63.32	0.007	0.785
rs28381709	rs28381709	18256	CA/CC	2/611	Intron 11	0.002	103.4/138.3	65.76/65.92/0	-0.202	0.484
rs12708980	rs12708980	18413	GG/GT/TT	103/274/230	Intron 11	0.394	138/139.9/136.4	68.08/61.64/70.25	0.013	0.580
rs12720889	rs12720889	18597	AA/AT/TT	315/240/59	Intron 11	0.290	139.38/135.99/137.78	65.68/66.64/65.25	-0.013	0.602
CTP18663	Novel	18663	CC/CT	618/1	Intron 11	0.001	137.87/179.03	65.80/NA	0.368	0.362
CTP18717	rs143024882	18717	CA/CC	2/607	Intron 11	0.002	159.57/137.44	70.71/65.78/0	0.172	0.547
rs12447620	rs12447620	20354	AA/GA/GG	13/124/451	Intron 11	0.128	119.11/137.84/137.28	60.16/60.17/64.91	-0.010	0.764
rs12708983	rs12708983	20446	CC/TC/TT	3/41/572	Intron 11	0.038	100.78/131.17/138.84	15.52/57.98/66.43	-0.053	0.354
CTP20593	Novel	20593	GA/GG	1/618	Intron 11	0.001	106.63/137.98	NA/65.76	-0.246	0.543
CTP20804	Novel	20804	CC/CT	613/6	Intron 11	0.005	137.92/139.59	65.77/70.78/0	-0.004	0.979
rs4784745	rs4784745	20910	AA/AG/GG	293/264/59	Intron 11	0.313	137.8/138.88/137.01	62.97/68.86/66.8	-0.003	0.902
rs5880	rs5880	21126	CC/CG/GG	7/57/555	Exon 12	0.057	143.53/134.35/138.23	67.43/59.46/66.45	-0.004	0.939
rs1800774	rs1800774	21580	CC/TC/TT	236/273/101	Intron 12	0.388	137.37/139.44/134.37	70.3/60.38/68.12	-0.004	0.850
rs5882	rs5882	22127	AA/GA/GG	289/259/66	Exon 14	0.317	135.95/141.01/134.4	65/67.3/63.07	0.010	0.686
rs111379440	rs111379440	22327	CC/CT	611/2	Intron 14	0.002	138.1/144.1	65.96/2.83/0	0.094	0.745
rs12720882	rs12720882	22349	AA/GA	605/11	Intron 14	0.009	138.07/141.93	65.46/86.8/0	-0.008	0.951
CTP22888delA	Novel	22888	WD/WW	1/616	Intron 14	0.001	300.67/137.64	NA/65.46	0.861	0.032
rs12720887	rs12720887	22997	CC/CT	597/16	Intron 14	0.013	138.03/141.51	65.76/72.3/0	-0.005	0.965
rs9923854	rs9923854	23037	GG/GT/TT	4/133/478	Intron 14	0.114	114.45/139.35/137.11	27.89/65.05/65.45	0.010	0.792
rs1800777	rs1800777	23353	AA/AG/GG	4/36/578	Exon 15	0.035	165.17/133.62/138.02	65/60.08/66.16	0.018	0.761
rs1801706	rs1801706	23696	AA/GA/GG	18/174/419	Exon 16-UTR	0.171	126.49/140.94/136.55	41.76/69.37/64.38	0.008	0.795
rs289742	rs289742	23796	CC/GC/GG	471/133/12	3' flanking	0.127	137.42/140.63/121.31	65.74/66.08/60.38	0.003	0.930
rs289743	rs289743	23830	AA/GA/GG	304/248/60	3' flanking	0.300	136.95/140.83/133.03	65.24/67.34/64.23	0.002	0.932
rs289744	rs289744	24136	AA/CA/CC	306/247/62	3' flanking	0.300	136.72/139.71/133.89	65.17/66.37/63.3	0.003	0.900
rs12720917	rs12720917	25425	CC/TC/TT	15/181/418	3' flanking	0.172	152.17/137.94/136.73	59.75/64.83/65.72	0.025	0.413
rs289745	rs289745	25565	AA/CA/CC	214/303/101	3' flanking	0.409	140.92/137.51/132.77	71.11/63.9/59.83	-0.018	0.458

*CTP12123 was excluded due to missing values.

TABLE B1.11. Association results of LDL-C levels with 104 CETP SNPs in NHWs (n=623)

CETP Variant	RefSNP ID	Position in Ref (NM_000078)	Genotypes (GTs)	GT Count	Locations	MAF	Adjusted Mean of plasma LDL-C	Standard Deviation	Beta	*P*
rs9989419	rs9989419	-8834	AA/GA/GG	103/285/226	5' flanking	0.400	135.69/139.14/135.56	41.56/38.94/42.08	0.726	0.749
rs247617	rs247617	-3257	AA/CA/CC	82/264/270	5' flanking	0.347	137.54/139.45/134.91	39.86/41.35/40.08	2.195	0.342
rs183130	rs183130	-2610	CC/TC/TT	271/263/82	5' flanking	0.347	134.65/139.47/137.5	39.66/41.37/39.86	2.359	0.305
rs6499863	rs6499863	-1956	AA/GA/GG	14/184/420	5' flanking	0.172	143.33/140.74/135.61	41.19/40.73/40.41	4.781	0.118
rs12149545	rs12149545	-812	AA/GA/GG	69/273/280	5' flanking	0.330	136.96/139.2/134.97	40.92/41.88/39.8	2.085	0.385
rs12708967	rs12708967	-762	CC/CT/TT	23/209/389	5' flanking	0.205	128.41/136.99/137.67	35.62/40.01/41.56	-2.154	0.451
rs3764261	rs3764261	-648	GG/GT/TT	271/272/63	5' flanking	0.328	134.96/138.7/141.15	40.1/41.72/42.73	3.327	0.179
rs17231506	rs17231506	557	CC/TC/TT	273/270/78	5' flanking	0.343	134.91/138.81/138.04	40/41.95/40.22	2.249	0.338
rs12708968	rs12708968	848	CC/CT/TT	3/95/519	5' flanking	0.082	128.5/132.21/137.69	29.9/44.18/39.96	-5.402	0.197
rs4783961	rs4783961	923	AA/AG/GG	181/313/127	5' flanking	0.457	137.68/137.12/135.86	39.95/41.11/41.68	-0.881	0.701
rs17245715	rs17245715	1019	CC/CT/TT	522/96/3	5' flanking	0.082	137.72/132.34/128.44	39.88/44.28/29.9	-5.311	0.202
rs4783962	rs4783962	1067	CC/TC/TT	402/196/22	5' flanking	0.194	138.13/133.82/142.18	41.78/37.5/50.15	-1.961	0.498
rs1800775	rs1800775	1265	AA/CA/CC	161/315/147	5' flanking	0.489	137.99/136.47/137.02	41.68/41.07/39.46	-0.510	0.823
rs17231534	rs17231534	2133	CA/CC	56/567	Intron 1	0.045	142.15/136.48	42.79/40.58/0	5.710	0.309
rs3816117	rs3816117	2187	CC/CT/TT	162/311/147	Intron 1	0.488	137.58/137.14/136.64	41.64/40.36/39.75	-0.469	0.835
rs711752	rs711752	2240	AA/AG/GG	121/306/192	Intron 1	0.443	136.42/137/137.1	41.18/41.72/39.45	-0.312	0.892
rs5030708	rs5030708	2308	CC/CT	582/39	Intron 1	0.031	137.25/134.69	40.61/44.44/0	-2.568	0.698
rs708272	rs708272	2317	AA/GA/GG	120/306/192	Intron 1	0.442	136.57/137.06/137.09	41.32/41.71/39.45	-0.236	0.918
rs1864163	rs1864163	3262	AA/GA/GG	43/242/334	Intron 2	0.265	136.32/138.2/136.72	30.46/42.63/40.19	0.593	0.816
CTP3412	Novel	3412	AA/GA	616/1	Intron 2	0.001	137.23/118.83	40.91/NA	-18.531	0.645
rs4369653	rs4369653	3581	AA/AG/GG	329/235/42	Intron 2	0.263	137.77/135.79/136.95	40.57/39.88/42.3	-1.160	0.652
rs7194225	rs7194225	3686	CC/CG/GG	4/103/515	Intron 2	0.089	143.41/138.96/136.73	52.69/41.21/40.53	2.407	0.548
CTP4559	Novel	4559	CC/CT	618/2	Intron 2	0.002	137.12/97.42	40.81/42.28/0	-39.820	0.160
rs9929488	rs9929488	4602	CC/GC/GG	52/248/309	Intron 2	0.289	136.44/138.36/136.19	35.68/41.87/41.27	0.984	0.698
rs7203984	rs7203984	5288	AA/CA/CC	389/188/31	Intron 2	0.206	137.34/137.56/135.87	40.52/41.97/32.9	-0.228	0.934
rs11508026	rs11508026	5358	CC/CT/TT	192/266/158	Intron 2	0.472	136.14/137.58/137.04	40.81/41.11/41.01	0.493	0.818
rs17231569	rs17231569	5810	DD/WD/WW	29/176/412	Intron 2	0.190	137.13/136.84/137.32	32.68/42.57/40.74	-0.301	0.915
rs708273	rs708273	5979	AA/AG/GG	40/244/332	Intron 2	0.263	136.12/137.45/137.16	42.06/39.31/41.35	-0.114	0.965
rs820299	rs820299	6314	AA/AG/GG	260/270/84	Intron 2	0.357	137.53/136.08/139.76	41.54/39.29/43.4	0.440	0.850
rs12720922	rs12720922	6914	AA/AG/GG	31/175/412	Intron 2	0.192	134.31/136.52/137.62	32.95/42.78/40.68	-1.370	0.621
rs12708969	Novel	7616	GG/TG/TT	188/318/113	Intron 2	0.439	137.02/137.1/136.9	39.37/41.55/41.04	-0.044	0.985
rs60545348	rs60545348	8017	AA/CA/CC	330/247/43	Intron 2	0.269	137.84/135.86/137.38	40.62/41.09/41.86	-1.066	0.680
rs9924087	Novel	8274	AA/GA/GG	5/102/513	Intron 2	0.090	129.03/137.91/136.87	55.41/41.44/40.54	0.156	0.969
rs12597002	rs12597002	8436	AA/AC/CC	42/247/330	Intron 2	0.267	135.61/137.02/137.07	41.45/40.19/41.32	-0.401	0.877
rs9926440	rs9926440	8695	CC/CG/GG	57/260/303	Intron 2	0.302	132.47/138.13/136.73	40.49/41.83/38.68	-0.741	0.760
rs9939224	rs9939224	8764	GG/GT/TT	396/191/31	Intron 2	0.205	137.43/135.31/137.53	39.62/43.83/32.16	-1.110	0.685
rs11076174	rs11076174	9178	CC/TC/TT	4/85/532	Intron 2	0.075	137.5/138.15/136.63	33.17/47.77/39.38	1.330	0.754
rs891142	rs891142	10009	CC/CT	617/2	Intron 5	0.002	137.11/126.66	40.82/57.42/0	-10.456	0.712
rs139040281	rs139040281	10459	AA/CA	619/2	Intron 5	0.002	136.87/165.72	40.85/34.93/0	28.855	0.307
rs7205804	rs7205804	10921	AA/AG/GG	126/308/184	Intron 5	0.453	136.91/136.78/137.87	42.24/40.93/39.87	-0.540	0.814
rs12708972	rs12708972	10924	CC/TC	609/11	Intron 5	0.009	136.82/141.34	40.95/35.33/0	4.568	0.708
rs34523084	rs34523084	11194	CC/TC	605/9	Intron 6	0.007	137.43/109.95	40.35/68.32/0	-27.482	0.041
rs1532624	rs1532624	11510	AA/CA/CC	125/310/185	Intron 7	0.452	137.78/136.92/137.54	40.62/40.85/40.04	0.046	0.984
rs12708974	rs12708974	11581	CC/TC/TT	499/112/11	Intron 7	0.108	137.95/134.07/124.57	40.5/43.28/28.73	-4.769	0.179
rs117040820	rs117040820	11793	CC/CT	598/20	Intron 7	0.016	137.43/126.18	40.84/41.91/0	-11.290	0.214
rs12720873	rs12720873	12103	AA/AG/GG	1/46/573	Intron 8	0.039	142.7/136.74/136.9	NA/42.67/40.78	0.096	0.987
CTP12123	Novel	12123	AT/TT	1/618	Intron 8	0.001	2.87/137.18	NA/40.50	-134.652	0.001
rs148654654	rs148654654	12178	CC/TC	610/9	Intron 8	0.007	136.64/156.91	40.53/53.8/0	20.298	0.130
rs289712	rs289712	12336	CC/CT/TT	330/246/40	Intron 8	0.265	137.03/137.18/136.34	42/39.16/41.85	-0.101	0.969
rs11076175	rs11076175	12409	AA/AG/GG	418/171/28	Intron 8	0.184	137.4/136.47/138.17	40.03/42.99/33.05	-0.326	0.907
rs7499892	rs7499892	12621	CC/CT/TT	419/171/29	Intron 8	0.185	137.22/136.26/137.01	40.55/42.98/32.68	-0.559	0.842
rs187766748	rs187766748	12746	AA/AG	608/8	Intron 8	0.006	137.25/129.41	40.74/16.49/0	-7.921	0.576
rs187468344	rs187468344	13071	CC/TC	608/7	Intron 8	0.006	137.19/112.74	40.66/56.04/0	-24.543	0.107
rs9930761	rs9930761	13223	CC/CT/TT	3/95/525	Intron 8	0.081	172.41/134.66/137.21	34.11/41.24/40.76	-0.103	0.980
rs28381707	rs28381707	13327	GG/GT	614/6	Exon 9	0.005	136.94/136.93	40.65/64.23/0	-0.014	0.999
rs5883	rs5883	13384	CC/CT/TT	535/83/2	Exon 9	0.070	137.27/134.53/173.4	40.68/41.97/47.8	-0.784	0.862
rs289714	rs289714	13482	CC/CT/TT	21/183/417	Intron 9	0.181	133.13/137.59/137.03	38.55/41.76/40.63	-0.379	0.897
rs11644475	rs11644475	13683	AA/GA/GG	577/45/1	Intron 9	0.038	136.99/136.91/142.64	40.72/42.70/NA	0.163	0.978
rs158478	rs158478	13765	AA/CA/CC	158/291/152	Intron 9	0.495	135.09/137.85/134.93	42.5/39.92/40.26	-0.053	0.981
CTP13868	Novel	13868	GA/GG	2/621	Intron 9	0.002	212.95/136.75	92.91/40.48/0	76.229	0.007
rs158479	rs158479	14079	AA/GA/GG	157/306/155	Intron 9	0.498	135.46/139.12/134.78	40.68/40.59/40.34	-0.327	0.884
rs181381869	rs181381869	14123	CC/CT	609/14	Intron 9	0.011	137.02/135.69	40.95/34.93/0	-1.337	0.901
CTP15277	Novel	15277	AA/AG	622/1	Intron 10	0.001	137.06/92.6	40.79/NA	-44.577	0.265
rs289717	rs289717	15419	CC/CT/TT	290/267/66	Intron 10	0.320	137.24/136.29/138.75	42.4/38.94/41.56	0.163	0.946
rs35874588	rs35874588	15688	DD/WD/WW	305/252/59	Intron 10	0.300	136.82/138.91/131.41	38.31/44.45/38.2	-0.902	0.715
rs289718	rs289718	15963	CC/CT/TT	64/250/308	Intron 10	0.304	130.84/139.18/136.94	38.54/43.64/38.11	-1.187	0.620
rs289719	rs289719	15972	AA/GA/GG	61/250/308	Intron 10	0.300	130.85/138.85/136.9	39.39/44.42/38.11	-1.207	0.622
rs2033254	rs2033254	16016	CC/TC/TT	94/276/251	Intron 10	0.374	134.46/139.99/134.58	41.76/39.43/41.98	1.196	0.602
rs183439140	rs183439140	16059	CC/CT	615/6	Intron 10	0.005	136.79/154.49	40.75/48.52/0	17.791	0.279
rs72771489	rs72771489	16148	GA/GG	11/610	Intron 10	0.009	156.57/136.61	32.2/40.88/0	20.045	0.099
rs56208677	rs56208677	16263	CC/TC/TT	530/86/5	Intron 10	0.077	137.64/133.75/120.29	40.17/44.88/37.79	-4.873	0.244
rs71387147	rs71387147	16413	GG/GT/TT	3/94/522	Intron 10	0.081	146.67/138.6/136.59	61.39/37.99/41.37	2.386	0.572
CTP16508	Novel	16508	CG/GG	4/616	Intron 10	0.003	91.05/137.2	64.6/40.59/0	-46.391	0.021

Table B1.11. Continued

CETP Variant	RefSNP ID	Position in Ref (NM_000078)	Genotypes (GTs)	GT Count	Locations	MAF	Adjusted Mean of plasma LDL-C	Standard Deviation	Beta	*P*
rs117427818	rs117427818	16517	AA/GA/GG	7/53/561	Intron 10	0.054	128.47/131.49/137.66	34.99/40.03/41.01	-5.611	0.228
rs142980129	rs142980129	16550	GG/GT	617/6	Intron 10	0.005	136.82/154.47	40.71/48.52/0	17.740	0.280
CTP16598	Novel	16598	CC/CT	612/3	Intron 10	0.002	136.83/165.51	40.69/57.59/0	28.825	0.213
rs4784744	rs4784744	17216	AA/GA/GG	66/266/288	Intron 10	0.321	138.75/136.47/137.25	41.56/39.03/42.45	0.223	0.927
rs12720898	rs12720898	17274	CC/CT/TT	555/64/3	Intron 10	0.056	137.91/128.13/114.68	40.72/39.24/10.6	-10.214	0.034
rs291044	rs291044	17483	AA/AG/GG	66/267/290	Intron 10	0.320	138.75/136.29/137.24	41.56/38.94/42.4	0.163	0.946
rs28381709	rs28381709	18256	CA/CC	2/614	Intron 11	0.002	101.31/137.28	69.58/40.44/0	-36.551	0.196
rs12708980	rs12708980	18413	GG/GT/TT	104/274/233	Intron 11	0.394	135.56/139.78/134.88	41.27/39.28/42.66	1.192	0.601
rs12720889	rs12720889	18597	AA/AT/TT	318/241/59	Intron 11	0.290	137.49/136.96/133.37	38.34/43.7/41.68	-1.495	0.542
CTP18663	Novel	18663	CC/CT	622/1	Intron 11	0.001	136.91/191.7	40.78/NA	54.887	0.170
CTP18717	rs143024882	18717	CA/CC	3/610	Intron 11	0.002	105.87/137.03	98.2/40.62/0	-31.212	0.179
rs12447620	rs12447620	20354	AA/GA/GG	13/125/454	Intron 11	0.128	130.41/135.96/137.1	35.12/44.11/40.45	-1.869	0.585
rs12708983	rs12708983	20446	CC/TC/TT	3/41/576	Intron 11	0.038	134.31/135.9/136.98	21.74/38/41.16	-1.141	0.841
CTP20593	Novel	20593	GA/GG	1/622	Intron 11	0.001	111.54/137.03	NA/40.81	-25.602	0.522
CTP20804	Novel	20804	CC/CT	617/6	Intron 11	0.005	137.09/126.83	40.91/24.42/0	-10.336	0.529
rs4784745	rs4784745	20910	AA/AG/GG	293/266/61	Intron 11	0.313	137.99/135.95/138.29	42.04/39.09/42.71	-0.671	0.784
rs5880	rs5880	21126	CC/CG/GG	7/57/559	Exon 12	0.057	128.47/131.49/137.66	34.99/40.92/40.88	-5.642	0.215
rs1800774	rs1800774	21580	CC/TC/TT	239/274/101	Intron 12	0.388	134.05/139.36/138.11	42.44/38.79/43.11	2.696	0.238
rs5882	rs5882	22127	AA/GA/GG	292/260/66	Exon 14	0.317	137.93/137.55/130.56	39.46/42.66/39.84	-2.574	0.288
CTP22327	rs111379440	22327	CC/CT	615/2	Intron 14	0.002	137.27/117.56	40.83/80.04/0	-20.000	0.484
rs12720882	rs12720882	22349	AA/GA	609/11	Intron 14	0.009	136.56/155.52	40.97/32.85/0	19.226	0.116
CTP22888delA	Novel	22888	WD/WW	1/620	Intron 14	0.001	151.5/136.94	NA/40.87	14.590	0.715
rs12720887	rs12720887	22997	CC/CT	601/16	Intron 14	0.013	136.7/156.12	40.48/51.79/0	19.556	0.054
rs9923854	rs9923854	23037	GG/GT/TT	4/133/482	Intron 14	0.114	172.08/135.98/136.85	49.57/40.94/40.73	1.377	0.710
rs1800777	rs1800777	23353	AA/AG/GG	4/36/582	Exon 15	0.035	135.75/127.43/137.5	43/37.58/40.94	-7.194	0.208
rs1801706	rs1801706	23696	AA/GA/GG	18/174/423	UTR	0.171	133.35/134.85/137.65	34.83/41.96/40.31	-2.600	0.390
rs289742	rs289742	23796	CC/GC/GG	474/134/12	3' flanking	0.127	137.28/136.26/129.52	40.18/43.52/36.6	-1.870	0.578
rs289743	rs289743	23830	AA/GA/GG	307/249/60	3' flanking	0.300	138.07/136.78/132.43	39.64/41.9/40.74	-2.277	0.352
rs289744	rs289744	24136	AA/CA/CC	309/248/62	3' flanking	0.300	137.95/136.85/131.58	39.56/41.93/40.43	-2.459	0.309
rs12720917	rs12720917	25425	CC/TC/TT	15/182/420	3' flanking	0.172	132.58/136.77/137.52	43.01/41.78/40.02	-1.262	0.679
rs289745	rs289745	25565	AA/CA/CC	214/307/101	3' flanking	0.409	135.38/136.55/141.65	39.24/42.4/39.41	2.792	0.233

TABLE B1.12. Association results of TC levels with 104 *CETP* SNPs in NHWs (n=623)

CETP Variant	RefSNP ID	Position in Ref (NM_000078)	Genotypes (GTs)	GT Count	Locations	MAF	Adjusted Mean of plasma TC	Standard Deviation	Beta	*P*
rs9989419	rs9989419	-8834	AA/GA/GG	103/285/226	5'flanking	0.40	215.38/218.35/215.21	42.6/42.55/44.27	0.663	0.780
rs247617	rs247617	-3257	AA/CA/CC	82/264/270	5'flanking	0.35	218.68/219.09/213.87	44.3/43.93/41.92	3.188	0.186
rs183130	rs183130	-2610	CC/TC/TT	271/263/82	5'flanking	0.35	213.63/218.79/218.64	41.5/43.99/44.3	3.240	0.177
rs6499863	rs6499863	-1956	AA/GA/GG	14/184/420	5'flanking	0.17	215.97/220.23/215.29	44.65/43.22/42.97	3.739	0.246
rs12149545	rs12149545	-812	AA/GA/GG	69/273/280	5'flanking	0.33	218.18/220.14/213.78	45.83/44.64/41.86	3.614	0.150
rs12708967	rs12708967	-762	CC/CT/TT	23/209/389	5'flanking	0.21	206.77/215.11/218.72	40.5/42.41/44.38	-4.511	0.131
rs3764261	rs3764261	-648	GG/GT/TT	271/272/63	5'flanking	0.33	213.87/219.58/222.58	41.99/44.54/47.21	4.856	0.060
rs17231506	rs17231506	557	CC/TC/TT	273/270/78	5'flanking	0.34	213.79/219.45/219.49	41.91/44.73/44.72	3.683	0.134
rs12708968	rs12708968	848	CC/CT/TT	3/95/519	5'flanking	0.08	201.67/213.87/217.29	34.56/46.35/42.73	-3.995	0.362
rs4783961	rs4783961	923	AA/AG/GG	181/313/127	5'flanking	0.46	216.39/217.8/215.72	43.96/43.25/43.72	-0.179	0.941
rs17245715	rs17245715	1019	CC/CT/TT	522/96/3	5'flanking	0.08	217.44/214.1/201.66	42.67/46.68/34.56	-3.918	0.369
rs4783962	rs4783962	1067	CC/TC/TT	402/196/22	5'flanking	0.19	218.55/212.38/227.96	45.13/39.77/44.87	-2.157	0.478
rs1800775	rs1800775	1265	AA/CA/CC	161/315/147	5'flanking	0.49	217.79/217.79/214.41	44.57/44.35/40.82	-1.668	0.486
rs17231534	rs17231534	2133	CA/CC	56/567	Intron 1	0.04	220.14/216.68	42.59/43.66/0	3.494	0.552
rs3816117	rs3816117	2187	CC/CT/TT	162/311/147	Intron 1	0.49	217.64/217.05/214.32	44.43/42.36/43.07	-1.650	0.485
rs711752	rs711752	2240	AA/AG/GG	121/306/192	Intron 1	0.44	216.19/218.32/215.01	45.26/43.47/42.76	0.905	0.706
rs5030708	rs5030708	2308	CC/CT	582/39	Intron 1	0.03	216.85/221.23	43.29/47.6/0	4.392	0.525
rs708272	rs708272	2317	AA/GA/GG	120/306/192	Intron 1	0.44	216.28/218.34/215	45.44/43.4/42.76	0.964	0.688
rs1864163	rs1864163	3262	AA/GA/GG	43/242/334	Intron 2	0.26	209.49/217.86/216.89	35.68/44.51/42.85	-1.500	0.575
CTP3412	Novel	3412	AA/GA	616/1	Intron 2	0.00	217.33/193.77	43.62/NA	-23.845	0.571
rs4369653	rs4369653	3581	AA/AG/GG	329/235/42	Intron 2	0.26	216.75/217.75/212.67	42.77/42.66/41.09	-0.605	0.821
rs7194225	rs7194225	3686	CC/CG/GG	4/103/515	Intron 2	0.09	219.35/220.04/216.48	61.55/41.24/43.88	3.276	0.436
CTP4559	Novel	4559	CC/CT	618/2	Intron 2	0.00	217.05/176.72	43.51/62.93/0	-40.474	0.172
rs9929488	rs9929488	4602	CC/GC/GG	52/248/309	Intron 2	0.29	213.17/217.95/217.18	39.05/43.93/44.28	-0.861	0.745
rs7203984	rs7203984	5288	AA/CA/CC	389/188/31	Intron 2	0.21	217.82/217.56/208.69	44.04/43.68/38.06	-2.298	0.427
rs11508026	rs11508026	5358	CC/CT/TT	192/266/158	Intron 2	0.47	215.83/217.64/216.98	44.53/42.99/43.82	0.627	0.780
rs17231569	rs17231569	5810	DD/WD/WW	29/176/412	Intron 2	0.19	208.71/217.23/217.64	38.6/43.84/43.86	-2.293	0.435
rs708273	rs708273	5979	AA/AG/GG	40/244/332	Intron 2	0.26	210.76/217.92/216.44	40.36/43.57/43.06	-0.708	0.794
rs820299	rs820299	6314	AA/AG/GG	260/270/84	Intron 2	0.36	216.69/217.42/218.29	43.75/43.66/43.62	0.781	0.749
rs12720922	rs12720922	6914	AA/AG/GG	31/175/412	Intron 2	0.19	206.17/216.92/218.15	38.31/44.18/43.76	-3.529	0.224
rs12708969	Novel	7616	GG/TG/TT	188/318/113	Intron 2	0.44	215.19/218.35/216.45	42.38/43.36/45.66	0.970	0.691
rs60545348	rs60545348	8017	AA/CA/CC	330/247/43	Intron 2	0.27	216.82/218.03/213.05	42.96/44.99/40.63	-0.418	0.877
rs9924087	Novel	8274	AA/GA/GG	5/102/513	Intron 2	0.09	203.64/219.51/216.58	63.76/40.42/43.91	1.261	0.762
rs12597002	rs12597002	8436	AA/AC/CC	42/247/330	Intron 2	0.27	211.38/218.54/216.45	40.41/44.85/42.98	-0.303	0.911
rs9926440	rs9926440	8695	CC/CG/GG	57/260/303	Intron 2	0.30	213.2/217.63/216.02	42.42/42.87/42.83	-0.225	0.929
rs9939224	rs9939224	8764	GG/GT/TT	396/191/31	Intron 2	0.20	217.32/216.74/210.09	43.26/44.31/38.39	-2.003	0.483
rs11076174	rs11076174	9178	CC/TC/TT	4/85/532	Intron 2	0.07	211.57/221.94/216.07	38.24/46.17/42.85	4.534	0.310
rs891142	rs891142	10009	CC/CT	617/2	Intron 5	0.00	217.16/198.74	43.54/53.03/0	-18.500	0.532
rs139040281	rs139040281	10459	AA/CA	619/2	Intron 5	0.00	216.89/241.95	43.6/38.18/0	25.147	0.396
rs7205804	rs7205804	10921	AA/AG/GG	126/308/184	Intron 5	0.45	219.01/217.16/215.93	47.3/42.36/42.98	1.521	0.526
rs12708972	rs12708972	10924	CC/TC	609/11	Intron 5	0.01	216.84/220.2	43.69/38.19/0	3.390	0.791
rs34523084	rs34523084	11194	CC/TC	605/9	Intron 6	0.01	216.86/225.53	43.14/75.11/0	8.725	0.535
rs1532624	rs1532624	11510	AA/CA/CC	125/310/185	Intron 7	0.45	217.38/217.28/215.52	45.09/42.31/43.21	1.019	0.668
rs12708974	rs12708974	11581	CC/TC/TT	499/112/11	Intron 7	0.11	217.94/214.4/203.79	43.68/44.28/28.5	-4.654	0.210
rs117040820	rs117040820	11793	CC/CT	598/20	Intron 7	0.02	217.57/201.25	43.42/48.34/0	-16.449	0.084
rs12720873	rs12720873	12103	AA/AG/GG	1/46/573	Intron 8	0.04	215.87/219.84/216.67	NA/42.82/43.71	2.891	0.639
CTP12123	Novel	12123	AT/TT	1/618	Intron 8	0.00	138.68/217.12	NA/43.50	-78.863	0.060
rs148654654	rs148654654	12178	CC/TC	610/9	Intron 8	0.01	216.68/236.41	43.38/53.31/0	19.786	0.159
rs289712	rs289712	12336	CC/CT/TT	330/246/40	Intron 8	0.26	217.47/217.02/212.39	43.93/43.28/41.41	-1.520	0.579
rs11076175	rs11076175	12409	AA/AG/GG	418/171/28	Intron 8	0.18	217.09/216.94/208.83	42.98/44.35/39.28	-1.981	0.499
rs7499892	rs7499892	12621	CC/CT/TT	419/171/29	Intron 8	0.18	217.58/216.39/208.62	43.64/44.17/38.6	-2.735	0.352
rs187766748	rs187766748	12746	AA/AG	608/8	Intron 8	0.01	216.83/202.17	43.23/23.94/0	-14.948	0.314
rs187468344	rs187468344	13071	CC/TC	608/7	Intron 8	0.01	216.83/221.75	43.67/34.9/0	4.964	0.756
rs9930761	rs9930761	13223	CC/CT/TT	3/95/525	Intron 8	0.08	251.87/215.94/216.98	45/43.63/43.57	1.212	0.783
rs28381707	rs28381707	13327	GG/GT	614/6	Exon 9	0.00	216.81/223.91	43.34/64.78/0	7.154	0.677
rs5883	rs5883	13384	CC/CT/TT	535/83/2	Exon 9	0.07	216.98/216.42/257.3	43.5/44.05/59.4	1.396	0.767
rs289714	rs289714	13482	CC/CT/TT	21/183/417	Intron 9	0.18	208.2/216.26/217.87	36.14/44.86/43.43	-2.824	0.358
rs11644475	rs11644475	13683	AA/GA/GG	577/45/1	Intron 9	0.04	216.73/220.36/215.94	43.66/42.92/NA	3.315	0.594
rs158478	rs158478	13765	AA/CA/CC	158/291/152	Intron 9	0.50	216.28/216.54/216.45	45.8/43.57/40.53	0.087	0.971
CTP13868	Novel	13868	GA/GG	2/621	Intron 9	0.00	325.36/216.64	147.79/42.8/0	109.620	2.05E-04
rs158479	rs158479	14079	AA/GA/GG	157/306/155	Intron 9	0.50	216.29/218.06/213.78	41.2/43.81/43.42	-1.252	0.594
CTP14123	rs181381869	14123	CC/CT	609/14	Intron 9	0.01	217.02/215.73	43.75/34.96/0	-1.295	0.909
CTP15277	Novel	15277	AA/AG	622/1	Intron 10	0.00	217.12/139.1	43.49/NA	-78.734	0.060
rs289717	rs289717	15419	CC/CT/TT	290/267/66	Intron 10	0.32	216.68/216.75/219.3	44.45/43.8/38.75	0.890	0.725
CTP15688delC	rs35874588	15688	DD/WD/WW	305/252/59	Intron 10	0.30	215.53/220.45/212.21	41.51/46.51/41.28	0.849	0.743
rs289718	rs289718	15963	CC/CT/TT	64/250/308	Intron 10	0.30	210.92/219.64/215.55	41.08/45.6/41.22	-0.037	0.988
rs289719	rs289719	15972	AA/GA/GG	61/250/308	Intron 10	0.30	210.75/220.45/215.58	41.85/46.73/41.22	0.277	0.914
rs2033254	rs2033254	16016	CC/TC/TT	94/276/251	Intron 10	0.37	213.22/218.72/216.44	43.49/43.8/43.42	-0.727	0.762
rs183439140	rs183439140	16059	CC/CT	615/6	Intron 10	0.00	216.79/234.91	43.44/56.3/0	18.224	0.288
rs72771489	rs72771489	16148	GA/GG	11/610	Intron 10	0.01	231.3/216.71	35.04/43.66/0	14.767	0.247
rs56208677	rs56208677	16263	CC/TC/TT	530/86/5	Intron 10	0.08	217.79/212.06/214.16	42.65/48.55/50.54	-4.946	0.258
rs71387147	rs71387147	16413	GG/GT/TT	3/94/522	Intron 10	0.08	228.59/217.66/216.68	64.49/39.63/44.24	1.597	0.718
CTP16508	Novel	16508	CG/GG	4/616	Intron 10	0.00	240.9/216.75	97.45/43.15/0	24.310	0.248

Table B1.12. Continued

***CETP* Variant**	**RefSNP ID**	**Position in Ref (NM_000078)**	**Genotypes (GTs)**	**GT Count**	**Locations**	**MAF**	**Adjusted Mean of plasma TC**	**Standard Deviation**	**Beta**	***P***
rs117427818	rs117427818	16517	AA/GA/GG	7/53/561	Intron 10	0.05	198.93/208.64/218.05	43.98/45.04/43.45	-9.507	0.051
rs142980129	rs142980129	16550	GG/GT	617/6	Intron 10	0.00	216.82/234.89	43.41/56.3/0	18.186	0.290
CTP16598	Novel	16598	CC/CT	612/3	Intron 10	0.00	216.98/232.46	43.51/50.27/0	15.570	0.521
rs4784744	rs4784744	17216	AA/GA/GG	66/266/288	Intron 10	0.32	219.28/217.01/216.74	38.75/43.84/44.51	0.935	0.713
rs12720898	rs12720898	17274	CC/CT/TT	555/64/3	Intron 10	0.06	217.89/208.15/195.77	43.81/38.87/11.53	-10.098	0.046
rs291044	rs291044	17483	AA/AG/GG	66/267/290	Intron 10	0.32	219.3/216.75/216.68	38.75/43.8/44.45	0.890	0.725
rs28381709	rs28381709	18256	CA/CC	2/614	Intron 11	0.00	198.18/216.76	64.35/43.06/0	-18.881	0.523
rs12708980	rs12708980	18413	GG/GT/TT	104/274/233	Intron 11	0.39	214.77/218.8/216.82	43.27/43.76/43.75	-0.466	0.845
rs12720889	rs12720889	18597	AA/AT/TT	318/241/59	Intron 11	0.29	216.4/218.42/213.79	41.34/46.25/43.75	-0.055	0.983
CTP18663	Novel	18663	CC/CT	622/1	Intron 11	0.00	216.92/259.14	43.55/NA	42.334	0.312
CTP18717	rs143024882	18717	CA/CC	3/610	Intron 11	0.00	234.73/216.72	28.58/43.69/0	18.096	0.456
rs12447620	rs12447620	20354	AA/GA/GG	13/125/454	Intron 11	0.13	208.58/217.92/216.58	36.53/46.86/42.96	-0.415	0.908
rs12708983	rs12708983	20446	CC/TC/TT	3/41/576	Intron 11	0.04	211.38/214.17/217.13	17.62/41.87/43.82	-2.951	0.620
CTP20593	Novel	20593	GA/GG	1/622	Intron 11	0.00	223.8/216.98	NA/43.58	6.888	0.870
CTP20804	Novel	20804	CC/CT	617/6	Intron 11	0.00	217.19/196.17	43.59/29.94/0	-21.211	0.217
rs4784745	rs4784745	20910	AA/AG/GG	293/266/61	Intron 11	0.31	216.69/217.37/218.42	44.83/43.33/38.4	0.801	0.755
rs5880	rs5880	21126	CC/CG/GG	7/57/559	Exon 12	0.06	198.94/207.41/218.19	43.98/45.04/43.35	-10.436	0.028
rs1800774	rs1800774	21580	CC/TC/TT	239/274/101	Intron 12	0.39	215.6/219.25/214.63	43.36/43/45.93	0.337	0.887
rs5882	rs5882	22127	AA/GA/GG	292/260/66	Exon 14	0.32	216.61/219.48/209.04	42.05/45.8/41.4	-1.519	0.551
CTP22327	rs111379440	22327	CC/CT	615/2	Intron 14	0.00	217.39/186.24	43.52/94.75/0	-31.638	0.289
rs12720882	rs12720882	22349	AA/GA	609/11	Intron 14	0.01	216.61/233.15	43.66/40.2/0	16.820	0.190
CTP22888delA	Novel	22888	WD/WW	1/620	Intron 14	0.00	248.32/216.92	NA/43.60	31.502	0.451
rs12720887	rs12720887	22997	CC/CT	601/16	Intron 14	0.01	216.71/239.19	43.28/51.96/0	22.729	0.033
rs9923854	rs9923854	23037	GG/GT/TT	4/133/482	Intron 14	0.11	246.83/216.67/216.64	57.36/44.2/43.35	1.872	0.629
rs1800777	rs1800777	23353	AA/AG/GG	4/36/582	Exon 15	0.04	209.28/200.82/217.97	47.97/41.37/43.56	-13.229	0.027
rs1801706	rs1801706	23696	AA/GA/GG	18/174/423	Exon 16-UTR	0.17	209.36/216.05/217.27	37.41/43.65/43.41	-2.177	0.491
rs289742	rs289742	23796	CC/GC/GG	474/134/12	3' flanking	0.13	216.65/218.72/207.91	42.83/46.78/38.12	0.170	0.962
rs289743	rs289743	23830	AA/GA/GG	307/249/60	3' flanking	0.30	216.73/218.88/211.33	42.29/45.06/41.15	-0.907	0.723
rs289744	rs289744	24136	AA/CA/CC	309/248/62	3' flanking	0.30	216.54/218.8/210.3	42.17/45/41.01	-1.189	0.639
rs12720917	rs12720917	25425	CC/TC/TT	15/182/420	3' flanking	0.17	208.79/217.64/216.3	45.41/43.78/42.75	-0.154	0.961
rs289745	rs289745	25565	AA/CA/CC	214/307/101	3' flanking	0.41	216.57/217.19/217.29	43.42/43.76/43.81	0.420	0.864

TABLE B1.13. Association results of ApoA1 levels with 100 *CETP* SNPs in NHWs (n=623)

CETP Variant	RefSNP ID	Position in Ref (NM_000078)	Genotypes (GTs)	GT Count	Locations	MAF	Adjusted Mean of plasma APOA1	Standard Deviation	Beta	*P*
rs9989419	rs9989419	-8834	AA/GA/GG	72/201/157	5' flanking	0.400	145.02/151.23/149.24	34.64/33.59/32.85	-1.346	0.552
rs247617	rs247617	-3257	AA/CA/CC	54/182/196	5' flanking	0.347	150.49/153.65/145.84	40.5/29.94/33.15	3.941	0.083
rs183130	rs183130	-2610	CC/TC/TT	196/180/54	5' flanking	0.347	146.06/153.16/150.47	33.3/30.92/40.5	3.639	0.115
rs6499863	rs6499863	-1956	AA/GA/GG	12/127/295	5' flanking	0.172	142.12/150.05/149.66	25.5/36.58/32.23	-0.962	0.746
rs12149545	rs12149545	-812	AA/GA/GG	43/191/201	5' flanking	0.330	152.71/152.41/146.31	44.55/30.16/33.27	4.294	0.074
rs12708967	rs12708967	-762	CC/CT/TT	16/148/270	5' flanking	0.205	142.64/149.85/149.68	28.42/34.03/33.17	-1.198	0.668
rs3764261	rs3764261	-648	GG/GT/TT	196/190/40	5' flanking	0.328	146.39/152.94/148.59	33.29/30.84/43.2	3.222	0.189
rs17231506	rs17231506	557	CC/TC/TT	197/186/50	5' flanking	0.343	146.24/153.4/150.38	33.24/29.69/41.89	3.709	0.109
rs12708968	rs12708968	848	CC/CT/TT	2/70/358	5' flanking	0.082	154.93/152.3/148.93	53.67/33.45/33.41	3.336	0.414
rs4783961	rs4783961	923	AA/AG/GG	127/208/99	5' flanking	0.457	147.59/153.84/143.12	34.57/33.39/30.44	-1.729	0.430
rs17245715	rs17245715	1019	CC/CT/TT	361/71/2	5' flanking	0.082	148.82/153.02/154.99	33.34/33.23/53.67	4.081	0.312
rs4783962	rs4783962	1067	CC/TC/TT	277/139/16	5' flanking	0.194	151.22/147.86/138.98	34.83/31.79/17.77	-4.415	0.118
rs1800775	rs1800775	1265	AA/CA/CC	112/219/104	5' flanking	0.489	150.09/152.2/143.68	35.81/32.04/32.93	-3.108	0.164
rs17231534	rs17231534	2133	CA/CC	41/394	Intron 1	0.045	142.67/150.34	31.75/33.44/0	-7.676	0.154
rs3816117	rs3816117	2187	CC/CT/TT	112/218/104	Intron 1	0.488	150.98/151.35/144.29	34.54/32.88/32.91	-3.281	0.142
rs711752	rs711752	2240	AA/AG/GG	83/214/135	Intron 1	0.443	153.17/152.03/144.21	36.73/31.4/32.95	4.888	0.028
rs5030708	rs5030708	2308	CC/CT	407/28	Intron 1	0.031	149.75/147.72	33.78/26.55/0	-2.038	0.751
rs708272	rs708272	2317	AA/GA/GG	82/213/135	Intron 1	0.442	152.89/152.21/144.19	36.86/31.41/32.95	4.810	0.032
rs1864163	rs1864163	3262	AA/GA/GG	29/171/233	Intron 2	0.265	141.92/150.17/150.12	43.91/31.16/33.52	-2.092	0.413
*CTP3412	Novel	3412	NA	NA	Intron 2	NA	NA	NA	NA	NA
rs4369653	rs4369653	3581	AA/AG/GG	231/161/31	Intron 2	0.263	150.84/150.3/138.29	34.06/32.85/23.17	-3.707	0.141
rs7194225	rs7194225	3686	CC/CG/GG	3/74/357	Intron 2	0.089	137.93/152.26/149.1	17.01/36.44/32.83	1.842	0.637
CTP4559	Novel	4559	CC/CT	431/1	Intron 2	0.002	149.53/145.84	33.45/NA	-3.712	0.911
rs9929488	rs9929488	4602	CC/GC/GG	34/177/213	Intron 2	0.289	145.14/151.83/149.72	34.63/32.96/33.66	-0.374	0.882
rs7203984	rs7203984	5288	AA/CA/CC	272/132/22	Intron 2	0.206	150.26/150.86/137.01	34.57/29.55/38.23	-2.829	0.296
rs11508026	rs11508026	5358	CC/CT/TT	134/187/109	Intron 2	0.472	144.91/150.49/153.64	32.62/31.84/36.72	4.428	0.036
rs17231569	rs17231569	5810	DD/WD/WW	21/123/287	Intron 2	0.190	135.67/151.75/149.59	38.5/29.89/34.32	-2.143	0.435
rs708273	rs708273	5979	AA/AG/GG	31/166/236	Intron 2	0.263	134.15/150.73/150.68	27.59/33.37/33.85	-4.452	0.078
rs820299	rs820299	6314	AA/AG/GG	182/183/63	Intron 2	0.357	150.31/151.37/143.38	34.42/32.9/32.42	-2.382	0.293
rs12720922	rs12720922	6914	AA/AG/GG	22/121/289	Intron 2	0.192	136.59/152.12/149.75	37.84/29.99/34.27	-1.996	0.463
rs12708969	Novel	7616	GG/TG/TT	134/225/76	Intron 2	0.439	144.9/151.24/153.12	32.62/32.04/37.74	4.445	0.054
rs60545348	rs60545348	8017	AA/CA/CC	234/167/32	Intron 2	0.269	150.53/150.43/138.57	33.69/34.62/22.91	-3.346	0.184
rs9924087	Novel	8274	AA/GA/GG	4/74/356	Intron 2	0.090	137.37/153.27/148.98	13.94/36.93/32.76	2.336	0.540
rs12597002	rs12597002	8436	AA/AC/CC	31/166/236	Intron 2	0.267	138.81/150.6/150.42	24.06/33.33/33.46	-3.062	0.216
rs9926440	rs9926440	8695	CC/CG/GG	42/182/209	Intron 2	0.302	143.4/151.94/148.64	34.09/33.43/33.1	-0.391	0.871
rs9939224	rs9939224	8764	GG/GT/TT	276/135/22	Intron 2	0.205	149.44/151.57/138.05	33.94/30.96/39.01	-1.537	0.568
rs11076174	rs11076174	9178	CC/TC/TT	4/61/369	Intron 2	0.075	149.26/147.18/149.93	25.42/36.39/32.93	-2.216	0.583
rs891142	rs891142	10009	CC/CT	429/2	Intron 5	0.002	149.86/140.69	33.48/4.88/0	-9.181	0.694
CTP10459	rs139040281	10459	AA/CA	433/1	Intron 5	0.002	149.7/107.98	33.353/NA	-41.732	0.204
rs7205804	rs7205804	10921	AA/AG/GG	84/217/130	Intron 5	0.453	151.51/152.27/144.64	36.59/32.41/32.59	3.903	0.086
rs12708972	rs12708972	10924	CC/TC	427/7	Intron 5	0.009	149.46/156.5	33.48/25.25/0	7.104	0.572
rs34523084	rs34523084	11194	CC/TC	425/5	Intron 6	0.007	149.57/130.71	33.1/51.9/0	-18.997	0.199
rs1532624	rs1532624	11510	AA/CA/CC	84/219/131	Intron 7	0.452	151.29/152.1/144.43	36.66/32.38/32.51	3.911	0.084
rs12708974	rs12708974	11581	CC/TC/TT	342/83/9	Intron 7	0.108	149.1/150.74/160.19	33.75/32.35/29.18	2.945	0.381
rs117040820	rs117040820	11793	CC/CT	419/12	Intron 7	0.016	149.89/141.57	33.26/39.95/0	-8.351	0.387
rs12720873	rs12720873	12103	AA/AG/GG	1/33/400	Intron 8	0.039	137.7/153.37/149.28	NA/34.94/33.30	3.011	0.594
*CTP12123	Novel	12123	NA	NA	Intron 8	NA	NA	NA	NA	NA
rs148654654	rs148654654	12178	CC/TC	425/6	Intron 8	0.007	149.46/154.99	33.46/36.99/0	5.527	0.683
rs289712	rs289712	12336	CC/CT/TT	233/165/31	Intron 8	0.265	150.85/148.64/141.52	33.83/33.33/28.73	-3.561	0.159
rs11076175	rs11076175	12409	AA/AG/GG	292/119/21	Intron 8	0.184	149.93/151.55/135.65	34.52/29.16/38.5	-2.567	0.351
rs7499892	rs7499892	12621	CC/CT/TT	292/118/21	Intron 8	0.185	149.75/151.69/135.62	34.5/29.17/38.5	-2.382	0.387
rs187766748	rs187766748	12746	AA/AG	426/6	Intron 8	0.006	149.58/141.38	33.36/29.05/0	-8.313	0.540
rs187468344	rs187468344	13071	CC/TC	422/6	Intron 8	0.006	149.59/156.72	33.5/32.86/0	7.132	0.599
rs9930761	rs9930761	13223	CC/CT/TT	2/66/367	Intron 8	0.081	145.29/154.62/148.74	16.26/35.28/33.03	5.024	0.226
rs28381707	rs28381707	13327	GG/GT	428/5	Exon 9	0.005	149.38/164.51	33.44/28.07/0	15.246	0.304
rs5883	rs5883	13384	CC/CT/TT	373/58/2	Exon 9	0.070	148.92/154.19/145.33	32.97/36.59/16.26	4.404	0.314
rs289714	rs289714	13482	CC/CT/TT	14/128/293	Intron 9	0.181	137.32/147.13/151.29	33.38/29.93/34.6	-5.190	0.073
rs11644475	rs11644475	13683	AA/GA/GG	402/32/1	Intron 9	0.038	149.27/154.32/137.72	33.26/35.16/NA	3.856	0.500
rs158478	rs158478	13765	AA/CA/CC	110/199/113	Intron 9	0.495	144.69/151.17/150.86	36.18/30.96/34.94	-3.097	0.163
CTP13868	Novel	13868	GA/GG	1/434	Intron 9	0.002	138/149.64	NA/33.37	-11.653	0.723
rs158479	rs158479	14079	AA/GA/GG	113/213/107	Intron 9	0.498	148.33/152.43/144.95	32.06/32.87/35.4	-1.631	0.464
CTP14123	rs181381869	14123	CC/CT	423/12	Intron 9	0.011	149.62/149.53	33.53/26.59/0	-0.086	0.993
*CTP15277	Novel	15277	NA	NA	Intron 9	NA	NA	NA	NA	NA
rs289717	rs289717	15419	CC/CT/TT	201/184/50	Intron 10	0.320	150.39/149.54/146.8	34.72/32/33.03	-1.496	0.521
CTP15688delC	rs35874588	15688	DD/WD/WW	224/170/38	Intron 10	0.300	147.65/152.41/150.3	34.08/30.87/39.36	2.720	0.264
rs289718	rs289718	15963	CC/CT/TT	39/171/225	Intron 10	0.304	149.59/152.55/147.4	38.94/30.8/34.12	2.716	0.262
rs289719	rs289719	15972	AA/GA/GG	37/170/225	Intron 10	0.300	148.86/152.37/147.38	39.54/30.85/34.12	2.493	0.309
rs2033254	rs2033254	16016	CC/TC/TT	70/194/170	Intron 10	0.374	147.66/150.41/149.75	37.51/31.68/33.48	-0.697	0.755

Table B1.13. Continued

CETP Variant	RefSNP ID	Position in Ref (NM_000078)	Genotypes (GTs)	GT Count	Locations	MAF	Adjusted Mean of plasma APOA1	Standard Deviation	Beta	*P*
rs183439140	rs183439140	16059	CC/CT	432/2	Intron 10	0.005	149.63/143.93	33.35/54.24/0	-5.745	0.806
rs72771489	rs72771489	16148	GA/GG	9/425	Intron 10	0.009	138.89/149.83	38.41/33.25/0	-10.997	0.321
rs56208677	rs56208677	16263	CC/TC/TT	370/60/4	Intron 10	0.077	149.63/148.49/163.97	33.28/34.83/14.52	0.735	0.857
rs71387147	rs71387147	16413	GG/GT/TT	3/60/369	Intron 10	0.081	154.86/145.28/150.26	47.95/34.31/33.23	-3.691	0.378
CTP16508	Novel	16508	CG/GG	2/432	Intron 10	0.003	120.08/149.71	4.24/33.36/0	-29.686	0.202
rs117427818	rs117427818	16517	AA/GA/GG	4/36/393	Intron 10	0.054	110.52/153.83/149.78	30.15/29.75/33.48	-3.520	0.459
rs142980129	rs142980129	16550	GG/GT	433/2	Intron 10	0.005	149.64/143.98	33.31/54.24/0	-5.709	0.807
CTP16598	Novel	16598	CC/CT	429/2	Intron 10	0.002	149.82/130.35	33.47/12.09/0	-19.566	0.403
rs4784744	rs4784744	17216	AA/GA/GG	50/184/200	Intron 10	0.321	146.78/149.71/150.39	33.03/31.93/34.8	-1.444	0.536
rs12720898	rs12720898	17274	CC/CT/TT	393/38/3	Intron 10	0.056	148.83/156.78/150.86	32.99/36.69/29.2	6.271	0.199
rs291044	rs291044	17483	AA/AG/GG	50/184/201	Intron 10	0.320	146.8/149.54/150.39	33.03/32/34.72	-1.496	0.521
rs28381709	rs28381709	18256	CA/CC	1/431	Intron 11	0.002	217.98/149.52	NA/33.32	68.932	0.036
rs12708980	rs12708980	18413	GG/GT/TT	75/193/159	Intron 11	0.394	146.4/151.56/149.91	36.64/31.22/33.94	-1.168	0.599
rs12720889	rs12720889	18597	AA/AT/TT	232/165/36	Intron 11	0.290	146.99/152.48/153.06	33.83/30.93/40.19	4.078	0.097
*CTP18663	Novel	18663	NA	NA	Intron 11	NA	NA	NA	NA	NA
CTP18717	rs143024882	18717	CA/CC	2/426	Intron 11	0.002	123.5/149.44	17.39/33.3/0	-26.013	0.264
rs12447620	rs12447620	20354	AA/GA/GG	7/79/329	Intron 11	0.128	126.7/150.86/149.33	23.29/35.43/33.07	-2.180	0.539
rs12708983	rs12708983	20446	CC/TC/TT	1/22/411	Intron 11	0.038	86.53/156.94/149.33	NA/39.69/32.88	1.468	0.824
CTP20593	Novel	20593	GA/GG	1/434	Intron 11	0.001	203.34/149.49	NA/33.26	54.106	0.100
CTP20804	Novel	20804	CC/CT	430/5	Intron 11	0.005	149.82/132.56	33.46/16.03/0	-17.385	0.240
rs4784745	rs4784745	20910	AA/AG/GG	203/187/44	Intron 11	0.313	150.06/149.91/146.8	35.38/30.88/34.54	-1.099	0.646
rs5880	rs5880	21126	CC/CG/GG	4/38/393	Exon 12	0.057	110.58/152.03/149.78	30.15/29.91/33.55	-4.504	0.336
rs1800774	rs1800774	21580	CC/TC/TT	162/191/75	Intron 12	0.388	150.14/151.05/146.35	34.04/30.55/39.13	-1.412	0.528
rs5882	rs5882	22127	AA/GA/GG	210/178/44	Exon 14	0.317	147.92/152.02/148.67	34.25/30.9/39.1	1.731	0.470
CTP22327	rs111379440	22327	CC/CT	429/2	Intron 14	0.002	149.76/143.92	33.51/0.49/0	-5.924	0.801
rs12720882	rs12720882	22349	AA/GA	426/8	Intron 14	0.009	149.67/144.26	33.52/22.92/0	-5.482	0.642
CTP22888delA	Novel	22888	WD/WW	1/433	Intron 14	0.001	126.64/149.66	NA/33.39	-23.029	0.484
rs12720887	rs12720887	22997	CC/CT	418/13	Intron 14	0.013	149.61/153.42	33.49/32.74/0	3.809	0.681
rs9923854	rs9923854	23037	GG/GT/TT	4/94/333	Intron 14	0.114	145/153.6/148.57	16.84/31.74/34.02	3.935	0.269
rs1800777	rs1800777	23353	AA/AG/GG	2/21/411	Exon 15	0.035	134.43/141.27/150.1	23.76/28.7/33.62	-8.564	0.171
rs1801706	rs1801706	23696	AA/GA/GG	13/120/295	UTR	0.171	148.73/154.06/147.6	29.04/32.87/33.79	4.425	0.139
rs289742	rs289742	23796	CC/GC/GG	341/85/6	3' flanking	0.127	149.47/152.34/123.94	32.93/35.28/22.46	-0.951	0.787
rs289743	rs289743	23830	AA/GA/GG	224/167/39	3' flanking	0.300	147.51/152.08/151.5	34.38/30.48/39.5	3.025	0.215
rs289744	rs289744	24136	AA/CA/CC	225/166/40	3' flanking	0.300	147.37/152.06/151.28	34.36/30.5/39.07	3.022	0.212
rs12720917	rs12720917	25425	CC/TC/TT	9/132/290	3' flanking	0.172	149.69/151.05/148.74	21.75/34.18/33.46	1.847	0.546
rs289745	rs289745	25565	AA/CA/CC	150/210/74	3' flanking	0.409	153.3/149.22/143.68	35.52/31.4/33.4	-4.717	0.037

*CTP3412; *CTP12123; *CTP15277; *CTP18663 were excluded due to missing values.

TABLE B1.14. Association results of APOB levels with 100 *CETP* SNPs in NHWs (n=623)

CETP Variant	RefSNP ID	Position in Ref (NM_000078)	Genotypes (GTs)	GT Count	Locations	MAF	Adjusted Mean of plasma APOB	Standard Deviation	Beta	*P*
rs9989419	rs9989419	-8834	AA/GA/GG	72/200/157	5' flanking	0.400	85.69/89.83/86.66	23.15/23.78/24.43	0.065	0.884
rs247617	rs247617	-3257	AA/CA/CC	54/182/195	5' flanking	0.347	85.66/88.31/88.09	28.05/23.64/23.19	-0.268	0.560
rs183130	rs183130	-2610	CC/TC/TT	195/180/54	5' flanking	0.347	87.91/88.63/85.69	22.88/23.73/28.05	-0.212	0.643
rs6499863	rs6499863	-1956	AA/GA/GG	12/127/294	5' flanking	0.172	90.37/90.4/86.75	23.75/23.74/24.07	0.873	0.143
rs12149545	rs12149545	-812	AA/GA/GG	43/191/200	5' flanking	0.330	86.91/88.21/87.86	30.68/23.2/23.11	-0.111	0.817
rs12708967	rs12708967	-762	CC/CT/TT	16/148/269	5' flanking	0.205	80.58/87.72/88.54	20.88/23.54/24.34	-0.538	0.334
rs3764261	rs3764261	-648	GG/GT/TT	195/190/40	5' flanking	0.328	87.93/88.44/84.99	23.14/23.23/29.02	-0.248	0.609
rs17231506	rs17231506	557	CC/TC/TT	196/186/50	5' flanking	0.343	87.91/88.38/85.9	23.09/23.54/28.89	-0.204	0.662
rs12708968	rs12708968	848	CC/CT/TT	2/69/358	5' flanking	0.082	95.56/88.02/87.92	5.8/23.59/24.14	0.176	0.829
rs4783961	rs4783961	923	AA/AG/GG	127/208/98	5' flanking	0.457	85.84/88.45/89.49	25.55/23.23/23.44	0.558	0.202
rs17245715	rs17245715	1019	CC/CT/TT	361/70/2	5' flanking	0.082	87.81/87.73/95.5	24.08/23.51/5.8	0.130	0.873
rs4783962	rs4783962	1067	CC/TC/TT	277/138/16	5' flanking	0.194	87.79/88.3/87.19	24.11/23.92/20.32	0.091	0.871
rs1800775	rs1800775	1265	AA/CA/CC	112/218/104	5' flanking	0.489	88.94/87.19/88.34	25.37/24.26/21.73	-0.049	0.912
rs17231534	rs17231534	2133	CA/CC	41/393	Intron 1	0.045	87.28/87.98	25.38/23.81/0	-0.226	0.833
rs3816117	rs3816117	2187	CC/CT/TT	112/217/104	Intron 1	0.488	88.7/87.49/87.99	25.32/24.47/21.46	-0.060	0.894
rs711752	rs711752	2240	AA/AG/GG	83/213/135	Intron 1	0.443	88.28/88.33/87.02	25.49/24.77/21.88	0.155	0.731
rs5030708	rs5030708	2308	CC/CT	406/28	Intron 1	0.031	87.67/91.51	24.26/18.49/0	1.183	0.354
rs708272	rs708272	2317	AA/GA/GG	82/212/135	Intron 1	0.442	88.35/88.51/87	25.65/24.75/21.88	0.169	0.708
rs1864163	rs1864163	3262	AA/GA/GG	29/171/232	Intron 2	0.265	86.53/88.35/87.82	16.93/23.46/25.18	0.036	0.944
CTP3412	Novel	3412	NA	NA	Intron 2	NA	NA	NA	NA	NA
rs4369653	rs4369653	3581	AA/AG/GG	231/161/31	Intron 2	0.263	88.28/89.48/84.53	24.01/24.59/17.12	-0.090	0.857
rs7194225	rs7194225	3686	CC/CG/GG	3/74/356	Intron 2	0.089	119.61/86.5/88.05	25.18/25.99/23.34	0.219	0.777
CTP4559	Novel	4559	CC/CT	430/1	Intron 2	0.002	88.07/64.05	23.99/NA	-6.620	0.311
rs9929488	rs9929488	4602	CC/GC/GG	34/177/212	Intron 2	0.289	83.21/88.08/88.17	24.23/23.71/24.21	-0.408	0.415
rs7203984	rs7203984	5288	AA/CA/CC	271/132/22	Intron 2	0.206	88.15/87.65/84.64	24.83/23.07/16.17	-0.243	0.651
rs11508026	rs11508026	5358	CC/CT/TT	134/186/109	Intron 2	0.472	87.06/87.88/89.85	21.95/24.23/25.98	0.332	0.430
rs17231569	rs17231569	5810	DD/WD/WW	21/123/286	Intron 2	0.190	85.41/88.03/88.33	16.16/23.51/24.62	-0.187	0.733
rs708273	rs708273	5979	AA/AG/GG	31/165/236	Intron 2	0.263	85.31/88.86/87.68	17.49/24.54/24.35	0.021	0.966
rs820299	rs820299	6314	AA/AG/GG	182/182/63	Intron 2	0.357	88.08/87.89/87.06	23.42/24.87/22.72	-0.118	0.792
rs12720922	rs12720922	6914	AA/AG/GG	22/121/288	Intron 2	0.192	85.31/87.78/88.16	15.79/23.72/24.69	-0.197	0.717
rs12708969	Novel	7616	GG/TG/TT	134/224/76	Intron 2	0.439	87.05/87.78/89.87	21.95/24.64/25.37	0.321	0.485
rs60545348	rs60545348	8017	AA/CA/CC	234/166/32	Intron 2	0.269	87.7/89.05/85.42	24.43/24.28/17.71	0.049	0.921
rs9924087	Novel	8274	AA/GA/GG	4/74/355	Intron 2	0.090	96.49/86.87/88.14	50.29/25.26/23.32	-0.178	0.814
rs12597002	rs12597002	8436	AA/AC/CC	31/165/236	Intron 2	0.267	82.63/89.28/87.26	14.57/24.78/23.87	-0.039	0.937
rs9926440	rs9926440	8695	CC/CG/GG	42/182/208	Intron 2	0.302	85.46/88.89/87.19	25.59/23.63/23.74	0.009	0.984
rs9939224	rs9939224	8764	GG/GT/TT	275/135/22	Intron 2	0.205	87.93/87.79/88.77	24.54/22.77/22.66	0.070	0.896
rs11076174	rs11076174	9178	CC/TC/TT	4/61/368	Intron 2	0.075	98.94/93.89/86.71	44.09/21.01/24	1.950	0.015
rs891142	rs891142	10009	CC/CT	428/2	Intron 5	0.002	87.95/71.41	23.94/22.84/0	-4.510	0.330
CTP10459	rs139040281	10459	AA/CA	432/1	Intron 5	0.002	88.04/74.29	23.91/NA	-3.626	0.579
rs7205804	rs7205804	10921	AA/AG/GG	84/216/130	Intron 5	0.453	89.65/87.41/87.49	24.78/24.72/22.09	0.231	0.610
rs12708972	rs12708972	10924	CC/TC	426/7	Intron 5	0.009	87.77/95.96	23.99/22.01/0	2.324	0.352
rs34523084	rs34523084	11194	CC/TC	424/5	Intron 6	0.007	87.71/106.16	23.52/28.34/0	4.976	0.087
rs1532624	rs1532624	11510	AA/CA/CC	84/218/131	Intron 7	0.452	89.49/87.62/87.51	24.86/24.8/22.01	0.212	0.639
rs12708974	rs12708974	11581	CC/TC/TT	342/82/9	Intron 7	0.108	87.33/90.23/90.09	23.99/24.44/18.3	0.682	0.309
rs117040820	rs117040820	11793	CC/CT	418/12	Intron 7	0.016	88.38/78.95	24.11/12.17/0	-2.449	0.200
rs12720873	rs12720873	12103	AA/AG/GG	1/33/399	Intron 8	0.039	125.24/87.39/87.86	NA/2980/23.44	0.299	0.789
rs148654654	rs148654654	12178	CC/TC	424/6	Intron 8	0.007	87.92/86.51	23.89/20.77/0	-0.292	0.913
CTP12123	Novel	12123	NA	NA	Intron 8	NA	NA	NA	NA	NA
rs289712	rs289712	12336	CC/CT/TT	233/164/31	Intron 8	0.265	87.56/88.96/84.21	24.53/23.84/16.34	-0.012	0.980
rs11076175	rs11076175	12409	AA/AG/GG	291/119/21	Intron 8	0.184	88.12/87.93/85.3	24.52/23.52/16.16	-0.167	0.761
rs7499892	rs7499892	12621	CC/CT/TT	291/118/21	Intron 8	0.185	88.33/87.84/85.37	24.67/23.63/16.16	-0.218	0.692
rs187766748	rs187766748	12746	AA/AG	425/6	Intron 8	0.006	87.84/92.58	23.97/22.53/0	1.397	0.603
rs187468344	rs187468344	13071	CC/TC	421/6	Intron 8	0.006	88/95.46	24.09/19.21/0	2.175	0.420
rs9930761	rs9930761	13223	CC/CT/TT	2/66/366	Intron 8	0.081	132.79/87.49/87.75	12.59/24.72/23.68	0.609	0.461
rs28381707	rs28381707	13327	GG/GT	427/5	Exon 9	0.005	87.98/90.81	23.95/23.01/0	0.856	0.771
rs5883	rs5883	13384	CC/CT/TT	372/58/2	Exon 9	0.070	87.86/87.71/132.82	23.45/26.01/12.59	0.682	0.431
rs289714	rs289714	13482	CC/CT/TT	14/128/292	Intron 9	0.181	81.95/87.42/88.42	17.62/22.89/24.68	-0.436	0.450
rs11644475	rs11644475	13683	AA/GA/GG	401/32/1	Intron 9	0.038	87.88/87.2/125.25	23.38/30.27/NA	0.251	0.824
rs158478	rs158478	13765	AA/CA/CC	110/199/112	Intron 9	0.495	84.86/89.14/88.45	23.18/23.89/23.83	-0.493	0.259
CTP13868	Novel	13868	GA/GG	1/433	Intron 9	0.002	91.05/87.91	NA/23.96	1.119	0.864
rs158479	rs158479	14079	AA/GA/GG	112/213/107	Intron 9	0.498	88.58/89.12/84.8	24.13/23.67/24.4	-0.523	0.239
CTP14123	rs181381869	14123	CC/CT	422/12	Intron 9	0.011	88.38/71.69	23.98/16.35/0	-4.562	0.017
CTP15277	Novel	15277	NA	NA	Intron 9	NA	NA	NA	NA	NA
rs289717	rs289717	15419	CC/CT/TT	201/184/49	Intron 10	0.320	87.34/88.84/86.8	23.64/24.74/22.44	0.087	0.852
CTP15688delC	rs35874588	15688	DD/WD/WW	223/170/38	Intron 10	0.300	88.47/87.63/85.77	23.35/24.57/25.17	-0.360	0.460
rs289718	rs289718	15963	CC/CT/TT	39/171/224	Intron 10	0.304	85.88/87.51/88.58	24.87/24.67/23.28	-0.387	0.423
rs289719	rs289719	15972	AA/GA/GG	37/170/224	Intron 10	0.300	85.33/87.56/88.58	25.32/24.52/23.28	-0.425	0.383
rs2033254	rs2033254	16016	CC/TC/TT	70/194/169	Intron 10	0.374	87.26/89.44/86.6	24.01/23.11/24.86	0.268	0.547
rs183439140	rs183439140	16059	CC/CT	431/2	Intron 10	0.005	88.06/76.15	23.89/33.8/0	-3.328	0.473
rs72771489	rs72771489	16148	GA/GG	9/424	Intron 10	0.009	96.8/87.82	32.95/23.67/0	2.323	0.290
rs56208677	rs56208677	16263	CC/TC/TT	369/60/4	Intron 10	0.077	88.2/87.19/82.99	23.85/24.72/18.54	-0.359	0.657
rs71387147	rs71387147	16413	GG/GT/TT	3/60/368	Intron 10	0.081	90.78/88.77/87.87	30.83/21.57/24.32	0.326	0.695
CTP16508	Novel	16508	CG/GG	2/431	Intron 10	0.003	96.2/87.87	2.69/24.01/0	2.528	0.586
rs117427818	rs117427818	16517	AA/GA/GG	4/36/392	Intron 10	0.054	83.16/87.27/88.06	19.45/22.68/24.18	-0.301	0.752

Table B1.14. Continued

***CETP* Variant**	**RefSNP ID**	**Position in Ref (NM_000078)**	**Genotypes (GTs)**	**GT Count**	**Locations**	**MAF**	**Adjusted Mean of plasma APOB**	**Standard Deviation**	**Beta**	***P***
rs142980129	rs142980129	16550	GG/GT	432/2	Intron 10	0.005	87.97/75.98	23.94/33.8/0	-3.352	0.470
CTP16598	Novel	16598	CC/CT	428/2	Intron 10	0.002	87.89/95.87	24.06/22.2/0	2.327	0.617
rs4784744	rs4784744	17216	AA/GA/GG	49/184/200	Intron 10	0.321	86.79/88.89/87.25	22.44/24.75/23.67	0.108	0.817
rs12720898	rs12720898	17274	CC/CT/TT	392/38/3	Intron 10	0.056	88.27/83.07/91.29	24.08/22.71/11.08	-0.934	0.335
rs291044	rs291044	17483	AA/AG/GG	49/184/201	Intron 10	0.320	86.8/88.84/87.34	22.44/24.74/23.64	0.087	0.852
rs28381709	rs28381709	18256	CA/CC	1/430	Intron 11	0.002	99.09/87.93	NA/24	3.299	0.615
rs12708980	rs12708980	18413	GG/GT/TT	75/193/158	Intron 11	0.394	86.78/88.7/87.25	23.56/23.13/25.3	0.055	0.902
rs12720889	rs12720889	18597	AA/AT/TT	231/165/36	Intron 11	0.290	88.26/87.33/88.62	23.3/24.41/26.89	-0.130	0.791
CTP18717	rs143024882	18717	CA/CC	2/425	Intron 11	0.002	94.8/87.54	30.62/23.72/0	2.028	0.659
CTP18663	Novel	18663	NA	NA	Intron 11	NA	NA	NA	NA	NA
rs12447620	rs12447620	20354	AA/GA/GG	7/79/328	Intron 11	0.128	75.93/82.25/88.93	26.27/25.45/23.67	-1.918	0.007
rs12708983	rs12708983	20446	CC/TC/TT	1/22/410	Intron 11	0.038	92.53/85.97/88	NA/34.20/23.37	-0.608	0.644
CTP20593	Novel	20593	GA/GG	1/433	Intron 11	0.001	70.42/87.96	NA/23.94	-4.799	0.464
CTP20804	Novel	20804	CC/CT	429/5	Intron 11	0.005	88.02/78.64	23.96/22.76/0	-2.591	0.377
rs4784745	rs4784745	20910	AA/AG/GG	203/187/43	Intron 11	0.313	87.51/88.64/86.99	23.51/24.85/22.48	0.067	0.888
rs5880	rs5880	21126	CC/CG/GG	4/38/392	Exon 12	0.057	83.15/85.49/88.2	19.45/23.02/24.11	-0.679	0.468
rs1800774	rs1800774	21580	CC/TC/TT	161/191/75	Intron 12	0.388	86.64/88.64/88.36	25.16/23.08/23.78	0.332	0.454
rs5882	rs5882	22127	AA/GA/GG	209/178/44	Exon 14	0.317	89.16/87.12/85.37	22.92/24.69/25.07	-0.594	0.213
CTP22327	rs111379440	22327	CC/CT	428/2	Intron 14	0.002	87.98/75.18	24.06/18.81/0	-3.413	0.463
rs12720882	rs12720882	22349	AA/GA	425/8	Intron 14	0.009	87.79/94.07	23.96/25.54/0	1.754	0.454
CTP22888delA	Novel	22888	WD/WW	1/432	Intron 14	0.001	100.98/87.98	NA/23.91	3.781	0.562
rs12720887	rs12720887	22997	CC/CT	417/13	Intron 14	0.013	87.58/99.02	24.09/20.04/0	3.213	0.081
rs9923854	rs9923854	23037	GG/GT/TT	4/94/332	Intron 14	0.114	111.87/90.46/86.94	44.34/22.09/24.01	1.368	0.053
rs1800777	rs1800777	23353	AA/AG/GG	2/21/410	Exon 15	0.035	93.66/79.33/88.23	10.11/18.04/24.12	-1.471	0.238
rs1801706	rs1801706	23696	AA/GA/GG	13/120/294	Exon 16-UTR	0.171	94.73/88.4/87.36	28.02/23.01/24.07	0.552	0.352
rs289742	rs289742	23796	CC/GC/GG	340/85/6	3' flanking	0.127	89.49/82.7/73.97	23.3/24.98/28.16	-2.023	0.004
rs289743	rs289743	23830	AA/GA/GG	223/167/39	3' flanking	0.300	88.88/86.43/87.91	23.26/24.6/26	-0.397	0.414
rs289744	rs289744	24136	AA/CA/CC	224/166/40	3' flanking	0.300	88.88/86.7/87.68	23.21/24.58/25.74	-0.381	0.429
rs12720917	rs12720917	25425	CC/TC/TT	9/132/289	3' flanking	0.172	91.11/88.2/87.83	27.76/26.74/22.63	0.087	0.886
rs289745	rs289745	25565	AA/CA/CC	149/210/74	3' flanking	0.409	87.78/86.83/91.13	24.66/23.78/23.03	0.356	0.433

*CTP3412; *CTP12123; *CTP15277; *CTP18663 were excluded due to missing values.

TABLE B1.15. Association results of HDL-C levels with 104 *CETP* SNPs in African blacks (n=788)

RefSNP ID	Position in Ref. (NM_000078)	Location	Genotype (GT)	GT Counts	MAF	Adjusted mean of plasma HDL-C	Standart Deviation	Beta	*P*
rs247615	-9210	5' flanking	AA/AG/GG	431/260/39	0.230	47.32/48.71/47.98	12.13/13.57/12.67	0.25	0.277
rs9989419	-8834	5' flanking	AA/GA/GG	316/329/82	0.340	48.55/47.38/48.49	12.44/13.18/10.9	-0.11	0.573
rs183130	-2610	5' flanking	CC/CT/TT	420/268/45	0.244	46.03/50.09/52.19	11.66/13.73/12.71	1.03	2.25E-06
rs3764261	-648	5' flanking-Promoter	AA/CA/CC	81/305/336	0.323	50.08/49.17/46.39	13.06/13.48/11.71	0.62	0.002
rs148562851	187	5' flanking	AA/AG/GG	709/29/1	0.020	47.55/54.08/70.56	12.57/14.4/NA	2.08	0.001
rs12447924	220	5' flanking	CC/CT/TT	42/228/428	0.224	46.81/47.35/48.37	13.06/12.14/13.22	-0.26	0.269
rs17231506	557	5' flanking	CC/TC/TT	595/136/8	0.105	47.64/48.65/49.87	12.78/12.46/14.1	0.31	0.320
rs12708968	848	5' flanking	CC/TC/TT	1/90/639	0.063	57.66/45.83/48.1	NA/11.72/12.81	-0.57	0.159
rs4783961	923	5' flanking	AA/GA/GG	156/339/222	0.454	50.6/47.8/45.89	14.22/13.32/10.56	0.64	0.001
rs146122874	950	5' flanking	CC/TC/TT	703/30/2	0.022	47.52/55.23/52.67	12.6/13.45/27.65	1.92	0.002
rs4783962	1067	5' flanking	CC/CT/TT	593/125/8	0.097	47.92/47.43/48.19	12.82/12.39/18.08	-0.11	0.732
rs17237883	1153	5' flanking	AA/GA/GG	1/42/688	0.031	58.43/49.41/47.79	NA/14.02/12.65	0.56	0.313
rs114856405	1189	5' flanking	AA/CA/CC	3/46/687	0.036	43.75/47.84/47.89	1.99/12.82/12.74	-0.13	0.797
rs1800775	1265	5' flanking	AA/CA/CC	270/343/118	0.395	49.36/47.58/45.62	12.93/13.22/10.45	-0.53	0.006
rs17231520	1856	5' flanking	AA/GA/GG	6/121/611	0.090	58.82/53.53/46.54	8.03/14.95/11.99	1.99	1.86E-09
rs34065661	1964	Exon 1	CC/GC/GG	4/124/618	0.088	60.7/53.62/46.48	9.61/14.75/11.94	2.07	7.88E-10
rs5884	1986	Exon 1	AA/CA/CC	2/92/644	0.065	46.86/45.7/48.12	17.75/11.78/12.86	-0.66	0.092
rs34680782	2089	Intron 1	AA/CA/CC	2/25/705	0.020	40.57/50.96/47.75	1.91/12.57/12.75	0.47	0.470
rs17231534	2133	Intron 1	AA/CA/CC	26/209/501	0.177	49.14/47.92/47.66	15.69/13.23/12.39	0.10	0.695
rs3816117	2187	Intron 1	CC/CT/TT	269/332/117	0.394	49.31/47.46/45.54	12.89/13.32/10.47	-0.54	0.006
rs711752	2240	Intron 1	AA/GA/GG	45/250/436	0.232	51.82/49.87/46.29	12.62/14/11.82	0.91	3.70E-05
rs708272	2317	Intron 1	AA/GA/GG	47/253/433	0.236	51.27/49.82/46.22	12.56/13.96/11.85	0.88	6.33E-05
rs60195610	2692	Intron 1	CC/CT/TT	715/34/1	0.023	47.56/52.67/70.57	12.57/14.16/NA	1.67	0.006
rs9935228	3101	Intron 2	AA/GA/GG	609/115/9	0.091	48.21/45.73/47.6	13/11.63/8.15	-0.54	0.098
rs1864163	3262	Intron 2	AA/GA/GG	60/278/379	0.278	43.32/47.31/49.11	10.27/12.52/13.26	-0.70	0.001
rs75313088	3347	Intron 2	AA/GA/GG	3/45/688	0.036	43.08/47.78/47.88	2.95/12.96/12.74	-0.17	0.741
rs5817083	3381	Intron 2	DD/WD/WW	104/361/264	0.393	49.92/47.05/47.94	13.16/12.24/13.06	0.16	0.429
rs4369653	3581	Intron 2	AA/AG/GG	454/260/27	0.212	48.2/47.22/47.18	13.04/11.92/14.47	-0.23	0.340
rs7194225	3686	Intron 2	CC/CG/GG	28/211/484	0.185	53.45/47.78/47.61	14.43/12.79/12.4	0.36	0.133
rs114908369	4299	Intron 2	CA/CC	38/703	0.025	46.13/47.94	12.09/12.76	-0.52	0.394
rs9929488	4602	Intron 2	CC/GC/GG	161/349/214	0.463	46.02/48.67/48.02	12.39/12.64/13.1	-0.26	0.172
rs12720906	4791	Intron 2	GG/GT/TT	3/42/681	0.034	43.1/47.12/47.96	2.04/12.87/12.74	-0.35	0.493
rs12720926	4948	Intron 2	AA/AG	706/40	0.027	47.73/46.48	12.62/14.46	-0.43	0.472
rs17237939	4957	Intron 2	CC/CT/TT	667/64/3	0.049	47.97/46.48/45.82	12.88/11.88/10.93	-0.39	0.375
rs35585922	5215	Intron 2	DD/WD/WW	20/169/520	0.149	47.85/48.8/47.35	16.58/13.33/12.49	0.27	0.323
rs7203984	5288	Intron 2	AA/CA/CC	137/354/228	0.438	47.9/47.42/48.17	14.54/11.94/12.92	-0.08	0.669
rs11508026	5358	Intron 2	AA/AG	706/40	0.027	47.89/46.07	12.64/14.16	-0.60	0.318
rs80296794	5375	Intron 2	TC/TT	31/713	0.021	45.56/47.88	11.93/12.74	-0.68	0.315
rs112236143	5593	Intron 2	CA/CC	28/687	0.020	44.8/48.04	11.23/12.81	-0.95	0.181
rs708273	5979	Intron 2	AA/AG/GG	8/130/594	0.100	42.93/47.19/48.02	16.66/12.39/12.8	-0.36	0.257
rs17231583	5990	Intron 2	CC/GC/GG	2/23/705	0.020	43.26/46.32/47.87	2.12/12.03/12.74	-0.49	0.464
rs142058276	6022	Intron 2	II/WI/WW	3/114/610	0.082	55.78/52.66/46.88	3.69/13.52/12.29	1.66	2.06E-06
rs17231590	6221	Intron 2	AA/AG/GG	664/78/4	0.058	47.9/46.5/46.9	12.86/11.46/9	-0.33	0.410
rs17237953	6239	Intron 2	GG/GT/TT	669/51/3	0.039	47.6/48.28/54.63	12.95/10.87/13.75	0.41	0.395
rs35619327	6251	Intron 2	CC/TC	694/34	0.023	48.04/45.6	12.79/11.54	-0.71	0.272
rs820299	6314	Intron 2	AA/AG/GG	185/371/175	0.495	48.13/47.26/49.31	12.83/11.98/13.62	0.16	0.415
rs17237967	6427	Intron 2	AA/GA/GG	4/42/658	0.035	48.99/46.16/48	9.06/13.7/12.84	-0.36	0.480
rs8045855	6725	Intron 2	AA/AT/TT	240/342/134	0.423	46.67/48.18/48.09	12.91/12.37/13.32	0.25	0.201
rs12720922	6914	Intron 2	AA/GA/GG	91/335/303	0.352	47.08/48.84/47.42	13.12/12.4/12.8	0.09	0.643
rs12708969	7616	Intron 2	AA/CA/CC	13/125/561	0.106	43.83/46.57/48.21	14.42/11.43/12.79	-0.54	0.076

Table B1.15. Continued

RefSNP ID	Position in Ref. (NM_000078)	Location	Genotype (GT)	GT Counts	MAF	Adjusted mean of plasma HDL-C	Standart Deviation	Beta	*P*
rs9924087	8274	Intron 2	AA/GA/GG	45/204/472	0.207	51.04/49.13/47.21	13.63/12.41/12.59	0.57	0.011
rs12597002	8436	Intron 2	AA/CA/CC	5/131/597	0.097	49.66/46.77/48.23	15.57/12.51/12.65	-0.34	0.301
rs12720863	8742	Intron 2	AA/GA/GG	704/32/1	0.023	47.89/46.39/58.4	12.72/13.37/NA	-0.25	0.694
rs9939224	8764	Intron 2	GG/GT/TT	299/337/92	0.356	47.38/48.48/47.04	12.92/12.5/13.23	0.07	0.745
rs11076174	9178	Intron 2	CC/TC/TT	10/177/545	0.132	38.2/46.71/48.47	7/11.7/13.02	-0.71	0.013
rs13306230	9282	Intron 2	CA/CC	2/734	0.001	59.64/47.81	34.22/12.66	3.07	0.237
rs12708971	9493	Intron 3	CC/CT/TT	2/21/705	0.019	42.67/46.84/47.93	0.64/12.4/12.81	-0.43	0.534
rs891141	9755	Intron 4	AA/AC/CC	568/163/17	0.130	46.92/50.3/49.85	12.27/13.72/14.38	0.79	0.004
CTPp9841	9841	Intron 4	AG/GG	1/737	0.001	18.22/47.85	NA/12.7	-9.93	0.007
rs34716057	9878	Exon 5	AA/GA/GG	2/46/696	0.034	42.7/49.15/47.65	0.42/12.32/12.76	0.29	0.579
rs891143	10012	Intron 5	CC/TC/TT	599/122/5	0.090	47.01/51.79/52.52	12.27/14.47/7.67	1.29	1.13E-04
rs12720862	10779	Intron 5	AA/GA/GG	580/147/10	0.112	47.52/49/47.19	12.43/13.65/15.72	0.29	0.333
rs7205804	10921	Intron 5	AA/GA/GG	11/123/605	0.097	46.25/45.23/48.37	14.04/11.87/12.87	-0.76	0.015
rs12708973	10934	Intron 5	AA/AG	741/14	0.009	47.82/44.58	12.66/14.16	-1.03	0.298
rs148134355	10943	Intron 5	GA/GG	6/721	0.005	43.51/47.85	16.31/12.73	-1.42	0.350
rs34611098	10983	Exon 6	AG/GG	2/737	0.001	68.44/47.76	21.57/12.65	5.70	0.028
rs12720925	11456	Intron 7	CC/TC/TT	1/57/675	0.042	37.47/48.89/47.74	NA/12.13/12.82	0.24	0.625
rs1532624	11510	Intron 7	AA/CA/CC	10/126/601	0.097	46.55/45.26/48.45	14.32/11.26/12.93	-0.77	0.014
rs12720871	11795	Intron 7	CC/CG/GG	637/83/5	0.066	47.81/48.75/46.6	12.9/12.01/8.03	0.22	0.572
rs12720872	11913	Intron 7	CC/TC/TT	545/175/12	0.135	47.63/48.7/45.99	12.32/13.69/16.72	0.13	0.636
rs11076175	12409	Intron 8	AA/AG/GG	421/261/48	0.243	48.48/47.81/42.84	13.24/12.07/10.87	-0.51	0.020
rs7499892	12621	Intron 8	CC/CT/TT	284/332/104	0.377	48.65/48.02/45.63	14.03/11.95/11.49	-0.35	0.077
rs289713	12860	Intron 8	AA/AT/TT	149/336/221	0.451	47.81/47.63/47.94	12.69/12.59/13.31	-0.02	0.921
rs191754368	12913	Intron 8	CC/TC/TT	716/24/2	0.019	47.76/50.34/40.57	12.73/12.78/1.91	0.31	0.640
rs9930761	13223	Intron 8	CC/CT/TT	14/182/518	0.148	56.32/49.02/47.22	16.54/13.48/12.37	0.72	0.010
rs35878799	13279	Exon 9	CT/TT	17/715	0.011	48.21/47.83	12.76/12.77	0.13	0.890
rs5883	13384	Exon 9	CC/TC/TT	522/201/13	0.155	47.25/48.69/57.2	12.36/13.36/15.11	0.65	0.017
rs11076176	13477	Intron 9	GG/GT/TT	120/349/258	0.403	45.21/48/48.66	12.07/12.14/13.74	-0.43	0.027
rs289714	13482	Intron 9	AA/GA/GG	145/355/222	0.447	48.35/48.37/46.79	13.71/12.6/12.35	0.24	0.213
rs158479	14079	Intron 9	AA/GA/GG	74/320/330	0.325	49.71/47.5/47.73	13.57/12.38/12.64	0.16	0.432
rs12720892	14192	Intron 9	AA/GA/GG	3/58/693	0.043	38.41/48.84/47.71	8.75/12.99/12.68	0.03	0.945
rs158480	14258	Intron 9	AA/GA/GG	145/330/223	0.445	47.7/48.05/47.03	13.28/12.1/12.94	0.12	0.538
CTPp14448del4	14448	Intron 9	WD/WW	27/714	0.018	47.79/47.83	11.6/12.78	0.02	0.978
rs289715	14539	Intron 9	AA/TA/TT	36/251/437	0.224	47.03/49.06/47.21	15.23/11.89/13.02	0.30	0.200
rs2303789	15226	Intron 10	GG/GT/TT	4/86/646	0.065	43.39/49.13/47.66	11.54/12.11/12.83	0.28	0.468
rs289716	15407	Intron 10	AA/AT/TT	167/354/200	0.476	45.81/48.44/48.51	11.83/12.56/13.73	-0.36	0.059
rs289717	15419	Intron 10	AA/GA/GG	12/188/532	0.147	46.9/47.21/48.08	10.74/12.06/12.99	-0.21	0.442
rs12708976	15542	Intron 10	CC/TC/TT	672/64/2	0.047	47.77/48.81/48.19	12.78/11.66/10.68	0.32	0.484
rs12720942	15639	Intron 10	AA/GA/GG	647/88/4	0.066	47.68/49.14/43.48	12.82/12.11/11.54	0.28	0.461
rs736274	15800	Intron 10	AA/AT/TT	728/23/1	0.016	47.88/44.32/30.02	12.68/12.28/NA	-1.36	0.059
rs12720937	15913	Intron 10	CC/GC/GG	635/86/4	0.066	47.71/49.02/43.37	12.9/12.21/11.54	0.24	0.535
rs289718	15963	Intron 10	CC/CT/TT	235/337/148	0.438	48.48/48.6/45.29	13.69/12.44/11.95	-0.40	0.035
rs289719	15972	Intron 10	AA/GA/GG	178/371/189	0.493	48.31/48.75/45.54	13.59/12.54/12.13	0.41	0.033
rs2033254	16016	Intron 10	CC/TC/TT	83/297/345	0.317	46.19/47.73/48.49	12.91/12.18/13.22	-0.29	0.145
rs112205272	16146	Intron 10	AA/GA/GG	4/82/647	0.063	43.44/48.58/47.74	11.54/12.36/12.77	0.11	0.773
rs112409939	16363	Intron 10	AA/GA/GG	647/84/4	0.064	47.67/49.02/43.45	12.74/12.04/11.54	0.25	0.521
rs71387147	16413	Intron 10	GT/TT	34/645	0.025	46.77/48.21	12.98/12.92	-0.43	0.514
rs1968905	16979	Intron 10	GG/GT/TT	293/356/86	0.360	46.43/48.32/51.07	12.07/12.88/13.97	0.63	0.002
rs12720903	17154	Intron 10	AA/GA/GG	5/93/649	0.068	48.03/48.39/47.71	12.26/13.64/12.56	0.15	0.680
rs4784744	17216	Intron 10	AA/GA/GG	7/131/593	0.100	46.56/47.15/48.03	13.54/11.55/13	-0.23	0.483
rs291044	17483	Intron 10	AA/GA/GG	7/133/589	0.102	46.52/47.15/48.01	13.54/11.33/13.01	-0.22	0.495
rs114486472	17575	Intron 10	AA/AG/GG	1/25/702	0.020	42.35/45.42/47.98	NA/12.28/12.77	-0.77	0.270
rs34426213	17918	Intron 10	CC/CT/TT	663/55/3	0.042	47.78/48.79/42.87	12.79/13.13/6.76	0.13	0.784

Table B1.15. Continued

RefSNP ID	Position in Ref. (NM_000078)	Location	Genotype (GT)	GT Counts	MAF	Adjusted mean of plasma HDL-C	Standart Deviation	Beta	*P*
rs891144	17970	Intron 10	AA/GA/GG	38/240/465	0.215	46.47/47.94/47.74	13.49/12.52/12.82	-0.06	0.806
rs12708979	18388	Intron 11	AA/GA/GG	2/42/707	0.030	40.57/47.9/47.8	1.91/12.59/12.71	-0.14	0.797
rs12708980	18413	Intron 11	AA/AC/CC	312/286/97	0.342	49.07/47.08/45.78	13.09/12.71/12.52	-0.51	0.011
rs12720889	18597	Intron 11	AA/AT/TT	469/235/32	0.204	47.36/47.99/52.46	12.53/12.79/15.09	0.41	0.086
rs291043	18733	Intron 11	AA/AG/GG	620/107/10	0.086	47.93/46.86/49.4	12.89/11.83/13.24	-0.15	0.657
rs114203109	18970	Intron 11	GA/GG	63/659	0.042	44.68/48.14	10.57/12.95	-0.99	0.041
rs145189439	19734	Intron 11	CC/TC/TT	3/68/667	0.052	38.22/49/47.63	8.75/12.1/12.76	0.15	0.732
rs4784745	20910	Intron 11	AA/AG/GG	624/98/6	0.076	47.87/47.14/45.73	12.86/12/14.84	-0.23	0.527
rs34855278	21111	Exon 12	GA/GG	23/725	0.015	44.36/47.84	12.28/12.73	-1.09	0.163
rs114948973	21454	Intron 12	AA/AG/GG	1/25/696	0.019	52.12/49.69/47.77	NA/13.54/12.8	0.59	0.397
rs7195984	21498	Intron 12	AA/GA/GG	494/186/27	0.169	47.11/49.02/53.69	12.48/13.73/13.35	0.72	0.005
rs7196174	21579	Intron 12	GG/GT/TT	631/96/4	0.070	47.82/47.32/50.49	12.61/13.8/10.66	-0.09	0.802
rs1800774	21580	Intron 12	CC/TC/TT	449/237/42	0.217	48.72/46.57/46.21	12.85/12.4/13.01	-0.51	0.025
rs5882	22127	Exon 14	AA/GA/GG	83/288/353	0.310	46.62/47.15/48.65	12.45/12.71/12.89	-0.35	0.083
rs5886	22162	Exon 14	AA/GA/GG	4/114/613	0.082	49.75/48.01/47.74	12/14.09/12.53	0.07	0.839
rs289740	22985	Intron 14	CC/CT/TT	11/147/569	0.117	56.15/49.63/47.27	17.27/12.22/12.73	0.87	0.003
rs36051594	23201	Intron 14	AA/GA/GG	4/59/689	0.044	44.73/46.89/47.85	8.07/12.05/12.79	-0.30	0.501
rs1801706	23696	3'UTR-Exon 16	AA/GA/GG	27/203/501	0.176	52.91/48.7/47.26	16.02/12.85/12.47	0.57	0.021
rs289742	23796	3' flanking	CC/CG/GG	132/336/254	0.421	47.68/47.99/47.62	12.68/12.28/13.54	0.04	0.830
rs289743	23830	3' flanking	AA/GA/GG	86/295/352	0.315	46.27/47.26/48.75	12.8/12.54/12.89	-0.39	0.048
rs289744	24136	3' flanking	GG/GT/TT	349/290/77	0.306	48.62/47.2/46.7	12.96/12.65/13.11	-0.33	0.105
rs12720875	24499	3' flanking	AA/GA/GG	2/44/702	0.032	40.62/48.14/47.76	1.91/12.5/12.71	-0.06	0.915
rs66495554	24669	3' flanking	CC/TC/TT	482/226/31	0.193	48.66/46.35/45.6	13.01/12.04/12.24	-0.58	0.015
rs114646974	24881	3' flanking	AA/AG	719/5	0.003	47.92/29.44	12.74/6.95	-5.85	3.93E-04
rs138161274	24899	3' flanking	CC/GC	695/36	0.027	47.78/50.08	12.73/13.13	0.69	0.270
rs12720874	25064	3' flanking	CC/TC/TT	22/173/511	0.153	46.65/47.23/47.77	12.39/12.44/12.97	-0.16	0.551
rs12720916	25218	3' flanking	AA/GA/GG	707/33/1	0.025	47.94/46.17/42.37	12.69/12.83/NA	-0.57	0.354
rs289745	25565	3' flanking	GG/GT/TT	36/213/478	0.194	47.14/49.15/47.38	14.55/12.46/12.72	0.26	0.272

TABLE B1.16. Association results of TG levels with 104 *CETP* SNPs in African blacks (n=788)

RefSNP ID	Position	Location	Genotype (GT)	GT Counts	MAF	Adjusted mean of plasma TG	Standart Deviation	Beta	*P*
rs247615	-9210	5' flanking	AA/AG/GG	436/260/40	0.230	70.52/70.65/66.23	31.36/30.09/25.93	0.00	0.863
rs9989419	-8834	5' flanking	AA/GA/GG	317/335/82	0.340	70.2/68.9/73.53	31.29/27.64/37.92	0.00	0.733
rs183130	-2610	5' flanking	CC/CT/TT	423/272/44	0.244	71.43/67.25/74.4	30.66/28.32/40.1	-0.01	0.194
rs3764261	-648	5'flanking-Promoter	AA/CA/CC	81/310/338	0.323	69.6/68.76/71.79	33.53/28.96/31.52	-0.01	0.233
rs148562851	187	5' flanking	AA/AG/GG	715/29/1	0.020	70.07/76.3/46.05	30.16/40.57/NA	0.01	0.750
rs12447924	220	5' flanking	CC/CT/TT	43/231/430	0.224	74.24/68.92/70.54	29.99/28.68/32.14	0.00	0.562
rs17231506	557	5' flanking	CC/TC/TT	600/137/8	0.105	71.23/65.53/83.44	30.93/26.92/56.91	-0.02	0.145
rs12708968	848	5' flanking	CC/TC/TT	2/91/643	0.063	58.07/67.83/70.41	9.9/26.42/31.21	-0.01	0.563
rs4783961	923	5' flanking	AA/GA/GG	156/339/228	0.454	72.69/69.37/70.56	35.06/29.23/29.92	0.00	0.924
rs146122874	950	5' flanking	CC/TC/TT	709/30/2	0.022	69.95/74.26/69.15	30.18/40.9/44.55	0.00	0.879
rs4783962	1067	5' flanking	CC/CT/TT	597/128/7	0.097	69.88/72.54/80.58	30.51/31.48/34.52	0.02	0.154
rs17237883	1153	5' flanking	AA/GA/GG	1/41/695	0.031	79.6/71.54/69.94	NA/32.12/30.61	0.02	0.454
rs114856405	1189	5' flanking	AA/CA/CC	4/46/692	0.036	79.06/76.97/69.6	31.38/33.77/30.23	0.03	0.061
rs1800775	1265	5' flanking	AA/CA/CC	271/346/120	0.395	71.54/68.39/71.99	32.67/27.98/32.37	0.00	0.895
rs17231520	1856	5' flanking	AA/GA/GG	6/121/617	0.090	62.84/73.62/69.77	26.81/33.75/30.02	0.01	0.493
rs34065661	1964	Exon 1	CC/GC/GG	4/124/624	0.088	62.95/72.81/69.96	19.65/33.58/30.11	0.01	0.542
rs5884	1986	Exon 1	AA/CA/CC	3/93/648	0.065	79.25/67.67/70.57	41.02/25.08/31.24	0.00	0.781
rs34680782	2089	Intron 1	AA/CA/CC	2/25/711	0.020	49.7/66.82/70.29	4.95/33.75/30.51	-0.03	0.189
rs17231534	2133	Intron 1	AA/CA/CC	26/207/509	0.177	71.92/73.09/69.17	38.53/29.96/30.5	0.01	0.162
rs3816117	2187	Intron 1	CC/CT/TT	270/335/119	0.394	71.44/68.68/71.79	32.56/28.32/32.35	0.00	0.880
rs711752	2240	Intron 1	AA/GA/GG	44/251/442	0.232	74.17/68.81/70.98	38.64/29.52/30.62	0.00	0.688
rs708272	2317	Intron 1	AA/GA/GG	46/254/439	0.236	73.69/68.91/70.83	38.22/29.35/30.51	0.00	0.699
rs60195610	2692	Intron 1	CC/CT/TT	720/33/1	0.023	69.74/76.4/46.73	29.79/38.64/NA	0.01	0.531
rs9935228	3101	Intron 2	AA/GA/GG	612/116/11	0.091	70.65/65.25/84.46	31.14/24.86/45.85	-0.01	0.544
rs1864163	3262	Intron 2	AA/GA/GG	60/282/381	0.278	67.77/69.74/71	31.33/28.81/31.67	-0.01	0.394
rs75313088	3347	Intron 2	AA/GA/GG	4/45/693	0.036	71.16/77.84/69.68	32.89/34.39/30.29	0.03	0.102
rs5817083	3381	Intron 2	DD/WD/WW	105/364/266	0.393	71.37/72.2/67.59	38.42/29.21/28.99	0.01	0.273
rs4369653	3581	Intron 2	AA/AG/GG	457/260/28	0.212	70.74/69.97/68.52	31.46/28.71/29.85	0.00	0.902
rs7194225	3686	Intron 2	CC/CG/GG	28/209/492	0.185	68.22/73.85/68.93	36.17/29.98/30.69	0.01	0.144
rs114908369	4299	Intron 2	CA/CC	38/709	0.025	59.82/70.78	25.26/30.76	-0.07	0.003
rs9929488	4602	Intron 2	CC/GC/GG	159/355/216	0.463	69.93/70.48/69.27	30.45/30.24/31.69	0.00	0.712
rs12720906	4791	Intron 2	GG/GT/TT	4/42/686	0.034	77.63/76.93/69.83	30.25/35.06/30.43	0.03	0.147
rs12720926	4948	Intron 2	AA/AG	714/38	0.027	70.41/70.41	30.02/40.08	-0.01	0.521
rs17237939	4957	Intron 2	CC/CT/TT	673/64/3	0.049	70.28/69.83/44.94	30.7/25.77/8.33	-0.01	0.682
rs35585922	5215	Intron 2	DD/WD/WW	20/167/527	0.149	70.53/73.06/69.08	40.48/29.97/30.31	0.01	0.313
rs7203984	5288	Intron 2	AA/CA/CC	137/357/231	0.438	67.22/72.59/68.39	30.17/30.99/30.45	0.00	0.969
rs11508026	5358	Intron 2	AA/AG	714/38	0.027	70.07/69.9	29.5/40.59	-0.02	0.379
rs80296794	5375	Intron 2	TC/TT	32/718	0.021	74.99/70.23	30.52/30.71	0.03	0.297
rs112236143	5593	Intron 2	CA/CC	29/691	0.020	73.31/69.98	33.02/30.55	0.01	0.607
rs708273	5979	Intron 2	AA/AG/GG	8/132/598	0.100	79.8/69.32/70.31	39.66/28.95/30.86	0.00	0.739
rs17231583	5990	Intron 2	CC/GC/GG	3/24/709	0.020	65.1/84.52/69.99	18.58/35.78/30.44	0.05	0.052
rs142058276	6022	Intron 2	II/WI/WW	3/116/614	0.082	78.21/69.1/70.21	16.52/29.61/30.76	0.00	0.920
rs17231590	6221	Intron 2	AA/AG/GG	669/78/4	0.058	70.74/67.77/55.84	31.55/24.17/17.69	-0.01	0.548
rs17237953	6239	Intron 2	GG/GT/TT	672/53/3	0.039	70.41/68.22/106.87	30.32/32.83/86.73	0.00	0.871
rs35619327	6251	Intron 2	CC/TC	699/35	0.023	69.91/75.1	30.48/33.06	0.02	0.313
rs820299	6314	Intron 2	AA/AG/GG	187/373/178	0.495	66.02/73.67/68.22	27.7/31.58/30.86	0.00	0.544
rs17237967	6427	Intron 2	AA/GA/GG	4/41/664	0.035	68.08/70.28/70.35	46.94/26.07/31.1	0.00	0.982
rs8045855	6725	Intron 2	AA/AT/TT	241/344/135	0.423	69.28/72.76/66.07	29.64/32.11/27.24	0.00	0.577
rs12720922	6914	Intron 2	AA/GA/GG	89/341/304	0.352	66.46/70.71/70.49	29.19/29.68/31.97	-0.01	0.503
rs12708969	7616	Intron 2	AA/CA/CC	13/124/569	0.106	85.46/67.05/70.75	45.17/29.04/30.22	0.00	0.748
rs9924087	8274	Intron 2	AA/GA/GG	45/203/476	0.207	64.55/73.9/69.21	30.94/30.21/30.12	0.00	0.689
rs12597002	8436	Intron 2	AA/CA/CC	6/132/601	0.097	78.27/70.16/70.07	37.69/30.12/30.22	0.01	0.670
rs12720863	8742	Intron 2	AA/GA/GG	710/32/1	0.023	70.17/73.78/79.62	30.28/37.57/NA	0.02	0.507
rs9939224	8764	Intron 2	GG/GT/TT	300/343/91	0.356	71.38/70.57/67.73	32.27/29.56/29.2	-0.01	0.461
rs11076174	9178	Intron 2	CC/TC/TT	9/178/551	0.132	59.48/71.44/69.97	28.91/30.81/30.5	0.00	0.975
rs13306230	9282	Intron 2	CA/CC	2/740	0.001	71.39/70.12	1.41/30.57	0.04	0.684
rs12708971	9493	Intron 3	CC/CT/TT	3/22/709	0.019	77.98/84.53/69.75	37/37.26/30.35	0.05	0.034
rs891141	9755	Intron 4	AA/AC/CC	573/164/16	0.130	70.45/70.28/62.71	30.79/31.48/16.49	-0.01	0.607
CTPp9841	9841	Intron 4	AG/GG	1/743	0.001	138.85/70.15	NA/30.5	0.28	0.040
rs34716057	9878	Exon 5	AA/GA/GG	2/46/702	0.034	155.7/64.64/70.29	69.3/27.11/30.09	-0.01	0.779
rs891143	10012	Intron 5	CC/TC/TT	605/123/5	0.090	70.42/69.3/64.88	31.09/28.83/17.37	0.00	0.818
rs12720862	10779	Intron 5	AA/GA/GG	586/148/9	0.112	70.46/69.53/61.99	30.99/29.74/22.57	-0.01	0.547

Table B1.16. Continued

RefSNP ID	Position	Location	Genotype (GT)	GT Counts	MAF	Adjusted mean of plasma TG	Standart Deviation	Beta	*P*
rs7205804	10921	Intron 5	AA/GA/GG	11/124/608	0.097	70.98/69.05/70.46	25.07/31.27/30.23	0.00	0.746
rs12708973	10934	Intron 5	AA/AG	746/14	0.009	70.43/61.62	30.81/19.64	-0.03	0.412
rs148134355	10943	Intron 5	GA/GG	7/726	0.005	62.45/70.46	18.22/30.79	-0.02	0.716
rs34611098	10983	Exon 6	AG/GG	2/743	0.001	77.12/70.05	4.24/30.53	0.07	0.476
rs12720925	11456	Intron 7	CC/TC/TT	1/59/679	0.042	62.78/66.81/70.5	NA/30.48/30.68	-0.02	0.289
rs1532624	11510	Intron 7	AA/CA/CC	10/127/606	0.097	71.09/68.51/70.6	27.31/31.33/30.65	-0.01	0.511
rs12720871	11795	Intron 7	CC/CG/GG	641/84/6	0.066	69.9/71.19/86.47	30.2/31.16/62.27	0.01	0.556
rs12720872	11913	Intron 7	CC/TC/TT	550/177/11	0.135	70.03/70.9/67.44	30.5/31.17/23.73	0.00	0.805
rs11076175	12409	Intron 8	AA/AG/GG	424/264/47	0.243	70.6/69.7/70.04	31.46/29.32/31.34	0.00	0.877
rs7499892	12621	Intron 8	CC/CT/TT	284/337/105	0.377	70.87/69.51/71.9	30.88/28.8/34.72	0.00	0.869
rs289713	12860	Intron 8	AA/AT/TT	151/338/223	0.451	68.44/73.05/67.8	32.28/31.62/28.12	0.00	0.956
rs191754368	12913	Intron 8	CC/TC/TT	722/24/2	0.019	70.29/67.57/49.57	30.45/34.81/4.95	-0.03	0.188
rs9930761	13223	Intron 8	CC/CT/TT	14/180/526	0.148	71.23/73.29/69.16	42.53/29.94/30.51	0.01	0.158
rs35878799	13279	Exon 9	CT/TT	17/721	0.011	60.92/70.18	26.53/30.7	-0.05	0.114
rs5883	13384	Exon 9	CC/TC/TT	530/199/13	0.155	69.31/72.39/70.1	30.5/29.83/44.19	0.01	0.336
rs11076176	13477	Intron 9	GG/GT/TT	121/350/262	0.403	71.1/67.87/72.91	35.14/26.2/33.3	-0.01	0.217
rs289714	13482	Intron 9	AA/GA/GG	145/358/225	0.447	71.16/69.25/70.41	35.01/27.42/31.55	0.00	0.895
rs158479	14079	Intron 9	AA/GA/GG	73/324/333	0.325	71.48/70.33/69.88	38.29/29.24/29.55	0.00	0.859
rs12720892	14192	Intron 9	AA/GA/GG	3/60/697	0.043	70.92/69.1/70.47	18.01/33.25/30.48	-0.01	0.641
rs158480	14258	Intron 9	AA/GA/GG	149/335/222	0.445	70.28/69.88/71.4	30.03/28.77/33.82	0.00	0.988
CTPp14448del4	14448	Intron 9	WD/WW	27/721	0.018	70.89/70.06	30.14/30.54	0.00	0.949
rs289715	14539	Intron 9	AA/TA/TT	37/254/440	0.224	67.88/69.31/71.36	26.64/28.23/32.35	0.00	0.612
rs2303789	15226	Intron 10	GG/GT/TT	4/88/650	0.065	67.12/68.32/70.53	20.07/30.33/30.67	-0.01	0.529
rs289716	15407	Intron 10	AA/AT/TT	168/355/203	0.476	71.3/67.91/73.27	35/27.72/31.81	-0.01	0.263
rs289717	15419	Intron 10	AA/GA/GG	12/194/532	0.147	80.43/68.89/70.53	48.9/30.04/30.35	0.00	0.790
rs12708976	15542	Intron 10	CC/TC/TT	677/65/2	0.047	70.12/69.75/59.08	30.82/28.85/6.36	0.00	0.983
rs12720942	15639	Intron 10	AA/GA/GG	651/90/4	0.066	70.47/68.86/67.28	30.65/30.87/20.07	-0.01	0.580
rs736274	15800	Intron 10	AA/AT/TT	734/22/1	0.016	70.35/66.43/33.91	30.41/38.83/NA	-0.04	0.140
rs12720937	15913	Intron 10	CC/GC/GG	639/88/4	0.066	70.49/68.19/67.33	30.71/30.57/20.07	-0.01	0.461
rs289718	15963	Intron 10	CC/CT/TT	238/341/148	0.438	72.61/67.44/71.58	32.24/26.73/35.8	-0.01	0.310
rs289719	15972	Intron 10	AA/GA/GG	181/372/190	0.493	73.87/68.61/69.86	34.01/26.9/32.78	0.01	0.164
rs2033254	16016	Intron 10	CC/TC/TT	82/298/352	0.317	71.66/68.06/71.35	34.89/28.51/31.32	-0.01	0.420
rs112205272	16146	Intron 10	AA/GA/GG	4/84/651	0.063	67.23/67.84/70.35	20.07/30.19/30.62	-0.01	0.482
rs112409939	16363	Intron 10	AA/GA/GG	651/86/4	0.064	70.37/68.91/67.33	30.62/31.01/20.07	-0.01	0.662
rs71387147	16413	Intron 10	GT/TT	34/651	0.025	62.33/70.71	20.86/31.17/	-0.04	0.112
rs1968905	16979	Intron 10	GG/GT/TT	295/360/87	0.360	69.4/70.7/68.93	32.08/28.45/29.45	0.00	0.602
rs12720903	17154	Intron 10	AA/GA/GG	5/93/655	0.068	71.11/68.93/70.33	27.06/28.43/30.4	0.00	0.757
rs4784744	17216	Intron 10	AA/GA/GG	7/135/595	0.100	83.94/69.14/70.47	55.18/30.46/30.39	0.00	0.838
rs291044	17483	Intron 10	AA/GA/GG	7/137/591	0.102	83.98/68.47/70.52	55.18/30.31/30.41	-0.01	0.637
rs114486472	17575	Intron 10	AA/AG/GG	2/26/706	0.020	60/79.71/70	18.38/35.81/30.48	0.03	0.209
rs34426213	17918	Intron 10	CC/CT/TT	667/57/3	0.042	70.25/67.89/79.24	30.66/29.32/58.96	-0.01	0.750
rs891144	17970	Intron 10	AA/GA/GG	39/242/468	0.215	74.44/68.39/70.96	30.15/29.4/31.14	0.00	0.828
rs12708979	18388	Intron 11	AA/GA/GG	2/42/713	0.030	50.02/64.8/70.41	4.95/24/30.5	-0.03	0.132
rs12708980	18413	Intron 11	AA/AC/CC	318/287/95	0.342	70.21/70.89/70.61	30.12/31.61/31.76	-1.01E-05	0.999
rs12720889	18597	Intron 11	AA/AT/TT	476/232/33	0.204	69.65/70.37/73.87	29.04/31.67/37.07	0.00	0.863
rs291043	18733	Intron 11	AA/AG/GG	624/108/10	0.086	70.21/68.57/75.27	30.68/27.2/48.28	0.00	0.814
rs114203109	18970	Intron 11	GA/GG	63/664	0.042	73.2/70.35	32.41/30.73	0.01	0.468
rs145189439	19734	Intron 11	CC/TC/TT	3/70/671	0.052	70.62/66.24/70.76	18.01/30.13/30.59	-0.02	0.279
rs4784745	20910	Intron 11	AA/AG/GG	628/100/6	0.076	70.53/68.54/91.34	30.61/28.01/57.79	0.00	0.944
rs34855278	21111	Exon 12	GA/GG	22/731	0.015	66.43/70.19	38.83/30.21	-0.03	0.324
rs114948973	21454	Intron 12	AA/AG/GG	1/26/701	0.019	149.84/67.45/70.52	NA/24.53/30.77	0.01	0.631
rs7195984	21498	Intron 12	AA/GA/GG	499/187/27	0.169	70.13/70.65/72.6	31.89/26.34/30.33	0.01	0.323
rs7196174	21579	Intron 12	GG/GT/TT	637/96/4	0.070	70.42/68.4/67.44	31.21/27.06/27.04	-0.01	0.653
rs1800774	21580	Intron 12	CC/TC/TT	457/237/41	0.217	70.18/71.06/64.11	30.27/32.51/25.68	-0.01	0.486
rs5882	22127	Exon 14	AA/GA/GG	82/291/357	0.310	67.9/70.67/70.7	31.32/31.43/30.09	-0.01	0.395
rs5886	22162	Exon 14	AA/GA/GG	4/115/618	0.082	74.09/67.81/70.77	25.56/27.6/31.21	-0.01	0.505
rs289740	22985	Intron 14	CC/CT/TT	11/149/574	0.117	66.08/71.22/69.63	25.69/27.04/31.28	0.01	0.366
rs36051594	23201	Intron 14	AA/GA/GG	4/60/694	0.044	64.82/69.82/70.29	22.6/33.17/30.31	-0.01	0.629
rs1801706	23696	3'UTR-Exon 16	AA/GA/GG	27/203/507	0.176	73.9/70.7/69.94	39.34/29.19/30.63	0.00	0.641
rs289742	23796	3' flanking	CC/CG/GG	136/341/251	0.421	69.35/71.94/68.9	27.16/32.13/29.95	0.01	0.349
rs289743	23830	3' flanking	AA/GA/GG	84/297/358	0.315	67.34/71.66/70.06	30.89/32.03/29.54	0.00	0.601
rs289744	24136	3' flanking	GG/GT/TT	355/292/75	0.306	70.38/71.09/68.1	29.29/31.96/31.54	-0.01	0.487
rs12720875	24499	3' flanking	AA/GA/GG	2/44/708	0.032	49.69/68.23/70.42	4.95/32.01/30.5	-0.02	0.298
rs66495554	24669	3' flanking	CC/TC/TT	488/227/30	0.193	70.86/69.37/65.9	30.64/31.31/25.19	-0.01	0.259
rs114646974	24881	3' flanking	AA/AG	725/5	0.003	69.95/93.13	30.45/37.85	0.11	0.077

Table B1.16. Continued

RefSNP ID	Position	Location	Genotype (GT)	GT Counts	MAF	Adjusted mean of plasma TG	Standart Deviation	Beta	*P*
rs138161274	24899	3' flanking	CC/GC/GG	697/39/1	0.027	70.28/68.03/63.34	30.95/26.61/NA	0.00	0.941
rs12720874	25064	3' flanking	CC/TC/TT	22/174/515	0.153	76.24/69.07/71.1	33.19/28.59/31.59	0.00	0.875
rs12720916	25218	3' flanking	AA/GA/GG	711/34/2	0.025	69.96/74.54/59.93	30.72/28.5/18.38	0.02	0.373
rs289745	25565	3' flanking	GG/GT/TT	36/214/483	0.194	80.24/69.69/69.99	27.81/28.33/31.85	0.02	0.056

TABLE B1.17. Association results of LDL-C levels with 104 *CETP* SNPs in African blacks (n=788)

RefSNP ID	Position	Location	Genotype (GT)	GT Counts	MAF	Adjusted mean of plasma LDL-C	Standart Deviation	Beta	*P*
rs247615	-9210	5' flanking	AA/AG/GG	437/260/40	0.230	110.4/107.27/111.2	34.46/36.14/29.77	-0.18	0.437
rs9989419	-8834	5' flanking	AA/GA/GG	318/334/82	0.340	107.42/110.82/110.17	35.53/34.64/31.26	0.27	0.196
rs183130	-2610	5' flanking	CC/CT/TT	423/271/46	0.244	111.02/107.01/104.85	35.81/33.6/30.45	-0.39	0.083
rs3764261	-648	5' flanking	AA/CA/CC	82/308/339	0.323	105.99/107.4/111.83	31.38/33.87/35.9	-0.37	0.066
rs148562851	187	5' flanking	AA/AG/GG	717/29/1	0.020	109.2/106.69/124.24	34.8/34.52/NA	-0.16	0.806
rs12447924	220	5' flanking	CC/CT/TT	43/232/431	0.224	114.97/111.46/107.73	33.47/33.18/35.4	0.46	0.042
rs17231506	557	5' flanking	CC/TC/TT	599/139/9	0.105	109.6/107.76/108.19	35.26/32.49/32.59	-0.16	0.609
rs12708968	848	5' flanking	CC/TC/TT	2/88/647	0.063	123.7/108.49/109.13	23.9/36.2/34.54	-0.02	0.960
rs4783961	923	5' flanking	AA/GA/GG	160/338/227	0.454	106.58/107.25/113	32.2/35.27/35.05	-0.39	0.041
rs146122874	950	5' flanking	CC/TC/TT	711/30/2	0.022	109.11/109.21/83.96	34.65/33.91/49.85	-0.34	0.583
rs4783962	1067	5' flanking	CC/CT/TT	597/129/8	0.097	107.9/115.31/106.78	34.62/35.14/35.62	0.66	0.042
rs17237883	1153	5' flanking	AA/GA/GG	1/42/696	0.031	175.53/110.8/108.87	NA/33.03/34.68	0.54	0.336
rs114856405	1189	5' flanking	AA/CA/CC	4/46/694	0.036	118.7/111.91/108.89	36.19/28.88/34.75	0.48	0.318
rs1800775	1265	5' flanking	AA/CA/CC	275/343/121	0.395	108.19/108.27/114.37	33.05/34.86/36.64	0.27	0.158
rs17231520	1856	5' flanking	AA/GA/GG	7/121/618	0.090	92.23/106.8/109.86	26.8/33.23/35.09	-0.48	0.151
rs34065661	1964	Exon 1	CC/GC/GG	5/124/626	0.088	95.5/107.13/109.69	27.34/32.81/34.83	-0.35	0.295
rs5884	1986	Exon 1	AA/CA/CC	3/90/653	0.065	120.83/107.07/109.15	17.43/36.44/34.4	-0.15	0.702
rs34680782	2089	Intron 1	AA/CA/CC	2/26/712	0.020	74.86/109.5/109.14	28.21/37.42/34.44	-0.52	0.417
rs17231534	2133	Intron 1	AA/CA/CC	28/205/511	0.177	111.98/106.56/110.1	36.81/35.83/34.31	-0.23	0.358
rs3816117	2187	Intron 1	CC/CT/TT	273/332/120	0.394	108.21/108.36/114.04	32.92/35.18/36.59	0.26	0.188
rs711752	2240	Intron 1	AA/GA/GG	47/252/440	0.232	102.24/108.76/110.5	25.66/35/35.47	-0.32	0.150
rs708272	2317	Intron 1	AA/GA/GG	49/255/437	0.236	101.46/108.17/110.17	25.12/35.01/35.31	-0.35	0.113
rs60195610	2692	Intron 1	CC/CT/TT	722/33/1	0.023	109.05/110.52/124.12	34.47/36.54/NA	0.21	0.739
rs9935228	3101	Intron 2	AA/GA/GG	617/114/10	0.091	109.32/107.52/121.63	34.73/34.7/30.18	0.06	0.843
rs1864163	3262	Intron 2	AA/GA/GG	60/282/382	0.278	111.97/106.39/110.6	34.68/35.36/33.76	-0.17	0.438
rs75313088	3347	Intron 2	AA/GA/GG	4/45/694	0.036	96.17/114.07/108.79	13.53/29.96/34.94	0.34	0.496
rs5817083	3381	Intron 2	DD/WD/WW	108/363/265	0.393	110.45/109.08/109.37	30.75/37.19/33.17	0.04	0.859
rs4369653	3581	Intron 2	AA/AG/GG	458/260/29	0.212	108.86/109/114.11	34.83/34.19/29.68	0.15	0.530
rs7194225	3686	Intron 2	CC/CG/GG	30/208/492	0.185	108.22/106.98/110.35	37.34/35.7/33.93	-0.32	0.187
rs114908369	4299	Intron 2	CA/CC	38/711	0.025	109.42/109.21	32.81/34.81	0.05	0.931
rs9929488	4602	Intron 2	CC/GC/GG	161/356/215	0.463	109.26/107.35/111.99	37.42/33.5/34.43	-0.22	0.259
rs12720906	4791	Intron 2	GG/GT/TT	4/42/688	0.034	105.91/111.88/109.04	14.96/34.08/34.87	0.23	0.652
rs12720926	4948	Intron 2	AA/AG	715/39	0.027	109.59/98.76	34.65/28.54/	-1.22	0.044
rs17237939	4957	Intron 2	CC/CT/TT	676/63/3	0.049	108.79/113.98/114.21	34.55/35.63/44.77	0.55	0.222
rs35585922	5215	Intron 2	DD/WD/WW	22/171/524	0.149	113.6/107.58/108.9	36.51/37.5/33.78	-0.04	0.884
rs7203984	5288	Intron 2	AA/CA/CC	141/356/229	0.438	109.82/109.27/109.37	33.93/36.01/33.1	0.01	0.958
rs11508026	5358	Intron 2	AA/AG	715/39	0.027	109.8/98.46	34.67/28.32	-1.29	0.033
rs80296794	5375	Intron 2	TC/TT	30/721	0.021	122.42/108.89	33.69/34.26	1.60	0.020
rs112236143	5593	Intron 2	CA/CC	27/694	0.020	105.45/109.48	32.25/34.46	-0.48	0.515
rs708273	5979	Intron 2	AA/AG/GG	8/135/598	0.100	126.52/108.58/108.79	29.4/34.28/34.77	0.22	0.483
rs17231583	5990	Intron 2	CC/GC/GG	3/23/711	0.020	111.76/109.96/109.31	14.53/33.12/34.81	0.16	0.805
rs142058276	6022	Intron 2	II/WI/WW	3/115/617	0.082	101.08/105.04/110.11	6.71/35.18/34.68	-0.58	0.106
rs17231590	6221	Intron 2	AA/AG/GG	672/77/4	0.058	108.46/114.7/115.59	34.31/35.55/36.61	0.67	0.101
rs17237953	6239	Intron 2	GG/GT/TT	677/52/3	0.039	108.69/111.05/122.58	34.7/32.25/55.96	0.41	0.395
rs35619327	6251	Intron 2	CC/TC	703/33	0.023	109.22/105.59	34.57/34.41	-0.45	0.494
rs820299	6314	Intron 2	AA/AG/GG	184/375/179	0.495	108.91/107.61/113.68	33.89/34.23/35.99	0.26	0.179
rs17237967	6427	Intron 2	AA/GA/GG	4/40/666	0.035	118.74/114.86/108.8	39.84/33.23/34.54	0.69	0.175
rs8045855	6725	Intron 2	AA/AT/TT	243/345/135	0.423	110.81/108.15/108.62	33.8/35.96/32.77	-0.15	0.449
rs12720922	6914	Intron 2	AA/GA/GG	89/340/307	0.352	108.38/107.03/111.79	32.36/35.11/34.92	-0.29	0.154
rs12708969	7616	Intron 2	AA/CA/CC	13/122/571	0.106	120.95/105.61/110.28	25.54/32.84/35.68	-0.12	0.693
rs9924087	8274	Intron 2	AA/GA/GG	45/209/472	0.207	117.91/108.16/109.35	35.98/34.67/34.59	0.19	0.403
rs12597002	8436	Intron 2	AA/CA/CC	6/135/601	0.097	120.78/110.59/108.87	35.74/33.69/34.62	0.31	0.337
rs12720863	8742	Intron 2	AA/GA/GG	711/33/1	0.023	108.93/111.03/174.63	34.84/31.57/NA	0.67	0.291
rs9939224	8764	Intron 2	GG/GT/TT	303/342/91	0.356	111.44/107.04/108.04	34.76/35.15/31.94	-0.28	0.178
rs11076174	9178	Intron 2	CC/TC/TT	10/175/554	0.132	105.53/107.19/109.82	31.75/34.48/34.85	-0.27	0.353
rs13306230	9282	Intron 2	CA/CC	2/742	0.001	100.93/109.22	37.34/34.43	-0.97	0.710
rs12708971	9493	Intron 3	CC/CT/TT	3/21/712	0.019	96.82/108.73/109.12	11.14/34.26/34.68	-0.24	0.720
rs891141	9755	Intron 4	AA/AC/CC	574/164/17	0.130	109.72/107.39/110.45	34.54/34.28/36.84	-0.17	0.547
CTPp9841	9841	Intron 4	AG/GG	1/745	0.001	116.95/108.93	NA/34.59	1.19	0.750
rs34716057	9878	Exon 5	AA/GA/GG	2/45/705	0.034	111.28/107.37/109.26	21.92/34.11/34.64	-0.16	0.767
rs891143	10012	Intron 5	CC/TC/TT	606/123/5	0.090	109.7/107.28/109.06	34.53/36.17/9.71	-0.25	0.470
rs12720862	10779	Intron 5	AA/GA/GG	588/147/10	0.112	108.49/109.91/118.15	34.21/36.32/32.43	0.24	0.439
rs7205804	10921	Intron 5	AA/GA/GG	11/121/613	0.097	98.04/104.49/110.29	20.28/31.05/35.11	-0.64	0.043
rs12708973	10934	Intron 5	AA/AG	749/13	0.009	109.25/104.08	34.38/34.54	-0.61	0.556
rs148134355	10943	Intron 5	GA/GG	7/728	0.005	92.98/109.27	37.64/34.53	-2.13	0.135
rs34611098	10983	Exon 6	AG/GG	2/745	0.001	88.71/109.26	20.72/34.41	-2.38	0.360
rs12720925	11456	Intron 7	CC/TC/TT	1/60/680	0.042	104.19/107.89/109.32	NA/31.68/34.98	-0.12	0.808
rs1532624	11510	Intron 7	AA/CA/CC	10/124/611	0.097	98.11/106.16/109.97	21.11/32.24/35.37	-0.47	0.143
rs12720871	11795	Intron 7	CC/CG/GG	644/83/6	0.066	109.44/108.02/99.88	34.83/34.55/26.82	-0.28	0.472
rs12720872	11913	Intron 7	CC/TC/TT	552/176/12	0.135	108.34/110.67/121.28	34.29/35.6/36.41	0.37	0.198
rs11076175	12409	Intron 8	AA/AG/GG	426/265/46	0.243	109.67/108.82/107.73	34.35/36.15/29.47	-0.10	0.652
rs7499892	12621	Intron 8	CC/CT/TT	287/337/104	0.377	108.23/110.96/107.5	33.79/36.51/32.26	0.04	0.831

Table B1.17. Continued

RefSNP ID	**Position**	**Location**	**Genotype (GT)**	**GT Counts**	**MAF**	**Adjusted mean of plasma LDL-C**	**Standart Deviation**	**Beta**	***P***
rs289713	12860	Intron 8	AA/AT/TT	154/340/221	0.451	108.56/110.27/108.25	31.94/34.95/36.39	0.07	0.735
rs191754368	12913	Intron 8	CC/TC/TT	723/25/2	0.019	109.2/110.14/74.84	34.56/37.56/28.21	-0.49	0.455
rs9930761	13223	Intron 8	CC/CT/TT	16/184/523	0.148	122.23/108.4/109.02	31.75/35.77/34.07	0.16	0.571
rs35878799	13279	Exon 9	CT/TT	17/723	0.011	112.52/109.06	32.43/34.65	0.45	0.624
rs5883	13384	Exon 9	CC/TC/TT	527/202/15	0.155	109.43/107.3/126.95	34.13/35.96/31.58	0.06	0.837
rs11076176	13477	Intron 9	GG/GT/TT	121/349/265	0.403	109.08/109.33/109.02	33.9/34.91/33.91	0.01	0.956
rs289714	13482	Intron 9	AA/GA/GG	149/359/223	0.447	112.18/109.25/106.48	33.99/36.28/32.15	0.32	0.106
rs158479	14079	Intron 9	AA/GA/GG	75/327/328	0.325	111.24/109.1/108.62	35.07/34.58/34.55	0.13	0.552
rs12720892	14192	Intron 9	AA/GA/GG	3/60/699	0.043	116.29/111.55/109.04	17.01/35.31/34.46	0.33	0.465
rs158480	14258	Intron 9	AA/GA/GG	145/334/227	0.445	110.26/109.74/107.24	37.75/33.06/34.64	0.16	0.398
CTPp14448del4	14448	Intron 9	WD/WW	28/721	0.018	115.57/109.12	33.31/34.68	0.78	0.274
rs289715	14539	Intron 9	AA/TA/TT	36/251/445	0.224	112.67/108.13/109.83	37.31/34.33/34.66	-0.05	0.841
rs2303789	15226	Intron 10	GG/GT/TT	5/87/652	0.065	113.64/109.66/108.72	14.3/36.45/34.44	0.13	0.740
rs289716	15407	Intron 10	AA/AT/TT	171/355/202	0.476	107.83/108.25/111.69	31.93/35.37/35.2	-0.21	0.285
rs289717	15419	Intron 10	AA/GA/GG	12/196/532	0.147	130.69/108.48/109.04	39.62/32.63/35.46	0.29	0.308
rs12708976	15542	Intron 10	CC/TC/TT	678/65/3	0.047	108.99/111.23/108.03	34.57/37.14/3.15	0.17	0.707
rs12720942	15639	Intron 10	AA/GA/GG	653/89/5	0.066	108.94/110.12/113.91	34.66/36.29/14.3	0.15	0.686
rs736274	15800	Intron 10	AA/AT/TT	736/23/1	0.016	109.26/102.95/158.83	34.53/26.79/NA	-0.14	0.850
rs12720937	15913	Intron 10	CC/GC/GG	641/87/5	0.066	108.93/109.79/113.93	34.46/36.53/14.3	0.12	0.755
rs289718	15963	Intron 10	CC/CT/TT	238/339/151	0.438	112.2/107.62/106.73	35.98/34.63/31.6	-0.31	0.103
rs289719	15972	Intron 10	AA/GA/GG	181/371/193	0.493	111.81/108.99/107.46	34.87/34.84/33.08	0.24	0.214
rs2033254	16016	Intron 10	CC/TC/TT	84/297/352	0.317	105.65/108.19/110.76	32.22/35.03/35.05	-0.29	0.146
rs112205272	16146	Intron 10	AA/GA/GG	5/83/653	0.063	113.98/110.04/109.04	14.3/37.16/34.61	0.13	0.745
rs112409939	16363	Intron 10	AA/GA/GG	653/85/5	0.064	108.91/108.84/113.91	34.67/35.23/14.3	0.05	0.890
rs71387147	16413	Intron 10	GT/TT	35/651	0.025	99.21/110.26	34.84/35.09	-1.29	0.049
rs1968905	16979	Intron 10	GG/GT/TT	298/357/89	0.360	110.16/108.25/111.76	33.35/35.51/35.08	-0.03	0.894
rs12720903	17154	Intron 10	AA/GA/GG	5/93/657	0.068	120.62/108.52/109.3	33.09/37.2/34.31	0.02	0.959
rs4784744	17216	Intron 10	AA/GA/GG	7/136/595	0.100	128.52/105.81/109.98	35.1/31.13/35.6	-0.12	0.716
rs291044	17483	Intron 10	AA/GA/GG	7/138/591	0.102	128.51/105.23/109.94	35.1/29.53/35.54	-0.16	0.623
rs114486472	17575	Intron 10	AA/AG/GG	2/24/710	0.020	101.06/110.44/109.37	12.59/34.25/34.78	0.01	0.983
rs34426213	17918	Intron 10	CC/CT/TT	668/57/3	0.042	108.55/120.26/100.32	34.51/36.73/20.87	1.03	0.029
rs891144	17970	Intron 10	AA/GA/GG	39/243/469	0.215	117.99/109.19/108.78	36.64/35.03/34.37	0.26	0.254
rs12708979	18388	Intron 11	AA/GA/GG	2/42/715	0.030	74.4/116.01/108.85	28.21/44.24/33.85	0.20	0.712
rs12708980	18413	Intron 11	AA/AC/CC	318/287/97	0.342	109.92/109.61/104.5	35.73/33.94/33.84	-0.23	0.260
rs12720889	18597	Intron 11	AA/AT/TT	473/236/34	0.204	108.45/109.12/115.24	33.77/35.95/30.46	0.21	0.379
rs291043	18733	Intron 11	AA/AG/GG	623/110/10	0.086	109.81/103.86/122.05	35.07/30.77/32.26	-0.23	0.491
rs114203109	18970	Intron 11	GA/GG	62/668	0.042	100.2/110.37	31.43/35.02	-1.14	0.022
rs145189439	19734	Intron 11	CC/TC/TT	4/69/672	0.052	113.6/109.75/109.26	15.18/36.21/34.38	0.08	0.851
rs4784745	20910	Intron 11	AA/AG/GG	629/101/6	0.076	109.7/104.3/131.5	34.99/32.47/35.19	-0.20	0.584
rs34855278	21111	Exon 12	GA/GG	23/732	0.015	102.92/109.29	26.79/34.54	-0.67	0.397
rs114948973	21454	Intron 12	AA/AG/GG	1/26/702	0.019	119.87/120.22/108.9	NA/41.51/34.23	1.12	0.103
rs7195984	21498	Intron 12	AA/GA/GG	501/188/27	0.169	109.12/109.21/108.74	34.39/36.66/35.03	-0.03	0.918
rs7196174	21579	Intron 12	GG/GT/TT	639/96/4	0.070	108.89/111.35/118.01	34.38/36.45/32.51	0.31	0.414
rs1800774	21580	Intron 12	CC/TC/TT	457/237/42	0.217	111.11/106.17/104.34	36.33/30.6/32.51	-0.43	0.057
rs5882	22127	Exon 14	AA/GA/GG	83/292/357	0.310	109.5/106.74/111.33	33.82/32.48/36.36	-0.21	0.306
rs5886	22162	Exon 14	AA/GA/GG	4/115/620	0.082	117.86/108.51/109.45	35.89/36.12/34.62	-0.04	0.907
rs289740	22985	Intron 14	CC/CT/TT	11/149/576	0.117	105.68/108.89/109.44	22.46/35.31/34.71	-0.10	0.751
rs36051594	23201	Intron 14	AA/GA/GG	4/60/696	0.044	110.08/112.72/108.94	57.23/38.28/34.14	0.28	0.522
rs1801706	23696	3'UTR-Exon 16	AA/GA/GG	28/206/505	0.176	114.81/109.92/108.53	32.42/37.19/33.63	0.21	0.388
rs289742	23796	3' flanking	CC/CG/GG	132/343/255	0.421	107.74/111.33/107.58	33.63/35.26/33.79	0.07	0.731
rs289743	23830	3' flanking	AA/GA/GG	86/298/357	0.315	106.93/107.56/111.42	31.16/33.64/36.25	-0.28	0.165
rs289744	24136	3' flanking	GG/GT/TT	355/293/77	0.306	111.93/107.28/106.99	36.25/33.64/30.41	-0.33	0.108
rs12720875	24499	3' flanking	AA/GA/GG	2/44/710	0.032	74.51/117.97/108.84	28.21/43.12/33.75	0.42	0.426
rs66495554	24669	3' flanking	CC/TC/TT	489/227/31	0.193	111.07/106.05/104.09	36.05/31.76/29.87	-0.45	0.061
rs114646974	24881	3' flanking	AA/AG	729/4	0.003	109.35/82.12	34.53/30.26	-3.33	0.074
rs138161274	24899	3' flanking	CC/GC/GG	702/36/1	0.027	109.14/114.83/109.73	34.17/43.28/NA	0.49	0.415
rs12720874	25064	3' flanking	CC/TC/TT	21/174/519	0.153	108.25/112.46/108.08	34.72/34.02/34.19	0.32	0.218
rs12720916	25218	3' flanking	AA/GA/GG	715/32/2	0.025	109.27/109.73/101.17	34.99/29.64/12.59	0.04	0.952
rs289745	25565	3' flanking	GG/GT/TT	35/216/485	0.194	106.75/107.22/110.62	38.36/33.86/34.91	-0.31	0.189

TABLE B1.18. Association results of TC levels with 104 *CETP* SNPs in African blacks (n=788)

RefSNP ID	Position	Location	Genotype (GT)	GT Counts	MAF	Adjusted mean of plasma TC	Standart Deviation	Beta	*P*
rs247615	-9210	5' flanking	AA/AG/GG	431/259/39	0.230	173.28/170.64/171.73	39.09/40.04/31.77	-0.09	0.463
rs9989419	-8834	5' flanking	AA/GA/GG	317/327/82	0.340	171.03/172.97/174.12	39.94/39.03/34.42	0.10	0.337
rs183130	-2610	5' flanking	CC/CT/TT	419/268/45	0.244	172.55/171.28/172.37	39.96/38.42/34.75	-0.03	0.830
rs3764261	-648	5' flanking	AA/CA/CC	80/307/334	0.323	171.32/170.86/173.88	37.21/37.8/40.4	-0.09	0.407
rs148562851	187	5' flanking	AA/AG/GG	709/29/1	0.020	171.87/176.03/205.63	38.82/43.02/NA	0.28	0.427
rs12447924	220	5' flanking	CC/CT/TT	42/229/428	0.224	177.96/173.72/171.25	40.26/35.73/40.4	0.18	0.141
rs17231506	557	5' flanking	CC/TC/TT	595/136/8	0.105	172.5/170.87/174.06	39.37/37.17/33.29	-0.04	0.789
rs12708968	848	5' flanking	CC/TC/TT	1/90/638	0.063	206.47/169.42/172.24	NA/39.42/38.98	-0.11	0.605
rs4783961	923	5' flanking	AA/GA/GG	157/338/222	0.454	172.41/170.46/173.74	38.53/39.57/38.57	-0.05	0.616
rs146122874	950	5' flanking	CC/TC/TT	703/30/2	0.022	171.73/179.47/151.78	38.78/41.54/68.59	0.17	0.595
rs4783962	1067	5' flanking	CC/CT/TT	593/125/8	0.097	170.99/177.81/173.76	39.04/38.96/45.19	0.31	0.074
rs17237883	1153	5' flanking	AA/GA/GG	1/42/688	0.031	249.73/175.2/171.74	NA/33.61/39.2	0.39	0.194
rs114856405	1189	5' flanking	AA/CA/CC	3/46/687	0.036	183.1/176.98/171.71	47.95/33.63/39.03	0.31	0.234
rs1800775	1265	5' flanking	AA/CA/CC	271/343/117	0.395	173.23/170.54/175.03	38.13/38.61/40.86	0.01	0.955
rs17231520	1856	5' flanking	AA/GA/GG	7/121/610	0.090	171.04/175.61/171.42	28.81/39.13/39.05	0.18	0.294
rs34065661	1964	Exon 1	CC/GC/GG	5/124/618	0.088	178.11/175.84/171.24	20.7/38.5/38.84	0.25	0.156
rs5884	1986	Exon 1	AA/CA/CC	2/92/644	0.065	189.03/167.78/172.39	24.04/39.21/38.77	-0.19	0.359
rs34680782	2089	Intron 1	AA/CA/CC	2/26/704	0.020	127.38/178/171.89	31.11/43.55/38.62	-0.09	0.785
rs17231534	2133	Intron 1	AA/CA/CC	26/208/502	0.177	176.05/170.8/172.47	48.34/40.49/37.89	-0.04	0.740
rs3816117	2187	Intron 1	CC/CT/TT	269/332/116	0.394	172.97/170.63/174.56	38.09/38.96/40.91	0.00	0.970
rs711752	2240	Intron 1	AA/GA/GG	46/250/435	0.232	170.49/173.39/172.03	26.83/39.93/39.59	0.03	0.808
rs708272	2317	Intron 1	AA/GA/GG	48/253/432	0.236	169.07/172.77/171.58	26.43/40.04/39.41	0.01	0.938
rs60195610	2692	Intron 1	CC/CT/TT	716/33/1	0.023	171.59/179.17/205.51	38.41/44.81/NA	0.42	0.201
rs9935228	3101	Intron 2	AA/GA/GG	609/114/10	0.091	172.67/167.65/187.04	39.37/37.22/31.43	-0.07	0.670
rs1864163	3262	Intron 2	AA/GA/GG	60/278/378	0.278	169.61/169.01/174.7	36.97/39.95/38.17	-0.21	0.059
rs75313088	3347	Intron 2	AA/GA/GG	3/45/687	0.036	150.32/179.18/171.55	10.02/34.22/39.16	0.23	0.395
rs5817083	3381	Intron 2	DD/WD/WW	104/361/263	0.393	175.04/172.03/171.48	37.94/40.89/36.79	0.07	0.500
rs4369653	3581	Intron 2	AA/AG/GG	455/259/27	0.212	172.22/171.28/176.23	39.47/37.08/36.09	0.02	0.859
rs7194225	3686	Intron 2	CC/CG/GG	28/210/484	0.185	175.91/171.19/172.52	46.42/40.04/37.55	-0.03	0.810
rs114908369	4299	Intron 2	CA/CC	38/703	0.025	167.65/172.42	35.78/39.02	-0.24	0.452
rs9929488	4602	Intron 2	CC/GC/GG	162/348/214	0.463	170.91/170.97/174.86	43.18/37.94/37.28	-0.14	0.177
rs12720906	4791	Intron 2	GG/GT/TT	3/42/681	0.034	165.45/175.79/172.02	20.11/35.41/39.13	0.15	0.589
rs12720926	4948	Intron 2	AA/AG	707/39	0.027	172.26/163.67	38.95/31.15	-0.43	0.184
rs17237939	4957	Intron 2	CC/CT/TT	669/62/3	0.049	171.91/175.34/167.74	38.88/39.76/38.03	0.15	0.538
rs35585922	5215	Intron 2	DD/WD/WW	20/171/517	0.149	176.7/173.07/170.65	49.55/41.8/37.45	0.11	0.436
rs7203984	5288	Intron 2	AA/CA/CC	137/355/226	0.438	172.77/172.39/171.64	40.05/39.44/37.71	0.03	0.810
rs11508026	5358	Intron 2	AA/AG	707/39	0.027	172.58/162.78	38.98/30.64	-0.49	0.122
rs80296794	5375	Intron 2	TC/TT	29/715	0.021	183.2/171.82	38.36/38.44	0.63	0.085
rs112236143	5593	Intron 2	CA/CC	26/688	0.020	164.16/172.55	36.64/38.76/	-0.48	0.225
rs708273	5979	Intron 2	AA/AG/GG	8/130/594	0.100	184.6/170.69/171.99	34.33/37.44/39.26	0.04	0.831
rs17231583	5990	Intron 2	CC/GC/GG	2/23/704	0.020	170.17/175.4/172.15	27.58/33.64/39.07	0.15	0.677
rs142058276	6022	Intron 2	II/WI/WW	3/114/610	0.082	172.91/171.69/172.29	5.86/39.8/38.95	-0.02	0.914
rs17231590	6221	Intron 2	AA/AG/GG	666/76/4	0.058	171.56/175.54/172.72	38.71/39.38/31.14	0.19	0.368
rs17237953	6239	Intron 2	GG/GT/TT	670/52/3	0.039	171.54/172.84/197.76	39.18/34.38/51.01	0.22	0.384
rs35619327	6251	Intron 2	CC/TC	696/32	0.023	172.38/165.82	38.83/39.02	-0.38	0.290
rs820299	6314	Intron 2	AA/AG/GG	183/371/176	0.495	170.45/171.26/176.93	38.23/37.63/41.47	0.17	0.110
rs17237967	6427	Intron 2	AA/GA/GG	4/40/659	0.035	181.05/176.86/171.94	33.33/38.02/39.03	0.28	0.291
rs8045855	6725	Intron 2	AA/AT/TT	238/345/135	0.423	172.58/172/170.52	37.94/39.84/37.62	-0.06	0.592
rs12720922	6914	Intron 2	AA/GA/GG	91/335/302	0.352	169.19/171/174.54	35.93/39.55/38.8	-0.16	0.147
rs12708969	7616	Intron 2	AA/CA/CC	13/125/560	0.106	189.18/166.76/173.5	30.63/34.16/40.32	-0.08	0.614
rs9924087	8274	Intron 2	AA/GA/GG	45/206/471	0.207	181.82/173.99/171.04	42.56/38.95/38.25	0.22	0.062
rs12597002	8436	Intron 2	AA/CA/CC	5/131/598	0.097	193.32/172.31/172.2	41.27/36.97/38.81	0.10	0.563
rs12720863	8742	Intron 2	AA/GA/GG	704/32/1	0.023	171.96/172.26/248.72	39.23/32.06/NA	0.28	0.399
rs9939224	8764	Intron 2	GG/GT/TT	298/337/93	0.356	174.33/170.6/169.65	38.67/39.64/36.34	-0.15	0.173
rs11076174	9178	Intron 2	CC/TC/TT	10/177/545	0.132	160.04/168.5/173.55	37.62/38.67/38.92	-0.29	0.057
rs13306230	9282	Intron 2	CA/CC	2/734	0.001	173.41/172.12	2.83/38.77	0.22	0.876
rs12708971	9493	Intron 3	CC/CT/TT	2/21/705	0.019	152.08/174.89/172.04	7.78/35.1/39.04	-0.01	0.972
rs891141	9755	Intron 4	AA/AC/CC	567/164/17	0.130	171.89/172.2/174.69	39.07/38.02/34.97	0.05	0.728
CTPp9841	9841	Intron 4	AG/GG	1/737	0.001	163.36/171.87	NA/38.79/	-0.33	0.866
rs34716057	9878	Exon 5	AA/GA/GG	2/46/696	0.034	184.75/170.37/172.04	35.36/35.66/38.94	0.00	0.995
rs891143	10012	Intron 5	CC/TC/TT	598/123/5	0.090	171.91/173.63/175.49	38.85/40.57/11.41	0.10	0.583
rs12720862	10779	Intron 5	AA/GA/GG	582/145/10	0.112	171.26/173.42/180.09	38.45/40.53/33.63	0.14	0.385
rs7205804	10921	Intron 5	AA/GA/GG	11/121/607	0.097	166.39/164.03/173.77	26.86/32.97/39.45	-0.41	0.014
rs12708973	10934	Intron 5	AA/AG	741/14	0.009	172.21/159.79	38.46/41.46	-0.72	0.169
rs148134355	10943	Intron 5	GA/GG	6/721	0.005	152.23/172.25	40.39/38.82	-1.21	0.136
rs34611098	10983	Exon 6	AG/GG	2/737	0.001	171.58/172.1	0/38.71	0.11	0.934
rs12720925	11456	Intron 7	CC/TC/TT	1/57/675	0.042	152.78/170.67/172.27	NA/38.6/38.97	-0.11	0.676
rs1532624	11510	Intron 7	AA/CA/CC	10/124/603	0.097	167.63/165.74/173.56	26.42/34.6/39.84	-0.33	0.051
rs12720871	11795	Intron 7	CC/CG/GG	637/83/5	0.066	172.33/172.02/162.28	39.27/35.36/36.51	-0.06	0.786
rs12720872	11913	Intron 7	CC/TC/TT	547/173/12	0.135	171.27/173.88/182.49	38.7/39.15/40.44	0.18	0.231
rs11076175	12409	Intron 8	AA/AG/GG	420/262/48	0.243	173.21/172.18/165.06	37.95/40.89/33.84	-0.15	0.200
rs7499892	12621	Intron 8	CC/CT/TT	283/333/104	0.377	172.01/174.35/167.76	37.83/40.49/37.08	-0.06	0.556
rs289713	12860	Intron 8	AA/AT/TT	149/338/219	0.451	171.76/173.55/170.31	37.25/38.15/41.24	0.06	0.528
rs191754368	12913	Intron 8	CC/TC/TT	715/25/2	0.019	171.95/178.33/127.25	38.61/43.86/31.11	-0.10	0.776

Table B1.18. Continued

RefSNP ID	**Position**	**Location**	**Genotype (GT)**	**GT Counts**	**MAF**	**Adjusted mean of plasma TC**	**Standart Deviation**	**Beta**	***P***
rs9930761	13223	Intron 8	CC/CT/TT	14/184/516	0.148	195.82/173.99/170.77	44.71/39.36/37.95	0.30	0.043
rs35878799	13279	Exon 9	CT/TT	17/715	0.011	172.46/172.03	32.9/38.92	0.08	0.873
rs5883	13384	Exon 9	CC/TC/TT	520/203/13	0.155	171.26/172.4/201.97	37.96/39.98/41	0.22	0.119
rs11076176	13477	Intron 9	GG/GT/TT	121/348/258	0.403	169.3/171.87/173.64	39.23/38.28/39	-0.11	0.275
rs289714	13482	Intron 9	AA/GA/GG	145/356/221	0.447	176.06/172.79/167.71	40.07/39.07/37.01	0.22	0.031
rs158479	14079	Intron 9	AA/GA/GG	74/323/327	0.325	176.44/172.01/171.09	41.52/37.67/38.94	0.11	0.315
rs12720892	14192	Intron 9	AA/GA/GG	3/58/693	0.043	167.28/174.42/171.97	26.46/42.33/38.37	0.08	0.745
rs158480	14258	Intron 9	AA/GA/GG	142/331/224	0.445	172.64/172.66/169.31	42.54/36.38/40.39	0.10	0.347
CTPp14448del4	14448	Intron 9	WD/WW	27/713	0.018	179.1/171.8	38.86/38.91	0.40	0.294
rs289715	14539	Intron 9	AA/TA/TT	35/252/437	0.224	175.71/171.94/172.3	39.75/37.86/39.32	0.04	0.777
rs2303789	15226	Intron 10	GG/GT/TT	4/86/646	0.065	170.22/172.25/171.74	21.65/42.13/38.42	0.01	0.976
rs289716	15407	Intron 10	AA/AT/TT	168/355/198	0.476	168.81/171.24/176.61	36.74/39.25/39.69	-0.21	0.043
rs289717	15419	Intron 10	AA/GA/GG	12/189/531	0.147	193.67/170.46/172.33	40.93/35.85/40	0.08	0.584
rs12708976	15542	Intron 10	CC/TC/TT	672/64/2	0.047	171.95/173.99/166.86	38.59/42.27/4.95	0.06	0.791
rs12720942	15639	Intron 10	AA/GA/GG	647/88/4	0.066	171.95/172.9/170.74	38.59/41.98/21.65	0.03	0.888
rs736274	15800	Intron 10	AA/AT/TT	729/23/1	0.016	172.06/167.09/193.91	38.77/30.32/NA	-0.10	0.799
rs12720937	15913	Intron 10	CC/GC/GG	635/86/4	0.066	172/172.31/170.59	38.52/42.18/21.65	0.00	0.993
rs289718	15963	Intron 10	CC/CT/TT	233/338/149	0.438	176.77/170.4/167.31	40.13/38.85/36.69	-0.26	0.011
rs289719	15972	Intron 10	AA/GA/GG	177/371/190	0.493	176.46/172.35/167.83	39.3/38.33/37.96	0.23	0.021
rs2033254	16016	Intron 10	CC/TC/TT	84/297/344	0.317	167.34/170.16/174.87	38.44/39.38/38.62	-0.23	0.034
rs112205272	16146	Intron 10	AA/GA/GG	4/82/647	0.063	170.84/172.12/172.07	21.65/42.7/38.53	-0.02	0.936
rs112409939	16363	Intron 10	AA/GA/GG	647/84/4	0.064	171.87/171.55/171.01	38.58/40.56/21.65	-0.02	0.921
rs71387147	16413	Intron 10	GT/TT	34/645	0.025	159.94/173.71	36.48/39.47/	-0.74	0.033
rs1968905	16979	Intron 10	GG/GT/TT	292/357/86	0.360	171.4/171.62/177.76	37.79/39.15/40.64	0.11	0.298
rs12720903	17154	Intron 10	AA/GA/GG	5/92/650	0.068	183.25/171.72/172.13	39.68/40.29/38.64	0.03	0.866
rs4784744	17216	Intron 10	AA/GA/GG	7/132/591	0.100	191.88/167.79/173.09	42.57/34.24/40.04	-0.10	0.544
rs291044	17483	Intron 10	AA/GA/GG	7/134/587	0.102	191.82/167.08/173.04	42.57/32.94/40.02	-0.13	0.443
rs114486472	17575	Intron 10	AA/AG/GG	1/24/703	0.020	147.94/174.62/172.36	NA/34.59/38.9	0.03	0.935
rs34426213	17918	Intron 10	CC/CT/TT	663/55/3	0.042	171.52/182.92/156.65	38.85/40.17/30.02	0.43	0.084
rs891144	17970	Intron 10	AA/GA/GG	37/238/468	0.215	179.49/171.66/171.98	41.35/39.39/38.54	0.08	0.522
rs12708979	18388	Intron 11	AA/GA/GG	2/43/706	0.030	126.67/178.7/171.72	31.11/48.01/38.03	0.04	0.878
rs12708980	18413	Intron 11	AA/AC/CC	312/286/97	0.342	174.34/171.81/166.08	39.76/38.11/39.89	-0.21	0.054
rs12720889	18597	Intron 11	AA/AT/TT	467/237/32	0.204	170.24/173.47/182.31	38.02/39.42/37.77	0.24	0.059
rs291043	18733	Intron 11	AA/AG/GG	619/108/10	0.086	172.73/165.93/186.51	39.18/34.77/36.52	-0.14	0.436
rs114203109	18970	Intron 11	GA/GG	63/658	0.042	159.45/173.68	34.92/39.09	-0.76	0.003
rs145189439	19734	Intron 11	CC/TC/TT	3/68/667	0.052	167.09/172.11/172.23	26.46/42.28/38.53	-0.04	0.855
rs4784745	20910	Intron 11	AA/AG/GG	623/99/6	0.076	172.73/166.41/195.16	39.29/35.82/42.62	-0.13	0.494
rs34855278	21111	Exon 12	GA/GG	23/725	0.015	167.11/172.01	30.32/38.74	-0.23	0.584
rs114948973	21454	Intron 12	AA/AG/GG	1/25/695	0.019	202.67/183.24/171.84	NA/43.58/38.73	0.63	0.089
rs7195984	21498	Intron 12	AA/GA/GG	495/186/27	0.169	171.28/173.12/177.22	39.17/39.73/38.83	0.13	0.342
rs7196174	21579	Intron 12	GG/GT/TT	632/95/4	0.070	171.86/173.42/182.26	38.64/41.39/33.67	0.10	0.604
rs1800774	21580	Intron 12	CC/TC/TT	447/239/42	0.217	175.01/167.86/164.71	40.18/35.65/36.18	-0.32	0.007
rs5882	22127	Exon 14	AA/GA/GG	83/291/350	0.310	170.2/169.17/175.34	35.84/37.49/40.16	-0.19	0.073
rs5886	22162	Exon 14	AA/GA/GG	4/113/614	0.082	182.37/170.85/172.48	37.92/40.24/38.87	-0.04	0.818
rs289740	22985	Intron 14	CC/CT/TT	11/147/569	0.117	175.78/173.27/171.7	26.43/38.37/39.38	0.11	0.490
rs36051594	23201	Intron 14	AA/GA/GG	4/60/688	0.044	168.28/175.52/171.81	66.98/42.24/38.33	0.10	0.670
rs1801706	23696	3'UTR-Exon 16	AA/GA/GG	27/205/499	0.176	182.31/174.55/170.61	40.55/41.16/37.48	0.24	0.068
rs289742	23796	3' flanking	CC/CG/GG	129/338/255	0.421	170.01/175/170	37.48/39.02/38.79	0.05	0.650
rs289743	23830	3' flanking	AA/GA/GG	86/298/349	0.315	167.53/170.25/175.33	34.83/38.12/40.06	-0.22	0.036
rs289744	24136	3' flanking	GG/GT/TT	347/293/77	0.306	175.85/169.79/168.35	40.12/38.29/34.07	-0.23	0.030
rs12720875	24499	3' flanking	AA/GA/GG	2/45/701	0.032	126.71/181.43/171.68	31.11/46.49/37.92	0.19	0.500
rs66495554	24669	3' flanking	CC/TC/TT	480/228/31	0.193	175.06/167.2/164.2	40.15/35.78/33.57	-0.35	0.006
rs114646974	24881	3' flanking	AA/AG	721/4	0.003	172.35/130.99	38.75/18.64	-2.33	0.018
rs138161274	24899	3' flanking	CC/GC	696/35	0.027	172.16/177.51	38.32/47.86	0.24	0.484
rs12720874	25064	3' flanking	CC/TC/TT	21/171/515	0.153	169.03/174.77/171.19	39.05/37.21/38.58	0.10	0.460
rs12720916	25218	3' flanking	AA/GA/GG	708/32/1	0.025	172.21/172.85/148.36	39.24/30.5/NA	0.00	0.997
rs289745	25565	3' flanking	GG/GT/TT	36/211/480	0.194	169.6/171.27/173.23	40.48/37.73/39.49	-0.10	0.445

TABLE B1.19. Association results of ApoA1 levels with 104 *CETP* SNPs in African blacks (n=788)

RefSNP ID	Positio	Location	Genotype (GT)	GT Counts	MAF	Adjusted mean of plasma ApoA1	Standart Deviation	Beta	*P*
rs247615	-9210	5' flanking	AA/AG/GG	437/258/40	0.230	137.22/136.18/137.94	26.9/28.49/31.21	-0.16	0.777
rs9989419	-8834	5' flanking	AA/GA/GG	318/334/81	0.340	138.07/136.11/137.49	26.91/28.17/27.15	-0.28	0.574
rs183130	-2610	5' flanking	CC/CT/TT	422/271/45	0.244	134.94/138.17/146.19	26.67/29.31/24.22	1.44	0.008
rs3764261	-648	5' flanking-Promoter	AA/CA/CC	82/308/337	0.323	143.42/136.71/135.95	28.13/28.01/27.12	0.90	0.073
rs148562851	187	5' flanking	AA/AG/GG	715/29/1	0.020	136.35/148.81/167.18	27.73/25.07/NA	4.28	0.008
rs12447924	220	5' flanking	CC/CT/TT	44/227/435	0.224	134.55/137.06/137.69	26.08/26.61/28.77	-0.34	0.547
rs17231506	557	5' flanking	CC/TC/TT	598/139/8	0.105	136.76/136.79/144.78	27.26/28.88/43.48	0.24	0.761
rs12708968	848	5' flanking	CC/TC/TT	2/90/643	0.063	127.19/135.97/136.93	58.05/27.08/27.8	-0.43	0.663
rs4783961	923	5' flanking	AA/GA/GG	158/339/226	0.454	137.87/137.22/135.87	27.76/29.23/26.22	0.32	0.492
rs146122874	950	5' flanking	CC/TC/TT	710/30/2	0.022	136.28/148.48/151	27.81/25.08/21.5	3.73	0.014
rs4783962	1067	5' flanking	CC/CT/TT	600/125/8	0.097	136.82/137.81/132.11	28.25/25.48/26	0.12	0.878
rs17237883	1153	5' flanking	AA/GA/GG	1/44/693	0.031	223.55/137.64/136.63	NA/29.82/27.46	1.45	0.287
rs114856405	1189	5' flanking	AA/CA/CC	4/45/693	0.036	128.75/132.69/137.16	4.75/27.43/27.82	-1.43	0.237
rs1800775	1265	5' flanking	AA/CA/CC	273/346/118	0.395	137.89/136.24/137.12	27.75/28.22/26.49	-0.21	0.666
rs17231520	1856	5' flanking	AA/GA/GG	7/122/615	0.090	150.48/144.71/135.06	27.33/28.31/27.41	3.06	1.75E-04
rs34065661	1964	Exon 1	CC/GC/GG	5/126/626	0.088	156.52/144.35/134.89	29.98/27.96/27.43	3.19	1.14E-04
rs5884	1986	Exon 1	AA/CA/CC	3/92/649	0.065	124.02/135.4/137.06	41.1/27.05/27.82	-0.74	0.439
rs34680782	2089	Intron 1	AA/CA/CC	2/25/712	0.020	124.96/150.25/136.36	17.18/21.82/27.86	3.04	0.060
rs17231534	2133	Intron 1	AA/CA/CC	26/209/507	0.177	134.69/135.73/137.44	29.96/27.15/27.94	-0.52	0.398
rs3816117	2187	Intron 1	CC/CT/TT	271/335/117	0.394	137.55/136.43/137.03	27.52/28.4/26.66	-0.14	0.768
rs711752	2240	Intron 1	AA/GA/GG	46/252/440	0.232	145.39/138.37/135.3	25.97/29.54/26.8	1.33	0.016
rs708272	2317	Intron 1	AA/GA/GG	48/254/437	0.236	144.57/138.25/135.13	26.05/29.49/26.9	1.29	0.018
rs60195610	2692	Intron 1	CC/CT/TT	724/34/1	0.023	136.34/144.45/167.01	27.76/27.37/NA	2.94	0.052
rs9935228	3101	Intron 2	AA/GA/GG	614/115/11	0.091	137.12/134.04/140.52	27.67/27.91/36.83	-0.56	0.479
rs1864163	3262	Intron 2	AA/GA/GG	60/283/379	0.278	137.92/136.14/137.65	29.4/27.66/27.74	-0.19	0.720
rs75313088	3347	Intron 2	AA/GA/GG	4/44/693	0.036	127.88/132.89/137.08	5.49/27.58/27.74	-1.40	0.249
rs5817083	3381	Intron 2	DD/WD/WW	104/366/265	0.393	135.55/137.13/136.83	27.93/27.17/27.88	-0.13	0.788
rs4369653	3581	Intron 2	AA/AG/GG	465/257/28	0.212	137.07/136.25/141.43	28.14/27.36/27.04	0.10	0.861
rs7194225	3686	Intron 2	CC/CG/GG	28/211/489	0.185	139.88/135.22/137.38	26.76/26.37/28.11	-0.23	0.699
rs114908369	4299	Intron 2	CA/CC	38/709	0.025	135.69/136.97	30.59/27.48	-0.47	0.758
rs9929488	4602	Intron 2	CC/GC/GG	162/353/216	0.463	136.06/136.91/137.93	27.04/27.07/29.37	-0.29	0.537
rs12720906	4791	Intron 2	GG/GT/TT	4/41/687	0.034	125.28/134.3/137.21	9.52/26.25/28	-1.21	0.332
rs12720926	4948	Intron 2	AA/AG	716/41	0.027	136.57/135.32	27.63/30.01	-0.45	0.759
rs17237939	4957	Intron 2	CC/CT/TT	676/67/3	0.049	136.82/136.39/138.37	27.7/30.41/28.07	-0.11	0.921
rs35585922	5215	Intron 2	DD/WD/WW	20/171/523	0.149	130.57/138.12/136.59	32.76/28.27/27.82	-0.06	0.935
rs7203984	5288	Intron 2	AA/CA/CC	137/358/230	0.438	133.93/137.22/137.76	28.08/27.65/28.1	-0.58	0.234
rs11508026	5358	Intron 2	AA/AG	716/41	0.027	136.79/135.67	27.78/28.76	-0.38	0.794
rs80296794	5375	Intron 2	TC/TT	32/722	0.021	135.32/136.73	34.32/27.56	-0.57	0.729
rs112236143	5593	Intron 2	CA/CC	29/690	0.020	141.98/136.72	26.65/27.87	1.76	0.310
rs708273	5979	Intron 2	AA/AG/GG	8/131/599	0.100	130.12/136.76/136.85	26.92/27.51/28.02	-0.25	0.750
rs17231583	5990	Intron 2	CC/GC/GG	3/23/709	0.020	122.08/134.31/136.82	9.75/22.77/27.87	-1.32	0.399
rs142058276	6022	Intron 2	II/WI/WW	3/115/615	0.082	130.84/141.89/135.88	4.4/29.06/27.52	1.68	0.057
rs17231590	6221	Intron 2	AA/AG/GG	672/80/4	0.058	136.7/136.1/139.36	27.72/29.28/22.92	-0.10	0.923
rs17237953	6239	Intron 2	GG/GT/TT	676/53/3	0.039	136.74/134.91/185.8	27.53/30.96/36.62	0.97	0.411
rs35619327	6251	Intron 2	CC/TC	699/35	0.023	136.78/141.35	27.94/24.84	1.56	0.325
rs820299	6314	Intron 2	AA/AG/GG	185/375/176	0.495	136.89/137.38/136.75	26.01/28/28.08	-0.03	0.942
rs17237967	6427	Intron 2	AA/GA/GG	4/41/663	0.035	132.83/133.51/136.87	45.43/32.45/27.51	-1.08	0.389
rs8045855	6725	Intron 2	AA/AT/TT	242/348/135	0.423	135.04/137.53/137.21	26.49/28.75/28.22	0.42	0.390
rs12720922	6914	Intron 2	AA/GA/GG	89/341/304	0.352	133.42/139.5/135.64	24.34/28.81/27.14	0.13	0.788
rs12708969	7616	Intron 2	AA/CA/CC	13/123/568	0.106	140.3/134.49/137.42	34.29/27.67/27.54	-0.51	0.499
rs9924087	8274	Intron 2	AA/GA/GG	45/207/476	0.207	134.3/138.94/137.05	28.49/27.1/27.8	0.04	0.938
rs12597002	8436	Intron 2	AA/CA/CC	6/132/606	0.097	144.67/136.48/137.18	14.93/27.59/27.73	0.03	0.968
rs12720863	8742	Intron 2	AA/GA/GG	709/33/1	0.023	136.82/134.57/223.51	27.46/30.16/NA	0.81	0.600
rs9939224	8764	Intron 2	GG/GT/TT	300/343/91	0.356	135.89/138.87/133.58	27.21/28.87/24.72	0.02	0.962
rs11076174	9178	Intron 2	CC/TC/TT	10/177/551	0.132	123.43/135.84/137.61	26.07/26.22/28.18	-0.93	0.190
rs13306230	9282	Intron 2	CA/CC	2/740	0.001	139.52/136.8	10.68/27.79	1.09	0.866
rs12708971	9493	Intron 3	CC/CT/TT	3/21/710	0.019	129.69/134.88/137.07	5.81/23.62/28.01	-0.83	0.608
rs891141	9755	Intron 4	AA/AC/CC	577/164/17	0.130	135.8/139.43/134.56	27.27/28.96/33.18	0.71	0.298
CTPp9841	9841	Intron 4	AG/GG	1/743	0.001	90.84/136.86	NA/27.72	-15.63	0.087
rs34716057	9878	Exon 5	AA/GA/GG	2/48/705	0.034	138.91/137.17/136.58	20.86/30.16/27.72	0.22	0.865
rs891143	10012	Intron 5	CC/TC/TT	605/123/5	0.090	136.15/141.03/133.86	27.38/30.06/6.26	1.28	0.126
rs12720862	10779	Intron 5	AA/GA/GG	586/147/10	0.112	136.15/139.4/137.58	27.21/29.78/26.5	0.85	0.255
rs7205804	10921	Intron 5	AA/GA/GG	11/123/614	0.097	144.38/135.32/136.9	36.54/25.96/28.12	-0.02	0.980
rs12708973	10934	Intron 5	AA/AG	751/14	0.009	136.8/127.01	27.82/22.63	-3.18	0.196
rs148134355	10943	Intron 5	GA/GG	7/726	0.005	123.16/137.04	34.57/27.68	-4.75	0.171
rs34611098	10983	Exon 6	AG/GG	2/743	0.001	143.68/136.72	5.3/27.78	2.48	0.701
rs12720925	11456	Intron 7	CC/TC/TT	1/58/680	0.042	123.74/134.84/136.99	NA/28.2/27.76	-0.82	0.499
rs1532624	11510	Intron 7	AA/CA/CC	10/124/609	0.097	141.42/135.33/137.17	34.22/25.98/27.98	-0.25	0.745
rs12720871	11795	Intron 7	CC/CG/GG	642/83/6	0.066	136.97/137.84/132.38	27.96/28.3/15.57	0.06	0.950

Table B1.19. Continued

RefSNP ID	Positio	Location	Genotype (GT)	GT Counts	MAF	Adjusted mean of plasma ApoA1	Standart Deviation	Beta	*P*
rs12720872	11913	Intron 7	CC/TC/TT	550/176/12	0.135	136.01/139.19/140.75	26.87/29.84/38.14	0.93	0.184
rs11076175	12409	Intron 8	AA/AG/GG	423/264/48	0.243	136.69/138.8/131.05	27.82/27.84/24.94	-0.14	0.797
rs7499892	12621	Intron 8	CC/CT/TT	284/337/105	0.377	137.98/137.58/134.08	28.52/27.67/26.29	-0.51	0.304
rs289713	12860	Intron 8	AA/AT/TT	150/337/225	0.451	134.87/136.62/138.11	26.38/28.69/28.52	-0.52	0.282
rs191754368	12913	Intron 8	CC/TC/TT	722/24/2	0.019	136.42/150.11/124.93	27.78/22.23/17.18	2.94	0.073
rs9930761	13223	Intron 8	CC/CT/TT	14/184/522	0.148	133.95/138.72/136.59	28.26/28.02/28.01	0.40	0.563
rs35878799	13279	Exon 9	CT/TT	16/722	0.011	134.28/136.82	28.53/27.83	-0.85	0.713
rs5883	13384	Exon 9	CC/TC/TT	526/203/13	0.155	136.7/137.05/140.16	27.89/27.85/24.47	0.23	0.729
rs11076176	13477	Intron 9	GG/GT/TT	119/352/263	0.403	131.95/137.52/137.95	29.27/27.01/28.15	-0.84	0.086
rs289714	13482	Intron 9	AA/GA/GG	145/362/221	0.447	137.47/138.36/134.72	28.95/27.54/27.77	0.53	0.274
rs158479	14079	Intron 9	AA/GA/GG	72/331/332	0.325	139.17/135.99/137.23	24.16/29.02/27.44	0.05	0.921
rs12720892	14192	Intron 9	AA/GA/GG	3/58/704	0.043	114.08/133.06/136.95	9.37/29.27/27.52	-1.77	0.119
rs158480	14258	Intron 9	AA/GA/GG	146/336/226	0.445	136.64/137.33/134.86	29.21/28.04/26.82	0.33	0.492
CTPp14448del4	14448	Intron 9	WD/WW	27/719	0.018	135.38/136.68	26.24/27.66	-0.42	0.816
rs289715	14539	Intron 9	AA/TA/TT	37/255/438	0.224	135.67/139.18/135.67	30.11/27.58/27.83	0.64	0.267
rs2303789	15226	Intron 10	GG/GT/TT	4/85/653	0.065	122.4/134.55/137.24	17.42/28.61/27.71	-1.18	0.226
rs289716	15407	Intron 10	AA/AT/TT	167/357/203	0.476	134.12/138.13/137.02	27.89/27.79/28.34	-0.44	0.361
rs289717	15419	Intron 10	AA/GA/GG	12/192/534	0.147	138.47/136.7/136.93	17.68/29.78/27.31	-0.01	0.985
rs12708976	15542	Intron 10	CC/TC/TT	680/62/2	0.047	137.21/133.71/136.11	27.58/28.87/14.64	-1.06	0.353
rs12720942	15639	Intron 10	AA/GA/GG	654/87/4	0.066	137.25/134.89/122.56	27.64/28.51/17.42	-1.07	0.265
rs736274	15800	Intron 10	AA/AT/TT	738/23/1	0.016	136.88/132.41/92.5	27.73/28.79/NA	-2.39	0.180
rs12720937	15913	Intron 10	CC/GC/GG	642/85/4	0.066	137.35/134.83/122.42	27.83/28.83/17.42	-1.13	0.247
rs289718	15963	Intron 10	CC/CT/TT	237/343/147	0.438	137.29/137.98/133.59	28.47/27.04/29	-0.52	0.272
rs289719	15972	Intron 10	AA/GA/GG	181/378/189	0.493	136.38/139.03/132.48	29.57/26.41/28.8	0.66	0.164
rs2033254	16016	Intron 10	CC/TC/TT	82/298/351	0.317	135.99/135.85/137.95	25.65/28.38/27.65	-0.44	0.375
rs112205272	16146	Intron 10	AA/GA/GG	4/81/654	0.063	122.52/134.15/137.27	17.42/29.17/27.62	-1.31	0.184
rs112409939	16363	Intron 10	AA/GA/GG	654/83/4	0.064	137.3/134.69/122.55	27.6/28.96/17.42	-1.16	0.235
rs71387147	16413	Intron 10	GT/TT	35/650	0.025	136.31/137.57	32.69/27.92	-0.52	0.748
rs1968905	16979	Intron 10	GG/GT/TT	295/363/88	0.360	135.11/138.55/135.3	27.78/27.86/27.43	0.38	0.456
rs12720903	17154	Intron 10	AA/GA/GG	4/93/661	0.068	140.98/136.83/136.77	35.82/27.19/27.73	0.13	0.893
rs4784744	17216	Intron 10	AA/GA/GG	7/134/595	0.100	141.02/136.31/137	18.25/29.79/27.33	-0.08	0.919
rs291044	17483	Intron 10	AA/GA/GG	7/136/591	0.102	141.04/136.08/136.92	18.25/29.77/27.45	-0.12	0.881
rs114486472	17575	Intron 10	AA/AG/GG	2/25/707	0.020	126.98/130.76/137.15	6.86/23.89/28.01	-1.96	0.229
rs34426213	17918	Intron 10	CC/CT/TT	669/56/3	0.042	136.43/141.74/145.98	27.91/28.63/10.97	1.75	0.132
rs891144	17970	Intron 10	AA/GA/GG	38/242/474	0.215	136.98/136.03/137.07	27.99/28.02/27.82	-0.19	0.734
rs12708979	18388	Intron 11	AA/GA/GG	2/42/718	0.030	124.97/141.54/136.52	17.18/24.69/27.9	1.11	0.402
rs12708980	18413	Intron 11	AA/AC/CC	320/287/98	0.342	137.44/136.09/136.57	28.2/28.41/25.94	-0.21	0.668
rs12720889	18597	Intron 11	AA/AT/TT	477/236/33	0.204	136.82/136.6/136.52	27.98/27.69/24.81	-0.05	0.929
rs291043	18733	Intron 11	AA/AG/GG	626/111/10	0.086	136.39/135.64/148	27.13/29.35/36.3	0.32	0.688
rs114203109	18970	Intron 11	GA/GG	63/664	0.042	134.82/136.89	27.63/27.9	-0.68	0.573
rs145189439	19734	Intron 11	CC/TC/TT	3/69/677	0.052	113.81/133.24/137.02	9.37/28.79/27.78	-1.68	0.118
rs4784745	20910	Intron 11	AA/AG/GG	627/101/6	0.076	136.76/137.13/138.22	27.32/31.42/18.96	0.10	0.906
rs34855278	21111	Exon 12	GA/GG	23/734	0.015	132.41/136.78	28.79/27.83	-1.46	0.450
rs114948973	21454	Intron 12	AA/AG/GG	1/25/701	0.019	154.59/142.65/136.62	NA/25.77/27.89	2.16	0.211
rs7195984	21498	Intron 12	AA/GA/GG	498/188/27	0.169	135.7/138.42/147.81	27.53/28.36/28.43	1.35	0.031
rs7196174	21579	Intron 12	GG/GT/TT	640/94/4	0.070	136.88/134.57/155.14	27.84/28.32/16.12	-0.19	0.842
rs1800774	21580	Intron 12	CC/TC/TT	455/237/42	0.217	137.78/135.41/135.21	27.57/28.82/24.73	-0.61	0.281
rs5882	22127	Exon 14	AA/GA/GG	83/292/356	0.310	135.44/137.44/136.87	31.04/28.63/26.5	-0.13	0.789
rs5886	22162	Exon 14	AA/GA/GG	4/112/621	0.082	149.24/134.48/137	22.78/28.17/27.77	-0.46	0.603
rs289740	22985	Intron 14	CC/CT/TT	11/151/571	0.117	143.03/141.03/135.44	27.67/28.56/27.53	1.70	0.021
rs36051594	23201	Intron 14	AA/GA/GG	4/59/700	0.044	142.44/138.45/136.48	25.82/24.62/28.05	0.77	0.484
rs1801706	23696	3'UTR-Exon 16	AA/GA/GG	27/204/506	0.176	138.31/137.7/136.88	25.85/27.35/27.85	0.27	0.660
rs289742	23796	3' flanking	CC/CG/GG	135/340/253	0.421	138.46/136.44/136.9	27.05/27.11/29.18	0.22	0.648
rs289743	23830	3' flanking	AA/GA/GG	86/298/355	0.315	135.13/137.1/137.29	31.09/27.91/26.75	-0.29	0.553
rs289744	24136	3' flanking	GG/GT/TT	352/293/77	0.306	137.1/136.45/136.73	26.86/27.27/31.59	-0.14	0.781
rs12720875	24499	3' flanking	AA/GA/GG	2/44/713	0.032	124.98/141.99/136.44	17.18/25.1/27.91	1.28	0.328
rs66495554	24669	3' flanking	CC/TC/TT	488/227/31	0.193	138.35/134.03/134.71	27.78/27.68/24.65	-1.08	0.067
rs114646974	24881	3' flanking	AA/AG	725/5	0.003	136.92/111.78	27.84/16.13	-8.35	0.042
rs138161274	24899	3' flanking	CC/GC/GG	697/39/1	0.027	136.92/137.85/84.74	27.83/27.21/NA	-0.55	0.703
rs12720874	25064	3' flanking	CC/TC/TT	22/175/518	0.153	136.24/136.45/136.72	32.73/27.19/28.06	-0.08	0.897
rs12720916	25218	3' flanking	AA/GA/GG	712/33/2	0.025	137.14/130.48/126.93	27.78/26.36/6.86	-2.09	0.152
rs289745	25565	3' flanking	GG/GT/TT	35/214/484	0.194	134.22/139.26/136.07	31.3/25.77/28.56	0.43	0.459

TABLE B1.20. Association results of ApoB levels with 104 *CETP* SNPs in African blacks (n=788)

RefSNP ID	Position	Location	Genotype (GT)	GT Counts	MAF	Adjusted mean of plasma ApoB	Standart Deviation	Beta	*P*
rs247615	-9210	5' flanking	AA/AG/GG	439/257/39	0.230	66.08/67.91/64.43	21.62/21.95/24.77	0.25	0.692
rs9989419	-8834	5' flanking	AA/GA/GG	317/335/81	0.340	66.04/66.89/68.25	21.83/21.82/20.67	0.51	0.370
rs183130	-2610	5' flanking	CC/CT/TT	422/271/45	0.244	67.49/64.82/66.86	21.61/22.12/23.41	-0.77	0.221
rs3764261	-648	5' flanking	AA/CA/CC	81/309/337	0.323	67.87/65.44/67.98	20.23/21.86/22	-0.42	0.455
rs148562851	187	5' flanking	AA/AG/GG	715/29/1	0.020	66.58/65.27/75.73	21.91/21.53/NA	-0.26	0.887
rs12447924	220	5' flanking	CC/CT/TT	44/227/435	0.224	69.21/66.21/66.81	19.72/20.72/22.89	0.22	0.735
rs17231506	557	5' flanking	CC/TC/TT	597/140/8	0.105	66.51/67.01/62.33	21.66/22.99/18.32	-0.04	0.962
rs12708968	848	5' flanking	CC/TC/TT	2/89/644	0.063	79.85/67.69/66.27	22.64/18.83/22.33	1.01	0.369
rs4783961	923	5' flanking	AA/GA/GG	160/336/227	0.454	65.65/65.85/69.22	21.48/21.5/21.98	-0.93	0.074
rs146122874	950	5' flanking	CC/TC/TT	710/30/2	0.022	66.56/65.74/62.56	21.84/22.75/14.39	-0.54	0.755
rs4783962	1067	5' flanking	CC/CT/TT	599/126/8	0.097	66.99/64.76/58.49	22.01/19.98/20.96	-1.27	0.159
rs17237883	1153	5' flanking	GA/GG	44/694	0.031	69.6/66.25	24.47/21.62/	1.57	0.327
rs114856405	1189	5' flanking	AA/CA/CC	4/46/692	0.036	71.78/67.39/66.35	18.23/20.23/21.94	0.80	0.557
rs1800775	1265	5' flanking	AA/CA/CC	273/345/119	0.395	66.73/65.64/68.5	20.68/22.26/23.16	0.21	0.702
rs17231520	1856	5' flanking	AA/GA/GG	7/121/616	0.090	58.52/64.96/67.06	14.7/22.12/21.75	-1.26	0.171
rs34065661	1964	Exon 1	CC/GC/GG	5/125/628	0.088	64.91/65.08/67.15	7.5/22.15/21.87	-0.96	0.308
rs5884	1986	Exon 1	AA/CA/CC	3/91/650	0.065	81.34/67.04/66.38	16.85/19.19/22.23	0.81	0.457
rs34680782	2089	Intron 1	AA/CA/CC	2/26/711	0.020	62.65/69.63/66.38	32.41/18.8/21.97	1.03	0.569
rs17231534	2133	Intron 1	AA/CA/CC	28/205/509	0.177	69.45/63.93/67.62	19.35/21.47/21.98	-0.85	0.214
rs3816117	2187	Intron 1	CC/CT/TT	271/334/118	0.394	66.77/66.11/69.13	20.72/21.83/23.21	0.37	0.494
rs711752	2240	Intron 1	AA/GA/GG	46/252/440	0.232	66.27/65.8/67.23	18.89/22.55/21.76	-0.46	0.460
rs708272	2317	Intron 1	AA/GA/GG	48/254/437	0.236	65.46/65.7/67.27	19.19/22.39/21.77	-0.60	0.336
rs60195610	2692	Intron 1	CC/CT/TT	725/33/1	0.023	66.68/65.06/75.59	21.81/24.63/NA	-0.54	0.757
rs9935228	3101	Intron 2	AA/GA/GG	615/114/11	0.091	66.08/68.15/72.86	22.25/19.62/23.73	1.25	0.164
rs1864163	3262	Intron 2	AA/GA/GG	61/283/378	0.278	72.52/67.08/66.01	24.66/21.95/20.69	1.11	0.060
rs75313088	3347	Intron 2	AA/GA/GG	4/45/692	0.036	64.14/68.22/66.48	12.51/20.89/22.01	0.55	0.691
rs5817083	3381	Intron 2	DD/WD/WW	106/364/265	0.393	66.71/65.82/67.99	20.09/21.8/22.5	-0.46	0.415
rs4369653	3581	Intron 2	AA/AG/GG	463/258/29	0.212	66.46/66.67/70.55	22.55/20.83/20.83	0.48	0.470
rs7194225	3686	Intron 2	CC/CG/GG	30/208/490	0.185	70.12/65.2/67.06	21.58/21.04/22.08	-0.17	0.799
rs114908369	4299	Intron 2	CA/CC	38/709	0.025	68.53/66.54	23.36/21.68	0.93	0.587
rs9929488	4602	Intron 2	CC/GC/GG	164/352/215	0.463	68.08/65.48/67.33	23.61/20.95/22.11	0.09	0.860
rs12720906	4791	Intron 2	GG/GT/TT	4/42/686	0.034	57.36/64.75/66.62	19.95/25.01/21.71	-1.32	0.345
rs12720926	4948	Intron 2	AA/AG	717/40	0.027	67.11/59.41	21.98/19.79	-3.73	0.026
rs17237939	4957	Intron 2	CC/CT/TT	679/64/3	0.049	66.38/70.4/58.17	22.02/20.89/37.77	1.31	0.296
rs35585922	5215	Intron 2	DD/WD/WW	22/169/523	0.149	73.2/64.72/66.89	18.74/20.7/22.19	0.00	0.995
rs7203984	5288	Intron 2	AA/CA/CC	140/357/228	0.438	67.5/66.58/66.65	19.74/21.53/23.36	0.24	0.666
rs11508026	5358	Intron 2	AA/AG	717/40	0.027	67.06/59.85	21.98/19.41	-3.49	0.038
rs80296794	5375	Intron 2	TC/TT	30/724	0.021	74.57/66.53	21.76/21.77	3.93	0.041
rs112236143	5593	Intron 2	CA/CC	27/692	0.020	66.25/67.02	25.98/21.47	-0.49	0.807
rs708273	5979	Intron 2	AA/AG/GG	8/133/597	0.100	77.47/65.1/66.59	21.02/20.46/22.07	0.03	0.970
rs17231583	5990	Intron 2	CC/GC/GG	3/24/708	0.020	51.27/69.32/66.56	16.97/22.54/21.84	-0.33	0.851
rs142058276	6022	Intron 2	II/WI/WW	3/114/616	0.082	56.49/63.02/67.23	15.09/22.08/21.88	-2.13	0.034
rs17231590	6221	Intron 2	AA/AG/GG	675/77/4	0.058	66.41/68.92/60.12	21.85/21.9/30.92	0.71	0.533
rs17237953	6239	Intron 2	GG/GT/TT	679/53/2	0.039	66.1/70.29/60.46	21.87/22.88/29.17	1.56	0.263
rs35619327	6251	Intron 2	CC/TC	701/33	0.023	66.81/64.29	21.46/27.05	-1.45	0.431
rs820299	6314	Intron 2	AA/AG/GG	184/374/178	0.495	65.28/66.46/68.77	23.98/20.69/21.53	0.90	0.099
rs17237967	6427	Intron 2	AA/GA/GG	4/39/666	0.035	77.06/71.01/66.26	18.54/21.21/21.89	2.45	0.088
rs8045855	6725	Intron 2	AA/AT/TT	242/349/135	0.423	67.69/65.47/67.75	20.11/23.29/21.8	-0.18	0.748
rs12720922	6914	Intron 2	AA/GA/GG	90/340/304	0.352	67.93/65.1/67.87	22.66/22.28/20.98	-0.43	0.453
rs12708969	7616	Intron 2	AA/CA/CC	13/122/569	0.106	74.81/65.97/66.57	19.09/19.9/22.73	0.51	0.564
rs9924087	8274	Intron 2	AA/GA/GG	46/207/475	0.207	69.58/67.01/66.44	22.98/21.03/22.5	0.56	0.378
rs12597002	8436	Intron 2	AA/CA/CC	6/134/605	0.097	67.58/66.11/66.54	14.71/20.7/22.25	-0.07	0.938
rs12720863	8742	Intron 2	AA/GA	710/33	0.023	66.48/69.83	21.81/22.03	1.65	0.370
rs9939224	8764	Intron 2	GG/GT/TT	300/342/92	0.356	67.99/65.31/67.46	20.82/22.52/22.45	-0.51	0.368
rs11076174	9178	Intron 2	CC/TC/TT	10/176/551	0.132	63/66.83/66.53	19.68/23.16/21.56	-0.08	0.917
rs13306230	9282	Intron 2	CA/CC	2/740	0.001	103.03/66.35	23.48/21.76	17.41	0.017
rs12708971	9493	Intron 3	CC/CT/TT	3/22/709	0.019	64.34/68.94/66.74	14.42/23.54/21.7	0.52	0.770
rs891141	9755	Intron 4	AA/AC/CC	579/163/16	0.130	67.49/63.87/64.85	21.76/21.65/29.12	-1.45	0.062
CTPp9841	9841	Intron 4	AG/GG	1/743	0.001	118.5/66.46	NA/21.78	24.04	0.020
rs34716057	9878	Exon 5	AA/GA/GG	2/47/706	0.034	72.68/66.41/66.68	10.18/24.4/21.79	0.02	0.987
rs891143	10012	Intron 5	CC/TC/TT	606/122/5	0.090	67.28/64.18/64.1	21.8/22.18/5.51	-1.40	0.140
rs12720862	10779	Intron 5	AA/GA/GG	589/144/10	0.112	66.03/68.76/65.85	21.76/22.01/24.02	1.00	0.240
rs7205804	10921	Intron 5	AA/GA/GG	11/122/615	0.097	59.64/67.36/66.53	15.32/21.63/22.12	-0.17	0.848
rs12708973	10934	Intron 5	AA/AG	751/14	0.009	66.7/61.26	21.81/21.61	-2.64	0.342
rs148134355	10943	Intron 5	GA/GG	7/726	0.005	70.85/66.74	24.81/21.73	2.04	0.603
rs34611098	10983	Exon 6	AG/GG	2/743	0.001	97.22/66.39	31.08/21.74	14.64	0.045
rs12720925	11456	Intron 7	CC/TC/TT	1/60/678	0.042	70.09/69.13/66.37	NA/22.57/21.81	1.32	0.329
rs1532624	11510	Intron 7	AA/CA/CC	10/123/610	0.097	60.25/67.16/66.63	15.61/20.91/22.09	-0.19	0.834
rs12720871	11795	Intron 7	CC/CG/GG	641/84/6	0.066	66.65/67.37/60.43	21.59/23.92/15.91	-0.13	0.901
rs12720872	11913	Intron 7	CC/TC/TT	554/173/11	0.135	65.75/69.36/64.27	21.63/22.45/23.62	1.26	0.118
rs11076175	12409	Intron 8	AA/AG/GG	422/265/48	0.243	65.87/68.04/65.83	21.19/22.81/22.61	0.47	0.446
rs7499892	12621	Intron 8	CC/CT/TT	282/337/107	0.377	65.87/67.57/67.46	20.34/22.29/24.01	0.44	0.428
rs289713	12860	Intron 8	AA/AT/TT	153/338/221	0.451	66.53/67.65/66.39	18.8/21.81/23.04	0.14	0.786

Table B1.20. Continued

RefSNP ID	Position	Location	Genotype (GT)	GT Counts	MAF	Adjusted mean of plasma ApoB	Standart Deviation	Beta	*P*
rs191754368	12913	Intron 8	CC/TC/TT	721/25/2	0.019	66.39/70.4/62.64	21.92/18.69/32.41	1.29	0.482
rs9930761	13223	Intron 8	CC/CT/TT	16/182/522	0.148	74.65/66.27/66.52	16.19/20.2/22.27	0.58	0.447
rs35878799	13279	Exon 9	CT/TT	16/722	0.011	56.64/66.72	27.54/21.7	-5.11	0.050
rs5883	13384	Exon 9	CC/TC/TT	526/201/15	0.155	66.74/65.15/76.07	22.26/20.96/16.32	0.08	0.916
rs11076176	13477	Intron 9	GG/GT/TT	120/350/264	0.403	66.1/67.79/64.51	24/21.98/20.56	0.58	0.291
rs289714	13482	Intron 9	AA/GA/GG	146/360/222	0.447	66.9/66.74/65.85	19.53/21.69/23.62	0.33	0.541
rs158479	14079	Intron 9	AA/GA/GG	74/330/329	0.325	69.08/66.48/66.4	17.85/21.49/22.89	0.49	0.404
rs12720892	14192	Intron 9	AA/GA/GG	3/60/702	0.043	76.21/69.29/66.38	8.71/21.49/21.93	1.63	0.199
rs158480	14258	Intron 9	AA/GA/GG	144/337/226	0.445	65.42/67.45/65.85	23.66/21.39/21.97	-0.03	0.957
CTPp14448del4	14448	Intron 9	WD/WW	28/718	0.018	68.97/66.4	23.58/21.76	1.18	0.554
rs289715	14539	Intron 9	AA/TA/TT	36/255/439	0.224	65.9/65.49/67.31	21.4/21.57/21.94	-0.65	0.314
rs2303789	15226	Intron 10	GG/GT/TT	5/86/651	0.065	71.12/67.06/66.4	11.25/22.96/21.8	0.50	0.642
rs289716	15407	Intron 10	AA/AT/TT	170/355/202	0.476	67.37/66.2/67.12	21.72/21.94/21.4	0.04	0.943
rs289717	15419	Intron 10	AA/GA/GG	12/195/531	0.147	75.66/66.24/66.4	20.92/20.58/22.3	0.51	0.514
rs12708976	15542	Intron 10	CC/TC/TT	678/63/3	0.047	66.62/65.67/65.77	21.82/22.76/7.09	-0.41	0.742
rs12720942	15639	Intron 10	AA/GA/GG	652/88/5	0.066	66.47/66.69/71.08	21.78/22.95/11.25	0.31	0.768
rs736274	15800	Intron 10	AA/AT/TT	739/23/1	0.016	66.77/61.62/85.41	21.95/18.78/NA	-1.40	0.491
rs12720937	15913	Intron 10	CC/GC/GG	640/86/5	0.066	66.78/66.48/71.12	21.64/23.15/11.25	0.09	0.929
rs289718	15963	Intron 10	CC/CT/TT	237/340/150	0.438	66.79/65.54/67.92	21.47/21.95/22.06	0.17	0.747
rs289719	15972	Intron 10	AA/GA/GG	181/375/192	0.493	66.75/66.27/67.52	20.89/22.26/22.52	-0.18	0.744
rs2033254	16016	Intron 10	CC/TC/TT	83/297/351	0.317	66.3/66.71/66.72	22.49/22.3/21.03	-0.10	0.863
rs112205272	16146	Intron 10	AA/GA/GG	5/82/652	0.063	71.05/67.12/66.5	11.25/23.59/21.74	0.46	0.670
rs112409939	16363	Intron 10	AA/GA/GG	652/84/5	0.064	66.44/65.69/71.09	21.77/22.59/11.25	-0.04	0.968
rs71387147	16413	Intron 10	GT/TT	35/649	0.025	68.31/67.04	23.41/21.68	0.62	0.727
rs1968905	16979	Intron 10	GG/GT/TT	296/361/89	0.360	67.57/65.68/67.56	22.31/21.96/20.23	-0.27	0.639
rs12720903	17154	Intron 10	AA/GA/GG	4/93/661	0.068	64.47/67.08/66.7	22.56/24.13/21.58	0.03	0.976
rs4784744	17216	Intron 10	AA/GA/GG	7/136/593	0.100	74.85/67.12/66.51	15.57/21.09/22.06	0.67	0.455
rs291044	17483	Intron 10	AA/GA/GG	7/138/589	0.102	74.82/66.9/66.38	15.57/20.33/22.14	0.65	0.467
rs114486472	17575	Intron 10	AA/AG/GG	2/25/707	0.020	58.79/70.46/66.54	11.96/22.8/21.81	1.02	0.577
rs34426213	17918	Intron 10	CC/CT/TT	668/56/3	0.042	66.75/67.53/57.52	21.65/24.75/11.31	-0.17	0.898
rs891144	17970	Intron 10	AA/GA/GG	38/244/472	0.215	70.78/65.3/67.26	23.33/22.71/21.35	-0.15	0.816
rs12708979	18388	Intron 11	AA/GA/GG	2/43/717	0.030	62.66/69.86/66.49	32.41/21.77/21.84	1.21	0.415
rs12708980	18413	Intron 11	AA/AC/CC	321/287/97	0.342	67.27/67.59/63.54	21.29/22.38/22.9	-0.66	0.236
rs12720889	18597	Intron 11	AA/AT/TT	476/236/34	0.204	66.86/65.19/72.36	22.45/21.06/17.37	0.17	0.792
rs291043	18733	Intron 11	AA/AG/GG	624/112/10	0.086	66.36/65.93/76.66	21.68/21.79/24.36	0.55	0.543
rs114203109	18970	Intron 11	GA/GG	62/665	0.042	63.15/67.16	23.33/21.77	-1.98	0.150
rs145189439	19734	Intron 11	CC/TC/TT	4/70/675	0.052	73.54/67.81/66.55	8.74/22.92/21.94	0.83	0.483
rs4784745	20910	Intron 11	AA/AG/GG	626/102/6	0.076	66.48/67.33/78.22	21.75/22.62/13.56	0.92	0.357
rs34855278	21111	Exon 12	GA/GG	23/734	0.015	61.63/66.83	18.78/21.99	-2.48	0.259
rs114948973	21454	Intron 12	AA/AG/GG	1/25/701	0.019	73.67/69.39/66.77	NA/24.15/21.72	1.30	0.502
rs7195984	21498	Intron 12	AA/GA/GG	498/189/27	0.169	66.73/65.05/68.9	21.59/21.92/25.09	-0.29	0.679
rs7196174	21579	Intron 12	GG/GT/TT	640/94/4	0.070	66.35/67.91/71.48	21.67/23.31/14.07	0.83	0.434
rs1800774	21580	Intron 12	CC/TC/TT	457/235/42	0.217	66.82/66.33/63.94	21.53/22.73/21.04	-0.48	0.453
rs5882	22127	Exon 14	AA/GA/GG	82/291/358	0.310	67.44/66.75/66.22	23.36/21.72/21.62	0.28	0.626
rs5886	22162	Exon 14	AA/GA/GG	4/113/620	0.082	71.72/66.43/66.7	15.34/22.91/21.7	0.06	0.955
rs289740	22985	Intron 14	CC/CT/TT	11/151/571	0.117	60.31/66.51/66.63	24.91/21.7/21.86	-0.46	0.577
rs36051594	23201	Intron 14	AA/GA/GG	4/60/699	0.044	66.86/69.46/66.48	22.61/19.64/22.06	1.21	0.329
rs1801706	23696	3'UTR-Exon 16	AA/GA/GG	28/204/505	0.176	71.1/66.51/66.62	18.57/21.12/22.1	0.46	0.505
rs289742	23796	3' flanking	CC/CG/GG	134/343/251	0.421	64.29/68.05/66.26	20.2/22.25/21.76	-0.27	0.613
rs289743	23830	3' flanking	AA/GA/GG	85/297/357	0.315	66.03/67.14/66.37	22.36/21.8/21.53	0.06	0.913
rs289744	24136	3' flanking	GG/GT/TT	355/292/76	0.306	66.53/66.56/67.09	22.25/21.27/22.93	0.10	0.859
rs12720875	24499	3' flanking	AA/GA/GG	2/45/712	0.032	62.65/70.62/66.48	32.41/21.08/21.92	1.57	0.286
rs66495554	24669	3' flanking	CC/TC/TT	489/226/31	0.193	67.06/66.08/62.54	22.06/21.41/20.87	-0.71	0.286
rs114646974	24881	3' flanking	AA/AG	727/4	0.003	66.77/55.58	21.82/17.96	-5.41	0.296
rs138161274	24899	3' flanking	CC/GC/GG	699/37/1	0.027	66.83/64.09/65.81	21.64/24.88/NA	-1.30	0.433
rs12720874	25064	3' flanking	CC/TC/TT	20/175/521	0.153	60.74/66.53/67.19	18.17/22.63/21.68	-0.79	0.290
rs12720916	25218	3' flanking	AA/GA/GG	712/33/2	0.025	66.61/65.31/58.83	21.87/22.22/11.96	-0.86	0.603
rs289745	25565	3' flanking	GG/GT/TT	35/215/483	0.194	66.63/66.19/67.16	28.35/21.51/21.31	-0.37	0.577

TABLE B1.21. *CETP* 4-SNP sliding window haplotype association results for TG in NHWs (n=623)

Window	Window SNP	Genotype	MAF	Beta	p_value	hap_P
1	rs9989419	AA/GA/GG	0.400	0.027	0.244	0.572
1	rs247617	AA/CA/CC	0.347	-0.024	0.313	NA
1	rs183130	CC/TC/TT	0.347	-0.022	0.340	NA
1	rs6499863	AA/GA/GG	0.172	0.010	0.748	NA
2	rs247617	AA/CA/CC	0.347	-0.024	0.313	0.807
2	rs183130	CC/TC/TT	0.347	-0.022	0.340	NA
2	rs6499863	AA/GA/GG	0.172	0.010	0.748	NA
2	rs12149545	AA/GA/GG	0.330	-0.022	0.356	NA
3	rs183130	CC/TC/TT	0.347	-0.022	0.340	0.701
3	rs6499863	AA/GA/GG	0.172	0.010	0.748	NA
3	rs12149545	AA/GA/GG	0.330	-0.022	0.356	NA
3	rs12708967	CC/CT/TT	0.205	0.042	0.150	NA
4	rs6499863	AA/GA/GG	0.172	0.010	0.748	0.755
4	rs12149545	AA/GA/GG	0.330	-0.022	0.356	NA
4	rs12708967	CC/CT/TT	0.205	0.042	0.150	NA
4	rs3764261	GG/GT/TT	0.328	-0.021	0.405	NA
5	rs12149545	AA/GA/GG	0.330	-0.022	0.356	0.672
5	rs12708967	CC/CT/TT	0.205	0.042	0.150	NA
5	rs3764261	GG/GT/TT	0.328	-0.021	0.405	NA
5	rs17231506	CC/TC/TT	0.343	-0.019	0.420	NA
6	rs12708967	CC/CT/TT	0.205	0.042	0.150	0.611
6	rs3764261	GG/GT/TT	0.328	-0.021	0.405	NA
6	rs17231506	CC/TC/TT	0.343	-0.019	0.420	NA
6	rs12708968	CC/CT/TT	0.082	0.031	0.462	NA
7	rs3764261	GG/GT/TT	0.328	-0.021	0.405	0.712
7	rs17231506	CC/TC/TT	0.343	-0.019	0.420	NA
7	rs12708968	CC/CT/TT	0.082	0.031	0.462	NA
7	rs4783961	AA/AG/GG	0.457	-0.004	0.876	NA
8	rs17231506	CC/TC/TT	0.343	-0.019	0.420	0.528
8	rs12708968	CC/CT/TT	0.082	0.031	0.462	NA
8	rs4783961	AA/AG/GG	0.457	-0.004	0.876	NA
8	rs17245715	CC/CT/TT	0.082	0.031	0.464	NA
9	rs12708968	CC/CT/TT	0.082	0.031	0.462	0.505
9	rs4783961	AA/AG/GG	0.457	-0.004	0.876	NA
9	rs17245715	CC/CT/TT	0.082	0.031	0.464	NA
9	rs4783962	CC/TC/TT	0.194	-0.037	0.213	NA
10	rs4783961	AA/AG/GG	0.457	-0.004	0.876	0.696
10	rs17245715	CC/CT/TT	0.082	0.031	0.464	NA
10	rs4783962	CC/TC/TT	0.194	-0.037	0.213	NA
10	rs1800775	AA/CA/CC	0.489	-0.004	0.864	NA
11	rs17245715	CC/CT/TT	0.082	0.031	0.464	0.493
11	rs4783962	CC/TC/TT	0.194	-0.037	0.213	NA
11	rs1800775	AA/CA/CC	0.489	-0.004	0.864	NA
11	rs17231534	CA/CC	0.045	0.071	0.211	NA
12	rs4783962	CC/TC/TT	0.194	-0.037	0.213	0.450
12	rs1800775	AA/CA/CC	0.489	-0.004	0.864	NA
12	rs17231534	CA/CC	0.045	0.071	0.211	NA
12	rs3816117	CC/CT/TT	0.488	-0.005	0.842	NA
13	rs1800775	AA/CA/CC	0.489	-0.004	0.864	0.728
13	rs17231534	CA/CC	0.045	0.071	0.211	NA
13	rs3816117	CC/CT/TT	0.488	-0.005	0.842	NA
13	rs711752	AA/AG/GG	0.443	-0.016	0.499	NA
14	rs17231534	CA/CC	0.045	0.071	0.211	0.729
14	rs3816117	CC/CT/TT	0.488	-0.005	0.842	NA
14	rs711752	AA/AG/GG	0.443	-0.016	0.499	NA
14	rs5030708	CC/CT	0.031	0.000	0.999	NA
15	rs3816117	CC/CT/TT	0.488	-0.005	0.842	0.456
15	rs711752	AA/AG/GG	0.443	-0.016	0.499	NA
15	rs5030708	CC/CT	0.031	0.000	0.999	NA
15	rs708272	AA/GA/GG	0.442	-0.016	0.493	NA
16	rs711752	AA/AG/GG	0.443	-0.016	0.499	0.770
16	rs5030708	CC/CT	0.031	0.000	0.999	NA
16	rs708272	AA/GA/GG	0.442	-0.016	0.493	NA
16	rs1864163	AA/GA/GG	0.265	0.025	0.336	NA
17	rs5030708	CC/CT	0.031	0.000	0.999	0.811
17	rs708272	AA/GA/GG	0.442	-0.016	0.493	NA
17	rs1864163	AA/GA/GG	0.265	0.025	0.336	NA
17	CTP3412	AA/GA	0.001	0.562	0.166	NA
18	rs708272	AA/GA/GG	0.442	-0.016	0.493	0.306
18	rs1864163	AA/GA/GG	0.265	0.025	0.336	NA
18	CTP3412	AA/GA	0.001	0.562	0.166	NA
18	rs4369653	AA/AG/GG	0.263	-0.019	0.475	NA
19	rs1864163	AA/GA/GG	0.265	0.025	0.336	0.748

Table B1.21. Continued

Window	Window SNP	Genotype	MAF	Beta	p_value	hap_P
19	CTP3412	AA/GA	0.001	0.562	0.166	NA
19	rs4369653	AA/AG/GG	0.263	-0.019	0.475	NA
19	rs7194225	CC/CG/GG	0.089	0.017	0.681	NA
20	CTP3412	AA/GA	0.001	0.562	0.166	0.821
20	rs4369653	AA/AG/GG	0.263	-0.019	0.475	NA
20	rs7194225	CC/CG/GG	0.089	0.017	0.681	NA
20	CTP4559	CC/CT	0.002	-0.077	0.787	NA
21	rs4369653	AA/AG/GG	0.263	-0.019	0.475	0.936
21	rs7194225	CC/CG/GG	0.089	0.017	0.681	NA
21	CTP4559	CC/CT	0.002	-0.077	0.787	NA
21	rs9929488	CC/GC/GG	0.289	0.025	0.329	NA
22	rs7194225	CC/CG/GG	0.089	0.017	0.681	0.737
22	CTP4559	CC/CT	0.002	-0.077	0.787	NA
22	rs9929488	CC/GC/GG	0.289	0.025	0.329	NA
22	rs7203984	AA/CA/CC	0.206	0.025	0.364	NA
23	CTP4559	CC/CT	0.002	-0.077	0.787	0.706
23	rs9929488	CC/GC/GG	0.289	0.025	0.329	NA
23	rs7203984	AA/CA/CC	0.206	0.025	0.364	NA
23	rs11508026	CC/CT/TT	0.472	-0.004	0.859	NA
24	rs9929488	CC/GC/GG	0.289	0.025	0.329	0.783
24	rs7203984	AA/CA/CC	0.206	0.025	0.364	NA
24	rs11508026	CC/CT/TT	0.472	-0.004	0.859	NA
24	rs17231569	DD/WD/WW	0.190	0.023	0.418	NA
25	rs7203984	AA/CA/CC	0.206	0.025	0.364	0.867
25	rs11508026	CC/CT/TT	0.472	-0.004	0.859	NA
25	rs17231569	DD/WD/WW	0.190	0.023	0.418	NA
25	rs708273	AA/AG/GG	0.263	-0.008	0.755	NA
26	rs11508026	CC/CT/TT	0.472	-0.004	0.859	0.502
26	rs17231569	DD/WD/WW	0.190	0.023	0.418	NA
26	rs708273	AA/AG/GG	0.263	-0.008	0.755	NA
26	rs820299	AA/AG/GG	0.357	-0.003	0.910	NA
27	rs17231569	DD/WD/WW	0.190	0.023	0.418	0.517
27	rs708273	AA/AG/GG	0.263	-0.008	0.755	NA
27	rs820299	AA/AG/GG	0.357	-0.003	0.910	NA
27	rs12720922	AA/AG/GG	0.192	0.017	0.541	NA
28	rs708273	AA/AG/GG	0.263	-0.008	0.755	0.604
28	rs820299	AA/AG/GG	0.357	-0.003	0.910	NA
28	rs12720922	AA/AG/GG	0.192	0.017	0.541	NA
28	rs12708969	GG/TG/TT	0.439	-0.012	0.599	NA
29	rs820299	AA/AG/GG	0.357	-0.003	0.910	0.969
29	rs12720922	AA/AG/GG	0.192	0.017	0.541	NA
29	rs12708969	GG/TG/TT	0.439	-0.012	0.599	NA
29	rs60545348	AA/CA/CC	0.269	-0.007	0.787	NA
30	rs12720922	AA/AG/GG	0.192	0.017	0.541	0.968
30	rs12708969	GG/TG/TT	0.439	-0.012	0.599	NA
30	rs60545348	AA/CA/CC	0.269	-0.007	0.787	NA
30	rs9924087	AA/GA/GG	0.090	0.010	0.802	NA
31	rs12708969	GG/TG/TT	0.439	-0.012	0.599	0.872
31	rs60545348	AA/CA/CC	0.269	-0.007	0.787	NA
31	rs9924087	AA/GA/GG	0.090	0.010	0.802	NA
31	rs12597002	AA/AC/CC	0.267	-0.009	0.740	NA
32	rs60545348	AA/CA/CC	0.269	-0.007	0.787	0.914
32	rs9924087	AA/GA/GG	0.090	0.010	0.802	NA
32	rs12597002	AA/AC/CC	0.267	-0.009	0.740	NA
32	rs9926440	CC/CG/GG	0.302	0.023	0.357	NA
33	rs9924087	AA/GA/GG	0.090	0.010	0.802	0.897
33	rs12597002	AA/AC/CC	0.267	-0.009	0.740	NA
33	rs9926440	CC/CG/GG	0.302	0.023	0.357	NA
33	rs9939224	GG/GT/TT	0.205	0.018	0.521	NA
34	rs12597002	AA/AC/CC	0.267	-0.009	0.740	0.987
34	rs9926440	CC/CG/GG	0.302	0.023	0.357	NA
34	rs9939224	GG/GT/TT	0.205	0.018	0.521	NA
34	rs11076174	CC/TC/TT	0.075	0.022	0.612	NA
35	rs9926440	CC/CG/GG	0.302	0.023	0.357	0.859
35	rs9939224	GG/GT/TT	0.205	0.018	0.521	NA
35	rs11076174	CC/TC/TT	0.075	0.022	0.612	NA
35	rs891142	CC/CT	0.002	0.197	0.490	NA
36	rs9939224	GG/GT/TT	0.205	0.018	0.521	0.906
36	rs11076174	CC/TC/TT	0.075	0.022	0.612	NA
36	rs891142	CC/CT	0.002	0.197	0.490	NA
36	rs139040281	AA/CA	0.002	-0.153	0.591	NA
37	rs11076174	CC/TC/TT	0.075	0.022	0.612	0.878
37	rs891142	CC/CT	0.002	0.197	0.490	NA
37	s139040281	AA/CA	0.002	-0.153	0.591	NA
37	rs7205804	AA/AG/GG	0.453	-0.016	0.484	NA

Table B1.21. Continued

Window	Window SNP	Genotype	MAF	Beta	p_value	hap_P
38	rs891142	CC/CT	0.002	0.197	0.490	0.515
38	s139040281	AA/CA	0.002	-0.153	0.591	NA
38	rs7205804	AA/AG/GG	0.453	-0.016	0.484	NA
38	rs12708972	CC/TC	0.009	0.131	0.287	NA
39	s139040281	AA/CA	0.002	-0.153	0.591	0.790
39	rs7205804	AA/AG/GG	0.453	-0.016	0.484	NA
39	rs12708972	CC/TC	0.009	0.131	0.287	NA
39	rs34523084	CC/TC	0.007	-0.124	0.418	NA
40	rs7205804	AA/AG/GG	0.453	-0.016	0.484	0.798
40	rs12708972	CC/TC	0.009	0.131	0.287	NA
40	rs34523084	CC/TC	0.007	-0.124	0.418	NA
40	rs1532624	AA/CA/CC	0.452	-0.016	0.477	NA
41	rs12708972	CC/TC	0.009	0.131	0.287	0.746
41	rs34523084	CC/TC	0.007	-0.124	0.418	NA
41	rs1532624	AA/CA/CC	0.452	-0.016	0.477	NA
41	rs12708974	CC/TC/TT	0.108	0.017	0.634	NA
42	rs34523084	CC/TC	0.007	-0.124	0.418	0.690
42	rs1532624	AA/CA/CC	0.452	-0.016	0.477	NA
42	rs12708974	CC/TC/TT	0.108	0.017	0.634	NA
42	rs117040820	CC/CT	0.016	-0.074	0.418	NA
43	rs1532624	AA/CA/CC	0.452	-0.016	0.477	0.738
43	rs12708974	CC/TC/TT	0.108	0.017	0.634	NA
43	rs117040820	CC/CT	0.016	-0.074	0.418	NA
43	rs12720873	AA/AG/GG	0.039	-0.030	0.609	NA
44	rs12708974	CC/TC/TT	0.108	0.017	0.634	0.547
44	rs117040820	CC/CT	0.016	-0.074	0.418	NA
44	rs12720873	AA/AG/GG	0.039	-0.030	0.609	NA
44	rs148654654	CC/TC	0.007	-0.188	0.167	NA
45	rs117040820	CC/CT	0.016	-0.074	0.418	0.462
45	rs12720873	AA/AG/GG	0.039	-0.030	0.609	NA
45	rs148654654	CC/TC	0.007	-0.188	0.167	NA
45	rs289712	CC/CT/TT	0.265	-0.017	0.531	NA
46	rs12720873	AA/AG/GG	0.039	-0.030	0.609	0.557
46	rs148654654	CC/TC	0.007	-0.188	0.167	NA
46	rs289712	CC/CT/TT	0.265	-0.017	0.531	NA
46	rs11076175	AA/AG/GG	0.184	0.022	0.430	NA
47	rs148654654	CC/TC	0.007	-0.188	0.167	0.664
47	rs289712	CC/CT/TT	0.265	-0.017	0.531	NA
47	rs11076175	AA/AG/GG	0.184	0.022	0.430	NA
47	rs7499892	CC/CT/TT	0.185	0.019	0.496	NA
48	rs289712	CC/CT/TT	0.265	-0.017	0.531	0.778
48	rs11076175	AA/AG/GG	0.184	0.022	0.430	NA
48	rs7499892	CC/CT/TT	0.185	0.019	0.496	NA
48	rs187766748	AA/AG	0.006	-0.123	0.396	NA
49	rs11076175	AA/AG/GG	0.184	0.022	0.430	0.536
49	rs7499892	CC/CT/TT	0.185	0.019	0.496	NA
49	rs187766748	AA/AG	0.006	-0.123	0.396	NA
49	rs187468344	CC/TC	0.006	0.298	0.071	NA
50	rs7499892	CC/CT/TT	0.185	0.019	0.496	0.761
50	rs187766748	AA/AG	0.006	-0.123	0.396	NA
50	rs187468344	CC/TC	0.006	0.298	0.071	NA
50	rs9930761	CC/CT/TT	0.081	0.021	0.622	NA
51	rs187766748	AA/AG	0.006	-0.123	0.396	0.751
51	rs187468344	CC/TC	0.006	0.298	0.071	NA
51	rs9930761	CC/CT/TT	0.081	0.021	0.622	NA
51	rs28381707	GG/GT	0.005	0.021	0.901	NA
52	rs187468344	CC/TC	0.006	0.298	0.071	0.525
52	rs9930761	CC/CT/TT	0.081	0.021	0.622	NA
52	rs28381707	GG/GT	0.005	0.021	0.901	NA
52	rs5883	CC/CT/TT	0.070	0.021	0.646	NA
53	rs9930761	CC/CT/TT	0.081	0.021	0.622	0.933
53	rs28381707	GG/GT	0.005	0.021	0.901	NA
53	rs5883	CC/CT/TT	0.070	0.021	0.646	NA
53	rs289714	CC/CT/TT	0.181	0.023	0.442	NA
54	rs28381707	GG/GT	0.005	0.021	0.901	0.851
54	rs5883	CC/CT/TT	0.070	0.021	0.646	NA
54	rs289714	CC/CT/TT	0.181	0.023	0.442	NA
54	rs11644475	AA/GA/GG	0.038	-0.014	0.819	NA
55	rs5883	CC/CT/TT	0.070	0.021	0.646	0.689
55	rs289714	CC/CT/TT	0.181	0.023	0.442	NA
55	rs11644475	AA/GA/GG	0.038	-0.014	0.819	NA
55	rs158478	AA/CA/CC	0.495	0.010	0.663	NA
56	rs289714	CC/CT/TT	0.181	0.023	0.442	0.307
56	rs11644475	AA/GA/GG	0.038	-0.014	0.819	NA
56	rs158478	AA/CA/CC	0.495	0.010	0.663	NA

Table B1.21. Continued

Window	Window SNP	Genotype	MAF	Beta	p_value	hap_P
56	CTP13868	GA/GG	0.002	0.537	0.060	NA
57	rs11644475	AA/GA/GG	0.038	-0.014	0.819	0.493
57	rs158478	AA/CA/CC	0.495	0.010	0.663	NA
57	CTP13868	GA/GG	0.002	0.537	0.060	NA
57	rs158479	AA/GA/GG	0.498	-0.005	0.843	NA
58	rs158478	AA/CA/CC	0.495	0.010	0.663	0.448
58	CTP13868	GA/GG	0.002	0.537	0.060	NA
58	rs158479	AA/GA/GG	0.498	-0.005	0.843	NA
58	rs181381869	CC/CT	0.011	-0.069	0.527	NA
59	CTP13868	GA/GG	0.002	0.537	0.060	0.636
59	rs158479	AA/GA/GG	0.498	-0.005	0.843	NA
59	rs181381869	CC/CT	0.011	-0.069	0.527	NA
59	CTP15277	AA/AG	0.001	-0.273	0.499	NA
60	rs158479	AA/GA/GG	0.498	-0.005	0.843	0.971
60	CTP14123	CC/CT	0.011	-0.069	0.527	NA
60	CTP15277	AA/AG	0.001	-0.273	0.499	NA
60	rs289717	CC/CT/TT	0.320	0.007	0.785	NA
61	rs181381869	CC/CT	0.011	-0.069	0.527	0.874
61	CTP15277	AA/AG	0.001	-0.273	0.499	NA
61	rs289717	CC/CT/TT	0.320	0.007	0.785	NA
61	rs35874588	DD/WD/WW	0.300	0.008	0.761	NA
62	CTP15277	AA/AG	0.001	-0.273	0.499	0.314
62	rs289717	CC/CT/TT	0.320	0.007	0.785	NA
62	rs35874588	DD/WD/WW	0.300	0.008	0.761	NA
62	rs289718	CC/CT/TT	0.304	0.002	0.923	NA
63	rs289717	CC/CT/TT	0.320	0.007	0.785	0.240
63	rs35874588	DD/WD/WW	0.300	0.008	0.761	NA
63	rs289718	CC/CT/TT	0.304	0.002	0.923	NA
63	rs289719	AA/GA/GG	0.300	0.002	0.932	NA
64	rs35874588	DD/WD/WW	0.300	0.008	0.761	0.244
64	rs289718	CC/CT/TT	0.304	0.002	0.923	NA
64	rs289719	AA/GA/GG	0.300	0.002	0.932	NA
64	rs2033254	CC/TC/TT	0.374	-0.006	0.791	NA
65	rs289718	CC/CT/TT	0.304	0.002	0.923	0.969
65	rs289719	AA/GA/GG	0.300	0.002	0.932	NA
65	rs2033254	CC/TC/TT	0.374	-0.006	0.791	NA
65	rs183439140	CC/CT	0.005	0.001	0.994	NA
66	rs289719	AA/GA/GG	0.300	0.002	0.932	0.988
66	rs2033254	CC/TC/TT	0.374	-0.006	0.791	NA
66	rs183439140	CC/CT	0.005	0.001	0.994	NA
66	rs72771489	GA/GG	0.009	0.039	0.751	NA
67	rs2033254	CC/TC/TT	0.374	-0.006	0.791	0.089
67	rs183439140	CC/CT	0.005	0.001	0.994	NA
67	rs72771489	GA/GG	0.009	0.039	0.751	NA
67	rs56208677	CC/TC/TT	0.077	-0.102	0.016	NA
68	rs183439140	CC/CT	0.005	0.001	0.994	0.116
68	rs72771489	GA/GG	0.009	0.039	0.751	NA
68	rs56208677	CC/TC/TT	0.077	-0.102	0.016	NA
68	rs71387147	GG/GT/TT	0.081	0.003	0.949	NA
69	rs72771489	GA/GG	0.009	0.039	0.751	0.119
69	rs56208677	CC/TC/TT	0.077	-0.102	0.016	NA
69	rs71387147	GG/GT/TT	0.081	0.003	0.949	NA
69	CTP16508	CG/GG	0.003	0.059	0.800	NA
70	rs56208677	CC/TC/TT	0.077	-0.102	0.016	0.212
70	rs71387147	GG/GT/TT	0.081	0.003	0.949	NA
70	CTP16508	CG/GG	0.003	0.059	0.800	NA
70	rs117427818	AA/GA/GG	0.054	0.005	0.909	NA
71	rs71387147	GG/GT/TT	0.081	0.003	0.949	0.997
71	CTP16508	CG/GG	0.003	0.059	0.800	NA
71	rs117427818	AA/GA/GG	0.054	0.005	0.909	NA
71	rs142980129	GG/GT	0.005	0.000	0.998	NA
72	CTP16508	CG/GG	0.003	0.059	0.800	0.982
72	rs117427818	AA/GA/GG	0.054	0.005	0.909	NA
72	rs142980129	GG/GT	0.005	0.000	0.998	NA
72	CTP16598	CC/CT	0.002	-0.117	0.617	NA
73	rs117427818	AA/GA/GG	0.054	0.005	0.909	0.978
73	rs142980129	GG/GT	0.005	0.000	0.998	NA
73	CTP16598	CC/CT	0.002	-0.117	0.617	NA
73	rs4784744	AA/GA/GG	0.321	0.007	0.765	NA
74	rs142980129	GG/GT	0.005	0.000	0.998	0.983
74	CTP16598	CC/CT	0.002	-0.117	0.617	NA
74	rs4784744	AA/GA/GG	0.321	0.007	0.765	NA
74	rs12720898	CC/CT/TT	0.056	-0.003	0.944	NA
75	CTP16598	CC/CT	0.002	-0.117	0.617	0.960
75	rs4784744	AA/GA/GG	0.321	0.007	0.765	NA

Table B1.21. Continued

Window	Window SNP	Genotype	MAF	Beta	p_value	hap_P
75	rs12720898	CC/CT/TT	0.056	-0.003	0.944	NA
75	rs291044	AA/AG/GG	0.320	0.007	0.785	NA
76	rs4784744	AA/GA/GG	0.321	0.007	0.765	0.929
76	rs12720898	CC/CT/TT	0.056	-0.003	0.944	NA
76	rs291044	AA/AG/GG	0.320	0.007	0.785	NA
76	rs28381709	CA/CC	0.002	-0.202	0.484	NA
77	rs12720898	CC/CT/TT	0.056	-0.003	0.944	0.791
77	rs291044	AA/AG/GG	0.320	0.007	0.785	NA
77	rs28381709	CA/CC	0.002	-0.202	0.484	NA
77	rs12708980	GG/GT/TT	0.394	0.013	0.580	NA
78	rs291044	AA/AG/GG	0.320	0.007	0.785	0.391
78	rs28381709	CA/CC	0.002	-0.202	0.484	NA
78	rs12708980	GG/GT/TT	0.394	0.013	0.580	NA
78	rs12720889	AA/AT/TT	0.290	-0.013	0.602	NA
79	rs28381709	CA/CC	0.002	-0.202	0.484	0.938
79	rs12708980	GG/GT/TT	0.394	0.013	0.580	NA
79	rs12720889	AA/AT/TT	0.290	-0.013	0.602	NA
79	CTP18663	CC/CT	0.001	0.368	0.362	NA
80	rs12708980	GG/GT/TT	0.394	0.013	0.580	0.592
80	rs12720889	AA/AT/TT	0.290	-0.013	0.602	NA
80	CTP18663	CC/CT	0.001	0.368	0.362	NA
80	rs143024882	CA/CC	0.002	0.172	0.547	NA
81	rs12720889	AA/AT/TT	0.290	-0.013	0.602	0.572
81	CTP18663	CC/CT	0.001	0.368	0.362	NA
81	rs143024882	CA/CC	0.002	0.172	0.547	NA
81	rs12447620	AA/GA/GG	0.128	-0.010	0.764	NA
82	CTP18663	CC/CT	0.001	0.368	0.362	0.595
82	CTP18717	CA/CC	0.002	0.172	0.547	NA
82	rs12447620	AA/GA/GG	0.128	-0.010	0.764	NA
82	rs12708983	CC/TC/TT	0.038	-0.053	0.354	NA
83	rs143024882	CA/CC	0.002	0.172	0.547	0.826
83	rs12447620	AA/GA/GG	0.128	-0.010	0.764	NA
83	rs12708983	CC/TC/TT	0.038	-0.053	0.354	NA
83	CTP20593	GA/GG	0.001	-0.246	0.543	NA
84	rs12447620	AA/GA/GG	0.128	-0.010	0.764	0.813
84	rs12708983	CC/TC/TT	0.038	-0.053	0.354	NA
84	CTP20593	GA/GG	0.001	-0.246	0.543	NA
84	CTP20804	CC/CT	0.005	-0.004	0.979	NA
85	rs12708983	CC/TC/TT	0.038	-0.053	0.354	0.793
85	CTP20593	GA/GG	0.001	-0.246	0.543	NA
85	CTP20804	CC/CT	0.005	-0.004	0.979	NA
85	rs4784745	AA/AG/GG	0.313	-0.003	0.902	NA
86	CTP20593	GA/GG	0.001	-0.246	0.543	0.992
86	CTP20804	CC/CT	0.005	-0.004	0.979	NA
86	rs4784745	AA/AG/GG	0.313	-0.003	0.902	NA
86	rs5880	CC/CG/GG	0.057	-0.004	0.939	NA
87	CTP20804	CC/CT	0.005	-0.004	0.979	0.999
87	rs4784745	AA/AG/GG	0.313	-0.003	0.902	NA
87	rs5880	CC/CG/GG	0.057	-0.004	0.939	NA
87	rs1800774	CC/TC/TT	0.388	-0.004	0.850	NA
88	rs4784745	AA/AG/GG	0.313	-0.003	0.902	0.869
88	rs5880	CC/CG/GG	0.057	-0.004	0.939	NA
88	rs1800774	CC/TC/TT	0.388	-0.004	0.850	NA
88	rs5882	AA/GA/GG	0.317	0.010	0.686	NA
89	rs5880	CC/CG/GG	0.057	-0.004	0.939	0.997
89	rs1800774	CC/TC/TT	0.388	-0.004	0.850	NA
89	rs5882	AA/GA/GG	0.317	0.010	0.686	NA
89	rs111379440	CC/CT	0.002	0.094	0.745	NA
90	rs1800774	CC/TC/TT	0.388	-0.004	0.850	0.986
90	rs5882	AA/GA/GG	0.317	0.010	0.686	NA
90	rs111379440	CC/CT	0.002	0.094	0.745	NA
90	rs12720882	AA/GA	0.009	-0.008	0.951	NA
91	rs5882	AA/GA/GG	0.317	0.010	0.686	0.733
91	rs111379440	CC/CT	0.002	0.094	0.745	NA
91	rs12720882	AA/GA	0.009	-0.008	0.951	NA
91	CTP22888delA	WD/WW	0.001	0.861	0.032	NA
92	rs111379440	CC/CT	0.002	0.094	0.745	0.810
92	rs12720882	AA/GA	0.009	-0.008	0.951	NA
92	CTP22888delA	WD/WW	0.001	0.861	0.032	NA
92	rs12720887	CC/CT	0.013	-0.005	0.965	NA
93	rs12720882	AA/GA	0.009	-0.008	0.951	0.968
93	CTP22888delA	WD/WW	0.001	0.861	0.032	NA
93	rs12720887	CC/CT	0.013	-0.005	0.965	NA
93	rs9923854	GG/GT/TT	0.114	0.010	0.792	NA
94	CTP22888delA	WD/WW	0.001	0.861	0.032	0.341

Table B1.21. Continued

Window	Window SNP	Genotype	MAF	Beta	p_value	hap_P
94	rs12720887	CC/CT	0.013	-0.005	0.965	NA
94	rs9923854	GG/GT/TT	0.114	0.010	0.792	NA
94	rs1800777	AA/AG/GG	0.035	0.018	0.761	NA
95	rs12720887	CC/CT	0.013	-0.005	0.965	0.601
95	rs9923854	GG/GT/TT	0.114	0.010	0.792	NA
95	rs1800777	AA/AG/GG	0.035	0.018	0.761	NA
95	rs1801706	AA/GA/GG	0.171	0.008	0.795	NA
96	rs9923854	GG/GT/TT	0.114	0.010	0.792	0.992
96	rs1800777	AA/AG/GG	0.035	0.018	0.761	NA
96	rs1801706	AA/GA/GG	0.171	0.008	0.795	NA
96	rs289742	CC/GC/GG	0.127	0.003	0.930	NA
97	rs1800777	AA/AG/GG	0.035	0.018	0.761	0.981
97	rs1801706	AA/GA/GG	0.171	0.008	0.795	NA
97	rs289742	CC/GC/GG	0.127	0.003	0.930	NA
97	rs289743	AA/GA/GG	0.300	0.002	0.932	NA
98	rs1801706	AA/GA/GG	0.171	0.008	0.795	0.968
98	rs289742	CC/GC/GG	0.127	0.003	0.930	NA
98	rs289743	AA/GA/GG	0.300	0.002	0.932	NA
98	rs289744	AA/CA/CC	0.300	0.003	0.900	NA
99	rs289742	CC/GC/GG	0.127	0.003	0.930	0.848
99	rs289743	AA/GA/GG	0.300	0.002	0.932	NA
99	rs289744	AA/CA/CC	0.300	0.003	0.900	NA
99	rs12720917	CC/TC/TT	0.172	0.025	0.413	NA
100	rs289743	AA/GA/GG	0.300	0.002	0.932	0.710
100	rs289744	AA/CA/CC	0.300	0.003	0.900	NA
100	rs12720917	CC/TC/TT	0.172	0.025	0.413	NA
100	rs289745	AA/CA/CC	0.409	-0.018	0.458	NA

TABLE B1.22. *CETP* 4-SNP sliding window haplotype association results for HDL-C, LDL-C and TC in NHWs (n=623)

				HDL-C			**LDL-C**			**TC**		
Window	**Window SNP**	**Genotype**	**MAF**	**Beta**	***P***	**Hap *P***	**Beta**	***P***	**Hap *P***	**Beta**	***P***	**Hap *P***
1	rs9989419	AA/GA/GG	0.400	-0.026	0.014	0.003	0.726	0.749	0.309	0.663	0.780	0.321
1	rs247617	AA/CA/CC	0.347	0.043	7.41E-05	NA	2.195	0.342	NA	3.188	0.186	NA
1	rs183130	CC/TC/TT	0.347	0.040	1.91E-04	NA	2.359	0.305	NA	3.240	0.177	NA
1	rs6499863	AA/GA/GG	0.172	-0.014	0.350	NA	4.781	0.118	NA	3.739	0.246	NA
2	rs247617	AA/CA/CC	0.347	0.043	7.41E-05	0.002	2.195	0.342	0.235	3.188	0.186	0.230
2	rs183130	CC/TC/TT	0.347	0.040	1.91E-04	NA	2.359	0.305	NA	3.240	0.177	NA
2	rs6499863	AA/GA/GG	0.172	-0.014	0.350	NA	4.781	0.118	NA	3.739	0.246	NA
2	rs12149545	AA/GA/GG	0.330	0.042	1.66E-04	NA	2.085	0.385	NA	3.614	0.150	NA
3	rs183130	CC/TC/TT	0.347	0.040	1.91E-04	0.006	2.359	0.305	0.500	3.240	0.177	0.469
3	rs6499863	AA/GA/GG	0.172	-0.014	0.350	NA	4.781	0.118	NA	3.739	0.246	NA
3	rs12149545	AA/GA/GG	0.330	0.042	1.66E-04	NA	2.085	0.385	NA	3.614	0.150	NA
3	rs12708967	CC/CT/TT	0.205	-0.034	0.011	NA	-2.154	0.451	NA	-4.511	0.131	NA
4	rs6499863	AA/GA/GG	0.172	-0.014	0.350	0.006	4.781	0.118	0.127	3.739	0.246	0.113
4	rs12149545	AA/GA/GG	0.330	0.042	1.66E-04	NA	2.085	0.385	NA	3.614	0.150	NA
4	rs12708967	CC/CT/TT	0.205	-0.034	0.011	NA	-2.154	0.451	NA	-4.511	0.131	NA
4	rs3764261	GG/GT/TT	0.328	0.043	0.000	NA	3.327	0.179	NA	4.856	0.060	NA
5	rs12149545	AA/GA/GG	0.330	0.042	1.66E-04	0.002	2.085	0.385	0.246	3.614	0.150	0.099
5	rs12708967	CC/CT/TT	0.205	-0.034	0.011	NA	-2.154	0.451	NA	-4.511	0.131	NA
5	rs3764261	GG/GT/TT	0.328	0.043	1.63E-04	NA	3.327	0.179	NA	4.856	0.060	NA
5	rs17231506	CC/TC/TT	0.343	0.042	1.25E-04	NA	2.249	0.338	NA	3.683	0.134	NA
6	rs12708967	CC/CT/TT	0.205	-0.034	0.011	0.002	-2.154	0.451	0.142	-4.511	0.131	0.078
6	rs3764261	GG/GT/TT	0.328	0.043	1.63E-04	NA	3.327	0.179	NA	4.856	0.060	NA
6	rs17231506	CC/TC/TT	0.343	0.042	1.25E-04	NA	2.249	0.338	NA	3.683	0.134	NA
6	rs12708968	CC/CT/TT	0.082	-0.016	0.432	NA	-5.402	0.197	NA	-3.995	0.362	NA
7	rs3764261	GG/GT/TT	0.328	0.043	1.63E-04	0.001	3.327	0.179	0.153	4.856	0.060	0.070
7	rs17231506	CC/TC/TT	0.343	0.042	1.25E-04	NA	2.249	0.338	NA	3.683	0.134	NA
7	rs12708968	CC/CT/TT	0.082	-0.016	0.432	NA	-5.402	0.197	NA	-3.995	0.362	NA
7	rs4783961	AA/AG/GG	0.457	-0.013	0.216	NA	-0.881	0.701	NA	-0.179	0.941	NA
8	rs17231506	CC/TC/TT	0.343	0.042	1.25E-04	3.60E-04	2.249	0.338	0.511	3.683	0.134	0.216
8	rs12708968	CC/CT/TT	0.082	-0.016	0.432	NA	-5.402	0.197	NA	-3.995	0.362	NA
8	rs4783961	AA/AG/GG	0.457	-0.013	0.216	NA	-0.881	0.701	NA	-0.179	0.941	NA
8	rs17245715	CC/CT/TT	0.082	-0.014	0.462	NA	-5.311	0.202	NA	-3.918	0.369	NA
9	rs12708968	CC/CT/TT	0.082	-0.016	0.432	0.647	-5.402	0.197	0.388	-3.995	0.362	0.478
9	rs4783961	AA/AG/GG	0.457	-0.013	0.216	NA	-0.881	0.701	NA	-0.179	0.941	NA
9	rs17245715	CC/CT/TT	0.082	-0.014	0.462	NA	-5.311	0.202	NA	-3.918	0.369	NA
9	rs4783962	CC/TC/TT	0.194	-0.005	0.702	NA	-1.961	0.498	NA	-2.157	0.478	NA
10	rs4783961	AA/AG/GG	0.457	-0.013	0.216	0.060	-0.881	0.701	0.516	-0.179	0.941	0.347
10	rs17245715	CC/CT/TT	0.082	-0.014	0.462	NA	-5.311	0.202	NA	-3.918	0.369	NA
10	rs4783962	CC/TC/TT	0.194	-0.005	0.702	NA	-1.961	0.498	NA	-2.157	0.478	NA
10	rs1800775	AA/CA/CC	0.489	-0.027	0.013	NA	-0.510	0.823	NA	-1.668	0.486	NA
11	rs17245715	CC/CT/TT	0.082	-0.014	0.462	0.002	-5.311	0.202	0.054	-3.918	0.369	0.040
11	rs4783962	CC/TC/TT	0.194	-0.005	0.702	NA	-1.961	0.498	NA	-2.157	0.478	NA
11	rs1800775	AA/CA/CC	0.489	-0.027	0.013	NA	-0.510	0.823	NA	-1.668	0.486	NA
11	rs17231534	CA/CC	0.045	-0.057	0.030	NA	5.710	0.309	NA	3.494	0.552	NA
12	rs4783962	CC/TC/TT	0.194	-0.005	0.702	0.002	-1.961	0.498	0.218	-2.157	0.478	0.067
12	rs1800775	AA/CA/CC	0.489	-0.027	0.013	NA	-0.510	0.823	NA	-1.668	0.486	NA
12	rs17231534	CA/CC	0.045	-0.057	0.030	NA	5.710	0.309	NA	3.494	0.552	NA
12	rs3816117	CC/CT/TT	0.488	-0.025	0.018	NA	-0.469	0.835	NA	-1.650	0.485	NA
13	rs1800775	AA/CA/CC	0.489	-0.027	0.013	0.003	-0.510	0.823	0.219	-1.668	0.486	0.081
13	rs17231534	CA/CC	0.045	-0.057	0.030	NA	5.710	0.309	NA	3.494	0.552	NA
13	rs3816117	CC/CT/TT	0.488	-0.025	0.018	NA	-0.469	0.835	NA	-1.650	0.485	NA
13	rs711752	AA/AG/GG	0.443	0.033	0.002	NA	-0.312	0.892	NA	0.905	0.706	NA
14	rs17231534	CA/CC	0.045	-0.057	0.030	0.011	5.710	0.309	0.829	3.494	0.552	0.854
14	rs3816117	CC/CT/TT	0.488	-0.025	0.018	NA	-0.469	0.835	NA	-1.650	0.485	NA
14	rs711752	AA/AG/GG	0.443	0.033	0.002	NA	-0.312	0.892	NA	0.905	0.706	NA
14	rs5030708	CC/CT	0.031	-0.024	0.446	NA	-2.568	0.698	NA	4.392	0.525	NA
15	rs3816117	CC/CT/TT	0.488	-0.025	0.018	0.020	-0.469	0.835	0.914	-1.650	0.485	0.773
15	rs711752	AA/AG/GG	0.443	0.033	0.002	NA	-0.312	0.892	NA	0.905	0.706	NA
15	rs5030708	CC/CT	0.031	-0.024	0.446	NA	-2.568	0.698	NA	4.392	0.525	NA
15	rs708272	AA/GA/GG	0.442	0.033	0.002	NA	-0.236	0.918	NA	0.964	0.688	NA
16	rs711752	AA/AG/GG	0.443	0.033	0.002	0.007	-0.312	0.892	0.977	0.905	0.706	0.844
16	rs5030708	CC/CT	0.031	-0.024	0.446	NA	-2.568	0.698	NA	4.392	0.525	NA
16	rs708272	AA/GA/GG	0.442	0.033	0.002	NA	-0.236	0.918	NA	0.964	0.688	NA
16	rs1864163	AA/GA/GG	0.265	-0.035	0.003	NA	0.593	0.816	NA	-1.500	0.575	NA

Table B1.22. Continued

				HDL-C			LDL-C			TC		
Window	**Window SNP**	**Genotype**	**MAF**	**Beta**	***P***	**Hap *P***	**Beta**	***P***	**Hap *P***	**Beta**	***P***	**Hap *P***
17	rs5030708	CC/CT	0.031	-0.024	0.446	0.010	-2.568	0.698	0.975	4.392	0.525	0.858
17	rs708272	AA/GA/GG	0.442	0.033	0.002	NA	-0.236	0.918	NA	0.964	0.688	NA
17	rs1864163	AA/GA/GG	0.265	-0.035	0.003	NA	0.593	0.816	NA	-1.500	0.575	NA
17	CTP3412	AA/GA	0.001	-0.369	0.050	NA	-18.531	0.645	NA	-23.845	0.571	NA
18	rs708272	AA/GA/GG	0.442	0.033	0.002	0.027	-0.236	0.918	0.590	0.964	0.688	0.832
18	rs1864163	AA/GA/GG	0.265	-0.035	0.003	NA	0.593	0.816	NA	-1.500	0.575	NA
18	CTP3412	AA/GA	0.001	-0.369	0.050	NA	-18.531	0.645	NA	-23.845	0.571	NA
18	rs4369653	AA/AG/GG	0.263	-0.012	0.327	NA	-1.160	0.652	NA	-0.605	0.821	NA
19	rs1864163	AA/GA/GG	0.265	-0.035	0.003	0.046	0.593	0.816	0.960	-1.500	0.575	0.965
19	CTP3412	AA/GA	0.001	-0.369	0.050	NA	-18.531	0.645	NA	-23.845	0.571	NA
19	rs4369653	AA/AG/GG	0.263	-0.012	0.327	NA	-1.160	0.652	NA	-0.605	0.821	NA
19	rs7194225	CC/CG/GG	0.089	-0.001	0.944	NA	2.407	0.548	NA	3.276	0.436	NA
20	CTP3412	AA/GA	0.001	-0.369	0.050	0.571	-18.531	0.645	0.497	-23.845	0.571	0.454
20	rs4369653	AA/AG/GG	0.263	-0.012	0.327	NA	-1.160	0.652	NA	-0.605	0.821	NA
20	rs7194225	CC/CG/GG	0.089	-0.001	0.944	NA	2.407	0.548	NA	3.276	0.436	NA
20	CTP4559	CC/CT	0.002	0.025	0.850	NA	-39.820	0.160	NA	-40.474	0.172	NA
21	rs4369653	AA/AG/GG	0.263	-0.012	0.327	0.176	-1.160	0.652	0.690	-0.605	0.821	0.532
21	rs7194225	CC/CG/GG	0.089	-0.001	0.944	NA	2.407	0.548	NA	3.276	0.436	NA
21	CTP4559	CC/CT	0.002	0.025	0.850	NA	-39.820	0.160	NA	-40.474	0.172	NA
21	rs9929488	CC/GC/GG	0.289	-0.018	0.117	NA	0.984	0.698	NA	-0.861	0.745	NA
22	rs7194225	CC/CG/GG	0.089	-0.001	0.944	0.071	2.407	0.548	0.012	3.276	0.436	0.101
22	CTP4559	CC/CT	0.002	0.025	0.850	NA	-39.820	0.160	NA	-40.474	0.172	NA
22	rs9929488	CC/GC/GG	0.289	-0.018	0.117	NA	0.984	0.698	NA	-0.861	0.745	NA
22	rs7203984	AA/CA/CC	0.206	-0.032	0.011	NA	-0.228	0.934	NA	-2.298	0.427	NA
23	CTP4559	CC/CT	0.002	0.025	0.850	0.006	-39.820	0.160	0.069	-40.474	0.172	0.535
23	rs9929488	CC/GC/GG	0.289	-0.018	0.117	NA	0.984	0.698	NA	-0.861	0.745	NA
23	rs7203984	AA/CA/CC	0.206	-0.032	0.011	NA	-0.228	0.934	NA	-2.298	0.427	NA
23	rs11508026	CC/CT/TT	0.472	0.025	0.012	NA	0.493	0.818	NA	0.627	0.780	NA
24	rs9929488	CC/GC/GG	0.289	-0.018	0.117	0.007	0.984	0.698	0.288	-0.861	0.745	0.851
24	rs7203984	AA/CA/CC	0.206	-0.032	0.011	NA	-0.228	0.934	NA	-2.298	0.427	NA
24	rs11508026	CC/CT/TT	0.472	0.025	0.012	NA	0.493	0.818	NA	0.627	0.780	NA
24	rs17231569	DD/WD/WW	0.190	-0.031	0.019	NA	-0.301	0.915	NA	-2.293	0.435	NA
25	rs7203984	AA/CA/CC	0.206	-0.032	0.011	0.022	-0.228	0.934	0.997	-2.298	0.427	0.855
25	rs11508026	CC/CT/TT	0.472	0.025	0.012	NA	0.493	0.818	NA	0.627	0.780	NA
25	rs17231569	DD/WD/WW	0.190	-0.031	0.019	NA	-0.301	0.915	NA	-2.293	0.435	NA
25	rs708273	AA/AG/GG	0.263	-0.012	0.344	NA	-0.114	0.965	NA	-0.708	0.794	NA
26	rs11508026	CC/CT/TT	0.472	0.025	0.012	0.014	0.493	0.818	0.972	0.627	0.780	0.838
26	rs17231569	DD/WD/WW	0.190	-0.031	0.019	NA	-0.301	0.915	NA	-2.293	0.435	NA
26	rs708273	AA/AG/GG	0.263	-0.012	0.344	NA	-0.114	0.965	NA	-0.708	0.794	NA
26	rs820299	AA/AG/GG	0.357	-0.010	0.337	NA	0.440	0.850	NA	0.781	0.749	NA
27	rs17231569	DD/WD/WW	0.190	-0.031	0.019	0.025	-0.301	0.915	0.609	-2.293	0.435	0.303
27	rs708273	AA/AG/GG	0.263	-0.012	0.344	NA	-0.114	0.965	NA	-0.708	0.794	NA
27	rs820299	AA/AG/GG	0.357	-0.010	0.337	NA	0.440	0.850	NA	0.781	0.749	NA
27	rs12720922	AA/AG/GG	0.192	-0.030	0.022	NA	-1.370	0.621	NA	-3.529	0.224	NA
28	rs708273	AA/AG/GG	0.263	-0.012	0.344	0.033	-0.114	0.965	0.876	-0.708	0.794	0.561
28	rs820299	AA/AG/GG	0.357	-0.010	0.337	NA	0.440	0.850	NA	0.781	0.749	NA
28	rs12720922	AA/AG/GG	0.192	-0.030	0.022	NA	-1.370	0.621	NA	-3.529	0.224	NA
28	rs12708969	GG/TG/TT	0.439	0.028	0.009	NA	-0.044	0.985	NA	0.970	0.691	NA
29	rs820299	AA/AG/GG	0.357	-0.010	0.337	0.069	0.440	0.850	0.175	0.781	0.749	0.715
29	rs12720922	AA/AG/GG	0.192	-0.030	0.022	NA	-1.370	0.621	NA	-3.529	0.224	NA
29	rs12708969	GG/TG/TT	0.439	0.028	0.009	NA	-0.044	0.985	NA	0.970	0.691	NA
29	rs60545348	AA/CA/CC	0.269	-0.014	0.232	NA	-1.066	0.680	NA	-0.418	0.877	NA
30	rs12720922	AA/AG/GG	0.192	-0.030	0.022	0.073	-1.370	0.621	0.176	-3.529	0.224	0.697
30	rs12708969	GG/TG/TT	0.439	0.028	0.009	NA	-0.044	0.985	NA	0.970	0.691	NA
30	rs60545348	AA/CA/CC	0.269	-0.014	0.232	NA	-1.066	0.680	NA	-0.418	0.877	NA
30	rs9924087	AA/GA/GG	0.090	0.003	0.875	NA	0.156	0.969	NA	1.261	0.762	NA
31	rs12708969	GG/TG/TT	0.439	0.028	0.009	0.033	-0.044	0.985	0.912	0.970	0.691	0.768
31	rs60545348	AA/CA/CC	0.269	-0.014	0.232	NA	-1.066	0.680	NA	-0.418	0.877	NA
31	rs9924087	AA/GA/GG	0.090	0.003	0.875	NA	0.156	0.969	NA	1.261	0.762	NA
31	rs12597002	AA/AC/CC	0.267	-0.011	0.367	NA	-0.401	0.877	NA	-0.303	0.911	NA
32	rs60545348	AA/CA/CC	0.269	-0.014	0.232	0.045	-1.066	0.680	0.508	-0.418	0.877	0.913
32	rs9924087	AA/GA/GG	0.090	0.003	0.875	NA	0.156	0.969	NA	1.261	0.762	NA
32	rs12597002	AA/AC/CC	0.267	-0.011	0.367	NA	-0.401	0.877	NA	-0.303	0.911	NA
32	rs9926440	CC/CG/GG	0.302	-0.027	0.019	NA	-0.741	0.760	NA	-0.225	0.929	NA
33	rs9924087	AA/GA/GG	0.090	0.003	0.875	0.073	0.156	0.969	0.709	1.261	0.762	0.795
33	rs12597002	AA/AC/CC	0.267	-0.011	0.367	NA	-0.401	0.877	NA	-0.303	0.911	NA
33	rs9926440	CC/CG/GG	0.302	-0.027	0.019	NA	-0.741	0.760	NA	-0.225	0.929	NA
33	rs9939224	GG/GT/TT	0.205	-0.034	0.008	NA	-1.110	0.685	NA	-2.003	0.483	NA
34	rs12597002	AA/AC/CC	0.267	-0.011	0.367	0.090	-0.401	0.877	0.480	-0.303	0.911	0.117
34	rs9926440	CC/CG/GG	0.302	-0.027	0.019	NA	-0.741	0.760	NA	-0.225	0.929	NA
34	rs9939224	GG/GT/TT	0.205	-0.034	0.008	NA	-1.110	0.685	NA	-2.003	0.483	NA

Table B1.22. Continued

				HDL-C			LDL-C			TC		
Window	Window SNP	Genotype	MAF	Beta	*P*	Hap *P*	Beta	*P*	Hap *P*	Beta	*P*	Hap *P*
34	rs11076174	CC/TC/TT	0.075	-0.023	0.254	NA	1.330	0.754	NA	4.534	0.310	NA
35	rs9926440	CC/CG/GG	0.302	-0.027	0.019	0.102	-0.741	0.760	0.962	-0.225	0.929	0.472
35	rs9939224	GG/GT/TT	0.205	-0.034	0.008	NA	-1.110	0.685	NA	-2.003	0.483	NA
35	rs11076174	CC/TC/TT	0.075	-0.023	0.254	NA	1.330	0.754	NA	4.534	0.310	NA
35	rs891142	CC/CT	0.002	-0.103	0.436	NA	-10.456	0.712	NA	-18.500	0.532	NA
36	rs9939224	GG/GT/TT	0.205	-0.034	0.008	0.081	-1.110	0.685	0.885	-2.003	0.483	0.411
36	rs11076174	CC/TC/TT	0.075	-0.023	0.254	NA	1.330	0.754	NA	4.534	0.310	NA
36	rs891142	CC/CT	0.002	-0.103	0.436	NA	-10.456	0.712	NA	-18.500	0.532	NA
36	rs139040281	AA/CA	0.002	0.138	0.299	NA	28.855	0.307	NA	25.147	0.396	NA
37	rs11076174	CC/TC/TT	0.075	-0.023	0.254	0.030	1.330	0.754	0.955	4.534	0.310	0.539
37	rs891142	CC/CT	0.002	-0.103	0.436	NA	-10.456	0.712	NA	-18.500	0.532	NA
37	rs139040281	AA/CA	0.002	0.138	0.299	NA	28.855	0.307	NA	25.147	0.396	NA
37	rs7205804	AA/AG/GG	0.453	0.031	0.004	NA	-0.540	0.814	NA	1.521	0.526	NA
38	rs891142	CC/CT	0.002	-0.103	0.436	0.013	-10.456	0.712	0.844	-18.500	0.532	0.721
38	rs139040281	AA/CA	0.002	0.138	0.299	NA	28.855	0.307	NA	25.147	0.396	NA
38	rs7205804	AA/AG/GG	0.453	0.031	0.004	NA	-0.540	0.814	NA	1.521	0.526	NA
38	rs12708972	CC/TC	0.009	-0.020	0.723	NA	4.568	0.708	NA	3.390	0.791	NA
39	rs139040281	AA/CA	0.002	0.138	0.299	0.009	28.855	0.307	0.752	25.147	0.396	0.591
39	rs7205804	AA/AG/GG	0.453	0.031	0.004	NA	-0.540	0.814	NA	1.521	0.526	NA
39	rs12708972	CC/TC	0.009	-0.020	0.723	NA	4.568	0.708	NA	3.390	0.791	NA
39	rs34523084	CC/TC	0.007	-0.119	0.058	NA	-27.482	0.041	NA	8.725	0.535	NA
40	rs7205804	AA/AG/GG	0.453	0.031	0.004	0.005	-0.540	0.814	0.536	1.521	0.526	0.707
40	rs12708972	CC/TC	0.009	-0.020	0.723	NA	4.568	0.708	NA	3.390	0.791	NA
40	rs34523084	CC/TC	0.007	-0.119	0.058	NA	-27.482	0.041	NA	8.725	0.535	NA
40	rs1532624	AA/CA/CC	0.452	0.032	0.003	NA	0.046	0.984	NA	1.019	0.668	NA
41	rs12708972	CC/TC	0.009	-0.020	0.723	0.002	4.568	0.708	0.310	3.390	0.791	0.435
41	rs34523084	CC/TC	0.007	-0.119	0.058	NA	-27.482	0.041	NA	8.725	0.535	NA
41	rs1532624	AA/CA/CC	0.452	0.032	0.003	NA	0.046	0.984	NA	1.019	0.668	NA
41	rs12708974	CC/TC/TT	0.108	-0.010	0.539	NA	-4.769	0.179	NA	-4.654	0.210	NA
42	rs34523084	CC/TC	0.007	-0.119	0.058	0.001	-27.482	0.041	0.056	8.725	0.535	0.137
42	rs1532624	AA/CA/CC	0.452	0.032	0.003	NA	0.046	0.984	NA	1.019	0.668	NA
42	rs12708974	CC/TC/TT	0.108	-0.010	0.539	NA	-4.769	0.179	NA	-4.654	0.210	NA
42	rs117040820	CC/CT	0.016	-0.021	0.625	NA	-11.290	0.214	NA	-16.449	0.084	NA
43	rs1532624	AA/CA/CC	0.452	0.032	0.003	0.002	0.046	0.984	0.332	1.019	0.668	0.127
43	rs12708974	CC/TC/TT	0.108	-0.010	0.539	NA	-4.769	0.179	NA	-4.654	0.210	NA
43	rs117040820	CC/CT	0.016	-0.021	0.625	NA	-11.290	0.214	NA	-16.449	0.084	NA
43	rs12720873	AA/AG/GG	0.039	0.026	0.345	NA	0.096	0.987	NA	2.891	0.639	NA
44	rs12708974	CC/TC/TT	0.108	-0.010	0.539	0.700	-4.769	0.179	0.291	-4.654	0.210	0.167
44	rs117040820	CC/CT	0.016	-0.021	0.625	NA	-11.290	0.214	NA	-16.449	0.084	NA
44	rs12720873	AA/AG/GG	0.039	0.026	0.345	NA	0.096	0.987	NA	2.891	0.639	NA
44	CTP12123	AT/TT	0.001	-0.621	0.001	NA	-134.652	0.001	NA	-78.863	0.060	NA
45	rs117040820	CC/CT	0.016	-0.021	0.625	0.581	-11.290	0.214	0.645	-16.449	0.084	0.301
45	rs12720873	AA/AG/GG	0.039	0.026	0.345	NA	0.096	0.987	NA	2.891	0.639	NA
45	CTP12123	AT/TT	0.001	-0.621	0.001	NA	-134.652	0.001	NA	-78.863	0.060	NA
45	rs148654654	CC/TC	0.007	0.129	0.039	NA	20.298	0.130	NA	19.786	0.159	NA
46	rs12720873	AA/AG/GG	0.039	0.026	0.345	0.588	0.096	0.987	0.981	2.891	0.639	0.826
46	CTP12123	AT/TT	0.001	-0.621	0.001	NA	-134.652	0.001	NA	-78.863	0.060	NA
46	rs148654654	CC/TC	0.007	0.129	0.039	NA	20.298	0.130	NA	19.786	0.159	NA
46	rs289712	CC/CT/TT	0.265	-0.009	0.461	NA	-0.101	0.969	NA	-1.520	0.579	NA
47	CTP12123	AT/TT	0.001	-0.621	0.001	0.019	-134.652	0.001	0.978	-78.863	0.060	0.697
47	rs148654654	CC/TC	0.007	0.129	0.039	NA	20.298	0.130	NA	19.786	0.159	NA
47	rs289712	CC/CT/TT	0.265	-0.009	0.461	NA	-0.101	0.969	NA	-1.520	0.579	NA
47	rs11076175	AA/AG/GG	0.184	-0.034	0.010	NA	-0.326	0.907	NA	-1.981	0.499	NA
48	rs148654654	CC/TC	0.007	0.129	0.039	0.009	20.298	0.130	0.525	19.786	0.159	0.329
48	rs289712	CC/CT/TT	0.265	-0.009	0.461	NA	-0.101	0.969	NA	-1.520	0.579	NA
48	rs11076175	AA/AG/GG	0.184	-0.034	0.010	NA	-0.326	0.907	NA	-1.981	0.499	NA
48	rs7499892	CC/CT/TT	0.185	-0.033	0.011	NA	-0.559	0.842	NA	-2.735	0.352	NA
49	rs289712	CC/CT/TT	0.265	-0.009	0.461	0.015	-0.101	0.969	0.969	-1.520	0.579	0.574
49	rs11076175	AA/AG/GG	0.184	-0.034	0.010	NA	-0.326	0.907	NA	-1.981	0.499	NA
49	rs7499892	CC/CT/TT	0.185	-0.033	0.011	NA	-0.559	0.842	NA	-2.735	0.352	NA
49	rs187766748	AA/AG	0.006	-0.059	0.377	NA	-7.921	0.576	NA	-14.948	0.314	NA
50	rs11076175	AA/AG/GG	0.184	-0.034	0.010	0.011	-0.326	0.907	0.348	-1.981	0.499	0.680
50	rs7499892	CC/CT/TT	0.185	-0.033	0.011	NA	-0.559	0.842	NA	-2.735	0.352	NA
50	rs187766748	AA/AG	0.006	-0.059	0.377	NA	-7.921	0.576	NA	-14.948	0.314	NA
50	rs187468344	CC/TC	0.006	-0.111	0.120	NA	-24.543	0.107	NA	4.964	0.756	NA
51	rs7499892	CC/CT/TT	0.185	-0.033	0.011	0.056	-0.559	0.842	0.461	-2.735	0.352	0.692
51	rs187766748	AA/AG	0.006	-0.059	0.377	NA	-7.921	0.576	NA	-14.948	0.314	NA
51	rs187468344	CC/TC	0.006	-0.111	0.120	NA	-24.543	0.107	NA	4.964	0.756	NA
51	rs9930761	CC/CT/TT	0.081	0.013	0.523	NA	-0.103	0.980	NA	1.212	0.783	NA
52	rs187766748	AA/AG	0.006	-0.059	0.377	0.751	-7.921	0.576	0.427	-14.948	0.314	0.955
52	rs187468344	CC/TC	0.006	-0.111	0.120	NA	-24.543	0.107	NA	4.964	0.756	NA

Table B1.22. Continued

				HDL-C			LDL-C			TC		
Window	**Window SNP**	**Genotype**	**MAF**	**Beta**	***P***	**Hap *P***	**Beta**	***P***	**Hap *P***	**Beta**	***P***	**Hap *P***
52	rs9930761	CC/CT/TT	0.081	0.013	0.523	NA	-0.103	0.980	NA	1.212	0.783	NA
52	rs28381707	GG/GT	0.005	0.145	0.059	NA	-0.014	0.999	NA	7.154	0.677	NA
53	rs187468344	CC/TC	0.006	-0.111	0.120	0.655	-24.543	0.107	0.666	4.964	0.756	0.950
53	rs9930761	CC/CT/TT	0.081	0.013	0.523	NA	-0.103	0.980	NA	1.212	0.783	NA
53	rs28381707	GG/GT	0.005	0.145	0.059	NA	-0.014	0.999	NA	7.154	0.677	NA
53	rs5883	CC/CT/TT	0.070	0.022	0.304	NA	-0.784	0.862	NA	1.396	0.767	NA
54	rs9930761	CC/CT/TT	0.081	0.013	0.523	0.045	-0.103	0.980	0.991	1.212	0.783	0.892
54	rs28381707	GG/GT	0.005	0.145	0.059	NA	-0.014	0.999	NA	7.154	0.677	NA
54	rs5883	CC/CT/TT	0.070	0.022	0.304	NA	-0.784	0.862	NA	1.396	0.767	NA
54	rs289714	CC/CT/TT	0.181	-0.025	0.064	NA	-0.379	0.897	NA	-2.824	0.358	NA
55	rs28381707	GG/GT	0.005	0.145	0.059	0.101	-0.014	0.999	0.999	7.154	0.677	0.861
55	rs5883	CC/CT/TT	0.070	0.022	0.304	NA	-0.784	0.862	NA	1.396	0.767	NA
55	rs289714	CC/CT/TT	0.181	-0.025	0.064	NA	-0.379	0.897	NA	-2.824	0.358	NA
55	rs11644475	AA/GA/GG	0.038	0.023	0.412	NA	0.163	0.978	NA	3.315	0.594	NA
56	rs5883	CC/CT/TT	0.070	0.022	0.304	0.191	-0.784	0.862	0.998	1.396	0.767	0.875
56	rs289714	CC/CT/TT	0.181	-0.025	0.064	NA	-0.379	0.897	NA	-2.824	0.358	NA
56	rs11644475	AA/GA/GG	0.038	0.023	0.412	NA	0.163	0.978	NA	3.315	0.594	NA
56	rs158478	AA/CA/CC	0.495	-0.003	0.754	NA	-0.053	0.981	NA	0.087	0.971	NA
57	rs289714	CC/CT/TT	0.181	-0.025	0.064	0.100	-0.379	0.897	0.115	-2.824	0.358	0.004
57	rs11644475	AA/GA/GG	0.038	0.023	0.412	NA	0.163	0.978	NA	3.315	0.594	NA
57	rs158478	AA/CA/CC	0.495	-0.003	0.754	NA	-0.053	0.981	NA	0.087	0.971	NA
57	CTP13868	GA/GG	0.002	0.179	0.176	NA	76.229	0.007	NA	109.620	0.000	NA
58	rs11644475	AA/GA/GG	0.038	0.023	0.412	0.653	0.163	0.978	0.860	3.315	0.594	0.588
58	rs158478	AA/CA/CC	0.495	-0.003	0.754	NA	-0.053	0.981	NA	0.087	0.971	NA
58	CTP13868	GA/GG	0.002	0.179	0.176	NA	76.229	0.007	NA	109.620	0.000	NA
58	rs158479	AA/GA/GG	0.498	0.004	0.735	NA	-0.327	0.884	NA	-1.252	0.594	NA
59	rs158478	AA/CA/CC	0.495	-0.003	0.754	0.631	-0.053	0.981	0.856	0.087	0.971	0.646
59	CTP13868	GA/GG	0.002	0.179	0.176	NA	76.229	0.007	NA	109.620	0.000	NA
59	rs158479	AA/GA/GG	0.498	0.004	0.735	NA	-0.327	0.884	NA	-1.252	0.594	NA
59	rs181381869	CC/CT	0.011	0.050	0.318	NA	-1.337	0.901	NA	-1.295	0.909	NA
60	CTP13868	GA/GG	0.002	0.179	0.176	0.775	76.229	0.007	0.481	109.620	0.000	0.269
60	rs158479	AA/GA/GG	0.498	0.004	0.735	NA	-0.327	0.884	NA	-1.252	0.594	NA
60	rs181381869	CC/CT	0.011	0.050	0.318	NA	-1.337	0.901	NA	-1.295	0.909	NA
60	CTP15277	AA/AG	0.001	-0.295	0.115	NA	-44.577	0.265	NA	-78.734	0.060	NA
61	rs158479	AA/GA/GG	0.498	0.004	0.735	0.318	-0.327	0.884	0.996	-1.252	0.594	0.886
61	rs181381869	CC/CT	0.011	0.050	0.318	NA	-1.337	0.901	NA	-1.295	0.909	NA
61	CTP15277	AA/AG	0.001	-0.295	0.115	NA	-44.577	0.265	NA	-78.734	0.060	NA
61	rs289717	CC/CT/TT	0.320	-0.015	0.186	NA	0.163	0.946	NA	0.890	0.725	NA
62	rs181381869	CC/CT	0.011	0.050	0.318	0.161	-1.337	0.901	0.992	-1.295	0.909	0.867
62	CTP15277	AA/AG	0.001	-0.295	0.115	NA	-44.577	0.265	NA	-78.734	0.060	NA
62	rs289717	CC/CT/TT	0.320	-0.015	0.186	NA	0.163	0.946	NA	0.890	0.725	NA
62	rs35874588	DD/WD/WW	0.300	0.022	0.055	NA	-0.902	0.715	NA	0.849	0.743	NA
63	CTP15277	AA/AG	0.001	-0.295	0.115	0.201	-44.577	0.265	0.786	-78.734	0.060	0.294
63	rs289717	CC/CT/TT	0.320	-0.015	0.186	NA	0.163	0.946	NA	0.890	0.725	NA
63	rs35874588	DD/WD/WW	0.300	0.022	0.055	NA	-0.902	0.715	NA	0.849	0.743	NA
63	rs289718	CC/CT/TT	0.304	0.023	0.043	NA	-1.187	0.620	NA	-0.037	0.988	NA
64	rs289717	CC/CT/TT	0.320	-0.015	0.186	0.249	0.163	0.946	0.920	0.890	0.725	0.665
64	rs35874588	DD/WD/WW	0.300	0.022	0.055	NA	-0.902	0.715	NA	0.849	0.743	NA
64	rs289718	CC/CT/TT	0.304	0.023	0.043	NA	-1.187	0.620	NA	-0.037	0.988	NA
64	rs289719	AA/GA/GG	0.300	0.023	0.043	NA	-1.207	0.622	NA	0.277	0.914	NA
65	rs35874588	DD/WD/WW	0.300	0.022	0.055	0.257	-0.902	0.715	0.911	0.849	0.743	0.676
65	rs289718	CC/CT/TT	0.304	0.023	0.043	NA	-1.187	0.620	NA	-0.037	0.988	NA
65	rs289719	AA/GA/GG	0.300	0.023	0.043	NA	-1.207	0.622	NA	0.277	0.914	NA
65	rs2033254	CC/TC/TT	0.374	-0.007	0.529	NA	1.196	0.602	NA	-0.727	0.762	NA
66	rs289718	CC/CT/TT	0.304	0.023	0.043	0.195	-1.187	0.620	0.636	-0.037	0.988	0.775
66	rs289719	AA/GA/GG	0.300	0.023	0.043	NA	-1.207	0.622	NA	0.277	0.914	NA
66	rs2033254	CC/TC/TT	0.374	-0.007	0.529	NA	1.196	0.602	NA	-0.727	0.762	NA
66	rs183439140	CC/CT	0.005	0.080	0.296	NA	17.791	0.279	NA	18.224	0.288	NA
67	rs289719	AA/GA/GG	0.300	0.023	0.043	0.291	-1.207	0.622	0.233	0.277	0.914	0.455
67	rs2033254	CC/TC/TT	0.374	-0.007	0.529	NA	1.196	0.602	NA	-0.727	0.762	NA
67	rs183439140	CC/CT	0.005	0.080	0.296	NA	17.791	0.279	NA	18.224	0.288	NA
67	rs72771489	GA/GG	0.009	-0.018	0.759	NA	20.045	0.099	NA	14.767	0.247	NA
68	rs2033254	CC/TC/TT	0.374	-0.007	0.529	0.178	1.196	0.602	0.109	-0.727	0.762	0.305
68	rs183439140	CC/CT	0.005	0.080	0.296	NA	17.791	0.279	NA	18.224	0.288	NA
68	rs72771489	GA/GG	0.009	-0.018	0.759	NA	20.045	0.099	NA	14.767	0.247	NA
68	rs56208677	CC/TC/TT	0.077	0.033	0.096	NA	-4.873	0.244	NA	-4.946	0.258	NA
69	rs183439140	CC/CT	0.005	0.080	0.296	0.266	17.791	0.279	0.151	18.224	0.288	0.298
69	rs72771489	GA/GG	0.009	-0.018	0.759	NA	20.045	0.099	NA	14.767	0.247	NA
69	rs56208677	CC/TC/TT	0.077	0.033	0.096	NA	-4.873	0.244	NA	-4.946	0.258	NA
69	rs71387147	GG/GT/TT	0.081	-0.021	0.279	NA	2.386	0.572	NA	1.597	0.718	NA
70	rs72771489	GA/GG	0.009	-0.018	0.759	0.143	20.045	0.099	0.662	14.767	0.247	0.299

Table B1.22. Continued

				HDL-C			LDL-C			TC		
Window	**Window SNP**	**Genotype**	**MAF**	**Beta**	***P***	**Hap *P***	**Beta**	***P***	**Hap *P***	**Beta**	***P***	**Hap *P***
70	rs56208677	CC/TC/TT	0.077	0.033	0.096	NA	-4.873	0.244	NA	-4.946	0.258	NA
70	rs71387147	GG/GT/TT	0.081	-0.021	0.279	NA	2.386	0.572	NA	1.597	0.718	NA
70	CTP16508	CG/GG	0.003	-0.142	0.129	NA	-46.391	0.021	NA	24.310	0.248	NA
71	rs56208677	CC/TC/TT	0.077	0.033	0.096	0.115	-4.873	0.244	0.064	-4.946	0.258	0.188
71	rs71387147	GG/GT/TT	0.081	-0.021	0.279	NA	2.386	0.572	NA	1.597	0.718	NA
71	CTP16508	CG/GG	0.003	-0.142	0.129	NA	-46.391	0.021	NA	24.310	0.248	NA
71	rs117427818	AA/GA/GG	0.054	-0.024	0.281	NA	-5.611	0.228	NA	-9.507	0.051	NA
72	rs71387147	GG/GT/TT	0.081	-0.021	0.279	0.477	2.386	0.572	0.574	1.597	0.718	0.123
72	CTP16508	CG/GG	0.003	-0.142	0.129	NA	-46.391	0.021	NA	24.310	0.248	NA
72	rs117427818	AA/GA/GG	0.054	-0.024	0.281	NA	-5.611	0.228	NA	-9.507	0.051	NA
72	rs142980129	GG/GT	0.005	0.080	0.295	NA	17.740	0.280	NA	18.186	0.290	NA
73	CTP16508	CG/GG	0.003	-0.142	0.129	0.547	-46.391	0.021	0.535	24.310	0.248	0.050
73	rs117427818	AA/GA/GG	0.054	-0.024	0.281	NA	-5.611	0.228	NA	-9.507	0.051	NA
73	rs142980129	GG/GT	0.005	0.080	0.295	NA	17.740	0.280	NA	18.186	0.290	NA
73	CTP16598	CC/CT	0.002	-0.077	0.477	NA	28.825	0.213	NA	15.570	0.521	NA
74	rs117427818	AA/GA/GG	0.054	-0.024	0.281	0.268	-5.611	0.228	0.269	-9.507	0.051	0.161
74	rs142980129	GG/GT	0.005	0.080	0.295	NA	17.740	0.280	NA	18.186	0.290	NA
74	CTP16598	CC/CT	0.002	-0.077	0.477	NA	28.825	0.213	NA	15.570	0.521	NA
74	rs4784744	AA/GA/GG	0.321	-0.015	0.178	NA	0.223	0.927	NA	0.935	0.713	NA
75	rs142980129	GG/GT	0.005	0.080	0.295	0.586	17.740	0.280	0.025	18.186	0.290	0.055
75	CTP16598	CC/CT	0.002	-0.077	0.477	NA	28.825	0.213	NA	15.570	0.521	NA
75	rs4784744	AA/GA/GG	0.321	-0.015	0.178	NA	0.223	0.927	NA	0.935	0.713	NA
75	rs12720898	CC/CT/TT	0.056	0.015	0.520	NA	-10.214	0.034	NA	-10.098	0.046	NA
76	CTP16598	CC/CT	0.002	-0.077	0.477	0.476	28.825	0.213	0.087	15.570	0.521	0.201
76	rs4784744	AA/GA/GG	0.321	-0.015	0.178	NA	0.223	0.927	NA	0.935	0.713	NA
76	rs12720898	CC/CT/TT	0.056	0.015	0.520	NA	-10.214	0.034	NA	-10.098	0.046	NA
76	rs291044	AA/AG/GG	0.320	-0.015	0.186	NA	0.163	0.946	NA	0.890	0.725	NA
77	rs4784744	AA/GA/GG	0.321	-0.015	0.178	0.097	0.223	0.927	0.169	0.935	0.713	0.248
77	rs12720898	CC/CT/TT	0.056	0.015	0.520	NA	-10.214	0.034	NA	-10.098	0.046	NA
77	rs291044	AA/AG/GG	0.320	-0.015	0.186	NA	0.163	0.946	NA	0.890	0.725	NA
77	rs28381709	CA/CC	0.002	0.368	0.006	NA	-36.551	0.196	NA	-18.881	0.523	NA
78	rs12720898	CC/CT/TT	0.056	0.015	0.520	0.415	-10.214	0.034	0.322	-10.098	0.046	0.293
78	rs291044	AA/AG/GG	0.320	-0.015	0.186	NA	0.163	0.946	NA	0.890	0.725	NA
78	rs28381709	CA/CC	0.002	0.368	0.006	NA	-36.551	0.196	NA	-18.881	0.523	NA
78	rs12708980	GG/GT/TT	0.394	-0.007	0.484	NA	1.192	0.601	NA	-0.466	0.845	NA
79	rs291044	AA/AG/GG	0.320	-0.015	0.186	0.316	0.163	0.946	0.502	0.890	0.725	0.506
79	rs28381709	CA/CC	0.002	0.368	0.006	NA	-36.551	0.196	NA	-18.881	0.523	NA
79	rs12708980	GG/GT/TT	0.394	-0.007	0.484	NA	1.192	0.601	NA	-0.466	0.845	NA
79	rs12720889	AA/AT/TT	0.290	0.025	0.031	NA	-1.495	0.542	NA	-0.055	0.983	NA
80	rs28381709	CA/CC	0.002	0.368	0.006	0.103	-36.551	0.196	0.917	-18.881	0.523	0.987
80	rs12708980	GG/GT/TT	0.394	-0.007	0.484	NA	1.192	0.601	NA	-0.466	0.845	NA
80	rs12720889	AA/AT/TT	0.290	0.025	0.031	NA	-1.495	0.542	NA	-0.055	0.983	NA
80	CTP18663	CC/CT	0.001	-0.382	0.041	NA	54.887	0.170	NA	42.334	0.312	NA
81	rs12708980	GG/GT/TT	0.394	-0.007	0.484	0.115	1.192	0.601	0.842	-0.466	0.845	0.694
81	rs12720889	AA/AT/TT	0.290	0.025	0.031	NA	-1.495	0.542	NA	-0.055	0.983	NA
81	CTP18663	CC/CT	0.001	-0.382	0.041	NA	54.887	0.170	NA	42.334	0.312	NA
81	rs143024882	CA/CC	0.002	-0.114	0.295	NA	-31.212	0.179	NA	18.096	0.456	NA
82	rs12720889	AA/AT/TT	0.290	0.025	0.031	0.078	-1.495	0.542	0.806	-0.055	0.983	0.734
82	CTP18663	CC/CT	0.001	-0.382	0.041	NA	54.887	0.170	NA	42.334	0.312	NA
82	rs143024882	CA/CC	0.002	-0.114	0.295	NA	-31.212	0.179	NA	18.096	0.456	NA
82	rs12447620	AA/GA/GG	0.128	0.021	0.193	NA	-1.869	0.585	NA	-0.415	0.908	NA
83	CTP18663	CC/CT	0.001	-0.382	0.041	0.140	54.887	0.170	0.909	42.334	0.312	0.654
83	rs143024882	CA/CC	0.002	-0.114	0.295	NA	-31.212	0.179	NA	18.096	0.456	NA
83	rs12447620	AA/GA/GG	0.128	0.021	0.193	NA	-1.869	0.585	NA	-0.415	0.908	NA
83	rs12708983	CC/TC/TT	0.038	0.019	0.488	NA	-1.141	0.841	NA	-2.951	0.620	NA
84	rs143024882	CA/CC	0.002	-0.114	0.295	0.682	-31.212	0.179	0.471	18.096	0.456	0.847
84	rs12447620	AA/GA/GG	0.128	0.021	0.193	NA	-1.869	0.585	NA	-0.415	0.908	NA
84	rs12708983	CC/TC/TT	0.038	0.019	0.488	NA	-1.141	0.841	NA	-2.951	0.620	NA
84	CTP20593	GA/GG	0.001	0.399	0.033	NA	-25.602	0.522	NA	6.888	0.870	NA
85	rs12447620	AA/GA/GG	0.128	0.021	0.193	0.458	-1.869	0.585	0.810	-0.415	0.908	0.691
85	rs12708983	CC/TC/TT	0.038	0.019	0.488	NA	-1.141	0.841	NA	-2.951	0.620	NA
85	CTP20593	GA/GG	0.001	0.399	0.033	NA	-25.602	0.522	NA	6.888	0.870	NA
85	CTP20804	CC/CT	0.005	-0.161	0.036	NA	-10.336	0.529	NA	-21.211	0.217	NA
86	rs12708983	CC/TC/TT	0.038	0.019	0.488	0.408	-1.141	0.841	0.842	-2.951	0.620	0.680
86	CTP20593	GA/GG	0.001	0.399	0.033	NA	-25.602	0.522	NA	6.888	0.870	NA
86	CTP20804	CC/CT	0.005	-0.161	0.036	NA	-10.336	0.529	NA	-21.211	0.217	NA
86	rs4784745	AA/AG/GG	0.313	-0.013	0.266	NA	-0.671	0.784	NA	0.801	0.755	NA
87	CTP20593	GA/GG	0.001	0.399	0.033	0.105	-25.602	0.522	0.457	6.888	0.870	0.102
87	CTP20804	CC/CT	0.005	-0.161	0.036	NA	-10.336	0.529	NA	-21.211	0.217	NA
87	rs4784745	AA/AG/GG	0.313	-0.013	0.266	NA	-0.671	0.784	NA	0.801	0.755	NA
87	rs5880	CC/CG/GG	0.057	-0.032	0.133	NA	-5.642	0.215	NA	-10.436	0.028	NA

Table B1.22. Continued

				HDL-C			LDL-C			TC		
Window	**Window SNP**	**Genotype**	**MAF**	**Beta**	***P***	**Hap *P***	**Beta**	***P***	**Hap *P***	**Beta**	***P***	**Hap *P***
88	CTP20804	CC/CT	0.005	-0.161	0.036	0.049	-10.336	0.529	0.264	-21.211	0.217	0.102
88	rs4784745	AA/AG/GG	0.313	-0.013	0.266	NA	-0.671	0.784	NA	0.801	0.755	NA
88	rs5880	CC/CG/GG	0.057	-0.032	0.133	NA	-5.642	0.215	NA	-10.436	0.028	NA
88	rs1800774	CC/TC/TT	0.388	-0.003	0.811	NA	2.696	0.238	NA	0.337	0.887	NA
89	rs4784745	AA/AG/GG	0.313	-0.013	0.266	0.250	-0.671	0.784	0.295	0.801	0.755	0.185
89	rs5880	CC/CG/GG	0.057	-0.032	0.133	NA	-5.642	0.215	NA	-10.436	0.028	NA
89	rs1800774	CC/TC/TT	0.388	-0.003	0.811	NA	2.696	0.238	NA	0.337	0.887	NA
89	rs5882	AA/GA/GG	0.317	0.013	0.252	NA	-2.574	0.288	NA	-1.519	0.551	NA
90	rs5880	CC/CG/GG	0.057	-0.032	0.133	0.163	-5.642	0.215	0.168	-10.436	0.028	0.066
90	rs1800774	CC/TC/TT	0.388	-0.003	0.811	NA	2.696	0.238	NA	0.337	0.887	NA
90	rs5882	AA/GA/GG	0.317	0.013	0.252	NA	-2.574	0.288	NA	-1.519	0.551	NA
90	rs111379440	CC/CT	0.002	-0.206	0.121	NA	-20.000	0.484	NA	-31.638	0.289	NA
91	rs1800774	CC/TC/TT	0.388	-0.003	0.811	0.345	2.696	0.238	0.499	0.337	0.887	0.974
91	rs5882	AA/GA/GG	0.317	0.013	0.252	NA	-2.574	0.288	NA	-1.519	0.551	NA
91	rs111379440	CC/CT	0.002	-0.206	0.121	NA	-20.000	0.484	NA	-31.638	0.289	NA
91	rs12720882	AA/GA	0.009	-0.041	0.471	NA	19.226	0.116	NA	16.820	0.190	NA
92	rs5882	AA/GA/GG	0.317	0.013	0.252	0.140	-2.574	0.288	0.317	-1.519	0.551	0.576
92	rs111379440	CC/CT	0.002	-0.206	0.121	NA	-20.000	0.484	NA	-31.638	0.289	NA
92	rs12720882	AA/GA	0.009	-0.041	0.471	NA	19.226	0.116	NA	16.820	0.190	NA
92	CTP22888delA	WD/WW	0.001	-0.285	0.128	NA	14.590	0.715	NA	31.502	0.451	NA
93	rs111379440	CC/CT	0.002	-0.206	0.121	0.109	-20.000	0.484	0.069	-31.638	0.289	0.060
93	rs12720882	AA/GA	0.009	-0.041	0.471	NA	19.226	0.116	NA	16.820	0.190	NA
93	CTP22888delA	WD/WW	0.001	-0.285	0.128	NA	14.590	0.715	NA	31.502	0.451	NA
93	rs12720887	CC/CT	0.013	0.065	0.172	NA	19.556	0.054	NA	22.729	0.033	NA
94	rs12720882	AA/GA	0.009	-0.041	0.471	0.440	19.226	0.116	0.078	16.820	0.190	0.056
94	CTP22888delA	WD/WW	0.001	-0.285	0.128	NA	14.590	0.715	NA	31.502	0.451	NA
94	rs12720887	CC/CT	0.013	0.065	0.172	NA	19.556	0.054	NA	22.729	0.033	NA
94	rs9923854	GG/GT/TT	0.114	0.005	0.760	NA	1.377	0.710	NA	1.872	0.629	NA
95	CTP22888delA	WD/WW	0.001	-0.285	0.128	0.064	14.590	0.715	0.228	31.502	0.451	0.042
95	rs12720887	CC/CT	0.013	0.065	0.172	NA	19.556	0.054	NA	22.729	0.033	NA
95	rs9923854	GG/GT/TT	0.114	0.005	0.760	NA	1.377	0.710	NA	1.872	0.629	NA
95	rs1800777	AA/AG/GG	0.035	-0.061	0.023	NA	-7.194	0.208	NA	-13.229	0.027	NA
96	rs12720887	CC/CT	0.013	0.065	0.172	0.106	19.556	0.054	0.071	22.729	0.033	0.018
96	rs9923854	GG/GT/TT	0.114	0.005	0.760	NA	1.377	0.710	NA	1.872	0.629	NA
96	rs1800777	AA/AG/GG	0.035	-0.061	0.023	NA	-7.194	0.208	NA	-13.229	0.027	NA
96	rs1801706	AA/GA/GG	0.171	0.009	0.508	NA	-2.600	0.390	NA	-2.177	0.491	NA
97	rs9923854	GG/GT/TT	0.114	0.005	0.760	0.107	1.377	0.710	0.138	1.872	0.629	0.057
97	rs1800777	AA/AG/GG	0.035	-0.061	0.023	NA	-7.194	0.208	NA	-13.229	0.027	NA
97	rs1801706	AA/GA/GG	0.171	0.009	0.508	NA	-2.600	0.390	NA	-2.177	0.491	NA
97	rs289742	CC/GC/GG	0.127	0.022	0.165	NA	-1.870	0.578	NA	0.170	0.962	NA
98	rs1800777	AA/AG/GG	0.035	-0.061	0.023	0.062	-7.194	0.208	0.334	-13.229	0.027	0.105
98	rs1801706	AA/GA/GG	0.171	0.009	0.508	NA	-2.600	0.390	NA	-2.177	0.491	NA
98	rs289742	CC/GC/GG	0.127	0.022	0.165	NA	-1.870	0.578	NA	0.170	0.962	NA
98	rs289743	AA/GA/GG	0.300	0.020	0.077	NA	-2.277	0.352	NA	-0.907	0.723	NA
99	rs1801706	AA/GA/GG	0.171	0.009	0.508	0.253	-2.600	0.390	0.530	-2.177	0.491	0.748
99	rs289742	CC/GC/GG	0.127	0.022	0.165	NA	-1.870	0.578	NA	0.170	0.962	NA
99	rs289743	AA/GA/GG	0.300	0.020	0.077	NA	-2.277	0.352	NA	-0.907	0.723	NA
99	rs289744	AA/CA/CC	0.300	0.018	0.113	NA	-2.459	0.309	NA	-1.189	0.639	NA
100	rs289742	CC/GC/GG	0.127	0.022	0.165	0.495	-1.870	0.578	0.899	0.170	0.962	0.949
100	rs289743	AA/GA/GG	0.300	0.020	0.077	NA	-2.277	0.352	NA	-0.907	0.723	NA
100	rs289744	AA/CA/CC	0.300	0.018	0.113	NA	-2.459	0.309	NA	-1.189	0.639	NA
100	rs12720917	CC/TC/TT	0.172	0.001	0.919	NA	-1.262	0.679	NA	-0.154	0.961	NA
101	rs289743	AA/GA/GG	0.300	0.020	0.077	0.672	-2.277	0.352	0.500	-0.907	0.723	0.728
101	rs289744	AA/CA/CC	0.300	0.018	0.113	NA	-2.459	0.309	NA	-1.189	0.639	NA
101	rs12720917	CC/TC/TT	0.172	0.001	0.919	NA	-1.262	0.679	NA	-0.154	0.961	NA
101	rs289745	AA/CA/CC	0.409	-0.014	0.215	NA	2.792	0.233	NA	0.420	0.864	NA

TABLE B1.23. *CETP* 4-SNP sliding window haplotype association results for ApoA1 and ApoB in NHWs (n=623)

				APOA1			APOB		
Window	Window SNP	Genotype	MAF	Beta	p_value	hap_P	Beta	p_value	hap_P
1	rs9989419	AA/GA/GG	0.400	-1.346	0.552	0.676	0.065	0.884	0.748
1	rs247617	AA/CA/CC	0.347	3.941	0.083	NA	-0.268	0.560	NA
1	rs183130	CC/TC/TT	0.347	3.639	0.115	NA	-0.212	0.643	NA
1	rs6499863	AA/GA/GG	0.172	-0.962	0.746	NA	0.873	0.143	NA
2	rs247617	AA/CA/CC	0.347	3.941	0.083	0.398	-0.268	0.560	0.428
2	rs183130	CC/TC/TT	0.347	3.639	0.115	NA	-0.212	0.643	NA
2	rs6499863	AA/GA/GG	0.172	-0.962	0.746	NA	0.873	0.143	NA
2	rs12149545	AA/GA/GG	0.330	4.294	0.074	NA	-0.111	0.817	NA
3	rs183130	CC/TC/TT	0.347	3.639	0.115	0.475	-0.212	0.643	0.370
3	rs6499863	AA/GA/GG	0.172	-0.962	0.746	NA	0.873	0.143	NA
3	rs12149545	AA/GA/GG	0.330	4.294	0.074	NA	-0.111	0.817	NA
3	rs12708967	CC/CT/TT	0.205	-1.198	0.668	NA	-0.538	0.334	NA
4	rs6499863	AA/GA/GG	0.172	-0.962	0.746	0.429	0.873	0.143	0.476
4	rs12149545	AA/GA/GG	0.330	4.294	0.074	NA	-0.111	0.817	NA
4	rs12708967	CC/CT/TT	0.205	-1.198	0.668	NA	-0.538	0.334	NA
4	rs3764261	GG/GT/TT	0.328	3.222	0.189	NA	-0.248	0.609	NA
5	rs12149545	AA/GA/GG	0.330	4.294	0.074	0.310	-0.111	0.817	0.404
5	rs12708967	CC/CT/TT	0.205	-1.198	0.668	NA	-0.538	0.334	NA
5	rs3764261	GG/GT/TT	0.328	3.222	0.189	NA	-0.248	0.609	NA
5	rs17231506	CC/TC/TT	0.343	3.709	0.109	NA	-0.204	0.662	NA
6	rs12708967	CC/CT/TT	0.205	-1.198	0.668	0.292	-0.538	0.334	0.508
6	rs3764261	GG/GT/TT	0.328	3.222	0.189	NA	-0.248	0.609	NA
6	rs17231506	CC/TC/TT	0.343	3.709	0.109	NA	-0.204	0.662	NA
6	rs12708968	CC/CT/TT	0.082	3.336	0.414	NA	0.176	0.829	NA
7	rs3764261	GG/GT/TT	0.328	3.222	0.189	0.302	-0.248	0.609	0.472
7	rs17231506	CC/TC/TT	0.343	3.709	0.109	NA	-0.204	0.662	NA
7	rs12708968	CC/CT/TT	0.082	3.336	0.414	NA	0.176	0.829	NA
7	rs4783961	AA/AG/GG	0.457	-1.729	0.430	NA	0.558	0.202	NA
8	rs17231506	CC/TC/TT	0.343	3.709	0.109	0.272	-0.204	0.662	0.706
8	rs12708968	CC/CT/TT	0.082	3.336	0.414	NA	0.176	0.829	NA
8	rs4783961	AA/AG/GG	0.457	-1.729	0.430	NA	0.558	0.202	NA
8	rs17245715	CC/CT/TT	0.082	4.081	0.312	NA	0.130	0.873	NA
9	rs12708968	CC/CT/TT	0.082	3.336	0.414	0.470	0.176	0.829	0.607
9	rs4783961	AA/AG/GG	0.457	-1.729	0.430	NA	0.558	0.202	NA
9	rs17245715	CC/CT/TT	0.082	4.081	0.312	NA	0.130	0.873	NA
9	rs4783962	CC/TC/TT	0.194	-4.415	0.118	NA	0.091	0.871	NA
10	rs4783961	AA/AG/GG	0.457	-1.729	0.430	0.578	0.558	0.202	0.382
10	rs17245715	CC/CT/TT	0.082	4.081	0.312	NA	0.130	0.873	NA
10	rs4783962	CC/TC/TT	0.194	-4.415	0.118	NA	0.091	0.871	NA
10	rs1800775	AA/CA/CC	0.489	-3.108	0.164	NA	-0.049	0.912	NA
11	rs17245715	CC/CT/TT	0.082	4.081	0.312	0.264	0.130	0.873	0.922
11	rs4783962	CC/TC/TT	0.194	-4.415	0.118	NA	0.091	0.871	NA
11	rs1800775	AA/CA/CC	0.489	-3.108	0.164	NA	-0.049	0.912	NA
11	rs17231534	CA/CC	0.045	-7.676	0.154	NA	-0.226	0.833	NA
12	rs4783962	CC/TC/TT	0.194	-4.415	0.118	0.048	0.091	0.871	0.785
12	rs1800775	AA/CA/CC	0.489	-3.108	0.164	NA	-0.049	0.912	NA
12	rs17231534	CA/CC	0.045	-7.676	0.154	NA	-0.226	0.833	NA
12	rs3816117	CC/CT/TT	0.488	-3.281	0.142	NA	-0.060	0.894	NA
13	rs1800775	AA/CA/CC	0.489	-3.108	0.164	0.062	-0.049	0.912	0.773
13	rs17231534	CA/CC	0.045	-7.676	0.154	NA	-0.226	0.833	NA
13	rs3816117	CC/CT/TT	0.488	-3.281	0.142	NA	-0.060	0.894	NA
13	rs711752	AA/AG/GG	0.443	4.888	0.028	NA	0.155	0.731	NA
14	rs17231534	CA/CC	0.045	-7.676	0.154	0.233	-0.226	0.833	0.879
14	rs3816117	CC/CT/TT	0.488	-3.281	0.142	NA	-0.060	0.894	NA
14	rs711752	AA/AG/GG	0.443	4.888	0.028	NA	0.155	0.731	NA
14	rs5030708	CC/CT	0.031	-2.038	0.751	NA	1.183	0.354	NA
15	rs3816117	CC/CT/TT	0.488	-3.281	0.142	0.122	-0.060	0.894	0.755
15	rs711752	AA/AG/GG	0.443	4.888	0.028	NA	0.155	0.731	NA
15	rs5030708	CC/CT	0.031	-2.038	0.751	NA	1.183	0.354	NA
15	rs708272	AA/GA/GG	0.442	4.810	0.032	NA	0.169	0.708	NA
16	rs711752	AA/AG/GG	0.443	4.888	0.028	0.147	0.155	0.731	0.774
16	rs5030708	CC/CT	0.031	-2.038	0.751	NA	1.183	0.354	NA
16	rs708272	AA/GA/GG	0.442	4.810	0.032	NA	0.169	0.708	NA
16	rs1864163	AA/GA/GG	0.265	-2.092	0.413	NA	0.036	0.944	NA
17	rs5030708	CC/CT	0.031	-2.038	0.751	0.343	1.183	0.354	0.461
17	rs708272	AA/GA/GG	0.442	4.810	0.032	NA	0.169	0.708	NA
17	rs1864163	AA/GA/GG	0.265	-2.092	0.413	NA	0.036	0.944	NA
17	rs4369653	AA/AG/GG	0.263	-3.707	0.141	NA	-0.090	0.857	NA
18	rs708272	AA/GA/GG	0.442	4.810	0.032	0.005	0.169	0.708	0.420
18	rs1864163	AA/GA/GG	0.265	-2.092	0.413	NA	0.036	0.944	NA
18	rs4369653	AA/AG/GG	0.263	-3.707	0.141	NA	-0.090	0.857	NA

Table B1.23. Continued

				APOA1			APOB		
Window	**Window SNP**	**Genotype**	**MAF**	**Beta**	**p_value**	**hap_P**	**Beta**	**p_value**	**hap_P**
18	rs7194225	CC/CG/GG	0.089	1.842	0.637	NA	0.219	0.777	NA
19	rs1864163	AA/GA/GG	0.265	-2.092	0.413	0.071	0.036	0.944	0.671
19	rs4369653	AA/AG/GG	0.263	-3.707	0.141	NA	-0.090	0.857	NA
19	rs7194225	CC/CG/GG	0.089	1.842	0.637	NA	0.219	0.777	NA
19	CTP4559	CC/CT	0.002	-3.712	0.911	NA	-6.620	0.311	NA
20	rs4369653	AA/AG/GG	0.263	-3.707	0.141	0.430	-0.090	0.857	0.799
20	rs7194225	CC/CG/GG	0.089	1.842	0.637	NA	0.219	0.777	NA
20	CTP4559	CC/CT	0.002	-3.712	0.911	NA	-6.620	0.311	NA
20	rs9929488	CC/GC/GG	0.289	-0.374	0.882	NA	-0.408	0.415	NA
21	rs7194225	CC/CG/GG	0.089	1.842	0.637	0.753	0.219	0.777	0.121
21	CTP4559	CC/CT	0.002	-3.712	0.911	NA	-6.620	0.311	NA
21	rs9929488	CC/GC/GG	0.289	-0.374	0.882	NA	-0.408	0.415	NA
21	rs7203984	AA/CA/CC	0.206	-2.829	0.296	NA	-0.243	0.651	NA
22	CTP4559	CC/CT	0.002	-3.712	0.911	0.240	-6.620	0.311	0.748
22	rs9929488	CC/GC/GG	0.289	-0.374	0.882	NA	-0.408	0.415	NA
22	rs7203984	AA/CA/CC	0.206	-2.829	0.296	NA	-0.243	0.651	NA
22	rs11508026	CC/CT/TT	0.472	4.428	0.036	NA	0.332	0.430	NA
23	rs9929488	CC/GC/GG	0.289	-0.374	0.882	0.288	-0.408	0.415	0.833
23	rs7203984	AA/CA/CC	0.206	-2.829	0.296	NA	-0.243	0.651	NA
23	rs11508026	CC/CT/TT	0.472	4.428	0.036	NA	0.332	0.430	NA
23	rs17231569	DD/WD/WW	0.190	-2.143	0.435	NA	-0.187	0.733	NA
24	rs7203984	AA/CA/CC	0.206	-2.829	0.296	0.006	-0.243	0.651	0.815
24	rs11508026	CC/CT/TT	0.472	4.428	0.036	NA	0.332	0.430	NA
24	rs17231569	DD/WD/WW	0.190	-2.143	0.435	NA	-0.187	0.733	NA
24	rs708273	AA/AG/GG	0.263	-4.452	0.078	NA	0.021	0.966	NA
25	rs11508026	CC/CT/TT	0.472	4.428	0.036	0.012	0.332	0.430	0.865
25	rs17231569	DD/WD/WW	0.190	-2.143	0.435	NA	-0.187	0.733	NA
25	rs708273	AA/AG/GG	0.263	-4.452	0.078	NA	0.021	0.966	NA
25	rs820299	AA/AG/GG	0.357	-2.382	0.293	NA	-0.118	0.792	NA
26	rs17231569	DD/WD/WW	0.190	-2.143	0.435	0.182	-0.187	0.733	0.987
26	rs708273	AA/AG/GG	0.263	-4.452	0.078	NA	0.021	0.966	NA
26	rs820299	AA/AG/GG	0.357	-2.382	0.293	NA	-0.118	0.792	NA
26	rs12720922	AA/AG/GG	0.192	-1.996	0.463	NA	-0.197	0.717	NA
27	rs708273	AA/AG/GG	0.263	-4.452	0.078	0.076	0.021	0.966	0.922
27	rs820299	AA/AG/GG	0.357	-2.382	0.293	NA	-0.118	0.792	NA
27	rs12720922	AA/AG/GG	0.192	-1.996	0.463	NA	-0.197	0.717	NA
27	rs12708969	GG/TG/TT	0.439	4.445	0.054	NA	0.321	0.485	NA
28	rs820299	AA/AG/GG	0.357	-2.382	0.293	0.206	-0.118	0.792	0.913
28	rs12720922	AA/AG/GG	0.192	-1.996	0.463	NA	-0.197	0.717	NA
28	rs12708969	GG/TG/TT	0.439	4.445	0.054	NA	0.321	0.485	NA
28	rs60545348	AA/CA/CC	0.269	-3.346	0.184	NA	0.049	0.921	NA
29	rs12720922	AA/AG/GG	0.192	-1.996	0.463	0.180	-0.197	0.717	0.909
29	rs12708969	GG/TG/TT	0.439	4.445	0.054	NA	0.321	0.485	NA
29	rs60545348	AA/CA/CC	0.269	-3.346	0.184	NA	0.049	0.921	NA
29	rs9924087	AA/GA/GG	0.090	2.336	0.540	NA	-0.178	0.814	NA
30	rs12708969	GG/TG/TT	0.439	4.445	0.054	0.139	0.321	0.485	0.717
30	rs60545348	AA/CA/CC	0.269	-3.346	0.184	NA	0.049	0.921	NA
30	rs9924087	AA/GA/GG	0.090	2.336	0.540	NA	-0.178	0.814	NA
30	rs12597002	AA/AC/CC	0.267	-3.062	0.216	NA	-0.039	0.937	NA
31	rs60545348	AA/CA/CC	0.269	-3.346	0.184	0.333	0.049	0.921	0.556
31	rs9924087	AA/GA/GG	0.090	2.336	0.540	NA	-0.178	0.814	NA
31	rs12597002	AA/AC/CC	0.267	-3.062	0.216	NA	-0.039	0.937	NA
31	rs9926440	CC/CG/GG	0.302	-0.391	0.871	NA	0.009	0.984	NA
32	rs9924087	AA/GA/GG	0.090	2.336	0.540	0.629	-0.178	0.814	0.739
32	rs12597002	AA/AC/CC	0.267	-3.062	0.216	NA	-0.039	0.937	NA
32	rs9926440	CC/CG/GG	0.302	-0.391	0.871	NA	0.009	0.984	NA
32	rs9939224	GG/GT/TT	0.205	-1.537	0.568	NA	0.070	0.896	NA
33	rs12597002	AA/AC/CC	0.267	-3.062	0.216	0.210	-0.039	0.937	0.149
33	rs9926440	CC/CG/GG	0.302	-0.391	0.871	NA	0.009	0.984	NA
33	rs9939224	GG/GT/TT	0.205	-1.537	0.568	NA	0.070	0.896	NA
33	rs11076174	CC/TC/TT	0.075	-2.216	0.583	NA	1.950	0.015	NA
34	rs9926440	CC/CG/GG	0.302	-0.391	0.871	0.944	0.009	0.984	0.057
34	rs9939224	GG/GT/TT	0.205	-1.537	0.568	NA	0.070	0.896	NA
34	rs11076174	CC/TC/TT	0.075	-2.216	0.583	NA	1.950	0.015	NA
34	rs891142	CC/CT	0.002	-9.181	0.694	NA	-4.510	0.330	NA
35	rs9939224	GG/GT/TT	0.205	-1.537	0.568	0.668	0.070	0.896	0.024
35	rs11076174	CC/TC/TT	0.075	-2.216	0.583	NA	1.950	0.015	NA
35	rs891142	CC/CT	0.002	-9.181	0.694	NA	-4.510	0.330	NA
35	CTP10459	AA/CA	0.002	-41.732	0.204	NA	-3.626	0.579	NA
36	rs11076174	CC/TC/TT	0.075	-2.216	0.583	0.240	1.950	0.015	0.031
36	rs891142	CC/CT	0.002	-9.181	0.694	NA	-4.510	0.330	NA
36	rs139040281	AA/CA	0.002	-41.732	0.204	NA	-3.626	0.579	NA
36	rs7205804	AA/AG/GG	0.453	3.903	0.086	NA	0.231	0.610	NA
37	rs891142	CC/CT	0.002	-9.181	0.694	0.181	-4.510	0.330	0.783

Table B1.23. Continued

				APOA1			APOB		
Window	**Window SNP**	**Genotype**	**MAF**	**Beta**	**p_value**	**hap_P**	**Beta**	**p_value**	**hap_P**
37	rs139040281	AA/CA	0.002	-41.732	0.204	NA	-3.626	0.579	NA
37	rs7205804	AA/AG/GG	0.453	3.903	0.086	NA	0.231	0.610	NA
37	rs12708972	CC/TC	0.009	7.104	0.572	NA	2.324	0.352	NA
38	rs139040281	AA/CA	0.002	-41.732	0.204	0.166	-3.626	0.579	0.208
38	rs7205804	AA/AG/GG	0.453	3.903	0.086	NA	0.231	0.610	NA
38	rs12708972	CC/TC	0.009	7.104	0.572	NA	2.324	0.352	NA
38	rs34523084	CC/TC	0.007	-18.997	0.199	NA	4.976	0.087	NA
39	rs7205804	AA/AG/GG	0.453	3.903	0.086	0.217	0.231	0.610	0.152
39	rs12708972	CC/TC	0.009	7.104	0.572	NA	2.324	0.352	NA
39	rs34523084	CC/TC	0.007	-18.997	0.199	NA	4.976	0.087	NA
39	rs1532624	AA/CA/CC	0.452	3.911	0.084	NA	0.212	0.639	NA
40	rs12708972	CC/TC	0.009	7.104	0.572	0.370	2.324	0.352	0.196
40	rs34523084	CC/TC	0.007	-18.997	0.199	NA	4.976	0.087	NA
40	rs1532624	AA/CA/CC	0.452	3.911	0.084	NA	0.212	0.639	NA
40	rs12708974	CC/TC/TT	0.108	2.945	0.381	NA	0.682	0.309	NA
41	rs34523084	CC/TC	0.007	-18.997	0.199	0.218	4.976	0.087	0.216
41	rs1532624	AA/CA/CC	0.452	3.911	0.084	NA	0.212	0.639	NA
41	rs12708974	CC/TC/TT	0.108	2.945	0.381	NA	0.682	0.309	NA
41	rs117040820	CC/CT	0.016	-8.351	0.387	NA	-2.449	0.200	NA
42	rs1532624	AA/CA/CC	0.452	3.911	0.084	0.292	0.212	0.639	0.599
42	rs12708974	CC/TC/TT	0.108	2.945	0.381	NA	0.682	0.309	NA
42	rs117040820	CC/CT	0.016	-8.351	0.387	NA	-2.449	0.200	NA
42	rs12720873	AA/AG/GG	0.039	3.011	0.594	NA	0.299	0.789	NA
43	rs12708974	CC/TC/TT	0.108	2.945	0.381	0.745	0.682	0.309	0.630
43	rs117040820	CC/CT	0.016	-8.351	0.387	NA	-2.449	0.200	NA
43	rs12720873	AA/AG/GG	0.039	3.011	0.594	NA	0.299	0.789	NA
43	rs148654654	CC/TC	0.007	5.527	0.683	NA	-0.292	0.913	NA
44	rs117040820	CC/CT	0.016	-8.351	0.387	0.553	-2.449	0.200	0.792
44	rs12720873	AA/AG/GG	0.039	3.011	0.594	NA	0.299	0.789	NA
44	rs148654654	CC/TC	0.007	5.527	0.683	NA	-0.292	0.913	NA
44	rs289712	CC/CT/TT	0.265	-3.561	0.159	NA	-0.012	0.980	NA
45	rs12720873	AA/AG/GG	0.039	3.011	0.594	0.341	0.299	0.789	0.998
45	rs148654654	CC/TC	0.007	5.527	0.683	NA	-0.292	0.913	NA
45	rs289712	CC/CT/TT	0.265	-3.561	0.159	NA	-0.012	0.980	NA
45	rs11076175	AA/AG/GG	0.184	-2.567	0.351	NA	-0.167	0.761	NA
46	rs148654654	CC/TC	0.007	5.527	0.683	0.200	-0.292	0.913	0.986
46	rs289712	CC/CT/TT	0.265	-3.561	0.159	NA	-0.012	0.980	NA
46	rs11076175	AA/AG/GG	0.184	-2.567	0.351	NA	-0.167	0.761	NA
46	rs7499892	CC/CT/TT	0.185	-2.382	0.387	NA	-0.218	0.692	NA
47	rs289712	CC/CT/TT	0.265	-3.561	0.159	0.211	-0.012	0.980	0.909
47	rs11076175	AA/AG/GG	0.184	-2.567	0.351	NA	-0.167	0.761	NA
47	rs7499892	CC/CT/TT	0.185	-2.382	0.387	NA	-0.218	0.692	NA
47	rs187766748	AA/AG	0.006	-8.313	0.540	NA	1.397	0.603	NA
48	rs11076175	AA/AG/GG	0.184	-2.567	0.351	0.612	-0.167	0.761	0.549
48	rs7499892	CC/CT/TT	0.185	-2.382	0.387	NA	-0.218	0.692	NA
48	rs187766748	AA/AG	0.006	-8.313	0.540	NA	1.397	0.603	NA
48	rs187468344	CC/TC	0.006	7.132	0.599	NA	2.175	0.420	NA
49	rs7499892	CC/CT/TT	0.185	-2.382	0.387	0.530	-0.218	0.692	0.785
49	rs187766748	AA/AG	0.006	-8.313	0.540	NA	1.397	0.603	NA
49	rs187468344	CC/TC	0.006	7.132	0.599	NA	2.175	0.420	NA
49	rs9930761	CC/CT/TT	0.081	5.024	0.226	NA	0.609	0.461	NA
50	rs187766748	AA/AG	0.006	-8.313	0.540	0.402	1.397	0.603	0.505
50	rs187468344	CC/TC	0.006	7.132	0.599	NA	2.175	0.420	NA
50	rs9930761	CC/CT/TT	0.081	5.024	0.226	NA	0.609	0.461	NA
50	rs28381707	GG/GT	0.005	15.246	0.304	NA	0.856	0.771	NA
51	rs187468344	CC/TC	0.006	7.132	0.599	0.234	2.175	0.420	0.677
51	rs9930761	CC/CT/TT	0.081	5.024	0.226	NA	0.609	0.461	NA
51	rs28381707	GG/GT	0.005	15.246	0.304	NA	0.856	0.771	NA
51	rs5883	CC/CT/TT	0.070	4.404	0.314	NA	0.682	0.431	NA
52	rs9930761	CC/CT/TT	0.081	5.024	0.226	0.133	0.609	0.461	0.810
52	rs28381707	GG/GT	0.005	15.246	0.304	NA	0.856	0.771	NA
52	rs5883	CC/CT/TT	0.070	4.404	0.314	NA	0.682	0.431	NA
52	rs289714	CC/CT/TT	0.181	-5.190	0.073	NA	-0.436	0.450	NA
53	rs28381707	GG/GT	0.005	15.246	0.304	0.316	0.856	0.771	0.879
53	rs5883	CC/CT/TT	0.070	4.404	0.314	NA	0.682	0.431	NA
53	rs289714	CC/CT/TT	0.181	-5.190	0.073	NA	-0.436	0.450	NA
53	rs11644475	AA/GA/GG	0.038	3.856	0.500	NA	0.251	0.824	NA
54	rs5883	CC/CT/TT	0.070	4.404	0.314	0.397	0.682	0.431	0.781
54	rs289714	CC/CT/TT	0.181	-5.190	0.073	NA	-0.436	0.450	NA
54	rs11644475	AA/GA/GG	0.038	3.856	0.500	NA	0.251	0.824	NA
54	rs158478	AA/CA/CC	0.495	-3.097	0.163	NA	-0.493	0.259	NA
55	rs289714	CC/CT/TT	0.181	-5.190	0.073	0.403	-0.436	0.450	0.864
55	rs11644475	AA/GA/GG	0.038	3.856	0.500	NA	0.251	0.824	NA
55	rs158478	AA/CA/CC	0.495	-3.097	0.163	NA	-0.493	0.259	NA

Table B1.23. Continued

				APOA1			APOB		
Window	**Window SNP**	**Genotype**	**MAF**	**Beta**	**p_value**	**hap_P**	**Beta**	**p_value**	**hap_P**
55	CTP13868	GA/GG	0.002	-11.653	0.723	NA	1.119	0.864	NA
56	rs11644475	AA/GA/GG	0.038	3.856	0.500	0.377	0.251	0.824	0.552
56	rs158478	AA/CA/CC	0.495	-3.097	0.163	NA	-0.493	0.259	NA
56	CTP13868	GA/GG	0.002	-11.653	0.723	NA	1.119	0.864	NA
56	rs158479	AA/GA/GG	0.498	-1.631	0.464	NA	-0.523	0.239	NA
57	rs158478	AA/CA/CC	0.495	-3.097	0.163	0.406	-0.493	0.259	0.076
57	CTP13868	GA/GG	0.002	-11.653	0.723	NA	1.119	0.864	NA
57	rs158479	AA/GA/GG	0.498	-1.631	0.464	NA	-0.523	0.239	NA
57	rs181381869	CC/CT	0.011	-0.086	0.993	NA	-4.562	0.017	NA
58	CTP13868	GA/GG	0.002	-11.653	0.723	0.501	1.119	0.864	0.077
58	rs158479	AA/GA/GG	0.498	-1.631	0.464	NA	-0.523	0.239	NA
58	rs181381869	CC/CT	0.011	-0.086	0.993	NA	-4.562	0.017	NA
58	rs289717	CC/CT/TT	0.320	-1.496	0.521	NA	0.087	0.852	NA
59	rs158479	AA/GA/GG	0.498	-1.631	0.464	0.761	-0.523	0.239	0.026
59	rs181381869	CC/CT	0.011	-0.086	0.993	NA	-4.562	0.017	NA
59	rs289717	CC/CT/TT	0.320	-1.496	0.521	NA	0.087	0.852	NA
59	rs35874588	DD/WD/WW	0.300	2.720	0.264	NA	-0.360	0.460	NA
60	rs181381869	CC/CT	0.011	-0.086	0.993	0.743	-4.562	0.017	0.150
60	rs289717	CC/CT/TT	0.320	-1.496	0.521	NA	0.087	0.852	NA
60	rs35874588	DD/WD/WW	0.300	2.720	0.264	NA	-0.360	0.460	NA
60	rs289718	CC/CT/TT	0.304	2.716	0.262	NA	-0.387	0.423	NA
61	rs289717	CC/CT/TT	0.320	-1.496	0.521	0.560	0.087	0.852	0.899
61	rs35874588	DD/WD/WW	0.300	2.720	0.264	NA	-0.360	0.460	NA
61	rs289718	CC/CT/TT	0.304	2.716	0.262	NA	-0.387	0.423	NA
61	rs289719	AA/GA/GG	0.300	2.493	0.309	NA	-0.425	0.383	NA
62	rs35874588	DD/WD/WW	0.300	2.720	0.264	0.552	-0.360	0.460	0.892
62	rs289718	CC/CT/TT	0.304	2.716	0.262	NA	-0.387	0.423	NA
62	rs289719	AA/GA/GG	0.300	2.493	0.309	NA	-0.425	0.383	NA
62	rs2033254	CC/TC/TT	0.374	-0.697	0.755	NA	0.268	0.547	NA
63	rs289718	CC/CT/TT	0.304	2.716	0.262	0.666	-0.387	0.423	0.830
63	rs289719	AA/GA/GG	0.300	2.493	0.309	NA	-0.425	0.383	NA
63	rs2033254	CC/TC/TT	0.374	-0.697	0.755	NA	0.268	0.547	NA
63	rs183439140	CC/CT	0.005	-5.745	0.806	NA	-3.328	0.473	NA
64	rs289719	AA/GA/GG	0.300	2.493	0.309	0.688	-0.425	0.383	0.700
64	rs2033254	CC/TC/TT	0.374	-0.697	0.755	NA	0.268	0.547	NA
64	rs183439140	CC/CT	0.005	-5.745	0.806	NA	-3.328	0.473	NA
64	rs72771489	GA/GG	0.009	-10.997	0.321	NA	2.323	0.290	NA
65	rs2033254	CC/TC/TT	0.374	-0.697	0.755	0.885	0.268	0.547	0.674
65	rs183439140	CC/CT	0.005	-5.745	0.806	NA	-3.328	0.473	NA
65	rs72771489	GA/GG	0.009	-10.997	0.321	NA	2.323	0.290	NA
65	rs56208677	CC/TC/TT	0.077	0.735	0.857	NA	-0.359	0.657	NA
66	rs183439140	CC/CT	0.005	-5.745	0.806	0.590	-3.328	0.473	0.873
66	rs72771489	GA/GG	0.009	-10.997	0.321	NA	2.323	0.290	NA
66	rs56208677	CC/TC/TT	0.077	0.735	0.857	NA	-0.359	0.657	NA
66	rs71387147	GG/GT/TT	0.081	-3.691	0.378	NA	0.326	0.695	NA
67	rs72771489	GA/GG	0.009	-10.997	0.321	0.382	2.323	0.290	0.626
67	rs56208677	CC/TC/TT	0.077	0.735	0.857	NA	-0.359	0.657	NA
67	rs71387147	GG/GT/TT	0.081	-3.691	0.378	NA	0.326	0.695	NA
67	CTP16508	CG/GG	0.003	-29.686	0.202	NA	2.528	0.586	NA
68	rs56208677	CC/TC/TT	0.077	0.735	0.857	0.553	-0.359	0.657	0.935
68	rs71387147	GG/GT/TT	0.081	-3.691	0.378	NA	0.326	0.695	NA
68	CTP16508	CG/GG	0.003	-29.686	0.202	NA	2.528	0.586	NA
68	rs117427818	AA/GA/GG	0.054	-3.520	0.459	NA	-0.301	0.752	NA
69	rs71387147	GG/GT/TT	0.081	-3.691	0.378	0.462	0.326	0.695	0.961
69	CTP16508	CG/GG	0.003	-29.686	0.202	NA	2.528	0.586	NA
69	rs117427818	AA/GA/GG	0.054	-3.520	0.459	NA	-0.301	0.752	NA
69	rs142980129	GG/GT	0.005	-5.709	0.807	NA	-3.352	0.470	NA
70	CTP16508	CG/GG	0.003	-29.686	0.202	0.307	2.528	0.586	0.912
70	rs117427818	AA/GA/GG	0.054	-3.520	0.459	NA	-0.301	0.752	NA
70	rs142980129	GG/GT	0.005	-5.709	0.807	NA	-3.352	0.470	NA
70	CTP16598	CC/CT	0.002	-19.566	0.403	NA	2.327	0.617	NA
71	rs117427818	AA/GA/GG	0.054	-3.520	0.459	0.577	-0.301	0.752	0.985
71	rs142980129	GG/GT	0.005	-5.709	0.807	NA	-3.352	0.470	NA
71	CTP16598	CC/CT	0.002	-19.566	0.403	NA	2.327	0.617	NA
71	rs4784744	AA/GA/GG	0.321	-1.444	0.536	NA	0.108	0.817	NA
72	rs142980129	GG/GT	0.005	-5.709	0.807	0.410	-3.352	0.470	0.858
72	CTP16598	CC/CT	0.002	-19.566	0.403	NA	2.327	0.617	NA
72	rs4784744	AA/GA/GG	0.321	-1.444	0.536	NA	0.108	0.817	NA
72	rs12720898	CC/CT/TT	0.056	6.271	0.199	NA	-0.934	0.335	NA
73	CTP16598	CC/CT	0.002	-19.566	0.403	0.504	2.327	0.617	0.658
73	rs4784744	AA/GA/GG	0.321	-1.444	0.536	NA	0.108	0.817	NA
73	rs12720898	CC/CT/TT	0.056	6.271	0.199	NA	-0.934	0.335	NA
73	rs291044	AA/AG/GG	0.320	-1.496	0.521	NA	0.087	0.852	NA
74	rs4784744	AA/GA/GG	0.321	-1.444	0.536	0.259	0.108	0.817	0.642

Table B1.23. Continued

				APOA1			APOB		
Window	**Window SNP**	**Genotype**	**MAF**	**Beta**	**p_value**	**hap_P**	**Beta**	**p_value**	**hap_P**
74	rs12720898	CC/CT/TT	0.056	6.271	0.199	NA	-0.934	0.335	NA
74	rs291044	AA/AG/GG	0.320	-1.496	0.521	NA	0.087	0.852	NA
74	rs28381709	CA/CC	0.002	68.932	0.036	NA	3.299	0.615	NA
75	rs12720898	CC/CT/TT	0.056	6.271	0.199	0.641	-0.934	0.335	0.914
75	rs291044	AA/AG/GG	0.320	-1.496	0.521	NA	0.087	0.852	NA
75	rs28381709	CA/CC	0.002	68.932	0.036	NA	3.299	0.615	NA
75	rs12708980	GG/GT/TT	0.394	-1.168	0.599	NA	0.055	0.902	NA
76	rs291044	AA/AG/GG	0.320	-1.496	0.521	0.431	0.087	0.852	0.703
76	rs28381709	CA/CC	0.002	68.932	0.036	NA	3.299	0.615	NA
76	rs12708980	GG/GT/TT	0.394	-1.168	0.599	NA	0.055	0.902	NA
76	rs12720889	AA/AT/TT	0.290	4.078	0.097	NA	-0.130	0.791	NA
77	rs28381709	CA/CC	0.002	68.932	0.036	0.500	3.299	0.615	0.916
77	rs12708980	GG/GT/TT	0.394	-1.168	0.599	NA	0.055	0.902	NA
77	rs12720889	AA/AT/TT	0.290	4.078	0.097	NA	-0.130	0.791	NA
77	rs143024882	CA/CC	0.002	-26.013	0.264	NA	2.028	0.659	NA
78	rs12708980	GG/GT/TT	0.394	-1.168	0.599	0.408	0.055	0.902	0.094
78	rs12720889	AA/AT/TT	0.290	4.078	0.097	NA	-0.130	0.791	NA
78	rs143024882	CA/CC	0.002	-26.013	0.264	NA	2.028	0.659	NA
78	rs12447620	AA/GA/GG	0.128	-2.180	0.539	NA	-1.918	0.007	NA
79	rs12720889	AA/AT/TT	0.290	4.078	0.097	0.361	-0.130	0.791	0.079
79	rs143024882	CA/CC	0.002	-26.013	0.264	NA	2.028	0.659	NA
79	rs12447620	AA/GA/GG	0.128	-2.180	0.539	NA	-1.918	0.007	NA
79	rs12708983	CC/TC/TT	0.038	1.468	0.824	NA	-0.608	0.644	NA
80	rs143024882	CA/CC	0.002	-26.013	0.264	0.867	2.028	0.659	0.062
80	rs12447620	AA/GA/GG	0.128	-2.180	0.539	NA	-1.918	0.007	NA
80	rs12708983	CC/TC/TT	0.038	1.468	0.824	NA	-0.608	0.644	NA
80	CTP20593	GA/GG	0.001	54.106	0.100	NA	-4.799	0.464	NA
81	rs12447620	AA/GA/GG	0.128	-2.180	0.539	0.821	-1.918	0.007	0.030
81	rs12708983	CC/TC/TT	0.038	1.468	0.824	NA	-0.608	0.644	NA
81	CTP20593	GA/GG	0.001	54.106	0.100	NA	-4.799	0.464	NA
81	CTP20804	CC/CT	0.005	-17.385	0.240	NA	-2.591	0.377	NA
82	rs12708983	CC/TC/TT	0.038	1.468	0.824	0.921	-0.608	0.644	0.681
82	CTP20593	GA/GG	0.001	54.106	0.100	NA	-4.799	0.464	NA
82	CTP20804	CC/CT	0.005	-17.385	0.240	NA	-2.591	0.377	NA
82	rs4784745	AA/AG/GG	0.313	-1.099	0.646	NA	0.067	0.888	NA
83	CTP20593	GA/GG	0.001	54.106	0.100	0.621	-4.799	0.464	0.607
83	CTP20804	CC/CT	0.005	-17.385	0.240	NA	-2.591	0.377	NA
83	rs4784745	AA/AG/GG	0.313	-1.099	0.646	NA	0.067	0.888	NA
83	rs5880	CC/CG/GG	0.057	-4.504	0.336	NA	-0.679	0.468	NA
84	CTP20804	CC/CT	0.005	-17.385	0.240	0.444	-2.591	0.377	0.591
84	rs4784745	AA/AG/GG	0.313	-1.099	0.646	NA	0.067	0.888	NA
84	rs5880	CC/CG/GG	0.057	-4.504	0.336	NA	-0.679	0.468	NA
84	rs1800774	CC/TC/TT	0.388	-1.412	0.528	NA	0.332	0.454	NA
85	rs4784745	AA/AG/GG	0.313	-1.099	0.646	0.337	0.067	0.888	0.815
85	rs5880	CC/CG/GG	0.057	-4.504	0.336	NA	-0.679	0.468	NA
85	rs1800774	CC/TC/TT	0.388	-1.412	0.528	NA	0.332	0.454	NA
85	rs5882	AA/GA/GG	0.317	1.731	0.470	NA	-0.594	0.213	NA
86	rs5880	CC/CG/GG	0.057	-4.504	0.336	0.411	-0.679	0.468	0.685
86	rs1800774	CC/TC/TT	0.388	-1.412	0.528	NA	0.332	0.454	NA
86	rs5882	AA/GA/GG	0.317	1.731	0.470	NA	-0.594	0.213	NA
86	rs111379440	CC/CT	0.002	-5.924	0.801	NA	-3.413	0.463	NA
87	rs1800774	CC/TC/TT	0.388	-1.412	0.528	0.511	0.332	0.454	0.742
87	rs5882	AA/GA/GG	0.317	1.731	0.470	NA	-0.594	0.213	NA
87	rs111379440	CC/CT	0.002	-5.924	0.801	NA	-3.413	0.463	NA
87	rs12720882	AA/GA	0.009	-5.482	0.642	NA	1.754	0.454	NA
88	rs5882	AA/GA/GG	0.317	1.731	0.470	0.607	-0.594	0.213	0.468
88	rs111379440	CC/CT	0.002	-5.924	0.801	NA	-3.413	0.463	NA
88	rs12720882	AA/GA	0.009	-5.482	0.642	NA	1.754	0.454	NA
88	CTP22888delA	WD/WW	0.001	-23.029	0.484	NA	3.781	0.562	NA
89	rs111379440	CC/CT	0.002	-5.924	0.801	0.713	-3.413	0.463	0.186
89	rs12720882	AA/GA	0.009	-5.482	0.642	NA	1.754	0.454	NA
89	CTP22888delA	WD/WW	0.001	-23.029	0.484	NA	3.781	0.562	NA
89	rs12720887	CC/CT	0.013	3.809	0.681	NA	3.213	0.081	NA
90	rs12720882	AA/GA	0.009	-5.482	0.642	0.612	1.754	0.454	0.043
90	CTP22888delA	WD/WW	0.001	-23.029	0.484	NA	3.781	0.562	NA
90	rs12720887	CC/CT	0.013	3.809	0.681	NA	3.213	0.081	NA
90	rs9923854	GG/GT/TT	0.114	3.935	0.269	NA	1.368	0.053	NA
91	CTP22888delA	WD/WW	0.001	-23.029	0.484	0.486	3.781	0.562	0.082
91	rs12720887	CC/CT	0.013	3.809	0.681	NA	3.213	0.081	NA
91	rs9923854	GG/GT/TT	0.114	3.935	0.269	NA	1.368	0.053	NA
91	rs1800777	AA/AG/GG	0.035	-8.564	0.171	NA	-1.471	0.238	NA
92	rs12720887	CC/CT	0.013	3.809	0.681	0.431	3.213	0.081	0.066
92	rs9923854	GG/GT/TT	0.114	3.935	0.269	NA	1.368	0.053	NA
92	rs1800777	AA/AG/GG	0.035	-8.564	0.171	NA	-1.471	0.238	NA

Table B1.23. Continued

				APOA1			APOB		
Window	**Window SNP**	**Genotype**	**MAF**	**Beta**	**p_value**	**hap_P**	**Beta**	**p_value**	**hap_P**
92	rs1801706	AA/GA/GG	0.171	4.425	0.139	NA	0.552	0.352	NA
93	rs9923854	GG/GT/TT	0.114	3.935	0.269	0.457	1.368	0.053	0.007
93	rs1800777	AA/AG/GG	0.035	-8.564	0.171	NA	-1.471	0.238	NA
93	rs1801706	AA/GA/GG	0.171	4.425	0.139	NA	0.552	0.352	NA
93	rs289742	CC/GC/GG	0.127	-0.951	0.787	NA	-2.023	0.004	NA
94	rs1800777	AA/AG/GG	0.035	-8.564	0.171	0.352	-1.471	0.238	0.029
94	rs1801706	AA/GA/GG	0.171	4.425	0.139	NA	0.552	0.352	NA
94	rs289742	CC/GC/GG	0.127	-0.951	0.787	NA	-2.023	0.004	NA
94	rs289743	AA/GA/GG	0.300	3.025	0.215	NA	-0.397	0.414	NA
95	rs1801706	AA/GA/GG	0.171	4.425	0.139	0.406	0.552	0.352	0.034
95	rs289742	CC/GC/GG	0.127	-0.951	0.787	NA	-2.023	0.004	NA
95	rs289743	AA/GA/GG	0.300	3.025	0.215	NA	-0.397	0.414	NA
95	rs289744	AA/CA/CC	0.300	3.022	0.212	NA	-0.381	0.429	NA
96	rs289742	CC/GC/GG	0.127	-0.951	0.787	0.657	-2.023	0.004	0.048
96	rs289743	AA/GA/GG	0.300	3.025	0.215	NA	-0.397	0.414	NA
96	rs289744	AA/CA/CC	0.300	3.022	0.212	NA	-0.381	0.429	NA
96	rs12720917	CC/TC/TT	0.172	1.847	0.546	NA	0.087	0.886	NA
97	rs289743	AA/GA/GG	0.300	3.025	0.215	0.224	-0.397	0.414	0.882
97	rs289744	AA/CA/CC	0.300	3.022	0.212	NA	-0.381	0.429	NA
97	rs12720917	CC/TC/TT	0.172	1.847	0.546	NA	0.087	0.886	NA
97	rs289745	AA/CA/CC	0.409	-4.717	0.037	NA	0.356	0.433	NA

TABLE B1.24. Summary of *CETP* 4-SNP sliding haplotypes (100 SNPs included) for ApoA1 and ApoB in NHWs

							ApoA1				ApoB			
	Window	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**	**coef**	**se**	**t.stat**	**pval**
Geno.2	1	A	A	T	G	0.035	-3.402	7.190	-0.473	0.636	-0.860	1.444	-0.595	0.552
Geno.3	1	A	C	C	A	0.134	-2.320	3.758	-0.617	0.537	0.643	0.740	0.868	0.386
Geno.4	1	A	C	C	G	0.231	-4.374	3.098	-1.412	0.159	-0.017	0.616	-0.027	0.978
Geno.7	1	G	C	C	A	0.040	-7.588	6.851	-1.108	0.269	1.258	1.347	0.935	0.351
Geno.8	1	G	C	C	G	0.261	-3.968	3.060	-1.297	0.195	-0.083	0.609	-0.137	0.891
haplo.base	1	G	A	T	G	0.299	NA	NA	NA	NA	NA	NA	NA	NA
Geno.21	2	A	T	G	A	0.317	4.495	2.510	1.790	0.074	0.084	0.500	0.168	0.867
Geno.31	2	A	T	G	G	0.017	-6.238	8.658	-0.720	0.472	-1.277	1.717	-0.743	0.458
Geno.5	2	C	C	A	G	0.173	0.532	3.126	0.170	0.865	0.794	0.622	1.277	0.202
Geno.rare	2	*	*	*	*	0.001	-11.887	0.060	-197.621	0.000	7.649	6.487	1.179	0.239
haplo.base1	2	C	C	G	G	0.492	NA	NA	NA	NA	NA	NA	NA	NA
Geno.22	3	C	A	G	T	0.172	-4.023	3.354	-1.200	0.231	0.692	0.667	1.037	0.300
Geno.41	3	C	G	G	C	0.206	-4.294	3.191	-1.346	0.179	-0.398	0.636	-0.625	0.532
Geno.51	3	C	G	G	T	0.286	-4.727	2.830	-1.670	0.096	0.129	0.563	0.228	0.820
Geno.81	3	T	G	G	T	0.016	-13.293	9.299	-1.430	0.154	-2.057	1.937	-1.062	0.289
Geno.rare1	3	*	*	*	*	0.003	4.354	0.227	19.147	0.000	5.792	4.266	1.358	0.175
haplo.base2	3	T	G	A	T	0.317	NA	NA	NA	NA	NA	NA	NA	NA
Geno.23	4	A	G	T	G	0.174	-4.527	3.428	-1.321	0.187	0.574	0.681	0.844	0.399
Geno.6	4	G	G	C	G	0.207	-4.490	3.269	-1.374	0.170	-0.516	0.648	-0.795	0.427
Geno.71	4	G	G	T	G	0.285	-4.920	2.917	-1.687	0.092	-0.044	0.581	-0.076	0.940
Geno.82	4	G	G	T	T	0.015	-14.958	9.503	-1.574	0.116	-1.890	1.892	-0.999	0.318
Geno.rare2	4	*	*	*	*	0.009	-8.062	12.862	-0.627	0.531	-2.654	2.572	-1.032	0.303
haplo.base3	4	G	A	T	T	0.310	NA	NA	NA	NA	NA	NA	NA	NA
Geno.32	5	A	T	T	T	0.310	4.833	2.629	1.838	0.067	-0.179	0.523	-0.342	0.733
Geno.42	5	G	C	G	C	0.207	0.204	2.981	0.069	0.945	-0.729	0.592	-1.232	0.219
Geno.83	5	G	T	T	T	0.013	-9.111	10.018	-0.910	0.364	-1.903	1.986	-0.958	0.339
Geno.rare3	5	*	*	*	*	0.012	-6.751	10.493	-0.643	0.520	-3.029	2.088	-1.450	0.148
haplo.base4	5	G	T	G	C	0.458	NA	NA	NA	NA	NA	NA	NA	NA
Geno.24	6	C	G	C	T	0.207	1.068	3.053	0.350	0.727	-0.753	0.606	-1.243	0.214
Geno.33	6	T	G	C	C	0.085	5.962	4.295	1.388	0.166	-0.106	0.859	-0.124	0.902
Geno.84	6	T	T	T	T	0.323	5.224	2.704	1.932	0.054	-0.305	0.537	-0.568	0.571
Geno.rare4	6	*	*	*	*	0.012	-6.009	11.029	-0.545	0.586	-2.958	2.134	-1.386	0.166
haplo.base5	6	T	G	C	T	0.373	NA	NA	NA	NA	NA	NA	NA	NA
Geno.25	7	G	C	C	G	0.085	5.756	4.288	1.342	0.180	-0.140	0.862	-0.162	0.871
Geno.34	7	G	C	T	A	0.199	-0.054	3.063	-0.018	0.986	-0.813	0.614	-1.324	0.186
Geno.85	7	T	T	T	A	0.323	4.845	2.680	1.808	0.071	-0.311	0.533	-0.584	0.559
Geno.rare5	7	*	*	*	*	0.012	-5.613	0.372	-15.096	0.000	-3.000	2.096	-1.431	0.153
haplo.base6	7	G	C	T	G	0.381	NA	NA	NA	NA	NA	NA	NA	NA
Geno.35	8	C	C	G	T	0.086	6.085	4.269	1.426	0.155	-0.220	0.855	-0.257	0.797
Geno.43	8	C	T	A	C	0.202	-0.466	3.087	-0.151	0.880	-0.845	0.613	-1.379	0.169
Geno.61	8	T	T	A	C	0.330	4.561	2.603	1.753	0.080	-0.471	0.518	-0.909	0.364
Geno.rare6	8	*	*	*	*	0.001	-15.473	0.074	-210.501	0.000	-1.974	6.530	-0.302	0.763
haplo.base7	8	C	T	G	C	0.380	NA	NA	NA	NA	NA	NA	NA	NA
Geno.36	9	C	G	T	C	0.086	2.889	4.118	0.701	0.483	0.329	0.823	0.400	0.690
Geno.52	9	T	G	C	C	0.182	-0.986	3.010	-0.328	0.743	0.967	0.598	1.618	0.106
Geno.62	9	T	G	C	T	0.198	-4.328	2.910	-1.487	0.138	0.291	0.580	0.502	0.616
Geno.rare7	9	*	*	*	*	0.001	-16.708	0.016	-1070.957	0.000	-1.052	6.512	-0.162	0.872
haplo.base8	9	T	A	C	C	0.533	NA	NA	NA	NA	NA	NA	NA	NA
Geno.26	10	A	C	C	C	0.120	-1.945	3.660	-0.531	0.595	-0.922	0.725	-1.273	0.204
Geno.37	10	G	C	C	A	0.010	-6.784	11.729	-0.578	0.563	2.897	2.315	1.252	0.211
Geno.44	10	G	C	C	C	0.173	-1.191	3.178	-0.375	0.708	0.623	0.630	0.990	0.323
Geno.63	10	G	C	T	C	0.198	-4.886	3.045	-1.604	0.109	0.050	0.604	0.083	0.934
Geno.72	10	G	T	C	A	0.086	2.551	4.208	0.606	0.545	0.083	0.838	0.099	0.921
haplo.base9	10	A	C	C	A	0.413	NA	NA	NA	NA	NA	NA	NA	NA
Geno.1	11	C	C	A	A	0.043	-6.940	5.870	-1.182	0.238	-0.642	1.136	-0.565	0.573
Geno.45	11	C	C	C	C	0.291	-1.681	2.730	-0.616	0.538	-0.201	0.543	-0.370	0.711
Geno.64	11	C	T	C	C	0.196	-5.010	3.063	-1.635	0.103	-0.010	0.610	-0.017	0.986
Geno.73	11	T	C	A	C	0.086	2.140	4.207	0.509	0.611	0.085	0.846	0.100	0.920
Geno.rare8	11	*	*	*	*	0.004	-27.945	0.221	-126.371	0.000	4.526	4.768	0.949	0.343
haplo.base10	11	C	C	A	C	0.379	NA	NA	NA	NA	NA	NA	NA	NA
Geno.11	12	C	A	A	C	0.045	-8.138	5.536	-1.470	0.142	-0.571	1.110	-0.515	0.607
Geno.53	12	C	C	C	T	0.291	-2.252	2.604	-0.865	0.388	-0.195	0.522	-0.374	0.708
Geno.9	12	T	C	C	T	0.196	-5.738	2.953	-1.943	0.053	0.017	0.593	0.028	0.977
Geno.rare9	12	*	*	*	*	0.007	-29.568	0.205	-143.910	0.000	3.018	2.680	1.126	0.261
haplo.base11	12	C	A	C	C	0.461	NA	NA	NA	NA	NA	NA	NA	NA
Geno.12	13	A	A	C	G	0.045	-4.810	5.593	-0.860	0.390	-0.454	1.122	-0.404	0.686
Geno.27	13	A	C	C	A	0.440	4.028	2.290	1.759	0.079	0.149	0.461	0.324	0.746
Geno.38	13	A	C	C	G	0.021	-1.996	7.901	-0.253	0.801	-0.518	1.567	-0.330	0.741
Geno.rare10	13	*	*	*	*	0.007	-25.514	0.355	-71.800	0.000	3.103	2.689	1.154	0.249
haplo.base12	13	C	C	T	G	0.487	NA	NA	NA	NA	NA	NA	NA	NA
Geno.13	14	A	C	G	C	0.047	-5.470	5.529	-0.989	0.323	-0.112	1.102	-0.101	0.919

Table B1.24. Continued

							ApoA1				ApoB			
	Window	loc.1	loc.2	loc.3	loc.4	hap.freq	coef	se	t.stat	pval	coef	se	t.stat	pval
Geno.39	14	C	C	A	C	0.441	4.218	2.347	1.797	0.073	0.205	0.467	0.438	0.661
Geno.46	14	C	C	G	C	0.021	-1.865	8.038	-0.232	0.817	-0.428	1.574	-0.272	0.786
Geno.65	14	C	T	G	T	0.032	-0.120	6.505	-0.018	0.985	1.256	1.297	0.968	0.334
haplo.base13	14	C	T	G	C	0.459	NA	NA	NA	NA	NA	NA	NA	NA
Geno.14	15	C	A	C	A	0.440	4.425	2.342	1.889	0.060	0.200	0.467	0.429	0.668
Geno.310	15	C	G	C	G	0.069	-4.621	4.734	-0.976	0.330	-0.244	0.932	-0.262	0.793
Geno.66	15	T	G	T	G	0.032	-0.222	6.486	-0.034	0.973	1.253	1.294	0.969	0.333
haplo.base14	15	T	G	C	G	0.459	NA	NA	NA	NA	NA	NA	NA	NA
Geno.47	16	G	C	G	A	0.233	-4.276	2.831	-1.511	0.132	-0.193	0.564	-0.341	0.733
Geno.54	16	G	C	G	G	0.296	-5.801	2.674	-2.169	0.031	-0.246	0.529	-0.464	0.643
Geno.67	16	G	T	G	A	0.032	-4.506	6.485	-0.695	0.488	1.065	1.293	0.824	0.410
haplo.base15	16	A	C	A	G	0.440	NA	NA	NA	NA	NA	NA	NA	NA
Geno.48	17	C	G	A	A	0.194	-4.423	2.998	-1.475	0.141	-0.257	0.593	-0.434	0.665
Geno.55	17	C	G	A	G	0.039	-2.292	6.710	-0.342	0.733	-0.428	1.289	-0.332	0.740
Geno.68	17	C	G	G	A	0.105	-4.010	4.068	-0.986	0.325	-0.400	0.803	-0.498	0.619
Geno.74	17	C	G	G	G	0.191	-6.673	3.122	-2.137	0.033	-0.293	0.616	-0.476	0.635
Geno.86	17	T	G	A	G	0.032	-4.191	6.498	-0.645	0.519	0.946	1.291	0.733	0.464
Geno.rare11	17	*	*	*	*	0.004	18.521	0.190	97.458	0.000	-9.395	4.214	-2.229	0.026
haplo.base16	17	C	A	G	A	0.436	NA	NA	NA	NA	NA	NA	NA	NA
Geno.49	18	G	A	A	G	0.188	-4.456	2.989	-1.491	0.137	-0.331	0.598	-0.554	0.580
Geno.69	18	G	A	G	G	0.075	-7.240	4.593	-1.576	0.116	0.477	0.909	0.524	0.600
Geno.75	18	G	G	A	C	0.092	-2.553	3.999	-0.638	0.524	-0.112	0.809	-0.139	0.890
Geno.87	18	G	G	A	G	0.019	-18.191	9.370	-1.941	0.053	-2.174	1.772	-1.227	0.221
Geno.91	18	G	G	G	G	0.185	-5.458	3.095	-1.764	0.079	-0.303	0.616	-0.492	0.623
Geno.rare12	18	*	*	*	*	0.004	54.775	0.318	172.364	0.000	-7.174	3.612	-1.986	0.048
haplo.base17	18	A	G	A	G	0.436	NA	NA	NA	NA	NA	NA	NA	NA
Geno.28	19	A	A	G	C	0.192	-3.615	3.255	-1.111	0.267	-0.602	0.627	-0.960	0.337
Geno.410	19	A	G	G	C	0.071	-6.511	5.295	-1.230	0.220	1.308	1.020	1.282	0.201
Geno.56	19	G	A	C	C	0.091	-1.879	4.076	-0.461	0.645	-0.061	0.821	-0.074	0.941
Geno.88	19	G	G	G	C	0.190	-4.922	3.549	-1.387	0.166	-0.799	0.672	-1.188	0.236
Geno.rare13	19	*	*	*	*	0.003	56.000	0.097	578.978	0.000	-2.044	4.845	-0.422	0.673
haplo.base18	19	G	A	G	C	0.454	NA	NA	NA	NA	NA	NA	NA	NA
Geno.15	20	A	C	C	C	0.093	-0.254	4.036	-0.063	0.950	-0.026	0.810	-0.032	0.975
Geno.29	20	A	G	C	C	0.200	-3.629	3.032	-1.197	0.232	-0.467	0.607	-0.769	0.442
Geno.610	20	G	G	C	G	0.262	-5.125	2.814	-1.821	0.069	-0.179	0.555	-0.322	0.747
Geno.rare14	20	*	*	*	*	0.001	-7.907	0.064	-123.129	0.000	-6.823	6.510	-1.048	0.295
haplo.base19	20	A	G	C	G	0.444	NA	NA	NA	NA	NA	NA	NA	NA
Geno.16	21	C	C	C	A	0.093	1.492	3.947	0.378	0.706	0.029	0.779	0.037	0.970
Geno.411	21	G	C	C	C	0.197	-1.992	2.790	-0.714	0.476	-0.263	0.551	-0.477	0.634
Geno.rare15	21	*	*	*	*	0.012	-7.048	0.127	-55.305	0.000	-4.916	2.072	-2.372	0.018
haplo.base20	21	G	C	G	A	0.698	NA	NA	NA	NA	NA	NA	NA	NA
Geno.17	22	C	C	A	C	0.054	1.479	4.811	0.307	0.759	-0.897	0.958	-0.937	0.349
Geno.210	22	C	C	A	T	0.038	1.699	6.469	0.263	0.793	-1.133	1.338	-0.847	0.398
Geno.311	22	C	C	C	C	0.197	-4.694	3.064	-1.532	0.126	-0.474	0.617	-0.769	0.442
Geno.412	22	C	G	A	C	0.269	-6.004	2.805	-2.140	0.033	-0.273	0.571	-0.478	0.633
Geno.rare16	22	*	*	*	*	0.009	-8.751	0.747	-11.718	0.000	-2.840	2.486	-1.143	0.254
haplo.base21	22	C	G	A	T	0.434	NA	NA	NA	NA	NA	NA	NA	NA
Geno.18	23	C	A	C	W	0.053	1.401	4.837	0.290	0.772	-0.895	0.958	-0.935	0.350
Geno.211	23	C	A	T	W	0.038	1.433	6.546	0.219	0.827	-1.113	1.332	-0.835	0.404
Geno.312	23	C	C	C	D	0.185	-4.513	3.109	-1.452	0.147	-0.403	0.621	-0.648	0.517
Geno.413	23	C	C	C	W	0.012	-12.621	10.489	-1.203	0.230	-2.077	2.081	-0.998	0.319
Geno.611	23	G	A	C	W	0.269	-6.082	2.856	-2.129	0.034	-0.307	0.571	-0.537	0.592
Geno.rare17	23	*	*	*	*	0.008	-8.949	13.171	-0.679	0.497	-2.282	2.655	-0.859	0.391
haplo.base22	23	G	A	T	W	0.434	NA	NA	NA	NA	NA	NA	NA	NA
Geno.19	24	A	C	W	A	0.263	-5.275	2.660	-1.983	0.048	-0.142	0.537	-0.264	0.792
Geno.212	24	A	C	W	G	0.059	-1.681	4.450	-0.378	0.706	-0.685	0.899	-0.762	0.447
Geno.57	24	C	C	D	G	0.191	-4.962	2.886	-1.719	0.086	-0.282	0.583	-0.485	0.628
Geno.612	24	C	C	W	G	0.015	-10.366	9.210	-1.125	0.261	-1.707	1.860	-0.918	0.359
Geno.rare18	24	*	*	*	*	0.001	-105.074	0.033	-3153.062	0.000	5.653	6.607	0.856	0.393
haplo.base23	24	A	T	W	G	0.471	NA	NA	NA	NA	NA	NA	NA	NA
Geno.110	25	C	D	G	A	0.191	-4.918	3.053	-1.611	0.108	-0.347	0.617	-0.562	0.574
Geno.313	25	C	W	A	G	0.263	-5.246	2.847	-1.843	0.066	-0.212	0.575	-0.369	0.712
Geno.414	25	C	W	G	A	0.016	-9.925	9.140	-1.086	0.278	-1.992	1.867	-1.067	0.287
Geno.58	25	C	W	G	G	0.058	-1.698	4.511	-0.376	0.707	-0.686	0.916	-0.749	0.454
Geno.89	25	T	W	G	G	0.039	0.142	6.359	0.022	0.982	-0.371	1.297	-0.286	0.775
Geno.rare19	25	*	*	*	*	0.001	-105.035	0.056	-1867.851	0.000	5.662	6.588	0.859	0.391
haplo.base24	25	T	W	G	A	0.432	NA	NA	NA	NA	NA	NA	NA	NA
Geno.213	26	D	G	A	A	0.191	-4.544	2.983	-1.523	0.128	-0.253	0.597	-0.425	0.671
Geno.76	26	W	A	G	G	0.262	-5.271	2.732	-1.929	0.054	-0.123	0.546	-0.225	0.822
Geno.111	26	W	G	G	G	0.095	-0.620	3.933	-0.158	0.875	-0.308	0.793	-0.389	0.698
Geno.rare20	26	*	*	*	*	0.004	-19.855	0.022	-912.542	0.000	0.642	6.616	0.097	0.923
haplo.base25	26	W	G	A	G	0.448	NA	NA	NA	NA	NA	NA	NA	NA
Geno.415	27	A	G	G	G	0.262	-5.616	2.768	-2.029	0.043	-0.223	0.555	-0.401	0.688
Geno.59	27	G	A	A	G	0.191	-4.645	3.014	-1.541	0.124	-0.364	0.604	-0.603	0.547
Geno.613	27	G	A	G	G	0.016	-10.287	9.223	-1.115	0.265	-1.723	1.894	-0.910	0.364

Table B1.24. Continued

							ApoA1				ApoB			
	Window	loc.1	loc.2	loc.3	loc.4	hap.freq	coef	se	t.stat	pval	coef	se	t.stat	pval
Geno.810	27	G	G	G	G	0.098	-1.275	3.930	-0.324	0.746	-0.405	0.789	-0.514	0.608
Geno.rare21	27	*	*	*	*	0.002	-49.764	0.050	-1001.291	0.000	2.303	6.600	0.349	0.727
haplo.base26	27	G	A	G	T	0.431	NA	NA	NA	NA	NA	NA	NA	NA
Geno.112	28	A	A	G	A	0.187	-5.111	3.031	-1.686	0.092	-0.408	0.605	-0.674	0.501
Geno.416	28	A	G	G	A	0.016	-9.834	9.244	-1.064	0.288	-1.737	1.893	-0.918	0.359
Geno.77	28	G	G	G	A	0.099	-0.732	3.931	-0.186	0.852	-0.506	0.790	-0.641	0.522
Geno.811	28	G	G	G	C	0.261	-5.636	2.769	-2.036	0.042	-0.195	0.554	-0.353	0.725
Geno.rare22	28	*	*	*	*	0.005	17.753	0.329	53.960	0.000	1.161	3.272	0.355	0.723
haplo.base27	28	A	G	T	A	0.432	NA	NA	NA	NA	NA	NA	NA	NA
Geno.113	29	A	G	A	G	0.188	-5.162	3.019	-1.710	0.088	-0.409	0.604	-0.677	0.499
Geno.510	29	G	G	A	A	0.095	-0.348	3.956	-0.088	0.930	-0.458	0.794	-0.577	0.564
Geno.614	29	G	G	A	G	0.018	-10.659	8.701	-1.225	0.221	-1.739	1.752	-0.993	0.321
Geno.78	29	G	G	C	G	0.262	-5.595	2.758	-2.028	0.043	-0.200	0.553	-0.362	0.717
Geno.rare23	29	*	*	*	*	0.005	16.952	0.347	48.877	0.000	1.077	3.280	0.328	0.743
haplo.base28	29	G	T	A	G	0.432	NA	NA	NA	NA	NA	NA	NA	NA
Geno.214	30	G	A	A	C	0.094	-0.533	3.974	-0.134	0.893	-0.355	0.798	-0.444	0.657
Geno.314	30	G	A	G	C	0.205	-5.464	2.964	-1.843	0.066	-0.474	0.595	-0.797	0.426
Geno.511	30	G	C	G	A	0.262	-5.644	2.776	-2.033	0.043	-0.278	0.554	-0.502	0.616
Geno.rare24	30	*	*	*	*	0.006	14.526	0.170	85.309	0.000	3.170	2.934	1.081	0.280
haplo.base29	30	T	A	G	C	0.433	NA	NA	NA	NA	NA	NA	NA	NA
Geno.215	31	A	A	C	C	0.092	-1.425	4.264	-0.334	0.738	-0.310	0.792	-0.392	0.695
Geno.315	31	A	G	C	C	0.195	-4.499	3.073	-1.464	0.144	-0.269	0.602	-0.447	0.655
Geno.615	31	C	G	A	C	0.013	6.478	0.359	18.039	0.000	3.235	2.228	1.452	0.147
Geno.79	31	C	G	A	G	0.247	-6.484	3.014	-2.152	0.032	-0.404	0.569	-0.710	0.478
Geno.rare25	31	*	*	*	*	0.008	25.070	0.282	88.875	0.000	3.359	2.928	1.147	0.252
haplo.base30	31	A	G	C	G	0.445	NA	NA	NA	NA	NA	NA	NA	NA
Geno.216	32	A	C	C	G	0.091	-0.064	4.263	-0.015	0.988	-0.425	0.816	-0.521	0.603
Geno.417	32	G	A	C	T	0.012	6.361	15.468	0.411	0.681	3.171	2.376	1.334	0.183
Geno.512	32	G	A	G	G	0.248	-5.219	3.190	-1.636	0.103	-0.338	0.587	-0.575	0.565
Geno.710	32	G	C	C	T	0.195	-3.796	3.174	-1.196	0.232	-0.212	0.606	-0.349	0.727
Geno.rare26	32	*	*	*	*	0.010	0.331	14.707	0.023	0.982	1.974	2.515	0.785	0.433
haplo.base31	32	G	C	G	G	0.445	NA	NA	NA	NA	NA	NA	NA	NA
Geno.217	33	A	C	T	C	0.015	4.198	11.556	0.363	0.717	2.892	2.125	1.361	0.174
Geno.418	33	A	G	G	T	0.245	-6.687	2.942	-2.273	0.024	-0.420	0.584	-0.719	0.473
Geno.513	33	C	C	G	T	0.098	-2.080	3.863	-0.538	0.591	-0.449	0.806	-0.558	0.577
Geno.616	33	C	C	T	C	0.065	-5.592	4.793	-1.167	0.244	1.408	0.925	1.522	0.129
Geno.711	33	C	C	T	T	0.126	-3.832	3.605	-1.063	0.288	-1.258	0.717	-1.754	0.080
Geno.rare27	33	*	*	*	*	0.004	71.091	0.115	617.517	0.000	-0.295	6.783	-0.044	0.965
haplo.base32	33	C	G	G	T	0.448	NA	NA	NA	NA	NA	NA	NA	NA
Geno.218	34	C	G	T	C	0.101	1.716	3.788	0.453	0.651	-0.328	0.750	-0.437	0.662
Geno.316	34	C	T	C	C	0.079	-2.191	4.063	-0.539	0.590	1.781	0.799	2.228	0.026
Geno.419	34	C	T	T	C	0.124	-0.674	3.427	-0.197	0.844	-1.054	0.675	-1.560	0.119
Geno.rare28	34	*	*	*	*	0.002	-9.245	0.063	-146.834	0.000	-4.501	4.577	-0.983	0.326
haplo.base33	34	G	G	T	C	0.693	NA	NA	NA	NA	NA	NA	NA	NA
Geno.420	35	T	C	C	A	0.079	-2.456	4.041	-0.608	0.544	1.797	0.795	2.259	0.024
Geno.514	35	T	T	C	A	0.125	-1.028	3.364	-0.306	0.760	-1.042	0.665	-1.567	0.118
Geno.rare29	35	*	*	*	*	0.003	-20.676	0.061	-341.126	0.000	-4.170	3.734	-1.117	0.265
haplo.base34	35	G	T	C	A	0.792	NA	NA	NA	NA	NA	NA	NA	NA
Geno.114	36	C	C	A	G	0.079	-0.106	4.233	-0.025	0.980	2.274	0.839	2.711	0.007
Geno.219	36	T	C	A	A	0.443	3.914	2.358	1.660	0.098	0.655	0.471	1.390	0.165
Geno.rare30	36	*	*	*	*	0.003	-16.543	0.149	-110.845	0.000	-3.237	3.760	-0.861	0.390
haplo.base35	36	T	C	A	G	0.474	NA	NA	NA	NA	NA	NA	NA	NA
Geno.115	37	C	A	A	C	0.443	4.156	2.232	1.862	0.063	0.306	0.451	0.678	0.498
Geno.rare31	37	*	*	*	*	0.012	1.351	0.190	7.112	0.000	0.526	2.093	0.251	0.802
haplo.base36	37	C	A	G	C	0.545	NA	NA	NA	NA	NA	NA	NA	NA
Geno.116	38	A	A	C	C	0.445	3.925	2.258	1.738	0.083	0.334	0.450	0.742	0.459
Geno.rare32	38	*	*	*	*	0.015	-5.110	9.241	-0.553	0.581	3.093	1.847	1.675	0.095
haplo.base37	38	A	G	C	C	0.540	NA	NA	NA	NA	NA	NA	NA	NA
Geno.117	39	A	C	C	A	0.447	3.831	2.257	1.697	0.090	0.277	0.447	0.619	0.536
Geno.rare33	39	*	*	*	*	0.014	-2.282	9.599	-0.238	0.812	3.613	1.918	1.884	0.060
haplo.base38	39	G	C	C	C	0.539	NA	NA	NA	NA	NA	NA	NA	NA
Geno.118	40	C	C	A	C	0.329	3.736	2.474	1.510	0.132	0.111	0.489	0.227	0.820
Geno.220	40	C	C	A	T	0.116	4.400	3.495	1.259	0.209	0.788	0.694	1.137	0.256
Geno.rare34	40	*	*	*	*	0.014	-2.076	10.640	-0.195	0.845	3.645	1.917	1.902	0.058
haplo.base39	40	C	C	C	C	0.541	NA	NA	NA	NA	NA	NA	NA	NA
Geno.119	41	C	A	C	C	0.315	4.155	2.500	1.662	0.097	0.167	0.496	0.336	0.737
Geno.221	41	C	A	C	T	0.014	-6.476	9.577	-0.676	0.499	-2.200	1.901	-1.158	0.248
Geno.317	41	C	A	T	C	0.116	4.079	3.487	1.170	0.243	0.734	0.693	1.059	0.290
Geno.rare35	41	*	*	*	*	0.006	-17.620	19.450	-0.906	0.365	5.248	3.088	1.700	0.090
haplo.base40	41	C	C	C	C	0.549	NA	NA	NA	NA	NA	NA	NA	NA
Geno.222	42	A	C	C	G	0.315	4.534	2.532	1.791	0.074	0.176	0.504	0.349	0.727
Geno.318	42	A	C	T	G	0.014	-5.613	9.607	-0.584	0.559	-2.239	1.912	-1.171	0.242
Geno.421	42	A	T	C	G	0.116	4.731	3.517	1.345	0.179	0.696	0.701	0.993	0.321
Geno.515	42	C	C	C	A	0.040	4.908	5.684	0.863	0.388	0.388	1.130	0.343	0.732

Table B1.24. Continued

							ApoA1				ApoB			
	Window	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**	**coef**	**se**	**t.stat**	**pval**
haplo.base41	42	C	C	C	G	0.514	NA	NA	NA	NA	NA	NA	NA	NA
Geno.120	43	C	C	A	C	0.040	3.319	5.635	0.589	0.556	0.323	1.117	0.289	0.773
Geno.422	43	C	T	G	C	0.014	-7.161	9.619	-0.744	0.457	-2.259	1.909	-1.183	0.237
Geno.617	43	T	C	G	C	0.116	2.993	3.383	0.885	0.377	0.625	0.673	0.929	0.353
Geno.rare36	43	*	*	*	*	0.007	6.220	13.485	0.461	0.645	-0.179	2.684	-0.067	0.947
haplo.base42	43	C	C	G	C	0.822	NA	NA	NA	NA	NA	NA	NA	NA
Geno.121	44	C	A	C	C	0.040	1.914	5.643	0.339	0.735	0.214	1.121	0.191	0.849
Geno.423	44	C	G	C	T	0.264	-3.464	2.549	-1.359	0.175	-0.043	0.510	-0.084	0.933
Geno.618	44	T	G	C	C	0.014	-8.789	9.578	-0.918	0.359	-2.409	1.904	-1.265	0.207
Geno.rare37	44	*	*	*	*	0.007	4.101	13.430	0.305	0.760	-0.353	2.694	-0.131	0.896
haplo.base43	44	C	G	C	C	0.675	NA	NA	NA	NA	NA	NA	NA	NA
Geno.122	45	A	C	C	A	0.040	0.800	5.698	0.140	0.888	0.253	1.137	0.223	0.824
Geno.424	45	G	C	C	G	0.183	-4.604	2.958	-1.557	0.120	-0.133	0.592	-0.225	0.822
Geno.516	45	G	C	T	A	0.265	-4.721	2.716	-1.738	0.083	-0.042	0.547	-0.076	0.939
Geno.rare38	45	*	*	*	*	0.007	2.915	13.487	0.216	0.829	-0.316	2.706	-0.117	0.907
haplo.base44	45	G	C	C	A	0.505	NA	NA	NA	NA	NA	NA	NA	NA
Geno.319	46	C	C	G	T	0.181	-4.803	2.900	-1.656	0.098	-0.219	0.580	-0.378	0.705
Geno.425	46	C	T	A	C	0.265	-4.906	2.657	-1.847	0.065	-0.076	0.538	-0.142	0.887
Geno.rare39	46	*	*	*	*	0.008	0.021	0.194	0.106	0.915	-0.171	2.510	-0.068	0.946
haplo.base45	46	C	C	A	C	0.545	NA	NA	NA	NA	NA	NA	NA	NA
Geno.320	47	C	G	T	A	0.178	-4.177	2.950	-1.416	0.158	-0.287	0.589	-0.486	0.627
Geno.517	47	T	A	C	A	0.265	-4.836	2.667	-1.813	0.070	-0.081	0.537	-0.151	0.880
Geno.rare40	47	*	*	*	*	0.008	-10.210	0.120	-85.440	0.000	1.323	2.484	0.533	0.594
haplo.base46	47	C	A	C	A	0.549	NA	NA	NA	NA	NA	NA	NA	NA
Geno.518	48	G	T	A	C	0.173	-2.741	2.809	-0.976	0.330	-0.281	0.557	-0.504	0.615
Geno.rare41	48	*	*	*	*	0.015	-1.900	9.220	-0.206	0.837	1.722	1.830	0.941	0.347
haplo.base47	48	A	C	A	C	0.812	NA	NA	NA	NA	NA	NA	NA	NA
Geno.123	49	C	A	C	C	0.072	5.072	4.482	1.132	0.258	0.828	0.902	0.918	0.359
Geno.619	49	T	A	C	T	0.165	-2.223	2.939	-0.756	0.450	-0.135	0.587	-0.230	0.818
Geno.rare42	49	*	*	*	*	0.021	0.422	8.427	0.050	0.960	0.362	1.704	0.212	0.832
haplo.base48	49	C	A	C	T	0.742	NA	NA	NA	NA	NA	NA	NA	NA
Geno.124	50	A	C	C	G	0.079	5.180	4.163	1.244	0.214	0.551	0.827	0.666	0.505
Geno.rare43	50	*	*	*	*	0.020	4.759	8.380	0.568	0.570	1.595	1.670	0.955	0.340
haplo.base49	50	A	C	T	G	0.901	NA	NA	NA	NA	NA	NA	NA	NA
Geno.223	51	C	C	G	T	0.070	4.744	4.367	1.086	0.278	0.606	0.869	0.697	0.486
Geno.rare44	51	*	*	*	*	0.022	10.513	7.946	1.323	0.187	0.885	1.585	0.558	0.577
haplo.base50	51	C	T	G	C	0.908	NA	NA	NA	NA	NA	NA	NA	NA
Geno.426	52	C	G	T	T	0.071	3.721	4.361	0.853	0.394	0.590	0.871	0.677	0.499
Geno.620	52	T	G	C	C	0.172	-5.120	2.956	-1.732	0.084	-0.365	0.590	-0.618	0.537
Geno.rare45	52	*	*	*	*	0.015	10.233	9.433	1.085	0.279	0.146	1.891	0.077	0.938
haplo.base51	52	T	G	C	T	0.743	NA	NA	NA	NA	NA	NA	NA	NA
Geno.125	53	G	C	C	A	0.179	-4.706	2.907	-1.619	0.106	-0.374	0.581	-0.644	0.520
Geno.427	53	G	T	T	A	0.031	3.679	6.504	0.566	0.572	0.945	1.302	0.726	0.468
Geno.519	53	G	T	T	G	0.039	3.473	5.680	0.611	0.541	0.243	1.131	0.215	0.830
Geno.rare46	53	*	*	*	*	0.006	13.723	0.169	81.398	0.000	0.715	3.231	0.221	0.825
haplo.base52	53	G	C	T	A	0.745	NA	NA	NA	NA	NA	NA	NA	NA
Geno.126	54	C	C	A	A	0.179	-5.321	3.065	-1.736	0.083	-0.501	0.611	-0.819	0.413
Geno.224	54	C	T	A	A	0.315	-1.154	2.600	-0.444	0.657	-0.337	0.525	-0.642	0.521
Geno.621	54	T	T	A	C	0.032	3.082	6.539	0.471	0.638	0.920	1.307	0.704	0.482
Geno.812	54	T	T	G	C	0.039	2.864	5.769	0.497	0.620	0.109	1.148	0.095	0.925
haplo.base53	54	C	T	A	C	0.435	NA	NA	NA	NA	NA	NA	NA	NA
Geno.127	55	C	A	A	G	0.179	-5.603	3.026	-1.852	0.065	-0.571	0.604	-0.945	0.345
Geno.428	55	T	A	A	G	0.315	-1.416	2.550	-0.555	0.579	-0.414	0.515	-0.804	0.422
Geno.813	55	T	G	C	G	0.039	2.597	5.751	0.452	0.652	0.042	1.145	0.037	0.970
Geno.rare47	55	*	*	*	*	0.001	-14.345	0.053	-269.974	0.000	0.648	6.528	0.099	0.921
haplo.base54	55	T	A	C	G	0.466	NA	NA	NA	NA	NA	NA	NA	NA
Geno.128	56	A	A	G	A	0.012	-15.906	0.513	-31.015	0.000	-1.026	2.101	-0.488	0.626
Geno.429	56	A	C	G	A	0.456	1.830	2.194	0.834	0.405	0.482	0.447	1.079	0.281
Geno.712	56	G	C	G	A	0.039	4.535	5.747	0.789	0.431	0.436	1.154	0.378	0.706
Geno.rare48	56	*	*	*	*	0.011	6.355	0.327	19.444	0.000	-2.381	2.206	-1.079	0.281
haplo.base55	56	A	A	G	G	0.482	NA	NA	NA	NA	NA	NA	NA	NA
Geno.129	57	A	G	A	C	0.012	-17.898	0.101	-177.375	0.000	-1.670	2.067	-0.808	0.420
Geno.225	57	A	G	G	C	0.469	-2.053	2.221	-0.924	0.356	-0.312	0.444	-0.703	0.483
Geno.321	57	A	G	G	T	0.014	-1.004	0.153	-6.561	0.000	-4.744	1.894	-2.505	0.013
Geno.rare49	57	*	*	*	*	0.011	4.230	0.159	26.682	0.000	-2.908	2.195	-1.325	0.186
haplo.base56	57	C	G	A	C	0.495	NA	NA	NA	NA	NA	NA	NA	NA
Geno.226	58	G	A	C	C	0.183	4.981	3.025	1.647	0.100	0.796	0.604	1.319	0.188
Geno.322	58	G	A	C	T	0.324	0.003	2.460	0.001	0.999	0.139	0.496	0.280	0.780
Geno.713	58	G	G	T	C	0.014	0.883	0.387	2.284	0.023	-4.294	1.914	-2.244	0.025
Geno.rare50	58	*	*	*	*	0.003	-10.978	0.050	-218.970	0.000	4.551	4.639	0.981	0.327
haplo.base57	58	G	G	C	C	0.476	NA	NA	NA	NA	NA	NA	NA	NA
Geno.130	59	A	C	C	D	0.010	7.946	1.802	4.409	0.000	0.525	2.300	0.228	0.820
Geno.227	59	A	C	C	W	0.173	4.884	3.178	1.537	0.125	0.421	0.630	0.668	0.504
Geno.323	59	A	C	T	D	0.325	-0.053	2.572	-0.021	0.983	-0.211	0.518	-0.407	0.684

Table B1.24. Continued

							ApoA1				**ApoB**			
	Window	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**	**coef**	**se**	**t.stat**	**pval**
Geno.520	59	G	C	C	W	0.111	-0.073	3.701	-0.020	0.984	-1.707	0.735	-2.324	0.021
Geno.714	59	G	T	C	D	0.013	1.171	9.823	0.119	0.905	-4.345	1.903	-2.283	0.023
Geno.rare51	59	*	*	*	*	0.002	-9.309	0.088	-105.677	0.000	7.781	6.240	1.247	0.213
haplo.base58	59	G	C	C	D	0.365	NA	NA	NA	NA	NA	NA	NA	NA
Geno.324	60	C	C	W	C	0.283	2.674	2.664	1.003	0.316	-0.486	0.531	-0.916	0.360
Geno.521	60	C	T	D	T	0.326	-0.501	2.550	-0.196	0.844	-0.259	0.515	-0.504	0.615
Geno.622	60	T	C	D	T	0.014	-0.258	0.391	-0.661	0.509	-4.724	1.912	-2.470	0.014
Geno.rare52	60	*	*	*	*	0.005	-10.731	0.138	-77.498	0.000	-1.145	3.264	-0.351	0.726
haplo.base59	60	C	C	D	T	0.372	NA	NA	NA	NA	NA	NA	NA	NA
Geno.430	61	C	W	C	A	0.282	2.773	2.681	1.034	0.302	-0.387	0.534	-0.724	0.469
Geno.814	61	T	D	T	G	0.326	-0.491	2.558	-0.192	0.848	-0.076	0.513	-0.148	0.882
Geno.rare53	61	*	*	*	*	0.006	-10.145	0.158	-64.108	0.000	-0.579	2.938	-0.197	0.844
haplo.base60	61	C	D	T	G	0.386	NA	NA	NA	NA	NA	NA	NA	NA
Geno.325	62	D	T	G	T	0.327	-0.725	2.567	-0.282	0.778	-0.118	0.514	-0.229	0.819
Geno.431	62	W	C	A	T	0.282	2.667	2.685	0.993	0.321	-0.406	0.535	-0.758	0.449
Geno.rare54	62	*	*	*	*	0.006	-10.242	0.160	-64.073	0.000	-0.593	2.939	-0.202	0.840
haplo.base61	62	D	T	G	C	0.385	NA	NA	NA	NA	NA	NA	NA	NA
Geno.228	63	C	A	T	C	0.283	2.541	2.691	0.944	0.346	-0.399	0.534	-0.747	0.456
Geno.815	63	T	G	T	C	0.329	-0.725	2.574	-0.282	0.778	-0.106	0.515	-0.207	0.836
Geno.rare55	63	*	*	*	*	0.003	-6.567	0.086	-76.203	0.000	-2.093	3.785	-0.553	0.581
haplo.base62	63	T	G	C	C	0.385	NA	NA	NA	NA	NA	NA	NA	NA
Geno.432	64	A	T	C	G	0.281	2.170	2.697	0.804	0.422	-0.374	0.537	-0.697	0.486
Geno.623	64	G	C	C	A	0.010	-10.694	11.077	-0.965	0.335	2.210	2.198	1.005	0.315
Geno.10	64	G	T	C	G	0.332	-0.825	2.586	-0.319	0.750	-0.059	0.516	-0.114	0.909
Geno.rare56	64	*	*	*	*	0.002	-5.454	0.143	-38.056	0.000	-3.466	4.617	-0.751	0.453
haplo.base63	64	G	C	C	G	0.375	NA	NA	NA	NA	NA	NA	NA	NA
Geno.131	65	C	C	A	C	0.010	-11.243	11.111	-1.012	0.312	2.413	2.201	1.096	0.274
Geno.229	65	C	C	G	C	0.296	-0.709	2.472	-0.287	0.774	0.359	0.490	0.733	0.464
Geno.326	65	C	C	G	T	0.078	0.268	4.101	0.065	0.948	-0.216	0.813	-0.266	0.791
Geno.rare57	65	*	*	*	*	0.002	-5.861	0.099	-59.038	0.000	-3.276	5.088	-0.644	0.520
haplo.base64	65	T	C	G	C	0.613	NA	NA	NA	NA	NA	NA	NA	NA
Geno.327	66	C	G	C	G	0.075	-3.966	4.229	-0.938	0.349	0.289	0.836	0.346	0.729
Geno.624	66	C	G	T	T	0.078	0.018	4.088	0.004	0.997	-0.290	0.810	-0.357	0.721
Geno.rare58	66	*	*	*	*	0.013	-10.419	10.041	-1.038	0.300	1.254	1.989	0.630	0.529
haplo.base65	66	C	G	C	T	0.834	NA	NA	NA	NA	NA	NA	NA	NA
Geno.328	67	G	C	G	G	0.075	-4.006	4.211	-0.951	0.342	0.305	0.837	0.365	0.715
Geno.816	67	G	T	T	G	0.077	0.279	4.079	0.068	0.945	-0.313	0.815	-0.384	0.701
Geno.rare59	67	*	*	*	*	0.013	-14.829	0.229	-64.719	0.000	2.347	1.991	1.179	0.239
haplo.base66	67	G	C	T	G	0.835	NA	NA	NA	NA	NA	NA	NA	NA
Geno.230	68	C	G	G	G	0.076	-4.016	4.196	-0.957	0.339	0.258	0.836	0.309	0.757
Geno.433	68	C	T	G	A	0.050	-3.469	4.825	-0.719	0.473	-0.380	0.959	-0.397	0.692
Geno.92	68	T	T	G	G	0.077	0.278	4.111	0.068	0.946	-0.399	0.820	-0.486	0.627
Geno.rare60	68	*	*	*	*	0.002	-30.545	0.059	-515.997	0.000	2.448	4.615	0.530	0.596
haplo.base67	68	C	T	G	G	0.794	NA	NA	NA	NA	NA	NA	NA	NA
Geno.231	69	G	G	G	G	0.076	-4.087	4.162	-0.982	0.327	0.292	0.830	0.352	0.725
Geno.522	69	T	G	A	G	0.050	-3.532	4.798	-0.736	0.462	-0.345	0.954	-0.362	0.718
Geno.rare61	69	*	*	*	*	0.005	-18.656	0.079	-235.946	0.000	-0.387	3.270	-0.118	0.906
haplo.base68	69	T	G	G	G	0.869	NA	NA	NA	NA	NA	NA	NA	NA
Geno.329	70	G	A	G	C	0.050	-3.283	4.783	-0.686	0.493	-0.364	0.949	-0.383	0.702
Geno.rare62	70	*	*	*	*	0.007	-18.712	0.076	-247.221	0.000	0.472	2.668	0.177	0.860
haplo.base69	70	G	G	G	C	0.943	NA	NA	NA	NA	NA	NA	NA	NA
Geno.232	71	A	G	C	G	0.051	-4.591	4.871	-0.942	0.346	-0.275	0.968	-0.284	0.777
Geno.330	71	G	G	C	A	0.327	-2.144	2.385	-0.899	0.369	0.070	0.478	0.147	0.883
Geno.rare63	71	*	*	*	*	0.005	-14.542	0.136	-106.976	0.000	-0.483	3.278	-0.147	0.883
haplo.base70	71	G	G	C	G	0.617	NA	NA	NA	NA	NA	NA	NA	NA
Geno.132	72	G	C	A	C	0.327	-1.173	2.347	-0.500	0.618	0.045	0.470	0.096	0.923
Geno.434	72	G	C	G	T	0.048	6.814	5.101	1.336	0.182	-0.844	1.016	-0.830	0.407
Geno.rare64	72	*	*	*	*	0.005	-14.476	0.074	-195.634	0.000	-0.339	3.272	-0.103	0.918
haplo.base71	72	G	C	G	C	0.620	NA	NA	NA	NA	NA	NA	NA	NA
Geno.133	73	C	A	C	A	0.326	-1.202	2.349	-0.512	0.609	0.049	0.470	0.105	0.916
Geno.523	73	C	G	T	G	0.051	5.704	4.903	1.163	0.245	-0.903	0.976	-0.926	0.355
Geno.rare65	73	*	*	*	*	0.003	-13.381	0.089	-150.424	0.000	3.011	3.764	0.800	0.424
haplo.base72	73	C	G	C	G	0.619	NA	NA	NA	NA	NA	NA	NA	NA
Geno.134	74	A	C	A	C	0.326	-0.817	2.344	-0.349	0.728	0.045	0.470	0.095	0.924
Geno.625	74	G	T	G	C	0.051	6.070	4.894	1.240	0.216	-0.907	0.975	-0.930	0.353
Geno.rare66	74	*	*	*	*	0.002	34.177	0.057	595.411	0.000	3.890	4.612	0.843	0.400
haplo.base73	74	G	C	G	C	0.621	NA	NA	NA	NA	NA	NA	NA	NA
Geno.233	75	C	A	C	T	0.318	-0.497	2.601	-0.191	0.849	0.055	0.519	0.106	0.916
Geno.626	75	C	G	C	T	0.227	1.658	2.934	0.565	0.572	0.100	0.586	0.172	0.864
Geno.715	75	T	G	C	T	0.051	6.517	4.952	1.316	0.189	-0.880	0.990	-0.889	0.375
Geno.rare67	75	*	*	*	*	0.010	8.515	0.315	27.054	0.000	0.414	2.495	0.166	0.868
haplo.base74	75	C	G	C	G	0.394	NA	NA	NA	NA	NA	NA	NA	NA
Geno.234	76	A	C	T	A	0.318	-0.196	2.560	-0.077	0.939	0.066	0.515	0.128	0.898
Geno.716	76	G	C	T	T	0.272	3.666	2.630	1.394	0.164	-0.078	0.529	-0.147	0.883

Table B1.24. Continued

							ApoA1				ApoB			
	Window	loc.1	loc.2	loc.3	loc.4	hap.freq	coef	se	t.stat	pval	coef	se	t.stat	pval
Geno.rare68	76	*	*	*	*	0.014	7.477	0.385	19.422	0.000	2.180	1.919	1.136	0.257
haplo.base75	76	G	C	G	A	0.396	NA	NA	NA	NA	NA	NA	NA	NA
Geno.627	77	C	T	A	C	0.322	-0.519	2.657	-0.196	0.845	0.023	0.524	0.044	0.965
Geno.717	77	C	T	T	C	0.272	3.427	2.665	1.286	0.199	-0.125	0.530	-0.236	0.813
Geno.rare69	77	*	*	*	*	0.004	7.823	0.081	96.777	0.000	2.423	3.831	0.633	0.527
haplo.base76	77	C	G	A	C	0.402	NA	NA	NA	NA	NA	NA	NA	NA
Geno.135	78	G	A	C	A	0.018	-7.183	9.538	-0.753	0.452	-0.924	2.062	-0.448	0.654
Geno.524	78	T	A	C	G	0.319	-0.660	2.701	-0.244	0.807	0.008	0.530	0.015	0.988
Geno.628	78	T	T	C	A	0.091	0.149	4.122	0.036	0.971	-2.024	0.835	-2.424	0.016
Geno.718	78	T	T	C	G	0.183	5.045	3.146	1.603	0.110	0.767	0.626	1.226	0.221
Geno.rare70	78	*	*	*	*	0.006	-11.316	0.365	-30.984	0.000	2.225	3.801	0.585	0.559
haplo.base77	78	G	A	C	G	0.384	NA	NA	NA	NA	NA	NA	NA	NA
Geno.331	79	A	C	A	T	0.021	-6.286	8.536	-0.736	0.462	-0.574	1.717	-0.334	0.738
Geno.525	79	T	C	A	C	0.028	2.297	6.635	0.346	0.729	-0.632	1.310	-0.483	0.629
Geno.629	79	T	C	A	T	0.064	0.197	4.718	0.042	0.967	-2.456	0.950	-2.586	0.010
Geno.719	79	T	C	G	T	0.183	5.202	2.918	1.783	0.075	0.752	0.576	1.304	0.193
Geno.rare71	79	*	*	*	*	0.002	-23.945	0.112	-214.590	0.000	1.977	4.659	0.424	0.671
haplo.base78	79	A	C	G	T	0.702	NA	NA	NA	NA	NA	NA	NA	NA
Geno.235	80	C	A	C	G	0.028	1.044	6.613	0.158	0.875	-0.856	1.302	-0.658	0.511
Geno.435	80	C	A	T	G	0.083	-3.268	3.982	-0.821	0.412	-2.082	0.782	-2.665	0.008
Geno.rare72	80	*	*	*	*	0.003	0.395	0.076	5.169	0.000	-0.639	3.757	-0.170	0.865
haplo.base79	80	C	G	T	G	0.886	NA	NA	NA	NA	NA	NA	NA	NA
Geno.136	81	A	C	G	C	0.028	0.952	6.609	0.144	0.885	-0.903	1.300	-0.694	0.488
Geno.332	81	A	T	G	C	0.083	-3.359	3.979	-0.844	0.399	-2.128	0.781	-2.726	0.007
Geno.rare73	81	*	*	*	*	0.007	-5.846	0.171	-34.125	0.000	-3.375	2.651	-1.273	0.204
haplo.base80	81	G	T	G	C	0.882	NA	NA	NA	NA	NA	NA	NA	NA
Geno.137	82	C	G	C	A	0.028	1.035	6.622	0.156	0.876	-0.630	1.313	-0.480	0.631
Geno.526	82	T	G	C	G	0.314	-1.283	2.395	-0.536	0.593	0.062	0.478	0.130	0.897
Geno.rare74	82	*	*	*	*	0.007	-5.673	0.170	-33.385	0.000	-2.982	2.676	-1.114	0.266
haplo.base81	82	T	G	C	A	0.651	NA	NA	NA	NA	NA	NA	NA	NA
Geno.333	83	G	C	A	C	0.053	-5.459	4.795	-1.138	0.256	-0.712	0.952	-0.747	0.455
Geno.527	83	G	C	G	G	0.315	-1.974	2.444	-0.808	0.420	-0.002	0.488	-0.004	0.997
Geno.rare75	83	*	*	*	*	0.007	-6.463	0.115	-56.387	0.000	-3.043	2.676	-1.137	0.256
haplo.base82	83	G	C	A	G	0.625	NA	NA	NA	NA	NA	NA	NA	NA
Geno.138	84	C	A	C	T	0.053	-4.445	4.916	-0.904	0.366	-0.981	0.980	-1.001	0.317
Geno.236	84	C	A	G	C	0.280	2.440	2.710	0.900	0.368	-0.651	0.544	-1.197	0.232
Geno.436	84	C	G	G	C	0.315	-0.669	2.707	-0.247	0.805	-0.302	0.545	-0.553	0.580
Geno.rare76	84	*	*	*	*	0.006	-17.421	0.283	-61.636	0.000	-2.972	3.467	-0.857	0.392
haplo.base83	84	C	A	G	T	0.346	NA	NA	NA	NA	NA	NA	NA	NA
Geno.237	85	A	C	T	A	0.051	-4.812	5.020	-0.959	0.338	-0.877	1.003	-0.875	0.382
Geno.437	85	A	G	C	G	0.285	1.645	2.707	0.608	0.544	-0.618	0.545	-1.134	0.257
Geno.93	85	G	G	C	A	0.300	-1.178	2.757	-0.427	0.669	-0.237	0.559	-0.425	0.671
Geno.101	85	G	G	C	G	0.019	-3.742	8.520	-0.439	0.661	-1.539	1.880	-0.819	0.413
Geno.rare77	85	*	*	*	*	0.003	-39.060	0.155	-252.146	0.000	0.406	5.303	0.076	0.939
haplo.base84	85	A	G	T	A	0.342	NA	NA	NA	NA	NA	NA	NA	NA
Geno.238	86	C	T	A	C	0.050	-5.074	5.043	-1.006	0.315	-0.854	1.003	-0.851	0.395
Geno.630	86	G	C	A	C	0.300	-1.276	2.755	-0.463	0.643	-0.254	0.558	-0.455	0.649
Geno.720	86	G	C	G	C	0.302	1.201	2.659	0.452	0.652	-0.672	0.535	-1.257	0.210
Geno.rare78	86	*	*	*	*	0.006	-23.450	0.243	-96.314	0.000	-2.202	3.647	-0.604	0.546
haplo.base85	86	G	T	A	C	0.342	NA	NA	NA	NA	NA	NA	NA	NA
Geno.139	87	C	A	C	A	0.290	0.107	2.701	0.039	0.969	-0.142	0.542	-0.263	0.793
Geno.334	87	C	G	C	A	0.302	2.093	2.603	0.804	0.422	-0.544	0.518	-1.050	0.294
Geno.rare79	87	*	*	*	*	0.015	-10.993	9.521	-1.155	0.249	0.388	1.915	0.203	0.840
haplo.base86	87	T	A	C	A	0.393	NA	NA	NA	NA	NA	NA	NA	NA
Geno.438	88	G	C	A	W	0.306	1.638	2.362	0.694	0.488	-0.532	0.473	-1.124	0.261
Geno.rare80	88	*	*	*	*	0.013	-6.600	0.126	-52.330	0.000	0.800	1.984	0.403	0.687
haplo.base87	88	A	C	A	W	0.682	NA	NA	NA	NA	NA	NA	NA	NA
Geno.335	89	C	A	W	T	0.015	3.596	9.042	0.398	0.691	3.202	1.818	1.762	0.079
Geno.rare81	89	*	*	*	*	0.013	-7.090	1.561	-4.542	0.000	1.088	1.975	0.551	0.582
haplo.base88	89	C	A	W	C	0.972	NA	NA	NA	NA	NA	NA	NA	NA
Geno.239	90	A	W	C	G	0.118	3.855	3.526	1.093	0.275	1.431	0.700	2.045	0.042
Geno.528	90	A	W	T	T	0.015	4.203	9.287	0.453	0.651	3.404	1.852	1.838	0.067
Geno.rare82	90	*	*	*	*	0.011	-6.591	0.783	-8.414	0.000	2.245	2.172	1.034	0.302
haplo.base89	90	A	W	C	T	0.857	NA	NA	NA	NA	NA	NA	NA	NA
Geno.240	91	W	C	G	G	0.118	3.401	3.538	0.961	0.337	1.340	0.704	1.904	0.058
Geno.336	91	W	C	T	A	0.029	-7.877	6.264	-1.258	0.209	-1.105	1.239	-0.892	0.373
Geno.631	91	W	T	T	G	0.015	3.588	9.212	0.390	0.697	3.240	1.849	1.752	0.080
Geno.rare83	91	*	*	*	*	0.001	-22.560	0.039	-577.970	0.000	4.168	6.471	0.644	0.520
haplo.base90	91	W	C	T	G	0.837	NA	NA	NA	NA	NA	NA	NA	NA
Geno.140	92	C	G	G	A	0.118	3.675	3.546	1.036	0.301	1.289	0.704	1.831	0.068
Geno.337	92	C	T	A	G	0.028	-7.767	6.367	-1.220	0.223	-1.147	1.239	-0.926	0.355
Geno.439	92	C	T	G	A	0.051	4.385	4.999	0.877	0.381	-0.985	0.983	-1.002	0.317
Geno.721	92	T	T	G	G	0.015	4.250	9.287	0.458	0.647	3.150	1.835	1.717	0.087
haplo.base91	92	C	T	G	G	0.787	NA	NA	NA	NA	NA	NA	NA	NA

Table B1.24. Continued

							ApoA1				ApoB			
	Window	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**	**coef**	**se**	**t.stat**	**pval**
Geno.141	93	G	G	A	C	0.118	3.547	3.587	0.989	0.323	0.923	0.701	1.315	0.189
Geno.338	93	T	A	G	C	0.029	-7.894	6.319	-1.249	0.212	-1.640	1.319	-1.243	0.214
Geno.529	93	T	G	A	C	0.051	4.284	4.980	0.860	0.390	-1.243	0.971	-1.280	0.201
Geno.817	93	T	G	G	G	0.112	-0.459	3.543	-0.130	0.897	-2.024	0.707	-2.864	0.004
haplo.base92	93	T	G	G	C	0.689	NA	NA	NA	NA	NA	NA	NA	NA
Geno.142	94	A	G	C	A	0.029	-7.652	6.258	-1.223	0.222	-1.843	1.314	-1.402	0.162
Geno.339	94	G	A	C	G	0.173	4.556	2.944	1.547	0.123	0.439	0.580	0.756	0.450
Geno.632	94	G	G	G	G	0.112	-0.075	3.523	-0.021	0.983	-2.030	0.714	-2.845	0.005
Geno.rare84	94	*	*	*	*	0.001	-4.741	0.032	-150.047	0.000	3.742	4.919	0.761	0.447
haplo.base93	94	G	G	C	A	0.685	NA	NA	NA	NA	NA	NA	NA	NA
Geno.143	95	A	C	G	C	0.173	4.920	2.931	1.679	0.094	0.512	0.579	0.885	0.377
Geno.440	95	G	G	G	C	0.112	0.125	3.521	0.035	0.972	-1.871	0.703	-2.662	0.008
Geno.rare85	95	*	*	*	*	0.001	-4.231	0.029	-144.268	0.000	2.347	6.475	0.363	0.717
haplo.base94	95	G	C	A	A	0.713	NA	NA	NA	NA	NA	NA	NA	NA
Geno.144	96	C	A	A	C	0.073	0.220	4.789	0.046	0.963	-0.078	0.988	-0.079	0.937
Geno.340	96	C	G	C	C	0.065	7.832	5.244	1.494	0.136	1.612	0.997	1.617	0.107
Geno.441	96	C	G	C	T	0.109	3.154	3.907	0.807	0.420	-0.099	0.747	-0.133	0.894
Geno.633	96	G	G	C	C	0.036	-2.806	7.288	-0.385	0.700	-2.866	1.290	-2.221	0.027
Geno.722	96	G	G	C	T	0.076	1.626	4.902	0.332	0.740	-1.333	0.911	-1.463	0.144
haplo.base95	96	C	A	A	T	0.641	NA	NA	NA	NA	NA	NA	NA	NA
Geno.145	97	A	A	C	A	0.055	-8.818	5.892	-1.496	0.135	0.000	1.645	0.000	1.000
Geno.241	97	A	A	C	C	0.018	15.043	11.711	1.284	0.200	1.181	3.246	0.364	0.716
Geno.442	97	A	A	T	C	0.321	-6.775	2.955	-2.292	0.022	0.557	0.692	0.804	0.422
Geno.530	97	G	C	C	A	0.081	2.365	4.701	0.503	0.615	-0.293	1.030	-0.284	0.776
Geno.634	97	G	C	C	C	0.021	-4.223	9.198	-0.459	0.646	1.919	2.525	0.760	0.448
Geno.723	97	G	C	T	A	0.132	-0.177	3.937	-0.045	0.964	0.202	0.871	0.232	0.817
Geno.818	97	G	C	T	C	0.054	-3.012	5.504	-0.547	0.584	-1.378	1.171	-1.176	0.240
haplo.base96	97	A	A	T	A	0.319	NA	NA	NA	NA	NA	NA	NA	NA

TABLE B1.25. Summary of *CETP* 4-SNP sliding haplotypes (104 SNPs included) for TC, HDL-C and LDL-C in NHWs

							TC				HDL-C				LDL-C			
	Window	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**	**coef**	**se**	**t.stat**	**pval**	**coef**	**se**	**t.stat**	**pval**
Geno.1	1	A	A	T	G	0.029	0.612	8.069	0.076	0.940	0.029	0.036	0.815	0.415	2.511	7.658	0.328	0.743
Geno.2	1	A	C	C	A	0.139	-0.307	3.913	-0.079	0.937	-0.031	0.017	-1.800	0.072	1.494	3.699	0.404	0.686
Geno.3	1	A	C	C	G	0.231	-2.047	3.217	-0.636	0.525	-0.054	0.014	-3.801	0.000	-1.832	3.055	-0.600	0.549
Geno.6	1	G	C	C	A	0.033	7.167	8.157	0.879	0.380	-0.049	0.034	-1.430	0.153	8.879	7.415	1.197	0.232
Geno.7	1	G	C	C	G	0.251	-6.021	3.197	-1.883	0.060	-0.026	0.014	-1.795	0.073	-4.434	3.039	-1.459	0.145
haplo.base	1	G	A	T	G	0.318	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.21	2	A	T	G	A	0.330	4.680	2.615	1.789	0.074	0.043	0.012	3.673	0.000	3.412	2.505	1.362	0.174
Geno.31	2	A	T	G	G	0.017	0.694	9.345	0.074	0.941	0.020	0.041	0.479	0.632	2.447	8.947	0.273	0.785
Geno.5	2	C	C	A	G	0.171	5.224	3.420	1.528	0.127	0.003	0.015	0.221	0.825	6.143	3.260	1.884	0.060
haplo.base1	2	C	C	G	G	0.482	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.22	3	C	A	G	T	0.171	0.659	3.495	0.189	0.850	-0.039	0.016	-2.455	0.014	2.707	3.338	0.811	0.418
Geno.4	3	C	G	G	C	0.204	-5.540	3.217	-1.722	0.085	-0.054	0.015	-3.662	0.000	-2.724	3.080	-0.884	0.377
Geno.51	3	C	G	G	T	0.277	-4.078	2.901	-1.406	0.160	-0.035	0.013	-2.590	0.010	-3.903	2.775	-1.406	0.160
Geno.8	3	T	G	G	T	0.016	-1.973	1.075	-1.835	0.067	-0.027	0.044	-0.622	0.534	0.150	1.031	0.145	0.884
Geno.rare	3	*	*	*	*	0.002	0.526	0.066	8.003	0.000	0.038	0.169	0.225	0.822	2.621	0.063	41.534	0.000
haplo.base2	3	T	G	A	T	0.330	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.32	4	A	G	T	G	0.172	-0.795	3.688	-0.216	0.829	-0.042	0.016	-2.567	0.010	1.306	3.522	0.371	0.711
Geno.61	4	G	G	C	G	0.206	-7.150	3.367	-2.123	0.034	-0.056	0.015	-3.705	0.000	-4.209	3.224	-1.305	0.192
Geno.81	4	G	G	T	G	0.277	-5.635	3.101	-1.817	0.070	-0.037	0.014	-2.690	0.007	-5.376	2.965	-1.813	0.070
Geno.9	4	G	G	T	T	0.016	-4.864	9.947	-0.489	0.625	-0.027	0.044	-0.619	0.536	-1.711	9.530	-0.180	0.858
Geno.rare1	4	*	*	*	*	0.010	-25.892	13.016	-1.989	0.047	-0.041	0.058	-0.707	0.480	-24.694	12.430	-1.987	0.047
haplo.base3	4	G	A	T	T	0.321	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.23	5	A	T	T	T	0.320	4.037	2.792	1.446	0.149	0.039	0.012	3.152	0.002	3.058	2.676	1.142	0.254
Geno.33	5	G	C	G	C	0.205	-3.381	3.212	-1.053	0.293	-0.017	0.014	-1.204	0.229	-1.422	3.082	-0.461	0.645
Geno.71	5	G	T	T	T	0.014	1.859	10.205	0.182	0.855	0.025	0.045	0.541	0.589	2.687	9.793	0.274	0.784
Geno.rare2	5	*	*	*	*	0.012	-20.917	11.221	-1.864	0.063	-0.019	0.050	-0.378	0.706	-20.247	10.761	-1.882	0.060
haplo.base4	5	G	T	G	C	0.449	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.24	6	C	G	C	T	0.206	-3.979	3.256	-1.222	0.222	-0.017	0.015	-1.184	0.237	-2.243	3.145	-0.713	0.476
Geno.34	6	T	G	C	C	0.082	-3.671	4.651	-0.789	0.430	0.001	0.021	0.049	0.961	-5.344	4.465	-1.197	0.232
Geno.82	6	T	T	T	T	0.334	3.155	2.884	1.094	0.274	0.039	0.013	3.000	0.003	1.947	2.762	0.705	0.481
Geno.rare3	6	*	*	*	*	0.012	-21.350	0.339	-62.897	0.000	-0.019	0.051	-0.369	0.712	-20.988	11.000	-1.908	0.057
haplo.base5	6	T	G	C	T	0.367	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.25	7	G	C	C	G	0.081	-3.953	4.653	-0.849	0.396	-0.001	0.021	-0.044	0.965	-5.321	4.455	-1.194	0.233
Geno.35	7	G	C	T	A	0.198	-4.391	3.312	-1.326	0.185	-0.027	0.015	-1.800	0.072	-1.651	3.173	-0.521	0.603
Geno.83	7	T	T	T	A	0.334	3.053	2.870	1.064	0.288	0.036	0.013	2.796	0.005	2.170	2.750	0.789	0.430
Geno.rare4	7	*	*	*	*	0.012	-21.547	0.329	-65.430	0.000	-0.022	0.052	-0.423	0.673	-20.825	0.328	-63.574	0.000
haplo.base6	7	G	C	T	G	0.375	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.36	8	C	C	G	T	0.082	-3.476	4.645	-0.748	0.455	-0.001	0.020	-0.033	0.974	-4.992	4.453	-1.121	0.263
Geno.41	8	C	T	A	C	0.200	-4.621	3.332	-1.387	0.166	-0.027	0.015	-1.844	0.066	-1.809	3.191	-0.567	0.571
Geno.62	8	T	T	A	C	0.343	1.765	2.788	0.633	0.527	0.034	0.012	2.724	0.007	0.938	2.672	0.351	0.726
haplo.base7	8	C	T	G	C	0.374	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.37	9	C	G	T	C	0.082	-3.762	4.464	-0.843	0.400	-0.019	0.020	-0.932	0.352	-5.345	4.273	-1.251	0.211
Geno.52	9	T	G	C	C	0.180	3.093	3.289	0.940	0.347	-0.014	0.015	-0.969	0.333	2.359	3.145	0.750	0.454
Geno.63	9	T	G	C	T	0.193	-1.886	3.128	-0.603	0.547	-0.009	0.014	-0.668	0.505	-1.977	2.994	-0.660	0.509
haplo.base8	9	T	A	C	C	0.544	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.26	10	A	C	C	C	0.124	-6.479	3.772	-1.718	0.086	-0.049	0.017	-2.896	0.004	-3.742	3.619	-1.034	0.302
Geno.38	10	G	C	C	A	0.010	1.501	12.723	0.118	0.906	0.004	0.056	0.067	0.946	-1.696	12.338	-0.137	0.891
Geno.42	10	G	C	C	C	0.171	1.939	3.439	0.564	0.573	-0.027	0.015	-1.756	0.080	1.861	3.297	0.564	0.573
Geno.53	10	G	C	T	C	0.193	-3.443	3.255	-1.058	0.291	-0.022	0.015	-1.488	0.137	-2.871	3.121	-0.920	0.358
Geno.64	10	G	T	C	A	0.082	-5.025	4.520	-1.112	0.267	-0.029	0.020	-1.426	0.155	-6.049	4.333	-1.396	0.163
haplo.base9	10	A	C	C	A	0.419	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.11	11	C	C	A	A	0.043	-1.797	6.030	-0.298	0.766	-0.085	0.028	-3.080	0.002	1.389	5.776	0.240	0.810
Geno.43	11	C	C	C	C	0.294	-2.724	2.829	-0.963	0.336	-0.045	0.013	-3.561	0.000	-1.120	2.712	-0.413	0.680
Geno.65	11	C	T	C	C	0.193	-3.853	3.253	-1.185	0.237	-0.027	0.014	-1.868	0.062	-3.011	3.118	-0.966	0.335
Geno.72	11	T	C	A	C	0.082	-5.154	4.533	-1.137	0.256	-0.035	0.020	-1.731	0.084	-5.861	4.342	-1.350	0.178
Geno.rare5	11	*	*	*	*	0.002	90.624	0.064	1419.201	0.000	0.057	0.109	0.519	0.604	83.003	0.052	1591.941	0.000
haplo.base10	11	C	C	A	C	0.386	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.12	12	C	A	A	C	0.043	-0.316	5.973	-0.053	0.958	-0.075	0.027	-2.812	0.005	2.708	5.741	0.472	0.637
Geno.66	12	C	C	C	T	0.293	-1.473	2.746	-0.536	0.592	-0.038	0.012	-3.105	0.002	0.183	2.639	0.070	0.945
Geno.10	12	T	C	C	T	0.192	-2.175	3.179	-0.684	0.494	-0.022	0.014	-1.527	0.127	-1.342	3.056	-0.439	0.661
Geno.rare6	12	*	*	*	*	0.007	44.432	0.124	359.552	0.000	0.067	0.075	0.887	0.375	32.635	0.114	286.706	0.000
haplo.base11	12	C	A	C	C	0.464	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.13	13	A	A	C	G	0.043	1.337	6.046	0.221	0.825	-0.042	0.027	-1.572	0.117	3.044	5.803	0.525	0.600
Geno.27	13	A	C	C	A	0.444	1.870	2.433	0.769	0.442	0.030	0.011	2.756	0.006	0.623	2.335	0.267	0.790
Geno.39	13	A	C	C	G	0.021	0.085	8.335	0.010	0.992	0.056	0.037	1.512	0.131	-3.095	7.987	-0.387	0.699
Geno.rare7	13	*	*	*	*	0.007	42.648	0.284	150.429	0.000	0.097	0.076	1.276	0.203	33.111	0.270	122.458	0.000
haplo.base12	13	C	C	T	G	0.485	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.14	14	A	C	G	C	0.045	4.567	6.020	0.759	0.448	-0.039	0.027	-1.467	0.143	5.556	5.765	0.964	0.336
Geno.310	14	C	C	A	C	0.444	1.741	2.491	0.699	0.485	0.029	0.011	2.597	0.010	0.152	2.384	0.064	0.949
Geno.54	14	C	C	G	C	0.022	-1.227	8.234	-0.149	0.882	0.045	0.037	1.218	0.224	-4.429	7.889	-0.561	0.575
Geno.73	14	C	T	G	T	0.031	5.403	7.017	0.770	0.442	-0.009	0.031	-0.301	0.764	-2.400	6.715	-0.357	0.721
haplo.base13	14	C	T	G	C	0.458	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.15	15	C	A	C	A	0.443	1.629	2.490	0.654	0.513	0.031	0.011	2.754	0.006	-0.088	2.385	-0.037	0.970
Geno.311	15	C	G	C	G	0.069	3.265	4.950	0.660	0.510	-0.013	0.022	-0.584	0.559	2.770	4.741	0.584	0.559
Geno.67	15	T	G	T	G	0.031	5.491	7.007	0.784	0.434	-0.011	0.031	-0.342	0.732	-2.283	6.709	-0.340	0.734
haplo.base14	15	T	G	C	G	0.457	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA

Table B1.25. Continued

Geno.44	16	G	C	G	A	0.234	-1.890	3.006	-0.629	0.530	-0.045	0.013	-3.371	0.001	0.686	2.879	0.238	0.812
Geno.55	16	G	C	G	G	0.292	-0.740	2.809	-0.263	0.792	-0.022	0.012	-1.783	0.075	0.213	2.690	0.079	0.937
Geno.68	16	G	T	G	A	0.031	3.672	7.016	0.523	0.601	-0.043	0.031	-1.387	0.166	-2.214	6.719	-0.330	0.742
haplo.base15	16	A	C	A	G	0.443	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.28	17	C	G	A	A	0.233	-1.752	3.010	-0.582	0.561	-0.043	0.013	-3.230	0.001	0.780	2.883	0.270	0.787
Geno.45	17	C	G	G	A	0.292	-0.654	2.816	-0.232	0.816	-0.022	0.013	-1.737	0.083	0.240	2.693	0.089	0.929
Geno.69	17	T	G	A	A	0.031	3.739	7.017	0.533	0.594	-0.042	0.031	-1.361	0.174	-2.178	6.719	-0.324	0.746
haplo.base16	17	C	A	G	A	0.442	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.312	18	G	A	A	A	0.189	-2.746	3.254	-0.844	0.399	-0.046	0.014	-3.199	0.001	0.212	3.079	0.069	0.945
Geno.46	18	G	A	A	G	0.075	0.824	5.450	0.151	0.880	-0.038	0.023	-1.641	0.101	0.244	5.063	0.048	0.962
Geno.610	18	G	G	A	A	0.105	0.649	4.411	0.147	0.883	-0.015	0.019	-0.800	0.424	-1.177	4.137	-0.285	0.776
Geno.74	18	G	G	A	G	0.188	-1.364	3.408	-0.400	0.689	-0.026	0.015	-1.732	0.084	-0.590	3.205	-0.184	0.854
Geno.rare8	18	*	*	*	*	0.003	-27.008	0.114	-236.545	0.000	-0.102	0.125	-0.813	0.416	-65.940	0.145	-455.622	0.000
haplo.base17	18	A	G	A	A	0.440	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.29	19	A	A	A	G	0.195	-1.011	3.475	-0.291	0.771	-0.040	0.015	-2.625	0.009	0.602	3.290	0.183	0.855
Geno.47	19	A	A	G	G	0.068	-1.168	6.168	-0.189	0.850	-0.045	0.026	-1.698	0.090	1.161	5.663	0.205	0.838
Geno.611	19	G	A	A	C	0.087	3.059	4.434	0.690	0.491	-0.017	0.020	-0.855	0.393	2.591	4.235	0.612	0.541
Geno.91	19	G	A	G	G	0.194	-0.437	3.646	-0.120	0.905	-0.018	0.016	-1.146	0.252	-1.479	3.453	-0.428	0.669
Geno.rare9	19	*	*	*	*	0.003	-15.329	0.140	-109.848	0.000	-0.130	0.144	-0.902	0.367	-19.735	0.068	-291.886	0.000
haplo.base18	19	G	A	A	G	0.454	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.16	20	A	A	C	C	0.089	2.964	4.223	0.702	0.483	-0.004	0.019	-0.231	0.818	1.922	4.056	0.474	0.636
Geno.48	20	A	G	G	C	0.262	-0.113	2.823	-0.040	0.968	-0.013	0.013	-1.013	0.311	-0.834	2.670	-0.312	0.755
Geno.rare10	20	*	*	*	*	0.002	-34.211	0.023	-1470.059	0.000	-0.109	0.132	-0.824	0.410	-32.313	0.022	-1443.880	0.000
haplo.base19	20	A	A	G	C	0.647	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.17	21	A	C	C	C	0.090	1.889	4.347	0.435	0.664	-0.013	0.019	-0.691	0.490	1.691	4.183	0.404	0.686
Geno.210	21	A	G	C	C	0.202	-2.886	3.193	-0.904	0.366	-0.033	0.014	-2.312	0.021	0.061	3.053	0.020	0.984
Geno.56	21	G	G	C	G	0.260	-0.967	3.030	-0.319	0.750	-0.025	0.014	-1.826	0.068	-0.606	2.882	-0.210	0.834
Geno.rare11	21	*	*	*	*	0.002	-41.116	0.060	-683.877	0.000	0.009	0.132	0.065	0.948	-39.310	0.057	-690.119	0.000
haplo.base20	21	A	G	C	G	0.447	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.18	22	C	C	C	A	0.090	2.098	4.213	0.498	0.619	-0.007	0.019	-0.355	0.723	1.718	4.030	0.426	0.670
Geno.49	22	G	C	C	C	0.198	-1.939	2.926	-0.663	0.508	-0.028	0.013	-2.158	0.031	0.773	2.790	0.277	0.782
Geno.rare12	22	*	*	*	*	0.011	-27.068	0.110	-245.292	0.000	-0.087	0.054	-1.623	0.105	-37.081	0.100	-370.425	0.000
haplo.base21	22	G	C	G	A	0.701	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.19	23	C	C	A	C	0.054	1.654	5.150	0.321	0.748	0.008	0.023	0.352	0.725	-0.167	4.877	-0.034	0.973
Geno.211	23	C	C	A	T	0.036	-2.052	7.135	-0.288	0.774	-0.054	0.032	-1.670	0.095	-2.559	6.754	-0.379	0.705
Geno.313	23	C	C	C	C	0.198	-2.051	3.242	-0.633	0.527	-0.045	0.014	-3.102	0.002	0.460	3.085	0.149	0.882
Geno.57	23	C	G	A	C	0.267	-0.144	3.051	-0.047	0.962	-0.034	0.014	-2.491	0.013	-0.647	2.927	-0.221	0.825
Geno.rare13	23	*	*	*	*	0.008	-26.011	0.613	-42.425	0.000	-0.157	0.066	-2.386	0.017	-44.308	0.476	-93.003	0.000
haplo.base22	23	C	G	A	T	0.437	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.110	24	C	A	C	W	0.054	2.286	5.142	0.445	0.657	0.007	0.023	0.298	0.766	0.727	4.879	0.149	0.882
Geno.212	24	C	A	T	W	0.035	-1.924	7.174	-0.268	0.789	-0.052	0.032	-1.626	0.104	-2.558	6.801	-0.376	0.707
Geno.314	24	C	C	C	D	0.185	-2.361	3.289	-0.718	0.473	-0.045	0.015	-3.080	0.002	0.105	3.134	0.034	0.973
Geno.410	24	C	C	C	W	0.014	1.144	10.600	0.108	0.914	-0.013	0.047	-0.270	0.787	2.563	10.109	0.254	0.800
Geno.612	24	G	A	C	W	0.268	-0.495	3.051	-0.162	0.871	-0.035	0.014	-2.535	0.012	-1.241	2.920	-0.425	0.671
Geno.rare14	24	*	*	*	*	0.006	-21.112	0.538	-39.247	0.000	-0.187	0.073	-2.581	0.010	-40.796	0.486	-84.012	0.000
haplo.base23	24	G	A	T	W	0.438	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.111	25	A	C	W	A	0.265	-0.785	2.933	-0.268	0.789	-0.027	0.013	-2.092	0.037	-0.819	2.792	-0.293	0.769
Geno.213	25	A	C	W	G	0.057	3.392	5.136	0.660	0.509	0.013	0.022	0.609	0.543	0.354	4.846	0.073	0.942
Geno.58	25	C	C	D	G	0.189	-2.804	3.116	-0.900	0.368	-0.042	0.014	-3.063	0.002	-0.689	2.986	-0.231	0.818
Geno.613	25	C	C	W	G	0.016	-0.119	9.803	-0.012	0.990	0.001	0.044	0.014	0.989	1.361	9.419	0.145	0.885
haplo.base24	25	A	T	W	G	0.472	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.112	26	C	D	G	A	0.189	-2.712	3.270	-0.829	0.407	-0.050	0.014	-3.458	0.001	-0.978	3.133	-0.312	0.755
Geno.315	26	C	W	A	G	0.264	-1.066	3.096	-0.344	0.731	-0.034	0.014	-2.509	0.012	-0.800	2.956	-0.270	0.787
Geno.411	26	C	W	G	A	0.017	7.233	9.686	0.747	0.455	-0.022	0.043	-0.519	0.604	-8.054	9.317	-0.864	0.388
Geno.59	26	C	W	G	G	0.057	3.466	5.078	0.682	0.495	0.008	0.022	0.371	0.710	1.232	4.848	0.254	0.799
Geno.84	26	T	W	G	G	0.035	-0.111	7.158	-0.016	0.988	-0.055	0.031	-1.746	0.081	-1.132	6.851	-0.165	0.869
haplo.base25	26	T	W	G	A	0.437	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.214	27	D	G	A	A	0.189	-2.972	3.157	-0.941	0.347	-0.045	0.014	-3.177	0.002	-0.504	3.029	-0.166	0.868
Geno.75	27	W	A	G	G	0.264	-1.071	2.936	-0.365	0.715	-0.026	0.013	-2.011	0.045	-0.215	2.812	-0.077	0.939
Geno.113	27	W	G	G	G	0.091	2.633	4.358	0.604	0.546	-0.017	0.019	-0.889	0.374	1.900	4.166	0.456	0.648
Geno.rare15	27	*	*	*	*	0.004	-25.391	0.087	-291.574	0.000	0.009	0.093	0.094	0.925	-20.537	0.084	-245.332	0.000
haplo.base26	27	W	G	A	G	0.452	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.510	28	A	G	G	G	0.263	-1.222	2.919	-0.419	0.676	-0.028	0.013	-2.099	0.036	-0.271	2.796	-0.097	0.923
Geno.614	28	G	A	A	G	0.190	-3.331	3.139	-1.061	0.289	-0.046	0.014	-3.214	0.001	-0.804	3.014	-0.267	0.790
Geno.76	28	G	A	G	G	0.016	-0.778	0.761	-1.023	0.307	0.000	0.044	0.009	0.993	0.821	0.701	1.172	0.242
Geno.101	28	G	G	G	G	0.092	2.391	4.307	0.555	0.579	-0.017	0.019	-0.892	0.373	1.561	4.118	0.379	0.705
Geno.rare16	28	*	*	*	*	0.003	-30.087	0.010	-2881.756	0.000	0.060	0.000	1.6E+15	0.000	-24.553	0.010	-2478.897	0.000
haplo.base27	28	G	A	G	T	0.435	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.114	29	A	A	G	A	0.187	-3.195	3.150	-1.014	0.311	-0.041	0.014	-2.884	0.004	0.068	3.065	0.022	0.982
Geno.511	29	A	G	G	A	0.016	-0.674	0.752	-0.897	0.370	0.001	0.044	0.016	0.987	0.691	9.516	0.073	0.942
Geno.102	29	G	G	G	A	0.092	1.695	4.246	0.399	0.690	-0.017	0.019	-0.899	0.369	1.365	4.098	0.333	0.739
Geno.115	29	G	G	G	C	0.263	-0.882	2.898	-0.304	0.761	-0.027	0.013	-2.020	0.044	-0.106	2.832	-0.038	0.970
Geno.rare17	29	*	*	*	*	0.006	-19.169	0.110	-174.285	0.000	-0.063	0.089	-0.711	0.477	-40.763	0.259	-157.465	0.000
haplo.base28	29	A	G	T	A	0.436	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.215	30	A	G	A	G	0.186	-3.123	3.213	-0.972	0.331	-0.042	0.014	-2.925	0.004	0.096	3.065	0.031	0.975
Geno.77	30	G	G	A	A	0.090	0.635	4.309	0.147	0.883	-0.015	0.019	-0.771	0.441	0.495	4.112	0.120	0.904
Geno.85	30	G	G	A	G	0.017	0.063	9.343	0.007	0.995	-0.004	0.042	-0.104	0.917	1.544	8.912	0.173	0.863
Geno.103	30	G	G	C	G	0.263	-0.824	2.962	-0.278	0.781	-0.027	0.013	-2.066	0.039	-0.105	2.826	-0.037	0.970
Geno.rare18	30	*	*	*	*	0.007	-20.725	0.335	-61.802	0.000	-0.039	0.081	-0.478	0.633	-38.555	0.326	-118.345	0.000
haplo.base29	30	G	T	A	G	0.437	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.216	31	G	A	A	C	0.090	0.296	4.313	0.069	0.945	-0.015	0.019	-0.773	0.440	-0.061	4.135	-0.015	0.988
Geno.316	31	G	A	G	C	0.202	-2.639	3.158	-0.836	0.404	-0.040	0.014	-2.840	0.005	0.253	3.028	0.084	0.933

Table B1.25. Continued

Geno.512	31	G	C	G	A	0.266	-1.430	2.965	-0.482	0.630	-0.027	0.013	-2.048	0.041	-0.434	2.841	-0.153	0.879
Geno.rare19	31	*	*	*	*	0.004	17.694	0.123	143.833	0.000	-0.115	0.093	-1.229	0.220	-17.099	0.119	-143.172	0.000
haplo.base30	31	T	A	G	C	0.439	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.217	32	A	A	C	C	0.090	0.890	4.304	0.207	0.836	-0.015	0.019	-0.766	0.444	0.416	4.103	0.101	0.919
Geno.317	32	A	G	C	C	0.190	-1.793	3.353	-0.535	0.593	-0.041	0.015	-2.771	0.006	1.144	3.092	0.370	0.711
Geno.615	32	C	G	A	C	0.017	0.384	13.147	0.029	0.977	-0.055	0.055	-1.004	0.316	-19.155	10.794	-1.775	0.076
Geno.78	32	C	G	A	G	0.248	-1.169	3.254	-0.359	0.720	-0.024	0.014	-1.649	0.100	1.530	2.975	0.514	0.607
Geno.rare20	32	*	*	*	*	0.004	18.729	0.207	90.426	0.000	-0.114	0.093	-1.226	0.221	-17.587	0.210	-83.739	0.000
haplo.base31	32	A	G	C	G	0.450	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.218	33	A	C	C	G	0.087	-0.543	4.555	-0.119	0.905	-0.014	0.019	-0.717	0.474	0.132	4.225	0.031	0.975
Geno.412	33	G	A	C	T	0.016	-5.658	12.839	-0.441	0.660	-0.047	0.056	-0.840	0.401	-16.829	10.557	-1.594	0.111
Geno.513	33	G	A	G	G	0.247	-1.246	3.215	-0.388	0.698	-0.023	0.015	-1.615	0.107	0.839	2.984	0.281	0.779
Geno.79	33	G	C	C	T	0.190	-1.910	3.297	-0.579	0.563	-0.043	0.015	-2.868	0.004	0.483	3.099	0.156	0.876
Geno.rare21	33	*	*	*	*	0.008	25.841	1.627	15.886	0.000	-0.011	0.073	-0.147	0.883	13.690	0.111	122.800	0.000
haplo.base32	33	G	C	G	G	0.451	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.219	34	A	C	T	C	0.017	-8.419	11.543	-0.729	0.466	-0.038	0.049	-0.779	0.436	-17.744	9.770	-1.816	0.070
Geno.413	34	A	G	G	T	0.245	-2.227	3.086	-0.722	0.471	-0.026	0.014	-1.815	0.070	0.286	2.990	0.096	0.924
Geno.514	34	C	C	G	T	0.091	-1.631	4.359	-0.374	0.708	-0.016	0.019	-0.863	0.388	-1.235	4.331	-0.285	0.776
Geno.616	34	C	C	T	C	0.058	6.357	5.388	1.180	0.239	-0.035	0.025	-1.399	0.162	6.675	5.111	1.306	0.192
Geno.710	34	C	C	T	T	0.130	-5.527	3.652	-1.514	0.131	-0.048	0.017	-2.920	0.004	-2.426	3.563	-0.681	0.496
Geno.rare22	34	*	*	*	*	0.005	82.135	20.742	3.960	0.000	0.081	0.179	0.451	0.652	44.250	0.172	257.125	0.000
haplo.base33	34	C	G	G	T	0.453	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.220	35	C	G	T	C	0.096	1.747	4.217	0.414	0.679	-0.007	0.018	-0.406	0.685	0.090	4.035	0.022	0.982
Geno.318	35	C	T	C	C	0.075	4.045	4.524	0.894	0.372	-0.028	0.020	-1.392	0.165	1.075	4.337	0.248	0.804
Geno.414	35	C	T	T	C	0.129	-4.728	3.557	-1.329	0.184	-0.038	0.016	-2.394	0.017	-2.060	3.416	-0.603	0.547
Geno.rare23	35	*	*	*	*	0.002	-18.450	0.049	-378.385	0.000	-0.119	0.131	-0.907	0.365	-10.758	0.047	-230.872	0.000
haplo.base34	35	G	G	T	C	0.699	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.515	36	T	C	C	A	0.075	4.042	4.503	0.898	0.370	-0.026	0.020	-1.324	0.186	1.226	4.314	0.284	0.776
Geno.617	36	T	T	C	A	0.129	-4.743	3.512	-1.350	0.177	-0.036	0.016	-2.322	0.021	-1.922	3.370	-0.570	0.569
Geno.rare24	36	*	*	*	*	0.003	3.102	0.030	102.076	0.000	0.005	0.131	0.039	0.969	8.999	0.029	309.437	0.000
haplo.base35	36	G	T	C	A	0.793	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.116	37	C	C	A	G	0.075	6.031	4.708	1.281	0.201	-0.005	0.021	-0.248	0.804	1.276	4.509	0.283	0.777
Geno.221	37	T	C	A	A	0.451	2.655	2.494	1.065	0.287	0.031	0.011	2.763	0.006	-0.210	2.388	-0.088	0.930
Geno.rare25	37	*	*	*	*	0.003	6.060	0.125	48.333	0.000	0.036	0.093	0.390	0.696	9.208	0.120	76.909	0.000
haplo.base36	37	T	C	A	G	0.471	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.117	38	C	A	A	C	0.451	1.773	2.372	0.747	0.455	0.031	0.011	2.932	0.003	-0.328	2.269	-0.144	0.885
Geno.rare26	38	*	*	*	*	0.012	4.380	0.195	22.453	0.000	0.006	0.049	0.128	0.899	5.692	0.186	30.532	0.000
haplo.base37	38	C	A	G	C	0.536	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.118	39	A	A	C	C	0.452	1.314	2.407	0.546	0.585	0.031	0.011	2.854	0.004	-0.303	2.303	-0.132	0.895
Geno.rare27	39	*	*	*	*	0.018	8.466	9.098	0.930	0.352	-0.031	0.040	-0.778	0.437	-6.554	8.714	-0.752	0.452
haplo.base38	39	A	G	C	C	0.530	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.119	40	A	C	C	A	0.452	1.294	2.398	0.539	0.590	0.030	0.011	2.849	0.005	-0.342	2.295	-0.149	0.882
Geno.rare28	40	*	*	*	*	0.016	6.626	9.523	0.696	0.487	-0.050	0.042	-1.181	0.238	-10.158	9.115	-1.114	0.266
haplo.base39	40	G	C	C	C	0.532	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.120	41	C	C	A	C	0.343	2.378	2.600	0.915	0.361	0.039	0.011	3.422	0.001	1.413	2.484	0.569	0.570
Geno.222	41	C	C	A	T	0.108	-3.481	3.856	-0.903	0.367	0.005	0.017	0.289	0.773	-4.426	3.688	-1.200	0.231
Geno.rare29	41	*	*	*	*	0.016	6.162	9.519	0.647	0.518	-0.051	0.042	-1.215	0.225	-10.259	9.111	-1.126	0.261
haplo.base40	41	C	C	C	C	0.533	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.121	42	C	A	C	C	0.327	3.432	2.641	1.300	0.194	0.043	0.012	3.645	0.000	2.165	2.518	0.860	0.390
Geno.223	42	C	A	C	T	0.016	-16.451	9.448	-1.741	0.082	-0.014	0.042	-0.340	0.734	-12.527	9.041	-1.386	0.166
Geno.319	42	C	A	T	C	0.108	-3.758	3.840	-0.979	0.328	0.004	0.017	0.239	0.811	-4.780	3.670	-1.303	0.193
Geno.rare30	42	*	*	*	*	0.007	8.476	13.980	0.606	0.545	-0.105	0.062	-1.695	0.090	-28.134	13.362	-2.106	0.036
haplo.base41	42	C	C	C	C	0.542	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.224	43	A	C	C	G	0.327	3.889	2.702	1.439	0.151	0.047	0.012	3.967	0.000	2.327	2.587	0.900	0.369
Geno.320	43	A	C	T	G	0.016	-16.193	9.469	-1.710	0.088	-0.007	0.042	-0.167	0.867	-11.970	9.096	-1.316	0.189
Geno.415	43	A	T	C	G	0.108	-3.514	3.875	-0.907	0.365	0.010	0.017	0.597	0.551	-4.276	3.717	-1.150	0.250
Geno.516	43	C	C	C	A	0.039	3.202	6.236	0.513	0.608	0.044	0.028	1.592	0.112	-0.132	5.984	-0.022	0.982
haplo.base42	43	C	C	C	G	0.510	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.122	44	C	C	A	T	0.039	1.481	6.127	0.242	0.809	0.024	0.027	0.858	0.391	-1.153	5.876	-0.196	0.845
Geno.416	44	C	T	G	T	0.016	-17.316	9.464	-1.830	0.068	-0.021	0.043	-0.496	0.620	-12.506	9.076	-1.378	0.169
Geno.618	44	T	C	G	T	0.108	-5.135	3.710	-1.384	0.167	-0.010	0.017	-0.571	0.568	-5.239	3.556	-1.473	0.141
haplo.base43	44	C	C	G	T	0.837	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.123	45	C	A	T	C	0.039	2.495	6.105	0.409	0.683	0.026	0.027	0.957	0.339	-0.206	5.857	-0.035	0.972
Geno.517	45	T	G	T	C	0.016	-15.929	9.431	-1.689	0.092	-0.018	0.042	-0.423	0.672	-11.175	9.049	-1.235	0.217
Geno.rare31	45	*	*	*	*	0.008	9.434	13.948	0.676	0.499	0.055	0.062	0.878	0.380	4.174	13.382	0.312	0.755
haplo.base44	45	C	G	T	C	0.937	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.124	46	A	T	C	C	0.039	2.791	6.134	0.455	0.649	0.025	0.027	0.926	0.355	0.221	5.878	0.038	0.970
Geno.518	46	G	T	C	T	0.264	-0.932	2.750	-0.339	0.735	-0.005	0.012	-0.413	0.680	0.573	2.630	0.218	0.828
Geno.rare32	46	*	*	*	*	0.008	9.850	13.985	0.704	0.482	0.054	0.062	0.875	0.382	4.650	13.405	0.347	0.729
haplo.base45	46	G	T	C	C	0.690	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.321	47	T	C	C	G	0.183	-2.682	3.166	-0.847	0.397	-0.041	0.014	-2.978	0.003	-0.453	3.044	-0.149	0.882
Geno.417	47	T	C	T	A	0.264	-1.903	2.894	-0.657	0.511	-0.018	0.013	-1.430	0.153	0.362	2.769	0.131	0.896
Geno.rare33	47	*	*	*	*	0.008	9.282	0.114	81.578	0.000	0.045	0.062	0.727	0.467	4.675	0.107	43.692	0.000
haplo.base46	47	T	C	C	A	0.545	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.322	48	C	C	G	T	0.183	-3.406	3.094	-1.101	0.271	-0.040	0.014	-2.943	0.003	-0.498	2.966	-0.168	0.867
Geno.418	48	C	T	A	C	0.265	-2.312	2.874	-0.805	0.421	-0.020	0.013	-1.566	0.118	-0.065	2.747	-0.024	0.981
Geno.rare34	48	*	*	*	*	0.008	17.830	0.109	163.940	0.000	0.083	0.062	1.333	0.183	18.780	0.104	181.413	0.000
haplo.base47	48	C	C	A	C	0.543	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.323	49	C	G	T	A	0.178	-2.989	3.128	-0.955	0.340	-0.040	0.014	-2.875	0.004	-0.257	2.999	-0.086	0.932
Geno.519	49	T	A	C	A	0.265	-2.507	2.879	-0.871	0.384	-0.021	0.013	-1.685	0.092	-0.261	2.755	-0.095	0.925
Geno.rare35	49	*	*	*	*	0.007	-12.984	14.815	-0.876	0.381	-0.090	0.066	-1.364	0.173	-6.610	14.196	-0.466	0.642
haplo.base48	49	C	A	C	A	0.549	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA

Table B1.25. Continued

Geno.520	50	G	T	A	C	0.174	-2.288	2.977	-0.769	0.442	-0.030	0.013	-2.245	0.025	0.585	2.850	0.205	0.837
Geno.rare36	50	*	*	*	*	0.013	-4.955	0.098	-50.591	0.000	-0.099	0.048	-2.054	0.040	-14.361	0.094	-153.155	0.000
haplo.base49	50	A	C	A	C	0.814	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.125	51	C	A	C	C	0.071	2.254	4.852	0.465	0.642	0.012	0.022	0.563	0.574	0.881	4.658	0.189	0.850
Geno.619	51	T	A	C	T	0.164	-1.865	3.139	-0.594	0.553	-0.027	0.014	-1.904	0.057	1.229	3.003	0.409	0.682
Geno.rare37	51	*	*	*	*	0.022	-7.930	9.081	-0.873	0.383	-0.072	0.043	-1.695	0.091	-13.411	8.781	-1.527	0.127
haplo.base50	51	C	A	C	T	0.744	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.126	52	A	C	C	G	0.080	1.093	4.392	0.249	0.804	0.012	0.020	0.625	0.532	-0.528	4.206	-0.126	0.900
Geno.rare38	52	*	*	*	*	0.017	-1.488	9.483	-0.157	0.875	-0.016	0.042	-0.383	0.702	-11.574	9.184	-1.260	0.208
haplo.base51	52	A	C	T	G	0.903	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.127	53	C	C	G	C	0.011	0.556	11.259	0.049	0.961	-0.037	0.050	-0.738	0.461	3.622	10.772	0.336	0.737
Geno.225	53	C	C	G	T	0.069	1.302	4.716	0.276	0.783	0.021	0.021	0.999	0.318	-1.108	4.520	-0.245	0.807
Geno.rare39	53	*	*	*	*	0.011	6.195	12.175	0.509	0.611	0.009	0.055	0.156	0.876	-13.097	11.794	-1.111	0.267
haplo.base52	53	C	T	G	C	0.909	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.128	54	C	G	C	C	0.010	-1.166	11.860	-0.098	0.922	-0.067	0.053	-1.261	0.208	4.674	11.342	0.412	0.680
Geno.419	54	C	G	T	T	0.069	0.835	4.734	0.176	0.860	0.019	0.021	0.898	0.369	-0.905	4.536	-0.200	0.842
Geno.620	54	T	G	C	C	0.171	-2.751	3.148	-0.874	0.383	-0.019	0.014	-1.366	0.172	-0.766	3.015	-0.254	0.800
Geno.rare40	54	*	*	*	*	0.006	7.215	0.269	26.863	0.000	0.156	0.084	1.860	0.063	-1.033	0.256	-4.028	0.000
haplo.base53	54	T	G	C	T	0.744	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.129	55	G	C	C	A	0.181	-2.741	3.079	-0.890	0.374	-0.023	0.014	-1.673	0.095	-0.477	2.949	-0.162	0.872
Geno.420	55	G	T	T	A	0.032	-1.769	6.919	-0.256	0.798	0.016	0.031	0.530	0.597	-1.965	6.623	-0.297	0.767
Geno.521	55	G	T	T	G	0.038	2.875	6.211	0.463	0.644	0.016	0.030	0.543	0.587	0.013	5.940	0.002	0.998
Geno.rare41	55	*	*	*	*	0.005	6.743	0.122	55.416	0.000	0.137	0.075	1.824	0.069	-0.081	0.116	-0.698	0.486
haplo.base54	55	G	C	T	A	0.745	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.130	56	C	C	A	A	0.181	-2.424	3.290	-0.737	0.462	-0.016	0.015	-1.108	0.269	-0.619	3.153	-0.196	0.844
Geno.226	56	C	T	A	A	0.323	0.840	2.793	0.301	0.764	0.018	0.012	1.439	0.151	-0.335	2.680	-0.125	0.901
Geno.621	56	T	T	A	C	0.032	-1.153	7.019	-0.164	0.870	0.023	0.031	0.733	0.464	-2.144	6.721	-0.319	0.750
Geno.86	56	T	T	G	C	0.038	3.195	6.302	0.507	0.612	0.027	0.028	0.973	0.331	-0.126	6.041	-0.021	0.983
haplo.base55	56	C	T	A	C	0.426	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.227	57	C	A	A	G	0.181	-2.541	3.209	-0.792	0.429	-0.019	0.014	-1.309	0.191	-0.547	3.090	-0.177	0.860
Geno.522	57	T	A	A	G	0.323	1.436	2.700	0.532	0.595	0.016	0.012	1.343	0.180	0.178	2.602	0.068	0.946
Geno.87	57	T	G	C	G	0.038	3.794	6.204	0.612	0.541	0.026	0.028	0.934	0.351	0.402	5.980	0.067	0.946
Geno.rare42	57	*	*	*	*	0.002	109.673	0.031	3550.215	0.000	0.188	0.209	0.900	0.368	76.319	0.040	1929.323	0.000
haplo.base56	57	T	A	C	G	0.456	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.228	58	A	A	G	A	0.013	6.895	0.515	13.390	0.000	0.040	0.049	0.810	0.418	8.385	0.500	16.759	0.000
Geno.523	58	A	C	G	A	0.450	0.175	2.358	0.074	0.941	-0.005	0.011	-0.431	0.666	0.442	2.260	0.195	0.845
Geno.88	58	G	C	G	A	0.038	3.882	6.265	0.620	0.536	0.022	0.028	0.780	0.435	0.792	6.006	0.132	0.895
Geno.rare43	58	*	*	*	*	0.008	19.749	0.263	75.064	0.000	0.052	0.059	0.881	0.379	10.974	0.251	43.717	0.000
haplo.base57	58	A	A	G	G	0.492	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.229	59	A	G	A	C	0.013	6.475	0.135	48.004	0.000	0.042	0.049	0.871	0.384	8.041	0.146	55.256	0.000
Geno.324	59	A	G	G	C	0.480	-0.407	2.358	-0.172	0.863	0.002	0.011	0.147	0.883	-0.445	2.255	-0.197	0.844
Geno.421	59	A	G	G	T	0.011	-0.955	0.160	-5.955	0.000	0.053	0.050	1.050	0.294	-1.123	0.153	-7.339	0.000
Geno.rare44	59	*	*	*	*	0.008	19.177	0.124	154.598	0.000	0.054	0.059	0.919	0.358	10.491	0.117	89.877	0.000
haplo.base58	59	C	G	A	C	0.487	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.622	60	G	G	C	A	0.487	-0.959	2.383	-0.402	0.688	0.003	0.011	0.239	0.811	-0.059	2.281	-0.026	0.980
Geno.711	60	G	G	T	A	0.011	-1.462	0.172	-8.513	0.000	0.051	0.050	1.020	0.308	-1.182	0.164	-7.205	0.000
Geno.rare45	60	*	*	*	*	0.002	45.856	0.025	1857.191	0.000	0.024	0.132	0.180	0.857	35.945	0.024	1523.348	0.000
haplo.base59	60	G	A	C	A	0.499	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.131	61	A	C	A	C	0.183	2.385	3.265	0.731	0.465	0.015	0.014	1.009	0.313	0.772	3.122	0.247	0.805
Geno.230	61	A	C	A	T	0.319	1.382	2.680	0.516	0.606	-0.010	0.012	-0.841	0.401	0.253	2.568	0.098	0.922
Geno.92	61	G	T	A	C	0.011	-0.321	11.342	-0.028	0.977	0.049	0.051	0.980	0.328	-1.100	10.871	-0.101	0.919
Geno.rare46	61	*	*	*	*	0.002	-20.015	NA	NA	NA	-0.132	0.000	-8.86E+16	0.000	-8.979	NA	NA	NA
haplo.base60	61	G	C	A	C	0.484	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.231	62	C	A	C	W	0.299	2.015	2.850	0.707	0.480	0.021	0.013	1.674	0.095	-0.722	2.728	-0.265	0.791
Geno.325	62	C	A	T	D	0.319	2.025	2.810	0.721	0.471	-0.004	0.013	-0.284	0.777	-0.016	2.693	-0.006	0.995
Geno.712	62	T	A	C	D	0.011	-0.210	11.325	-0.019	0.985	0.053	0.050	1.045	0.296	-1.466	10.852	-0.135	0.893
haplo.base61	62	C	A	C	D	0.369	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.326	63	A	C	W	C	0.299	1.327	2.804	0.473	0.636	0.021	0.013	1.650	0.099	-1.221	2.692	-0.454	0.650
Geno.524	63	A	T	D	T	0.319	1.433	2.781	0.515	0.606	-0.005	0.012	-0.409	0.682	-0.361	2.669	-0.135	0.892
Geno.rare47	63	*	*	*	*	0.007	-26.212	0.152	-171.906	0.000	-0.033	0.071	-0.470	0.638	-13.524	0.141	-95.794	0.000
haplo.base62	63	A	C	D	T	0.375	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.327	64	C	W	C	A	0.299	1.033	2.815	0.367	0.714	0.019	0.013	1.537	0.125	-1.435	2.697	-0.532	0.595
Geno.623	64	T	D	T	G	0.320	1.132	2.784	0.406	0.685	-0.006	0.012	-0.511	0.610	-0.537	2.668	-0.201	0.841
Geno.rare48	64	*	*	*	*	0.007	-16.676	0.152	-109.514	0.000	0.004	0.071	0.058	0.954	-6.838	0.146	-46.756	0.000
haplo.base63	64	C	D	T	G	0.374	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.328	65	D	T	G	T	0.320	0.932	2.793	0.334	0.739	-0.005	0.013	-0.430	0.668	-0.740	2.677	-0.276	0.782
Geno.525	65	W	C	A	T	0.299	0.944	2.816	0.335	0.737	0.020	0.013	1.570	0.117	-1.524	2.699	-0.565	0.572
Geno.rare49	65	*	*	*	*	0.007	-16.817	0.152	-110.372	0.000	0.005	0.071	0.067	0.947	-6.986	0.146	-47.965	0.000
haplo.base64	65	D	T	G	C	0.374	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.329	66	C	A	T	C	0.299	0.204	2.809	0.073	0.942	0.018	0.013	1.465	0.143	-2.030	2.688	-0.755	0.450
Geno.713	66	T	G	T	C	0.322	0.855	2.791	0.306	0.759	-0.006	0.013	-0.440	0.660	-0.754	2.672	-0.282	0.778
Geno.rare50	66	*	*	*	*	0.006	16.263	0.138	117.842	0.000	0.074	0.076	0.967	0.334	15.443	0.133	116.225	0.000
haplo.base65	66	T	G	C	C	0.374	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.330	67	A	T	C	G	0.296	0.555	2.824	0.196	0.844	0.018	0.013	1.444	0.149	-1.548	2.701	-0.573	0.567
Geno.89	67	G	T	C	G	0.325	0.996	2.799	0.356	0.722	-0.006	0.013	-0.464	0.643	-0.567	2.677	-0.212	0.832
Geno.rare51	67	*	*	*	*	0.014	16.439	10.287	1.598	0.111	0.021	0.046	0.464	0.643	18.820	9.831	1.914	0.056
haplo.base66	67	G	C	C	G	0.365	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.232	68	C	C	G	C	0.288	0.317	2.629	0.121	0.904	-0.016	0.012	-1.372	0.171	2.484	2.513	0.988	0.323
Geno.331	68	C	C	G	T	0.077	-4.534	4.400	-1.031	0.303	0.029	0.020	1.488	0.137	-3.835	4.205	-0.912	0.362
Geno.rare52	68	*	*	*	*	0.014	15.463	10.286	1.503	0.133	0.016	0.046	0.359	0.720	19.631	9.824	1.998	0.046
haplo.base67	68	T	C	G	C	0.622	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.332	69	C	G	C	G	0.080	1.459	4.432	0.329	0.742	-0.019	0.020	-0.953	0.341	2.178	4.237	0.514	0.607

Table B1.25. Continued

Geno.624	69	C	G	T	T	0.077	-4.367	4.376	-0.998	0.319	0.031	0.020	1.601	0.110	-4.129	4.189	-0.986	0.325
Geno.rare53	69	*	*	*	*	0.014	15.568	10.805	1.441	0.150	0.021	0.048	0.430	0.668	18.991	10.318	1.841	0.066
haplo.base68	69	C	G	C	T	0.829	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.422	70	G	C	G	G	0.079	1.627	4.441	0.366	0.714	-0.022	0.020	-1.100	0.272	2.127	4.253	0.500	0.617
Geno.93	70	G	T	T	G	0.077	-4.144	4.384	-0.945	0.345	0.032	0.020	1.649	0.100	-4.560	4.199	-1.086	0.278
Geno.rare54	70	*	*	*	*	0.012	16.928	0.190	89.156	0.000	-0.048	0.056	-0.860	0.390	1.739	0.172	10.100	0.000
haplo.base69	70	G	C	T	G	0.832	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.333	71	C	G	G	G	0.080	0.969	4.419	0.219	0.827	-0.022	0.020	-1.102	0.271	1.676	4.211	0.398	0.691
Geno.526	71	C	T	G	A	0.053	-9.317	4.877	-1.910	0.057	-0.018	0.022	-0.846	0.398	-6.176	4.662	-1.325	0.186
Geno.810	71	T	T	G	G	0.076	-5.057	4.401	-1.149	0.251	0.032	0.020	1.612	0.107	-5.414	4.202	-1.288	0.198
Geno.rare55	71	*	*	*	*	0.003	22.397	0.042	528.955	0.000	-0.142	0.146	-0.968	0.334	-47.473	0.036	-1314.970	0.000
haplo.base70	71	C	T	G	G	0.787	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.334	72	G	G	G	G	0.080	1.687	4.395	0.384	0.701	-0.024	0.020	-1.237	0.217	2.335	4.213	0.554	0.580
Geno.625	72	T	G	A	G	0.053	-8.617	4.880	-1.766	0.078	-0.023	0.022	-1.033	0.302	-5.145	4.678	-1.100	0.272
Geno.rare56	72	*	*	*	*	0.008	20.521	0.110	185.966	0.000	-0.014	0.070	-0.197	0.844	-7.933	0.085	-92.798	0.000
haplo.base71	72	T	G	G	G	0.859	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.423	73	G	A	G	C	0.053	-8.650	4.866	-1.778	0.076	-0.022	0.022	-0.986	0.324	-5.216	4.669	-1.117	0.264
Geno.rare57	73	*	*	*	*	0.010	19.114	0.111	171.595	0.000	-0.026	0.056	-0.469	0.639	0.256	0.081	3.166	0.002
haplo.base72	73	G	G	G	C	0.937	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.132	74	A	G	C	G	0.054	-9.169	4.939	-1.857	0.064	-0.031	0.022	-1.403	0.161	-5.380	4.739	-1.135	0.257
Geno.335	74	G	G	C	A	0.321	0.122	2.554	0.048	0.962	-0.018	0.011	-1.589	0.113	-0.130	2.447	-0.053	0.958
Geno.rare58	74	*	*	*	*	0.007	17.089	0.118	144.958	0.000	0.020	0.065	0.308	0.758	21.298	0.120	177.751	0.000
haplo.base73	74	G	G	C	G	0.618	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.133	75	G	C	A	C	0.321	0.164	2.527	0.065	0.948	-0.014	0.011	-1.268	0.205	-0.525	2.415	-0.217	0.828
Geno.424	75	G	C	G	T	0.051	-12.964	5.361	-2.418	0.016	0.003	0.024	0.138	0.890	-13.282	5.126	-2.591	0.010
Geno.rare59	75	*	*	*	*	0.007	17.528	0.085	207.370	0.000	0.023	0.062	0.367	0.714	21.515	0.081	265.535	0.000
haplo.base74	75	G	C	G	C	0.621	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.134	76	C	A	C	A	0.320	0.145	2.537	0.057	0.955	-0.014	0.011	-1.268	0.205	-0.524	2.426	-0.216	0.829
Geno.527	76	C	G	T	G	0.056	-9.968	5.112	-1.950	0.052	0.009	0.023	0.398	0.691	-10.223	4.887	-2.092	0.037
Geno.rare60	76	*	*	*	*	0.003	15.926	0.051	311.219	0.000	-0.070	0.107	-0.653	0.514	27.997	0.049	567.411	0.000
haplo.base75	76	C	G	C	G	0.620	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.135	77	A	C	A	C	0.320	-0.013	2.538	-0.005	0.996	-0.012	0.011	-1.079	0.281	-0.825	2.429	-0.340	0.734
Geno.626	77	G	T	G	C	0.056	-10.163	5.114	-1.987	0.047	0.011	0.023	0.501	0.617	-10.589	4.893	-2.164	0.031
Geno.rare61	77	*	*	*	*	0.002	-7.180	0.045	-161.270	0.000	0.225	0.131	1.714	0.087	-15.641	0.043	-366.858	0.000
haplo.base76	77	G	C	G	C	0.621	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.233	78	C	A	C	T	0.312	0.928	2.796	0.332	0.740	-0.006	0.013	-0.481	0.631	-0.554	2.676	-0.207	0.836
Geno.627	78	C	G	C	T	0.236	3.070	3.027	1.014	0.311	0.020	0.014	1.430	0.153	1.020	2.895	0.352	0.725
Geno.94	78	T	G	C	T	0.056	-9.114	5.189	-1.756	0.080	0.017	0.023	0.732	0.464	-10.168	4.972	-2.045	0.041
Geno.rare62	78	*	*	*	*	0.010	2.523	0.351	7.189	0.000	0.038	0.059	0.643	0.520	-2.194	0.340	-6.456	0.000
haplo.base77	78	C	G	C	G	0.386	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.234	79	A	C	T	A	0.311	0.915	2.772	0.330	0.741	-0.005	0.013	-0.391	0.696	-0.670	2.653	-0.253	0.801
Geno.95	79	G	C	T	T	0.288	0.723	2.760	0.262	0.794	0.018	0.013	1.415	0.157	-1.200	2.641	-0.454	0.650
Geno.rare63	79	*	*	*	*	0.016	14.965	0.448	33.415	0.000	-0.022	0.043	-0.504	0.614	12.987	0.446	29.090	0.000
haplo.base78	79	G	C	G	A	0.385	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.628	80	C	T	A	C	0.316	0.903	2.809	0.321	0.748	-0.005	0.013	-0.390	0.697	-0.634	2.688	-0.236	0.814
Geno.714	80	C	T	T	C	0.287	0.242	2.792	0.087	0.931	0.020	0.012	1.636	0.102	-1.690	2.673	-0.632	0.527
Geno.rare64	80	*	*	*	*	0.004	4.767	0.091	52.605	0.000	0.137	0.106	1.295	0.196	-7.543	0.087	-87.134	0.000
haplo.base79	80	C	G	A	C	0.394	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.629	81	T	A	C	C	0.313	0.699	2.838	0.246	0.805	-0.005	0.013	-0.378	0.706	-0.301	2.716	-0.111	0.912
Geno.715	81	T	T	C	C	0.288	0.210	2.780	0.076	0.940	0.021	0.012	1.722	0.086	-1.887	2.664	-0.708	0.479
Geno.rare65	81	*	*	*	*	0.004	22.659	0.078	289.137	0.000	-0.090	0.092	-0.984	0.326	-10.602	0.074	-143.535	0.000
haplo.base80	81	G	A	C	C	0.394	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.235	82	A	C	C	A	0.018	7.733	10.686	0.724	0.470	-0.005	0.044	-0.123	0.902	6.316	9.722	0.650	0.516
Geno.528	82	T	C	C	A	0.110	-1.283	3.856	-0.333	0.739	0.027	0.017	1.566	0.118	-3.582	3.664	-0.978	0.329
Geno.630	82	T	C	C	G	0.180	0.934	3.162	0.295	0.768	0.022	0.014	1.596	0.111	-0.578	3.006	-0.192	0.847
Geno.rare66	82	*	*	*	*	0.003	24.402	0.154	158.805	0.000	-0.167	0.107	-1.559	0.119	-10.396	0.127	-82.168	0.000
haplo.base81	82	A	C	C	G	0.689	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.236	83	C	C	A	C	0.038	-2.635	5.922	-0.445	0.657	0.020	0.027	0.766	0.444	-1.454	5.677	-0.256	0.798
Geno.336	83	C	C	A	T	0.089	0.989	4.126	0.240	0.811	0.020	0.018	1.112	0.267	-2.029	3.933	-0.516	0.606
Geno.rare67	83	*	*	*	*	0.003	24.055	0.050	480.087	0.000	-0.175	0.107	-1.636	0.102	-10.052	0.047	-212.123	0.000
haplo.base82	83	C	C	G	T	0.870	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.237	84	C	A	C	G	0.038	-2.706	5.925	-0.457	0.648	0.021	0.027	0.797	0.426	-1.563	5.668	-0.276	0.783
Geno.425	84	C	A	T	G	0.088	0.862	4.141	0.208	0.835	0.018	0.018	0.979	0.328	-1.939	3.940	-0.492	0.623
Geno.rare68	84	*	*	*	*	0.003	15.186	0.050	304.008	0.000	0.018	0.107	0.172	0.863	-30.139	0.047	-642.156	0.000
haplo.base83	84	C	G	T	G	0.871	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.136	85	A	C	G	C	0.038	-3.026	5.922	-0.511	0.610	0.020	0.027	0.758	0.449	-1.508	5.674	-0.266	0.790
Geno.337	85	A	T	G	C	0.088	0.529	4.138	0.128	0.898	0.017	0.018	0.920	0.358	-1.883	3.944	-0.477	0.633
Geno.rare69	85	*	*	*	*	0.006	-17.206	0.104	-165.356	0.000	-0.075	0.076	-0.985	0.325	-12.934	0.099	-130.623	0.000
haplo.base84	85	G	T	G	C	0.869	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.137	86	C	G	C	A	0.038	-2.967	5.967	-0.497	0.619	0.013	0.027	0.499	0.618	-1.591	5.718	-0.278	0.781
Geno.631	86	T	G	C	G	0.310	0.581	2.568	0.226	0.821	-0.013	0.012	-1.085	0.278	-0.739	2.459	-0.301	0.764
Geno.rare70	86	*	*	*	*	0.006	-17.085	0.109	-156.618	0.000	-0.083	0.076	-1.085	0.278	-12.874	0.105	-122.752	0.000
haplo.base85	86	T	G	C	A	0.646	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.338	87	G	C	A	C	0.057	-10.756	4.836	-2.224	0.027	-0.040	0.022	-1.854	0.064	-6.313	4.645	-1.359	0.175
Geno.632	87	G	C	G	G	0.310	-0.455	2.593	-0.175	0.861	-0.018	0.012	-1.564	0.118	-1.350	2.489	-0.542	0.588
Geno.rare71	87	*	*	*	*	0.006	-18.464	0.102	-181.468	0.000	-0.090	0.076	-1.176	0.240	-13.682	0.098	-139.085	0.000
haplo.base86	87	G	C	A	G	0.627	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.138	88	C	A	C	T	0.057	-12.153	4.996	-2.433	0.015	-0.038	0.022	-1.679	0.094	-8.410	4.794	-1.754	0.080
Geno.238	88	C	A	G	C	0.297	-3.078	2.892	-1.064	0.288	0.007	0.013	0.517	0.605	-4.712	2.759	-1.708	0.088
Geno.426	88	C	G	G	C	0.311	-1.930	2.916	-0.662	0.508	-0.015	0.013	-1.125	0.261	-3.634	2.796	-1.299	0.194
Geno.rare72	88	*	*	*	*	0.005	-23.915	0.253	-94.451	0.000	-0.166	0.077	-2.176	0.030	-13.685	0.232	-59.005	0.000
haplo.base87	88	C	A	G	T	0.330	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA

Table B1.25. Continued

Geno.239	89	A	C	T	A	0.056	-11.686	5.016	-2.330	0.020	-0.038	0.023	-1.657	0.098	-8.010	4.809	-1.666	0.096
Geno.427	89	A	G	C	G	0.300	-3.392	2.820	-1.203	0.229	0.007	0.013	0.564	0.573	-4.971	2.703	-1.839	0.066
Geno.96	89	G	G	C	A	0.299	-2.514	2.892	-0.869	0.385	-0.014	0.013	-1.082	0.280	-4.168	2.773	-1.503	0.133
Geno.104	89	G	G	C	G	0.014	2.274	0.776	2.932	0.003	-0.054	0.047	-1.148	0.251	2.187	0.734	2.978	0.003
Geno.rare73	89	*	*	*	*	0.002	-38.395	0.115	-332.677	0.000	-0.063	0.110	-0.575	0.565	-29.222	0.110	-264.819	0.000
haplo.base88	89	A	G	T	A	0.328	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.240	90	C	T	A	C	0.055	-12.175	5.070	-2.402	0.017	-0.038	0.023	-1.659	0.098	-8.432	4.863	-1.734	0.083
Geno.633	90	G	C	A	C	0.300	-2.375	2.968	-0.800	0.424	-0.014	0.013	-1.044	0.297	-4.158	2.840	-1.464	0.144
Geno.716	90	G	C	G	C	0.313	-3.093	2.851	-1.085	0.278	0.005	0.013	0.415	0.678	-4.636	2.734	-1.696	0.090
Geno.rare74	90	*	*	*	*	0.004	-37.343	0.072	-521.714	0.000	-0.132	0.131	-1.010	0.313	-29.756	0.071	-418.905	0.000
haplo.base89	90	G	T	A	C	0.328	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.139	91	C	A	C	A	0.290	-0.340	2.868	-0.119	0.906	-0.005	0.013	-0.385	0.700	-3.029	2.736	-1.107	0.269
Geno.339	91	C	G	C	A	0.313	-1.024	2.738	-0.374	0.709	0.012	0.012	0.928	0.354	-3.160	2.616	-1.208	0.228
Geno.rare75	91	*	*	*	*	0.013	2.577	0.395	6.524	0.000	-0.059	0.049	-1.216	0.225	5.420	0.377	14.372	0.000
haplo.base90	91	T	A	C	A	0.384	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.529	92	G	C	A	W	0.316	-1.044	2.498	-0.418	0.676	0.012	0.011	1.111	0.267	-2.143	2.391	-0.896	0.370
Geno.rare76	92	*	*	*	*	0.011	10.351	0.122	84.809	0.000	-0.077	0.052	-1.475	0.141	12.195	0.117	104.218	0.000
haplo.base91	92	A	C	A	W	0.673	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.340	93	C	A	W	T	0.013	22.756	0.044	518.979	0.000	0.062	0.047	1.317	0.188	19.697	0.042	468.028	0.000
Geno.rare77	93	*	*	*	*	0.011	11.421	0.036	321.084	0.000	-0.080	0.052	-1.549	0.122	13.646	0.034	400.217	0.000
haplo.base92	93	C	A	W	C	0.976	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.241	94	A	W	C	G	0.113	2.532	3.862	0.656	0.512	0.005	0.017	0.273	0.785	1.976	3.689	0.535	0.593
Geno.530	94	A	W	T	T	0.012	25.357	10.955	2.315	0.021	0.063	0.047	1.339	0.181	21.661	10.660	2.032	0.043
Geno.rare78	94	*	*	*	*	0.011	16.884	3.008	5.614	0.000	-0.059	0.057	-1.036	0.301	17.622	12.046	1.463	0.144
haplo.base93	94	A	W	C	T	0.865	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.242	95	W	C	G	G	0.113	1.334	3.869	0.345	0.730	0.000	0.017	0.024	0.981	1.238	3.728	0.332	0.740
Geno.341	95	W	C	T	A	0.035	-12.327	5.951	-2.072	0.039	-0.059	0.027	-2.228	0.026	-6.483	5.734	-1.131	0.259
Geno.634	95	W	T	T	G	0.012	24.022	0.292	82.224	0.000	0.059	0.047	1.262	0.207	21.180	10.853	1.952	0.051
Geno.rare79	95	*	*	*	*	0.002	12.034	0.016	761.695	0.000	-0.287	NA	NA	NA	4.239	0.358	11.836	0.000
haplo.base94	95	W	C	T	G	0.838	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.140	96	C	G	G	A	0.113	0.963	3.858	0.249	0.803	0.000	0.017	0.025	0.980	0.814	3.710	0.219	0.826
Geno.342	96	C	T	A	G	0.034	-13.011	6.024	-2.160	0.031	-0.066	0.028	-2.386	0.017	-7.652	5.886	-1.300	0.194
Geno.428	96	C	T	G	A	0.056	-10.258	5.150	-1.992	0.047	0.006	0.023	0.252	0.801	-10.625	4.995	-2.127	0.034
Geno.811	96	T	T	G	G	0.012	23.906	0.314	76.112	0.000	0.038	0.053	0.728	0.467	20.332	10.639	1.911	0.056
Geno.rare80	96	*	*	*	*	0.002	-8.402	0.018	-469.414	0.000	0.196	0.129	1.522	0.129	5.634	0.115	48.882	0.000
haplo.base95	96	C	T	G	G	0.783	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.141	97	G	G	A	C	0.114	0.303	3.886	0.078	0.938	0.004	0.017	0.251	0.802	-0.080	3.729	-0.022	0.983
Geno.343	97	T	A	G	C	0.034	-14.529	6.236	-2.330	0.020	-0.061	0.027	-2.232	0.026	-9.106	6.351	-1.434	0.152
Geno.531	97	T	G	A	C	0.056	-10.479	5.164	-2.029	0.043	0.013	0.023	0.575	0.565	-11.027	4.978	-2.215	0.027
Geno.717	97	T	G	G	G	0.126	-0.985	3.547	-0.278	0.781	0.022	0.016	1.371	0.171	-2.947	3.466	-0.850	0.396
haplo.base96	97	T	G	G	C	0.668	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.142	98	A	G	C	A	0.034	-14.779	6.162	-2.398	0.017	-0.057	0.027	-2.141	0.033	-8.840	5.861	-1.508	0.132
Geno.344	98	G	A	C	G	0.173	-3.314	3.182	-1.041	0.298	0.009	0.014	0.641	0.522	-3.622	3.056	-1.185	0.236
Geno.635	98	G	G	G	G	0.127	-0.846	3.559	-0.238	0.812	0.022	0.016	1.398	0.162	-2.687	3.413	-0.787	0.431
haplo.base97	98	G	G	C	A	0.664	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.143	99	A	C	G	C	0.173	-2.393	3.173	-0.754	0.451	0.013	0.014	0.894	0.372	-3.071	3.038	-1.011	0.313
Geno.429	99	G	G	G	C	0.128	-0.078	3.539	-0.022	0.982	0.024	0.016	1.518	0.129	-2.177	3.392	-0.642	0.521
haplo.base98	99	G	C	A	A	0.699	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.144	100	C	A	A	C	0.071	4.013	5.856	0.685	0.493	-0.003	0.024	-0.105	0.916	0.572	5.463	0.105	0.917
Geno.345	100	C	G	C	C	0.064	-3.736	5.372	-0.695	0.487	0.023	0.024	0.994	0.320	-5.185	5.181	-1.001	0.317
Geno.430	100	C	G	C	T	0.110	-1.051	4.096	-0.257	0.798	0.006	0.018	0.321	0.748	-1.777	3.925	-0.453	0.651
Geno.718	100	G	G	C	C	0.036	-1.293	7.945	-0.163	0.871	-0.011	0.033	-0.333	0.739	-0.151	7.255	-0.021	0.983
Geno.812	100	G	G	C	T	0.091	0.951	4.797	0.198	0.843	0.039	0.021	1.892	0.059	-3.021	4.483	-0.674	0.501
haplo.base99	100	C	A	A	T	0.627	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Geno.145	101	A	A	C	A	0.051	7.607	7.315	1.040	0.299	-0.012	0.031	-0.384	0.701	3.317	7.182	0.462	0.644
Geno.243	101	A	A	C	C	0.022	-2.970	11.867	-0.250	0.802	0.040	0.050	0.796	0.426	-6.815	13.127	-0.519	0.604
Geno.346	101	A	A	T	A	0.309	-1.006	3.589	-0.280	0.779	0.015	0.015	0.963	0.336	-3.099	3.470	-0.893	0.372
Geno.532	101	G	C	C	A	0.081	-9.475	5.901	-1.606	0.109	0.029	0.022	1.303	0.193	-11.976	5.618	-2.132	0.033
Geno.636	101	G	C	C	C	0.018	20.978	13.008	1.613	0.107	-0.036	0.062	-0.582	0.561	20.463	11.172	1.832	0.067
Geno.719	101	G	C	T	A	0.150	2.150	4.005	0.537	0.592	0.027	0.017	1.575	0.116	-1.373	3.838	-0.358	0.721
Geno.813	101	G	C	T	C	0.052	-6.958	7.737	-0.899	0.369	0.027	0.029	0.900	0.369	-7.975	7.418	-1.075	0.283
haplo.base100	101	A	A	T	C	0.317	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA

TABLE B1.26. Summary of *CETP* 4-SNP sliding haplotypes (103 SNPs included) for TG in NHWs

	Window	loc.1	loc.2	loc.3	loc.4	hap.freq	TG coef	se	t.stat	pval
Geno.1	1	A	A	T	G	0.029	-0.084	0.080	-1.050	0.294
Geno.2	1	A	C	C	A	0.138	0.014	0.038	0.382	0.702
Geno.3	1	A	C	C	G	0.232	0.041	0.031	1.328	0.185
Geno.6	1	G	C	C	A	0.033	0.007	0.073	0.090	0.928
Geno.7	1	G	C	C	G	0.250	-0.010	0.031	-0.335	0.738
haplo.base	1	G	A	T	G	0.318	NA	NA	NA	NA
Geno.21	2	A	T	G	A	0.330	-0.024	0.025	-0.963	0.336
Geno.31	2	A	T	G	G	0.017	-0.002	0.090	-0.021	0.983
Geno.5	2	C	C	A	G	0.170	-0.003	0.033	-0.087	0.930
haplo.base1	2	C	C	G	G	0.482	NA	NA	NA	NA
Geno.22	3	C	A	G	T	0.170	0.021	0.035	0.589	0.556
Geno.4	3	C	G	G	C	0.206	0.051	0.032	1.606	0.109
Geno.51	3	C	G	G	T	0.276	0.005	0.029	0.185	0.853
Geno.8	3	T	G	G	T	0.016	0.051	0.098	0.522	0.602
Geno.rare	3	*	*	*	*	0.002	-0.036	0.361	-0.100	0.921
haplo.base2	3	T	G	A	T	0.330	NA	NA	NA	NA
Geno.32	4	A	G	T	G	0.171	0.019	0.036	0.537	0.592
Geno.61	4	G	G	C	G	0.207	0.045	0.033	1.392	0.164
Geno.81	4	G	G	T	G	0.276	0.002	0.030	0.052	0.959
Geno.9	4	G	G	T	T	0.016	0.024	0.096	0.249	0.803
Geno.rare1	4	*	*	*	*	0.010	-0.038	0.126	-0.304	0.761
haplo.base3	4	G	A	T	T	0.322	NA	NA	NA	NA
Geno.23	5	A	T	T	T	0.321	-0.006	0.027	-0.233	0.816
Geno.33	5	G	C	G	C	0.207	0.039	0.031	1.245	0.214
Geno.71	5	G	T	T	T	0.014	0.035	0.099	0.358	0.721
Geno.rare2	5	*	*	*	*	0.012	-0.015	0.108	-0.134	0.893
haplo.base4	5	G	T	G	C	0.447	NA	NA	NA	NA
Geno.24	6	C	G	C	T	0.207	0.044	0.032	1.390	0.165
Geno.34	6	T	G	C	C	0.081	0.032	0.045	0.719	0.472
Geno.82	6	T	T	T	T	0.335	0.003	0.028	0.095	0.924
Geno.rare3	6	*	*	*	*	0.012	-0.011	0.112	-0.101	0.919
haplo.base5	6	T	G	C	T	0.365	NA	NA	NA	NA
Geno.25	7	G	C	C	G	0.081	0.027	0.045	0.603	0.547
Geno.35	7	G	C	T	A	0.199	0.039	0.033	1.198	0.232
Geno.83	7	T	T	T	A	0.335	-0.001	0.028	-0.019	0.985
Geno.rare4	7	*	*	*	*	0.012	-0.011	0.113	-0.100	0.921
haplo.base6	7	G	C	T	G	0.373	NA	NA	NA	NA
Geno.36	8	C	C	G	T	0.082	0.034	0.045	0.750	0.454
Geno.41	8	C	T	A	C	0.202	0.037	0.032	1.140	0.255
Geno.62	8	T	T	A	C	0.344	-0.002	0.027	-0.088	0.930
haplo.base7	8	C	T	G	C	0.372	NA	NA	NA	NA
Geno.37	9	C	G	T	C	0.082	0.025	0.043	0.587	0.558
Geno.52	9	T	G	C	C	0.180	0.012	0.032	0.367	0.714
Geno.63	9	T	G	C	T	0.192	-0.036	0.030	-1.205	0.229
haplo.base8	9	T	A	C	C	0.545	NA	NA	NA	NA
Geno.26	10	A	C	C	C	0.125	0.027	0.036	0.734	0.463
Geno.38	10	G	C	C	A	0.010	0.075	0.122	0.619	0.536
Geno.42	10	G	C	C	C	0.169	0.016	0.033	0.477	0.634
Geno.53	10	G	C	T	C	0.193	-0.027	0.032	-0.855	0.393
Geno.64	10	G	T	C	A	0.082	0.031	0.044	0.709	0.478
haplo.base9	10	A	C	C	A	0.420	NA	NA	NA	NA
Geno.11	11	C	C	A	A	0.042	0.080	0.060	1.336	0.182
Geno.43	11	C	C	C	C	0.293	0.025	0.028	0.917	0.360
Geno.65	11	C	T	C	C	0.193	-0.023	0.032	-0.735	0.463
Geno.72	11	T	C	A	C	0.082	0.036	0.044	0.828	0.408
Geno.rare5	11	*	*	*	*	0.003	0.052	0.290	0.180	0.857
haplo.base10	11	C	C	A	C	0.388	NA	NA	NA	NA
Geno.12	12	C	A	A	C	0.044	0.073	0.058	1.266	0.206
Geno.66	12	C	C	C	T	0.293	0.019	0.027	0.712	0.477
Geno.10	12	T	C	C	T	0.192	-0.027	0.031	-0.879	0.380
Geno.rare6	12	*	*	*	*	0.007	0.071	0.165	0.430	0.667
haplo.base11	12	C	A	C	C	0.465	NA	NA	NA	NA
Geno.13	13	A	A	C	G	0.044	0.069	0.059	1.177	0.240
Geno.27	13	A	C	C	A	0.444	-0.004	0.024	-0.151	0.880
Geno.39	13	A	C	C	G	0.021	0.041	0.081	0.500	0.618
Geno.rare7	13	*	*	*	*	0.006	0.075	0.166	0.454	0.650
haplo.base12	13	C	C	T	G	0.485	NA	NA	NA	NA
Geno.14	14	A	C	G	C	0.045	0.068	0.058	1.174	0.241
Geno.310	14	C	C	A	C	0.444	-0.006	0.024	-0.260	0.795
Geno.54	14	C	C	G	C	0.022	0.048	0.080	0.598	0.550
Geno.73	14	C	T	G	T	0.030	0.001	0.069	0.020	0.984
haplo.base13	14	C	T	G	C	0.458	NA	NA	NA	NA
Geno.15	15	C	A	C	A	0.443	-0.006	0.024	-0.265	0.791
Geno.311	15	C	G	C	G	0.069	0.070	0.048	1.475	0.141
Geno.67	15	T	G	T	G	0.030	0.003	0.069	0.042	0.966
haplo.base14	15	T	G	C	G	0.458	NA	NA	NA	NA
Geno.44	16	G	C	G	A	0.235	0.029	0.029	1.017	0.310

Table B1.26. Continued

	Window	loc.1	loc.2	loc.3	loc.4	hap.freq	TG coef	se	t.stat	pval
Geno.55	16	G	C	G	G	0.292	0.003	0.027	0.111	0.911
Geno.68	16	G	T	G	A	0.030	0.010	0.069	0.143	0.886
haplo.base15	16	A	C	A	G	0.443	NA	NA	NA	NA
Geno.28	17	C	G	A	A	0.234	0.028	0.029	0.952	0.342
Geno.45	17	C	G	G	A	0.293	0.005	0.027	0.166	0.868
Geno.69	17	T	G	A	A	0.030	0.010	0.069	0.138	0.890
haplo.base16	17	C	A	G	A	0.442	NA	NA	NA	NA
Geno.312	18	G	A	A	A	0.191	0.020	0.031	0.658	0.511
Geno.46	18	G	A	A	G	0.073	0.050	0.050	0.993	0.321
Geno.610	18	G	G	A	A	0.105	0.051	0.041	1.237	0.217
Geno.74	18	G	G	A	G	0.186	-0.021	0.032	-0.666	0.506
Geno.rare8	18	*	*	*	*	0.003	0.368	0.264	1.397	0.163
haplo.base17	18	A	G	A	A	0.440	NA	NA	NA	NA
Geno.29	19	A	A	A	G	0.196	0.027	0.033	0.836	0.403
Geno.47	19	A	A	G	G	0.066	-0.001	0.057	-0.010	0.992
Geno.611	19	G	A	A	C	0.088	0.020	0.042	0.461	0.645
Geno.91	19	G	A	G	G	0.193	-0.012	0.034	-0.356	0.722
Geno.rare9	19	*	*	*	*	0.002	0.304	0.409	0.744	0.457
haplo.base18	19	G	A	A	G	0.454	NA	NA	NA	NA
Geno.16	20	A	A	C	C	0.090	0.014	0.041	0.338	0.736
Geno.48	20	A	G	G	C	0.259	-0.017	0.027	-0.632	0.528
Geno.rare10	20	*	*	*	*	0.002	0.133	0.285	0.467	0.641
haplo.base19	20	A	A	G	C	0.649	NA	NA	NA	NA
Geno.17	21	A	C	C	C	0.090	0.018	0.042	0.441	0.659
Geno.210	21	A	G	C	C	0.203	0.016	0.031	0.505	0.614
Geno.56	21	G	G	C	G	0.258	-0.009	0.029	-0.314	0.753
Geno.rare11	21	*	*	*	*	0.002	-0.069	0.285	-0.241	0.810
haplo.base20	21	A	G	C	G	0.447	NA	NA	NA	NA
Geno.18	22	C	C	C	A	0.090	0.024	0.041	0.583	0.560
Geno.49	22	G	C	C	C	0.199	0.028	0.028	0.989	0.323
Geno.rare12	22	*	*	*	*	0.010	-0.034	0.117	-0.292	0.770
haplo.base21	22	G	C	G	A	0.700	NA	NA	NA	NA
Geno.19	23	C	C	A	C	0.055	-0.006	0.050	-0.111	0.912
Geno.211	23	C	C	A	T	0.036	0.103	0.070	1.481	0.139
Geno.313	23	C	C	C	C	0.199	0.037	0.031	1.161	0.246
Geno.57	23	C	G	A	C	0.265	0.014	0.030	0.455	0.649
Geno.rare13	23	*	*	*	*	0.007	0.019	0.144	0.132	0.895
haplo.base22	23	C	G	A	T	0.439	NA	NA	NA	NA
Geno.110	24	C	A	C	W	0.055	-0.011	0.050	-0.220	0.826
Geno.212	24	C	A	T	W	0.036	0.104	0.070	1.489	0.137
Geno.314	24	C	C	C	D	0.186	0.037	0.032	1.174	0.241
Geno.410	24	C	C	C	W	0.014	0.057	0.102	0.559	0.576
Geno.612	24	G	A	C	W	0.266	0.015	0.030	0.489	0.625
Geno.rare14	24	*	*	*	*	0.006	0.037	0.166	0.225	0.822
haplo.base23	24	G	A	T	W	0.439	NA	NA	NA	NA
Geno.111	25	A	C	W	A	0.263	-0.001	0.028	-0.018	0.985
Geno.213	25	A	C	W	G	0.057	-0.032	0.048	-0.676	0.499
Geno.58	25	C	C	D	G	0.190	0.023	0.030	0.751	0.453
Geno.613	25	C	C	W	G	0.016	0.030	0.095	0.311	0.756
haplo.base24	25	A	T	W	G	0.473	NA	NA	NA	NA
Geno.112	26	C	D	G	A	0.190	0.039	0.031	1.246	0.213
Geno.315	26	C	W	A	G	0.263	0.017	0.030	0.576	0.565
Geno.411	26	C	W	G	A	0.016	0.064	0.095	0.668	0.504
Geno.59	26	C	W	G	G	0.057	-0.024	0.048	-0.508	0.612
Geno.84	26	T	W	G	G	0.036	0.117	0.069	1.703	0.089
haplo.base25	26	T	W	G	A	0.438	NA	NA	NA	NA
Geno.214	27	D	G	A	A	0.190	0.023	0.031	0.768	0.443
Geno.75	27	W	A	G	G	0.262	0.003	0.028	0.090	0.928
Geno.113	27	W	G	G	G	0.091	0.009	0.042	0.220	0.826
Geno.rare15	27	*	*	*	*	0.004	-0.210	0.201	-1.042	0.298
haplo.base26	27	W	G	A	G	0.453	NA	NA	NA	NA
Geno.510	28	A	G	G	G	0.262	0.006	0.029	0.219	0.827
Geno.614	28	G	A	A	G	0.190	0.027	0.031	0.878	0.380
Geno.76	28	G	A	G	G	0.016	0.039	0.095	0.413	0.679
Geno.101	28	G	G	G	G	0.093	0.016	0.042	0.375	0.708
Geno.rare16	28	*	*	*	*	0.003	-0.329	0.363	-0.907	0.365
haplo.base27	28	G	A	G	T	0.436	NA	NA	NA	NA
Geno.114	29	A	A	G	A	0.188	0.023	0.031	0.748	0.455
Geno.511	29	A	G	G	A	0.016	0.040	0.095	0.422	0.673
Geno.102	29	G	G	G	A	0.093	0.022	0.042	0.526	0.599
Geno.115	29	G	G	G	C	0.262	0.004	0.029	0.142	0.887
Geno.rare17	29	*	*	*	*	0.005	-0.042	0.193	-0.218	0.828
haplo.base28	29	A	G	T	A	0.437	NA	NA	NA	NA
Geno.215	30	A	G	A	G	0.187	0.023	0.031	0.734	0.463
Geno.615	30	G	G	A	A	0.090	0.019	0.042	0.449	0.654
Geno.77	30	G	G	A	G	0.018	0.035	0.091	0.383	0.702
Geno.92	30	G	G	C	G	0.262	0.004	0.029	0.148	0.882
Geno.rare18	30	*	*	*	*	0.006	-0.064	0.190	-0.335	0.738
haplo.base29	30	G	T	A	G	0.438	NA	NA	NA	NA
Geno.216	31	G	A	A	C	0.090	0.019	0.042	0.451	0.652

Table B1.26. Continued

	Window	loc.1	loc.2	loc.3	loc.4	hap.freq	TG coef	se	t.stat	pval
Geno.316	31	G	A	G	C	0.203	0.024	0.031	0.797	0.426
Geno.512	31	G	C	G	A	0.264	0.001	0.029	0.023	0.981
Geno.rare19	31	*	*	*	*	0.003	0.141	0.233	0.605	0.545
haplo.base30	31	T	A	G	C	0.439	NA	NA	NA	NA
Geno.217	32	A	A	C	C	0.091	0.021	0.041	0.508	0.612
Geno.317	32	A	G	C	C	0.192	0.028	0.031	0.898	0.370
Geno.616	32	C	G	A	C	0.016	-0.031	0.112	-0.272	0.786
Geno.78	32	C	G	A	G	0.248	0.004	0.030	0.123	0.902
Geno.rare20	32	*	*	*	*	0.003	0.146	0.234	0.624	0.533
haplo.base31	32	A	G	C	G	0.450	NA	NA	NA	NA
Geno.218	33	A	C	C	G	0.089	0.018	0.043	0.422	0.673
Geno.412	33	G	A	C	T	0.015	-0.072	0.126	-0.576	0.565
Geno.513	33	G	A	G	G	0.248	0.005	0.030	0.168	0.867
Geno.79	33	G	C	C	T	0.191	0.031	0.031	0.972	0.331
Geno.rare21	33	*	*	*	*	0.007	0.107	0.164	0.656	0.512
haplo.base32	33	G	C	G	G	0.451	NA	NA	NA	NA
Geno.219	34	A	C	T	C	0.017	0.007	0.115	0.058	0.954
Geno.413	34	A	G	G	T	0.247	-0.001	0.031	-0.035	0.972
Geno.514	34	C	C	G	T	0.094	0.023	0.042	0.557	0.578
Geno.617	34	C	C	T	C	0.057	0.029	0.054	0.542	0.588
Geno.710	34	C	C	T	T	0.131	0.021	0.036	0.582	0.561
Geno.rare22	34	*	*	*	*	0.002	-0.070	0.360	-0.194	0.846
haplo.base33	34	C	G	G	T	0.452	NA	NA	NA	NA
Geno.220	35	C	G	T	C	0.096	0.022	0.040	0.555	0.579
Geno.318	35	C	T	C	C	0.074	0.026	0.044	0.588	0.557
Geno.414	35	C	T	T	C	0.130	0.020	0.034	0.588	0.557
Geno.rare23	35	*	*	*	*	0.002	0.213	0.285	0.747	0.456
haplo.base34	35	G	G	T	C	0.699	NA	NA	NA	NA
Geno.515	36	T	C	C	A	0.074	0.024	0.044	0.540	0.589
Geno.618	36	T	T	C	A	0.129	0.018	0.034	0.541	0.589
Geno.rare24	36	*	*	*	*	0.003	0.031	0.285	0.108	0.914
haplo.base35	36	G	T	C	A	0.794	NA	NA	NA	NA
Geno.116	37	C	C	A	G	0.074	0.013	0.046	0.280	0.779
Geno.221	37	T	C	A	A	0.451	-0.016	0.024	-0.643	0.520
Geno.rare25	37	*	*	*	*	0.003	0.014	0.202	0.070	0.944
haplo.base36	37	T	C	A	G	0.472	NA	NA	NA	NA
Geno.117	38	C	A	A	C	0.451	-0.015	0.023	-0.633	0.527
Geno.rare26	38	*	*	*	*	0.012	0.093	0.106	0.882	0.378
haplo.base37	38	C	A	G	C	0.537	NA	NA	NA	NA
Geno.118	39	A	A	C	C	0.453	-0.016	0.023	-0.674	0.501
Geno.rare27	39	*	*	*	*	0.016	0.004	0.092	0.040	0.968
haplo.base38	39	A	G	C	C	0.531	NA	NA	NA	NA
Geno.119	40	A	C	C	A	0.453	-0.014	0.023	-0.595	0.552
Geno.rare28	40	*	*	*	*	0.015	0.023	0.097	0.239	0.811
haplo.base39	40	G	C	C	C	0.532	NA	NA	NA	NA
Geno.120	41	C	C	A	C	0.344	-0.023	0.025	-0.939	0.348
Geno.222	41	C	C	A	T	0.108	0.008	0.037	0.209	0.835
Geno.rare29	41	*	*	*	*	0.015	0.024	0.097	0.245	0.807
haplo.base40	41	C	C	C	C	0.533	NA	NA	NA	NA
Geno.121	42	C	A	C	C	0.328	-0.022	0.025	-0.873	0.383
Geno.223	42	C	A	C	T	0.016	-0.077	0.092	-0.844	0.399
Geno.319	42	C	A	T	C	0.108	0.004	0.037	0.115	0.909
Geno.rare30	42	*	*	*	*	0.006	-0.131	0.153	-0.858	0.391
haplo.base41	42	C	C	C	C	0.542	NA	NA	NA	NA
Geno.224	43	A	C	C	G	0.328	-0.024	0.026	-0.942	0.347
Geno.320	43	A	C	T	G	0.016	-0.080	0.092	-0.870	0.385
Geno.415	43	A	T	C	G	0.108	0.002	0.038	0.066	0.947
Geno.516	43	C	C	C	A	0.039	-0.042	0.060	-0.691	0.490
haplo.base42	43	C	C	C	G	0.509	NA	NA	NA	NA
Geno.122	44	C	C	A	C	0.039	-0.035	0.059	-0.583	0.560
Geno.416	44	C	T	G	C	0.016	-0.077	0.092	-0.843	0.400
Geno.619	44	T	C	G	C	0.108	0.009	0.036	0.263	0.792
Geno.rare31	44	*	*	*	*	0.007	-0.189	0.135	-1.397	0.163
haplo.base43	44	C	C	G	C	0.830	NA	NA	NA	NA
Geno.123	45	C	A	C	C	0.039	-0.040	0.059	-0.667	0.505
Geno.417	45	C	G	C	T	0.264	-0.021	0.027	-0.781	0.435
Geno.711	45	T	G	C	C	0.016	-0.087	0.092	-0.948	0.344
Geno.rare32	45	*	*	*	*	0.007	-0.196	0.134	-1.457	0.146
haplo.base44	45	C	G	C	C	0.674	NA	NA	NA	NA
Geno.124	46	A	C	C	A	0.039	-0.031	0.060	-0.524	0.601
Geno.418	46	G	C	C	G	0.183	0.018	0.031	0.583	0.560
Geno.517	46	G	C	T	A	0.264	-0.012	0.028	-0.418	0.676
Geno.rare33	46	*	*	*	*	0.007	-0.190	0.161	-1.182	0.238
haplo.base45	46	G	C	C	A	0.506	NA	NA	NA	NA
Geno.321	47	C	C	G	T	0.184	0.019	0.030	0.644	0.520
Geno.419	47	C	T	A	C	0.265	-0.011	0.028	-0.397	0.692
Geno.rare34	47	*	*	*	*	0.008	-0.111	0.134	-0.823	0.411
haplo.base46	47	C	C	A	C	0.543	NA	NA	NA	NA
Geno.322	48	C	G	T	A	0.178	0.024	0.030	0.787	0.432
Geno.518	48	T	A	C	A	0.265	-0.009	0.028	-0.333	0.739

Table B1.26. Continued

	Window	loc.1	loc.2	loc.3	loc.4	hap.freq	TG coef	se	t.stat	pval
Geno.rare35	48	*	*	*	*	0.007	-0.040	0.143	-0.282	0.778
haplo.base47	48	C	A	C	A	0.550	NA	NA	NA	NA
Geno.519	49	G	T	A	C	0.175	0.018	0.029	0.614	0.539
Geno.rare36	49	*	*	*	*	0.012	0.101	0.108	0.932	0.352
haplo.base48	49	A	C	A	C	0.813	NA	NA	NA	NA
Geno.125	50	C	A	C	C	0.071	0.043	0.047	0.906	0.365
Geno.620	50	T	A	C	T	0.165	0.021	0.030	0.673	0.501
Geno.rare37	50	*	*	*	*	0.021	0.019	0.091	0.206	0.837
haplo.base49	50	C	A	C	T	0.743	NA	NA	NA	NA
Geno.126	51	A	C	C	G	0.081	0.023	0.043	0.535	0.593
Geno.rare38	51	*	*	*	*	0.016	0.051	0.096	0.534	0.593
haplo.base50	51	A	C	T	G	0.903	NA	NA	NA	NA
Geno.127	52	C	C	G	C	0.011	0.023	0.108	0.211	0.833
Geno.225	52	C	C	G	T	0.069	0.024	0.046	0.516	0.606
Geno.rare39	52	*	*	*	*	0.010	0.165	0.130	1.272	0.204
haplo.base51	52	C	T	G	C	0.910	NA	NA	NA	NA
Geno.128	53	C	G	C	C	0.010	0.032	0.115	0.283	0.777
Geno.420	53	C	G	T	T	0.070	0.023	0.046	0.492	0.623
Geno.621	53	T	G	C	C	0.171	0.024	0.031	0.788	0.431
Geno.rare40	53	*	*	*	*	0.006	0.015	0.179	0.083	0.934
haplo.base52	53	T	G	C	T	0.743	NA	NA	NA	NA
Geno.129	54	G	C	C	A	0.182	0.025	0.030	0.845	0.399
Geno.421	54	G	T	T	A	0.032	0.057	0.067	0.842	0.400
Geno.520	54	G	T	T	G	0.038	-0.007	0.060	-0.125	0.901
Geno.rare41	54	*	*	*	*	0.005	0.032	0.181	0.176	0.861
haplo.base53	54	G	C	T	A	0.744	NA	NA	NA	NA
Geno.130	55	C	C	A	A	0.182	0.017	0.032	0.536	0.592
Geno.226	55	C	T	A	A	0.323	-0.021	0.027	-0.778	0.437
Geno.622	55	T	T	A	C	0.032	0.055	0.068	0.806	0.421
Geno.85	55	T	T	G	C	0.038	-0.016	0.061	-0.259	0.796
haplo.base54	55	C	T	A	C	0.425	NA	NA	NA	NA
Geno.227	56	C	A	A	G	0.182	0.013	0.031	0.417	0.677
Geno.623	56	T	A	A	G	0.323	-0.022	0.026	-0.825	0.410
Geno.103	56	T	G	C	G	0.038	-0.017	0.060	-0.286	0.775
Geno.rare42	56	*	*	*	*	0.002	0.518	0.315	1.644	0.101
haplo.base55	56	T	A	C	G	0.456	NA	NA	NA	NA
Geno.228	57	A	A	G	A	0.013	-0.087	0.106	-0.821	0.412
Geno.521	57	A	C	G	A	0.449	0.006	0.023	0.244	0.807
Geno.86	57	G	C	G	A	0.038	-0.010	0.061	-0.157	0.875
Geno.rare43	57	*	*	*	*	0.008	0.203	0.128	1.582	0.114
haplo.base56	57	A	A	G	G	0.492	NA	NA	NA	NA
Geno.229	58	A	G	A	C	0.013	-0.091	0.105	-0.872	0.383
Geno.323	58	A	G	G	C	0.480	-0.003	0.023	-0.133	0.894
Geno.422	58	A	G	G	T	0.011	-0.069	0.109	-0.634	0.526
Geno.rare44	58	*	*	*	*	0.008	0.198	0.128	1.546	0.123
haplo.base57	58	C	G	A	C	0.487	NA	NA	NA	NA
Geno.624	59	G	G	C	A	0.488	-0.001	0.023	-0.045	0.964
Geno.712	59	G	G	T	A	0.011	-0.068	0.109	-0.624	0.533
Geno.rare45	59	*	*	*	*	0.002	0.263	0.284	0.925	0.355
haplo.base58	59	G	A	C	A	0.498	NA	NA	NA	NA
Geno.131	60	A	C	A	C	0.184	0.001	0.031	0.029	0.977
Geno.230	60	A	C	A	T	0.317	0.004	0.026	0.156	0.876
Geno.93	60	G	T	A	C	0.011	-0.067	0.109	-0.611	0.542
Geno.rare46	60	*	*	*	*	0.002	0.089	0.409	0.218	0.827
haplo.base59	60	G	C	A	C	0.485	NA	NA	NA	NA
Geno.231	61	C	A	C	W	0.301	0.013	0.027	0.471	0.638
Geno.324	61	C	A	T	D	0.317	0.012	0.027	0.443	0.658
Geno.713	61	T	A	C	D	0.011	-0.062	0.109	-0.569	0.569
haplo.base60	61	C	A	C	D	0.370	NA	NA	NA	NA
Geno.325	62	A	C	W	C	0.300	0.011	0.027	0.393	0.695
Geno.522	62	A	T	D	T	0.317	0.009	0.027	0.344	0.731
Geno.rare47	62	*	*	*	*	0.007	-0.255	0.153	-1.663	0.097
haplo.base61	62	A	C	D	T	0.376	NA	NA	NA	NA
Geno.326	63	C	W	C	A	0.300	0.012	0.027	0.441	0.659
Geno.625	63	T	D	T	G	0.318	0.009	0.027	0.317	0.751
Geno.rare48	63	*	*	*	*	0.007	-0.280	0.153	-1.827	0.068
haplo.base62	63	C	D	T	G	0.375	NA	NA	NA	NA
Geno.327	64	D	T	G	T	0.318	0.007	0.027	0.255	0.799
Geno.523	64	W	C	A	T	0.300	0.011	0.027	0.414	0.679
Geno.rare49	64	*	*	*	*	0.007	-0.279	0.152	-1.836	0.067
haplo.base63	64	D	T	G	C	0.375	NA	NA	NA	NA
Geno.328	65	C	A	T	C	0.300	0.006	0.027	0.230	0.818
Geno.714	65	T	G	T	C	0.320	0.006	0.027	0.207	0.836
Geno.rare50	65	*	*	*	*	0.006	-0.062	0.166	-0.376	0.707
haplo.base64	65	T	G	C	C	0.375	NA	NA	NA	NA
Geno.329	66	A	T	C	G	0.298	0.006	0.027	0.220	0.826
Geno.87	66	G	T	C	G	0.323	0.006	0.027	0.217	0.828
Geno.rare51	66	*	*	*	*	0.014	0.028	0.100	0.285	0.776
haplo.base65	66	G	C	C	G	0.366	NA	NA	NA	NA

Table B1.26. Continued

	Window	loc.1	loc.2	loc.3	loc.4	hap.freq	TG coef	se	t.stat	pval
Geno.232	67	C	C	G	C	0.289	0.020	0.025	0.775	0.439
Geno.330	67	C	C	G	T	0.077	-0.097	0.043	-2.283	0.023
Geno.rare52	67	*	*	*	*	0.014	0.017	0.099	0.172	0.864
haplo.base66	67	T	C	G	C	0.621	NA	NA	NA	NA
Geno.331	68	C	G	C	G	0.079	-0.002	0.043	-0.049	0.961
Geno.626	68	C	G	T	T	0.077	-0.102	0.042	-2.410	0.016
Geno.rare53	68	*	*	*	*	0.014	0.009	0.103	0.089	0.929
haplo.base67	68	C	G	C	T	0.830	NA	NA	NA	NA
Geno.423	69	G	C	G	G	0.078	-0.004	0.043	-0.084	0.933
Geno.94	69	G	T	T	G	0.076	-0.101	0.042	-2.380	0.018
Geno.rare54	69	*	*	*	*	0.011	0.029	0.124	0.231	0.817
haplo.base68	69	G	C	T	G	0.834	NA	NA	NA	NA
Geno.332	70	C	G	G	G	0.079	-0.008	0.043	-0.194	0.846
Geno.524	70	C	T	G	A	0.053	-0.002	0.047	-0.053	0.958
Geno.88	70	T	T	G	G	0.076	-0.102	0.043	-2.391	0.017
Geno.rare55	70	*	*	*	*	0.002	0.044	0.000	3.74E+14	0.000
haplo.base69	70	C	T	G	G	0.789	NA	NA	NA	NA
Geno.333	71	G	G	G	G	0.079	0.001	0.043	0.028	0.977
Geno.627	71	T	G	A	G	0.053	0.008	0.047	0.160	0.873
Geno.rare56	71	*	*	*	*	0.007	0.022	0.175	0.123	0.902
haplo.base70	71	T	G	G	G	0.861	NA	NA	NA	NA
Geno.424	72	G	A	G	C	0.053	0.007	0.047	0.148	0.883
Geno.rare57	72	*	*	*	*	0.010	-0.014	0.125	-0.108	0.914
haplo.base71	72	G	G	G	C	0.937	NA	NA	NA	NA
Geno.132	73	A	G	C	G	0.054	0.008	0.048	0.176	0.860
Geno.334	73	G	G	C	A	0.319	0.008	0.025	0.318	0.751
Geno.rare58	73	*	*	*	*	0.007	-0.036	0.139	-0.258	0.796
haplo.base72	73	G	G	C	G	0.620	NA	NA	NA	NA
Geno.133	74	G	C	A	C	0.319	0.007	0.025	0.268	0.789
Geno.425	74	G	C	G	T	0.052	-0.002	0.052	-0.032	0.974
Geno.rare59	74	*	*	*	*	0.007	-0.037	0.135	-0.274	0.784
haplo.base73	74	G	C	G	C	0.622	NA	NA	NA	NA
Geno.134	75	C	A	C	A	0.318	0.006	0.025	0.238	0.812
Geno.525	75	C	G	T	G	0.057	-0.002	0.049	-0.044	0.965
Geno.rare60	75	*	*	*	*	0.003	-0.095	0.232	-0.409	0.683
haplo.base74	75	C	G	C	G	0.622	NA	NA	NA	NA
Geno.135	76	A	C	A	C	0.318	0.005	0.025	0.218	0.827
Geno.628	76	G	T	G	C	0.057	-0.002	0.049	-0.049	0.961
Geno.rare61	76	*	*	*	*	0.002	-0.143	0.284	-0.503	0.615
haplo.base75	76	G	C	G	C	0.623	NA	NA	NA	NA
Geno.233	77	C	A	C	T	0.310	-0.006	0.027	-0.203	0.839
Geno.629	77	C	G	C	T	0.237	-0.013	0.030	-0.429	0.668
Geno.89	77	T	G	C	T	0.057	-0.004	0.050	-0.086	0.932
Geno.rare62	77	*	*	*	*	0.010	0.150	0.129	1.165	0.244
haplo.base76	77	C	G	C	G	0.387	NA	NA	NA	NA
Geno.234	78	A	C	T	A	0.309	-0.004	0.027	-0.130	0.897
Geno.95	78	G	C	T	T	0.289	-0.008	0.027	-0.310	0.757
Geno.rare63	78	*	*	*	*	0.016	0.155	0.094	1.644	0.101
haplo.base77	78	G	C	G	A	0.386	NA	NA	NA	NA
Geno.630	79	C	T	A	C	0.314	-0.006	0.027	-0.216	0.829
Geno.715	79	C	T	T	C	0.288	-0.015	0.027	-0.560	0.576
Geno.rare64	79	*	*	*	*	0.004	0.054	0.233	0.230	0.818
haplo.base78	79	C	G	A	C	0.395	NA	NA	NA	NA
Geno.631	80	T	A	C	C	0.312	-0.008	0.027	-0.273	0.785
Geno.716	80	T	T	C	C	0.289	-0.015	0.027	-0.571	0.568
Geno.rare65	80	*	*	*	*	0.004	0.241	0.229	1.052	0.293
haplo.base79	80	G	A	C	C	0.395	NA	NA	NA	NA
Geno.235	81	A	C	C	A	0.018	0.119	0.098	1.212	0.226
Geno.526	81	T	C	C	A	0.110	-0.023	0.037	-0.626	0.532
Geno.632	81	T	C	C	G	0.181	-0.001	0.030	-0.021	0.983
Geno.rare66	81	*	*	*	*	0.002	0.238	0.283	0.839	0.402
haplo.base80	81	A	C	C	G	0.688	NA	NA	NA	NA
Geno.236	82	C	C	A	C	0.038	-0.050	0.057	-0.882	0.378
Geno.335	82	C	C	A	T	0.088	0.006	0.041	0.143	0.886
Geno.rare67	82	*	*	*	*	0.002	0.235	0.283	0.831	0.406
haplo.base81	82	C	C	G	T	0.871	NA	NA	NA	NA
Geno.237	83	C	A	C	G	0.038	-0.051	0.057	-0.896	0.371
Geno.426	83	C	A	T	G	0.087	0.007	0.041	0.176	0.860
Geno.rare68	83	*	*	*	*	0.002	0.032	0.284	0.112	0.911
haplo.base82	83	C	G	T	G	0.872	NA	NA	NA	NA
Geno.136	84	A	C	G	C	0.038	-0.052	0.057	-0.907	0.365
Geno.336	84	A	T	G	C	0.087	0.006	0.041	0.158	0.874
Geno.rare69	84	*	*	*	*	0.006	-0.042	0.165	-0.253	0.800
haplo.base83	84	G	T	G	C	0.869	NA	NA	NA	NA
Geno.137	85	C	G	C	A	0.038	-0.056	0.058	-0.967	0.334
Geno.527	85	T	G	C	G	0.308	-0.008	0.025	-0.305	0.761
Geno.rare70	85	*	*	*	*	0.006	-0.046	0.165	-0.279	0.781
haplo.base84	85	T	G	C	A	0.649	NA	NA	NA	NA
Geno.337	86	G	C	A	C	0.057	-0.006	0.047	-0.119	0.905

Table B1.26. Continued

	Window	loc.1	loc.2	loc.3	loc.4	hap.freq	TG coef	se	t.stat	pval
Geno.633	86	G	C	G	G	0.307	-0.004	0.025	-0.169	0.866
Geno.rare71	86	*	*	*	*	0.006	-0.041	0.165	-0.248	0.804
haplo.base85	86	G	C	A	G	0.630	NA	NA	NA	NA
Geno.138	87	C	A	C	T	0.057	-0.002	0.049	-0.042	0.967
Geno.238	87	C	A	G	C	0.298	0.007	0.028	0.251	0.802
Geno.427	87	C	G	G	C	0.308	-0.001	0.029	-0.033	0.974
Geno.rare72	87	*	*	*	*	0.005	-0.003	0.166	-0.017	0.986
haplo.base86	87	C	A	G	T	0.332	NA	NA	NA	NA
Geno.239	88	A	C	T	A	0.056	-0.005	0.049	-0.111	0.911
Geno.428	88	A	G	C	G	0.301	0.001	0.028	0.043	0.965
Geno.96	88	G	G	C	A	0.296	-0.006	0.029	-0.221	0.825
Geno.104	88	G	G	C	G	0.014	0.128	0.102	1.246	0.213
Geno.rare73	88	*	*	*	*	0.003	-0.104	0.253	-0.412	0.681
haplo.base87	88	A	G	T	A	0.329	NA	NA	NA	NA
Geno.240	89	C	T	A	C	0.056	-0.003	0.049	-0.064	0.949
Geno.634	89	G	C	A	C	0.297	-0.003	0.029	-0.102	0.919
Geno.717	89	G	C	G	C	0.314	0.007	0.028	0.248	0.804
Geno.rare74	89	*	*	*	*	0.004	-0.038	0.384	-0.098	0.922
haplo.base88	89	G	T	A	C	0.329	NA	NA	NA	NA
Geno.139	90	C	A	C	A	0.287	-0.002	0.028	-0.064	0.949
Geno.338	90	C	G	C	A	0.314	0.008	0.027	0.282	0.778
Geno.rare75	90	*	*	*	*	0.013	-0.013	0.106	-0.120	0.905
haplo.base89	90	T	A	C	A	0.386	NA	NA	NA	NA
Geno.528	91	G	C	A	W	0.317	0.011	0.024	0.451	0.652
Geno.rare76	91	*	*	*	*	0.011	0.075	0.113	0.660	0.509
haplo.base90	91	A	C	A	W	0.672	NA	NA	NA	NA
Geno.339	92	C	A	W	T	0.013	-0.004	0.102	-0.037	0.970
Geno.rare77	92	*	*	*	*	0.011	0.070	0.113	0.622	0.534
haplo.base91	92	C	A	W	C	0.976	NA	NA	NA	NA
Geno.241	93	A	W	C	G	0.114	0.014	0.038	0.360	0.719
Geno.529	93	A	W	T	T	0.012	0.018	0.110	0.165	0.869
Geno.rare78	93	*	*	*	*	0.011	0.038	0.122	0.309	0.758
haplo.base92	93	A	W	C	T	0.863	NA	NA	NA	NA
Geno.242	94	W	C	G	G	0.115	0.013	0.038	0.355	0.722
Geno.340	94	W	C	T	A	0.036	0.021	0.058	0.365	0.715
Geno.635	94	W	T	T	G	0.013	-0.002	0.102	-0.022	0.983
Geno.rare79	94	*	*	*	*	0.001	0.862	0.000	7.17E+15	0.000
haplo.base93	94	W	C	T	G	0.836	NA	NA	NA	NA
Geno.140	95	C	G	G	A	0.113	0.019	0.038	0.494	0.622
Geno.341	95	C	T	A	G	0.034	0.038	0.060	0.630	0.529
Geno.429	95	C	T	G	A	0.056	0.013	0.051	0.256	0.798
Geno.810	95	T	T	G	G	0.012	0.060	0.111	0.540	0.589
Geno.rare80	95	*	*	*	*	0.003	-0.466	0.250	-1.863	0.063
haplo.base94	95	C	T	G	G	0.782	NA	NA	NA	NA
Geno.141	96	G	G	A	C	0.115	0.013	0.038	0.343	0.732
Geno.342	96	T	A	G	C	0.035	0.024	0.059	0.411	0.681
Geno.530	96	T	G	A	C	0.057	0.006	0.050	0.113	0.910
Geno.718	96	T	G	G	G	0.127	0.006	0.034	0.163	0.870
haplo.base95	96	T	G	G	C	0.665	NA	NA	NA	NA
Geno.142	97	A	G	C	A	0.036	0.019	0.058	0.336	0.737
Geno.343	97	G	A	C	G	0.174	0.009	0.031	0.283	0.777
Geno.636	97	G	G	G	G	0.127	0.004	0.034	0.122	0.903
haplo.base96	97	G	G	C	A	0.662	NA	NA	NA	NA
Geno.143	98	A	C	G	C	0.174	0.007	0.030	0.245	0.806
Geno.430	98	G	G	G	C	0.127	0.004	0.034	0.103	0.918
haplo.base97	98	G	C	A	A	0.698	NA	NA	NA	NA
Geno.144	99	C	A	A	C	0.071	0.076	0.054	1.403	0.161
Geno.344	99	C	G	C	C	0.065	0.000	0.051	0.000	1.000
Geno.431	99	C	G	C	T	0.110	0.019	0.039	0.495	0.621
Geno.719	99	G	G	C	C	0.037	0.003	0.068	0.049	0.961
Geno.811	99	G	G	C	T	0.091	0.014	0.044	0.315	0.753
haplo.base98	99	C	A	A	T	0.627	NA	NA	NA	NA
Geno.145	100	A	A	C	A	0.049	0.130	0.071	1.827	0.068
Geno.243	100	A	A	C	C	0.022	-0.028	0.122	-0.230	0.818
Geno.345	100	A	A	T	A	0.312	0.009	0.033	0.268	0.789
Geno.531	100	G	C	C	A	0.085	-0.024	0.050	-0.470	0.639
Geno.637	100	G	C	C	C	0.016	0.146	0.123	1.183	0.237
Geno.720	100	G	C	T	A	0.146	0.034	0.038	0.901	0.368
Geno.812	100	G	C	T	C	0.056	-0.012	0.064	-0.180	0.857
haplo.base99	100	A	A	T	C	0.315	NA	NA	NA	NA

TABLE B1.27. *CETP* 4-SNP sliding window haplotype association results for HDL-C, TG, LDL-C, TC in African blacks (n=788)

				HDL-C			TG			LDL-C			TC		
Window	**Winow SNP**	**Genotype**	**MAF**	**Beta**	***P***	**Hap_P**	**Beta**	***P***	**Hap_P**	**Beta**	***P***	**Hap_P**	**Beta**	***P***	**Hap_P**
1	rs247615	AA/AG/GG	0.230	0.246	0.277	2.482E-05	-0.001	0.863	0.736	-0.179	0.437	0.246	-0.090	0.463	0.258
1	rs9989419	AA/GA/GG	0.340	-0.114	0.573	NA	0.003	0.733	NA	0.267	0.196	NA	0.105	0.337	NA
1	rs183130	CC/CT/TT	0.244	1.035	0.000	NA	-0.011	0.194	NA	-0.388	0.083	NA	-0.026	0.830	NA
1	rs3764261	AA/CA/CC	0.323	0.617	0.002	NA	-0.009	0.233	NA	-0.375	0.066	NA	-0.090	0.407	NA
2	rs9989419	AA/GA/GG	0.340	-0.114	0.573	1.627E-06	0.003	0.733	0.711	0.267	0.196	0.109	0.105	0.337	0.092
2	rs183130	CC/CT/TT	0.244	1.035	0.000	NA	-0.011	0.194	NA	-0.388	0.083	NA	-0.026	0.830	NA
2	rs3764261	AA/CA/CC	0.323	0.617	0.002	NA	-0.009	0.233	NA	-0.375	0.066	NA	-0.090	0.407	NA
2	rs148562851	AA/AG/GG	0.020	2.076	0.001	NA	0.008	0.750	NA	-0.163	0.806	NA	0.277	0.427	NA
3	rs183130	CC/CT/TT	0.244	1.035	0.000	9.395E-06	-0.011	0.194	0.303	-0.388	0.083	0.190	-0.026	0.830	0.260
3	rs3764261	AA/CA/CC	0.323	0.617	0.002	NA	-0.009	0.233	NA	-0.375	0.066	NA	-0.090	0.407	NA
3	rs148562851	AA/AG/GG	0.020	2.076	0.001	NA	0.008	0.750	NA	-0.163	0.806	NA	0.277	0.427	NA
3	rs12447924	CC/CT/TT	0.224	-0.256	0.269	NA	0.005	0.562	NA	0.460	0.042	NA	0.178	0.141	NA
4	rs3764261	AA/CA/CC	0.323	0.617	0.002	4.089E-04	-0.009	0.233	0.707	-0.375	0.066	0.165	-0.090	0.407	0.523
4	rs148562851	AA/AG/GG	0.020	2.076	0.001	NA	0.008	0.750	NA	-0.163	0.806	NA	0.277	0.427	NA
4	rs12447924	CC/CT/TT	0.224	-0.256	0.269	NA	0.005	0.562	NA	0.460	0.042	NA	0.178	0.141	NA
4	rs17231506	CC/TC/TT	0.105	0.312	0.320	NA	-0.017	0.145	NA	-0.160	0.609	NA	-0.045	0.789	NA
5	rs148562851	AA/AG/GG	0.020	2.076	0.001	8.517E-03	0.008	0.750	0.565	-0.163	0.806	0.392	0.277	0.427	0.447
5	rs12447924	CC/CT/TT	0.224	-0.256	0.269	NA	0.005	0.562	NA	0.460	0.042	NA	0.178	0.141	NA
5	rs17231506	CC/TC/TT	0.105	0.312	0.320	NA	-0.017	0.145	NA	-0.160	0.609	NA	-0.045	0.789	NA
5	rs12708968	CC/TC/TT	0.063	-0.568	0.159	NA	-0.009	0.563	NA	-0.021	0.960	NA	-0.112	0.605	NA
6	rs12447924	CC/CT/TT	0.224	-0.256	0.269	4.639E-04	0.005	0.562	0.225	0.460	0.042	0.189	0.178	0.141	0.557
6	rs17231506	CC/TC/TT	0.105	0.312	0.320	NA	-0.017	0.145	NA	-0.160	0.609	NA	-0.045	0.789	NA
6	rs12708968	CC/TC/TT	0.063	-0.568	0.159	NA	-0.009	0.563	NA	-0.021	0.960	NA	-0.112	0.605	NA
6	rs4783961	AA/GA/GG	0.454	0.643	0.001	NA	0.001	0.924	NA	-0.388	0.041	NA	-0.051	0.616	NA
7	rs17231506	CC/TC/TT	0.105	0.312	0.320	1.738E-04	-0.017	0.145	0.343	-0.160	0.609	0.082	-0.045	0.789	0.140
7	rs12708968	CC/TC/TT	0.063	-0.568	0.159	NA	-0.009	0.563	NA	-0.021	0.960	NA	-0.112	0.605	NA
7	rs4783961	AA/GA/GG	0.454	0.643	0.001	NA	0.001	0.924	NA	-0.388	0.041	NA	-0.051	0.616	NA
7	rs146122874	CC/TC/TT	0.022	1.918	0.002	NA	0.003	0.879	NA	-0.338	0.583	NA	0.173	0.595	NA
8	rs12708968	CC/TC/TT	0.063	-0.568	0.159	3.235E-05	-0.009	0.563	0.693	-0.021	0.960	0.002	-0.112	0.605	0.003
8	rs4783961	AA/GA/GG	0.454	0.643	0.001	NA	0.001	0.924	NA	-0.388	0.041	NA	-0.051	0.616	NA
8	rs146122874	CC/TC/TT	0.022	1.918	0.002	NA	0.003	0.879	NA	-0.338	0.583	NA	0.173	0.595	NA
8	rs4783962	CC/CT/TT	0.097	-0.111	0.732	NA	0.017	0.154	NA	0.658	0.042	NA	0.309	0.074	NA
9	rs4783961	AA/GA/GG	0.454	0.643	0.001	3.238E-05	0.001	0.924	0.632	-0.388	0.041	0.001	-0.051	0.616	0.001
9	rs146122874	CC/TC/TT	0.022	1.918	0.002	NA	0.003	0.879	NA	-0.338	0.583	NA	0.173	0.595	NA
9	rs4783962	CC/CT/TT	0.097	-0.111	0.732	NA	0.017	0.154	NA	0.658	0.042	NA	0.309	0.074	NA
9	rs17237883	AA/GA/GG	0.031	0.561	0.313	NA	0.016	0.454	NA	0.541	0.336	NA	0.386	0.194	NA
10	rs146122874	CC/TC/TT	0.022	1.918	0.002	4.953E-03	0.003	0.879	0.088	-0.338	0.583	0.019	0.173	0.595	0.013
10	rs4783962	CC/CT/TT	0.097	-0.111	0.732	NA	0.017	0.154	NA	0.658	0.042	NA	0.309	0.074	NA
10	rs17237883	AA/GA/GG	0.031	0.561	0.313	NA	0.016	0.454	NA	0.541	0.336	NA	0.386	0.194	NA
10	rs114856405	AA/CA/CC	0.036	-0.128	0.797	NA	0.034	0.061	NA	0.481	0.318	NA	0.313	0.234	NA
11	rs4783962	CC/CT/TT	0.097	-0.111	0.732	6.975E-02	0.017	0.154	0.261	0.658	0.042	0.100	0.309	0.074	0.141
11	rs17237883	AA/GA/GG	0.031	0.561	0.313	NA	0.016	0.454	NA	0.541	0.336	NA	0.386	0.194	NA
11	rs114856405	AA/CA/CC	0.036	-0.128	0.797	NA	0.034	0.061	NA	0.481	0.318	NA	0.313	0.234	NA
11	rs1800775	AA/CA/CC	0.395	-0.530	0.006	NA	-0.001	0.895	NA	0.272	0.158	NA	0.006	0.955	NA
12	rs17237883	AA/GA/GG	0.031	0.561	0.313	1.641E-07	0.016	0.454	0.275	0.541	0.336	0.220	0.386	0.194	0.287
12	rs114856405	AA/CA/CC	0.036	-0.128	0.797	NA	0.034	0.061	NA	0.481	0.318	NA	0.313	0.234	NA
12	rs1800775	AA/CA/CC	0.395	-0.530	0.006	NA	-0.001	0.895	NA	0.272	0.158	NA	0.006	0.955	NA
12	rs17231520	AA/GA/GG	0.090	1.986	0.000	NA	0.009	0.493	NA	-0.481	0.151	NA	0.185	0.294	NA
13	rs114856405	AA/CA/CC	0.036	-0.128	0.797	1.909E-08	0.034	0.061	0.280	0.481	0.318	0.228	0.313	0.234	0.379
13	rs1800775	AA/CA/CC	0.395	-0.530	0.006	NA	-0.001	0.895	NA	0.272	0.158	NA	0.006	0.955	NA
13	rs17231520	AA/GA/GG	0.090	1.986	0.000	NA	0.009	0.493	NA	-0.481	0.151	NA	0.185	0.294	NA
13	rs34065661	CC/GC/GG	0.088	2.070	0.000	NA	0.008	0.542	NA	-0.354	0.295	NA	0.253	0.156	NA
14	rs1800775	AA/CA/CC	0.395	-0.530	0.006	1.709E-08	-0.001	0.895	0.990	0.272	0.158	0.497	0.006	0.955	0.646
14	rs17231520	AA/GA/GG	0.090	1.986	0.000	NA	0.009	0.493	NA	-0.481	0.151	NA	0.185	0.294	NA
14	rs34065661	CC/GC/GG	0.088	2.070	0.000	NA	0.008	0.542	NA	-0.354	0.295	NA	0.253	0.156	NA
14	rs5884	AA/CA/CC	0.065	-0.661	0.092	NA	-0.004	0.781	NA	-0.150	0.702	NA	-0.192	0.359	NA
15	rs17231520	AA/GA/GG	0.090	1.986	0.000	3.099E-08	0.009	0.493	0.671	-0.481	0.151	0.426	0.185	0.294	0.537
15	rs34065661	CC/GC/GG	0.088	2.070	0.000	NA	0.008	0.542	NA	-0.354	0.295	NA	0.253	0.156	NA
15	rs5884	AA/CA/CC	0.065	-0.661	0.092	NA	-0.004	0.781	NA	-0.150	0.702	NA	-0.192	0.359	NA
15	rs34680782	AA/CA/CC	0.020	0.470	0.470	NA	-0.032	0.189	NA	-0.523	0.417	NA	-0.093	0.785	NA
16	rs34065661	CC/GC/GG	0.088	2.070	0.000	1.391E-08	0.008	0.542	0.381	-0.354	0.295	0.467	0.253	0.156	0.587
16	rs5884	AA/CA/CC	0.065	-0.661	0.092	NA	-0.004	0.781	NA	-0.150	0.702	NA	-0.192	0.359	NA
16	rs34680782	AA/CA/CC	0.020	0.470	0.470	NA	-0.032	0.189	NA	-0.523	0.417	NA	-0.093	0.785	NA
16	rs17231534	AA/CA/CC	0.177	0.097	0.695	NA	0.013	0.162	NA	-0.229	0.358	NA	-0.044	0.740	NA
17	rs5884	AA/CA/CC	0.065	-0.661	0.092	4.022E-03	-0.004	0.781	0.434	-0.150	0.702	0.302	-0.192	0.359	0.437
17	rs34680782	AA/CA/CC	0.020	0.470	0.470	NA	-0.032	0.189	NA	-0.523	0.417	NA	-0.093	0.785	NA
17	rs17231534	AA/CA/CC	0.177	0.097	0.695	NA	0.013	0.162	NA	-0.229	0.358	NA	-0.044	0.740	NA
17	rs3816117	CC/CT/TT	0.394	-0.538	0.006	NA	-0.001	0.880	NA	0.256	0.188	NA	0.004	0.970	NA
18	rs34680782	AA/CA/CC	0.020	0.470	0.470	2.959E-04	-0.032	0.189	0.395	-0.523	0.417	0.327	-0.093	0.785	0.996
18	rs17231534	AA/CA/CC	0.177	0.097	0.695	NA	0.013	0.162	NA	-0.229	0.358	NA	-0.044	0.740	NA

Table B1.27. Continued

				HDL-C			TG			LDL-C			TC		
Window	**Winow SNP**	**Genotype**	**MAF**	**Beta**	***P***	**Hap_P**	**Beta**	***P***	**Hap_P**	**Beta**	***P***	**Hap_P**	**Beta**	***P***	**Hap_P**
18	rs3816117	CC/CT/TT	0.394	-0.538	0.006	NA	-0.001	0.880	NA	0.256	0.188	NA	0.004	0.970	NA
18	rs711752	AA/GA/GG	0.232	0.915	0.000	NA	-0.003	0.688	NA	-0.323	0.150	NA	0.029	0.808	NA
19	rs17231534	AA/CA/CC	0.177	0.097	0.695	3.904E-04	0.013	0.162	0.666	-0.229	0.358	0.170	-0.044	0.740	0.446
19	rs3816117	CC/CT/TT	0.394	-0.538	0.006	NA	-0.001	0.880	NA	0.256	0.188	NA	0.004	0.970	NA
19	rs711752	AA/GA/GG	0.232	0.915	0.000	NA	-0.003	0.688	NA	-0.323	0.150	NA	0.029	0.808	NA
19	rs708272	AA/GA/GG	0.236	0.879	0.000	NA	-0.003	0.699	NA	-0.353	0.113	NA	0.009	0.938	NA
20	rs3816117	CC/CT/TT	0.394	-0.538	0.006	4.691E-04	-0.001	0.880	0.657	0.256	0.188	0.401	0.004	0.970	0.809
20	rs711752	AA/GA/GG	0.232	0.915	0.000	NA	-0.003	0.688	NA	-0.323	0.150	NA	0.029	0.808	NA
20	rs708272	AA/GA/GG	0.236	0.879	0.000	NA	-0.003	0.699	NA	-0.353	0.113	NA	0.009	0.938	NA
20	rs60195610	CC/CT/TT	0.023	1.665	0.006	NA	0.014	0.531	NA	0.209	0.739	NA	0.420	0.201	NA
21	rs711752	AA/GA/GG	0.232	0.915	0.000	3.680E-04	-0.003	0.688	0.624	-0.323	0.150	0.577	0.029	0.808	0.847
21	rs708272	AA/GA/GG	0.236	0.879	0.000	NA	-0.003	0.699	NA	-0.353	0.113	NA	0.009	0.938	NA
21	rs60195610	CC/CT/TT	0.023	1.665	0.006	NA	0.014	0.531	NA	0.209	0.739	NA	0.420	0.201	NA
21	rs9935228	AA/GA/GG	0.091	-0.539	0.098	NA	-0.007	0.544	NA	0.064	0.843	NA	-0.073	0.670	NA
22	rs708272	AA/GA/GG	0.236	0.879	0.000	8.442E-05	-0.003	0.699	0.785	-0.353	0.113	0.204	0.009	0.938	0.170
22	rs60195610	CC/CT/TT	0.023	1.665	0.006	NA	0.014	0.531	NA	0.209	0.739	NA	0.420	0.201	NA
22	rs9935228	AA/GA/GG	0.091	-0.539	0.098	NA	-0.007	0.544	NA	0.064	0.843	NA	-0.073	0.670	NA
22	rs1864163	AA/GA/GG	0.278	-0.704	0.001	NA	-0.007	0.394	NA	-0.166	0.438	NA	-0.215	0.059	NA
23	rs60195610	CC/CT/TT	0.023	1.665	0.006	2.412E-04	0.014	0.531	0.605	0.209	0.739	0.567	0.420	0.201	0.151
23	rs9935228	AA/GA/GG	0.091	-0.539	0.098	NA	-0.007	0.544	NA	0.064	0.843	NA	-0.073	0.670	NA
23	rs1864163	AA/GA/GG	0.278	-0.704	0.001	NA	-0.007	0.394	NA	-0.166	0.438	NA	-0.215	0.059	NA
23	rs75313088	AA/GA/GG	0.036	-0.166	0.741	NA	0.030	0.102	NA	0.335	0.496	NA	0.228	0.395	NA
24	rs9935228	AA/GA/GG	0.091	-0.539	0.098	7.362E-04	-0.007	0.544	0.492	0.064	0.843	0.888	-0.073	0.670	0.378
24	rs1864163	AA/GA/GG	0.278	-0.704	0.001	NA	-0.007	0.394	NA	-0.166	0.438	NA	-0.215	0.059	NA
24	rs75313088	AA/GA/GG	0.036	-0.166	0.741	NA	0.030	0.102	NA	0.335	0.496	NA	0.228	0.395	NA
24	rs5817083	DD/WD/WW	0.393	0.159	0.429	NA	0.008	0.273	NA	0.036	0.859	NA	0.072	0.500	NA
25	rs1864163	AA/GA/GG	0.278	-0.704	0.001	2.269E-02	-0.007	0.394	0.538	-0.166	0.438	0.977	-0.215	0.059	0.757
25	rs75313088	AA/GA/GG	0.036	-0.166	0.741	NA	0.030	0.102	NA	0.335	0.496	NA	0.228	0.395	NA
25	rs5817083	DD/WD/WW	0.393	0.159	0.429	NA	0.008	0.273	NA	0.036	0.859	NA	0.072	0.500	NA
25	rs4369653	AA/AG/GG	0.212	-0.228	0.340	NA	-0.001	0.902	NA	0.150	0.530	NA	0.022	0.859	NA
26	rs75313088	AA/GA/GG	0.036	-0.166	0.741	7.225E-01	0.030	0.102	0.374	0.335	0.496	0.262	0.228	0.395	0.331
26	rs5817083	DD/WD/WW	0.393	0.159	0.429	NA	0.008	0.273	NA	0.036	0.859	NA	0.072	0.500	NA
26	rs4369653	AA/AG/GG	0.212	-0.228	0.340	NA	-0.001	0.902	NA	0.150	0.530	NA	0.022	0.859	NA
26	rs7194225	CC/CG/GG	0.185	0.364	0.133	NA	0.013	0.144	NA	-0.325	0.187	NA	-0.031	0.810	NA
27	rs5817083	DD/WD/WW	0.393	0.159	0.429	7.103E-01	0.008	0.273	0.081	0.036	0.859	0.308	0.072	0.500	0.323
27	rs4369653	AA/AG/GG	0.212	-0.228	0.340	NA	-0.001	0.902	NA	0.150	0.530	NA	0.022	0.859	NA
27	rs7194225	CC/CG/GG	0.185	0.364	0.133	NA	0.013	0.144	NA	-0.325	0.187	NA	-0.031	0.810	NA
27	rs114908369	CA/CC	0.025	-0.522	0.394	NA	-0.068	0.003	NA	0.053	0.931	NA	-0.245	0.452	NA
28	rs4369653	AA/AG/GG	0.212	-0.228	0.340	7.631E-02	-0.001	0.902	0.048	0.150	0.530	0.866	0.022	0.859	0.700
28	rs7194225	CC/CG/GG	0.185	0.364	0.133	NA	0.013	0.144	NA	-0.325	0.187	NA	-0.031	0.810	NA
28	rs114908369	CA/CC	0.025	-0.522	0.394	NA	-0.068	0.003	NA	0.053	0.931	NA	-0.245	0.452	NA
28	rs9929488	CC/GC/GG	0.463	-0.260	0.172	NA	0.003	0.712	NA	-0.217	0.259	NA	-0.137	0.177	NA
29	rs7194225	CC/CG/GG	0.185	0.364	0.133	1.436E-01	0.013	0.144	0.009	-0.325	0.187	0.852	-0.031	0.810	0.839
29	rs114908369	CA/CC	0.025	-0.522	0.394	NA	-0.068	0.003	NA	0.053	0.931	NA	-0.245	0.452	NA
29	rs9929488	CC/GC/GG	0.463	-0.260	0.172	NA	0.003	0.712	NA	-0.217	0.259	NA	-0.137	0.177	NA
29	rs12720906	GG/GT/TT	0.034	-0.354	0.493	NA	0.027	0.147	NA	0.228	0.652	NA	0.148	0.589	NA
30	rs114908369	CA/CC	0.025	-0.522	0.394	3.489E-01	-0.068	0.003	0.013	0.053	0.931	0.188	-0.245	0.452	0.347
30	rs9929488	CC/GC/GG	0.463	-0.260	0.172	NA	0.003	0.712	NA	-0.217	0.259	NA	-0.137	0.177	NA
30	rs12720906	GG/GT/TT	0.034	-0.354	0.493	NA	0.027	0.147	NA	0.228	0.652	NA	0.148	0.589	NA
30	rs12720926	AA/AG	0.027	-0.430	0.472	NA	-0.015	0.521	NA	-1.224	0.044	NA	-0.426	0.184	NA
31	rs9929488	CC/GC/GG	0.463	-0.260	0.172	2.100E-01	0.003	0.712	0.511	-0.217	0.259	0.151	-0.137	0.177	0.376
31	rs12720906	GG/GT/TT	0.034	-0.354	0.493	NA	0.027	0.147	NA	0.228	0.652	NA	0.148	0.589	NA
31	rs12720926	AA/AG	0.027	-0.430	0.472	NA	-0.015	0.521	NA	-1.224	0.044	NA	-0.426	0.184	NA
31	rs17237939	CC/CT/TT	0.049	-0.394	0.375	NA	-0.007	0.682	NA	0.549	0.222	NA	0.147	0.538	NA
32	rs12720906	GG/GT/TT	0.034	-0.354	0.493	7.231E-01	0.027	0.147	0.542	0.228	0.652	0.288	0.148	0.589	0.602
32	rs12720926	AA/AG	0.027	-0.430	0.472	NA	-0.015	0.521	NA	-1.224	0.044	NA	-0.426	0.184	NA
32	rs17237939	CC/CT/TT	0.049	-0.394	0.375	NA	-0.007	0.682	NA	0.549	0.222	NA	0.147	0.538	NA
32	rs35585922	DD/WD/WW	0.149	0.266	0.323	NA	0.010	0.313	NA	-0.039	0.884	NA	0.112	0.436	NA
33	rs12720926	AA/AG	0.027	-0.430	0.472	4.077E-01	-0.015	0.521	0.076	-1.224	0.044	0.253	-0.426	0.184	0.610
33	rs17237939	CC/CT/TT	0.049	-0.394	0.375	NA	-0.007	0.682	NA	0.549	0.222	NA	0.147	0.538	NA
33	rs35585922	DD/WD/WW	0.149	0.266	0.323	NA	0.010	0.313	NA	-0.039	0.884	NA	0.112	0.436	NA
33	rs7203984	AA/CA/CC	0.438	-0.084	0.669	NA	0.000	0.969	NA	0.010	0.958	NA	0.025	0.810	NA
34	rs17237939	CC/CT/TT	0.049	-0.394	0.375	3.894E-01	-0.007	0.682	0.045	0.549	0.222	0.218	0.147	0.538	0.522
34	rs35585922	DD/WD/WW	0.149	0.266	0.323	NA	0.010	0.313	NA	-0.039	0.884	NA	0.112	0.436	NA
34	rs7203984	AA/CA/CC	0.438	-0.084	0.669	NA	0.000	0.969	NA	0.010	0.958	NA	0.025	0.810	NA
34	rs11508026	AA/AG	0.027	-0.596	0.318	NA	-0.020	0.379	NA	-1.294	0.033	NA	-0.494	0.122	NA
35	rs35585922	DD/WD/WW	0.149	0.266	0.323	3.964E-01	0.010	0.313	0.031	-0.039	0.884	0.045	0.112	0.436	0.206
35	rs7203984	AA/CA/CC	0.438	-0.084	0.669	NA	0.000	0.969	NA	0.010	0.958	NA	0.025	0.810	NA
35	rs11508026	AA/AG	0.027	-0.596	0.318	NA	-0.020	0.379	NA	-1.294	0.033	NA	-0.494	0.122	NA
35	rs80296794	TC/TT	0.021	-0.678	0.315	NA	0.026	0.297	NA	1.599	0.020	NA	0.630	0.085	NA
36	rs7203984	AA/CA/CC	0.438	-0.084	0.669	4.309E-01	0.000	0.969	0.622	0.010	0.958	0.036	0.025	0.810	0.138
36	rs11508026	AA/AG	0.027	-0.596	0.318	NA	-0.020	0.379	NA	-1.294	0.033	NA	-0.494	0.122	NA
36	rs80296794	TC/TT	0.021	-0.678	0.315	NA	0.026	0.297	NA	1.599	0.020	NA	0.630	0.085	NA
36	rs112236143	CA/CC	0.020	-0.950	0.181	NA	0.013	0.607	NA	-0.475	0.515	NA	-0.476	0.225	NA

Table B1.27. Continued

				HDL-C			TG			LDL-C			TC		
Window	**Winow SNP**	**Genotype**	**MAF**	**Beta**	***P***	**Hap_P**	**Beta**	***P***	**Hap_P**	**Beta**	***P***	**Hap_P**	**Beta**	***P***	**Hap_P**
37	rs11508026	AA/AG	0.027	-0.596	0.318	3.660E-01	-0.020	0.379	0.531	-1.294	0.033	0.051	-0.494	0.122	0.240
37	rs80296794	TC/TT	0.021	-0.678	0.315	NA	0.026	0.297	NA	1.599	0.020	NA	0.630	0.085	NA
37	rs112236143	CA/CC	0.020	-0.950	0.181	NA	0.013	0.607	NA	-0.475	0.515	NA	-0.476	0.225	NA
37	rs708273	AA/AG/GG	0.100	-0.362	0.257	NA	0.004	0.739	NA	0.224	0.483	NA	0.036	0.831	NA
38	rs80296794	TC/TT	0.021	-0.678	0.315	5.497E-01	0.026	0.297	0.219	1.599	0.020	0.283	0.630	0.085	0.530
38	rs112236143	CA/CC	0.020	-0.950	0.181	NA	0.013	0.607	NA	-0.475	0.515	NA	-0.476	0.225	NA
38	rs708273	AA/AG/GG	0.100	-0.362	0.257	NA	0.004	0.739	NA	0.224	0.483	NA	0.036	0.831	NA
38	rs17231583	CC/GC/GG	0.020	-0.492	0.464	NA	0.045	0.052	NA	0.157	0.805	NA	0.148	0.677	NA
39	rs112236143	CA/CC	0.020	-0.950	0.181	2.252E-04	0.013	0.607	0.238	-0.475	0.515	0.619	-0.476	0.225	0.841
39	rs708273	AA/AG/GG	0.100	-0.362	0.257	NA	0.004	0.739	NA	0.224	0.483	NA	0.036	0.831	NA
39	rs17231583	CC/GC/GG	0.020	-0.492	0.464	NA	0.045	0.052	NA	0.157	0.805	NA	0.148	0.677	NA
39	rs142058276	II/WI/WW	0.082	1.663	0.000	NA	-0.001	0.920	NA	-0.582	0.106	NA	-0.020	0.914	NA
40	rs708273	AA/AG/GG	0.100	-0.362	0.257	3.534E-04	0.004	0.739	0.554	0.224	0.483	0.393	0.036	0.831	0.967
40	rs17231583	CC/GC/GG	0.020	-0.492	0.464	NA	0.045	0.052	NA	0.157	0.805	NA	0.148	0.677	NA
40	rs142058276	II/WI/WW	0.082	1.663	0.000	NA	-0.001	0.920	NA	-0.582	0.106	NA	-0.020	0.914	NA
40	rs17231590	AA/AG/GG	0.058	-0.330	0.410	NA	-0.009	0.548	NA	0.667	0.101	NA	0.194	0.368	NA
41	rs17231583	CC/GC/GG	0.020	-0.492	0.464	9.286E-05	0.045	0.052	0.406	0.157	0.805	0.249	0.148	0.677	0.802
41	rs142058276	II/WI/WW	0.082	1.663	0.000	NA	-0.001	0.920	NA	-0.582	0.106	NA	-0.020	0.914	NA
41	rs17231590	AA/AG/GG	0.058	-0.330	0.410	NA	-0.009	0.548	NA	0.667	0.101	NA	0.194	0.368	NA
41	rs17237953	GG/GT/TT	0.039	0.412	0.395	NA	-0.003	0.871	NA	0.415	0.395	NA	0.224	0.384	NA
42	rs142058276	II/WI/WW	0.082	1.663	0.000	2.003E-04	-0.001	0.920	0.882	-0.582	0.106	0.304	-0.020	0.914	0.735
42	rs17231590	AA/AG/GG	0.058	-0.330	0.410	NA	-0.009	0.548	NA	0.667	0.101	NA	0.194	0.368	NA
42	rs17237953	GG/GT/TT	0.039	0.412	0.395	NA	-0.003	0.871	NA	0.415	0.395	NA	0.224	0.384	NA
42	rs35619327	CC/TC	0.023	-0.708	0.272	NA	0.024	0.313	NA	-0.453	0.494	NA	-0.376	0.290	NA
43	rs17231590	AA/AG/GG	0.058	-0.330	0.410	7.447E-01	-0.009	0.548	0.775	0.667	0.101	0.196	0.194	0.368	0.305
43	rs17237953	GG/GT/TT	0.039	0.412	0.395	NA	-0.003	0.871	NA	0.415	0.395	NA	0.224	0.384	NA
43	rs35619327	CC/TC	0.023	-0.708	0.272	NA	0.024	0.313	NA	-0.453	0.494	NA	-0.376	0.290	NA
43	rs820299	AA/AG/GG	0.495	0.156	0.415	NA	0.004	0.544	NA	0.264	0.179	NA	0.166	0.110	NA
44	rs17237953	GG/GT/TT	0.039	0.412	0.395	7.576E-01	-0.003	0.871	0.791	0.415	0.395	0.292	0.224	0.384	0.264
44	rs35619327	CC/TC	0.023	-0.708	0.272	NA	0.024	0.313	NA	-0.453	0.494	NA	-0.376	0.290	NA
44	rs820299	AA/AG/GG	0.495	0.156	0.415	NA	0.004	0.544	NA	0.264	0.179	NA	0.166	0.110	NA
44	rs17237967	AA/GA/GG	0.035	-0.355	0.480	NA	0.000	0.982	NA	0.688	0.175	NA	0.283	0.291	NA
45	rs35619327	CC/TC	0.023	-0.708	0.272	5.390E-01	0.024	0.313	0.790	-0.453	0.494	0.442	-0.376	0.290	0.417
45	rs820299	AA/AG/GG	0.495	0.156	0.415	NA	0.004	0.544	NA	0.264	0.179	NA	0.166	0.110	NA
45	rs17237967	AA/GA/GG	0.035	-0.355	0.480	NA	0.000	0.982	NA	0.688	0.175	NA	0.283	0.291	NA
45	rs8045855	AA/AT/TT	0.423	0.249	0.201	NA	-0.004	0.577	NA	-0.149	0.449	NA	-0.056	0.592	NA
46	rs820299	AA/AG/GG	0.495	0.156	0.415	5.843E-01	0.004	0.544	0.840	0.264	0.179	0.335	0.166	0.110	0.359
46	rs17237967	AA/GA/GG	0.035	-0.355	0.480	NA	0.000	0.982	NA	0.688	0.175	NA	0.283	0.291	NA
46	rs8045855	AA/AT/TT	0.423	0.249	0.201	NA	-0.004	0.577	NA	-0.149	0.449	NA	-0.056	0.592	NA
46	rs12720922	AA/GA/GG	0.352	0.093	0.643	NA	-0.005	0.503	NA	-0.293	0.154	NA	-0.156	0.147	NA
47	rs17237967	AA/GA/GG	0.035	-0.355	0.480	2.069E-01	0.000	0.982	0.874	0.688	0.175	0.513	0.283	0.291	0.375
47	rs8045855	AA/AT/TT	0.423	0.249	0.201	NA	-0.004	0.577	NA	-0.149	0.449	NA	-0.056	0.592	NA
47	rs12720922	AA/GA/GG	0.352	0.093	0.643	NA	-0.005	0.503	NA	-0.293	0.154	NA	-0.156	0.147	NA
47	rs12708969	AA/CA/CC	0.106	-0.539	0.076	NA	-0.004	0.748	NA	-0.124	0.693	NA	-0.083	0.614	NA
48	rs8045855	AA/AT/TT	0.423	0.249	0.201	1.050E-02	-0.004	0.577	0.952	-0.149	0.449	0.222	-0.056	0.592	0.144
48	rs12720922	AA/GA/GG	0.352	0.093	0.643	NA	-0.005	0.503	NA	-0.293	0.154	NA	-0.156	0.147	NA
48	rs12708969	AA/CA/CC	0.106	-0.539	0.076	NA	-0.004	0.748	NA	-0.124	0.693	NA	-0.083	0.614	NA
48	rs9924087	AA/GA/GG	0.207	0.569	0.011	NA	0.003	0.689	NA	0.190	0.403	NA	0.223	0.062	NA
49	rs12720922	AA/GA/GG	0.352	0.093	0.643	9.067E-02	-0.005	0.503	0.938	-0.293	0.154	0.636	-0.156	0.147	0.275
49	rs12708969	AA/CA/CC	0.106	-0.539	0.076	NA	-0.004	0.748	NA	-0.124	0.693	NA	-0.083	0.614	NA
49	rs9924087	AA/GA/GG	0.207	0.569	0.011	NA	0.003	0.689	NA	0.190	0.403	NA	0.223	0.062	NA
49	rs12597002	AA/CA/CC	0.097	-0.338	0.301	NA	0.005	0.670	NA	0.311	0.337	NA	0.100	0.563	NA
50	rs12708969	AA/CA/CC	0.106	-0.539	0.076	5.577E-02	-0.004	0.748	0.903	-0.124	0.693	0.479	-0.083	0.614	0.240
50	rs9924087	AA/GA/GG	0.207	0.569	0.011	NA	0.003	0.689	NA	0.190	0.403	NA	0.223	0.062	NA
50	rs12597002	AA/CA/CC	0.097	-0.338	0.301	NA	0.005	0.670	NA	0.311	0.337	NA	0.100	0.563	NA
50	rs12720863	AA/GA/GG	0.023	-0.248	0.694	NA	0.016	0.507	NA	0.665	0.291	NA	0.284	0.399	NA
51	rs9924087	AA/GA/GG	0.207	0.569	0.011	1.425E-01	0.003	0.689	0.920	0.190	0.403	0.514	0.223	0.062	0.189
51	rs12597002	AA/CA/CC	0.097	-0.338	0.301	NA	0.005	0.670	NA	0.311	0.337	NA	0.100	0.563	NA
51	rs12720863	AA/GA/GG	0.023	-0.248	0.694	NA	0.016	0.507	NA	0.665	0.291	NA	0.284	0.399	NA
51	rs9939224	GG/GT/TT	0.356	0.066	0.745	NA	-0.006	0.461	NA	-0.277	0.178	NA	-0.147	0.173	NA
52	rs12597002	AA/CA/CC	0.097	-0.338	0.301	2.617E-02	0.005	0.670	0.948	0.311	0.337	0.528	0.100	0.563	0.309
52	rs12720863	AA/GA/GG	0.023	-0.248	0.694	NA	0.016	0.507	NA	0.665	0.291	NA	0.284	0.399	NA
52	rs9939224	GG/GT/TT	0.356	0.066	0.745	NA	-0.006	0.461	NA	-0.277	0.178	NA	-0.147	0.173	NA
52	rs11076174	CC/TC/TT	0.132	-0.709	0.013	NA	0.000	0.975	NA	-0.271	0.353	NA	-0.290	0.057	NA
53	rs12720863	AA/GA/GG	0.023	-0.248	0.694	2.829E-02	0.016	0.507	0.859	0.665	0.291	0.571	0.284	0.399	0.318
53	rs9939224	GG/GT/TT	0.356	0.066	0.745	NA	-0.006	0.461	NA	-0.277	0.178	NA	-0.147	0.173	NA
53	rs11076174	CC/TC/TT	0.132	-0.709	0.013	NA	0.000	0.975	NA	-0.271	0.353	NA	-0.290	0.057	NA
53	rs13306230	CA/CC	0.001	3.072	0.237	NA	0.040	0.684	NA	-0.969	0.710	NA	0.216	0.876	NA
54	rs9939224	GG/GT/TT	0.356	0.066	0.745	2.403E-02	-0.006	0.461	0.265	-0.277	0.178	0.672	-0.147	0.173	0.366
54	rs11076174	CC/TC/TT	0.132	-0.709	0.013	NA	0.000	0.975	NA	-0.271	0.353	NA	-0.290	0.057	NA
54	rs13306230	CA/CC	0.001	3.072	0.237	NA	0.040	0.684	NA	-0.969	0.710	NA	0.216	0.876	NA
54	rs12708971	CC/CT/TT	0.019	-0.433	0.534	NA	0.051	0.034	NA	-0.235	0.720	NA	-0.013	0.972	NA
55	rs11076174	CC/TC/TT	0.132	-0.709	0.013	7.193E-03	0.000	0.975	0.285	-0.271	0.353	0.778	-0.290	0.057	0.433
55	rs13306230	CA/CC	0.001	3.072	0.237	NA	0.040	0.684	NA	-0.969	0.710	NA	0.216	0.876	NA

Table B1.27. Continued

				HDL-C			TG			LDL-C			TC		
Window	**Winow SNP**	**Genotype**	**MAF**	**Beta**	***P***	**Hap_P**	**Beta**	***P***	**Hap_P**	**Beta**	***P***	**Hap_P**	**Beta**	***P***	**Hap_P**
55	rs12708971	CC/CT/TT	0.019	-0.433	0.534	NA	0.051	0.034	NA	-0.235	0.720	NA	-0.013	0.972	NA
55	rs891141	AA/AC/CC	0.130	0.792	0.004	NA	-0.005	0.607	NA	-0.166	0.547	NA	0.051	0.728	NA
56	rs13306230	CA/CC	0.001	3.072	0.237	2.818E-02	0.040	0.684	0.059	-0.969	0.710	0.921	0.216	0.876	0.987
56	rs12708971	CC/CT/TT	0.019	-0.433	0.534	NA	0.051	0.034	NA	-0.235	0.720	NA	-0.013	0.972	NA
56	rs891141	AA/AC/CC	0.130	0.792	0.004	NA	-0.005	0.607	NA	-0.166	0.547	NA	0.051	0.728	NA
56	CTPp9841	AG/GG	0.001	-9.930	0.007	NA	0.283	0.040	NA	1.191	0.750	NA	-0.332	0.866	NA
57	rs12708971	CC/CT/TT	0.019	-0.433	0.534	2.002E-02	0.051	0.034	0.173	-0.235	0.720	0.882	-0.013	0.972	0.986
57	rs891141	AA/AC/CC	0.130	0.792	0.004	NA	-0.005	0.607	NA	-0.166	0.547	NA	0.051	0.728	NA
57	CTPp9841	AG/GG	0.001	-9.930	0.007	NA	0.283	0.040	NA	1.191	0.750	NA	-0.332	0.866	NA
57	rs34716057	AA/GA/GG	0.034	0.287	0.579	NA	-0.005	0.779	NA	-0.156	0.767	NA	-0.002	0.995	NA
58	rs891141	AA/AC/CC	0.130	0.792	0.004	3.333E-03	-0.005	0.607	0.891	-0.166	0.547	0.615	0.051	0.728	0.935
58	CTPp9841	AG/GG	0.001	-9.930	0.007	NA	0.283	0.040	NA	1.191	0.750	NA	-0.332	0.866	NA
58	rs34716057	AA/GA/GG	0.034	0.287	0.579	NA	-0.005	0.779	NA	-0.156	0.767	NA	-0.002	0.995	NA
58	rs891143	CC/TC/TT	0.090	1.294	0.000	NA	-0.003	0.818	NA	-0.246	0.470	NA	0.099	0.583	NA
59	CTPp9841	AG/GG	0.001	-9.930	0.007	4.919E-04	0.283	0.040	0.904	1.191	0.750	0.786	-0.332	0.866	0.720
59	rs34716057	AA/GA/GG	0.034	0.287	0.579	NA	-0.005	0.779	NA	-0.156	0.767	NA	-0.002	0.995	NA
59	rs891143	CC/TC/TT	0.090	1.294	0.000	NA	-0.003	0.818	NA	-0.246	0.470	NA	0.099	0.583	NA
59	rs12720862	AA/GA/GG	0.112	0.291	0.333	NA	-0.007	0.547	NA	0.236	0.439	NA	0.140	0.385	NA
60	rs34716057	AA/GA/GG	0.034	0.287	0.579	2.976E-04	-0.005	0.779	0.954	-0.156	0.767	0.256	-0.002	0.995	0.154
60	rs891143	CC/TC/TT	0.090	1.294	0.000	NA	-0.003	0.818	NA	-0.246	0.470	NA	0.099	0.583	NA
60	rs12720862	AA/GA/GG	0.112	0.291	0.333	NA	-0.007	0.547	NA	0.236	0.439	NA	0.140	0.385	NA
60	rs7205804	AA/GA/GG	0.097	-0.762	0.015	NA	-0.004	0.746	NA	-0.641	0.043	NA	-0.408	0.014	NA
61	rs891143	CC/TC/TT	0.090	1.294	0.000	2.752E-04	-0.003	0.818	0.853	-0.246	0.470	0.249	0.099	0.583	0.074
61	rs12720862	AA/GA/GG	0.112	0.291	0.333	NA	-0.007	0.547	NA	0.236	0.439	NA	0.140	0.385	NA
61	rs7205804	AA/GA/GG	0.097	-0.762	0.015	NA	-0.004	0.746	NA	-0.641	0.043	NA	-0.408	0.014	NA
61	rs12708973	AA/AG	0.009	-1.030	0.298	NA	-0.031	0.412	NA	-0.608	0.556	NA	-0.718	0.169	NA
62	rs12720862	AA/GA/GG	0.112	0.291	0.333	3.948E-02	-0.007	0.547	0.723	0.236	0.439	0.098	0.140	0.385	0.014
62	rs7205804	AA/GA/GG	0.097	-0.762	0.015	NA	-0.004	0.746	NA	-0.641	0.043	NA	-0.408	0.014	NA
62	rs12708973	AA/AG	0.009	-1.030	0.298	NA	-0.031	0.412	NA	-0.608	0.556	NA	-0.718	0.169	NA
62	rs148134355	GA/GG	0.005	-1.418	0.350	NA	-0.019	0.716	NA	-2.129	0.135	NA	-1.206	0.136	NA
63	rs7205804	AA/GA/GG	0.097	-0.762	0.015	2.329E-02	-0.004	0.746	0.744	-0.641	0.043	0.044	-0.408	0.014	0.007
63	rs12708973	AA/AG	0.009	-1.030	0.298	NA	-0.031	0.412	NA	-0.608	0.556	NA	-0.718	0.169	NA
63	rs148134355	GA/GG	0.005	-1.418	0.350	NA	-0.019	0.716	NA	-2.129	0.135	NA	-1.206	0.136	NA
63	rs34611098	AG/GG	0.001	5.704	0.028	NA	0.070	0.476	NA	-2.379	0.360	NA	0.113	0.934	NA
64	rs12708973	AA/AG	0.009	-1.030	0.298	6.962E-01	-0.031	0.412	0.325	-0.608	0.556	0.290	-0.718	0.169	0.160
64	rs148134355	GA/GG	0.005	-1.418	0.350	NA	-0.019	0.716	NA	-2.129	0.135	NA	-1.206	0.136	NA
64	rs34611098	AG/GG	0.001	5.704	0.028	NA	0.070	0.476	NA	-2.379	0.360	NA	0.113	0.934	NA
64	rs12720925	CC/TC/TT	0.042	0.240	0.625	NA	-0.019	0.289	NA	-0.118	0.808	NA	-0.109	0.676	NA
65	rs148134355	GA/GG	0.005	-1.418	0.350	1.169E-01	-0.019	0.716	0.567	-2.129	0.135	0.139	-1.206	0.136	0.114
65	rs34611098	AG/GG	0.001	5.704	0.028	NA	0.070	0.476	NA	-2.379	0.360	NA	0.113	0.934	NA
65	rs12720925	CC/TC/TT	0.042	0.240	0.625	NA	-0.019	0.289	NA	-0.118	0.808	NA	-0.109	0.676	NA
65	rs1532624	AA/CA/CC	0.097	-0.769	0.014	NA	-0.008	0.511	NA	-0.468	0.143	NA	-0.329	0.051	NA
66	rs34611098	AG/GG	0.001	5.704	0.028	3.140E-02	0.070	0.476	0.667	-2.379	0.360	0.395	0.113	0.934	0.315
66	rs12720925	CC/TC/TT	0.042	0.240	0.625	NA	-0.019	0.289	NA	-0.118	0.808	NA	-0.109	0.676	NA
66	rs1532624	AA/CA/CC	0.097	-0.769	0.014	NA	-0.008	0.511	NA	-0.468	0.143	NA	-0.329	0.051	NA
66	rs12720871	CC/CG/GG	0.066	0.218	0.572	NA	0.008	0.556	NA	-0.275	0.472	NA	-0.056	0.786	NA
67	rs12720925	CC/TC/TT	0.042	0.240	0.625	2.022E-01	-0.019	0.289	0.739	-0.118	0.808	0.392	-0.109	0.676	0.261
67	rs1532624	AA/CA/CC	0.097	-0.769	0.014	NA	-0.008	0.511	NA	-0.468	0.143	NA	-0.329	0.051	NA
67	rs12720871	CC/CG/GG	0.066	0.218	0.572	NA	0.008	0.556	NA	-0.275	0.472	NA	-0.056	0.786	NA
67	rs12720872	CC/TC/TT	0.135	0.134	0.636	NA	0.003	0.805	NA	0.370	0.198	NA	0.182	0.231	NA
68	rs1532624	AA/CA/CC	0.097	-0.769	0.014	4.931E-03	-0.008	0.511	0.940	-0.468	0.143	0.344	-0.329	0.051	0.100
68	rs12720871	CC/CG/GG	0.066	0.218	0.572	NA	0.008	0.556	NA	-0.275	0.472	NA	-0.056	0.786	NA
68	rs12720872	CC/TC/TT	0.135	0.134	0.636	NA	0.003	0.805	NA	0.370	0.198	NA	0.182	0.231	NA
68	rs11076175	AA/AG/GG	0.243	-0.514	0.020	NA	-0.001	0.877	NA	-0.101	0.652	NA	-0.150	0.200	NA
69	rs12720871	CC/CG/GG	0.066	0.218	0.572	2.294E-01	0.008	0.556	0.990	-0.275	0.472	0.387	-0.056	0.786	0.506
69	rs12720872	CC/TC/TT	0.135	0.134	0.636	NA	0.003	0.805	NA	0.370	0.198	NA	0.182	0.231	NA
69	rs11076175	AA/AG/GG	0.243	-0.514	0.020	NA	-0.001	0.877	NA	-0.101	0.652	NA	-0.150	0.200	NA
69	rs7499892	CC/CT/TT	0.377	-0.351	0.077	NA	-0.001	0.869	NA	0.043	0.831	NA	-0.062	0.556	NA
70	rs12720872	CC/TC/TT	0.135	0.134	0.636	7.881E-02	0.003	0.805	0.994	0.370	0.198	0.272	0.182	0.231	0.371
70	rs11076175	AA/AG/GG	0.243	-0.514	0.020	NA	-0.001	0.877	NA	-0.101	0.652	NA	-0.150	0.200	NA
70	rs7499892	CC/CT/TT	0.377	-0.351	0.077	NA	-0.001	0.869	NA	0.043	0.831	NA	-0.062	0.556	NA
70	rs289713	AA/AT/TT	0.451	-0.019	0.921	NA	0.000	0.956	NA	0.066	0.735	NA	0.065	0.528	NA
71	rs11076175	AA/AG/GG	0.243	-0.514	0.020	9.162E-02	-0.001	0.877	0.872	-0.101	0.652	0.691	-0.150	0.200	0.684
71	rs7499892	CC/CT/TT	0.377	-0.351	0.077	NA	-0.001	0.869	NA	0.043	0.831	NA	-0.062	0.556	NA
71	rs289713	AA/AT/TT	0.451	-0.019	0.921	NA	0.000	0.956	NA	0.066	0.735	NA	0.065	0.528	NA
71	rs191754368	CC/TC/TT	0.019	0.309	0.640	NA	-0.033	0.188	NA	-0.493	0.455	NA	-0.099	0.776	NA
72	rs7499892	CC/CT/TT	0.377	-0.351	0.077	7.273E-03	-0.001	0.869	0.694	0.043	0.831	0.903	-0.062	0.556	0.565
72	rs289713	AA/AT/TT	0.451	-0.019	0.921	NA	0.000	0.956	NA	0.066	0.735	NA	0.065	0.528	NA
72	rs191754368	CC/TC/TT	0.019	0.309	0.640	NA	-0.033	0.188	NA	-0.493	0.455	NA	-0.099	0.776	NA
72	rs9930761	CC/CT/TT	0.148	0.717	0.010	NA	0.015	0.158	NA	0.155	0.571	NA	0.295	0.043	NA
73	rs289713	AA/AT/TT	0.451	-0.019	0.921	2.947E-02	0.000	0.956	0.311	0.066	0.735	0.882	0.065	0.528	0.335
73	rs191754368	CC/TC/TT	0.019	0.309	0.640	NA	-0.033	0.188	NA	-0.493	0.455	NA	-0.099	0.776	NA
73	rs9930761	CC/CT/TT	0.148	0.717	0.010	NA	0.015	0.158	NA	0.155	0.571	NA	0.295	0.043	NA
73	rs35878799	CT/TT	0.011	0.126	0.890	NA	-0.054	0.114	NA	0.446	0.624	NA	0.077	0.873	NA

Table B1.27. Continued

				HDL-C			TG			LDL-C			TC		
Window	**Winow SNP**	**Genotype**	**MAF**	**Beta**	***P***	**Hap_P**	**Beta**	***P***	**Hap_P**	**Beta**	***P***	**Hap_P**	**Beta**	***P***	**Hap_P**
74	rs191754368	CC/TC/TT	0.019	0.309	0.640	1.774E-01	-0.033	0.188	0.221	-0.493	0.455	0.820	-0.099	0.776	0.483
74	rs9930761	CC/CT/TT	0.148	0.717	0.010	NA	0.015	0.158	NA	0.155	0.571	NA	0.295	0.043	NA
74	rs35878799	CT/TT	0.011	0.126	0.890	NA	-0.054	0.114	NA	0.446	0.624	NA	0.077	0.873	NA
74	rs5883	CC/TC/TT	0.155	0.650	0.017	NA	0.010	0.336	NA	0.056	0.837	NA	0.225	0.119	NA
75	rs9930761	CC/CT/TT	0.148	0.717	0.010	7.545E-02	0.015	0.158	0.392	0.155	0.571	0.965	0.295	0.043	0.423
75	rs35878799	CT/TT	0.011	0.126	0.890	NA	-0.054	0.114	NA	0.446	0.624	NA	0.077	0.873	NA
75	rs5883	CC/TC/TT	0.155	0.650	0.017	NA	0.010	0.336	NA	0.056	0.837	NA	0.225	0.119	NA
75	rs11076176	GG/GT/TT	0.403	-0.434	0.027	NA	-0.009	0.217	NA	0.011	0.956	NA	-0.113	0.275	NA
76	rs35878799	CT/TT	0.011	0.126	0.890	6.766E-02	-0.054	0.114	0.327	0.446	0.624	0.267	0.077	0.873	0.225
76	rs5883	CC/TC/TT	0.155	0.650	0.017	NA	0.010	0.336	NA	0.056	0.837	NA	0.225	0.119	NA
76	rs11076176	GG/GT/TT	0.403	-0.434	0.027	NA	-0.009	0.217	NA	0.011	0.956	NA	-0.113	0.275	NA
76	rs289714	AA/GA/GG	0.447	0.242	0.213	NA	-0.001	0.895	NA	0.317	0.106	NA	0.224	0.031	NA
77	rs5883	CC/TC/TT	0.155	0.650	0.017	1.160E-01	0.010	0.336	0.291	0.056	0.837	0.567	0.225	0.119	0.571
77	rs11076176	GG/GT/TT	0.403	-0.434	0.027	NA	-0.009	0.217	NA	0.011	0.956	NA	-0.113	0.275	NA
77	rs289714	AA/GA/GG	0.447	0.242	0.213	NA	-0.001	0.895	NA	0.317	0.106	NA	0.224	0.031	NA
77	rs158479	AA/GA/GG	0.325	0.161	0.432	NA	-0.001	0.859	NA	0.125	0.552	NA	0.112	0.315	NA
78	rs11076176	GG/GT/TT	0.403	-0.434	0.027	5.173E-01	-0.009	0.217	0.352	0.011	0.956	0.431	-0.113	0.275	0.471
78	rs289714	AA/GA/GG	0.447	0.242	0.213	NA	-0.001	0.895	NA	0.317	0.106	NA	0.224	0.031	NA
78	rs158479	AA/GA/GG	0.325	0.161	0.432	NA	-0.001	0.859	NA	0.125	0.552	NA	0.112	0.315	NA
78	rs12720892	AA/GA/GG	0.043	0.032	0.945	NA	-0.008	0.641	NA	0.332	0.465	NA	0.079	0.745	NA
79	rs289714	AA/GA/GG	0.447	0.242	0.213	3.050E-03	-0.001	0.895	0.386	0.317	0.106	0.529	0.224	0.031	0.350
79	rs158479	AA/GA/GG	0.325	0.161	0.432	NA	-0.001	0.859	NA	0.125	0.552	NA	0.112	0.315	NA
79	rs12720892	AA/GA/GG	0.043	0.032	0.945	NA	-0.008	0.641	NA	0.332	0.465	NA	0.079	0.745	NA
79	rs158480	AA/GA/GG	0.445	0.119	0.538	NA	0.000	0.988	NA	0.164	0.398	NA	0.098	0.347	NA
80	rs158479	AA/GA/GG	0.325	0.161	0.432	7.425E-01	-0.001	0.859	0.840	0.125	0.552	0.443	0.112	0.315	0.321
80	rs12720892	AA/GA/GG	0.043	0.032	0.945	NA	-0.008	0.641	NA	0.332	0.465	NA	0.079	0.745	NA
80	rs158480	AA/GA/GG	0.445	0.119	0.538	NA	0.000	0.988	NA	0.164	0.398	NA	0.098	0.347	NA
80	CTPp14448del4	WD/WW	0.018	0.020	0.978	NA	0.002	0.949	NA	0.783	0.274	NA	0.403	0.294	NA
81	rs12720892	AA/GA/GG	0.043	0.032	0.945	8.872E-01	-0.008	0.641	0.990	0.332	0.465	0.538	0.079	0.745	0.787
81	rs158480	AA/GA/GG	0.445	0.119	0.538	NA	0.000	0.988	NA	0.164	0.398	NA	0.098	0.347	NA
81	CTPp14448del4	WD/WW	0.018	0.020	0.978	NA	0.002	0.949	NA	0.783	0.274	NA	0.403	0.294	NA
81	rs289715	AA/TA/TT	0.224	0.299	0.200	NA	-0.004	0.612	NA	-0.047	0.841	NA	0.035	0.777	NA
82	rs158480	AA/GA/GG	0.445	0.119	0.538	7.448E-01	0.000	0.988	0.980	0.164	0.398	0.523	0.098	0.347	0.780
82	CTPp14448del4	WD/WW	0.018	0.020	0.978	NA	0.002	0.949	NA	0.783	0.274	NA	0.403	0.294	NA
82	rs289715	AA/TA/TT	0.224	0.299	0.200	NA	-0.004	0.612	NA	-0.047	0.841	NA	0.035	0.777	NA
82	rs2303789	GG/GT/TT	0.065	0.283	0.468	NA	-0.009	0.529	NA	0.127	0.740	NA	0.006	0.976	NA
83	CTPp14448del4	WD/WW	0.018	0.020	0.978	2.447E-01	0.002	0.949	0.619	0.783	0.274	0.507	0.403	0.294	0.210
83	rs289715	AA/TA/TT	0.224	0.299	0.200	NA	-0.004	0.612	NA	-0.047	0.841	NA	0.035	0.777	NA
83	rs2303789	GG/GT/TT	0.065	0.283	0.468	NA	-0.009	0.529	NA	0.127	0.740	NA	0.006	0.976	NA
83	rs289716	AA/AT/TT	0.476	-0.364	0.059	NA	-0.008	0.263	NA	-0.206	0.285	NA	-0.207	0.043	NA
84	rs289715	AA/TA/TT	0.224	0.299	0.200	2.110E-01	-0.004	0.612	0.640	-0.047	0.841	0.241	0.035	0.777	0.096
84	rs2303789	GG/GT/TT	0.065	0.283	0.468	NA	-0.009	0.529	NA	0.127	0.740	NA	0.006	0.976	NA
84	rs289716	AA/AT/TT	0.476	-0.364	0.059	NA	-0.008	0.263	NA	-0.206	0.285	NA	-0.207	0.043	NA
84	rs289717	AA/GA/GG	0.147	-0.213	0.442	NA	-0.003	0.790	NA	0.285	0.308	NA	0.081	0.584	NA
85	rs2303789	GG/GT/TT	0.065	0.283	0.468	2.320E-01	-0.009	0.529	0.584	0.127	0.740	0.259	0.006	0.976	0.101
85	rs289716	AA/AT/TT	0.476	-0.364	0.059	NA	-0.008	0.263	NA	-0.206	0.285	NA	-0.207	0.043	NA
85	rs289717	AA/GA/GG	0.147	-0.213	0.442	NA	-0.003	0.790	NA	0.285	0.308	NA	0.081	0.584	NA
85	rs12708976	CC/TC/TT	0.047	0.316	0.484	NA	0.000	0.983	NA	0.167	0.707	NA	0.064	0.791	NA
86	rs289716	AA/AT/TT	0.476	-0.364	0.059	2.140E-01	-0.008	0.263	0.729	-0.206	0.285	0.255	-0.207	0.043	0.095
86	rs289717	AA/GA/GG	0.147	-0.213	0.442	NA	-0.003	0.790	NA	0.285	0.308	NA	0.081	0.584	NA
86	rs12708976	CC/TC/TT	0.047	0.316	0.484	NA	0.000	0.983	NA	0.167	0.707	NA	0.064	0.791	NA
86	rs12720942	AA/GA/GG	0.066	0.284	0.461	NA	-0.008	0.580	NA	0.154	0.686	NA	0.029	0.888	NA
87	rs289717	AA/GA/GG	0.147	-0.213	0.442	2.934E-01	-0.003	0.790	0.462	0.285	0.308	0.849	0.081	0.584	0.978
87	rs12708976	CC/TC/TT	0.047	0.316	0.484	NA	0.000	0.983	NA	0.167	0.707	NA	0.064	0.791	NA
87	rs12720942	AA/GA/GG	0.066	0.284	0.461	NA	-0.008	0.580	NA	0.154	0.686	NA	0.029	0.888	NA
87	rs736274	AA/AT/TT	0.016	-1.360	0.059	NA	-0.041	0.140	NA	-0.137	0.850	NA	-0.097	0.799	NA
88	rs12708976	CC/TC/TT	0.047	0.316	0.484	2.240E-01	0.000	0.983	0.335	0.167	0.707	0.979	0.064	0.791	0.989
88	rs12720942	AA/GA/GG	0.066	0.284	0.461	NA	-0.008	0.580	NA	0.154	0.686	NA	0.029	0.888	NA
88	rs736274	AA/AT/TT	0.016	-1.360	0.059	NA	-0.041	0.140	NA	-0.137	0.850	NA	-0.097	0.799	NA
88	rs12720937	CC/GC/GG	0.066	0.243	0.535	NA	-0.011	0.461	NA	0.119	0.755	NA	-0.002	0.993	NA
89	rs12720942	AA/GA/GG	0.066	0.284	0.461	1.037E-02	-0.008	0.580	0.302	0.154	0.686	0.310	0.029	0.888	0.059
89	rs736274	AA/AT/TT	0.016	-1.360	0.059	NA	-0.041	0.140	NA	-0.137	0.850	NA	-0.097	0.799	NA
89	rs12720937	CC/GC/GG	0.066	0.243	0.535	NA	-0.011	0.461	NA	0.119	0.755	NA	-0.002	0.993	NA
89	rs289718	CC/CT/TT	0.438	-0.403	0.035	NA	-0.007	0.310	NA	-0.309	0.103	NA	-0.258	0.011	NA
90	rs736274	AA/AT/TT	0.016	-1.360	0.059	1.693E-02	-0.041	0.140	0.294	-0.137	0.850	0.375	-0.097	0.799	0.070
90	rs12720937	CC/GC/GG	0.066	0.243	0.535	NA	-0.011	0.461	NA	0.119	0.755	NA	-0.002	0.993	NA
90	rs289718	CC/CT/TT	0.438	-0.403	0.035	NA	-0.007	0.310	NA	-0.309	0.103	NA	-0.258	0.011	NA
90	rs289719	AA/GA/GG	0.493	0.412	0.033	NA	0.010	0.164	NA	0.239	0.214	NA	0.234	0.021	NA
91	rs12720937	CC/GC/GG	0.066	0.243	0.535	1.812E-01	-0.011	0.461	0.765	0.119	0.755	0.501	-0.002	0.993	0.124
91	rs289718	CC/CT/TT	0.438	-0.403	0.035	NA	-0.007	0.310	NA	-0.309	0.103	NA	-0.258	0.011	NA
91	rs289719	AA/GA/GG	0.493	0.412	0.033	NA	0.010	0.164	NA	0.239	0.214	NA	0.234	0.021	NA
91	rs2033254	CC/TC/TT	0.317	-0.294	0.145	NA	-0.006	0.420	NA	-0.294	0.146	NA	-0.227	0.034	NA
92	rs289718	CC/CT/TT	0.438	-0.403	0.035	2.373E-01	-0.007	0.310	0.796	-0.309	0.103	0.510	-0.258	0.011	0.134
92	rs289719	AA/GA/GG	0.493	0.412	0.033	NA	0.010	0.164	NA	0.239	0.214	NA	0.234	0.021	NA

Table B1.27. Continued

				HDL-C			TG			LDL-C			TC		
Window	**Winow SNP**	**Genotype**	**MAF**	**Beta**	***P***	**Hap_P**	**Beta**	***P***	**Hap_P**	**Beta**	***P***	**Hap_P**	**Beta**	***P***	**Hap_P**
92	rs2033254	CC/TC/TT	0.317	-0.294	0.145	NA	-0.006	0.420	NA	-0.294	0.146	NA	-0.227	0.034	NA
92	rs112205272	AA/GA/GG	0.063	0.114	0.773	NA	-0.010	0.482	NA	0.127	0.745	NA	-0.017	0.936	NA
93	rs289719	AA/GA/GG	0.493	0.412	0.033	7.339E-02	0.010	0.164	0.625	0.239	0.214	0.235	0.234	0.021	0.039
93	rs2033254	CC/TC/TT	0.317	-0.294	0.145	NA	-0.006	0.420	NA	-0.294	0.146	NA	-0.227	0.034	NA
93	rs112205272	AA/GA/GG	0.063	0.114	0.773	NA	-0.010	0.482	NA	0.127	0.745	NA	-0.017	0.936	NA
93	rs112409939	AA/GA/GG	0.064	0.250	0.521	NA	-0.006	0.662	NA	0.053	0.890	NA	-0.021	0.921	NA
94	rs2033254	CC/TC/TT	0.317	-0.294	0.145	2.090E-01	-0.006	0.420	0.366	-0.294	0.146	0.053	-0.227	0.034	0.013
94	rs112205272	AA/GA/GG	0.063	0.114	0.773	NA	-0.010	0.482	NA	0.127	0.745	NA	-0.017	0.936	NA
94	rs112409939	AA/GA/GG	0.064	0.250	0.521	NA	-0.006	0.662	NA	0.053	0.890	NA	-0.021	0.921	NA
94	rs71387147	GT/TT	0.025	-0.430	0.514	NA	-0.039	0.112	NA	-1.286	0.049	NA	-0.743	0.033	NA
95	rs112205272	AA/GA/GG	0.063	0.114	0.773	1.340E-02	-0.010	0.482	0.436	0.127	0.745	0.265	-0.017	0.936	0.149
95	rs112409939	AA/GA/GG	0.064	0.250	0.521	NA	-0.006	0.662	NA	0.053	0.890	NA	-0.021	0.921	NA
95	rs71387147	GT/TT	0.025	-0.430	0.514	NA	-0.039	0.112	NA	-1.286	0.049	NA	-0.743	0.033	NA
95	rs1968905	GG/GT/TT	0.360	0.634	0.002	NA	0.004	0.602	NA	-0.027	0.894	NA	0.114	0.298	NA
96	rs112409939	AA/GA/GG	0.064	0.250	0.521	2.062E-02	-0.006	0.662	0.582	0.053	0.890	0.463	-0.021	0.921	0.292
96	rs71387147	GT/TT	0.025	-0.430	0.514	NA	-0.039	0.112	NA	-1.286	0.049	NA	-0.743	0.033	NA
96	rs1968905	GG/GT/TT	0.360	0.634	0.002	NA	0.004	0.602	NA	-0.027	0.894	NA	0.114	0.298	NA
96	rs12720903	AA/GA/GG	0.068	0.152	0.680	NA	-0.004	0.757	NA	0.019	0.959	NA	0.033	0.866	NA
97	rs71387147	GT/TT	0.025	-0.430	0.514	4.022E-02	-0.039	0.112	0.654	-1.286	0.049	0.554	-0.743	0.033	0.351
97	rs1968905	GG/GT/TT	0.360	0.634	0.002	NA	0.004	0.602	NA	-0.027	0.894	NA	0.114	0.298	NA
97	rs12720903	AA/GA/GG	0.068	0.152	0.680	NA	-0.004	0.757	NA	0.019	0.959	NA	0.033	0.866	NA
97	rs4784744	AA/GA/GG	0.100	-0.226	0.483	NA	-0.002	0.838	NA	-0.118	0.716	NA	-0.104	0.544	NA
98	rs1968905	GG/GT/TT	0.360	0.634	0.002	2.012E-02	0.004	0.602	0.940	-0.027	0.894	0.976	0.114	0.298	0.715
98	rs12720903	AA/GA/GG	0.068	0.152	0.680	NA	-0.004	0.757	NA	0.019	0.959	NA	0.033	0.866	NA
98	rs4784744	AA/GA/GG	0.100	-0.226	0.483	NA	-0.002	0.838	NA	-0.118	0.716	NA	-0.104	0.544	NA
98	rs291044	AA/GA/GG	0.102	-0.218	0.495	NA	-0.006	0.637	NA	-0.157	0.623	NA	-0.131	0.443	NA
99	rs12720903	AA/GA/GG	0.068	0.152	0.680	7.539E-01	-0.004	0.757	0.810	0.019	0.959	0.956	0.033	0.866	0.930
99	rs4784744	AA/GA/GG	0.100	-0.226	0.483	NA	-0.002	0.838	NA	-0.118	0.716	NA	-0.104	0.544	NA
99	rs291044	AA/GA/GG	0.102	-0.218	0.495	NA	-0.006	0.637	NA	-0.157	0.623	NA	-0.131	0.443	NA
99	rs114486472	AA/AG/GG	0.020	-0.769	0.270	NA	0.030	0.209	NA	0.014	0.983	NA	0.030	0.935	NA
100	rs4784744	AA/GA/GG	0.100	-0.226	0.483	8.404E-01	-0.002	0.838	0.596	-0.118	0.716	0.350	-0.104	0.544	0.531
100	rs291044	AA/GA/GG	0.102	-0.218	0.495	NA	-0.006	0.637	NA	-0.157	0.623	NA	-0.131	0.443	NA
100	rs114486472	AA/AG/GG	0.020	-0.769	0.270	NA	0.030	0.209	NA	0.014	0.983	NA	0.030	0.935	NA
100	rs34426213	CC/CT/TT	0.042	0.130	0.784	NA	-0.006	0.750	NA	1.026	0.029	NA	0.433	0.084	NA
101	rs291044	AA/GA/GG	0.102	-0.218	0.495	9.281E-01	-0.006	0.637	0.732	-0.157	0.623	0.417	-0.131	0.443	0.738
101	rs114486472	AA/AG/GG	0.020	-0.769	0.270	NA	0.030	0.209	NA	0.014	0.983	NA	0.030	0.935	NA
101	rs34426213	CC/CT/TT	0.042	0.130	0.784	NA	-0.006	0.750	NA	1.026	0.029	NA	0.433	0.084	NA
101	rs891144	AA/GA/GG	0.215	-0.056	0.806	NA	-0.002	0.828	NA	0.263	0.254	NA	0.079	0.522	NA
102	rs114486472	AA/AG/GG	0.020	-0.769	0.270	9.689E-01	0.030	0.209	0.400	0.014	0.983	0.504	0.030	0.935	0.784
102	rs34426213	CC/CT/TT	0.042	0.130	0.784	NA	-0.006	0.750	NA	1.026	0.029	NA	0.433	0.084	NA
102	rs891144	AA/GA/GG	0.215	-0.056	0.806	NA	-0.002	0.828	NA	0.263	0.254	NA	0.079	0.522	NA
102	rs12708979	AA/GA/GG	0.030	-0.137	0.797	NA	-0.030	0.132	NA	0.199	0.712	NA	0.043	0.878	NA
103	rs34426213	CC/CT/TT	0.042	0.130	0.784	2.025E-01	-0.006	0.750	0.386	1.026	0.029	0.124	0.433	0.084	0.081
103	rs891144	AA/GA/GG	0.215	-0.056	0.806	NA	-0.002	0.828	NA	0.263	0.254	NA	0.079	0.522	NA
103	rs12708979	AA/GA/GG	0.030	-0.137	0.797	NA	-0.030	0.132	NA	0.199	0.712	NA	0.043	0.878	NA
103	rs12708980	AA/AC/CC	0.342	-0.512	0.011	NA	0.000	0.999	NA	-0.227	0.260	NA	-0.205	0.054	NA
104	rs891144	AA/GA/GG	0.215	-0.056	0.806	1.973E-01	-0.002	0.828	0.502	0.263	0.254	0.348	0.079	0.522	0.137
104	rs12708979	AA/GA/GG	0.030	-0.137	0.797	NA	-0.030	0.132	NA	0.199	0.712	NA	0.043	0.878	NA
104	rs12708980	AA/AC/CC	0.342	-0.512	0.011	NA	0.000	0.999	NA	-0.227	0.260	NA	-0.205	0.054	NA
104	rs12720889	AA/AT/TT	0.204	0.407	0.086	NA	0.002	0.863	NA	0.207	0.379	NA	0.237	0.059	NA
105	rs12708979	AA/GA/GG	0.030	-0.137	0.797	1.802E-01	-0.030	0.132	0.734	0.199	0.712	0.781	0.043	0.878	0.272
105	rs12708980	AA/AC/CC	0.342	-0.512	0.011	NA	0.000	0.999	NA	-0.227	0.260	NA	-0.205	0.054	NA
105	rs12720889	AA/AT/TT	0.204	0.407	0.086	NA	0.002	0.863	NA	0.207	0.379	NA	0.237	0.059	NA
105	rs291043	AA/AG/GG	0.086	-0.147	0.657	NA	-0.003	0.814	NA	-0.227	0.491	NA	-0.136	0.436	NA
106	rs12708980	AA/AC/CC	0.342	-0.512	0.011	7.156E-02	0.000	0.999	0.957	-0.227	0.260	0.252	-0.205	0.054	0.021
106	rs12720889	AA/AT/TT	0.204	0.407	0.086	NA	0.002	0.863	NA	0.207	0.379	NA	0.237	0.059	NA
106	rs291043	AA/AG/GG	0.086	-0.147	0.657	NA	-0.003	0.814	NA	-0.227	0.491	NA	-0.136	0.436	NA
106	rs114203109	GA/GG	0.042	-0.994	0.041	NA	0.013	0.468	NA	-1.140	0.022	NA	-0.765	0.003	NA
107	rs12720889	AA/AT/TT	0.204	0.407	0.086	2.063E-01	0.002	0.863	0.080	0.207	0.379	0.251	0.237	0.059	0.022
107	rs291043	AA/AG/GG	0.086	-0.147	0.657	NA	-0.003	0.814	NA	-0.227	0.491	NA	-0.136	0.436	NA
107	rs114203109	GA/GG	0.042	-0.994	0.041	NA	0.013	0.468	NA	-1.140	0.022	NA	-0.765	0.003	NA
107	rs145189439	CC/TC/TT	0.052	0.148	0.732	NA	-0.017	0.279	NA	0.079	0.851	NA	-0.042	0.855	NA
108	rs291043	AA/AG/GG	0.086	-0.147	0.657	1.709E-01	-0.003	0.814	0.584	-0.227	0.491	0.170	-0.136	0.436	0.027
108	rs114203109	GA/GG	0.042	-0.994	0.041	NA	0.013	0.468	NA	-1.140	0.022	NA	-0.765	0.003	NA
108	rs145189439	CC/TC/TT	0.052	0.148	0.732	NA	-0.017	0.279	NA	0.079	0.851	NA	-0.042	0.855	NA
108	rs4784745	AA/AG/GG	0.076	-0.227	0.527	NA	0.001	0.944	NA	-0.198	0.584	NA	-0.131	0.494	NA
109	rs114203109	GA/GG	0.042	-0.994	0.041	2.058E-01	0.013	0.468	0.197	-1.140	0.022	0.211	-0.765	0.003	0.043
109	rs145189439	CC/TC/TT	0.052	0.148	0.732	NA	-0.017	0.279	NA	0.079	0.851	NA	-0.042	0.855	NA
109	rs4784745	AA/AG/GG	0.076	-0.227	0.527	NA	0.001	0.944	NA	-0.198	0.584	NA	-0.131	0.494	NA
109	rs34855278	GA/GG	0.015	-1.092	0.163	NA	-0.029	0.324	NA	-0.667	0.397	NA	-0.226	0.584	NA
110	rs145189439	CC/TC/TT	0.052	0.148	0.732	5.147E-01	-0.017	0.279	0.692	0.079	0.851	0.525	-0.042	0.855	0.492
110	rs4784745	AA/AG/GG	0.076	-0.227	0.527	NA	0.001	0.944	NA	-0.198	0.584	NA	-0.131	0.494	NA
110	rs34855278	GA/GG	0.015	-1.092	0.163	NA	-0.029	0.324	NA	-0.667	0.397	NA	-0.226	0.584	NA
110	rs114948973	AA/AG/GG	0.019	0.592	0.397	NA	0.012	0.631	NA	1.125	0.103	NA	0.630	0.089	NA

Table B1.27. Continued

				HDL-C			TG			LDL-C			TC		
Window	**Winow SNP**	**Genotype**	**MAF**	**Beta**	***P***	**Hap_P**	**Beta**	***P***	**Hap_P**	**Beta**	***P***	**Hap_P**	**Beta**	***P***	**Hap_P**
111	rs4784745	AA/AG/GG	0.076	-0.227	0.527	3.470E-02	0.001	0.944	0.705	-0.198	0.584	0.493	-0.131	0.494	0.349
111	rs34855278	GA/GG	0.015	-1.092	0.163	NA	-0.029	0.324	NA	-0.667	0.397	NA	-0.226	0.584	NA
111	rs114948973	AA/AG/GG	0.019	0.592	0.397	NA	0.012	0.631	NA	1.125	0.103	NA	0.630	0.089	NA
111	rs7195984	AA/GA/GG	0.169	0.722	0.005	NA	0.009	0.323	NA	-0.026	0.918	NA	0.128	0.342	NA
112	rs34855278	GA/GG	0.015	-1.092	0.163	2.774E-02	-0.029	0.324	0.723	-0.667	0.397	0.418	-0.226	0.584	0.375
112	rs114948973	AA/AG/GG	0.019	0.592	0.397	NA	0.012	0.631	NA	1.125	0.103	NA	0.630	0.089	NA
112	rs7195984	AA/GA/GG	0.169	0.722	0.005	NA	0.009	0.323	NA	-0.026	0.918	NA	0.128	0.342	NA
112	rs7196174	GG/GT/TT	0.070	-0.094	0.802	NA	-0.006	0.653	NA	0.309	0.414	NA	0.104	0.604	NA
113	rs114948973	AA/AG/GG	0.019	0.592	0.397	2.465E-02	0.012	0.631	0.798	1.125	0.103	0.248	0.630	0.089	0.077
113	rs7195984	AA/GA/GG	0.169	0.722	0.005	NA	0.009	0.323	NA	-0.026	0.918	NA	0.128	0.342	NA
113	rs7196174	GG/GT/TT	0.070	-0.094	0.802	NA	-0.006	0.653	NA	0.309	0.414	NA	0.104	0.604	NA
113	rs1800774	CC/TC/TT	0.217	-0.507	0.025	NA	-0.006	0.486	NA	-0.433	0.057	NA	-0.321	0.007	NA
114	rs7195984	AA/GA/GG	0.169	0.722	0.005	1.784E-02	0.009	0.323	0.874	-0.026	0.918	0.467	0.128	0.342	0.227
114	rs7196174	GG/GT/TT	0.070	-0.094	0.802	NA	-0.006	0.653	NA	0.309	0.414	NA	0.104	0.604	NA
114	rs1800774	CC/TC/TT	0.217	-0.507	0.025	NA	-0.006	0.486	NA	-0.433	0.057	NA	-0.321	0.007	NA
114	rs5882	AA/GA/GG	0.310	-0.350	0.083	NA	-0.006	0.395	NA	-0.208	0.306	NA	-0.192	0.073	NA
115	rs7196174	GG/GT/TT	0.070	-0.094	0.802	1.761E-01	-0.006	0.653	0.757	0.309	0.414	0.392	0.104	0.604	0.109
115	rs1800774	CC/TC/TT	0.217	-0.507	0.025	NA	-0.006	0.486	NA	-0.433	0.057	NA	-0.321	0.007	NA
115	rs5882	AA/GA/GG	0.310	-0.350	0.083	NA	-0.006	0.395	NA	-0.208	0.306	NA	-0.192	0.073	NA
115	rs5886	AA/GA/GG	0.082	0.071	0.839	NA	-0.009	0.505	NA	-0.042	0.907	NA	-0.043	0.818	NA
116	rs1800774	CC/TC/TT	0.217	-0.507	0.025	5.024E-03	-0.006	0.486	0.774	-0.433	0.057	0.348	-0.321	0.007	0.076
116	rs5882	AA/GA/GG	0.310	-0.350	0.083	NA	-0.006	0.395	NA	-0.208	0.306	NA	-0.192	0.073	NA
116	rs5886	AA/GA/GG	0.082	0.071	0.839	NA	-0.009	0.505	NA	-0.042	0.907	NA	-0.043	0.818	NA
116	rs289740	CC/CT/TT	0.117	0.871	0.003	NA	0.010	0.366	NA	-0.095	0.751	NA	0.110	0.490	NA
117	rs5882	AA/GA/GG	0.310	-0.350	0.083	2.929E-02	-0.006	0.395	0.713	-0.208	0.306	0.642	-0.192	0.073	0.206
117	rs5886	AA/GA/GG	0.082	0.071	0.839	NA	-0.009	0.505	NA	-0.042	0.907	NA	-0.043	0.818	NA
117	rs289740	CC/CT/TT	0.117	0.871	0.003	NA	0.010	0.366	NA	-0.095	0.751	NA	0.110	0.490	NA
117	rs36051594	AA/GA/GG	0.044	-0.297	0.501	NA	-0.008	0.629	NA	0.285	0.522	NA	0.100	0.670	NA
118	rs5886	AA/GA/GG	0.082	0.071	0.839	1.931E-03	-0.009	0.505	0.834	-0.042	0.907	0.345	-0.043	0.818	0.072
118	rs289740	CC/CT/TT	0.117	0.871	0.003	NA	0.010	0.366	NA	-0.095	0.751	NA	0.110	0.490	NA
118	rs36051594	AA/GA/GG	0.044	-0.297	0.501	NA	-0.008	0.629	NA	0.285	0.522	NA	0.100	0.670	NA
118	rs1801706	AA/GA/GG	0.176	0.572	0.021	NA	0.004	0.641	NA	0.215	0.388	NA	0.240	0.068	NA
119	rs289740	CC/CT/TT	0.117	0.871	0.003	1.551E-03	0.010	0.366	0.645	-0.095	0.751	0.668	0.110	0.490	0.100
119	rs36051594	AA/GA/GG	0.044	-0.297	0.501	NA	-0.008	0.629	NA	0.285	0.522	NA	0.100	0.670	NA
119	rs1801706	AA/GA/GG	0.176	0.572	0.021	NA	0.004	0.641	NA	0.215	0.388	NA	0.240	0.068	NA
119	rs289742	CC/CG/GG	0.421	0.042	0.830	NA	0.007	0.349	NA	0.067	0.731	NA	0.047	0.650	NA
120	rs36051594	AA/GA/GG	0.044	-0.297	0.501	3.973E-02	-0.008	0.629	0.753	0.285	0.522	0.523	0.100	0.670	0.147
120	rs1801706	AA/GA/GG	0.176	0.572	0.021	NA	0.004	0.641	NA	0.215	0.388	NA	0.240	0.068	NA
120	rs289742	CC/CG/GG	0.421	0.042	0.830	NA	0.007	0.349	NA	0.067	0.731	NA	0.047	0.650	NA
120	rs289743	AA/GA/GG	0.315	-0.395	0.048	NA	-0.004	0.601	NA	-0.280	0.165	NA	-0.222	0.036	NA
121	rs1801706	AA/GA/GG	0.176	0.572	0.021	7.350E-02	0.004	0.641	0.084	0.215	0.388	0.383	0.240	0.068	0.129
121	rs289742	CC/CG/GG	0.421	0.042	0.830	NA	0.007	0.349	NA	0.067	0.731	NA	0.047	0.650	NA
121	rs289743	AA/GA/GG	0.315	-0.395	0.048	NA	-0.004	0.601	NA	-0.280	0.165	NA	-0.222	0.036	NA
121	rs289744	GG/GT/TT	0.306	-0.334	0.105	NA	-0.005	0.487	NA	-0.330	0.108	NA	-0.235	0.030	NA
122	rs289742	CC/CG/GG	0.421	0.042	0.830	1.399E-01	0.007	0.349	0.091	0.067	0.731	0.328	0.047	0.650	0.110
122	rs289743	AA/GA/GG	0.315	-0.395	0.048	NA	-0.004	0.601	NA	-0.280	0.165	NA	-0.222	0.036	NA
122	rs289744	GG/GT/TT	0.306	-0.334	0.105	NA	-0.005	0.487	NA	-0.330	0.108	NA	-0.235	0.030	NA
122	rs12720875	AA/GA/GG	0.032	-0.056	0.915	NA	-0.021	0.298	NA	0.422	0.426	NA	0.186	0.500	NA
123	rs289743	AA/GA/GG	0.315	-0.395	0.048	6.271E-02	-0.004	0.601	0.202	-0.280	0.165	0.427	-0.222	0.036	0.124
123	rs289744	GG/GT/TT	0.306	-0.334	0.105	NA	-0.005	0.487	NA	-0.330	0.108	NA	-0.235	0.030	NA
123	rs12720875	AA/GA/GG	0.032	-0.056	0.915	NA	-0.021	0.298	NA	0.422	0.426	NA	0.186	0.500	NA
123	rs66495554	CC/TC/TT	0.193	-0.577	0.015	NA	-0.010	0.259	NA	-0.451	0.061	NA	-0.350	0.006	NA
124	rs289744	GG/GT/TT	0.306	-0.334	0.105	4.009E-03	-0.005	0.487	0.158	-0.330	0.108	0.136	-0.235	0.030	0.009
124	rs12720875	AA/GA/GG	0.032	-0.056	0.915	NA	-0.021	0.298	NA	0.422	0.426	NA	0.186	0.500	NA
124	rs66495554	CC/TC/TT	0.193	-0.577	0.015	NA	-0.010	0.259	NA	-0.451	0.061	NA	-0.350	0.006	NA
124	rs114646974	AA/AG	0.003	-5.846	0.000	NA	0.109	0.077	NA	-3.335	0.074	NA	-2.329	0.018	NA
125	rs12720875	AA/GA/GG	0.032	-0.056	0.915	1.481E-03	-0.021	0.298	0.099	0.422	0.426	0.071	0.186	0.500	0.005
125	rs66495554	CC/TC/TT	0.193	-0.577	0.015	NA	-0.010	0.259	NA	-0.451	0.061	NA	-0.350	0.006	NA
125	rs114646974	AA/AG	0.003	-5.846	0.000	NA	0.109	0.077	NA	-3.335	0.074	NA	-2.329	0.018	NA
125	rs138161274	CC/GC	0.027	0.694	0.270	NA	-0.002	0.941	NA	0.490	0.415	NA	0.237	0.484	NA
126	rs66495554	CC/TC/TT	0.193	-0.577	0.015	5.735E-03	-0.010	0.259	0.512	-0.451	0.061	0.068	-0.350	0.006	0.008
126	rs114646974	AA/AG	0.003	-5.846	0.000	NA	0.109	0.077	NA	-3.335	0.074	NA	-2.329	0.018	NA
126	rs138161274	CC/GC	0.027	0.694	0.270	NA	-0.002	0.941	NA	0.490	0.415	NA	0.237	0.484	NA
126	rs12720874	CC/TC/TT	0.153	-0.159	0.551	NA	0.002	0.875	NA	0.324	0.218	NA	0.103	0.460	NA
127	rs114646974	AA/AG	0.003	-5.846	0.000	2.216E-02	0.109	0.077	0.423	-3.335	0.074	0.120	-2.329	0.018	0.084
127	rs138161274	CC/GC	0.027	0.694	0.270	NA	-0.002	0.941	NA	0.490	0.415	NA	0.237	0.484	NA
127	rs12720874	CC/TC/TT	0.153	-0.159	0.551	NA	0.002	0.875	NA	0.324	0.218	NA	0.103	0.460	NA
127	rs12720916	AA/GA/GG	0.025	-0.571	0.354	NA	0.019	0.373	NA	0.037	0.952	NA	0.001	0.997	NA
128	rs138161274	CC/GC	0.027	0.694	0.270	3.907E-01	-0.002	0.941	0.447	0.490	0.415	0.099	0.237	0.484	0.191
128	rs12720874	CC/TC/TT	0.153	-0.159	0.551	NA	0.002	0.875	NA	0.324	0.218	NA	0.103	0.460	NA
128	rs12720916	AA/GA/GG	0.025	-0.571	0.354	NA	0.019	0.373	NA	0.037	0.952	NA	0.001	0.997	NA
128	rs289745	GG/GT/TT	0.194	0.258	0.272	NA	0.017	0.056	NA	-0.313	0.189	NA	-0.096	0.445	NA

TABLE B1.28. *CETP* 4-SNP sliding window haplotype association results for ApoA1 and ApoB in African blacks (n=788)

				ApoA1			ApoB		
wind	**Winow SNP**	**Genotype**	**MAF**	**Beta**	***P***	**Hap_P**	**Beta**	***P***	**Hap_P**
1	rs247615	AA/AG/GG	0.230	-0.159	0.777	0.085	0.254	0.692	0.719
1	rs9989419	AA/GA/GG	0.340	-0.283	0.574	NA	0.513	0.370	NA
1	rs183130	CC/CT/TT	0.244	1.444	0.008	NA	-0.768	0.221	NA
1	rs3764261	AA/CA/CC	0.323	0.898	0.073	NA	-0.424	0.455	NA
2	rs9989419	AA/GA/GG	0.340	-0.283	0.574	0.019	0.513	0.370	0.844
2	rs183130	CC/CT/TT	0.244	1.444	0.008	NA	-0.768	0.221	NA
2	rs3764261	AA/CA/CC	0.323	0.898	0.073	NA	-0.424	0.455	NA
2	rs148562851	AA/AG/GG	0.020	4.275	0.008	NA	-0.261	0.887	NA
3	rs183130	CC/CT/TT	0.244	1.444	0.008	0.028	-0.768	0.221	0.883
3	rs3764261	AA/CA/CC	0.323	0.898	0.073	NA	-0.424	0.455	NA
3	rs148562851	AA/AG/GG	0.020	4.275	0.008	NA	-0.261	0.887	NA
3	rs12447924	CC/CT/TT	0.224	-0.341	0.547	NA	0.217	0.735	NA
4	rs3764261	AA/CA/CC	0.323	0.898	0.073	0.108	-0.424	0.455	0.969
4	rs148562851	AA/AG/GG	0.020	4.275	0.008	NA	-0.261	0.887	NA
4	rs12447924	CC/CT/TT	0.224	-0.341	0.547	NA	0.217	0.735	NA
4	rs17231506	CC/TC/TT	0.105	0.236	0.761	NA	-0.042	0.962	NA
5	rs148562851	AA/AG/GG	0.020	4.275	0.008	0.117	-0.261	0.887	0.921
5	rs12447924	CC/CT/TT	0.224	-0.341	0.547	NA	0.217	0.735	NA
5	rs17231506	CC/TC/TT	0.105	0.236	0.761	NA	-0.042	0.962	NA
5	rs12708968	CC/TC/TT	0.063	-0.428	0.663	NA	1.008	0.369	NA
6	rs12447924	CC/CT/TT	0.224	-0.341	0.547	0.882	0.217	0.735	0.266
6	rs17231506	CC/TC/TT	0.105	0.236	0.761	NA	-0.042	0.962	NA
6	rs12708968	CC/TC/TT	0.063	-0.428	0.663	NA	1.008	0.369	NA
6	rs4783961	AA/GA/GG	0.454	0.325	0.492	NA	-0.932	0.074	NA
7	rs17231506	CC/TC/TT	0.105	0.236	0.761	0.203	-0.042	0.962	0.387
7	rs12708968	CC/TC/TT	0.063	-0.428	0.663	NA	1.008	0.369	NA
7	rs4783961	AA/GA/GG	0.454	0.325	0.492	NA	-0.932	0.074	NA
7	rs146122874	CC/TC/TT	0.022	3.732	0.014	NA	-0.536	0.755	NA
8	rs12708968	CC/TC/TT	0.063	-0.428	0.663	0.125	1.008	0.369	0.120
8	rs4783961	AA/GA/GG	0.454	0.325	0.492	NA	-0.932	0.074	NA
8	rs146122874	CC/TC/TT	0.022	3.732	0.014	NA	-0.536	0.755	NA
8	rs4783962	CC/CT/TT	0.097	0.123	0.878	NA	-1.266	0.159	NA
9	rs4783961	AA/GA/GG	0.454	0.325	0.492	0.083	-0.932	0.074	0.053
9	rs146122874	CC/TC/TT	0.022	3.732	0.014	NA	-0.536	0.755	NA
9	rs4783962	CC/CT/TT	0.097	0.123	0.878	NA	-1.266	0.159	NA
9	rs17237883	AA/GA/GG	0.031	1.447	0.287	NA	1.572	0.327	NA
10	rs146122874	CC/TC/TT	0.022	3.732	0.014	0.094	-0.536	0.755	0.581
10	rs4783962	CC/CT/TT	0.097	0.123	0.878	NA	-1.266	0.159	NA
10	rs17237883	AA/GA/GG	0.031	1.447	0.287	NA	1.572	0.327	NA
10	rs114856405	AA/CA/CC	0.036	-1.430	0.237	NA	0.796	0.557	NA
11	rs4783962	CC/CT/TT	0.097	0.123	0.878	0.333	-1.266	0.159	0.429
11	rs17237883	AA/GA/GG	0.031	1.447	0.287	NA	1.572	0.327	NA
11	rs114856405	AA/CA/CC	0.036	-1.430	0.237	NA	0.796	0.557	NA
11	rs1800775	AA/CA/CC	0.395	-0.208	0.666	NA	0.208	0.702	NA
12	rs17237883	AA/GA/GG	0.031	1.447	0.287	0.002	1.572	0.327	0.539
12	rs114856405	AA/CA/CC	0.036	-1.430	0.237	NA	0.796	0.557	NA
12	rs1800775	AA/CA/CC	0.395	-0.208	0.666	NA	0.208	0.702	NA
12	rs17231520	AA/GA/GG	0.090	3.059	0.000	NA	-1.263	0.171	NA
13	rs114856405	AA/CA/CC	0.036	-1.430	0.237	0.002	0.796	0.557	0.535
13	rs1800775	AA/CA/CC	0.395	-0.208	0.666	NA	0.208	0.702	NA
13	rs17231520	AA/GA/GG	0.090	3.059	0.000	NA	-1.263	0.171	NA
13	rs34065661	CC/GC/GG	0.088	3.192	0.000	NA	-0.957	0.308	NA
14	rs1800775	AA/CA/CC	0.395	-0.208	0.666	0.006	0.208	0.702	0.454
14	rs17231520	AA/GA/GG	0.090	3.059	0.000	NA	-1.263	0.171	NA
14	rs34065661	CC/GC/GG	0.088	3.192	0.000	NA	-0.957	0.308	NA
14	rs5884	AA/CA/CC	0.065	-0.739	0.439	NA	0.809	0.457	NA
15	rs17231520	AA/GA/GG	0.090	3.059	0.000	0.001	-1.263	0.171	0.268
15	rs34065661	CC/GC/GG	0.088	3.192	0.000	NA	-0.957	0.308	NA
15	rs5884	AA/CA/CC	0.065	-0.739	0.439	NA	0.809	0.457	NA
15	rs34680782	AA/CA/CC	0.020	3.043	0.060	NA	1.030	0.569	NA
16	rs34065661	CC/GC/GG	0.088	3.192	0.000	0.001	-0.957	0.308	0.443
16	rs5884	AA/CA/CC	0.065	-0.739	0.439	NA	0.809	0.457	NA
16	rs34680782	AA/CA/CC	0.020	3.043	0.060	NA	1.030	0.569	NA
16	rs17231534	AA/CA/CC	0.177	-0.519	0.398	NA	-0.854	0.214	NA
17	rs5884	AA/CA/CC	0.065	-0.739	0.439	0.234	0.809	0.457	0.689
17	rs34680782	AA/CA/CC	0.020	3.043	0.060	NA	1.030	0.569	NA
17	rs17231534	AA/CA/CC	0.177	-0.519	0.398	NA	-0.854	0.214	NA
17	rs3816117	CC/CT/TT	0.394	-0.143	0.768	NA	0.370	0.494	NA

Table B1.28. Continued

				ApoA1			ApoB		
wind	**Winow SNP**	**Genotype**	**MAF**	**Beta**	***P***	**Hap_P**	**Beta**	***P***	**Hap_P**
18	rs34680782	AA/CA/CC	0.020	3.043	0.060	0.045	1.030	0.569	0.551
18	rs17231534	AA/CA/CC	0.177	-0.519	0.398	NA	-0.854	0.214	NA
18	rs3816117	CC/CT/TT	0.394	-0.143	0.768	NA	0.370	0.494	NA
18	rs711752	AA/GA/GG	0.232	1.330	0.016	NA	-0.462	0.460	NA
19	rs17231534	AA/CA/CC	0.177	-0.519	0.398	0.200	-0.854	0.214	0.429
19	rs3816117	CC/CT/TT	0.394	-0.143	0.768	NA	0.370	0.494	NA
19	rs711752	AA/GA/GG	0.232	1.330	0.016	NA	-0.462	0.460	NA
19	rs708272	AA/GA/GG	0.236	1.288	0.018	NA	-0.595	0.336	NA
20	rs3816117	CC/CT/TT	0.394	-0.143	0.768	0.080	0.370	0.494	0.466
20	rs711752	AA/GA/GG	0.232	1.330	0.016	NA	-0.462	0.460	NA
20	rs708272	AA/GA/GG	0.236	1.288	0.018	NA	-0.595	0.336	NA
20	rs60195610	CC/CT/TT	0.023	2.944	0.052	NA	-0.541	0.757	NA
21	rs711752	AA/GA/GG	0.232	1.330	0.016	0.103	-0.462	0.460	0.358
21	rs708272	AA/GA/GG	0.236	1.288	0.018	NA	-0.595	0.336	NA
21	rs60195610	CC/CT/TT	0.023	2.944	0.052	NA	-0.541	0.757	NA
21	rs9935228	AA/GA/GG	0.091	-0.560	0.479	NA	1.249	0.164	NA
22	rs708272	AA/GA/GG	0.236	1.288	0.018	0.338	-0.595	0.336	0.211
22	rs60195610	CC/CT/TT	0.023	2.944	0.052	NA	-0.541	0.757	NA
22	rs9935228	AA/GA/GG	0.091	-0.560	0.479	NA	1.249	0.164	NA
22	rs1864163	AA/GA/GG	0.278	-0.190	0.720	NA	1.108	0.060	NA
23	rs60195610	CC/CT/TT	0.023	2.944	0.052	0.340	-0.541	0.757	0.196
23	rs9935228	AA/GA/GG	0.091	-0.560	0.479	NA	1.249	0.164	NA
23	rs1864163	AA/GA/GG	0.278	-0.190	0.720	NA	1.108	0.060	NA
23	rs75313088	AA/GA/GG	0.036	-1.398	0.249	NA	0.545	0.691	NA
24	rs9935228	AA/GA/GG	0.091	-0.560	0.479	0.293	1.249	0.164	0.543
24	rs1864163	AA/GA/GG	0.278	-0.190	0.720	NA	1.108	0.060	NA
24	rs75313088	AA/GA/GG	0.036	-1.398	0.249	NA	0.545	0.691	NA
24	rs5817083	DD/WD/WW	0.393	-0.133	0.788	NA	-0.458	0.415	NA
25	rs1864163	AA/GA/GG	0.278	-0.190	0.720	0.428	1.108	0.060	0.363
25	rs75313088	AA/GA/GG	0.036	-1.398	0.249	NA	0.545	0.691	NA
25	rs5817083	DD/WD/WW	0.393	-0.133	0.788	NA	-0.458	0.415	NA
25	rs4369653	AA/AG/GG	0.212	0.104	0.861	NA	0.483	0.470	NA
26	rs75313088	AA/GA/GG	0.036	-1.398	0.249	0.902	0.545	0.691	0.296
26	rs5817083	DD/WD/WW	0.393	-0.133	0.788	NA	-0.458	0.415	NA
26	rs4369653	AA/AG/GG	0.212	0.104	0.861	NA	0.483	0.470	NA
26	rs7194225	CC/CG/GG	0.185	-0.234	0.699	NA	-0.173	0.799	NA
27	rs5817083	DD/WD/WW	0.393	-0.133	0.788	0.991	-0.458	0.415	0.200
27	rs4369653	AA/AG/GG	0.212	0.104	0.861	NA	0.483	0.470	NA
27	rs7194225	CC/CG/GG	0.185	-0.234	0.699	NA	-0.173	0.799	NA
27	rs114908369	CA/CC	0.025	-0.467	0.758	NA	0.932	0.587	NA
28	rs4369653	AA/AG/GG	0.212	0.104	0.861	0.974	0.483	0.470	0.260
28	rs7194225	CC/CG/GG	0.185	-0.234	0.699	NA	-0.173	0.799	NA
28	rs114908369	CA/CC	0.025	-0.467	0.758	NA	0.932	0.587	NA
28	rs9929488	CC/GC/GG	0.463	-0.291	0.537	NA	0.095	0.860	NA
29	rs7194225	CC/CG/GG	0.185	-0.234	0.699	0.769	-0.173	0.799	0.027
29	rs114908369	CA/CC	0.025	-0.467	0.758	NA	0.932	0.587	NA
29	rs9929488	CC/GC/GG	0.463	-0.291	0.537	NA	0.095	0.860	NA
29	rs12720906	GG/GT/TT	0.034	-1.212	0.332	NA	-1.324	0.345	NA
30	rs114908369	CA/CC	0.025	-0.467	0.758	0.748	0.932	0.587	0.173
30	rs9929488	CC/GC/GG	0.463	-0.291	0.537	NA	0.095	0.860	NA
30	rs12720906	GG/GT/TT	0.034	-1.212	0.332	NA	-1.324	0.345	NA
30	rs12720926	AA/AG	0.027	-0.450	0.759	NA	-3.733	0.026	NA
31	rs9929488	CC/GC/GG	0.463	-0.291	0.537	0.701	0.095	0.860	0.138
31	rs12720906	GG/GT/TT	0.034	-1.212	0.332	NA	-1.324	0.345	NA
31	rs12720926	AA/AG	0.027	-0.450	0.759	NA	-3.733	0.026	NA
31	rs17237939	CC/CT/TT	0.049	-0.107	0.921	NA	1.306	0.296	NA
32	rs12720906	GG/GT/TT	0.034	-1.212	0.332	0.871	-1.324	0.345	0.137
32	rs12720926	AA/AG	0.027	-0.450	0.759	NA	-3.733	0.026	NA
32	rs17237939	CC/CT/TT	0.049	-0.107	0.921	NA	1.306	0.296	NA
32	rs35585922	DD/WD/WW	0.149	-0.055	0.935	NA	-0.005	0.995	NA
33	rs12720926	AA/AG	0.027	-0.450	0.759	0.878	-3.733	0.026	0.151
33	rs17237939	CC/CT/TT	0.049	-0.107	0.921	NA	1.306	0.296	NA
33	rs35585922	DD/WD/WW	0.149	-0.055	0.935	NA	-0.005	0.995	NA
33	rs7203984	AA/CA/CC	0.438	-0.579	0.234	NA	0.236	0.666	NA
34	rs17237939	CC/CT/TT	0.049	-0.107	0.921	0.898	1.306	0.296	0.189
34	rs35585922	DD/WD/WW	0.149	-0.055	0.935	NA	-0.005	0.995	NA
34	rs7203984	AA/CA/CC	0.438	-0.579	0.234	NA	0.236	0.666	NA
34	rs11508026	AA/AG	0.027	-0.384	0.794	NA	-3.492	0.038	NA
35	rs35585922	DD/WD/WW	0.149	-0.055	0.935	0.880	-0.005	0.995	0.056
35	rs7203984	AA/CA/CC	0.438	-0.579	0.234	NA	0.236	0.666	NA
35	rs11508026	AA/AG	0.027	-0.384	0.794	NA	-3.492	0.038	NA
35	rs80296794	TC/TT	0.021	-0.573	0.729	NA	3.934	0.041	NA
36	rs7203984	AA/CA/CC	0.438	-0.579	0.234	0.687	0.236	0.666	0.058
36	rs11508026	AA/AG	0.027	-0.384	0.794	NA	-3.492	0.038	NA

Table B1.28. Continued

				ApoA1			ApoB		
wind	**Winow SNP**	**Genotype**	**MAF**	**Beta**	***P***	**Hap_P**	**Beta**	***P***	**Hap_P**
36	rs80296794	TC/TT	0.021	-0.573	0.729	NA	3.934	0.041	NA
36	rs112236143	CA/CC	0.020	1.760	0.310	NA	-0.494	0.807	NA
37	rs11508026	AA/AG	0.027	-0.384	0.794	0.849	-3.492	0.038	0.167
37	rs80296794	TC/TT	0.021	-0.573	0.729	NA	3.934	0.041	NA
37	rs112236143	CA/CC	0.020	1.760	0.310	NA	-0.494	0.807	NA
37	rs708273	AA/AG/GG	0.100	-0.252	0.750	NA	0.033	0.970	NA
38	rs80296794	TC/TT	0.021	-0.573	0.729	0.759	3.934	0.041	0.600
38	rs112236143	CA/CC	0.020	1.760	0.310	NA	-0.494	0.807	NA
38	rs708273	AA/AG/GG	0.100	-0.252	0.750	NA	0.033	0.970	NA
38	rs17231583	CC/GC/GG	0.020	-1.320	0.399	NA	-0.330	0.851	NA
39	rs112236143	CA/CC	0.020	1.760	0.310	0.364	-0.494	0.807	0.435
39	rs708273	AA/AG/GG	0.100	-0.252	0.750	NA	0.033	0.970	NA
39	rs17231583	CC/GC/GG	0.020	-1.320	0.399	NA	-0.330	0.851	NA
39	rs142058276	II/WI/WW	0.082	1.682	0.057	NA	-2.129	0.034	NA
40	rs708273	AA/AG/GG	0.100	-0.252	0.750	0.470	0.033	0.970	0.365
40	rs17231583	CC/GC/GG	0.020	-1.320	0.399	NA	-0.330	0.851	NA
40	rs142058276	II/WI/WW	0.082	1.682	0.057	NA	-2.129	0.034	NA
40	rs17231590	AA/AG/GG	0.058	-0.096	0.923	NA	0.709	0.533	NA
41	rs17231583	CC/GC/GG	0.020	-1.320	0.399	0.247	-0.330	0.851	0.231
41	rs142058276	II/WI/WW	0.082	1.682	0.057	NA	-2.129	0.034	NA
41	rs17231590	AA/AG/GG	0.058	-0.096	0.923	NA	0.709	0.533	NA
41	rs17237953	GG/GT/TT	0.039	0.974	0.411	NA	1.557	0.263	NA
42	rs142058276	II/WI/WW	0.082	1.682	0.057	0.302	-2.129	0.034	0.156
42	rs17231590	AA/AG/GG	0.058	-0.096	0.923	NA	0.709	0.533	NA
42	rs17237953	GG/GT/TT	0.039	0.974	0.411	NA	1.557	0.263	NA
42	rs35619327	CC/TC	0.023	1.557	0.325	NA	-1.446	0.431	NA
43	rs17231590	AA/AG/GG	0.058	-0.096	0.923	0.780	0.709	0.533	0.367
43	rs17237953	GG/GT/TT	0.039	0.974	0.411	NA	1.557	0.263	NA
43	rs35619327	CC/TC	0.023	1.557	0.325	NA	-1.446	0.431	NA
43	rs820299	AA/AG/GG	0.495	-0.035	0.942	NA	0.901	0.099	NA
44	rs17237953	GG/GT/TT	0.039	0.974	0.411	0.672	1.557	0.263	0.120
44	rs35619327	CC/TC	0.023	1.557	0.325	NA	-1.446	0.431	NA
44	rs820299	AA/AG/GG	0.495	-0.035	0.942	NA	0.901	0.099	NA
44	rs17237967	AA/GA/GG	0.035	-1.079	0.389	NA	2.448	0.088	NA
45	rs35619327	CC/TC	0.023	1.557	0.325	0.123	-1.446	0.431	0.124
45	rs820299	AA/AG/GG	0.495	-0.035	0.942	NA	0.901	0.099	NA
45	rs17237967	AA/GA/GG	0.035	-1.079	0.389	NA	2.448	0.088	NA
45	rs8045855	AA/AT/TT	0.423	0.415	0.390	NA	-0.176	0.748	NA
46	rs820299	AA/AG/GG	0.495	-0.035	0.942	0.552	0.901	0.099	0.086
46	rs17237967	AA/GA/GG	0.035	-1.079	0.389	NA	2.448	0.088	NA
46	rs8045855	AA/AT/TT	0.423	0.415	0.390	NA	-0.176	0.748	NA
46	rs12720922	AA/GA/GG	0.352	0.135	0.788	NA	-0.427	0.453	NA
47	rs17237967	AA/GA/GG	0.035	-1.079	0.389	0.050	2.448	0.088	0.393
47	rs8045855	AA/AT/TT	0.423	0.415	0.390	NA	-0.176	0.748	NA
47	rs12720922	AA/GA/GG	0.352	0.135	0.788	NA	-0.427	0.453	NA
47	rs12708969	AA/CA/CC	0.106	-0.513	0.499	NA	0.509	0.564	NA
48	rs8045855	AA/AT/TT	0.423	0.415	0.390	0.076	-0.176	0.748	0.200
48	rs12720922	AA/GA/GG	0.352	0.135	0.788	NA	-0.427	0.453	NA
48	rs12708969	AA/CA/CC	0.106	-0.513	0.499	NA	0.509	0.564	NA
48	rs9924087	AA/GA/GG	0.207	0.043	0.938	NA	0.563	0.378	NA
49	rs12720922	AA/GA/GG	0.352	0.135	0.788	0.386	-0.427	0.453	0.778
49	rs12708969	AA/CA/CC	0.106	-0.513	0.499	NA	0.509	0.564	NA
49	rs9924087	AA/GA/GG	0.207	0.043	0.938	NA	0.563	0.378	NA
49	rs12597002	AA/CA/CC	0.097	0.032	0.968	NA	-0.071	0.938	NA
50	rs12708969	AA/CA/CC	0.106	-0.513	0.499	0.939	0.509	0.564	0.671
50	rs9924087	AA/GA/GG	0.207	0.043	0.938	NA	0.563	0.378	NA
50	rs12597002	AA/CA/CC	0.097	0.032	0.968	NA	-0.071	0.938	NA
50	rs12720863	AA/GA/GG	0.023	0.805	0.600	NA	1.651	0.370	NA
51	rs9924087	AA/GA/GG	0.207	0.043	0.938	0.963	0.563	0.378	0.614
51	rs12597002	AA/CA/CC	0.097	0.032	0.968	NA	-0.071	0.938	NA
51	rs12720863	AA/GA/GG	0.023	0.805	0.600	NA	1.651	0.370	NA
51	rs9939224	GG/GT/TT	0.356	0.024	0.962	NA	-0.512	0.368	NA
52	rs12597002	AA/CA/CC	0.097	0.032	0.968	0.692	-0.071	0.938	0.794
52	rs12720863	AA/GA/GG	0.023	0.805	0.600	NA	1.651	0.370	NA
52	rs9939224	GG/GT/TT	0.356	0.024	0.962	NA	-0.512	0.368	NA
52	rs11076174	CC/TC/TT	0.132	-0.931	0.190	NA	-0.085	0.917	NA
53	rs12720863	AA/GA/GG	0.023	0.805	0.600	0.579	1.651	0.370	0.088
53	rs9939224	GG/GT/TT	0.356	0.024	0.962	NA	-0.512	0.368	NA
53	rs11076174	CC/TC/TT	0.132	-0.931	0.190	NA	-0.085	0.917	NA
53	rs13306230	CA/CC	0.001	1.089	0.866	NA	17.408	0.017	NA
54	rs9939224	GG/GT/TT	0.356	0.024	0.962	0.567	-0.512	0.368	0.052
54	rs11076174	CC/TC/TT	0.132	-0.931	0.190	NA	-0.085	0.917	NA
54	rs13306230	CA/CC	0.001	1.089	0.866	NA	17.408	0.017	NA
54	rs12708971	CC/CT/TT	0.019	-0.831	0.608	NA	0.522	0.770	NA

Table B1.28. Continued

				ApoA1			ApoB		
wind	**Winow SNP**	**Genotype**	**MAF**	**Beta**	***P***	**Hap_P**	**Beta**	***P***	**Hap_P**
55	rs11076174	CC/TC/TT	0.132	-0.931	0.190	0.595	-0.085	0.917	0.010
55	rs13306230	CA/CC	0.001	1.089	0.866	NA	17.408	0.017	NA
55	rs12708971	CC/CT/TT	0.019	-0.831	0.608	NA	0.522	0.770	NA
55	rs891141	AA/AC/CC	0.130	0.710	0.298	NA	-1.454	0.062	NA
56	rs13306230	CA/CC	0.001	1.089	0.866	0.514	17.408	0.017	0.001
56	rs12708971	CC/CT/TT	0.019	-0.831	0.608	NA	0.522	0.770	NA
56	rs891141	AA/AC/CC	0.130	0.710	0.298	NA	-1.454	0.062	NA
56	CTPp9841	AG/GG	0.001	-15.630	0.087	NA	24.037	0.020	NA
57	rs12708971	CC/CT/TT	0.019	-0.831	0.608	0.649	0.522	0.770	0.237
57	rs891141	AA/AC/CC	0.130	0.710	0.298	NA	-1.454	0.062	NA
57	CTPp9841	AG/GG	0.001	-15.630	0.087	NA	24.037	0.020	NA
57	rs34716057	AA/GA/GG	0.034	0.215	0.865	NA	0.024	0.987	NA
58	rs891141	AA/AC/CC	0.130	0.710	0.298	0.695	-1.454	0.062	0.175
58	CTPp9841	AG/GG	0.001	-15.630	0.087	NA	24.037	0.020	NA
58	rs34716057	AA/GA/GG	0.034	0.215	0.865	NA	0.024	0.987	NA
58	rs891143	CC/TC/TT	0.090	1.283	0.126	NA	-1.402	0.140	NA
59	CTPp9841	AG/GG	0.001	-15.630	0.087	0.221	24.037	0.020	0.377
59	rs34716057	AA/GA/GG	0.034	0.215	0.865	NA	0.024	0.987	NA
59	rs891143	CC/TC/TT	0.090	1.283	0.126	NA	-1.402	0.140	NA
59	rs12720862	AA/GA/GG	0.112	0.849	0.255	NA	0.999	0.240	NA
60	rs34716057	AA/GA/GG	0.034	0.215	0.865	0.348	0.024	0.987	0.529
60	rs891143	CC/TC/TT	0.090	1.283	0.126	NA	-1.402	0.140	NA
60	rs12720862	AA/GA/GG	0.112	0.849	0.255	NA	0.999	0.240	NA
60	rs7205804	AA/GA/GG	0.097	-0.020	0.980	NA	-0.169	0.848	NA
61	rs891143	CC/TC/TT	0.090	1.283	0.126	0.229	-1.402	0.140	0.398
61	rs12720862	AA/GA/GG	0.112	0.849	0.255	NA	0.999	0.240	NA
61	rs7205804	AA/GA/GG	0.097	-0.020	0.980	NA	-0.169	0.848	NA
61	rs12708973	AA/AG	0.009	-3.181	0.196	NA	-2.643	0.342	NA
62	rs12720862	AA/GA/GG	0.112	0.849	0.255	0.200	0.999	0.240	0.642
62	rs7205804	AA/GA/GG	0.097	-0.020	0.980	NA	-0.169	0.848	NA
62	rs12708973	AA/AG	0.009	-3.181	0.196	NA	-2.643	0.342	NA
62	rs148134355	GA/GG	0.005	-4.747	0.171	NA	2.039	0.603	NA
63	rs7205804	AA/GA/GG	0.097	-0.020	0.980	0.243	-0.169	0.848	0.916
63	rs12708973	AA/AG	0.009	-3.181	0.196	NA	-2.643	0.342	NA
63	rs148134355	GA/GG	0.005	-4.747	0.171	NA	2.039	0.603	NA
63	rs34611098	AG/GG	0.001	2.481	0.701	NA	14.638	0.045	NA
64	rs12708973	AA/AG	0.009	-3.181	0.196	0.213	-2.643	0.342	0.755
64	rs148134355	GA/GG	0.005	-4.747	0.171	NA	2.039	0.603	NA
64	rs34611098	AG/GG	0.001	2.481	0.701	NA	14.638	0.045	NA
64	rs12720925	CC/TC/TT	0.042	-0.818	0.499	NA	1.316	0.329	NA
65	rs148134355	GA/GG	0.005	-4.747	0.171	0.687	2.039	0.603	0.431
65	rs34611098	AG/GG	0.001	2.481	0.701	NA	14.638	0.045	NA
65	rs12720925	CC/TC/TT	0.042	-0.818	0.499	NA	1.316	0.329	NA
65	rs1532624	AA/CA/CC	0.097	-0.254	0.745	NA	-0.186	0.834	NA
66	rs34611098	AG/GG	0.001	2.481	0.701	0.962	14.638	0.045	0.268
66	rs12720925	CC/TC/TT	0.042	-0.818	0.499	NA	1.316	0.329	NA
66	rs1532624	AA/CA/CC	0.097	-0.254	0.745	NA	-0.186	0.834	NA
66	rs12720871	CC/CG/GG	0.066	0.059	0.950	NA	-0.131	0.901	NA
67	rs12720925	CC/TC/TT	0.042	-0.818	0.499	0.701	1.316	0.329	0.485
67	rs1532624	AA/CA/CC	0.097	-0.254	0.745	NA	-0.186	0.834	NA
67	rs12720871	CC/CG/GG	0.066	0.059	0.950	NA	-0.131	0.901	NA
67	rs12720872	CC/TC/TT	0.135	0.934	0.184	NA	1.263	0.118	NA
68	rs1532624	AA/CA/CC	0.097	-0.254	0.745	0.753	-0.186	0.834	0.460
68	rs12720871	CC/CG/GG	0.066	0.059	0.950	NA	-0.131	0.901	NA
68	rs12720872	CC/TC/TT	0.135	0.934	0.184	NA	1.263	0.118	NA
68	rs11076175	AA/AG/GG	0.243	-0.140	0.797	NA	0.471	0.446	NA
69	rs12720871	CC/CG/GG	0.066	0.059	0.950	0.453	-0.131	0.901	0.400
69	rs12720872	CC/TC/TT	0.135	0.934	0.184	NA	1.263	0.118	NA
69	rs11076175	AA/AG/GG	0.243	-0.140	0.797	NA	0.471	0.446	NA
69	rs7499892	CC/CT/TT	0.377	-0.506	0.304	NA	0.438	0.428	NA
70	rs12720872	CC/TC/TT	0.135	0.934	0.184	0.596	1.263	0.118	0.234
70	rs11076175	AA/AG/GG	0.243	-0.140	0.797	NA	0.471	0.446	NA
70	rs7499892	CC/CT/TT	0.377	-0.506	0.304	NA	0.438	0.428	NA
70	rs289713	AA/AT/TT	0.451	-0.519	0.282	NA	0.143	0.786	NA
71	rs11076175	AA/AG/GG	0.243	-0.140	0.797	0.209	0.471	0.446	0.969
71	rs7499892	CC/CT/TT	0.377	-0.506	0.304	NA	0.438	0.428	NA
71	rs289713	AA/AT/TT	0.451	-0.519	0.282	NA	0.143	0.786	NA
71	rs191754368	CC/TC/TT	0.019	2.941	0.073	NA	1.287	0.482	NA
72	rs7499892	CC/CT/TT	0.377	-0.506	0.304	0.313	0.438	0.428	0.846
72	rs289713	AA/AT/TT	0.451	-0.519	0.282	NA	0.143	0.786	NA
72	rs191754368	CC/TC/TT	0.019	2.941	0.073	NA	1.287	0.482	NA
72	rs9930761	CC/CT/TT	0.148	0.400	0.563	NA	0.576	0.447	NA
73	rs289713	AA/AT/TT	0.451	-0.519	0.282	0.411	0.143	0.786	0.389
73	rs191754368	CC/TC/TT	0.019	2.941	0.073	NA	1.287	0.482	NA

Table B1.28. Continued

				ApoA1			**ApoB**		
wind	**Winow SNP**	**Genotype**	**MAF**	**Beta**	***P***	**Hap_P**	**Beta**	***P***	**Hap_P**
73	rs9930761	CC/CT/TT	0.148	0.400	0.563	NA	0.576	0.447	NA
73	rs35878799	CT/TT	0.011	-0.851	0.713	NA	-5.106	0.050	NA
74	rs191754368	CC/TC/TT	0.019	2.941	0.073	0.270	1.287	0.482	0.297
74	rs9930761	CC/CT/TT	0.148	0.400	0.563	NA	0.576	0.447	NA
74	rs35878799	CT/TT	0.011	-0.851	0.713	NA	-5.106	0.050	NA
74	rs5883	CC/TC/TT	0.155	0.233	0.729	NA	0.080	0.916	NA
75	rs9930761	CC/CT/TT	0.148	0.400	0.563	0.197	0.576	0.447	0.190
75	rs35878799	CT/TT	0.011	-0.851	0.713	NA	-5.106	0.050	NA
75	rs5883	CC/TC/TT	0.155	0.233	0.729	NA	0.080	0.916	NA
75	rs11076176	GG/GT/TT	0.403	-0.836	0.086	NA	0.579	0.291	NA
76	rs35878799	CT/TT	0.011	-0.851	0.713	0.532	-5.106	0.050	0.077
76	rs5883	CC/TC/TT	0.155	0.233	0.729	NA	0.080	0.916	NA
76	rs11076176	GG/GT/TT	0.403	-0.836	0.086	NA	0.579	0.291	NA
76	rs289714	AA/GA/GG	0.447	0.530	0.274	NA	0.334	0.541	NA
77	rs5883	CC/TC/TT	0.155	0.233	0.729	0.752	0.080	0.916	0.472
77	rs11076176	GG/GT/TT	0.403	-0.836	0.086	NA	0.579	0.291	NA
77	rs289714	AA/GA/GG	0.447	0.530	0.274	NA	0.334	0.541	NA
77	rs158479	AA/GA/GG	0.325	0.051	0.921	NA	0.486	0.404	NA
78	rs11076176	GG/GT/TT	0.403	-0.836	0.086	0.341	0.579	0.291	0.441
78	rs289714	AA/GA/GG	0.447	0.530	0.274	NA	0.334	0.541	NA
78	rs158479	AA/GA/GG	0.325	0.051	0.921	NA	0.486	0.404	NA
78	rs12720892	AA/GA/GG	0.043	-1.767	0.119	NA	1.631	0.199	NA
79	rs289714	AA/GA/GG	0.447	0.530	0.274	0.204	0.334	0.541	0.729
79	rs158479	AA/GA/GG	0.325	0.051	0.921	NA	0.486	0.404	NA
79	rs12720892	AA/GA/GG	0.043	-1.767	0.119	NA	1.631	0.199	NA
79	rs158480	AA/GA/GG	0.445	0.331	0.492	NA	-0.030	0.957	NA
80	rs158479	AA/GA/GG	0.325	0.051	0.921	0.568	0.486	0.404	0.633
80	rs12720892	AA/GA/GG	0.043	-1.767	0.119	NA	1.631	0.199	NA
80	rs158480	AA/GA/GG	0.445	0.331	0.492	NA	-0.030	0.957	NA
80	CTPp14448del4	WD/WW	0.018	-0.415	0.816	NA	1.180	0.554	NA
81	rs12720892	AA/GA/GG	0.043	-1.767	0.119	0.591	1.631	0.199	0.556
81	rs158480	AA/GA/GG	0.445	0.331	0.492	NA	-0.030	0.957	NA
81	CTPp14448del4	WD/WW	0.018	-0.415	0.816	NA	1.180	0.554	NA
81	rs289715	AA/TA/TT	0.224	0.637	0.267	NA	-0.653	0.314	NA
82	rs158480	AA/GA/GG	0.445	0.331	0.492	0.752	-0.030	0.957	0.681
82	CTPp14448del4	WD/WW	0.018	-0.415	0.816	NA	1.180	0.554	NA
82	rs289715	AA/TA/TT	0.224	0.637	0.267	NA	-0.653	0.314	NA
82	rs2303789	GG/GT/TT	0.065	-1.176	0.226	NA	0.497	0.642	NA
83	CTPp14448del4	WD/WW	0.018	-0.415	0.816	0.626	1.180	0.554	0.724
83	rs289715	AA/TA/TT	0.224	0.637	0.267	NA	-0.653	0.314	NA
83	rs2303789	GG/GT/TT	0.065	-1.176	0.226	NA	0.497	0.642	NA
83	rs289716	AA/AT/TT	0.476	-0.438	0.361	NA	0.038	0.943	NA
84	rs289715	AA/TA/TT	0.224	0.637	0.267	0.671	-0.653	0.314	0.752
84	rs2303789	GG/GT/TT	0.065	-1.176	0.226	NA	0.497	0.642	NA
84	rs289716	AA/AT/TT	0.476	-0.438	0.361	NA	0.038	0.943	NA
84	rs289717	AA/GA/GG	0.147	-0.013	0.985	NA	0.506	0.514	NA
85	rs2303789	GG/GT/TT	0.065	-1.176	0.226	0.748	0.497	0.642	0.768
85	rs289716	AA/AT/TT	0.476	-0.438	0.361	NA	0.038	0.943	NA
85	rs289717	AA/GA/GG	0.147	-0.013	0.985	NA	0.506	0.514	NA
85	rs12708976	CC/TC/TT	0.047	-1.058	0.353	NA	-0.411	0.742	NA
86	rs289716	AA/AT/TT	0.476	-0.438	0.361	0.793	0.038	0.943	0.770
86	rs289717	AA/GA/GG	0.147	-0.013	0.985	NA	0.506	0.514	NA
86	rs12708976	CC/TC/TT	0.047	-1.058	0.353	NA	-0.411	0.742	NA
86	rs12720942	AA/GA/GG	0.066	-1.072	0.265	NA	0.313	0.768	NA
87	rs289717	AA/GA/GG	0.147	-0.013	0.985	0.515	0.506	0.514	0.717
87	rs12708976	CC/TC/TT	0.047	-1.058	0.353	NA	-0.411	0.742	NA
87	rs12720942	AA/GA/GG	0.066	-1.072	0.265	NA	0.313	0.768	NA
87	rs736274	AA/AT/TT	0.016	-2.395	0.180	NA	-1.397	0.491	NA
88	rs12708976	CC/TC/TT	0.047	-1.058	0.353	0.369	-0.411	0.742	0.629
88	rs12720942	AA/GA/GG	0.066	-1.072	0.265	NA	0.313	0.768	NA
88	rs736274	AA/AT/TT	0.016	-2.395	0.180	NA	-1.397	0.491	NA
88	rs12720937	CC/GC/GG	0.066	-1.132	0.247	NA	0.094	0.929	NA
89	rs12720942	AA/GA/GG	0.066	-1.072	0.265	0.258	0.313	0.768	0.907
89	rs736274	AA/AT/TT	0.016	-2.395	0.180	NA	-1.397	0.491	NA
89	rs12720937	CC/GC/GG	0.066	-1.132	0.247	NA	0.094	0.929	NA
89	rs289718	CC/CT/TT	0.438	-0.523	0.272	NA	0.171	0.747	NA
90	rs736274	AA/AT/TT	0.016	-2.395	0.180	0.290	-1.397	0.491	0.930
90	rs12720937	CC/GC/GG	0.066	-1.132	0.247	NA	0.094	0.929	NA
90	rs289718	CC/CT/TT	0.438	-0.523	0.272	NA	0.171	0.747	NA
90	rs289719	AA/GA/GG	0.493	0.665	0.164	NA	-0.176	0.744	NA
91	rs12720937	CC/GC/GG	0.066	-1.132	0.247	0.394	0.094	0.929	0.930
91	rs289718	CC/CT/TT	0.438	-0.523	0.272	NA	0.171	0.747	NA
91	rs289719	AA/GA/GG	0.493	0.665	0.164	NA	-0.176	0.744	NA
91	rs2033254	CC/TC/TT	0.317	-0.442	0.375	NA	-0.097	0.863	NA

Table B1.28. Continued

				ApoA1			ApoB		
wind	**Winow SNP**	**Genotype**	**MAF**	**Beta**	***P***	**Hap_P**	**Beta**	***P***	**Hap_P**
92	rs289718	CC/CT/TT	0.438	-0.523	0.272	0.361	0.171	0.747	0.900
92	rs289719	AA/GA/GG	0.493	0.665	0.164	NA	-0.176	0.744	NA
92	rs2033254	CC/TC/TT	0.317	-0.442	0.375	NA	-0.097	0.863	NA
92	rs112205272	AA/GA/GG	0.063	-1.311	0.184	NA	0.464	0.670	NA
93	rs289719	AA/GA/GG	0.493	0.665	0.164	0.465	-0.176	0.744	0.765
93	rs2033254	CC/TC/TT	0.317	-0.442	0.375	NA	-0.097	0.863	NA
93	rs112205272	AA/GA/GG	0.063	-1.311	0.184	NA	0.464	0.670	NA
93	rs112409939	AA/GA/GG	0.064	-1.162	0.235	NA	-0.043	0.968	NA
94	rs2033254	CC/TC/TT	0.317	-0.442	0.375	0.653	-0.097	0.863	0.951
94	rs112205272	AA/GA/GG	0.063	-1.311	0.184	NA	0.464	0.670	NA
94	rs112409939	AA/GA/GG	0.064	-1.162	0.235	NA	-0.043	0.968	NA
94	rs71387147	GT/TT	0.025	-0.519	0.748	NA	0.624	0.727	NA
95	rs112205272	AA/GA/GG	0.063	-1.311	0.184	0.642	0.464	0.670	0.956
95	rs112409939	AA/GA/GG	0.064	-1.162	0.235	NA	-0.043	0.968	NA
95	rs71387147	GT/TT	0.025	-0.519	0.748	NA	0.624	0.727	NA
95	rs1968905	GG/GT/TT	0.360	0.378	0.456	NA	-0.268	0.639	NA
96	rs112409939	AA/GA/GG	0.064	-1.162	0.235	0.780	-0.043	0.968	0.990
96	rs71387147	GT/TT	0.025	-0.519	0.748	NA	0.624	0.727	NA
96	rs1968905	GG/GT/TT	0.360	0.378	0.456	NA	-0.268	0.639	NA
96	rs12720903	AA/GA/GG	0.068	0.125	0.893	NA	0.031	0.976	NA
97	rs71387147	GT/TT	0.025	-0.519	0.748	0.934	0.624	0.727	0.975
97	rs1968905	GG/GT/TT	0.360	0.378	0.456	NA	-0.268	0.639	NA
97	rs12720903	AA/GA/GG	0.068	0.125	0.893	NA	0.031	0.976	NA
97	rs4784744	AA/GA/GG	0.100	-0.080	0.919	NA	0.667	0.455	NA
98	rs1968905	GG/GT/TT	0.360	0.378	0.456	0.889	-0.268	0.639	0.848
98	rs12720903	AA/GA/GG	0.068	0.125	0.893	NA	0.031	0.976	NA
98	rs4784744	AA/GA/GG	0.100	-0.080	0.919	NA	0.667	0.455	NA
98	rs291044	AA/GA/GG	0.102	-0.118	0.881	NA	0.645	0.467	NA
99	rs12720903	AA/GA/GG	0.068	0.125	0.893	0.739	0.031	0.976	0.861
99	rs4784744	AA/GA/GG	0.100	-0.080	0.919	NA	0.667	0.455	NA
99	rs291044	AA/GA/GG	0.102	-0.118	0.881	NA	0.645	0.467	NA
99	rs114486472	AA/AG/GG	0.020	-1.959	0.229	NA	1.018	0.577	NA
100	rs4784744	AA/GA/GG	0.100	-0.080	0.919	0.375	0.667	0.455	0.888
100	rs291044	AA/GA/GG	0.102	-0.118	0.881	NA	0.645	0.467	NA
100	rs114486472	AA/AG/GG	0.020	-1.959	0.229	NA	1.018	0.577	NA
100	rs34426213	CC/CT/TT	0.042	1.755	0.132	NA	-0.168	0.898	NA
101	rs291044	AA/GA/GG	0.102	-0.118	0.881	0.288	0.645	0.467	0.917
101	rs114486472	AA/AG/GG	0.020	-1.959	0.229	NA	1.018	0.577	NA
101	rs34426213	CC/CT/TT	0.042	1.755	0.132	NA	-0.168	0.898	NA
101	rs891144	AA/GA/GG	0.215	-0.193	0.734	NA	-0.150	0.816	NA
102	rs114486472	AA/AG/GG	0.020	-1.959	0.229	0.314	1.018	0.577	0.955
102	rs34426213	CC/CT/TT	0.042	1.755	0.132	NA	-0.168	0.898	NA
102	rs891144	AA/GA/GG	0.215	-0.193	0.734	NA	-0.150	0.816	NA
102	rs12708979	AA/GA/GG	0.030	1.112	0.402	NA	1.215	0.415	NA
103	rs34426213	CC/CT/TT	0.042	1.755	0.132	0.219	-0.168	0.898	0.264
103	rs891144	AA/GA/GG	0.215	-0.193	0.734	NA	-0.150	0.816	NA
103	rs12708979	AA/GA/GG	0.030	1.112	0.402	NA	1.215	0.415	NA
103	rs12708980	AA/AC/CC	0.342	-0.211	0.668	NA	-0.662	0.236	NA
104	rs891144	AA/GA/GG	0.215	-0.193	0.734	0.690	-0.150	0.816	0.787
104	rs12708979	AA/GA/GG	0.030	1.112	0.402	NA	1.215	0.415	NA
104	rs12708980	AA/AC/CC	0.342	-0.211	0.668	NA	-0.662	0.236	NA
104	rs12720889	AA/AT/TT	0.204	-0.052	0.929	NA	0.174	0.792	NA
105	rs12708979	AA/GA/GG	0.030	1.112	0.402	0.694	1.215	0.415	0.361
105	rs12708980	AA/AC/CC	0.342	-0.211	0.668	NA	-0.662	0.236	NA
105	rs12720889	AA/AT/TT	0.204	-0.052	0.929	NA	0.174	0.792	NA
105	rs291043	AA/AG/GG	0.086	0.324	0.688	NA	0.553	0.543	NA
106	rs12708980	AA/AC/CC	0.342	-0.211	0.668	0.760	-0.662	0.236	0.316
106	rs12720889	AA/AT/TT	0.204	-0.052	0.929	NA	0.174	0.792	NA
106	rs291043	AA/AG/GG	0.086	0.324	0.688	NA	0.553	0.543	NA
106	rs114203109	GA/GG	0.042	-0.681	0.573	NA	-1.978	0.150	NA
107	rs12720889	AA/AT/TT	0.204	-0.052	0.929	0.374	0.174	0.792	0.572
107	rs291043	AA/AG/GG	0.086	0.324	0.688	NA	0.553	0.543	NA
107	rs114203109	GA/GG	0.042	-0.681	0.573	NA	-1.978	0.150	NA
107	rs145189439	CC/TC/TT	0.052	-1.676	0.118	NA	0.827	0.483	NA
108	rs291043	AA/AG/GG	0.086	0.324	0.688	0.608	0.553	0.543	0.589
108	rs114203109	GA/GG	0.042	-0.681	0.573	NA	-1.978	0.150	NA
108	rs145189439	CC/TC/TT	0.052	-1.676	0.118	NA	0.827	0.483	NA
108	rs4784745	AA/AG/GG	0.076	0.105	0.906	NA	0.916	0.357	NA
109	rs114203109	GA/GG	0.042	-0.681	0.573	0.594	-1.978	0.150	0.360
109	rs145189439	CC/TC/TT	0.052	-1.676	0.118	NA	0.827	0.483	NA
109	rs4784745	AA/AG/GG	0.076	0.105	0.906	NA	0.916	0.357	NA
109	rs34855278	GA/GG	0.015	-1.464	0.450	NA	-2.483	0.259	NA
110	rs145189439	CC/TC/TT	0.052	-1.676	0.118	0.316	0.827	0.483	0.555
110	rs4784745	AA/AG/GG	0.076	0.105	0.906	NA	0.916	0.357	NA

Table B1.28. Continued

				ApoA1			ApoB		
wind	**Winow SNP**	**Genotype**	**MAF**	**Beta**	***P***	**Hap_P**	**Beta**	***P***	**Hap_P**
110	rs34855278	GA/GG	0.015	-1.464	0.450	NA	-2.483	0.259	NA
110	rs114948973	AA/AG/GG	0.019	2.161	0.211	NA	1.304	0.502	NA
111	rs4784745	AA/AG/GG	0.076	0.105	0.906	0.124	0.916	0.357	0.633
111	rs34855278	GA/GG	0.015	-1.464	0.450	NA	-2.483	0.259	NA
111	rs114948973	AA/AG/GG	0.019	2.161	0.211	NA	1.304	0.502	NA
111	rs7195984	AA/GA/GG	0.169	1.350	0.031	NA	-0.291	0.679	NA
112	rs34855278	GA/GG	0.015	-1.464	0.450	0.105	-2.483	0.259	0.508
112	rs114948973	AA/AG/GG	0.019	2.161	0.211	NA	1.304	0.502	NA
112	rs7195984	AA/GA/GG	0.169	1.350	0.031	NA	-0.291	0.679	NA
112	rs7196174	GG/GT/TT	0.070	-0.187	0.842	NA	0.828	0.434	NA
113	rs114948973	AA/AG/GG	0.019	2.161	0.211	0.090	1.304	0.502	0.840
113	rs7195984	AA/GA/GG	0.169	1.350	0.031	NA	-0.291	0.679	NA
113	rs7196174	GG/GT/TT	0.070	-0.187	0.842	NA	0.828	0.434	NA
113	rs1800774	CC/TC/TT	0.217	-0.608	0.281	NA	-0.479	0.453	NA
114	rs7195984	AA/GA/GG	0.169	1.350	0.031	0.144	-0.291	0.679	0.692
114	rs7196174	GG/GT/TT	0.070	-0.187	0.842	NA	0.828	0.434	NA
114	rs1800774	CC/TC/TT	0.217	-0.608	0.281	NA	-0.479	0.453	NA
114	rs5882	AA/GA/GG	0.310	-0.134	0.789	NA	0.275	0.626	NA
115	rs7196174	GG/GT/TT	0.070	-0.187	0.842	0.557	0.828	0.434	0.623
115	rs1800774	CC/TC/TT	0.217	-0.608	0.281	NA	-0.479	0.453	NA
115	rs5882	AA/GA/GG	0.310	-0.134	0.789	NA	0.275	0.626	NA
115	rs5886	AA/GA/GG	0.082	-0.457	0.603	NA	0.055	0.955	NA
116	rs1800774	CC/TC/TT	0.217	-0.608	0.281	0.089	-0.479	0.453	0.780
116	rs5882	AA/GA/GG	0.310	-0.134	0.789	NA	0.275	0.626	NA
116	rs5886	AA/GA/GG	0.082	-0.457	0.603	NA	0.055	0.955	NA
116	rs289740	CC/CT/TT	0.117	1.699	0.021	NA	-0.465	0.577	NA
117	rs5882	AA/GA/GG	0.310	-0.134	0.789	0.144	0.275	0.626	0.912
117	rs5886	AA/GA/GG	0.082	-0.457	0.603	NA	0.055	0.955	NA
117	rs289740	CC/CT/TT	0.117	1.699	0.021	NA	-0.465	0.577	NA
117	rs36051594	AA/GA/GG	0.044	0.769	0.484	NA	1.206	0.329	NA
118	rs5886	AA/GA/GG	0.082	-0.457	0.603	0.182	0.055	0.955	0.170
118	rs289740	CC/CT/TT	0.117	1.699	0.021	NA	-0.465	0.577	NA
118	rs36051594	AA/GA/GG	0.044	0.769	0.484	NA	1.206	0.329	NA
118	rs1801706	AA/GA/GG	0.176	0.268	0.660	NA	0.457	0.505	NA
119	rs289740	CC/CT/TT	0.117	1.699	0.021	0.071	-0.465	0.577	0.803
119	rs36051594	AA/GA/GG	0.044	0.769	0.484	NA	1.206	0.329	NA
119	rs1801706	AA/GA/GG	0.176	0.268	0.660	NA	0.457	0.505	NA
119	rs289742	CC/CG/GG	0.421	0.218	0.648	NA	-0.273	0.613	NA
120	rs36051594	AA/GA/GG	0.044	0.769	0.484	0.853	1.206	0.329	0.778
120	rs1801706	AA/GA/GG	0.176	0.268	0.660	NA	0.457	0.505	NA
120	rs289742	CC/CG/GG	0.421	0.218	0.648	NA	-0.273	0.613	NA
120	rs289743	AA/GA/GG	0.315	-0.292	0.553	NA	0.061	0.913	NA
121	rs1801706	AA/GA/GG	0.176	0.268	0.660	0.861	0.457	0.505	0.859
121	rs289742	CC/CG/GG	0.421	0.218	0.648	NA	-0.273	0.613	NA
121	rs289743	AA/GA/GG	0.315	-0.292	0.553	NA	0.061	0.913	NA
121	rs289744	GG/GT/TT	0.306	-0.140	0.781	NA	0.102	0.859	NA
122	rs289742	CC/CG/GG	0.421	0.218	0.648	0.749	-0.273	0.613	0.569
122	rs289743	AA/GA/GG	0.315	-0.292	0.553	NA	0.061	0.913	NA
122	rs289744	GG/GT/TT	0.306	-0.140	0.781	NA	0.102	0.859	NA
122	rs12720875	AA/GA/GG	0.032	1.278	0.328	NA	1.565	0.286	NA
123	rs289743	AA/GA/GG	0.315	-0.292	0.553	0.275	0.061	0.913	0.629
123	rs289744	GG/GT/TT	0.306	-0.140	0.781	NA	0.102	0.859	NA
123	rs12720875	AA/GA/GG	0.032	1.278	0.328	NA	1.565	0.286	NA
123	rs66495554	CC/TC/TT	0.193	-1.077	0.067	NA	-0.713	0.286	NA
124	rs289744	GG/GT/TT	0.306	-0.140	0.781	0.079	0.102	0.859	0.451
124	rs12720875	AA/GA/GG	0.032	1.278	0.328	NA	1.565	0.286	NA
124	rs66495554	CC/TC/TT	0.193	-1.077	0.067	NA	-0.713	0.286	NA
124	rs114646974	AA/AG	0.003	-8.351	0.042	NA	-5.410	0.296	NA
125	rs12720875	AA/GA/GG	0.032	1.278	0.328	0.063	1.565	0.286	0.454
125	rs66495554	CC/TC/TT	0.193	-1.077	0.067	NA	-0.713	0.286	NA
125	rs114646974	AA/AG	0.003	-8.351	0.042	NA	-5.410	0.296	NA
125	rs138161274	CC/GC	0.027	-0.546	0.703	NA	-1.295	0.433	NA
126	rs66495554	CC/TC/TT	0.193	-1.077	0.067	0.114	-0.713	0.286	0.517
126	rs114646974	AA/AG	0.003	-8.351	0.042	NA	-5.410	0.296	NA
126	rs138161274	CC/GC	0.027	-0.546	0.703	NA	-1.295	0.433	NA
126	rs12720874	CC/TC/TT	0.153	-0.085	0.897	NA	-0.789	0.290	NA
127	rs114646974	AA/AG	0.003	-8.351	0.042	0.192	-5.410	0.296	0.577
127	rs138161274	CC/GC	0.027	-0.546	0.703	NA	-1.295	0.433	NA
127	rs12720874	CC/TC/TT	0.153	-0.085	0.897	NA	-0.789	0.290	NA
127	rs12720916	AA/GA/GG	0.025	-2.091	0.152	NA	-0.860	0.603	NA
128	rs138161274	CC/GC	0.027	-0.546	0.703	0.747	-1.295	0.433	0.019
128	rs12720874	CC/TC/TT	0.153	-0.085	0.897	NA	-0.789	0.290	NA
128	rs12720916	AA/GA/GG	0.025	-2.091	0.152	NA	-0.860	0.603	NA
128	rs289745	GG/GT/TT	0.194	0.435	0.459	NA	-0.366	0.577	NA

TABLE B1.29.Summary of CETP 4-SNP sliding haplotypes for HDL-C and TG in African blacks (n=788)

							HDL-C									TG			
Window	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**	**Window**	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**
1	A	A	C	A	0.036	-0.043	0.595	-0.072	0.942	1	A	A	C	A	0.036	0.006	0.022	0.291	0.771
1	A	A	T	A	0.086	0.862	0.452	1.907	0.057	1	A	A	T	A	0.083	0.013	0.016	0.805	0.421
1	A	G	C	A	0.030	-1.281	0.643	-1.990	0.047	1	A	G	C	A	0.032	-0.015	0.023	-0.668	0.504
1	A	G	C	C	0.218	0.370	0.292	1.265	0.206	1	A	G	C	C	0.220	0.009	0.011	0.856	0.393
1	A	G	T	A	0.041	0.642	0.617	1.041	0.298	1	A	G	T	A	0.040	-0.026	0.021	-1.202	0.230
1	G	A	C	C	0.075	-0.929	0.480	-1.936	0.053	1	G	A	C	C	0.070	0.012	0.019	0.625	0.532
1	G	A	T	A	0.106	1.710	0.353	4.848	0.000	1	G	A	T	A	0.110	-0.014	0.013	-1.044	0.297
1	G	G	C	A	0.010	-0.202	1.414	-0.143	0.886	1	G	G	C	A	0.010	0.080	0.058	1.372	0.170
1	G	G	C	C	0.026	0.473	0.776	0.609	0.543	1	G	G	C	C	0.028	0.010	0.028	0.381	0.704
1	G	G	T	A	0.012	-2.263	1.425	-1.588	0.113	1	G	G	T	A	0.011	-0.019	0.054	-0.354	0.724
1	*	*	*	*	0.003	1.015	3.062	0.331	0.740	1	*	*	*	*	0.003	-0.077	0.129	-0.596	0.552
1	A	A	C	C	0.357	NA	NA	NA	NA	1	A	A	C	C	0.358	NA	NA	NA	NA
2	A	C	A	A	0.039	0.275	0.567	0.485	0.628	2	A	C	A	A	0.039	0.006	0.021	0.273	0.785
2	A	T	A	A	0.168	1.287	0.314	4.095	0.000	2	A	T	A	A	0.170	-0.005	0.011	-0.474	0.636
2	A	T	A	G	0.021	2.428	0.638	3.803	0.000	2	A	T	A	G	0.021	0.008	0.025	0.308	0.758
2	G	C	A	A	0.040	-1.081	0.541	-1.998	0.046	2	G	C	A	A	0.041	-0.002	0.020	-0.117	0.907
2	G	C	C	A	0.243	0.520	0.278	1.872	0.062	2	G	C	C	A	0.246	0.009	0.010	0.893	0.372
2	G	T	A	A	0.056	0.447	0.533	0.839	0.402	2	G	T	A	A	0.054	-0.024	0.019	-1.316	0.188
2	A	C	C	A	0.433	NA	NA	NA	NA	2	A	C	C	A	0.430	NA	NA	NA	NA
3	C	A	A	C	0.063	-0.471	0.421	-1.118	0.264	3	C	A	A	C	0.064	0.001	0.015	0.078	0.938
3	C	A	A	T	0.016	-1.189	0.789	-1.506	0.133	3	C	A	A	T	0.016	0.003	0.031	0.084	0.933
3	C	C	A	C	0.165	0.226	0.272	0.832	0.406	3	C	C	A	C	0.165	0.005	0.010	0.498	0.619
3	T	A	A	T	0.223	0.949	0.237	4.009	0.000	3	T	A	A	T	0.222	-0.010	0.009	-1.112	0.267
3	T	A	G	T	0.021	2.298	0.641	3.586	0.000	3	T	A	G	T	0.021	0.006	0.025	0.238	0.812
3	*	*	*	*	0.001	2.434	3.815	0.638	0.524	3	*	*	*	*	0.001	-0.287	0.115	-2.489	0.013
3	C	C	A	T	0.510	NA	NA	NA	NA	3	C	C	A	T	0.510	NA	NA	NA	NA
4	A	A	C	C	0.064	-0.393	0.453	-0.867	0.386	4	A	A	C	C	0.065	-0.008	0.017	-0.501	0.616
4	A	A	T	C	0.134	1.043	0.316	3.299	0.001	4	A	A	T	C	0.134	-0.002	0.012	-0.157	0.876
4	A	A	T	T	0.104	0.446	0.320	1.396	0.163	4	A	A	T	T	0.103	-0.015	0.012	-1.265	0.206
4	A	G	T	C	0.021	2.274	0.646	3.518	0.000	4	A	G	T	C	0.021	0.008	0.025	0.306	0.760
4	C	A	C	C	0.162	0.229	0.292	0.786	0.432	4	C	A	C	C	0.161	0.008	0.011	0.682	0.495
4	C	A	T	C	0.516	NA	NA	NA	NA	4	C	A	T	C	0.516	NA	NA	NA	NA
5	A	C	C	C	0.063	-0.495	0.403	-1.227	0.220	5	A	C	C	C	0.065	-0.009	0.015	-0.579	0.563
5	A	C	C	T	0.168	-0.043	0.261	-0.164	0.870	5	A	C	C	T	0.167	0.006	0.010	0.594	0.553
5	A	T	T	T	0.103	0.307	0.318	0.966	0.334	5	A	T	T	T	0.103	-0.016	0.012	-1.329	0.184
5	G	T	C	T	0.020	2.185	0.667	3.275	0.001	5	G	T	C	T	0.021	0.007	0.025	0.285	0.775
5	A	T	C	T	0.645	NA	NA	NA	NA	5	A	T	C	T	0.644	NA	NA	NA	NA
6	C	C	C	G	0.062	-0.840	0.418	-2.010	0.045	6	C	C	C	G	0.065	-0.014	0.015	-0.909	0.364
6	C	C	T	G	0.169	-0.401	0.277	-1.446	0.148	6	C	C	T	G	0.169	0.001	0.011	0.077	0.938
6	T	C	T	G	0.315	-0.769	0.229	-3.361	0.001	6	T	C	T	G	0.316	-0.011	0.009	-1.285	0.199
6	T	T	T	A	0.102	-0.063	0.340	-0.186	0.852	6	T	T	T	A	0.102	-0.023	0.013	-1.823	0.069
6	*	*	*	*	0.003	-7.690	0.000	-1.30E+17	0.000	6	*	*	*	*	0.001	0.198	0.000	7.53E+16	0.000
6	T	C	T	A	0.350	NA	NA	NA	NA	6	T	C	T	A	0.347	NA	NA	NA	NA
7	C	C	G	C	0.062	-0.268	0.411	-0.651	0.515	7	C	C	G	C	0.064	-0.008	0.015	-0.540	0.589
7	C	T	A	C	0.331	0.518	0.209	2.478	0.013	7	C	T	A	C	0.328	0.007	0.008	0.883	0.378
7	C	T	A	T	0.021	2.719	0.661	4.113	0.000	7	C	T	A	T	0.021	-0.004	0.024	-0.183	0.855
7	T	T	A	C	0.102	0.506	0.318	1.591	0.112	7	T	T	A	C	0.102	-0.016	0.012	-1.346	0.179
7	*	*	*	*	0.003	-1.581	1.668	-0.947	0.344	7	*	*	*	*	0.003	0.084	NA	NA	NA
7	C	T	G	C	0.481	NA	NA	NA	NA	7	C	T	G	C	0.483	NA	NA	NA	NA
8	C	G	C	C	0.062	-0.828	0.409	-2.022	0.044	8	C	G	C	C	0.064	-0.009	0.015	-0.607	0.544
8	T	A	T	C	0.021	2.205	NA	NA	NA	8	T	A	T	C	0.021	-0.005	0.042	-0.130	0.897
8	T	G	C	C	0.386	-0.603	0.201	-2.992	0.003	8	T	G	C	C	0.387	-0.003	0.008	-0.431	0.667
8	T	G	C	T	0.096	-0.135	0.306	-0.441	0.659	8	T	G	C	T	0.096	0.014	0.013	1.040	0.299
8	*	*	*	*	0.004	-3.196	NA	NA	NA	8	*	*	*	*	0.003	0.060	0.273	0.219	0.827
8	T	A	C	C	0.431	NA	NA	NA	NA	8	T	A	C	C	0.428	NA	NA	NA	NA
9	A	C	C	A	0.030	0.854	0.554	1.542	0.124	9	A	C	C	A	0.029	0.020	0.021	0.915	0.360
9	A	C	C	G	0.401	0.615	0.201	3.068	0.002	9	A	C	C	G	0.399	0.003	0.008	0.357	0.721
9	A	T	C	G	0.021	2.852	NA	NA	NA	9	A	T	C	G	0.021	0.000	0.037	0.006	0.996
9	G	C	T	G	0.096	0.517	0.326	1.587	0.113	9	G	C	T	G	0.096	0.018	0.013	1.359	0.175
9	*	*	*	*	0.004	-2.508	NA	NA	NA	9	*	*	*	*	0.003	0.060	0.213	0.282	0.778

Table B1.29. Continued

						HDL-C									TG			
Window	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**	**Window**	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**
9	G	C	C	G	0.448	NA	NA	NA	NA	9	G	C	C	G	0.452	NA	NA	NA	NA
10	C	C	A	C	0.030	0.620	0.551	1.124	0.261	10	C	C	A	C	0.029	0.019	0.021	0.914	0.361
10	C	C	G	A	0.035	-0.023	0.499	-0.047	0.963	10	C	C	G	A	0.035	0.027	0.019	1.400	0.162
10	C	T	G	C	0.097	0.032	0.319	0.101	0.920	10	C	T	G	C	0.095	0.017	0.012	1.362	0.174
10	T	C	G	C	0.022	2.479	0.655	3.787	0.000	10	T	C	G	C	0.021	-0.010	0.025	-0.416	0.678
10	*	*	*	*	0.002	-3.754	NA	NA	NA	10	*	*	*	*	0.002	0.217	0.124	1.745	0.081
10	C	C	G	C	0.815	NA	NA	NA	NA	10	C	C	G	C	0.817	NA	NA	NA	NA
11	C	A	C	A	0.030	0.264	0.560	0.471	0.638	11	C	A	C	A	0.029	0.019	0.021	0.871	0.384
11	C	G	A	A	0.036	-0.400	0.499	-0.801	0.424	11	C	G	A	A	0.036	0.035	0.018	1.898	0.058
11	C	G	C	C	0.300	-0.643	0.220	-2.923	0.004	11	C	G	C	C	0.302	-0.002	0.008	-0.299	0.765
11	T	G	C	C	0.095	-0.147	0.346	-0.425	0.671	11	T	G	C	C	0.095	0.017	0.013	1.329	0.184
11	*	*	*	*	0.004	-1.996	1.849	-1.079	0.281	11	*	*	*	*	0.003	0.026	0.079	0.329	0.742
11	C	G	C	A	0.535	NA	NA	NA	NA	11	C	G	C	A	0.534	NA	NA	NA	NA
12	A	C	A	G	0.030	0.544	0.553	0.984	0.326	12	A	C	A	G	0.029	0.020	0.021	0.930	0.353
12	G	A	A	G	0.036	-0.109	0.494	-0.221	0.825	12	G	A	A	G	0.036	0.037	0.019	1.996	0.046
12	G	C	A	A	0.090	1.844	0.340	5.426	0.000	12	G	C	A	A	0.089	0.013	0.013	0.954	0.341
12	G	C	C	G	0.396	-0.201	0.204	-0.989	0.323	12	G	C	C	G	0.398	0.004	0.008	0.570	0.569
12	G	C	A	G	0.448	NA	NA	NA	NA	12	G	C	A	G	0.447	NA	NA	NA	NA
13	A	A	G	G	0.036	-0.132	0.492	-0.268	0.789	13	A	A	G	G	0.037	0.035	0.019	1.917	0.056
13	C	A	A	C	0.090	1.869	0.335	5.573	0.000	13	C	A	A	C	0.089	0.007	0.013	0.543	0.587
13	C	C	G	G	0.397	-0.240	0.200	-1.200	0.231	13	C	C	G	G	0.399	0.003	0.008	0.328	0.743
13	C	A	G	G	0.477	NA	NA	NA	NA	13	C	A	G	G	0.475	NA	NA	NA	NA
14	A	A	C	C	0.088	1.789	0.343	5.209	0.000	14	A	A	C	C	0.088	0.005	0.013	0.383	0.702
14	A	G	G	A	0.063	-0.761	0.407	-1.871	0.062	14	A	G	G	A	0.065	-0.003	0.015	-0.170	0.865
14	C	G	G	C	0.397	-0.317	0.202	-1.571	0.117	14	C	G	G	C	0.399	-0.001	0.008	-0.114	0.910
14	*	*	*	*	0.002	1.385	3.911	0.354	0.723	14	*	*	*	*	0.002	-0.022	0.120	-0.187	0.852
14	A	G	G	C	0.449	NA	NA	NA	NA	14	A	G	G	C	0.446	NA	NA	NA	NA
15	A	C	C	C	0.088	2.019	0.348	5.800	0.000	15	A	C	C	C	0.086	0.002	0.013	0.151	0.880
15	G	G	A	C	0.063	-0.541	0.426	-1.271	0.204	15	G	G	A	C	0.064	-0.006	0.015	-0.423	0.672
15	G	G	C	A	0.020	0.711	0.646	1.102	0.271	15	G	G	C	A	0.019	-0.036	0.025	-1.418	0.157
15	*	*	*	*	0.003	-0.494	16.822	-0.029	0.977	15	*	*	*	*	0.004	0.053	0.106	0.497	0.620
15	G	G	C	C	0.826	NA	NA	NA	NA	15	G	G	C	C	0.827	NA	NA	NA	NA
16	C	C	C	C	0.088	2.104	0.335	6.280	0.000	16	C	C	C	C	0.087	0.010	0.013	0.782	0.434
16	G	A	C	C	0.065	-0.497	0.385	-1.290	0.197	16	G	A	C	C	0.066	-0.002	0.015	-0.106	0.915
16	G	C	A	C	0.020	0.674	0.630	1.069	0.285	16	G	C	A	C	0.020	-0.030	0.025	-1.197	0.232
16	G	C	C	A	0.177	0.363	0.246	1.477	0.140	16	G	C	C	A	0.175	0.014	0.010	1.435	0.152
16	G	C	C	C	0.650	NA	NA	NA	NA	16	G	C	C	C	0.651	NA	NA	NA	NA
17	A	C	C	C	0.065	-0.308	0.404	-0.762	0.446	17	A	C	C	C	0.066	-0.005	0.015	-0.331	0.741
17	C	A	C	T	0.020	0.801	0.647	1.238	0.216	17	C	A	C	T	0.020	-0.033	0.025	-1.350	0.178
17	C	C	A	C	0.176	0.473	0.268	1.764	0.078	17	C	C	A	C	0.173	0.010	0.010	1.030	0.303
17	C	C	C	C	0.364	0.759	0.219	3.464	0.001	17	C	C	C	C	0.363	-0.007	0.008	-0.776	0.438
17	*	*	*	*	0.001	-3.569	3.672	-0.972	0.331	17	*	*	*	*	0.001	-0.247	0.146	-1.692	0.091
17	C	C	C	T	0.374	NA	NA	NA	NA	17	C	C	C	T	0.376	NA	NA	NA	NA
18	A	C	T	G	0.020	0.759	0.645	1.177	0.239	18	A	C	T	G	0.020	-0.033	0.025	-1.327	0.185
18	C	A	C	G	0.177	0.510	0.267	1.912	0.056	18	C	A	C	G	0.174	0.009	0.010	0.890	0.374
18	C	C	C	A	0.234	1.047	0.243	4.312	0.000	18	C	C	C	A	0.231	-0.003	0.009	-0.361	0.718
18	C	C	C	G	0.193	0.081	0.266	0.303	0.762	18	C	C	C	G	0.197	-0.008	0.010	-0.817	0.414
18	C	C	T	G	0.375	NA	NA	NA	NA	18	C	C	T	G	0.377	NA	NA	NA	NA
19	A	C	G	G	0.177	0.460	0.265	1.733	0.083	19	A	C	G	G	0.174	0.010	0.010	1.026	0.305
19	C	C	A	A	0.236	0.987	0.240	4.110	0.000	19	C	C	A	A	0.233	-0.003	0.009	-0.311	0.756
19	C	C	G	G	0.192	0.037	0.264	0.139	0.890	19	C	C	G	G	0.195	-0.007	0.010	-0.678	0.498
19	*	*	*	*	0.002	-3.078	0.000	-8.50E+16	0.000	19	*	*	*	*	0.002	0.003	0.000	2.83E+15	0.000
19	C	T	G	G	0.394	NA	NA	NA	NA	19	C	T	G	G	0.396	NA	NA	NA	NA
20	C	A	A	C	0.214	0.876	0.246	3.564	0.000	20	C	A	A	C	0.211	-0.004	0.009	-0.392	0.695
20	C	A	A	T	0.022	1.974	0.629	3.140	0.002	20	C	A	A	T	0.022	0.008	0.024	0.310	0.757
20	C	G	G	C	0.369	0.237	0.213	1.113	0.266	20	C	G	G	C	0.371	0.002	0.008	0.290	0.772
20	*	*	*	*	0.002	-0.638	NA	NA	NA	20	*	*	*	*	0.002	0.109	0.096	1.135	0.257
20	T	G	G	C	0.394	NA	NA	NA	NA	20	T	G	G	C	0.394	NA	NA	NA	NA
21	A	A	C	A	0.214	0.709	0.226	3.136	0.002	21	A	A	C	A	0.211	-0.006	0.009	-0.653	0.514
21	A	A	T	A	0.021	2.035	0.670	3.040	0.002	21	A	A	T	A	0.020	0.003	0.025	0.109	0.914
21	G	G	C	G	0.089	-0.350	0.327	-1.071	0.284	21	G	G	C	G	0.092	-0.008	0.012	-0.705	0.481
21	*	*	*	*	0.003	-0.975	3.132	-0.311	0.756	21	*	*	*	*	0.003	0.094	0.102	0.922	0.357
21	G	G	C	A	0.673	NA	NA	NA	NA	21	G	G	C	A	0.672	NA	NA	NA	NA
22	A	C	A	A	0.025	-0.524	0.726	-0.721	0.471	22	A	C	A	A	0.024	-0.002	0.028	-0.087	0.931

Table B1.29. Continued

HDL-C										TG									
Window	loc.1	loc.2	loc.3	loc.4	hap.freq	coef	se	t.stat	pval	Window	loc.1	loc.2	loc.3	loc.4	hap.freq	coef	se	t.stat	pval
22	A	C	A	G	0.190	0.666	0.271	2.461	0.014	22	A	C	A	G	0.189	-0.009	0.010	-0.913	0.361
22	A	T	A	G	0.021	1.258	0.709	1.774	0.077	22	A	T	A	G	0.020	0.000	0.025	0.015	0.988
22	G	C	A	A	0.240	-0.539	0.258	-2.086	0.037	22	G	C	A	A	0.241	-0.009	0.010	-0.899	0.369
22	G	C	G	A	0.010	-1.414	1.068	-1.324	0.186	22	G	C	G	A	0.011	-0.049	0.044	-1.099	0.272
22	G	C	G	G	0.081	-0.465	0.355	-1.309	0.191	22	G	C	G	G	0.082	-0.007	0.014	-0.479	0.632
22	*	*	*	*	0.003	4.205	2.175	1.933	0.054	22	*	*	*	*	0.003	0.078	0.094	0.828	0.408
22	G	C	A	G	0.430	NA	NA	NA	NA	22	G	C	A	G	0.430	NA	NA	NA	NA
23	C	A	A	G	0.266	-0.812	0.223	-3.644	0.000	23	C	A	A	G	0.265	-0.004	0.009	-0.429	0.668
23	C	A	G	A	0.035	-0.573	0.498	-1.150	0.251	23	C	A	G	A	0.035	0.024	0.019	1.294	0.196
23	C	G	A	G	0.010	-1.696	1.045	-1.623	0.105	23	C	G	A	G	0.011	-0.041	0.045	-0.907	0.364
23	C	G	G	G	0.080	-0.708	0.350	-2.025	0.043	23	C	G	G	G	0.081	-0.002	0.014	-0.168	0.866
23	T	A	G	G	0.021	0.931	0.680	1.370	0.171	23	T	A	G	G	0.019	-0.002	0.028	-0.084	0.933
23	*	*	*	*	0.002	5.263	2.254	2.335	0.020	23	*	*	*	*	0.004	0.100	0.096	1.038	0.300
23	C	A	G	G	0.585	NA	NA	NA	NA	23	C	A	G	G	0.584	NA	NA	NA	NA
24	A	A	G	W	0.267	-0.590	0.244	-2.412	0.016	24	A	A	G	W	0.266	-0.006	0.010	-0.640	0.522
24	A	G	A	W	0.035	-0.401	0.514	-0.781	0.435	24	A	G	A	W	0.036	0.025	0.019	1.314	0.189
24	A	G	G	W	0.234	0.603	0.256	2.354	0.019	24	A	G	G	W	0.232	-0.009	0.010	-0.938	0.348
24	G	A	G	W	0.011	-1.384	1.010	-1.369	0.171	24	G	A	G	W	0.012	-0.067	0.039	-1.697	0.090
24	G	G	G	D	0.018	0.508	0.779	0.652	0.515	24	G	G	G	D	0.018	0.012	0.032	0.370	0.712
24	G	G	G	W	0.062	-0.943	0.424	-2.221	0.027	24	G	G	G	W	0.063	-0.006	0.016	-0.375	0.708
24	*	*	*	*	0.003	-0.263	1.981	-0.133	0.895	24	*	*	*	*	0.003	0.015	0.078	0.198	0.843
24	A	G	G	D	0.371	NA	NA	NA	NA	24	A	G	G	D	0.370	NA	NA	NA	NA
25	A	G	W	G	0.019	-0.435	0.986	-0.441	0.659	25	A	G	W	G	0.018	-0.025	0.034	-0.716	0.474
25	G	A	W	A	0.035	0.204	0.513	0.397	0.691	25	G	A	W	A	0.036	0.033	0.019	1.729	0.084
25	G	G	D	A	0.253	0.677	0.272	2.490	0.013	25	G	G	D	A	0.251	0.012	0.010	1.142	0.254
25	G	G	D	G	0.136	0.362	0.340	1.064	0.288	25	G	G	D	G	0.137	0.001	0.013	0.082	0.935
25	G	G	W	A	0.238	0.940	0.281	3.343	0.001	25	G	G	W	A	0.239	-0.004	0.010	-0.351	0.726
25	G	G	W	G	0.057	0.355	0.526	0.675	0.500	25	G	G	W	G	0.056	0.014	0.018	0.770	0.441
25	*	*	*	*	0.003	0.192	2.414	0.079	0.937	25	*	*	*	*	0.003	0.025	0.112	0.223	0.823
25	A	G	W	A	0.259	NA	NA	NA	NA	25	A	G	W	A	0.259	NA	NA	NA	NA
26	A	W	A	G	0.034	-0.278	0.507	-0.549	0.583	26	A	W	A	G	0.035	0.032	0.019	1.750	0.081
26	G	D	A	C	0.181	0.262	0.260	1.010	0.313	26	G	D	A	C	0.179	0.014	0.010	1.470	0.142
26	G	D	A	G	0.070	-0.158	0.414	-0.383	0.702	26	G	D	A	G	0.071	0.008	0.015	0.525	0.600
26	G	D	G	G	0.136	0.062	0.302	0.204	0.838	26	G	D	G	G	0.137	0.005	0.011	0.405	0.685
26	G	W	G	G	0.075	-0.460	0.396	-1.160	0.246	26	G	W	G	G	0.074	0.002	0.015	0.117	0.907
26	*	*	*	*	0.008	0.604	1.194	0.506	0.613	26	*	*	*	*	0.008	0.057	0.044	1.311	0.190
26	G	W	A	G	0.496	NA	NA	NA	NA	26	G	W	A	G	0.497	NA	NA	NA	NA
27	D	A	C	C	0.182	0.274	0.260	1.054	0.292	27	D	A	C	C	0.179	0.010	0.010	1.015	0.311
27	D	A	G	C	0.070	-0.153	0.413	-0.370	0.712	27	D	A	G	C	0.071	0.003	0.015	0.192	0.848
27	D	G	G	C	0.136	0.056	0.302	0.185	0.853	27	D	G	G	C	0.136	-0.001	0.011	-0.132	0.895
27	W	A	G	A	0.026	-0.508	0.610	-0.832	0.405	27	W	A	G	A	0.025	-0.065	0.023	-2.841	0.005
27	W	G	G	C	0.076	-0.427	0.395	-1.080	0.281	27	W	G	G	C	0.074	-0.004	0.015	-0.265	0.791
27	*	*	*	*	0.007	0.292	1.199	0.244	0.808	27	*	*	*	*	0.007	0.046	0.044	1.042	0.298
27	W	A	G	C	0.504	NA	NA	NA	NA	27	W	A	G	C	0.506	NA	NA	NA	NA
28	A	C	C	C	0.185	0.021	0.273	0.075	0.940	28	A	C	C	C	0.183	0.012	0.010	1.206	0.228
28	A	G	A	C	0.026	-0.764	0.614	-1.244	0.214	28	A	G	A	C	0.026	-0.064	0.023	-2.763	0.006
28	A	G	C	C	0.251	-0.665	0.251	-2.646	0.008	28	A	G	C	C	0.250	0.003	0.009	0.282	0.778
28	G	G	C	G	0.210	-0.449	0.272	-1.652	0.099	28	G	G	C	G	0.210	-0.001	0.010	-0.132	0.895
28	*	*	*	*	0.004	0.532	2.328	0.228	0.819	28	*	*	*	*	0.004	0.052	0.093	0.562	0.574
28	A	G	C	G	0.324	NA	NA	NA	NA	28	A	G	C	G	0.328	NA	NA	NA	NA
29	C	C	C	T	0.184	0.146	0.259	0.563	0.574	29	C	C	C	T	0.182	0.014	0.010	1.501	0.134
29	G	A	C	T	0.026	-0.640	0.612	-1.046	0.296	29	G	A	C	T	0.026	-0.061	0.023	-2.666	0.008
29	G	C	C	T	0.252	-0.546	0.235	-2.317	0.021	29	G	C	C	T	0.252	0.005	0.009	0.609	0.543
29	G	C	G	G	0.033	-0.547	0.521	-1.050	0.294	29	G	C	G	G	0.034	0.029	0.019	1.554	0.121
29	*	*	*	*	0.002	0.075	2.614	0.029	0.977	29	*	*	*	*	0.002	0.150	0.092	1.630	0.103
29	G	C	G	T	0.502	NA	NA	NA	NA	29	G	C	G	T	0.504	NA	NA	NA	NA
30	A	C	T	A	0.026	-0.698	0.614	-1.138	0.255	30	A	C	T	A	0.025	-0.062	0.023	-2.703	0.007
30	C	C	T	A	0.438	-0.299	0.199	-1.504	0.133	30	C	C	T	A	0.435	0.009	0.007	1.237	0.216
30	C	G	G	A	0.033	-0.598	0.523	-1.142	0.254	30	C	G	G	A	0.034	0.029	0.019	1.510	0.131
30	C	G	T	G	0.026	-0.712	0.605	-1.176	0.240	30	C	G	T	G	0.025	-0.013	0.023	-0.569	0.570
30	C	G	T	A	0.477	NA	NA	NA	NA	30	C	G	T	A	0.480	NA	NA	NA	NA
31	G	G	A	C	0.033	-0.242	0.517	-0.468	0.640	31	G	G	A	C	0.034	0.025	0.019	1.314	0.189
31	G	T	A	C	0.429	0.399	0.203	1.972	0.049	31	G	T	A	C	0.431	-0.005	0.008	-0.654	0.514
31	G	T	A	T	0.046	-0.184	0.448	-0.411	0.681	31	G	T	A	T	0.047	-0.011	0.017	-0.633	0.527

Table B1.29. Continued

HDL-C										TG									
Window	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**	**Window**	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**
31	G	T	G	C	0.026	-0.399	0.603	-0.662	0.508	31	G	T	G	C	0.025	-0.017	0.023	-0.743	0.458
31	C	T	A	C	0.465	NA	NA	NA	NA	31	C	T	A	C	0.462	NA	NA	NA	NA
32	G	A	C	W	0.031	-0.389	0.531	-0.733	0.464	32	G	A	C	W	0.033	0.030	0.019	1.548	0.122
32	T	A	C	D	0.148	0.229	0.268	0.857	0.392	32	T	A	C	D	0.145	0.011	0.010	1.119	0.263
32	T	A	T	W	0.045	-0.343	0.452	-0.758	0.449	32	T	A	T	W	0.046	-0.004	0.017	-0.236	0.814
32	T	G	C	W	0.026	-0.527	0.603	-0.874	0.382	32	T	G	C	W	0.025	-0.011	0.023	-0.489	0.625
32	*	*	*	*	0.002	0.254	2.422	0.105	0.917	32	*	*	*	*	0.002	-0.007	0.118	-0.059	0.953
32	T	A	C	W	0.747	NA	NA	NA	NA	32	T	A	C	W	0.750	NA	NA	NA	NA
33	A	C	D	A	0.151	0.247	0.274	0.904	0.366	33	A	C	D	A	0.148	0.007	0.010	0.644	0.520
33	A	C	W	A	0.261	-0.278	0.231	-1.202	0.230	33	A	C	W	A	0.264	-0.004	0.009	-0.510	0.610
33	A	T	W	C	0.047	-0.346	0.444	-0.778	0.437	33	A	T	W	C	0.047	-0.006	0.017	-0.344	0.731
33	G	C	W	A	0.026	-0.444	0.617	-0.720	0.472	33	G	C	W	A	0.023	-0.044	0.027	-1.662	0.097
33	A	C	W	C	0.515	NA	NA	NA	NA	33	*	*	*	*	0.002	0.242	0.088	2.756	0.006
34	C	D	A	A	0.151	0.243	0.274	0.885	0.376	33	A	C	W	C	0.515	NA	NA	NA	NA
34	C	W	A	A	0.261	-0.250	0.232	-1.078	0.281	34	C	D	A	A	0.148	0.007	0.010	0.698	0.485
34	C	W	A	G	0.026	-0.629	0.618	-1.018	0.309	34	C	W	A	A	0.264	-0.004	0.009	-0.425	0.671
34	T	W	C	A	0.047	-0.355	0.445	-0.797	0.426	34	C	W	A	G	0.023	-0.050	0.026	-1.903	0.057
34	C	W	C	A	0.515	NA	NA	NA	NA	34	T	W	C	A	0.047	-0.006	0.017	-0.350	0.726
35	D	A	A	T	0.151	0.252	0.273	0.924	0.356	34	*	*	*	*	0.003	0.251	0.082	3.074	0.002
35	W	A	A	T	0.261	-0.235	0.231	-1.017	0.309	34	C	W	C	A	0.515	NA	NA	NA	NA
35	W	A	G	T	0.026	-0.610	0.616	-0.990	0.323	35	D	A	A	T	0.148	0.009	0.010	0.866	0.387
35	W	C	A	C	0.020	-0.547	0.692	-0.792	0.429	35	W	A	A	T	0.264	-0.003	0.009	-0.307	0.759
35	W	C	A	T	0.542	NA	NA	NA	NA	35	W	A	G	T	0.023	-0.047	0.026	-1.794	0.073
36	A	A	T	C	0.412	-0.092	0.198	-0.466	0.641	35	W	C	A	C	0.021	0.027	0.025	1.077	0.282
36	A	G	T	C	0.026	-0.816	0.610	-1.339	0.181	35	*	*	*	*	0.003	0.254	0.083	3.073	0.002
36	C	A	C	C	0.020	-0.650	0.692	-0.939	0.348	35	W	C	A	T	0.541	NA	NA	NA	NA
36	C	A	T	A	0.018	-0.915	0.726	-1.261	0.208	36	A	A	T	C	0.411	0.001	0.007	0.197	0.844
36	C	A	T	C	0.523	NA	NA	NA	NA	36	A	G	T	C	0.025	-0.027	0.024	-1.130	0.259
37	A	C	C	G	0.018	-0.578	0.734	-0.787	0.432	36	C	A	C	C	0.021	0.025	0.025	1.013	0.311
37	A	T	A	G	0.017	-0.749	0.805	-0.931	0.352	36	C	A	T	A	0.020	0.005	0.027	0.205	0.838
37	A	T	C	A	0.097	-0.342	0.325	-1.053	0.293	36	C	A	T	C	0.523	NA	NA	NA	NA
37	G	T	C	G	0.026	-0.809	0.601	-1.347	0.179	37	A	C	C	G	0.019	0.034	0.027	1.256	0.210
37	*	*	*	*	0.004	-2.192	2.130	-1.029	0.304	37	A	T	A	G	0.018	0.026	0.028	0.914	0.361
37	A	T	C	G	0.839	NA	NA	NA	NA	37	A	T	C	A	0.096	0.008	0.012	0.622	0.534
38	C	C	G	G	0.017	-0.526	0.748	-0.703	0.482	37	G	T	C	G	0.025	-0.018	0.023	-0.779	0.436
38	T	A	G	G	0.017	-0.760	0.810	-0.938	0.348	37	*	*	*	*	0.004	-0.076	0.067	-1.123	0.262
38	T	C	A	G	0.095	-0.319	0.332	-0.961	0.337	37	A	T	C	G	0.837	NA	NA	NA	NA
38	T	C	G	C	0.017	-0.525	0.725	-0.725	0.469	38	C	C	G	G	0.019	0.035	0.027	1.315	0.189
38	*	*	*	*	0.006	-1.572	1.938	-0.811	0.418	38	T	A	G	G	0.018	0.028	0.028	0.989	0.323
38	T	C	G	G	0.849	NA	NA	NA	NA	38	T	C	A	G	0.096	0.010	0.012	0.778	0.437
39	A	G	G	W	0.016	-0.603	0.892	-0.676	0.500	38	T	C	G	C	0.020	0.050	0.024	2.070	0.039
39	C	A	G	W	0.097	-0.184	0.336	-0.547	0.585	38	*	*	*	*	0.005	-0.070	0.066	-1.058	0.290
39	C	G	C	W	0.017	-0.382	0.723	-0.529	0.597	38	T	C	G	G	0.842	NA	NA	NA	NA
39	C	G	G	I	0.081	1.619	0.355	4.560	0.000	39	A	G	G	W	0.017	0.039	0.031	1.281	0.200
39	*	*	*	*	0.004	-1.626	4.478	-0.363	0.717	39	C	A	G	W	0.098	0.008	0.012	0.653	0.514
39	C	G	G	W	0.784	NA	NA	NA	NA	39	C	G	C	W	0.020	0.050	0.024	2.098	0.036
40	A	G	W	A	0.096	-0.172	0.329	-0.522	0.602	39	C	G	G	I	0.082	0.003	0.013	0.233	0.816
40	G	C	W	A	0.016	-0.433	0.727	-0.596	0.551	39	*	*	*	*	0.003	-0.123	0.081	-1.519	0.129
40	G	G	I	A	0.082	1.612	0.355	4.534	0.000	39	C	G	G	W	0.780	NA	NA	NA	NA
40	G	G	W	G	0.053	-0.027	0.422	-0.065	0.948	40	A	G	W	A	0.097	0.005	0.013	0.376	0.707
40	*	*	*	*	0.005	-1.014	2.158	-0.470	0.638	40	G	C	W	A	0.019	0.046	0.025	1.856	0.064
40	G	G	W	A	0.748	NA	NA	NA	NA	40	G	G	I	A	0.083	0.000	0.013	-0.026	0.979
41	C	W	A	G	0.018	-0.359	0.672	-0.535	0.593	40	G	G	W	G	0.055	-0.009	0.016	-0.541	0.589
41	G	I	A	G	0.082	1.679	0.356	4.719	0.000	40	*	*	*	*	0.003	0.008	0.175	0.044	0.965
41	G	W	A	T	0.040	0.558	0.467	1.195	0.232	40	G	G	W	A	0.743	NA	NA	NA	NA
41	G	W	G	G	0.056	-0.074	0.400	-0.185	0.853	41	C	W	A	G	0.020	0.044	0.024	1.868	0.062
41	G	W	A	G	0.804	NA	NA	NA	NA	41	G	I	A	G	0.083	-0.001	0.013	-0.092	0.927
42	I	A	G	C	0.080	1.678	0.359	4.677	0.000	41	G	W	A	T	0.040	-0.001	0.018	-0.065	0.948
42	W	A	G	T	0.020	-0.618	0.697	-0.887	0.375	41	G	W	G	G	0.057	-0.010	0.015	-0.635	0.525
42	W	A	T	C	0.040	0.546	0.468	1.167	0.243	41	G	W	A	G	0.799	NA	NA	NA	NA
42	W	G	G	C	0.057	-0.078	0.397	-0.195	0.845	42	I	A	G	C	0.082	0.000	0.014	-0.005	0.996
42	*	*	*	*	0.002	1.494	2.632	0.568	0.570	42	W	A	G	T	0.023	0.031	0.025	1.211	0.226
42	W	A	G	C	0.801	NA	NA	NA	NA	42	W	A	T	C	0.040	-0.002	0.018	-0.096	0.923
43	A	G	C	A	0.427	-0.085	0.207	-0.411	0.681	42	W	G	G	C	0.057	-0.009	0.015	-0.601	0.548

Table B1.29. Continued

							HDL-C									TG			
Window	loc.1	loc.2	loc.3	loc.4	hap.freq	coef	se	t.stat	pval	Window	loc.1	loc.2	loc.3	loc.4	hap.freq	coef	se	t.stat	pval
43	A	G	T	A	0.022	-0.615	0.669	-0.919	0.358	42	*	*	*	*	0.001	-0.134	0.198	-0.678	0.498
43	A	T	C	G	0.040	0.293	0.483	0.607	0.544	42	W	A	G	C	0.796	NA	NA	NA	NA
43	G	G	C	A	0.057	-0.312	0.413	-0.757	0.449	43	A	G	C	A	0.426	-0.005	0.008	-0.655	0.513
43	A	G	C	G	0.454	NA	NA	NA	NA	43	A	G	T	A	0.024	0.021	0.024	0.867	0.386
44	G	C	A	A	0.035	-0.317	0.507	-0.626	0.531	43	A	T	C	G	0.041	-0.004	0.018	-0.229	0.819
44	G	C	A	G	0.448	-0.101	0.205	-0.492	0.623	43	G	G	C	A	0.057	-0.011	0.015	-0.711	0.477
44	G	T	A	G	0.022	-0.627	0.669	-0.938	0.349	43	A	G	C	G	0.452	NA	NA	NA	NA
44	T	C	G	G	0.040	0.294	0.484	0.607	0.544	44	G	C	A	A	0.035	-0.003	0.019	-0.138	0.890
44	G	C	G	G	0.455	NA	NA	NA	NA	44	G	C	A	G	0.448	-0.006	0.008	-0.821	0.412
45	C	A	A	A	0.036	-0.219	0.544	-0.403	0.687	44	G	T	A	G	0.024	0.021	0.024	0.863	0.389
45	C	A	G	A	0.089	-0.158	0.376	-0.420	0.675	44	T	C	G	G	0.041	-0.004	0.018	-0.223	0.824
45	C	A	G	T	0.353	0.047	0.218	0.216	0.829	44	G	C	G	G	0.453	NA	NA	NA	NA
45	C	G	G	T	0.071	0.691	0.399	1.731	0.084	45	C	A	A	A	0.036	-0.011	0.020	-0.562	0.574
45	T	A	G	A	0.023	-0.560	0.668	-0.838	0.402	45	C	A	G	A	0.090	-0.014	0.014	-0.974	0.330
45	*	*	*	*	0.002	-0.050	2.368	-0.021	0.983	45	C	A	G	T	0.351	-0.005	0.008	-0.606	0.544
45	C	G	G	A	0.427	NA	NA	NA	NA	45	C	G	G	T	0.073	-0.008	0.015	-0.529	0.597
46	A	A	A	G	0.036	-0.286	0.537	-0.532	0.595	45	T	A	G	A	0.024	0.020	0.024	0.831	0.406
46	A	G	A	G	0.112	-0.285	0.329	-0.869	0.385	45	*	*	*	*	0.002	0.088	0.098	0.902	0.367
46	A	G	T	A	0.351	0.073	0.218	0.335	0.737	45	C	G	G	A	0.424	NA	NA	NA	NA
46	G	G	T	G	0.074	0.514	0.371	1.387	0.166	46	A	A	A	G	0.037	-0.011	0.020	-0.558	0.577
46	*	*	*	*	0.002	0.508	2.637	0.193	0.847	46	A	G	A	G	0.114	0.001	0.012	0.078	0.938
46	G	G	A	G	0.424	NA	NA	NA	NA	46	A	G	T	A	0.351	-0.006	0.008	-0.691	0.490
47	A	A	G	C	0.032	-0.667	0.618	-1.079	0.281	46	G	G	T	G	0.075	0.001	0.014	0.064	0.949
47	G	A	G	A	0.073	-0.621	0.410	-1.515	0.130	46	*	*	*	*	0.001	0.114	0.097	1.168	0.243
47	G	T	A	A	0.012	-1.177	1.251	-0.941	0.347	46	G	G	A	G	0.422	NA	NA	NA	NA
47	G	T	A	C	0.338	0.060	0.220	0.272	0.785	47	A	A	G	C	0.033	-0.010	0.022	-0.474	0.635
47	G	T	G	A	0.023	-0.027	0.654	-0.041	0.967	47	G	A	G	A	0.069	0.003	0.016	0.194	0.846
47	G	T	G	C	0.050	0.778	0.452	1.722	0.086	47	G	T	A	A	0.015	-0.065	0.045	-1.445	0.149
47	*	*	*	*	0.003	2.499	2.461	1.015	0.310	47	G	T	A	C	0.336	-0.003	0.008	-0.312	0.755
47	G	A	G	C	0.468	NA	NA	NA	NA	47	G	T	G	A	0.023	0.008	0.030	0.268	0.789
48	A	G	A	G	0.075	-0.637	0.388	-1.642	0.101	47	G	T	G	C	0.051	-0.001	0.019	-0.071	0.944
48	A	G	C	A	0.203	0.340	0.259	1.311	0.190	47	*	*	*	*	0.002	0.094	0.095	0.994	0.321
48	A	G	C	G	0.295	-0.466	0.235	-1.983	0.048	47	G	A	G	C	0.471	NA	NA	NA	NA
48	T	A	A	G	0.011	-1.616	1.111	-1.454	0.146	48	A	G	A	G	0.073	-0.001	0.015	-0.063	0.949
48	T	G	A	G	0.023	-0.056	0.660	-0.084	0.933	48	A	G	C	A	0.201	0.004	0.010	0.426	0.670
48	T	G	C	G	0.051	0.685	0.453	1.512	0.131	48	A	G	C	G	0.299	0.006	0.009	0.628	0.530
48	*	*	*	*	0.001	-2.577	3.668	-0.702	0.483	48	T	A	A	G	0.012	-0.005	0.047	-0.111	0.912
48	T	A	C	G	0.341	NA	NA	NA	NA	48	T	G	A	G	0.023	0.005	0.028	0.169	0.866
49	A	A	G	C	0.012	-1.386	1.051	-1.319	0.187	48	T	G	C	G	0.052	0.005	0.018	0.297	0.766
49	G	A	G	C	0.098	-0.518	0.345	-1.503	0.133	48	*	*	*	*	0.001	0.170	0.121	1.401	0.162
49	G	C	A	C	0.204	0.346	0.261	1.327	0.185	48	T	A	C	G	0.339	NA	NA	NA	NA
49	G	C	G	A	0.097	-0.389	0.353	-1.103	0.271	49	A	A	G	C	0.011	0.018	0.043	0.424	0.672
49	G	C	G	C	0.245	-0.231	0.253	-0.911	0.362	49	G	A	G	C	0.097	-0.002	0.013	-0.144	0.886
49	*	*	*	*	0.001	-2.944	3.985	-0.739	0.460	49	G	C	A	C	0.203	0.006	0.010	0.618	0.537
49	A	C	G	C	0.344	NA	NA	NA	NA	49	G	C	G	A	0.096	0.007	0.013	0.539	0.590
50	A	G	C	A	0.109	-0.474	0.314	-1.509	0.132	49	G	C	G	C	0.250	0.006	0.010	0.652	0.514
50	C	A	C	A	0.204	0.451	0.236	1.908	0.057	49	*	*	*	*	0.002	0.090	0.104	0.868	0.386
50	C	G	A	A	0.097	-0.286	0.342	-0.838	0.403	49	A	C	G	C	0.341	NA	NA	NA	NA
50	C	G	C	G	0.023	-0.301	0.620	-0.486	0.627	50	A	G	C	A	0.107	-0.002	0.012	-0.156	0.876
50	C	G	C	A	0.567	NA	NA	NA	NA	50	C	A	C	A	0.202	0.005	0.009	0.522	0.602
51	A	C	A	G	0.204	0.429	0.258	1.659	0.098	50	C	G	A	A	0.097	0.007	0.013	0.558	0.577
51	G	A	A	G	0.096	-0.292	0.350	-0.835	0.404	50	C	G	C	G	0.023	0.017	0.024	0.721	0.471
51	G	C	A	G	0.316	-0.231	0.229	-1.009	0.313	50	C	G	C	A	0.570	NA	NA	NA	NA
51	G	C	G	G	0.023	-0.346	0.628	-0.551	0.582	51	A	C	A	G	0.203	0.006	0.010	0.599	0.549
51	*	*	*	*	0.001	-2.460	3.725	-0.660	0.509	51	G	A	A	G	0.096	0.008	0.013	0.583	0.560
51	G	C	A	T	0.358	NA	NA	NA	NA	51	G	C	A	G	0.320	0.003	0.009	0.399	0.690
52	A	A	G	T	0.096	-0.316	0.338	-0.935	0.350	51	G	C	G	G	0.023	0.019	0.024	0.777	0.437
52	C	A	T	C	0.135	-0.686	0.291	-2.356	0.019	51	*	*	*	*	0.002	0.068	0.101	0.676	0.499
52	C	A	T	T	0.223	0.345	0.239	1.445	0.149	51	G	C	A	T	0.356	NA	NA	NA	NA
52	C	G	G	T	0.023	-0.365	0.621	-0.588	0.557	52	A	A	G	T	0.096	0.004	0.013	0.301	0.764
52	C	A	G	T	0.522	NA	NA	NA	NA	52	C	A	T	C	0.133	-0.002	0.011	-0.150	0.881
53	A	T	C	C	0.135	-0.651	0.289	-2.249	0.025	52	C	A	T	T	0.223	-0.006	0.009	-0.673	0.501
53	A	T	T	C	0.221	0.362	0.236	1.537	0.125	52	C	G	G	T	0.023	0.014	0.024	0.606	0.545
53	G	G	T	C	0.023	-0.301	0.620	-0.486	0.627	52	*	*	*	*	0.001	-0.036	0.128	-0.281	0.778

Table B1.29. Continued

HDL-C										TG									
Window	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**	**Window**	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**
53	*	*	*	*	0.001	2.670	2.559	1.044	0.297	52	C	A	G	T	0.524	NA	NA	NA	NA
53	A	G	T	C	0.619	NA	NA	NA	NA	53	A	T	C	C	0.133	-0.002	0.011	-0.171	0.864
54	G	T	C	C	0.017	-0.583	0.707	-0.824	0.410	53	A	T	T	C	0.223	-0.008	0.009	-0.849	0.396
54	T	C	C	T	0.135	-0.678	0.290	-2.334	0.020	53	G	G	T	C	0.023	0.014	0.024	0.577	0.564
54	T	T	C	T	0.221	0.350	0.236	1.480	0.139	53	*	*	*	*	0.001	0.044	0.098	0.448	0.654
54	*	*	*	*	0.002	3.429	2.560	1.339	0.181	53	A	G	T	C	0.620	NA	NA	NA	NA
54	G	T	C	T	0.625	NA	NA	NA	NA	54	G	T	C	C	0.019	0.050	0.024	2.062	0.040
55	C	C	T	A	0.135	-0.655	0.290	-2.258	0.024	54	T	C	C	T	0.133	0.000	0.011	-0.041	0.967
55	T	C	C	A	0.017	-0.603	0.706	-0.853	0.394	54	T	T	C	T	0.223	-0.006	0.009	-0.644	0.520
55	T	C	T	C	0.130	0.608	0.279	2.179	0.030	54	*	*	*	*	0.001	0.045	0.098	0.456	0.648
55	*	*	*	*	0.002	3.565	2.548	1.399	0.162	54	G	T	C	T	0.624	NA	NA	NA	NA
55	T	C	T	A	0.716	NA	NA	NA	NA	55	C	C	T	A	0.133	0.000	0.011	0.038	0.970
56	C	C	A	G	0.017	-0.325	0.682	-0.476	0.634	55	T	C	C	A	0.019	0.051	0.024	2.116	0.035
56	C	T	C	G	0.130	0.795	0.275	2.889	0.004	55	T	C	T	C	0.129	-0.004	0.011	-0.422	0.673
56	*	*	*	*	0.002	-1.220	2.561	-0.476	0.634	55	*	*	*	*	0.001	0.044	0.097	0.448	0.654
56	C	T	A	G	0.851	NA	NA	NA	NA	55	T	C	T	A	0.718	NA	NA	NA	NA
57	C	A	G	G	0.017	-0.292	0.681	-0.429	0.668	56	C	C	A	G	0.019	0.051	0.024	2.127	0.034
57	T	A	G	A	0.033	0.349	0.513	0.680	0.497	56	C	T	C	G	0.128	-0.006	0.010	-0.596	0.551
57	T	C	G	G	0.131	0.827	0.272	3.035	0.002	56	*	*	*	*	0.002	0.124	0.096	1.289	0.198
57	T	A	G	G	0.818	NA	NA	NA	NA	56	C	T	A	G	0.851	NA	NA	NA	NA
58	A	G	A	C	0.033	0.383	0.519	0.738	0.461	57	C	A	G	G	0.019	0.050	0.024	2.101	0.036
58	C	G	G	C	0.038	-0.031	0.508	-0.061	0.951	57	T	A	G	A	0.033	-0.004	0.020	-0.228	0.819
58	C	G	G	T	0.094	1.212	0.329	3.684	0.000	57	T	C	G	G	0.130	-0.006	0.010	-0.540	0.589
58	A	G	G	C	0.834	NA	NA	NA	NA	57	T	A	G	G	0.817	NA	NA	NA	NA
59	G	A	C	A	0.033	0.465	0.524	0.888	0.375	58	A	G	A	C	0.033	-0.007	0.020	-0.341	0.733
59	G	G	C	G	0.113	0.511	0.299	1.711	0.088	58	C	G	G	C	0.038	-0.007	0.019	-0.355	0.723
59	G	G	T	A	0.090	1.375	0.337	4.074	0.000	58	C	G	G	T	0.094	-0.008	0.012	-0.635	0.526
59	G	G	C	A	0.764	NA	NA	NA	NA	58	A	G	G	C	0.835	NA	NA	NA	NA
60	A	C	A	G	0.033	0.353	0.510	0.693	0.489	59	G	A	C	A	0.033	-0.007	0.020	-0.341	0.733
60	G	C	A	A	0.098	-0.569	0.308	-1.848	0.065	59	G	G	C	G	0.112	-0.007	0.011	-0.651	0.515
60	G	C	G	G	0.112	0.436	0.300	1.455	0.146	59	G	G	T	A	0.091	-0.004	0.013	-0.330	0.741
60	G	T	A	G	0.090	1.284	0.334	3.839	0.000	59	G	G	C	A	0.763	NA	NA	NA	NA
60	G	C	A	G	0.667	NA	NA	NA	NA	60	A	C	A	G	0.033	-0.007	0.020	-0.347	0.728
61	C	A	A	A	0.097	-0.591	0.308	-1.920	0.055	60	G	C	A	A	0.098	-0.005	0.012	-0.449	0.654
61	C	G	G	A	0.112	0.404	0.300	1.348	0.178	60	G	C	G	G	0.111	-0.007	0.012	-0.646	0.518
61	T	A	G	A	0.090	1.252	0.334	3.749	0.000	60	G	T	A	G	0.091	-0.004	0.013	-0.345	0.731
61	*	*	*	*	0.009	-0.840	0.979	-0.858	0.391	60	G	C	A	G	0.666	NA	NA	NA	NA
61	C	A	G	A	0.691	NA	NA	NA	NA	61	C	A	A	A	0.098	-0.005	0.012	-0.451	0.652
62	A	A	A	G	0.097	-0.715	0.310	-2.310	0.021	61	C	G	G	A	0.111	-0.008	0.012	-0.684	0.494
62	G	G	A	G	0.112	0.237	0.299	0.793	0.428	61	T	A	G	A	0.091	-0.005	0.013	-0.370	0.712
62	*	*	*	*	0.013	-1.180	0.841	-1.403	0.161	61	*	*	*	*	0.009	-0.033	0.037	-0.877	0.381
62	A	G	A	G	0.777	NA	NA	NA	NA	61	C	A	G	A	0.690	NA	NA	NA	NA
63	A	A	G	G	0.096	-0.826	0.310	-2.669	0.008	62	A	A	A	G	0.098	-0.005	0.012	-0.422	0.673
63	*	*	*	*	0.015	-0.605	0.799	-0.757	0.449	62	G	G	A	G	0.111	-0.007	0.011	-0.642	0.521
63	G	A	G	G	0.890	NA	NA	NA	NA	62	*	*	*	*	0.014	-0.029	0.031	-0.927	0.354
64	A	G	G	C	0.039	0.280	0.496	0.566	0.572	62	A	G	A	G	0.776	NA	NA	NA	NA
64	*	*	*	*	0.015	-0.486	0.849	-0.573	0.567	63	A	A	G	G	0.097	-0.005	0.012	-0.413	0.680
64	A	G	G	T	0.946	NA	NA	NA	NA	63	*	*	*	*	0.015	-0.019	0.030	-0.657	0.512
65	G	G	C	C	0.040	0.232	0.493	0.472	0.637	63	G	A	G	G	0.888	NA	NA	NA	NA
65	G	G	T	A	0.098	-0.719	0.314	-2.293	0.022	64	A	G	G	C	0.039	-0.025	0.019	-1.352	0.177
65	*	*	*	*	0.006	0.271	1.445	0.187	0.851	64	*	*	*	*	0.015	-0.020	0.029	-0.687	0.492
65	G	G	T	C	0.856	NA	NA	NA	NA	64	A	G	G	T	0.946	NA	NA	NA	NA
66	G	C	C	C	0.040	0.154	0.486	0.318	0.751	65	G	G	C	C	0.040	-0.023	0.018	-1.257	0.209
66	G	T	A	C	0.098	-0.706	0.313	-2.252	0.025	65	G	G	T	A	0.099	-0.009	0.012	-0.797	0.426
66	G	T	C	G	0.064	0.152	0.382	0.399	0.690	65	*	*	*	*	0.006	-0.003	0.046	-0.055	0.956
66	*	*	*	*	0.001	5.609	2.568	2.184	0.029	65	G	G	T	C	0.855	NA	NA	NA	NA
66	G	T	C	C	0.796	NA	NA	NA	NA	66	G	C	C	C	0.041	-0.020	0.018	-1.104	0.270
67	C	C	C	C	0.040	0.151	0.490	0.309	0.758	66	G	T	A	C	0.099	-0.009	0.012	-0.747	0.455
67	T	A	C	C	0.098	-0.709	0.317	-2.236	0.026	66	G	T	C	G	0.066	0.007	0.014	0.458	0.647
67	T	C	C	T	0.135	0.103	0.285	0.363	0.717	66	*	*	*	*	0.002	0.064	0.098	0.659	0.510
67	T	C	G	C	0.064	0.143	0.384	0.371	0.711	66	G	T	C	C	0.793	NA	NA	NA	NA
67	T	C	C	C	0.662	NA	NA	NA	NA	67	C	C	C	C	0.041	-0.020	0.018	-1.103	0.270
68	A	C	C	A	0.099	-0.983	0.324	-3.033	0.003	67	T	A	C	C	0.099	-0.009	0.012	-0.740	0.460
68	C	C	C	G	0.246	-0.701	0.235	-2.980	0.003	67	T	C	C	T	0.135	0.001	0.011	0.076	0.940

Table B1.29. Continued

HDL-C										TG									
Window	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**	**Window**	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**
68	C	C	T	A	0.135	-0.163	0.295	-0.551	0.582	67	T	C	G	C	0.066	0.006	0.014	0.451	0.652
68	C	G	C	A	0.065	-0.115	0.389	-0.296	0.768	67	T	C	C	C	0.659	NA	NA	NA	NA
68	C	C	C	A	0.455	NA	NA	NA	NA	68	A	C	C	A	0.099	-0.008	0.012	-0.647	0.518
69	C	C	A	T	0.064	-0.240	0.412	-0.582	0.561	68	C	C	C	G	0.244	-0.002	0.009	-0.212	0.832
69	C	C	G	T	0.247	-0.529	0.233	-2.273	0.023	68	C	C	T	A	0.135	0.001	0.011	0.093	0.926
69	C	T	A	C	0.135	-0.023	0.295	-0.079	0.937	68	C	G	C	A	0.067	0.007	0.015	0.470	0.639
69	G	C	A	T	0.064	0.015	0.393	0.038	0.969	68	C	C	C	A	0.455	NA	NA	NA	NA
69	*	*	*	*	0.002	-2.212	2.514	-0.880	0.379	69	C	C	A	T	0.064	-0.006	0.016	-0.345	0.730
69	C	C	A	C	0.488	NA	NA	NA	NA	69	C	C	G	T	0.246	-0.001	0.009	-0.139	0.890
70	C	A	C	T	0.141	0.676	0.304	2.224	0.026	69	C	T	A	C	0.135	0.002	0.011	0.173	0.863
70	C	A	T	A	0.103	0.192	0.345	0.557	0.578	69	G	C	A	T	0.066	0.008	0.015	0.545	0.586
70	C	A	T	T	0.025	-0.221	0.678	-0.326	0.744	69	*	*	*	*	0.002	0.003	0.099	0.028	0.978
70	C	G	T	T	0.247	-0.328	0.247	-1.326	0.185	69	C	C	A	C	0.487	NA	NA	NA	NA
70	T	A	C	T	0.135	0.203	0.307	0.660	0.509	70	C	A	C	T	0.144	-0.003	0.012	-0.240	0.810
70	*	*	*	*	0.002	-1.708	0.000	-3.07E+15	0.000	70	C	A	T	A	0.105	-0.004	0.013	-0.315	0.753
70	C	A	C	A	0.348	NA	NA	NA	NA	70	C	A	T	T	0.025	0.010	0.027	0.373	0.709
71	A	C	T	C	0.276	0.446	0.248	1.797	0.073	70	C	G	T	T	0.246	-0.002	0.009	-0.209	0.834
71	A	T	A	C	0.102	0.217	0.351	0.618	0.537	70	T	A	C	T	0.135	0.001	0.012	0.095	0.925
71	A	T	T	C	0.026	-0.261	0.681	-0.384	0.701	70	*	*	*	*	0.002	0.060	NA	NA	NA
71	G	T	T	C	0.227	-0.385	0.252	-1.526	0.127	70	C	A	C	A	0.343	NA	NA	NA	NA
71	G	T	T	T	0.019	0.377	0.670	0.563	0.574	71	A	C	T	C	0.279	-0.002	0.010	-0.164	0.870
71	*	*	*	*	0.002	-1.707	NA	NA	NA	71	A	T	A	C	0.105	-0.006	0.014	-0.423	0.673
71	A	C	A	C	0.348	NA	NA	NA	NA	71	A	T	T	C	0.025	0.012	0.029	0.427	0.669
72	C	A	C	C	0.149	0.239	0.313	0.762	0.446	71	G	T	T	C	0.226	0.000	0.010	0.045	0.964
72	C	A	C	T	0.200	-0.731	0.296	-2.469	0.014	71	G	T	T	T	0.019	-0.032	0.025	-1.279	0.201
72	T	A	C	T	0.101	-0.330	0.354	-0.934	0.351	71	*	*	*	*	0.002	0.060	NA	NA	NA
72	T	T	C	T	0.257	-0.674	0.274	-2.455	0.014	71	A	C	A	C	0.344	NA	NA	NA	NA
72	T	T	T	T	0.018	-0.271	0.685	-0.396	0.692	72	C	A	C	C	0.146	0.011	0.012	0.911	0.362
72	*	*	*	*	0.002	3.816	NA	NA	NA	72	C	A	C	T	0.197	-0.008	0.012	-0.635	0.526
72	C	T	C	T	0.273	NA	NA	NA	NA	72	T	A	C	T	0.106	-0.004	0.014	-0.272	0.786
73	A	C	C	T	0.148	0.576	0.282	2.040	0.042	72	T	T	C	T	0.253	0.001	0.011	0.125	0.900
73	A	C	T	C	0.011	0.097	0.913	0.106	0.915	72	T	T	T	T	0.018	-0.030	0.026	-1.141	0.254
73	A	C	T	T	0.290	-0.288	0.218	-1.320	0.187	72	*	*	*	*	0.002	-0.049	0.000	-1.23E+16	0.000
73	T	T	T	T	0.017	-0.073	0.693	-0.105	0.917	72	C	T	C	T	0.279	NA	NA	NA	NA
73	*	*	*	*	0.003	4.297	2.346	1.831	0.067	73	A	C	C	T	0.145	0.010	0.011	0.950	0.343
73	T	C	T	T	0.531	NA	NA	NA	NA	73	A	C	T	C	0.011	-0.054	0.035	-1.565	0.118
74	C	C	T	T	0.153	0.658	0.271	2.426	0.015	73	A	C	T	T	0.292	-0.005	0.008	-0.605	0.545
74	C	T	C	C	0.011	0.165	0.918	0.179	0.858	73	T	T	T	T	0.017	-0.033	0.026	-1.259	0.208
74	T	T	T	C	0.018	0.265	0.682	0.389	0.697	73	*	*	*	*	0.002	-0.022	0.000	-2.51E+15	0.000
74	*	*	*	*	0.005	0.754	1.476	0.511	0.609	73	T	C	T	T	0.532	NA	NA	NA	NA
74	C	T	T	C	0.813	NA	NA	NA	NA	74	C	C	T	T	0.150	0.010	0.010	0.959	0.338
75	C	T	T	T	0.152	0.541	0.285	1.895	0.059	74	C	T	C	C	0.011	-0.056	0.035	-1.617	0.106
75	T	C	C	G	0.012	0.162	0.898	0.180	0.857	74	T	T	T	C	0.018	-0.034	0.025	-1.352	0.177
75	T	T	C	G	0.392	-0.305	0.207	-1.479	0.140	74	*	*	*	*	0.005	-0.003	0.056	-0.049	0.961
75	*	*	*	*	0.005	-0.113	1.517	-0.074	0.941	74	C	T	T	C	0.816	NA	NA	NA	NA
75	T	T	C	T	0.438	NA	NA	NA	NA	75	C	T	T	T	0.149	0.008	0.011	0.773	0.440
76	C	C	G	G	0.012	0.464	0.897	0.518	0.605	75	T	C	C	G	0.011	-0.053	0.034	-1.554	0.121
76	T	C	T	A	0.291	0.136	0.228	0.598	0.550	75	T	T	C	G	0.391	-0.005	0.008	-0.663	0.507
76	T	C	T	G	0.151	0.527	0.287	1.832	0.067	75	*	*	*	*	0.005	-0.013	0.054	-0.242	0.809
76	T	T	T	A	0.155	0.848	0.292	2.905	0.004	75	T	T	C	T	0.443	NA	NA	NA	NA
76	*	*	*	*	0.003	0.025	1.807	0.014	0.989	76	C	C	G	G	0.011	-0.048	0.034	-1.422	0.155
76	T	C	G	G	0.388	NA	NA	NA	NA	76	T	C	T	A	0.291	0.000	0.009	-0.010	0.992
77	C	G	G	A	0.047	-0.368	0.549	-0.671	0.503	76	T	C	T	G	0.156	0.016	0.011	1.511	0.131
77	C	T	A	A	0.119	-0.034	0.331	-0.103	0.918	76	T	T	T	A	0.151	0.011	0.011	0.948	0.343
77	C	T	A	G	0.173	0.151	0.279	0.543	0.587	76	*	*	*	*	0.003	-0.016	0.068	-0.235	0.814
77	C	T	G	A	0.011	0.625	1.316	0.475	0.635	76	T	C	G	G	0.387	NA	NA	NA	NA
77	C	T	G	G	0.140	0.451	0.312	1.444	0.149	77	C	G	G	A	0.047	-0.013	0.020	-0.657	0.512
77	T	T	A	A	0.149	0.802	0.301	2.666	0.008	77	C	T	A	A	0.119	0.006	0.012	0.489	0.625
77	*	*	*	*	0.008	-0.730	1.461	-0.500	0.617	77	C	T	A	G	0.173	-0.005	0.010	-0.470	0.639
77	C	G	G	G	0.354	NA	NA	NA	NA	77	C	T	G	A	0.011	-0.062	0.044	-1.418	0.157
78	G	G	A	G	0.046	-0.201	0.559	-0.360	0.719	77	C	T	G	G	0.144	0.021	0.011	1.847	0.065
78	G	G	G	A	0.043	0.280	0.478	0.585	0.558	77	T	T	A	A	0.146	0.012	0.011	1.057	0.291
78	T	A	A	G	0.267	0.504	0.260	1.937	0.053	77	*	*	*	*	0.008	0.024	0.055	0.430	0.667
78	T	A	G	G	0.179	0.153	0.288	0.530	0.596	77	C	G	G	G	0.352	NA	NA	NA	NA

Table B1.29. Continued

HDL-C										TG									
Window	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**	**Window**	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**
78	T	G	A	G	0.012	0.048	1.173	0.041	0.968	78	G	G	A	G	0.046	-0.009	0.020	-0.432	0.666
78	T	G	G	G	0.140	0.549	0.320	1.715	0.087	78	G	G	G	A	0.043	-0.003	0.018	-0.166	0.868
78	*	*	*	*	0.003	-0.101	1.801	-0.056	0.955	78	T	A	A	G	0.264	0.009	0.010	0.900	0.369
78	G	G	G	G	0.312	NA	NA	NA	NA	78	T	A	G	G	0.178	-0.003	0.011	-0.277	0.782
79	A	G	G	A	0.147	-0.819	0.321	-2.547	0.011	78	T	G	A	G	0.011	-0.080	0.047	-1.694	0.091
79	A	G	G	G	0.030	1.494	0.637	2.347	0.019	78	T	G	G	G	0.144	0.023	0.012	1.929	0.054
79	G	A	G	G	0.056	-0.702	0.482	-1.456	0.146	78	*	*	*	*	0.003	-0.015	0.068	-0.222	0.824
79	G	G	A	A	0.042	-0.277	0.476	-0.581	0.562	78	G	G	G	G	0.309	NA	NA	NA	NA
79	G	G	G	A	0.251	0.056	0.263	0.213	0.832	79	A	G	G	A	0.149	-0.018	0.012	-1.497	0.135
79	G	G	G	G	0.203	-0.880	0.284	-3.099	0.002	79	A	G	G	G	0.028	0.016	0.027	0.576	0.565
79	*	*	*	*	0.002	1.095	NA	NA	NA	79	G	A	G	G	0.056	-0.024	0.019	-1.286	0.199
79	A	A	G	G	0.270	NA	NA	NA	NA	79	G	G	A	A	0.042	-0.010	0.018	-0.557	0.577
80	A	G	G	W	0.326	0.080	0.226	0.355	0.723	79	G	G	G	A	0.256	0.002	0.010	0.153	0.878
80	G	A	A	W	0.041	-0.013	0.478	-0.026	0.979	79	G	G	G	G	0.200	-0.006	0.011	-0.523	0.601
80	G	G	A	D	0.018	-0.081	0.727	-0.112	0.911	79	*	*	*	*	0.002	-0.161	0.085	-1.898	0.058
80	G	G	G	W	0.232	-0.329	0.253	-1.302	0.193	79	A	A	G	G	0.267	NA	NA	NA	NA
80	*	*	*	*	0.002	0.835	3.396	0.246	0.806	80	A	G	G	W	0.324	0.001	0.008	0.123	0.902
80	G	G	A	W	0.380	NA	NA	NA	NA	80	G	A	A	W	0.042	-0.006	0.018	-0.324	0.746
81	A	A	W	T	0.042	0.041	0.468	0.087	0.931	80	G	G	A	D	0.018	0.001	0.027	0.037	0.971
81	G	A	D	A	0.019	0.021	0.723	0.030	0.976	80	G	G	G	W	0.228	0.000	0.009	-0.022	0.983
81	G	A	W	A	0.203	0.207	0.244	0.846	0.398	80	*	*	*	*	0.002	-0.134	0.136	-0.979	0.328
81	G	A	W	T	0.174	-0.054	0.271	-0.198	0.843	80	G	G	A	W	0.386	NA	NA	NA	NA
81	*	*	*	*	0.002	2.301	0.000	2.19E+16	0.000	81	A	A	W	T	0.043	-0.007	0.017	-0.389	0.698
81	G	G	W	T	0.560	NA	NA	NA	NA	81	G	A	D	A	0.018	0.002	0.027	0.062	0.951
82	A	D	A	T	0.018	0.031	0.726	0.042	0.966	81	G	A	W	A	0.206	-0.002	0.009	-0.265	0.791
82	A	W	A	T	0.204	0.213	0.246	0.867	0.386	81	G	A	W	T	0.178	0.001	0.010	0.104	0.917
82	A	W	T	G	0.064	0.272	0.395	0.687	0.492	81	*	*	*	*	0.002	-0.053	0.000	-3.18E+15	0.000
82	A	W	T	T	0.152	-0.175	0.291	-0.603	0.547	81	G	G	W	T	0.553	NA	NA	NA	NA
82	*	*	*	*	0.002	2.321	NA	NA	NA	82	A	D	A	T	0.018	0.002	0.028	0.066	0.947
82	G	W	T	T	0.561	NA	NA	NA	NA	82	A	W	A	T	0.206	-0.003	0.009	-0.290	0.772
83	D	A	T	T	0.018	0.292	0.725	0.402	0.688	82	A	W	T	G	0.064	-0.008	0.015	-0.505	0.613
83	W	A	T	T	0.203	0.469	0.256	1.831	0.068	82	A	W	T	T	0.156	0.003	0.011	0.291	0.771
83	W	T	G	A	0.064	0.506	0.398	1.272	0.204	82	*	*	*	*	0.002	-0.049	NA	NA	NA
83	W	T	T	T	0.299	0.421	0.230	1.832	0.067	82	G	W	T	T	0.554	NA	NA	NA	NA
83	W	T	T	A	0.414	NA	NA	NA	NA	83	D	A	T	T	0.018	0.006	0.028	0.234	0.815
84	A	T	T	G	0.222	0.042	0.268	0.155	0.877	83	W	A	T	T	0.206	0.001	0.010	0.090	0.929
84	T	G	A	G	0.064	0.098	0.409	0.240	0.810	83	W	T	G	A	0.065	-0.005	0.015	-0.358	0.720
84	T	T	A	A	0.146	-0.323	0.307	-1.053	0.293	83	W	T	T	T	0.300	0.012	0.009	1.398	0.162
84	T	T	A	G	0.267	-0.481	0.255	-1.889	0.059	83	W	T	T	A	0.410	NA	NA	NA	NA
84	T	T	T	G	0.299	NA	NA	NA	NA	84	A	T	T	G	0.224	-0.011	0.010	-1.120	0.263
85	G	A	G	C	0.018	-0.115	0.725	-0.158	0.874	84	T	G	A	G	0.065	-0.017	0.015	-1.103	0.270
85	G	A	G	T	0.047	0.115	0.457	0.252	0.801	84	T	T	A	A	0.148	-0.010	0.011	-0.911	0.362
85	T	A	A	C	0.146	-0.335	0.287	-1.166	0.244	84	T	T	A	G	0.261	-0.012	0.010	-1.271	0.204
85	T	A	G	C	0.267	-0.487	0.224	-2.172	0.030	84	T	T	T	G	0.300	NA	NA	NA	NA
85	T	T	G	C	0.522	NA	NA	NA	NA	85	G	A	G	C	0.018	-0.041	0.027	-1.526	0.127
86	A	A	C	A	0.146	-0.334	0.287	-1.166	0.244	85	G	A	G	T	0.047	-0.002	0.017	-0.144	0.885
86	A	G	C	A	0.266	-0.497	0.224	-2.215	0.027	85	T	A	A	C	0.148	-0.006	0.011	-0.523	0.601
86	A	G	C	G	0.019	0.032	0.711	0.045	0.964	85	T	A	G	C	0.261	-0.007	0.008	-0.777	0.437
86	A	G	T	G	0.047	0.105	0.457	0.230	0.818	85	T	T	G	C	0.526	NA	NA	NA	NA
86	T	G	C	A	0.522	NA	NA	NA	NA	86	A	A	C	A	0.148	-0.006	0.011	-0.531	0.596
87	A	C	A	A	0.146	-0.214	0.280	-0.766	0.444	86	A	G	C	A	0.260	-0.007	0.009	-0.856	0.392
87	G	C	A	T	0.017	-1.422	0.713	-1.995	0.046	86	A	G	C	G	0.019	-0.031	0.027	-1.175	0.240
87	G	C	G	A	0.019	0.114	0.710	0.161	0.872	86	A	G	T	G	0.047	-0.003	0.017	-0.168	0.866
87	G	T	G	A	0.047	0.229	0.451	0.507	0.612	86	T	G	C	A	0.526	NA	NA	NA	NA
87	G	C	A	A	0.773	NA	NA	NA	NA	87	A	C	A	A	0.148	-0.004	0.010	-0.426	0.670
88	C	A	T	C	0.017	-1.389	0.712	-1.952	0.051	87	G	C	A	T	0.016	-0.042	0.027	-1.546	0.122
88	C	G	A	G	0.019	0.158	0.708	0.222	0.824	87	G	C	G	A	0.019	-0.030	0.027	-1.129	0.259
88	T	G	A	G	0.046	0.281	0.446	0.631	0.529	87	G	T	G	A	0.047	-0.001	0.017	-0.086	0.932
88	C	A	A	C	0.918	NA	NA	NA	NA	87	G	C	A	A	0.771	NA	NA	NA	NA
89	A	A	C	T	0.376	-0.520	0.197	-2.632	0.009	88	C	A	T	C	0.016	-0.042	0.027	-1.519	0.129
89	A	T	C	C	0.017	-1.587	0.712	-2.230	0.026	88	C	G	A	G	0.019	-0.029	0.026	-1.088	0.277
89	G	A	G	T	0.065	0.045	0.386	0.118	0.906	88	T	G	A	G	0.047	0.000	0.017	-0.024	0.981
89	A	A	C	C	0.542	NA	NA	NA	NA	88	C	A	A	C	0.919	NA	NA	NA	NA
90	A	C	C	G	0.069	-0.285	0.389	-0.732	0.464	89	A	A	C	T	0.372	-0.008	0.007	-1.034	0.302

Table B1.29. Continued

HDL-C										TG									
Window	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**	**Window**	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**
90	A	C	T	G	0.373	-0.573	0.204	-2.810	0.005	89	A	T	C	C	0.016	-0.044	0.027	-1.611	0.107
90	A	G	T	G	0.065	-0.050	0.387	-0.128	0.898	89	G	A	G	T	0.066	-0.012	0.015	-0.805	0.421
90	T	C	C	A	0.017	-1.654	0.715	-2.314	0.021	89	A	A	C	C	0.547	NA	NA	NA	NA
90	A	C	C	A	0.475	NA	NA	NA	NA	90	A	C	C	G	0.069	-0.010	0.015	-0.709	0.478
91	C	C	G	T	0.070	-0.217	0.389	-0.558	0.577	90	A	C	T	G	0.370	-0.010	0.008	-1.359	0.174
91	C	T	G	C	0.256	-0.544	0.228	-2.389	0.017	90	A	G	T	G	0.066	-0.017	0.015	-1.152	0.250
91	C	T	G	T	0.116	-0.445	0.314	-1.419	0.156	90	T	C	C	A	0.016	-0.047	0.028	-1.707	0.088
91	G	T	G	C	0.065	0.016	0.387	0.042	0.967	90	A	C	C	A	0.479	NA	NA	NA	NA
91	*	*	*	*	0.002	-1.963	2.563	-0.766	0.444	91	C	C	G	T	0.069	-0.006	0.015	-0.399	0.690
91	C	C	A	T	0.491	NA	NA	NA	NA	91	C	T	G	C	0.251	-0.006	0.009	-0.699	0.485
92	C	G	T	G	0.070	-0.209	0.389	-0.538	0.591	91	C	T	G	T	0.117	-0.015	0.012	-1.252	0.211
92	T	G	C	A	0.062	-0.081	0.396	-0.205	0.837	91	G	T	G	C	0.066	-0.016	0.015	-1.113	0.266
92	T	G	C	G	0.259	-0.513	0.226	-2.265	0.024	91	*	*	*	*	0.002	0.004	0.098	0.041	0.968
92	T	G	T	G	0.116	-0.443	0.314	-1.410	0.159	91	C	C	A	T	0.494	NA	NA	NA	NA

TABLE B1.30. Summary of *CETP* 4-SNP sliding haplotypes for LDL-C and TC in African blacks (n=788)

							LDL-C										TC		
Window	loc.1	loc.2	loc.3	loc.4	hap.freq	coef	se	t.stat	pval	Window	loc.1	loc.2	loc.3	loc.4	hap.freq	coef	se	t.stat	pval
1	A	A	C	A	0.037	0.314	0.626	0.501	0.617	1	A	A	C	A	0.036	0.097	0.321	0.304	0.762
1	A	A	T	A	0.085	0.310	0.434	0.715	0.475	1	A	A	T	A	0.084	0.406	0.229	1.771	0.077
1	A	G	C	A	0.029	-0.947	0.690	-1.373	0.170	1	A	G	C	A	0.030	-0.584	0.357	-1.633	0.103
1	A	G	C	C	0.221	0.575	0.321	1.792	0.074	1	A	G	C	C	0.218	0.354	0.164	2.156	0.031
1	A	G	T	A	0.043	-0.734	0.544	-1.349	0.178	1	A	G	T	A	0.043	-0.290	0.285	-1.016	0.310
1	G	A	C	C	0.072	-0.158	0.583	-0.271	0.786	1	G	A	C	C	0.073	-0.103	0.280	-0.370	0.712
1	G	A	T	A	0.108	-0.376	0.366	-1.029	0.304	1	G	A	T	A	0.108	-0.007	0.190	-0.037	0.970
1	G	G	C	A	0.010	0.126	1.400	0.090	0.928	1	G	G	C	A	0.010	0.119	0.843	0.141	0.888
1	G	G	C	C	0.028	1.335	0.914	1.461	0.144	1	G	G	C	C	0.027	0.453	0.473	0.959	0.338
1	G	G	T	A	0.010	-0.591	1.541	-0.384	0.701	1	G	G	T	A	0.010	-0.358	0.753	-0.475	0.635
1	*	*	*	*	0.003	0.869	3.486	0.249	0.803	1	*	*	*	*	0.003	0.207	1.510	0.137	0.891
1	A	A	C	C	0.355	NA	NA	NA	NA	1	A	A	C	C	0.357	NA	NA	NA	NA
2	A	C	A	A	0.040	0.317	0.585	0.542	0.588	2	A	C	A	A	0.040	0.124	0.305	0.406	0.685
2	A	T	A	A	0.170	-0.037	0.301	-0.122	0.903	2	A	T	A	A	0.169	0.164	0.157	1.049	0.295
2	A	T	A	G	0.021	-0.068	0.662	-0.103	0.918	2	A	T	A	G	0.021	0.363	0.347	1.048	0.295
2	G	C	A	A	0.038	-0.618	0.572	-1.080	0.280	2	G	C	A	A	0.040	-0.423	0.293	-1.443	0.149
2	G	C	C	A	0.247	0.653	0.276	2.366	0.018	2	G	C	C	A	0.244	0.370	0.143	2.585	0.010
2	G	T	A	A	0.055	-0.669	0.507	-1.321	0.187	2	G	T	A	A	0.055	-0.253	0.262	-0.964	0.335
2	A	C	C	A	0.429	NA	NA	NA	NA	2	A	C	C	A	0.432	NA	NA	NA	NA
3	C	A	A	C	0.063	-0.324	0.439	-0.737	0.461	3	C	A	A	C	0.063	-0.184	0.233	-0.788	0.431
3	C	A	A	T	0.016	-0.078	0.930	-0.084	0.933	3	C	A	A	T	0.017	-0.413	0.476	-0.867	0.386
3	C	C	A	C	0.167	0.590	0.280	2.104	0.036	3	C	C	A	C	0.164	0.300	0.148	2.031	0.043
3	T	A	A	T	0.224	-0.269	0.242	-1.108	0.268	3	T	A	A	T	0.223	0.015	0.128	0.117	0.907
3	T	A	G	T	0.021	-0.135	0.662	-0.204	0.838	3	T	A	G	T	0.021	0.315	0.348	0.905	0.366
3	*	*	*	*	0.001	-1.742	3.958	-0.440	0.660	3	*	*	*	*	0.001	-0.884	1.931	-0.458	0.647
3	C	C	A	T	0.509	NA	NA	NA	NA	3	C	C	A	T	0.511	NA	NA	NA	NA
4	A	A	C	C	0.063	0.153	0.490	0.312	0.755	4	A	A	C	C	0.063	0.005	0.250	0.022	0.983
4	A	A	T	C	0.134	-0.576	0.338	-1.703	0.089	4	A	A	T	C	0.135	-0.120	0.172	-0.697	0.486
4	A	A	T	T	0.105	-0.128	0.323	-0.397	0.691	4	A	A	T	T	0.103	-0.003	0.173	-0.018	0.986
4	A	G	T	C	0.021	-0.185	0.661	-0.280	0.780	4	A	G	T	C	0.021	0.289	0.348	0.830	0.407
4	C	A	C	C	0.163	0.411	0.306	1.343	0.180	4	C	A	C	C	0.161	0.222	0.158	1.409	0.159
4	C	A	T	C	0.515	NA	NA	NA	NA	4	C	A	T	C	0.517	NA	NA	NA	NA
5	A	C	C	C	0.063	0.052	0.403	0.129	0.898	5	A	C	C	C	0.063	-0.073	0.214	-0.339	0.735
5	A	C	C	T	0.169	0.517	0.267	1.935	0.053	5	A	C	C	T	0.167	0.235	0.141	1.663	0.097
5	A	T	T	T	0.105	-0.033	0.319	-0.103	0.918	5	A	T	T	T	0.103	0.019	0.171	0.112	0.911
5	G	T	C	T	0.021	-0.063	0.662	-0.095	0.925	5	G	T	C	T	0.021	0.324	0.350	0.925	0.355
5	A	T	C	T	0.642	NA	NA	NA	NA	5	A	T	C	T	0.646	NA	NA	NA	NA
6	C	C	C	G	0.063	0.216	0.418	0.516	0.606	6	C	C	C	G	0.064	-0.091	0.222	-0.411	0.681
6	C	C	T	G	0.170	0.707	0.287	2.467	0.014	6	C	C	T	G	0.168	0.236	0.152	1.557	0.120
6	T	C	T	G	0.314	0.351	0.237	1.483	0.138	6	T	C	T	G	0.314	-0.008	0.126	-0.067	0.946
6	T	T	T	A	0.104	0.152	0.342	0.443	0.658	6	T	T	T	A	0.102	0.005	0.184	0.030	0.976
6	*	*	*	*	0.002	-2.551	3.247	-0.786	0.432	6	*	*	*	*	0.002	-1.191	2.330	-0.511	0.609
6	T	C	T	A	0.348	NA	NA	NA	NA	6	T	C	T	A	0.351	NA	NA	NA	NA
7	C	C	G	C	0.061	-0.145	0.409	-0.354	0.723	7	C	C	G	C	0.062	-0.103	0.220	-0.468	0.640
7	C	T	A	C	0.330	-0.494	0.207	-2.384	0.017	7	C	T	A	C	0.333	-0.111	0.114	-0.975	0.330
7	C	T	A	T	0.020	0.146	NA	NA	NA	7	C	T	A	T	0.020	0.654	0.407	1.607	0.108
7	T	T	A	C	0.104	-0.339	0.320	-1.057	0.291	7	T	T	A	C	0.102	-0.077	0.172	-0.448	0.654
7	*	*	*	*	0.004	-4.002	NA	NA	NA	7	*	*	*	*	0.004	-2.240	0.821	-2.730	0.006
7	C	T	G	C	0.481	NA	NA	NA	NA	7	C	T	G	C	0.479	NA	NA	NA	NA
8	C	G	C	C	0.062	0.254	0.409	0.620	0.535	8	C	G	C	C	0.062	-0.007	0.220	-0.031	0.975
8	T	A	T	C	0.020	0.886	0.769	1.152	0.250	8	T	A	T	C	0.020	0.827	0.394	2.102	0.036
8	T	G	C	C	0.384	0.302	0.207	1.455	0.146	8	T	G	C	C	0.385	0.016	0.110	0.149	0.882
8	T	G	C	T	0.097	1.039	0.340	3.056	0.002	8	T	G	C	T	0.095	0.449	0.179	2.507	0.012
8	*	*	*	*	0.006	-4.854	1.976	-2.456	0.014	8	*	*	*	*	0.006	-2.531	1.030	-2.457	0.014
8	T	A	C	C	0.432	NA	NA	NA	NA	8	T	A	C	C	0.433	NA	NA	NA	NA
9	A	C	C	A	0.030	0.514	0.556	0.925	0.355	9	A	C	C	A	0.030	0.430	0.294	1.463	0.144
9	A	C	C	G	0.402	-0.366	0.205	-1.781	0.075	9	A	C	C	G	0.403	-0.051	0.109	-0.468	0.640
9	A	T	C	G	0.020	0.585	0.799	0.732	0.464	9	A	T	C	G	0.020	0.842	0.413	2.040	0.042
9	G	C	T	G	0.097	0.761	0.352	2.166	0.031	9	G	C	T	G	0.095	0.428	0.184	2.331	0.020
9	*	*	*	*	0.006	-5.124	1.966	-2.606	0.009	9	*	*	*	*	0.006	-2.398	0.977	-2.455	0.014
9	G	C	C	G	0.446	NA	NA	NA	NA	9	G	C	C	G	0.447	NA	NA	NA	NA
10	C	C	A	C	0.030	0.670	0.557	1.204	0.229	10	C	C	A	C	0.030	0.463	0.294	1.576	0.115
10	C	C	G	A	0.036	0.574	0.484	1.185	0.236	10	C	C	G	A	0.035	0.357	0.264	1.354	0.176
10	C	T	G	C	0.098	0.818	0.323	2.535	0.011	10	C	T	G	C	0.097	0.387	0.170	2.270	0.023
10	T	C	G	C	0.022	0.301	0.640	0.470	0.638	10	T	C	G	C	0.022	0.525	0.339	1.550	0.122
10	*	*	*	*	0.001	-9.318	2.944	-3.165	0.002	10	*	*	*	*	0.001	-4.617	0.000	-1.43E+16	0.000
10	C	C	G	C	0.813	NA	NA	NA	NA	10	C	C	G	C	0.815	NA	NA	NA	NA
11	C	A	C	A	0.030	0.712	0.566	1.258	0.209	11	C	A	C	A	0.030	0.411	0.298	1.380	0.168
11	C	G	A	A	0.036	0.639	0.495	1.292	0.197	11	C	G	A	A	0.035	0.329	0.268	1.225	0.221
11	C	G	C	C	0.300	0.157	0.224	0.701	0.483	11	C	G	C	C	0.300	-0.065	0.119	-0.545	0.586
11	T	G	C	C	0.096	0.935	0.360	2.595	0.010	11	T	G	C	C	0.094	0.387	0.187	2.071	0.039
11	*	*	*	*	0.004	-2.266	2.137	-1.060	0.289	11	*	*	*	*	0.004	-0.845	1.023	-0.826	0.409
11	C	G	C	A	0.535	NA	NA	NA	NA	11	C	G	C	A	0.536	NA	NA	NA	NA
12	A	C	A	G	0.030	0.648	0.572	1.132	0.258	12	A	C	A	G	0.030	0.437	0.299	1.459	0.145
12	G	A	A	G	0.036	0.614	0.501	1.227	0.220	12	G	A	A	G	0.035	0.376	0.270	1.393	0.164
12	G	C	A	A	0.091	-0.301	0.347	-0.866	0.387	12	G	C	A	A	0.092	0.244	0.182	1.339	0.181

Table B1.30. Continued

LDL-C										TC									
Window	loc.1	loc.2	loc.3	loc.4	hap.freq	coef	se	t.stat	pval	Window	loc.1	loc.2	loc.3	loc.4	hap.freq	coef	se	t.stat	pval
12	G	C	C	G	0.396	0.297	0.212	1.405	0.160	12	G	C	C	G	0.395	0.092	0.112	0.826	0.409
12	G	C	A	G	0.447	NA	NA	NA	NA	12	G	C	A	G	0.448	NA	NA	NA	NA
13	A	A	G	G	0.036	0.580	0.497	1.167	0.244	13	A	A	G	G	0.035	0.353	0.269	1.312	0.190
13	C	A	A	C	0.091	-0.311	0.342	-0.910	0.363	13	C	A	A	C	0.091	0.231	0.180	1.286	0.199
13	C	C	G	G	0.397	0.257	0.207	1.245	0.214	13	C	C	G	G	0.396	0.062	0.109	0.569	0.569
13	C	A	G	G	0.476	NA	NA	NA	NA	13	C	A	G	G	0.477	NA	NA	NA	NA
14	A	A	C	C	0.089	-0.350	0.353	-0.992	0.321	14	A	A	C	C	0.090	0.200	0.185	1.081	0.280
14	A	G	G	A	0.063	-0.073	0.416	-0.175	0.861	14	A	G	G	A	0.063	-0.163	0.220	-0.741	0.459
14	C	G	G	C	0.397	0.186	0.209	0.888	0.375	14	C	G	G	C	0.396	0.007	0.111	0.064	0.949
14	*	*	*	*	0.002	-1.935	4.275	-0.453	0.651	14	*	*	*	*	0.002	-0.952	1.938	-0.492	0.623
14	A	G	G	C	0.449	NA	NA	NA	NA	14	A	G	G	C	0.449	NA	NA	NA	NA
15	A	C	C	C	0.089	-0.411	0.335	-1.229	0.220	15	A	C	C	C	0.090	0.211	0.177	1.194	0.233
15	G	G	A	C	0.063	-0.058	0.404	-0.143	0.886	15	G	G	A	C	0.063	-0.117	0.217	-0.541	0.589
15	G	G	C	A	0.020	-0.430	0.665	-0.647	0.518	15	G	G	C	A	0.020	-0.032	0.347	-0.092	0.927
15	*	*	*	*	0.003	-4.529	6.690	-0.677	0.499	15	*	*	*	*	0.003	-2.061	2.399	-0.859	0.391
15	G	G	C	C	0.826	NA	NA	NA	NA	15	G	G	C	C	0.824	NA	NA	NA	NA
16	C	C	C	C	0.089	-0.453	0.344	-1.318	0.188	16	C	C	C	C	0.090	0.232	0.181	1.285	0.199
16	G	A	C	C	0.065	-0.244	0.392	-0.622	0.534	16	G	A	C	C	0.065	-0.186	0.209	-0.888	0.375
16	G	C	A	C	0.020	-0.632	0.659	-0.959	0.338	16	G	C	A	C	0.021	-0.099	0.340	-0.290	0.772
16	G	C	C	A	0.175	-0.309	0.251	-1.231	0.219	16	G	C	C	A	0.177	-0.029	0.134	-0.215	0.830
16	G	C	C	C	0.651	NA	NA	NA	NA	16	G	C	C	C	0.647	NA	NA	NA	NA
17	A	C	C	C	0.064	-0.330	0.408	-0.810	0.418	17	A	C	C	C	0.065	-0.191	0.217	-0.882	0.378
17	C	A	C	T	0.019	-0.310	0.713	-0.434	0.664	17	C	A	C	T	0.020	-0.081	0.350	-0.231	0.817
17	C	C	A	C	0.173	-0.320	0.271	-1.182	0.238	17	C	C	A	C	0.176	-0.034	0.144	-0.239	0.812
17	C	C	C	C	0.367	-0.291	0.225	-1.297	0.195	17	C	C	C	C	0.365	0.018	0.118	0.148	0.882
17	*	*	*	*	0.002	-7.772	3.334	-2.331	0.020	17	*	*	*	*	0.001	-3.620	1.752	-2.066	0.039
17	C	C	C	T	0.374	NA	NA	NA	NA	17	C	C	C	T	0.373	NA	NA	NA	NA
18	A	C	T	G	0.020	-0.661	0.661	-0.999	0.318	18	A	C	T	G	0.021	-0.102	0.346	-0.296	0.767
18	C	A	C	G	0.175	-0.355	0.270	-1.312	0.190	18	C	A	C	G	0.177	-0.024	0.144	-0.163	0.870
18	C	C	C	A	0.235	-0.439	0.246	-1.783	0.075	18	C	C	C	A	0.235	0.015	0.131	0.112	0.911
18	C	C	C	G	0.194	-0.079	0.273	-0.290	0.772	18	C	C	C	G	0.194	-0.027	0.144	-0.186	0.853
18	C	C	T	G	0.374	NA	NA	NA	NA	18	C	C	T	G	0.373	NA	NA	NA	NA
19	A	C	G	G	0.175	-0.343	0.268	-1.279	0.201	19	A	C	G	G	0.176	-0.032	0.143	-0.222	0.824
19	C	C	A	A	0.237	-0.441	0.244	-1.810	0.071	19	C	C	A	A	0.237	-0.002	0.129	-0.016	0.987
19	C	C	G	G	0.192	-0.050	0.271	-0.186	0.853	19	C	C	G	G	0.192	-0.025	0.142	-0.176	0.860
19	*	*	*	*	0.002	-4.112	NA	NA	NA	19	*	*	*	*	0.002	-2.606	NA	NA	NA
19	C	T	G	G	0.395	NA	NA	NA	NA	19	C	T	G	G	0.393	NA	NA	NA	NA
20	C	A	A	C	0.215	-0.454	0.250	-1.818	0.069	20	C	A	A	C	0.214	-0.027	0.133	-0.206	0.837
20	C	A	A	T	0.022	-0.206	0.648	-0.317	0.751	20	C	A	A	T	0.022	0.287	0.341	0.842	0.400
20	C	G	G	C	0.368	-0.183	0.218	-0.840	0.401	20	C	G	G	C	0.369	-0.021	0.116	-0.186	0.853
20	*	*	*	*	0.002	2.058	0.000	1.53057E+16	0.000	20	*	*	*	*	0.002	1.116	0.000	2.97155E+15	0.000
20	T	G	G	C	0.394	NA	NA	NA	NA	20	T	G	G	C	0.393	NA	NA	NA	NA
21	A	A	C	A	0.215	-0.368	0.230	-1.604	0.109	21	A	A	C	A	0.214	-0.027	0.122	-0.221	0.825
21	A	A	T	A	0.021	-0.109	0.658	-0.165	0.869	21	A	A	T	A	0.021	0.338	0.287	1.177	0.239
21	G	G	C	G	0.090	-0.013	0.332	-0.038	0.970	21	G	G	C	G	0.090	-0.067	0.169	-0.400	0.689
21	*	*	*	*	0.002	1.242	0.000	2.79908E+15	0.000	21	*	*	*	*	0.003	0.392	NA	NA	NA
21	G	G	C	A	0.672	NA	NA	NA	NA	21	G	G	C	A	0.671	NA	NA	NA	NA
22	A	C	A	A	0.024	0.074	0.691	0.107	0.915	22	A	C	A	A	0.026	-0.068	0.350	-0.194	0.846
22	A	C	A	G	0.192	-0.637	0.267	-2.385	0.017	22	A	C	A	G	0.190	-0.166	0.142	-1.166	0.244
22	A	T	A	G	0.021	-0.216	0.656	-0.330	0.742	22	A	T	A	G	0.021	0.193	0.353	0.547	0.585
22	G	C	A	A	0.241	-0.576	0.264	-2.179	0.030	22	G	C	A	A	0.241	-0.371	0.140	-2.658	0.008
22	G	C	G	A	0.011	1.553	1.146	1.355	0.176	22	G	C	G	G	0.082	-0.282	0.194	-1.454	0.146
22	G	C	G	G	0.080	-0.422	0.374	-1.129	0.259	22	*	*	*	*	0.011	0.681	0.634	1.075	0.283
22	*	*	*	*	0.002	2.335	NA	NA	NA	22	G	C	A	G	0.428	NA	NA	NA	NA
22	G	C	A	G	0.429	NA	NA	NA	NA	23	C	A	A	G	0.266	-0.217	0.124	-1.758	0.079
23	C	A	A	G	0.265	-0.201	0.238	-0.845	0.398	23	C	A	G	A	0.035	0.118	0.268	0.440	0.660
23	C	A	G	A	0.036	0.256	0.496	0.516	0.606	23	C	G	A	G	0.010	0.317	0.684	0.463	0.644
23	C	G	A	G	0.011	1.483	1.224	1.212	0.226	23	C	G	G	G	0.080	-0.160	0.196	-0.815	0.415
23	C	G	G	G	0.078	-0.138	0.378	-0.365	0.715	23	T	A	G	G	0.019	0.843	0.401	2.105	0.036
23	T	A	G	G	0.019	0.905	0.764	1.185	0.236	23	*	*	*	*	0.004	-2.035	1.000	-2.034	0.042
23	*	*	*	*	0.004	-3.697	2.150	-1.720	0.086	23	C	A	G	G	0.586	NA	NA	NA	NA
23	C	A	G	G	0.587	NA	NA	NA	NA	24	A	A	G	W	0.267	-0.198	0.136	-1.455	0.146
24	A	A	G	W	0.266	-0.189	0.262	-0.720	0.472	24	A	G	A	W	0.035	0.165	0.276	0.600	0.549
24	A	G	A	W	0.036	0.306	0.512	0.597	0.550	24	A	G	G	W	0.234	0.137	0.139	0.986	0.324
24	A	G	G	W	0.232	0.136	0.267	0.510	0.610	24	G	A	G	W	0.011	0.063	0.699	0.090	0.928
24	G	A	G	W	0.012	1.152	1.314	0.877	0.381	24	G	G	G	D	0.018	0.372	0.491	0.757	0.449
24	G	G	G	D	0.018	0.354	0.983	0.360	0.719	24	G	G	G	W	0.062	-0.310	0.232	-1.338	0.181
24	G	G	G	W	0.061	-0.259	0.443	-0.585	0.558	24	*	*	*	*	0.003	-0.214	1.145	-0.187	0.852
24	*	*	*	*	0.003	-0.247	2.245	-0.110	0.912	24	A	G	G	D	0.370	NA	NA	NA	NA
24	A	G	G	D	0.373	NA	NA	NA	NA	25	A	G	W	G	0.019	-0.153	0.540	-0.284	0.776
25	A	G	W	G	0.020	-0.085	1.002	-0.085	0.932	25	G	A	W	A	0.035	0.336	0.276	1.216	0.224
25	G	A	W	A	0.036	0.416	0.511	0.813	0.417	25	G	G	D	A	0.253	0.159	0.149	1.069	0.285
25	G	G	D	A	0.253	0.012	0.284	0.042	0.967	25	G	G	D	G	0.135	0.216	0.186	1.163	0.245
25	G	G	D	G	0.138	0.332	0.352	0.944	0.345	25	G	G	W	A	0.239	0.230	0.155	1.490	0.137
25	G	G	W	A	0.239	0.174	0.299	0.583	0.560	25	G	G	W	G	0.057	0.119	0.291	0.409	0.683
25	G	G	W	G	0.054	0.074	0.576	0.128	0.898	25	*	*	*	*	0.003	-0.005	1.397	-0.003	0.997
25	*	*	*	*	0.003	-0.045	2.650	-0.017	0.987	25	A	G	W	A	0.259	NA	NA	NA	NA
25	A	G	W	A	0.257	NA	NA	NA	NA	26	A	W	A	G	0.034	0.196	0.270	0.728	0.467
26	A	W	A	G	0.035	0.295	0.497	0.594	0.553	26	G	D	A	C	0.181	-0.011	0.139	-0.077	0.939
26	G	D	A	C	0.180	-0.219	0.263	-0.835	0.404	26	G	D	A	G	0.070	-0.167	0.218	-0.767	0.443
26	G	D	A	G	0.070	-0.265	0.412	-0.643	0.520	26	G	D	G	G	0.135	0.230	0.162	1.425	0.155

Table B1.30. Continued

LDL-C										TC									
Window	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**	**Window**	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**
26	G	D	G	G	0.138	0.417	0.301	1.384	0.167	26	G	W	G	G	0.074	-0.338	0.217	-1.556	0.120
26	G	W	G	G	0.072	-0.495	0.419	-1.182	0.238	26	*	*	*	*	0.008	-0.485	0.652	-0.744	0.457
26	*	*	*	*	0.008	-1.644	1.330	-1.236	0.217	26	G	W	A	G	0.497	NA	NA	NA	NA
26	G	W	A	G	0.495	NA	NA	NA	NA	27	D	A	C	C	0.182	-0.035	0.138	-0.256	0.798
27	D	A	C	C	0.181	-0.247	0.262	-0.946	0.345	27	D	A	G	C	0.070	-0.198	0.218	-0.910	0.363
27	D	A	G	C	0.070	-0.296	0.411	-0.721	0.471	27	D	G	G	C	0.135	0.203	0.162	1.254	0.210
27	D	G	G	C	0.138	0.395	0.302	1.308	0.191	27	W	A	G	A	0.026	-0.284	0.326	-0.871	0.384
27	W	A	G	A	0.025	-0.033	0.621	-0.053	0.958	27	W	G	G	C	0.075	-0.376	0.216	-1.741	0.082
27	W	G	G	C	0.073	-0.549	0.414	-1.327	0.185	27	*	*	*	*	0.007	-0.537	0.656	-0.818	0.413
27	*	*	*	*	0.007	-1.584	1.327	-1.193	0.233	27	W	A	G	C	0.505	NA	NA	NA	NA
27	W	A	G	C	0.504	NA	NA	NA	NA	28	A	C	C	C	0.186	-0.111	0.146	-0.761	0.447
28	A	C	C	C	0.185	-0.323	0.275	-1.174	0.241	28	A	G	A	C	0.026	-0.322	0.331	-0.971	0.332
28	A	G	A	C	0.025	-0.028	0.630	-0.045	0.964	28	A	G	C	C	0.250	-0.185	0.135	-1.368	0.172
28	A	G	C	C	0.250	-0.138	0.259	-0.535	0.593	28	G	G	C	G	0.209	-0.087	0.148	-0.588	0.557
28	G	G	C	G	0.211	0.011	0.277	0.039	0.969	28	*	*	*	*	0.004	0.618	1.376	0.449	0.654
28	*	*	*	*	0.004	0.589	2.623	0.225	0.822	28	A	G	C	G	0.325	NA	NA	NA	NA
28	A	G	C	G	0.325	NA	NA	NA	NA	29	C	C	C	T	0.185	-0.076	0.138	-0.555	0.579
29	C	C	C	T	0.184	-0.318	0.259	-1.228	0.220	29	G	A	C	T	0.026	-0.282	0.328	-0.861	0.390
29	G	A	C	T	0.025	-0.024	0.625	-0.039	0.969	29	G	C	C	T	0.252	-0.136	0.126	-1.084	0.279
29	G	C	C	T	0.252	-0.109	0.241	-0.452	0.651	29	G	C	G	G	0.033	0.070	0.279	0.252	0.801
29	G	C	G	G	0.034	0.124	0.514	0.242	0.809	29	*	*	*	*	0.002	0.041	1.373	0.030	0.976
29	*	*	*	*	0.002	-1.256	2.688	-0.467	0.640	29	G	C	G	T	0.502	NA	NA	NA	NA
29	G	C	G	T	0.502	NA	NA	NA	NA	30	A	C	T	A	0.026	-0.318	0.326	-0.976	0.329
30	A	C	T	A	0.025	-0.123	0.619	-0.199	0.843	30	C	C	T	A	0.438	-0.144	0.105	-1.370	0.171
30	C	C	T	A	0.437	-0.288	0.202	-1.428	0.154	30	C	G	G	A	0.033	0.029	0.278	0.104	0.918
30	C	G	G	A	0.034	0.012	0.510	0.024	0.981	30	C	G	T	G	0.026	-0.498	0.323	-1.541	0.124
30	C	G	T	G	0.026	-1.337	0.615	-2.175	0.030	30	C	G	T	A	0.477	NA	NA	NA	NA
30	C	G	T	A	0.477	NA	NA	NA	NA	31	G	G	A	C	0.033	0.187	0.274	0.682	0.495
31	G	G	A	C	0.034	0.275	0.503	0.546	0.585	31	G	T	A	C	0.430	0.150	0.107	1.395	0.164
31	G	T	A	C	0.430	0.236	0.205	1.150	0.251	31	G	T	A	T	0.046	0.194	0.238	0.817	0.414
31	G	T	A	T	0.047	0.606	0.451	1.342	0.180	31	G	T	G	C	0.026	-0.336	0.323	-1.042	0.298
31	G	T	G	C	0.026	-1.044	0.613	-1.702	0.089	31	C	T	A	C	0.465	NA	NA	NA	NA
31	C	T	A	C	0.464	NA	NA	NA	NA	32	G	A	C	W	0.031	0.085	0.284	0.298	0.766
32	G	A	C	W	0.032	0.049	0.518	0.095	0.925	32	T	A	C	D	0.149	0.114	0.142	0.804	0.422
32	T	A	C	D	0.150	-0.043	0.265	-0.161	0.872	32	T	A	T	W	0.044	0.102	0.242	0.423	0.673
32	T	A	T	W	0.045	0.394	0.457	0.862	0.389	32	T	G	C	W	0.026	-0.385	0.321	-1.199	0.231
32	T	G	C	W	0.026	-1.179	0.610	-1.932	0.054	32	*	*	*	*	0.002	1.361	1.367	0.996	0.320
32	*	*	*	*	0.002	2.773	2.510	1.105	0.270	32	T	A	C	W	0.747	NA	NA	NA	NA
32	T	A	C	W	0.745	NA	NA	NA	NA	33	A	C	D	A	0.152	0.124	0.145	0.855	0.393
33	A	C	D	A	0.152	0.015	0.272	0.054	0.957	33	A	C	W	A	0.261	0.001	0.123	0.011	0.992
33	A	C	W	A	0.262	0.130	0.232	0.561	0.575	33	A	T	W	C	0.046	0.146	0.238	0.616	0.538
33	A	T	W	C	0.047	0.497	0.449	1.108	0.268	33	G	C	W	A	0.025	-0.369	0.330	-1.118	0.264
33	G	C	W	A	0.025	-1.122	0.628	-1.785	0.075	33	A	C	W	C	0.515	NA	NA	NA	NA
33	A	C	W	C	0.513	NA	NA	NA	NA	34	C	D	A	A	0.151	0.126	0.146	0.864	0.388
34	C	D	A	A	0.152	0.019	0.273	0.071	0.944	34	C	W	A	A	0.261	0.013	0.123	0.108	0.914
34	C	W	A	A	0.262	0.143	0.233	0.616	0.538	34	C	W	A	G	0.025	-0.438	0.335	-1.310	0.191
34	C	W	A	G	0.025	-1.187	0.633	-1.875	0.061	34	T	W	C	A	0.046	0.144	0.238	0.604	0.546
34	T	W	C	A	0.047	0.495	0.449	1.102	0.271	34	C	W	C	A	0.515	NA	NA	NA	NA
34	C	W	C	A	0.514	NA	NA	NA	NA	35	D	A	A	T	0.151	0.140	0.145	0.966	0.334
35	D	A	A	T	0.152	0.042	0.271	0.157	0.875	35	W	A	A	T	0.261	0.020	0.123	0.163	0.871
35	W	A	A	T	0.262	0.152	0.231	0.660	0.510	35	W	A	G	T	0.025	-0.420	0.333	-1.262	0.207
35	W	A	G	T	0.025	-1.160	0.630	-1.843	0.066	35	W	C	A	C	0.019	0.647	0.370	1.747	0.081
35	W	C	A	C	0.020	1.579	0.693	2.280	0.023	35	W	C	A	T	0.542	NA	NA	NA	NA
35	W	C	A	T	0.541	NA	NA	NA	NA	36	A	A	T	C	0.412	0.054	0.105	0.514	0.607
36	A	A	T	C	0.414	0.105	0.198	0.530	0.596	36	A	G	T	C	0.026	-0.476	0.329	-1.447	0.148
36	A	G	T	C	0.026	-1.194	0.619	-1.931	0.054	36	C	A	C	C	0.019	0.612	0.370	1.653	0.099
36	C	A	C	C	0.020	1.566	0.693	2.258	0.024	36	C	A	T	A	0.018	-0.438	0.388	-1.128	0.260
36	C	A	T	A	0.019	-0.427	0.729	-0.586	0.558	36	C	A	T	C	0.524	NA	NA	NA	NA
36	C	A	T	C	0.522	NA	NA	NA	NA	37	A	C	C	G	0.017	0.577	0.395	1.461	0.144
37	A	C	C	G	0.018	1.458	0.734	1.985	0.047	37	A	T	A	G	0.017	-0.565	0.420	-1.344	0.179
37	A	T	A	G	0.017	-0.722	0.782	-0.924	0.356	37	A	T	C	A	0.096	-0.003	0.171	-0.020	0.984
37	A	T	C	A	0.099	0.115	0.321	0.358	0.721	37	G	T	C	G	0.026	-0.499	0.323	-1.546	0.123
37	G	T	C	G	0.026	-1.239	0.609	-2.035	0.042	37	*	*	*	*	0.003	0.668	1.225	0.546	0.585
37	*	*	*	*	0.003	2.369	2.149	1.102	0.271	37	A	T	C	G	0.840	NA	NA	NA	NA
37	A	T	C	G	0.837	NA	NA	NA	NA	38	C	C	G	G	0.017	0.598	0.399	1.497	0.135
38	C	C	G	G	0.018	1.511	0.745	2.028	0.043	38	T	A	G	G	0.017	-0.504	0.423	-1.191	0.234
38	T	A	G	G	0.017	-0.610	0.787	-0.775	0.439	38	T	C	A	G	0.095	0.030	0.173	0.175	0.861
38	T	C	A	G	0.098	0.180	0.323	0.558	0.577	38	T	C	G	C	0.017	0.158	0.375	0.421	0.674
38	T	C	G	C	0.018	0.155	0.653	0.238	0.812	38	*	*	*	*	0.006	0.332	0.927	0.358	0.721
38	*	*	*	*	0.005	1.830	2.044	0.895	0.371	38	T	C	G	G	0.850	NA	NA	NA	NA
38	T	C	G	G	0.844	NA	NA	NA	NA	39	A	G	G	W	0.016	-0.305	0.499	-0.612	0.541
39	A	G	G	W	0.017	-0.355	0.798	-0.445	0.657	39	C	A	G	W	0.097	0.049	0.172	0.286	0.775
39	C	A	G	W	0.100	0.187	0.323	0.578	0.563	39	C	G	C	W	0.017	0.185	0.372	0.497	0.619
39	C	G	C	W	0.018	0.216	0.668	0.323	0.747	39	C	G	G	I	0.081	0.002	0.193	0.012	0.990
39	C	G	G	I	0.081	-0.539	0.362	-1.488	0.137	39	*	*	*	*	0.004	-1.137	1.454	-0.782	0.435
39	*	*	*	*	0.003	-1.826	3.365	-0.542	0.588	39	C	G	G	W	0.785	NA	NA	NA	NA
39	C	G	G	W	0.781	NA	NA	NA	NA	40	A	G	W	A	0.096	0.051	0.172	0.296	0.767
40	A	G	W	A	0.099	0.186	0.322	0.578	0.563	40	G	C	W	A	0.016	0.148	0.380	0.388	0.698
40	G	C	W	A	0.018	0.105	0.664	0.158	0.875	40	G	G	I	A	0.082	0.001	0.189	0.006	0.996
40	G	G	I	A	0.082	-0.509	0.358	-1.424	0.155	40	G	G	W	G	0.053	0.187	0.223	0.840	0.401
40	G	G	W	G	0.053	0.575	0.419	1.374	0.170	40	*	*	*	*	0.005	0.128	0.935	0.137	0.891

Table B1.30. Continued

LDL-C										TC									
Window	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**	**Window**	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**
40	*	*	*	*	0.004	0.976	2.440	0.400	0.689	40	G	G	W	A	0.748	NA	NA	NA	NA
40	G	G	W	A	0.744	NA	NA	NA	NA	41	C	W	A	G	0.018	0.133	0.361	0.369	0.713
41	C	W	A	G	0.019	0.110	0.643	0.171	0.864	41	G	I	A	G	0.083	0.012	0.189	0.065	0.949
41	G	I	A	G	0.082	-0.505	0.357	-1.413	0.158	41	G	W	A	T	0.040	0.233	0.251	0.928	0.353
41	G	W	A	T	0.040	0.376	0.477	0.787	0.431	41	G	W	G	G	0.056	0.190	0.216	0.883	0.378
41	G	W	G	G	0.056	0.608	0.407	1.494	0.136	41	G	W	A	G	0.803	NA	NA	NA	NA
41	G	W	A	G	0.803	NA	NA	NA	NA	42	I	A	G	C	0.081	0.034	0.195	0.175	0.861
42	I	A	G	C	0.081	-0.471	0.365	-1.291	0.197	42	W	A	G	T	0.020	-0.240	0.396	-0.607	0.544
42	W	A	G	T	0.021	-0.232	0.706	-0.329	0.742	42	W	A	T	C	0.040	0.233	0.253	0.922	0.357
42	W	A	T	C	0.040	0.364	0.477	0.763	0.446	42	W	G	G	C	0.056	0.203	0.215	0.941	0.347
42	W	G	G	C	0.056	0.615	0.405	1.517	0.130	42	*	*	*	*	0.002	-1.516	3.231	-0.469	0.639
42	*	*	*	*	0.002	-2.324	3.643	-0.638	0.524	42	W	A	G	C	0.801	NA	NA	NA	NA
42	W	A	G	C	0.801	NA	NA	NA	NA	43	A	G	C	A	0.428	-0.164	0.108	-1.520	0.129
43	A	G	C	A	0.425	-0.310	0.204	-1.520	0.129	43	A	G	T	A	0.022	-0.413	0.353	-1.169	0.243
43	A	G	T	A	0.022	-0.493	0.664	-0.743	0.458	43	A	T	C	G	0.040	0.140	0.255	0.548	0.584
43	A	T	C	G	0.040	0.293	0.483	0.607	0.544	43	G	G	C	A	0.056	0.100	0.218	0.456	0.648
43	G	G	C	A	0.057	0.494	0.414	1.195	0.232	43	A	G	C	G	0.454	NA	NA	NA	NA
43	A	G	C	G	0.456	NA	NA	NA	NA	44	G	C	A	A	0.035	0.199	0.270	0.736	0.462
44	G	C	A	A	0.034	0.554	0.516	1.074	0.283	44	G	C	A	G	0.449	-0.164	0.107	-1.531	0.126
44	G	C	A	G	0.447	-0.284	0.203	-1.404	0.161	44	G	T	A	G	0.022	-0.406	0.354	-1.148	0.251
44	G	T	A	G	0.022	-0.478	0.666	-0.718	0.473	44	T	C	G	G	0.040	0.137	0.255	0.539	0.590
44	T	C	G	G	0.040	0.286	0.484	0.590	0.555	44	G	C	G	G	0.454	NA	NA	NA	NA
44	G	C	G	G	0.456	NA	NA	NA	NA	45	C	A	A	A	0.036	0.246	0.296	0.831	0.406
45	C	A	A	A	0.035	0.695	0.563	1.235	0.217	45	C	A	G	A	0.088	-0.172	0.200	-0.859	0.391
45	C	A	G	A	0.091	-0.330	0.373	-0.886	0.376	45	C	A	G	T	0.353	-0.135	0.115	-1.173	0.241
45	C	A	G	T	0.350	-0.263	0.218	-1.205	0.229	45	C	G	G	T	0.071	0.228	0.213	1.069	0.286
45	C	G	G	T	0.072	0.339	0.402	0.844	0.399	45	T	A	G	A	0.022	-0.359	0.354	-1.013	0.311
45	T	A	G	A	0.023	-0.393	0.663	-0.593	0.553	45	*	*	*	*	0.002	0.195	1.280	0.152	0.879
45	*	*	*	*	0.002	0.140	2.423	0.058	0.954	45	C	G	G	A	0.427	NA	NA	NA	NA
45	C	G	G	A	0.428	NA	NA	NA	NA	46	A	A	A	G	0.036	0.243	0.292	0.831	0.406
46	A	A	A	G	0.036	0.704	0.553	1.272	0.204	46	A	G	A	G	0.112	-0.178	0.173	-1.028	0.304
46	A	G	A	G	0.114	-0.304	0.323	-0.941	0.347	46	A	G	T	A	0.352	-0.124	0.115	-1.078	0.281
46	A	G	T	A	0.349	-0.243	0.218	-1.116	0.265	46	G	G	T	G	0.075	0.232	0.197	1.174	0.241
46	G	G	T	G	0.075	0.354	0.372	0.951	0.342	46	*	*	*	*	0.001	0.405	1.424	0.284	0.776
46	*	*	*	*	0.001	0.183	2.629	0.070	0.944	46	G	G	A	G	0.424	NA	NA	NA	NA
46	G	G	A	G	0.425	NA	NA	NA	NA	47	A	A	G	C	0.032	0.273	0.330	0.829	0.407
47	A	A	G	C	0.032	0.737	0.594	1.242	0.215	47	G	A	G	A	0.072	-0.034	0.217	-0.155	0.877
47	G	A	G	A	0.069	-0.161	0.413	-0.389	0.697	47	G	T	A	A	0.014	-0.904	0.556	-1.627	0.104
47	G	T	A	A	0.013	-1.096	1.095	-1.001	0.317	47	G	T	A	C	0.338	-0.078	0.117	-0.672	0.502
47	G	T	A	C	0.335	-0.199	0.220	-0.905	0.366	47	G	T	G	A	0.024	0.201	0.361	0.558	0.577
47	G	T	G	A	0.023	0.453	0.713	0.635	0.525	47	G	T	G	C	0.051	0.343	0.248	1.382	0.167
47	G	T	G	C	0.052	0.425	0.466	0.913	0.361	47	*	*	*	*	0.003	0.334	1.508	0.221	0.825
47	*	*	*	*	0.003	-0.120	2.316	-0.052	0.959	47	G	A	G	C	0.468	NA	NA	NA	NA
47	G	A	G	C	0.474	NA	NA	NA	NA	48	A	G	A	G	0.075	-0.045	0.207	-0.215	0.830
48	A	G	A	G	0.072	-0.125	0.396	-0.315	0.753	48	A	G	C	A	0.203	0.216	0.140	1.544	0.123
48	A	G	C	A	0.205	0.273	0.263	1.038	0.300	48	A	G	C	G	0.293	0.062	0.125	0.498	0.619
48	A	G	C	G	0.297	0.333	0.237	1.403	0.161	48	T	A	A	G	0.011	-0.565	0.651	-0.869	0.385
48	T	A	A	G	0.011	0.012	1.204	0.010	0.992	48	T	G	A	G	0.023	0.359	0.366	0.980	0.327
48	T	G	A	G	0.022	0.797	0.722	1.105	0.270	48	T	G	C	G	0.051	0.410	0.246	1.667	0.096
48	T	G	C	G	0.052	0.618	0.464	1.332	0.183	48	*	*	*	*	0.002	3.421	1.654	2.069	0.039
48	*	*	*	*	0.001	7.207	3.267	2.206	0.028	48	T	A	C	G	0.342	NA	NA	NA	NA
48	T	A	C	G	0.339	NA	NA	NA	NA	49	A	A	G	C	0.011	-0.128	0.588	-0.218	0.827
49	A	A	G	C	0.011	0.587	1.083	0.542	0.588	49	G	A	G	C	0.099	0.034	0.183	0.187	0.852
49	G	A	G	C	0.095	0.061	0.350	0.173	0.862	49	G	C	A	C	0.205	0.236	0.139	1.694	0.091
49	G	C	A	C	0.207	0.311	0.262	1.185	0.236	49	G	C	G	A	0.096	0.188	0.188	0.998	0.318
49	G	C	G	A	0.098	0.470	0.354	1.328	0.185	49	G	C	G	C	0.244	0.113	0.135	0.837	0.403
49	G	C	G	C	0.247	0.336	0.254	1.325	0.186	49	*	*	*	*	0.001	3.446	1.577	2.185	0.029
49	*	*	*	*	0.002	2.431	2.508	0.969	0.333	49	A	C	G	C	0.344	NA	NA	NA	NA
49	A	C	G	C	0.340	NA	NA	NA	NA	50	A	G	C	A	0.109	0.010	0.166	0.060	0.953
50	A	G	C	A	0.105	0.006	0.316	0.018	0.986	50	C	A	C	A	0.205	0.257	0.126	2.040	0.042
50	C	A	C	A	0.206	0.266	0.238	1.119	0.264	50	C	G	A	A	0.096	0.190	0.183	1.035	0.301
50	C	G	A	A	0.099	0.407	0.338	1.205	0.228	50	C	G	C	G	0.023	0.347	0.330	1.050	0.294
50	C	G	C	G	0.024	0.762	0.619	1.230	0.219	50	C	G	C	A	0.567	NA	NA	NA	NA
50	C	G	C	A	0.566	NA	NA	NA	NA	51	A	C	A	G	0.205	0.232	0.138	1.685	0.092
51	A	C	A	G	0.207	0.268	0.260	1.029	0.304	51	G	A	A	G	0.096	0.206	0.187	1.099	0.272
51	G	A	A	G	0.098	0.484	0.352	1.374	0.170	51	G	C	A	G	0.316	0.062	0.121	0.512	0.609
51	G	C	A	G	0.315	0.175	0.232	0.754	0.451	51	G	C	G	G	0.023	0.371	0.334	1.111	0.267
51	G	C	G	G	0.024	0.841	0.628	1.339	0.181	51	*	*	*	*	0.001	3.374	0.000	6.84E+15	0.000
51	*	*	*	*	0.002	2.170	2.514	0.863	0.388	51	G	C	A	T	0.359	NA	NA	NA	NA
51	G	C	A	T	0.355	NA	NA	NA	NA	52	A	A	G	T	0.095	0.062	0.182	0.340	0.734
52	A	A	G	T	0.097	0.316	0.345	0.916	0.360	52	C	A	T	C	0.135	-0.297	0.156	-1.907	0.057
52	C	A	T	C	0.132	-0.290	0.296	-0.979	0.328	52	C	A	T	T	0.224	-0.037	0.127	-0.295	0.768
52	C	A	T	T	0.222	-0.153	0.241	-0.634	0.527	52	C	G	G	T	0.023	0.234	0.332	0.707	0.480
52	C	G	G	T	0.023	0.625	0.622	1.004	0.315	52	C	A	G	T	0.522	NA	NA	NA	NA
52	*	*	*	*	0.001	-2.985	3.497	-0.854	0.394	53	A	T	C	C	0.135	-0.308	0.155	-1.987	0.047
52	C	A	G	T	0.523	NA	NA	NA	NA	53	A	T	T	C	0.222	-0.051	0.125	-0.408	0.684
53	A	T	C	C	0.132	-0.330	0.296	-1.116	0.265	53	G	G	T	C	0.023	0.223	0.332	0.670	0.503
53	A	T	T	C	0.222	-0.206	0.238	-0.865	0.387	53	*	*	*	*	0.001	0.192	1.378	0.140	0.889
53	G	G	T	C	0.023	0.568	0.624	0.910	0.363	53	A	G	T	C	0.618	NA	NA	NA	NA
53	*	*	*	*	0.001	-0.923	2.675	-0.345	0.730	54	G	T	C	C	0.017	-0.075	0.368	-0.203	0.839
53	A	G	T	C	0.621	NA	NA	NA	NA	54	T	C	C	T	0.135	-0.319	0.155	-2.063	0.039

Table B1.30. Continued

LDL-C										TC									
Window	loc.1	loc.2	loc.3	loc.4	hap.freq	coef	se	t.stat	pval	Window	loc.1	loc.2	loc.3	loc.4	hap.freq	coef	se	t.stat	pval
54	G	T	C	C	0.018	-0.332	0.662	-0.501	0.616	54	T	T	C	T	0.222	-0.062	0.126	-0.493	0.622
54	T	C	C	T	0.132	-0.366	0.296	-1.235	0.217	54	*	*	*	*	0.001	0.182	1.377	0.132	0.895
54	T	T	C	T	0.222	-0.239	0.239	-1.001	0.317	54	G	T	C	T	0.624	NA	NA	NA	NA
54	*	*	*	*	0.001	-0.954	2.681	-0.356	0.722	55	C	C	T	A	0.135	-0.292	0.153	-1.904	0.057
54	G	T	C	T	0.626	NA	NA	NA	NA	55	T	C	C	A	0.017	-0.056	0.364	-0.154	0.877
55	C	C	T	A	0.132	-0.320	0.292	-1.096	0.273	55	T	C	T	C	0.131	-0.002	0.148	-0.016	0.987
55	T	C	C	A	0.018	-0.297	0.653	-0.455	0.649	55	*	*	*	*	0.001	0.174	1.376	0.126	0.899
55	T	C	T	C	0.130	-0.211	0.283	-0.746	0.456	55	T	C	T	A	0.715	NA	NA	NA	NA
55	*	*	*	*	0.001	-1.035	2.727	-0.379	0.704	56	C	C	A	G	0.017	-0.007	0.364	-0.020	0.984
55	T	C	T	A	0.718	NA	NA	NA	NA	56	C	T	C	G	0.130	0.052	0.146	0.358	0.721
56	C	C	A	G	0.018	-0.245	0.651	-0.377	0.707	56	*	*	*	*	0.002	0.056	1.379	0.041	0.968
56	C	T	C	G	0.129	-0.168	0.279	-0.602	0.547	56	C	T	A	G	0.850	NA	NA	NA	NA
56	*	*	*	*	0.002	-0.225	2.688	-0.084	0.933	57	C	A	G	G	0.017	-0.007	0.365	-0.020	0.984
56	C	T	A	G	0.851	NA	NA	NA	NA	57	T	A	G	A	0.034	0.004	0.274	0.015	0.988
57	C	A	G	G	0.018	-0.260	0.652	-0.398	0.691	57	T	C	G	G	0.132	0.055	0.146	0.378	0.706
57	T	A	G	A	0.033	-0.197	0.524	-0.375	0.707	57	T	A	G	G	0.817	NA	NA	NA	NA
57	T	C	G	G	0.131	-0.183	0.277	-0.662	0.508	58	A	G	A	C	0.034	0.010	0.273	0.037	0.971
57	T	A	G	G	0.818	NA	NA	NA	NA	58	C	G	G	C	0.038	0.154	0.271	0.569	0.570
58	A	G	A	C	0.033	-0.167	0.523	-0.319	0.750	58	C	G	G	T	0.096	0.053	0.171	0.309	0.758
58	C	G	G	C	0.038	0.429	0.513	0.838	0.403	58	A	G	G	C	0.833	NA	NA	NA	NA
58	C	G	G	T	0.095	-0.328	0.326	-1.008	0.314	59	G	A	C	A	0.034	0.024	0.274	0.089	0.929
58	A	G	G	C	0.834	NA	NA	NA	NA	59	G	G	C	G	0.112	0.160	0.161	0.996	0.319
59	G	A	C	A	0.033	-0.155	0.525	-0.296	0.768	59	G	G	T	A	0.091	0.128	0.179	0.716	0.474
59	G	G	C	G	0.112	0.209	0.304	0.688	0.492	59	G	G	C	A	0.762	NA	NA	NA	NA
59	G	G	T	A	0.090	-0.204	0.342	-0.596	0.551	60	A	C	A	G	0.033	-0.018	0.274	-0.066	0.947
59	G	G	C	A	0.764	NA	NA	NA	NA	60	G	C	A	A	0.097	-0.388	0.168	-2.312	0.021
60	A	C	A	G	0.032	-0.279	0.533	-0.524	0.601	60	G	C	G	G	0.112	0.117	0.161	0.729	0.466
60	G	C	A	A	0.095	-0.671	0.319	-2.101	0.036	60	G	T	A	G	0.091	0.088	0.180	0.489	0.625
60	G	C	G	G	0.112	0.133	0.305	0.437	0.662	60	G	C	A	G	0.667	NA	NA	NA	NA
60	G	T	A	G	0.090	-0.276	0.343	-0.806	0.420	61	C	A	A	A	0.097	-0.389	0.167	-2.330	0.020
60	G	C	A	G	0.670	NA	NA	NA	NA	61	C	G	G	A	0.112	0.105	0.161	0.656	0.512
61	C	A	A	A	0.096	-0.640	0.317	-2.020	0.044	61	T	A	G	A	0.092	0.078	0.179	0.438	0.662
61	C	G	G	A	0.112	0.137	0.305	0.449	0.653	61	*	*	*	*	0.009	-0.714	0.524	-1.363	0.173
61	T	A	G	A	0.091	-0.268	0.342	-0.783	0.434	61	C	A	G	A	0.691	NA	NA	NA	NA
61	*	*	*	*	0.009	-0.641	1.037	-0.618	0.537	62	A	A	A	G	0.097	-0.403	0.166	-2.428	0.015
61	C	A	G	A	0.693	NA	NA	NA	NA	62	G	G	A	G	0.111	0.097	0.159	0.610	0.542
62	A	A	A	G	0.096	-0.625	0.316	-1.979	0.048	62	*	*	*	*	0.013	-0.894	0.456	-1.961	0.050
62	G	G	A	G	0.112	0.164	0.302	0.542	0.588	62	A	G	A	G	0.778	NA	NA	NA	NA
62	*	*	*	*	0.013	-1.172	0.860	-1.363	0.173	63	A	A	G	G	0.095	-0.419	0.166	-2.525	0.012
62	A	G	A	G	0.779	NA	NA	NA	NA	63	*	*	*	*	0.015	-0.826	0.422	-1.960	0.050
63	A	A	G	G	0.094	-0.618	0.316	-1.958	0.051	63	G	A	G	G	0.890	NA	NA	NA	NA
63	*	*	*	*	0.015	-1.324	0.814	-1.626	0.104	64	A	G	G	C	0.039	-0.115	0.264	-0.438	0.662
63	G	A	G	G	0.891	NA	NA	NA	NA	64	*	*	*	*	0.015	-0.786	0.429	-1.833	0.067
64	A	G	G	C	0.040	-0.070	0.493	-0.142	0.887	64	A	G	G	T	0.947	NA	NA	NA	NA
64	*	*	*	*	0.015	-1.255	0.800	-1.569	0.117	65	G	G	C	C	0.040	-0.131	0.262	-0.499	0.618
64	A	G	G	T	0.946	NA	NA	NA	NA	65	G	G	T	A	0.098	-0.348	0.167	-2.082	0.038
65	G	G	C	C	0.041	-0.111	0.492	-0.225	0.822	65	*	*	*	*	0.005	-0.934	0.739	-1.263	0.207
65	G	G	T	A	0.097	-0.507	0.318	-1.592	0.112	65	G	G	T	C	0.857	NA	NA	NA	NA
65	*	*	*	*	0.006	-2.268	1.266	-1.792	0.074	66	G	C	C	C	0.040	-0.173	0.261	-0.664	0.507
65	G	G	T	C	0.857	NA	NA	NA	NA	66	G	T	A	C	0.096	-0.361	0.172	-2.095	0.036
66	G	C	C	C	0.042	-0.235	0.488	-0.482	0.630	66	G	T	C	G	0.063	-0.119	0.215	-0.555	0.579
66	G	T	A	C	0.097	-0.513	0.320	-1.606	0.109	66	*	*	*	*	0.003	0.416	1.248	0.333	0.739
66	G	T	C	G	0.065	-0.336	0.382	-0.879	0.380	66	G	T	C	C	0.798	NA	NA	NA	NA
66	*	*	*	*	0.001	-2.670	2.759	-0.968	0.334	67	C	C	C	C	0.040	-0.147	0.262	-0.562	0.574
66	G	T	C	C	0.795	NA	NA	NA	NA	67	T	A	C	C	0.098	-0.323	0.169	-1.913	0.056
67	C	C	C	C	0.042	-0.170	0.490	-0.347	0.729	67	T	C	C	T	0.134	0.134	0.152	0.885	0.376
67	T	A	C	C	0.097	-0.460	0.322	-1.426	0.154	67	T	C	G	C	0.065	-0.078	0.206	-0.379	0.705
67	T	C	C	T	0.135	0.291	0.288	1.011	0.313	67	T	C	C	C	0.663	NA	NA	NA	NA
67	T	C	G	C	0.065	-0.289	0.384	-0.751	0.453	68	A	C	C	A	0.098	-0.386	0.173	-2.225	0.026
67	T	C	C	C	0.661	NA	NA	NA	NA	68	C	C	C	G	0.246	-0.210	0.127	-1.652	0.099
68	A	C	C	A	0.097	-0.498	0.331	-1.503	0.133	68	C	C	T	A	0.134	0.069	0.158	0.434	0.665
68	C	C	C	G	0.243	-0.160	0.243	-0.658	0.511	68	C	G	C	A	0.065	-0.149	0.211	-0.709	0.479
68	C	C	T	A	0.135	0.252	0.300	0.840	0.401	68	C	C	C	A	0.456	NA	NA	NA	NA
68	C	G	C	A	0.066	-0.340	0.392	-0.868	0.386	69	C	C	A	T	0.063	0.181	0.223	0.814	0.416
68	C	C	C	A	0.459	NA	NA	NA	NA	69	C	C	G	T	0.248	-0.097	0.125	-0.772	0.440
69	C	C	A	T	0.064	0.685	0.421	1.627	0.104	69	C	T	A	C	0.135	0.161	0.158	1.023	0.306
69	C	C	G	T	0.245	0.047	0.239	0.197	0.844	69	G	C	A	T	0.064	-0.051	0.211	-0.241	0.810
69	C	T	A	C	0.135	0.426	0.298	1.427	0.154	69	*	*	*	*	0.002	-1.194	1.397	-0.855	0.393
69	G	C	A	T	0.065	-0.164	0.392	-0.419	0.675	69	C	C	A	C	0.488	NA	NA	NA	NA
69	*	*	*	*	0.002	-1.231	2.643	-0.466	0.641	70	C	A	C	T	0.142	-0.168	0.163	-1.028	0.304
69	C	C	A	C	0.489	NA	NA	NA	NA	70	C	A	T	A	0.102	0.021	0.187	0.112	0.911
70	C	A	C	T	0.141	-0.527	0.312	-1.689	0.092	70	C	A	T	T	0.025	0.235	0.364	0.645	0.519
70	C	A	T	A	0.104	-0.042	0.352	-0.120	0.904	70	C	G	T	T	0.247	-0.137	0.132	-1.033	0.302
70	C	A	T	T	0.025	0.687	0.697	0.985	0.325	70	T	A	C	T	0.134	0.146	0.165	0.882	0.378
70	C	G	T	T	0.244	-0.103	0.253	-0.407	0.684	70	*	*	*	*	0.003	-3.126	0.000	-2.46E+16	0.000
70	T	A	C	T	0.135	0.244	0.311	0.786	0.432	70	C	A	C	A	0.348	NA	NA	NA	NA
70	*	*	*	*	0.002	-3.727	NA	NA	NA	71	A	C	T	C	0.276	-0.038	0.136	-0.281	0.778
70	C	A	C	A	0.349	NA	NA	NA	NA	71	A	T	A	C	0.102	-0.021	0.193	-0.111	0.911
71	A	C	T	C	0.276	-0.164	0.258	-0.633	0.527	71	A	T	T	C	0.026	0.211	0.379	0.556	0.578
71	A	T	A	C	0.103	-0.065	0.365	-0.177	0.859	71	G	T	T	C	0.227	-0.143	0.136	-1.053	0.293
71	A	T	T	C	0.026	0.783	0.733	1.068	0.286	71	G	T	T	T	0.020	-0.146	0.354	-0.413	0.680

Table B1.30. Continued

LDL-C										TC									
Window	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**	**Window**	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**
71	G	T	T	C	0.224	-0.073	0.259	-0.280	0.779	71	*	*	*	*	0.002	-2.008	NA	NA	NA
71	G	T	T	T	0.019	-0.533	0.674	-0.791	0.429	71	A	C	A	C	0.348	NA	NA	NA	NA
71	*	*	*	*	0.002	-3.560	NA	NA	NA	72	C	A	C	C	0.150	0.273	0.171	1.597	0.111
71	A	C	A	C	0.349	NA	NA	NA	NA	72	C	A	C	T	0.199	0.000	0.166	0.001	0.999
72	C	A	C	C	0.151	0.283	0.320	0.884	0.377	72	T	A	C	T	0.101	-0.049	0.193	-0.253	0.800
72	C	A	C	T	0.197	0.220	0.313	0.702	0.483	72	T	T	C	T	0.256	0.019	0.152	0.125	0.901
72	T	A	C	T	0.104	0.024	0.359	0.068	0.946	72	T	T	T	T	0.018	-0.191	0.398	-0.480	0.632
72	T	T	C	T	0.251	0.277	0.289	0.958	0.338	72	*	*	*	*	0.002	1.370	2.848	0.481	0.631
72	T	T	T	T	0.018	-0.475	0.705	-0.674	0.500	72	C	T	C	T	0.274	NA	NA	NA	NA
72	*	*	*	*	0.002	1.411	NA	NA	NA	73	A	C	C	T	0.148	0.261	0.154	1.694	0.091
72	C	T	C	T	0.276	NA	NA	NA	NA	73	A	C	T	C	0.011	0.113	0.492	0.230	0.818
73	A	C	C	T	0.149	0.142	0.294	0.484	0.628	73	A	C	T	T	0.289	-0.033	0.118	-0.279	0.781
73	A	C	T	C	0.011	0.479	0.934	0.513	0.608	73	T	T	T	T	0.018	-0.288	0.393	-0.734	0.463
73	A	C	T	T	0.291	-0.003	0.225	-0.014	0.989	73	*	*	*	*	0.003	1.651	1.454	1.135	0.257
73	T	T	T	T	0.018	-0.719	0.888	-0.810	0.418	73	T	C	T	T	0.531	NA	NA	NA	NA
73	*	*	*	*	0.003	1.777	7.987	0.223	0.824	74	C	C	T	T	0.153	0.236	0.148	1.587	0.113
73	T	C	T	T	0.528	NA	NA	NA	NA	74	C	T	C	C	0.011	0.088	0.493	0.178	0.859
74	C	C	T	T	0.153	0.066	0.272	0.241	0.809	74	T	T	T	C	0.018	-0.184	0.410	-0.448	0.654
74	C	T	C	C	0.011	0.416	0.937	0.444	0.657	74	*	*	*	*	0.006	0.563	0.976	0.577	0.564
74	T	T	T	C	0.018	-0.694	0.710	-0.978	0.329	74	C	T	T	C	0.812	NA	NA	NA	NA
74	*	*	*	*	0.006	1.258	1.515	0.830	0.407	75	C	T	T	T	0.153	0.248	0.153	1.621	0.106
74	C	T	T	C	0.812	NA	NA	NA	NA	75	T	C	C	G	0.012	0.143	0.483	0.297	0.767
75	C	T	T	T	0.153	0.157	0.287	0.548	0.584	75	T	T	C	G	0.393	-0.051	0.112	-0.458	0.647
75	T	C	C	G	0.011	0.541	0.922	0.587	0.558	75	*	*	*	*	0.006	-0.278	0.794	-0.349	0.727
75	T	T	C	G	0.389	0.052	0.213	0.242	0.809	75	T	T	C	T	0.437	NA	NA	NA	NA
75	*	*	*	*	0.005	-0.136	1.569	-0.086	0.931	76	C	C	G	G	0.012	0.193	0.482	0.401	0.688
75	T	T	C	T	0.441	NA	NA	NA	NA	76	T	C	T	A	0.290	0.158	0.122	1.293	0.197
76	C	C	G	G	0.011	0.490	0.918	0.533	0.594	76	T	C	T	G	0.151	-0.113	0.156	-0.725	0.469
76	T	C	T	A	0.291	0.234	0.231	1.012	0.312	76	T	T	T	A	0.155	0.291	0.156	1.864	0.063
76	T	C	T	G	0.154	-0.474	0.296	-1.601	0.110	76	*	*	*	*	0.003	-0.813	0.988	-0.823	0.411
76	T	T	T	A	0.155	0.113	0.293	0.386	0.699	76	T	C	G	G	0.389	NA	NA	NA	NA
76	*	*	*	*	0.003	-1.721	1.948	-0.884	0.377	77	C	G	G	A	0.047	-0.137	0.275	-0.498	0.619
76	T	C	G	G	0.385	NA	NA	NA	NA	77	C	T	A	A	0.119	0.114	0.175	0.651	0.515
77	C	G	G	A	0.046	-0.301	0.524	-0.573	0.567	77	C	T	A	G	0.172	0.138	0.148	0.930	0.353
77	C	T	A	A	0.120	0.260	0.331	0.786	0.432	77	C	T	G	A	0.011	-0.156	0.550	-0.284	0.777
77	C	T	A	G	0.172	0.119	0.281	0.423	0.672	77	C	T	G	G	0.140	-0.133	0.166	-0.800	0.424
77	C	T	G	A	0.011	-0.263	1.038	-0.254	0.800	77	T	T	A	A	0.150	0.246	0.160	1.542	0.123
77	C	T	G	G	0.142	-0.541	0.313	-1.728	0.084	77	*	*	*	*	0.008	0.050	0.685	0.073	0.942
77	T	T	A	A	0.151	0.014	0.299	0.046	0.963	77	C	G	G	G	0.354	NA	NA	NA	NA
77	*	*	*	*	0.007	-0.164	1.396	-0.118	0.906	78	G	G	A	G	0.046	-0.143	0.283	-0.504	0.614
77	C	G	G	G	0.351	NA	NA	NA	NA	78	G	G	G	A	0.042	0.143	0.254	0.564	0.573
78	G	G	A	G	0.045	-0.389	0.548	-0.711	0.477	78	T	A	A	G	0.267	0.203	0.137	1.487	0.137
78	G	G	G	A	0.043	0.294	0.476	0.618	0.537	78	T	A	G	G	0.178	0.175	0.152	1.151	0.250
78	T	A	A	G	0.269	0.155	0.258	0.600	0.549	78	T	G	A	G	0.011	-0.108	0.545	-0.198	0.843
78	T	A	G	G	0.177	0.180	0.290	0.620	0.536	78	T	G	G	G	0.140	-0.111	0.169	-0.656	0.512
78	T	G	A	G	0.011	-0.105	1.029	-0.102	0.919	78	*	*	*	*	0.003	-0.810	0.970	-0.835	0.404
78	T	G	G	G	0.142	-0.515	0.320	-1.608	0.108	78	G	G	G	G	0.312	NA	NA	NA	NA
78	*	*	*	*	0.003	-1.696	1.919	-0.884	0.377	79	A	G	G	A	0.147	-0.048	0.174	-0.274	0.784
78	G	G	G	G	0.308	NA	NA	NA	NA	79	A	G	G	G	0.029	-0.043	0.371	-0.115	0.908
79	A	G	G	A	0.148	0.170	0.330	0.517	0.606	79	G	A	G	G	0.056	-0.326	0.257	-1.269	0.205
79	A	G	G	G	0.029	-0.696	0.707	-0.984	0.326	79	G	G	A	A	0.042	-0.026	0.257	-0.099	0.921
79	G	A	G	G	0.056	-0.458	0.501	-0.913	0.361	79	G	G	G	A	0.251	-0.146	0.142	-1.027	0.305
79	G	G	A	A	0.042	0.225	0.486	0.463	0.644	79	G	G	G	G	0.203	-0.369	0.152	-2.421	0.016
79	G	G	G	A	0.251	-0.256	0.267	-0.958	0.338	79	*	*	*	*	0.002	0.355	NA	NA	NA
79	G	G	G	G	0.201	-0.412	0.288	-1.433	0.152	79	A	A	G	G	0.270	NA	NA	NA	NA
79	*	*	*	*	0.002	1.234	0.000	2.05E+15	0.000	80	A	G	G	W	0.327	0.058	0.119	0.485	0.628
79	A	A	G	G	0.273	NA	NA	NA	NA	80	G	A	A	W	0.041	0.083	0.256	0.325	0.745
80	A	G	G	W	0.328	0.048	0.225	0.214	0.830	80	G	G	A	D	0.018	0.368	0.383	0.959	0.338
80	G	A	A	W	0.042	0.325	0.479	0.679	0.497	80	G	G	G	W	0.231	-0.220	0.132	-1.669	0.095
80	G	G	A	D	0.019	0.747	0.716	1.042	0.298	80	*	*	*	*	0.003	0.612	1.772	0.345	0.730
80	G	G	G	W	0.229	-0.330	0.250	-1.322	0.187	80	G	G	A	W	0.380	NA	NA	NA	NA
80	*	*	*	*	0.002	1.642	3.351	0.490	0.624	81	A	A	W	T	0.042	0.140	0.248	0.564	0.573
80	G	G	A	W	0.379	NA	NA	NA	NA	81	G	A	D	A	0.018	0.443	0.381	1.163	0.245
81	A	A	W	T	0.042	0.446	0.467	0.957	0.339	81	G	A	W	A	0.204	0.049	0.130	0.380	0.704
81	G	A	D	A	0.019	0.866	0.715	1.212	0.226	81	G	A	W	T	0.174	0.128	0.141	0.904	0.366
81	G	A	W	A	0.202	0.011	0.245	0.044	0.965	81	*	*	*	*	0.002	-0.634	NA	NA	NA
81	G	A	W	T	0.175	0.349	0.267	1.304	0.192	81	G	G	W	T	0.561	NA	NA	NA	NA
81	*	*	*	*	0.002	-1.635	NA	NA	NA	82	A	D	A	T	0.018	0.443	0.384	1.155	0.249
81	G	G	W	T	0.560	NA	NA	NA	NA	82	A	W	A	T	0.204	0.048	0.130	0.366	0.715
82	A	D	A	T	0.019	0.862	0.720	1.197	0.232	82	A	W	T	G	0.064	0.070	0.209	0.335	0.737
82	A	W	A	T	0.202	0.003	0.247	0.013	0.990	82	A	W	T	T	0.151	0.155	0.152	1.020	0.308
82	A	W	T	G	0.065	0.236	0.389	0.609	0.543	82	*	*	*	*	0.002	-0.597	0.000	-1.05E+15	0.000
82	A	W	T	T	0.152	0.431	0.287	1.502	0.133	82	G	W	T	T	0.561	NA	NA	NA	NA
82	*	*	*	*	0.002	-1.607	0.000	-2.00E+15	0.000	83	D	A	T	T	0.018	0.536	0.385	1.392	0.164
82	G	W	T	T	0.560	NA	NA	NA	NA	83	W	A	T	T	0.204	0.133	0.137	0.973	0.331
83	D	A	T	T	0.019	0.927	0.729	1.273	0.204	83	W	T	G	A	0.064	0.144	0.212	0.679	0.497
83	W	A	T	T	0.202	0.060	0.261	0.232	0.817	83	W	T	T	T	0.298	0.263	0.122	2.153	0.032
83	W	T	G	A	0.065	0.280	0.398	0.705	0.481	83	W	T	T	A	0.414	NA	NA	NA	NA
83	W	T	T	T	0.301	0.317	0.231	1.371	0.171	84	A	T	T	G	0.222	-0.101	0.143	-0.706	0.480
83	W	T	T	A	0.413	NA	NA	NA	NA	84	T	G	A	G	0.064	-0.104	0.218	-0.476	0.634
84	A	T	T	G	0.220	-0.202	0.270	-0.748	0.455	84	T	T	A	A	0.146	-0.067	0.163	-0.411	0.681

Table B1.30. Continued

LDL-C										TC									
Window	loc.1	loc.2	loc.3	loc.4	hap.freq	coef	se	t.stat	pval	Window	loc.1	loc.2	loc.3	loc.4	hap.freq	coef	se	t.stat	pval
84	T	G	A	G	0.065	-0.027	0.406	-0.067	0.947	84	T	T	A	G	0.268	-0.362	0.135	-2.681	0.007
84	T	T	A	A	0.149	0.067	0.307	0.218	0.828	84	T	T	T	G	0.299	NA	NA	NA	NA
84	T	T	A	G	0.263	-0.524	0.257	-2.041	0.042	85	G	A	G	C	0.018	-0.153	0.387	-0.396	0.692
84	T	T	T	G	0.301	NA	NA	NA	NA	85	G	A	G	T	0.046	-0.028	0.243	-0.115	0.909
85	G	A	G	C	0.018	0.095	0.739	0.129	0.898	85	T	A	A	C	0.146	-0.029	0.152	-0.187	0.851
85	G	A	G	T	0.048	0.054	0.449	0.121	0.904	85	T	A	G	C	0.268	-0.323	0.119	-2.709	0.007
85	T	A	A	C	0.149	0.137	0.288	0.475	0.635	85	T	T	G	C	0.522	NA	NA	NA	NA
85	T	A	G	C	0.262	-0.456	0.228	-2.000	0.046	86	A	A	C	A	0.146	-0.028	0.152	-0.186	0.852
85	T	T	G	C	0.523	NA	NA	NA	NA	86	A	G	C	A	0.267	-0.326	0.119	-2.740	0.006
86	A	A	C	A	0.149	0.137	0.288	0.477	0.633	86	A	G	C	G	0.019	-0.101	0.378	-0.268	0.789
86	A	G	C	A	0.262	-0.457	0.228	-2.006	0.045	86	A	G	T	G	0.046	-0.030	0.243	-0.124	0.901
86	A	G	C	G	0.018	0.100	0.724	0.138	0.890	86	T	G	C	A	0.522	NA	NA	NA	NA
86	A	G	T	G	0.048	0.056	0.448	0.124	0.901	87	A	C	A	A	0.145	0.085	0.148	0.578	0.563
86	T	G	C	A	0.523	NA	NA	NA	NA	87	G	C	A	T	0.017	-0.076	0.382	-0.199	0.842
87	A	C	A	A	0.149	0.300	0.277	1.083	0.279	87	G	C	G	A	0.018	-0.010	0.379	-0.026	0.979
87	G	C	A	T	0.016	-0.064	0.728	-0.088	0.930	87	G	T	G	A	0.046	0.074	0.240	0.309	0.758
87	G	C	G	A	0.018	0.234	0.721	0.325	0.745	87	G	C	A	A	0.773	NA	NA	NA	NA
87	G	T	G	A	0.048	0.195	0.442	0.442	0.659	88	C	A	T	C	0.017	-0.093	0.381	-0.244	0.807
87	G	C	A	A	0.769	NA	NA	NA	NA	88	C	G	A	G	0.018	-0.026	0.378	-0.070	0.945
88	C	A	T	C	0.016	-0.122	0.725	-0.168	0.866	88	T	G	A	G	0.046	0.055	0.238	0.231	0.817
88	C	G	A	G	0.018	0.184	0.720	0.255	0.799	88	C	A	A	C	0.919	NA	NA	NA	NA
88	T	G	A	G	0.048	0.132	0.438	0.301	0.764	89	A	A	C	T	0.376	-0.287	0.105	-2.718	0.007
88	C	A	A	C	0.918	NA	NA	NA	NA	89	A	T	C	C	0.017	-0.199	0.382	-0.522	0.602
89	A	A	C	T	0.373	-0.373	0.202	-1.844	0.066	89	G	A	G	T	0.065	-0.080	0.205	-0.388	0.698
89	A	T	C	C	0.016	-0.254	0.729	-0.348	0.728	89	A	A	C	C	0.543	NA	NA	NA	NA
89	G	A	G	T	0.066	0.005	0.383	0.013	0.990	90	A	C	C	G	0.069	-0.020	0.211	-0.094	0.925
89	A	A	C	C	0.544	NA	NA	NA	NA	90	A	C	T	G	0.374	-0.309	0.109	-2.842	0.005
90	A	C	C	G	0.069	0.101	0.402	0.252	0.801	90	A	G	T	G	0.065	-0.132	0.208	-0.635	0.526
90	A	C	T	G	0.371	-0.388	0.206	-1.881	0.060	90	T	C	C	A	0.017	-0.217	0.384	-0.566	0.571
90	A	G	T	G	0.066	-0.047	0.388	-0.122	0.903	90	A	C	C	A	0.475	NA	NA	NA	NA
90	T	C	C	A	0.016	-0.254	0.732	-0.346	0.729	91	C	C	G	T	0.069	-0.043	0.210	-0.206	0.837
90	A	C	C	A	0.476	NA	NA	NA	NA	91	C	T	G	C	0.257	-0.334	0.121	-2.762	0.006
91	C	C	G	T	0.069	0.036	0.403	0.088	0.930	91	C	T	G	T	0.116	-0.228	0.167	-1.367	0.172
91	C	T	G	C	0.252	-0.449	0.230	-1.956	0.051	91	G	T	G	C	0.065	-0.121	0.208	-0.580	0.562
91	C	T	G	T	0.118	-0.215	0.316	-0.680	0.497	91	*	*	*	*	0.002	-0.462	1.378	-0.335	0.737
91	G	T	G	C	0.066	-0.028	0.386	-0.072	0.943	91	C	C	A	T	0.491	NA	NA	NA	NA
91	*	*	*	*	0.002	0.053	2.622	0.020	0.984	92	C	G	T	G	0.069	-0.041	0.210	-0.196	0.845
91	C	C	A	T	0.492	NA	NA	NA	NA	92	T	G	C	A	0.062	-0.138	0.211	-0.654	0.513
92	C	G	T	G	0.069	0.039	0.403	0.098	0.922	92	T	G	C	G	0.260	-0.327	0.120	-2.728	0.007
92	T	G	C	A	0.063	-0.032	0.392	-0.083	0.934	92	T	G	T	G	0.116	-0.227	0.167	-1.360	0.174
92	T	G	C	G	0.255	-0.442	0.228	-1.939	0.053	92	*	*	*	*	0.002	-0.458	1.381	-0.331	0.740
92	T	G	T	G	0.118	-0.215	0.315	-0.683	0.495	92	C	A	T	G	0.491	NA	NA	NA	NA
92	*	*	*	*	0.002	0.066	2.626	0.025	0.980	93	G	C	A	G	0.064	-0.091	0.207	-0.440	0.660
92	C	A	T	G	0.492	NA	NA	NA	NA	93	G	C	G	A	0.257	-0.346	0.120	-2.878	0.004
93	G	C	A	G	0.065	0.001	0.385	0.003	0.998	93	G	T	G	A	0.185	-0.165	0.139	-1.184	0.237
93	G	C	G	A	0.252	-0.463	0.229	-2.023	0.043	93	A	T	G	A	0.493	NA	NA	NA	NA
93	G	T	G	A	0.187	-0.125	0.262	-0.478	0.633	94	C	A	G	T	0.064	-0.040	0.204	-0.198	0.843
93	A	T	G	A	0.494	NA	NA	NA	NA	94	C	G	A	T	0.256	-0.293	0.116	-2.526	0.012
94	C	A	G	T	0.066	0.037	0.381	0.098	0.922	94	T	G	A	G	0.025	-0.791	0.338	-2.340	0.020
94	C	G	A	T	0.251	-0.430	0.221	-1.942	0.053	94	T	G	A	T	0.654	NA	NA	NA	NA
94	T	G	A	G	0.026	-1.360	0.647	-2.103	0.036	95	A	G	T	G	0.064	0.057	0.208	0.275	0.783
94	T	G	A	T	0.657	NA	NA	NA	NA	95	G	A	G	G	0.025	-0.679	0.339	-2.004	0.045
95	A	G	T	G	0.065	0.106	0.387	0.274	0.784	95	G	A	T	T	0.360	0.097	0.111	0.867	0.386
95	G	A	G	G	0.026	-1.244	0.641	-1.941	0.053	95	G	A	T	G	0.550	NA	NA	NA	NA
95	G	A	T	T	0.360	-0.052	0.210	-0.247	0.805	96	A	G	G	G	0.025	-0.643	0.335	-1.919	0.055
95	G	A	T	G	0.548	NA	NA	NA	NA	96	A	T	G	A	0.068	0.044	0.201	0.217	0.829
96	A	G	G	G	0.026	-1.186	0.629	-1.884	0.060	96	A	T	T	G	0.361	0.094	0.114	0.828	0.408
96	A	T	G	A	0.068	-0.051	0.381	-0.135	0.893	96	G	T	G	G	0.062	0.012	0.212	0.057	0.954
96	A	T	T	G	0.361	-0.073	0.215	-0.341	0.733	96	A	T	G	G	0.483	NA	NA	NA	NA
96	G	T	G	G	0.064	0.004	0.394	0.010	0.992	97	G	G	G	A	0.026	-0.566	0.333	-1.702	0.089
96	A	T	G	G	0.482	NA	NA	NA	NA	97	T	G	A	G	0.068	0.051	0.201	0.252	0.801
97	G	G	G	A	0.026	-1.049	0.630	-1.664	0.097	97	T	G	G	A	0.075	0.080	0.195	0.409	0.683
97	T	G	A	G	0.068	-0.042	0.380	-0.111	0.911	97	T	T	G	G	0.360	0.104	0.114	0.917	0.359
97	T	G	G	A	0.076	0.124	0.368	0.337	0.736	97	T	G	G	G	0.471	NA	NA	NA	NA
97	T	T	G	G	0.360	-0.060	0.214	-0.282	0.778	98	G	A	G	G	0.068	0.065	0.201	0.323	0.747
97	T	G	G	G	0.470	NA	NA	NA	NA	98	G	G	A	A	0.102	-0.070	0.173	-0.405	0.686
98	G	A	G	G	0.068	-0.014	0.381	-0.037	0.971	98	T	G	G	G	0.360	0.107	0.114	0.943	0.346
98	G	G	A	A	0.104	-0.140	0.326	-0.428	0.669	98	G	G	G	G	0.468	NA	NA	NA	NA
98	T	G	G	G	0.360	-0.056	0.215	-0.261	0.794	99	A	G	G	G	0.068	0.025	0.196	0.127	0.899
98	G	G	G	G	0.467	NA	NA	NA	NA	99	G	A	A	G	0.102	-0.105	0.167	-0.626	0.531
99	A	G	G	G	0.067	0.049	0.385	0.127	0.899	99	G	G	G	A	0.018	0.042	0.378	0.112	0.911
99	G	A	A	G	0.103	-0.095	0.322	-0.294	0.769	99	G	G	G	G	0.811	NA	NA	NA	NA
99	G	G	G	A	0.019	0.053	0.670	0.078	0.938	100	A	A	G	C	0.103	-0.086	0.168	-0.509	0.611
99	*	*	*	*	0.002	-1.923	3.086	-0.623	0.533	100	G	G	A	C	0.016	0.036	0.393	0.092	0.927
99	G	G	G	G	0.810	NA	NA	NA	NA	100	G	G	G	T	0.041	0.406	0.251	1.616	0.107
100	A	A	G	C	0.104	-0.059	0.318	-0.186	0.852	100	*	*	*	*	0.002	-0.305	1.548	-0.197	0.844
100	G	G	A	C	0.018	0.003	0.690	0.004	0.997	100	G	G	G	C	0.838	NA	NA	NA	NA
100	G	G	G	T	0.042	0.974	0.472	2.064	0.039	101	A	G	C	G	0.101	-0.103	0.172	-0.597	0.551
100	*	*	*	*	0.002	0.178	3.076	0.058	0.954	101	G	A	C	G	0.017	0.007	0.387	0.019	0.985
100	G	G	G	C	0.834	NA	NA	NA	NA	101	G	G	C	A	0.168	-0.020	0.135	-0.145	0.885
101	A	G	C	G	0.103	-0.079	0.325	-0.244	0.807	101	G	G	T	A	0.041	0.359	0.250	1.437	0.151

Table B1.30. Continued

							LDL-C										TC		
Window	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**	**Window**	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**
101	G	A	C	G	0.018	-0.004	0.678	-0.006	0.995	101	*	*	*	*	0.001	0.307	1.596	0.192	0.848
101	G	G	C	A	0.171	0.050	0.255	0.196	0.844	101	G	G	C	G	0.672	NA	NA	NA	NA
101	G	G	T	A	0.043	0.897	0.469	1.912	0.056	102	A	C	G	G	0.017	0.031	0.387	0.080	0.936
101	G	G	C	G	0.665	NA	NA	NA	NA	102	G	C	A	G	0.168	0.002	0.134	0.012	0.990
102	A	C	G	G	0.018	0.022	0.681	0.032	0.975	102	G	C	G	A	0.031	0.066	0.281	0.236	0.813
102	G	C	A	G	0.171	0.086	0.253	0.340	0.734	102	G	T	A	G	0.041	0.381	0.249	1.531	0.126
102	G	C	G	A	0.030	0.272	0.540	0.504	0.614	102	*	*	*	*	0.001	0.340	1.518	0.224	0.823
102	G	T	A	G	0.042	0.926	0.468	1.979	0.048	102	G	C	G	G	0.741	NA	NA	NA	NA
102	*	*	*	*	0.001	1.434	3.003	0.478	0.633	103	C	A	G	A	0.135	-0.084	0.160	-0.526	0.599
102	G	C	G	G	0.737	NA	NA	NA	NA	103	C	A	G	C	0.033	-0.177	0.328	-0.538	0.591
103	C	A	G	A	0.137	-0.012	0.300	-0.041	0.968	103	C	G	A	C	0.031	-0.027	0.282	-0.097	0.923
103	C	A	G	C	0.034	-0.247	0.618	-0.400	0.689	103	C	G	G	C	0.239	-0.323	0.126	-2.568	0.010
103	C	G	A	C	0.030	0.146	0.542	0.269	0.788	103	T	A	G	C	0.042	0.301	0.246	1.224	0.221
103	C	G	G	C	0.236	-0.444	0.239	-1.858	0.064	103	C	G	G	A	0.519	NA	NA	NA	NA
103	T	A	G	C	0.043	0.846	0.461	1.834	0.067	104	A	G	A	A	0.137	-0.038	0.175	-0.219	0.827
103	C	G	G	A	0.519	NA	NA	NA	NA	104	A	G	C	A	0.072	0.202	0.218	0.926	0.355
104	A	G	A	A	0.139	0.014	0.330	0.043	0.966	104	G	A	C	A	0.031	0.017	0.286	0.058	0.954
104	A	G	C	A	0.073	0.553	0.412	1.341	0.180	104	G	G	A	T	0.204	0.161	0.149	1.087	0.278
104	G	A	C	A	0.030	0.185	0.550	0.336	0.737	104	G	G	C	A	0.241	-0.273	0.142	-1.916	0.056
104	G	G	A	T	0.204	0.162	0.281	0.579	0.563	104	*	*	*	*	0.002	0.517	1.338	0.387	0.699
104	G	G	C	A	0.237	-0.404	0.270	-1.498	0.134	104	G	G	A	A	0.313	NA	NA	NA	NA
104	*	*	*	*	0.002	0.783	2.482	0.315	0.753	105	A	C	A	A	0.031	-0.003	0.286	-0.009	0.993
104	G	G	A	A	0.313	NA	NA	NA	NA	105	G	A	A	G	0.078	-0.089	0.198	-0.448	0.654
105	A	C	A	A	0.030	0.113	0.548	0.205	0.837	105	G	A	T	A	0.203	0.167	0.142	1.174	0.241
105	G	A	A	G	0.079	-0.199	0.375	-0.530	0.596	105	G	C	A	A	0.303	-0.148	0.124	-1.198	0.231
105	G	A	T	A	0.204	0.125	0.268	0.466	0.642	105	*	*	*	*	0.010	-0.543	0.622	-0.872	0.383
105	G	C	A	A	0.302	-0.206	0.237	-0.868	0.386	105	G	A	A	A	0.374	NA	NA	NA	NA
105	*	*	*	*	0.010	-0.688	1.199	-0.573	0.567	106	A	A	G	G	0.079	-0.072	0.198	-0.362	0.717
105	G	A	A	A	0.375	NA	NA	NA	NA	106	A	T	A	G	0.203	0.185	0.142	1.309	0.191
106	A	A	G	G	0.079	-0.170	0.374	-0.454	0.650	106	C	A	A	A	0.043	-0.743	0.261	-2.845	0.005
106	A	T	A	G	0.204	0.161	0.268	0.601	0.548	106	C	A	A	G	0.293	-0.049	0.124	-0.393	0.695
106	C	A	A	A	0.042	-1.100	0.501	-2.194	0.029	106	*	*	*	*	0.010	-0.632	0.684	-0.923	0.356
106	C	A	A	G	0.292	-0.040	0.237	-0.167	0.867	106	A	A	A	G	0.372	NA	NA	NA	NA
106	*	*	*	*	0.009	-0.827	1.300	-0.636	0.525	107	A	A	A	T	0.042	-0.785	0.267	-2.940	0.003
106	A	A	A	G	0.374	NA	NA	NA	NA	107	A	A	G	C	0.047	-0.054	0.256	-0.209	0.834
107	A	A	A	T	0.041	-1.157	0.504	-2.297	0.022	107	A	G	G	T	0.086	-0.105	0.181	-0.579	0.563
107	A	A	G	C	0.049	0.027	0.456	0.060	0.952	107	T	A	G	T	0.202	0.208	0.130	1.599	0.110
107	A	G	G	T	0.086	-0.220	0.342	-0.645	0.519	107	*	*	*	*	0.005	-0.141	1.163	-0.121	0.903
107	T	A	G	T	0.202	0.160	0.245	0.652	0.515	107	A	A	G	T	0.619	NA	NA	NA	NA
107	*	*	*	*	0.004	0.066	2.173	0.030	0.976	108	A	A	T	A	0.041	-0.851	0.266	-3.201	0.001
107	A	A	G	T	0.617	NA	NA	NA	NA	108	A	G	C	A	0.048	-0.129	0.236	-0.548	0.584
108	A	A	T	A	0.040	-1.232	0.506	-2.435	0.015	108	G	G	T	G	0.079	-0.160	0.180	-0.889	0.374
108	A	G	C	A	0.050	-0.029	0.436	-0.067	0.947	108	*	*	*	*	0.011	-0.137	0.522	-0.262	0.794
108	G	G	T	G	0.079	-0.262	0.340	-0.770	0.441	108	A	G	T	A	0.821	NA	NA	NA	NA
108	*	*	*	*	0.011	-0.014	1.007	-0.013	0.989	109	A	T	A	G	0.042	-0.860	0.262	-3.284	0.001
108	A	G	T	A	0.820	NA	NA	NA	NA	109	G	C	A	G	0.048	-0.144	0.235	-0.614	0.539
109	A	T	A	G	0.041	-1.269	0.502	-2.526	0.012	109	G	T	A	A	0.015	-0.270	0.410	-0.660	0.510
109	G	C	A	G	0.050	-0.063	0.435	-0.144	0.886	109	G	T	G	G	0.076	-0.172	0.186	-0.921	0.357
109	G	T	A	A	0.015	-0.743	0.788	-0.943	0.346	109	*	*	*	*	0.002	0.907	1.314	0.690	0.490
109	G	T	G	G	0.077	-0.244	0.353	-0.692	0.489	109	G	T	A	G	0.817	NA	NA	NA	NA
109	*	*	*	*	0.002	1.406	2.680	0.524	0.600	110	C	A	G	G	0.050	-0.039	0.229	-0.170	0.865
109	G	T	A	G	0.816	NA	NA	NA	NA	110	T	A	A	G	0.015	-0.181	0.423	-0.428	0.669
110	C	A	G	G	0.052	0.084	0.424	0.197	0.844	110	T	A	G	A	0.019	0.599	0.366	1.634	0.103
110	T	A	A	G	0.015	-0.512	0.809	-0.632	0.527	110	T	G	G	G	0.076	-0.105	0.188	-0.559	0.577
110	T	A	G	A	0.019	1.090	0.689	1.582	0.114	110	T	A	G	G	0.840	NA	NA	NA	NA
110	T	G	G	G	0.076	-0.127	0.356	-0.358	0.720	111	A	A	G	A	0.015	-0.170	0.417	-0.407	0.684
110	T	A	G	G	0.837	NA	NA	NA	NA	111	A	G	A	A	0.019	0.628	0.366	1.716	0.087
111	A	A	G	A	0.015	-0.614	0.786	-0.781	0.435	111	A	G	G	G	0.170	0.131	0.132	0.988	0.323
111	A	G	A	A	0.019	1.076	0.687	1.567	0.118	111	G	G	G	A	0.076	-0.087	0.188	-0.465	0.642
111	A	G	G	G	0.169	-0.022	0.252	-0.088	0.930	111	A	G	G	A	0.720	NA	NA	NA	NA
111	G	G	G	A	0.077	-0.158	0.355	-0.446	0.655	112	A	G	A	G	0.015	-0.186	0.411	-0.452	0.651
111	A	G	G	A	0.719	NA	NA	NA	NA	112	G	A	A	G	0.018	0.533	0.381	1.400	0.162
112	A	G	A	G	0.014	-0.773	0.817	-0.946	0.344	112	G	G	G	G	0.116	0.158	0.158	1.003	0.316
112	G	A	A	G	0.018	0.995	0.708	1.406	0.160	112	G	G	G	T	0.070	0.032	0.199	0.158	0.874
112	G	G	G	G	0.115	-0.087	0.303	-0.286	0.775	112	*	*	*	*	0.002	2.356	NA	NA	NA
112	G	G	G	T	0.070	0.120	0.384	0.312	0.755	112	G	G	A	G	0.779	NA	NA	NA	NA
112	*	*	*	*	0.003	3.513	3.451	1.018	0.309	113	A	A	G	C	0.019	0.571	0.368	1.550	0.122
112	G	G	A	G	0.780	NA	NA	NA	NA	113	G	A	G	T	0.221	-0.299	0.126	-2.377	0.018
113	A	A	G	C	0.019	1.001	0.694	1.443	0.149	113	G	G	G	C	0.116	0.069	0.163	0.426	0.670
113	G	A	G	T	0.217	-0.443	0.240	-1.845	0.065	113	G	G	T	C	0.070	-0.014	0.205	-0.067	0.947
113	G	G	G	C	0.116	-0.198	0.313	-0.634	0.526	113	*	*	*	*	0.002	0.265	1.336	0.199	0.843
113	G	G	T	C	0.070	0.054	0.397	0.137	0.891	113	G	A	G	C	0.573	NA	NA	NA	NA
113	*	*	*	*	0.002	0.893	2.518	0.355	0.723	114	A	G	C	A	0.113	0.038	0.169	0.226	0.821
113	G	A	G	C	0.576	NA	NA	NA	NA	114	A	G	T	A	0.203	-0.328	0.133	-2.472	0.014
114	A	G	C	A	0.114	0.197	0.319	0.619	0.536	114	A	G	T	G	0.018	-0.273	0.397	-0.688	0.491
114	A	G	T	A	0.199	-0.508	0.252	-2.012	0.045	114	G	G	C	G	0.116	0.055	0.165	0.332	0.740
114	A	G	T	G	0.018	-0.124	0.750	-0.165	0.869	114	G	T	C	G	0.070	-0.022	0.208	-0.104	0.918
114	G	G	C	G	0.117	-0.211	0.316	-0.668	0.504	114	*	*	*	*	0.002	0.238	1.347	0.176	0.860
114	G	T	C	G	0.070	0.071	0.402	0.177	0.860	114	A	G	C	G	0.477	NA	NA	NA	NA
114	*	*	*	*	0.002	0.842	2.527	0.333	0.739	115	G	C	A	G	0.113	0.002	0.167	0.011	0.992
114	A	G	C	G	0.481	NA	NA	NA	NA	115	G	C	G	A	0.012	-0.747	0.486	-1.538	0.124

Table B1.30. Continued

LDL-C										TC									
Window	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**	**Window**	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**
115	G	C	A	G	0.114	0.188	0.316	0.596	0.551	115	G	T	A	G	0.203	-0.357	0.129	-2.769	0.006
115	G	C	G	A	0.012	-1.101	0.939	-1.173	0.241	115	G	T	G	G	0.018	-0.305	0.397	-0.769	0.442
115	G	T	A	G	0.200	-0.490	0.245	-1.999	0.046	115	T	C	G	A	0.071	-0.035	0.208	-0.168	0.866
115	G	T	G	G	0.018	-0.145	0.752	-0.193	0.847	115	*	*	*	*	0.001	-0.905	1.855	-0.488	0.626
115	T	C	G	A	0.071	0.067	0.395	0.170	0.865	115	G	C	G	G	0.582	NA	NA	NA	NA
115	*	*	*	*	0.001	-1.052	3.205	-0.328	0.743	116	C	A	G	T	0.114	0.012	0.169	0.074	0.941
115	G	C	G	G	0.584	NA	NA	NA	NA	116	C	G	A	T	0.081	-0.093	0.200	-0.466	0.642
116	C	A	G	T	0.114	0.162	0.320	0.505	0.614	116	C	G	G	C	0.115	0.046	0.167	0.276	0.783
116	C	G	A	T	0.081	-0.065	0.387	-0.167	0.868	116	T	A	G	T	0.203	-0.331	0.134	-2.475	0.014
116	C	G	G	C	0.114	-0.149	0.323	-0.462	0.645	116	T	G	G	T	0.018	-0.303	0.396	-0.764	0.445
116	T	A	G	T	0.200	-0.503	0.255	-1.974	0.049	116	*	*	*	*	0.002	-2.554	2.118	-1.206	0.228
116	T	G	G	T	0.018	-0.169	0.749	-0.226	0.821	116	C	G	G	T	0.467	NA	NA	NA	NA
116	*	*	*	*	0.003	-4.070	3.647	-1.116	0.265	117	A	G	T	G	0.317	-0.187	0.117	-1.594	0.111
116	C	G	G	T	0.470	NA	NA	NA	NA	117	G	A	T	G	0.080	-0.055	0.199	-0.274	0.784
117	A	G	T	G	0.314	-0.216	0.221	-0.979	0.328	117	G	G	C	G	0.114	0.086	0.168	0.513	0.608
117	G	A	T	G	0.081	-0.014	0.380	-0.038	0.970	117	G	G	T	A	0.045	0.043	0.237	0.180	0.857
117	G	G	C	G	0.113	-0.067	0.321	-0.208	0.835	117	*	*	*	*	0.003	-2.286	1.202	-1.902	0.058
117	G	G	T	A	0.045	0.193	0.451	0.427	0.669	117	G	G	T	G	0.441	NA	NA	NA	NA
117	*	*	*	*	0.003	-4.080	2.512	-1.624	0.105	118	A	T	G	A	0.016	-0.737	0.471	-1.565	0.118
117	G	G	T	G	0.444	NA	NA	NA	NA	118	A	T	G	G	0.067	0.229	0.214	1.072	0.284
118	A	T	G	A	0.016	-1.516	0.897	-1.690	0.091	118	G	C	G	G	0.116	0.190	0.161	1.182	0.238
118	A	T	G	G	0.067	0.403	0.404	0.998	0.319	118	G	T	A	G	0.045	0.177	0.233	0.762	0.446
118	G	C	G	G	0.116	-0.004	0.305	-0.014	0.989	118	G	T	G	A	0.162	0.405	0.143	2.825	0.005
118	G	T	A	G	0.044	0.333	0.448	0.743	0.458	118	G	T	G	G	0.594	NA	NA	NA	NA
118	G	T	G	A	0.162	0.446	0.270	1.652	0.099	119	C	G	G	C	0.114	0.252	0.167	1.510	0.132
118	G	T	G	G	0.594	NA	NA	NA	NA	119	T	A	G	C	0.045	0.200	0.239	0.834	0.405
119	C	G	G	C	0.113	0.105	0.319	0.330	0.742	119	T	G	A	G	0.178	0.302	0.142	2.132	0.033
119	T	A	G	C	0.045	0.380	0.459	0.828	0.408	119	T	G	G	C	0.254	0.061	0.128	0.475	0.635
119	T	G	A	G	0.178	0.275	0.268	1.025	0.306	119	*	*	*	*	0.003	-1.819	1.052	-1.728	0.084
119	T	G	G	C	0.258	0.109	0.243	0.450	0.653	119	T	G	G	G	0.406	NA	NA	NA	NA
119	*	*	*	*	0.003	-2.779	2.290	-1.213	0.225	120	A	G	C	G	0.044	0.045	0.245	0.183	0.855
119	T	G	G	G	0.403	NA	NA	NA	NA	120	G	A	G	G	0.178	0.194	0.141	1.374	0.170
120	A	G	C	G	0.044	0.263	0.461	0.570	0.569	120	G	G	G	A	0.322	-0.174	0.118	-1.473	0.141
120	G	A	G	G	0.178	0.208	0.266	0.781	0.435	120	G	G	G	G	0.083	0.137	0.200	0.686	0.493
120	G	G	G	A	0.319	-0.180	0.224	-0.806	0.420	120	*	*	*	*	0.001	1.859	1.939	0.959	0.338
120	G	G	G	G	0.084	0.419	0.380	1.102	0.271	120	G	G	C	G	0.371	NA	NA	NA	NA
120	*	*	*	*	0.001	1.302	3.951	0.330	0.742	121	A	G	G	G	0.178	0.192	0.140	1.372	0.171
120	G	G	C	G	0.374	NA	NA	NA	NA	121	G	G	A	G	0.015	-0.228	0.411	-0.553	0.580
121	A	G	G	G	0.178	0.188	0.265	0.710	0.478	121	G	G	A	T	0.307	-0.167	0.117	-1.421	0.156
121	G	G	A	G	0.015	0.330	0.787	0.419	0.676	121	G	G	G	G	0.081	0.164	0.200	0.818	0.414
121	G	G	A	T	0.304	-0.235	0.223	-1.052	0.293	121	*	*	*	*	0.002	-1.167	1.108	-1.053	0.293
121	G	G	G	G	0.082	0.450	0.381	1.181	0.238	121	G	C	G	G	0.416	NA	NA	NA	NA
121	*	*	*	*	0.002	-1.724	2.100	-0.821	0.412	122	C	G	G	A	0.032	0.249	0.285	0.874	0.382
121	G	C	G	G	0.419	NA	NA	NA	NA	122	G	A	G	G	0.015	-0.193	0.413	-0.469	0.639
122	C	G	G	A	0.031	0.567	0.547	1.036	0.301	122	G	A	T	G	0.307	-0.149	0.119	-1.252	0.211
122	G	A	G	G	0.015	0.401	0.784	0.512	0.609	122	G	G	G	G	0.262	0.191	0.127	1.499	0.134
122	G	A	T	G	0.304	-0.206	0.226	-0.910	0.363	122	*	*	*	*	0.002	-1.150	1.451	-0.793	0.428
122	G	G	G	G	0.262	0.275	0.242	1.138	0.256	122	C	G	G	G	0.383	NA	NA	NA	NA
122	*	*	*	*	0.002	-1.743	2.698	-0.646	0.519	123	A	G	G	C	0.014	-0.280	0.428	-0.655	0.513
122	C	G	G	G	0.386	NA	NA	NA	NA	123	A	T	G	C	0.125	-0.119	0.154	-0.772	0.440
123	A	G	G	C	0.014	0.364	0.814	0.447	0.655	123	A	T	G	T	0.183	-0.321	0.131	-2.461	0.014
123	A	T	G	C	0.125	-0.233	0.292	-0.800	0.424	123	G	G	A	C	0.031	0.173	0.282	0.612	0.541
123	A	T	G	T	0.180	-0.396	0.249	-1.591	0.112	123	G	G	G	T	0.011	-0.772	0.501	-1.543	0.123
123	G	G	A	C	0.030	0.465	0.543	0.856	0.392	123	*	*	*	*	0.003	-0.869	1.359	-0.639	0.523
123	G	G	G	T	0.012	-1.036	0.928	-1.116	0.265	123	G	G	G	C	0.632	NA	NA	NA	NA
123	*	*	*	*	0.003	-1.592	2.586	-0.616	0.538	124	G	A	C	A	0.032	0.156	0.281	0.554	0.580
123	G	G	G	C	0.636	NA	NA	NA	NA	124	G	G	T	A	0.013	-0.725	0.478	-1.516	0.130
124	G	A	C	A	0.032	0.314	0.530	0.593	0.554	124	T	G	C	A	0.126	-0.081	0.157	-0.514	0.607
124	G	G	T	A	0.013	-1.092	0.891	-1.226	0.221	124	T	G	T	A	0.184	-0.346	0.130	-2.665	0.008
124	T	G	C	A	0.126	-0.194	0.298	-0.650	0.516	124	*	*	*	*	0.003	-2.662	1.005	-2.649	0.008
124	T	G	T	A	0.181	-0.440	0.248	-1.778	0.076	124	G	G	C	A	0.642	NA	NA	NA	NA
124	*	*	*	*	0.003	-3.505	1.978	-1.772	0.077	125	A	C	A	C	0.033	0.125	0.274	0.455	0.650
124	G	G	C	A	0.645	NA	NA	NA	NA	125	G	C	A	G	0.023	0.244	0.339	0.719	0.473
125	A	C	A	C	0.032	0.366	0.528	0.692	0.489	125	G	T	A	C	0.196	-0.349	0.125	-2.791	0.005
125	G	C	A	G	0.025	0.605	0.606	0.998	0.319	125	*	*	*	*	0.003	-2.435	1.098	-2.218	0.027
125	G	T	A	C	0.193	-0.435	0.239	-1.824	0.069	125	G	C	A	C	0.745	NA	NA	NA	NA
125	*	*	*	*	0.003	-3.451	2.155	-1.601	0.110	126	C	A	C	C	0.131	0.038	0.162	0.234	0.815
125	G	C	A	C	0.747	NA	NA	NA	NA	126	C	A	G	T	0.023	0.200	0.343	0.585	0.559
126	C	A	C	C	0.132	0.245	0.305	0.802	0.423	126	T	A	C	C	0.017	0.313	0.518	0.604	0.546
126	C	A	G	T	0.025	0.567	0.614	0.924	0.356	126	T	A	C	T	0.180	-0.416	0.142	-2.928	0.004
126	T	A	C	C	0.016	0.926	0.976	0.948	0.343	126	*	*	*	*	0.003	-2.425	1.070	-2.267	0.024
126	T	A	C	T	0.177	-0.538	0.268	-2.007	0.045	126	C	A	C	T	0.646	NA	NA	NA	NA
126	*	*	*	*	0.003	-3.404	2.134	-1.595	0.111	127	A	C	C	A	0.148	0.172	0.144	1.198	0.231
126	C	A	C	T	0.646	NA	NA	NA	NA	127	A	C	T	G	0.023	0.024	0.328	0.075	0.941
127	A	C	C	A	0.149	0.450	0.274	1.647	0.100	127	A	G	T	A	0.023	0.359	0.340	1.058	0.291
127	A	C	T	G	0.024	0.135	0.594	0.227	0.820	127	*	*	*	*	0.003	-2.280	1.078	-2.116	0.035
127	A	G	T	A	0.025	0.765	0.606	1.262	0.207	127	A	C	T	A	0.803	NA	NA	NA	NA
127	*	*	*	*	0.003	-3.333	2.131	-1.564	0.118	128	C	C	A	G	0.026	-0.656	0.417	-1.572	0.116
127	A	C	T	A	0.800	NA	NA	NA	NA	128	C	C	A	T	0.125	0.270	0.166	1.628	0.104
128	C	C	A	G	0.026	-1.026	0.795	-1.290	0.197	128	C	T	A	G	0.167	-0.010	0.142	-0.072	0.943
128	C	C	A	T	0.126	0.606	0.317	1.912	0.056	128	C	T	G	T	0.023	0.004	0.329	0.012	0.990

Table B1.30. Continued

LDL-C										TC									
Window	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**	**Window**	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**
128	C	T	A	G	0.167	-0.191	0.271	-0.704	0.482	128	G	T	A	T	0.021	-0.030	0.364	-0.082	0.935
128	C	T	G	T	0.024	0.062	0.593	0.104	0.917	128	*	*	*	*	0.002	2.979	1.671	1.782	0.075
128	G	T	A	T	0.024	0.015	0.629	0.024	0.981	128	C	T	A	T	0.635	NA	NA	NA	NA
128	*	*	*	*	0.002	7.323	2.815	2.601	0.009										
128	C	T	A	T	0.632	NA	NA	NA	NA										

TABLE B1.31. Summary of *CETP* 4-SNP sliding haplotypes for ApoA1 and ApoB in African blacks (n=788)

ApoA1										ApoB									
Window	loc.1	loc.2	loc.3	loc.4	hap.freq	coef	se	t.stat	pval	Window	loc.1	loc.2	loc.3	loc.4	hap.freq	coef	se	t.stat	pval
1	A	A	C	A	0.038	0.194	1.401	0.138	0.890	1	A	A	C	A	0.036	1.296	1.714	0.756	0.450
1	A	A	T	A	0.086	-0.468	1.085	-0.431	0.667	1	A	A	T	A	0.086	-0.095	1.177	-0.080	0.936
1	A	G	C	A	0.030	-3.032	1.630	-1.860	0.063	1	A	G	C	A	0.030	0.036	1.744	0.021	0.984
1	A	G	C	C	0.219	-0.533	0.741	-0.719	0.472	1	A	G	C	C	0.220	0.760	0.821	0.926	0.355
1	A	G	T	A	0.041	2.303	1.439	1.600	0.110	1	A	G	T	A	0.043	0.653	1.554	0.420	0.674
1	G	A	C	C	0.076	-3.481	1.334	-2.609	0.009	1	G	A	C	C	0.073	2.671	1.375	1.943	0.052
1	G	A	T	A	0.105	2.039	0.959	2.127	0.034	1	G	A	T	A	0.106	-1.059	1.072	-0.988	0.323
1	G	G	C	A	0.011	0.136	2.716	0.050	0.960	1	G	G	C	A	0.011	3.810	3.044	1.252	0.211
1	G	G	C	C	0.024	0.388	2.332	0.166	0.868	1	G	G	C	C	0.025	-1.119	2.279	-0.491	0.624
1	G	G	T	A	0.014	-3.511	3.446	-1.019	0.309	1	G	G	T	A	0.010	3.590	5.247	0.684	0.494
1	*	*	*	*	0.000	-2.690	NA	NA	NA	1	*	*	*	*	0.002	-2.686	9.077	-0.296	0.767
1	A	A	C	C	0.356	NA	NA	NA	NA	1	A	A	C	C	0.357	NA	NA	NA	NA
2	A	C	A	A	0.038	0.634	1.420	0.447	0.655	2	A	C	A	A	0.038	0.834	1.598	0.522	0.602
2	A	T	A	A	0.170	0.608	0.769	0.791	0.429	2	A	T	A	A	0.169	-0.911	0.863	-1.056	0.291
2	A	T	A	G	0.021	4.489	1.621	2.769	0.006	2	A	T	A	G	0.021	-0.285	1.857	-0.154	0.878
2	G	C	A	A	0.041	-1.979	1.326	-1.493	0.136	2	G	C	A	A	0.041	0.618	1.474	0.419	0.675
2	G	C	C	A	0.244	-0.195	0.682	-0.286	0.775	2	G	C	C	A	0.244	0.337	0.778	0.433	0.665
2	G	T	A	A	0.054	2.677	1.350	1.982	0.048	2	G	T	A	A	0.055	0.208	1.446	0.144	0.885
2	A	C	C	A	0.432	NA	NA	NA	NA	2	A	C	C	A	0.432	NA	NA	NA	NA
3	C	A	A	C	0.064	-0.482	1.033	-0.467	0.641	3	C	A	A	C	0.063	0.293	1.187	0.247	0.805
3	C	A	A	T	0.016	-2.111	2.020	-1.045	0.296	3	C	A	A	T	0.016	1.549	2.320	0.667	0.505
3	C	C	A	C	0.163	0.203	0.680	0.299	0.765	3	C	C	A	C	0.164	-0.073	0.774	-0.094	0.925
3	T	A	A	T	0.223	1.231	0.598	2.060	0.040	3	T	A	A	T	0.223	-0.756	0.677	-1.117	0.265
3	T	A	G	T	0.021	4.529	1.620	2.796	0.005	3	T	A	G	T	0.021	-0.435	1.851	-0.235	0.814
3	*	*	*	*	0.001	7.679	9.423	0.815	0.415	3	*	*	*	*	0.001	-5.225	9.612	-0.544	0.587
3	C	C	A	T	0.511	NA	NA	NA	NA	3	C	C	A	T	0.511	NA	NA	NA	NA
4	A	A	C	C	0.064	0.379	1.126	0.336	0.737	4	A	A	C	C	0.063	0.069	1.274	0.054	0.957
4	A	A	T	C	0.134	0.957	0.804	1.190	0.234	4	A	A	T	C	0.133	-0.796	0.903	-0.881	0.379
4	A	A	T	T	0.104	0.453	0.798	0.567	0.571	4	A	A	T	T	0.105	-0.145	0.908	-0.160	0.873
4	A	G	T	C	0.021	4.380	1.627	2.692	0.007	4	A	G	T	C	0.021	-0.420	1.849	-0.227	0.820
4	C	A	C	C	0.160	-0.126	0.732	-0.173	0.863	4	C	A	C	C	0.160	0.011	0.823	0.013	0.990
4	C	A	T	C	0.517	NA	NA	NA	NA	4	C	A	T	C	0.517	NA	NA	NA	NA
5	A	C	C	C	0.064	-0.426	0.976	-0.436	0.663	5	A	C	C	C	0.064	1.010	1.123	0.899	0.369
5	A	C	C	T	0.166	-0.209	0.646	-0.324	0.746	5	A	C	C	T	0.166	-0.175	0.740	-0.236	0.814
5	A	T	T	T	0.104	0.269	0.788	0.341	0.733	5	A	T	T	T	0.105	-0.035	0.897	-0.039	0.969
5	G	T	C	T	0.021	4.241	1.637	2.591	0.010	5	G	T	C	T	0.021	-0.225	1.855	-0.121	0.904
5	A	T	C	T	0.645	NA	NA	NA	NA	5	A	T	C	T	0.645	NA	NA	NA	NA
6	C	C	C	G	0.065	-0.707	1.016	-0.696	0.487	6	C	C	C	G	0.064	1.656	1.161	1.427	0.154
6	C	C	T	G	0.166	-0.384	0.699	-0.549	0.583	6	C	C	T	G	0.167	0.567	0.794	0.713	0.476
6	T	C	T	G	0.316	-0.326	0.578	-0.563	0.573	6	T	C	T	G	0.315	1.414	0.667	2.120	0.034
6	T	T	T	A	0.103	-0.062	0.851	-0.073	0.942	6	T	T	T	A	0.103	0.776	0.967	0.803	0.422
6	*	*	*	*	0.002	-6.465	6.551	-0.987	0.324	6	*	*	*	*	0.002	-7.796	7.340	-1.062	0.289
6	T	C	T	A	0.348	NA	NA	NA	NA	6	T	C	T	A	0.348	NA	NA	NA	NA
7	C	C	G	C	0.063	-0.318	1.006	-0.316	0.752	7	C	C	G	C	0.062	0.627	1.154	0.543	0.587
7	C	T	A	C	0.329	0.107	0.525	0.204	0.838	7	C	T	A	C	0.330	-1.124	0.609	-1.848	0.065
7	C	T	A	T	0.021	4.250	1.664	2.553	0.011	7	C	T	A	T	0.021	-0.549	1.892	-0.290	0.772
7	T	T	A	C	0.103	0.313	0.794	0.394	0.694	7	T	T	A	C	0.104	-0.344	0.903	-0.381	0.703
7	*	*	*	*	0.003	1.625	NA	NA	NA	7	*	*	*	*	0.003	-4.599	4.491	-1.024	0.306
7	C	T	G	C	0.481	NA	NA	NA	NA	7	C	T	G	C	0.481	NA	NA	NA	NA
8	C	G	C	C	0.063	-0.550	1.008	-0.546	0.585	8	C	G	C	C	0.063	1.599	1.153	1.387	0.166
8	T	A	T	C	0.021	4.199	1.367	3.071	0.002	8	T	A	T	C	0.021	0.318	1.987	0.160	0.873
8	T	G	C	C	0.388	-0.312	0.512	-0.609	0.543	8	T	G	C	C	0.386	1.350	0.596	2.264	0.024
8	T	G	C	T	0.094	0.392	0.814	0.482	0.630	8	T	G	C	T	0.095	-0.486	0.979	-0.497	0.620
8	*	*	*	*	0.004	-3.742	NA	NA	NA	8	*	*	*	*	0.004	-4.379	8.601	-0.509	0.611
8	T	A	C	C	0.430	NA	NA	NA	NA	8	T	A	C	C	0.431	NA	NA	NA	NA
9	A	C	C	A	0.031	1.781	1.368	1.302	0.193	9	A	C	C	A	0.030	0.860	1.638	0.525	0.600
9	A	C	C	G	0.399	0.231	0.507	0.456	0.649	9	A	C	C	G	0.401	-1.560	0.588	-2.654	0.008
9	A	T	C	G	0.021	4.560	1.431	3.186	0.002	9	A	T	C	G	0.021	-0.936	2.091	-0.448	0.655
9	G	C	T	G	0.094	0.792	0.846	0.936	0.349	9	G	C	T	G	0.095	-1.827	1.022	-1.788	0.074

Table B1.31. Continued

ApoA1										ApoB									
Window	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**	**Window**	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**
9	*	*	*	*	0.004	-3.409	NA	NA	NA	9	*	*	*	*	0.005	-6.036	8.052	-0.750	0.454
9	G	C	C	G	0.451	NA	NA	NA	NA	9	G	C	C	G	0.449	NA	NA	NA	NA
10	C	C	A	C	0.031	1.621	1.355	1.196	0.232	10	C	C	A	C	0.030	1.433	1.621	0.884	0.377
10	C	C	G	A	0.035	-1.320	1.204	-1.096	0.273	10	C	C	G	A	0.036	0.723	1.358	0.533	0.594
10	C	T	G	C	0.096	0.301	0.803	0.375	0.708	10	C	T	G	C	0.096	-1.094	0.922	-1.186	0.236
10	T	C	G	C	0.022	4.231	1.613	2.622	0.009	10	T	C	G	C	0.022	-0.011	1.836	-0.006	0.995
10	*	*	*	*	0.001	-2.151	0.000	-4.00E+15	0.000	10	*	*	*	*	0.001	-9.926	0.000	-9.02E+15	0.000
10	C	C	G	C	0.815	NA	NA	NA	NA	10	C	C	G	C	0.815	NA	NA	NA	NA
11	C	A	C	A	0.031	1.277	1.369	0.933	0.351	11	C	A	C	A	0.030	1.717	1.637	1.049	0.294
11	C	G	A	A	0.036	-1.584	1.218	-1.300	0.194	11	C	G	A	A	0.036	1.043	1.377	0.757	0.449
11	C	G	C	C	0.301	-0.420	0.549	-0.765	0.444	11	C	G	C	C	0.301	0.820	0.626	1.310	0.191
11	T	G	C	C	0.094	0.517	0.864	0.598	0.550	11	T	G	C	C	0.094	-0.909	0.986	-0.923	0.357
11	*	*	*	*	0.004	-7.390	4.578	-1.614	0.107	11	*	*	*	*	0.004	-2.237	5.098	-0.439	0.661
11	C	G	C	A	0.535	NA	NA	NA	NA	11	C	G	C	A	0.535	NA	NA	NA	NA
12	A	C	A	G	0.031	1.804	1.366	1.321	0.187	12	A	C	A	G	0.030	1.592	1.644	0.969	0.333
12	G	A	A	G	0.036	-1.049	1.217	-0.862	0.389	12	G	A	A	G	0.036	0.819	1.383	0.592	0.554
12	G	C	A	A	0.091	3.174	0.846	3.750	0.000	12	G	C	A	A	0.091	-1.130	0.976	-1.158	0.247
12	G	C	C	G	0.395	0.350	0.514	0.681	0.496	12	G	C	C	G	0.396	0.153	0.587	0.261	0.794
12	G	C	A	G	0.446	NA	NA	NA	NA	12	G	C	A	G	0.447	NA	NA	NA	NA
13	A	A	G	G	0.036	-1.164	1.220	-0.954	0.340	13	A	A	G	G	0.037	0.734	1.384	0.530	0.596
13	C	A	A	C	0.091	3.033	0.836	3.628	0.000	13	C	A	A	C	0.091	-1.212	0.958	-1.265	0.206
13	C	C	G	G	0.396	0.199	0.508	0.391	0.696	13	C	C	G	G	0.397	0.051	0.579	0.088	0.930
13	C	A	G	G	0.476	NA	NA	NA	NA	13	C	A	G	G	0.475	NA	NA	NA	NA
14	A	A	C	C	0.090	3.023	0.871	3.470	0.001	14	A	A	C	C	0.089	-1.159	0.978	-1.185	0.236
14	A	G	G	A	0.064	-0.532	1.038	-0.513	0.608	14	A	G	G	A	0.063	0.846	1.152	0.734	0.463
14	C	G	G	C	0.396	0.234	0.515	0.454	0.650	14	C	G	G	C	0.397	0.053	0.585	0.091	0.928
14	*	*	*	*	0.002	4.523	11.196	0.404	0.686	14	*	*	*	*	0.002	-7.702	8.800	-0.875	0.382
14	A	G	G	C	0.448	NA	NA	NA	NA	14	A	G	G	C	0.448	NA	NA	NA	NA
15	A	C	C	C	0.088	2.802	0.847	3.309	0.001	15	A	C	C	C	0.090	-1.095	0.935	-1.171	0.242
15	G	G	A	C	0.063	-0.802	1.028	-0.780	0.436	15	G	G	A	C	0.064	0.936	1.121	0.835	0.404
15	G	G	C	A	0.019	3.176	1.631	1.947	0.052	15	G	G	C	A	0.020	1.016	1.798	0.565	0.572
15	*	*	*	*	0.004	7.177	8.234	0.872	0.384	15	*	*	*	*	0.002	-13.495	0.011	-1227.901	0.000
15	G	G	C	C	0.826	NA	NA	NA	NA	15	G	G	C	C	0.824	NA	NA	NA	NA
16	C	C	C	C	0.090	3.157	0.831	3.799	0.000	16	C	C	C	C	0.089	-1.185	0.958	-1.236	0.217
16	G	A	C	C	0.066	-0.552	0.957	-0.577	0.564	16	G	A	C	C	0.066	0.537	1.101	0.488	0.626
16	G	C	A	C	0.020	3.139	1.602	1.960	0.050	16	G	C	A	C	0.020	0.895	1.806	0.496	0.620
16	G	C	C	A	0.176	-0.100	0.625	-0.160	0.873	16	G	C	C	A	0.176	-0.957	0.713	-1.343	0.180
16	G	C	C	C	0.648	NA	NA	NA	NA	16	G	C	C	C	0.649	NA	NA	NA	NA
17	A	C	C	C	0.066	-0.493	0.991	-0.498	0.619	17	A	C	C	C	0.065	0.525	1.131	0.464	0.643
17	C	A	C	T	0.020	3.159	1.621	1.949	0.052	17	C	A	C	T	0.020	0.843	1.822	0.462	0.644
17	C	C	A	C	0.175	-0.163	0.670	-0.243	0.808	17	C	C	A	C	0.175	-0.834	0.761	-1.096	0.273
17	C	C	C	C	0.364	0.622	0.549	1.133	0.257	17	C	C	C	C	0.364	-0.281	0.633	-0.443	0.658
17	*	*	*	*	0.001	-7.765	0.013	-579.620	0.000	17	*	*	*	*	0.001	-10.202	0.016	-657.983	0.000
17	C	C	C	T	0.374	NA	NA	NA	NA	17	C	C	C	T	0.374	NA	NA	NA	NA
18	A	C	T	G	0.020	3.116	1.618	1.926	0.054	18	A	C	T	G	0.020	0.937	1.821	0.515	0.607
18	C	A	C	G	0.176	-0.097	0.668	-0.145	0.885	18	C	A	C	G	0.176	-0.861	0.760	-1.133	0.258
18	C	C	C	A	0.234	1.242	0.606	2.048	0.041	18	C	C	C	A	0.234	-0.581	0.693	-0.837	0.403
18	C	C	C	G	0.196	-0.278	0.656	-0.423	0.672	18	C	C	C	G	0.195	0.383	0.763	0.501	0.616
18	C	C	T	G	0.374	NA	NA	NA	NA	18	C	C	T	G	0.374	NA	NA	NA	NA
19	A	C	G	G	0.176	-0.266	0.666	-0.399	0.690	19	A	C	G	G	0.176	-0.958	0.755	-1.269	0.205
19	C	C	A	A	0.235	1.061	0.602	1.763	0.078	19	C	C	A	A	0.235	-0.755	0.685	-1.102	0.271
19	C	C	G	G	0.194	-0.466	0.653	-0.713	0.476	19	C	C	G	G	0.193	0.306	0.754	0.406	0.685
19	*	*	*	*	0.002	-2.931	NA	NA	NA	19	*	*	*	*	0.002	-5.718	NA	NA	NA
19	C	T	G	G	0.394	NA	NA	NA	NA	19	C	T	G	G	0.394	NA	NA	NA	NA
20	C	A	A	C	0.213	0.901	0.620	1.453	0.147	20	C	A	A	C	0.213	-0.656	0.705	-0.931	0.352
20	C	A	A	T	0.022	2.778	1.601	1.736	0.083	20	C	A	A	T	0.022	-1.628	1.834	-0.888	0.375
20	C	G	G	C	0.371	-0.357	0.535	-0.667	0.505	20	C	G	G	C	0.369	-0.281	0.615	-0.456	0.648
20	*	*	*	*	0.002	5.566	6.581	0.846	0.398	20	*	*	*	*	0.002	10.406	0.016	659.600	0.000
20	T	G	G	C	0.391	NA	NA	NA	NA	20	T	G	G	C	0.394	NA	NA	NA	NA
21	A	A	C	A	0.213	1.041	0.569	1.830	0.068	21	A	A	C	A	0.213	-0.381	0.646	-0.589	0.556
21	A	A	T	A	0.021	3.114	1.665	1.870	0.062	21	A	A	T	A	0.022	-1.374	1.783	-0.770	0.441
21	G	G	C	G	0.092	-0.274	0.799	-0.343	0.732	21	G	G	C	G	0.092	1.196	0.904	1.324	0.186
21	*	*	*	*	0.004	3.519	5.848	0.602	0.547	21	*	*	*	*	0.002	10.498	NA	NA	NA
21	G	G	C	A	0.671	NA	NA	NA	NA	21	G	G	C	A	0.671	NA	NA	NA	NA

Table B1.31. Continued

ApoA1										ApoB									
Window	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**	**Window**	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**
22	A	C	A	A	0.026	0.741	1.959	0.378	0.705	22	A	C	A	A	0.025	4.104	1.979	2.074	0.038
22	A	C	A	G	0.189	1.182	0.697	1.695	0.091	22	A	C	A	G	0.190	-0.741	0.767	-0.965	0.335
22	A	T	A	G	0.021	3.252	1.651	1.970	0.049	22	A	T	A	G	0.021	-0.703	1.837	-0.383	0.702
22	G	C	A	A	0.240	0.161	0.653	0.246	0.806	22	G	C	A	A	0.242	0.619	0.751	0.824	0.410
22	G	C	G	A	0.011	-0.577	2.847	-0.203	0.839	22	G	C	G	A	0.011	2.579	3.118	0.827	0.408
22	G	C	G	G	0.082	-0.213	0.892	-0.239	0.811	22	G	C	G	G	0.081	1.294	1.009	1.282	0.200
22	*	*	*	*	0.003	3.020	6.550	0.461	0.645	22	*	*	*	*	0.002	3.781	0.027	139.371	0.000
22	G	C	A	G	0.429	NA	NA	NA	NA	22	G	C	A	G	0.428	NA	NA	NA	NA
23	C	A	A	G	0.267	-0.225	0.575	-0.392	0.695	23	C	A	A	G	0.268	1.504	0.664	2.265	0.024
23	C	A	G	A	0.035	-1.624	1.240	-1.309	0.191	23	C	A	G	A	0.036	1.275	1.385	0.921	0.357
23	C	G	A	G	0.011	-1.515	2.646	-0.573	0.567	23	C	G	A	G	0.011	2.483	3.054	0.813	0.417
23	C	G	G	G	0.080	-0.578	0.886	-0.652	0.515	23	C	G	G	G	0.081	1.657	0.998	1.661	0.097
23	T	A	G	G	0.021	3.418	1.670	2.046	0.041	23	T	A	G	G	0.021	0.895	1.911	0.468	0.640
23	*	*	*	*	0.003	-2.162	5.993	-0.361	0.718	23	*	*	*	*	0.002	-11.533	7.807	-1.477	0.140
23	C	A	G	G	0.583	NA	NA	NA	NA	23	C	A	G	G	0.582	NA	NA	NA	NA
24	A	A	G	W	0.267	0.084	0.626	0.134	0.893	24	A	A	G	W	0.268	1.014	0.721	1.406	0.160
24	A	G	A	W	0.035	-1.216	1.260	-0.965	0.335	24	A	G	A	W	0.036	1.023	1.422	0.719	0.472
24	A	G	G	W	0.232	1.213	0.654	1.853	0.064	24	A	G	G	W	0.231	-0.254	0.749	-0.339	0.735
24	G	A	G	W	0.013	-2.185	2.419	-0.903	0.367	24	G	A	G	W	0.012	2.480	3.055	0.812	0.417
24	G	G	G	D	0.017	2.767	2.151	1.286	0.199	24	G	G	G	D	0.018	1.112	2.350	0.473	0.636
24	G	G	G	W	0.063	-1.125	1.048	-1.074	0.283	24	G	G	G	W	0.061	1.584	1.194	1.327	0.185
24	*	*	*	*	0.003	3.721	5.202	0.715	0.475	24	*	*	*	*	0.003	4.313	6.126	0.704	0.482
24	A	G	G	D	0.370	NA	NA	NA	NA	24	A	G	G	D	0.371	NA	NA	NA	NA
25	A	G	W	G	0.021	-3.885	2.415	-1.609	0.108	25	A	G	W	G	0.020	-0.593	2.765	-0.214	0.830
25	G	A	W	A	0.035	-1.389	1.258	-1.104	0.270	25	G	A	W	A	0.036	-0.110	1.420	-0.077	0.938
25	G	G	D	A	0.254	-0.059	0.694	-0.084	0.933	25	G	G	D	A	0.254	-1.026	0.783	-1.311	0.190
25	G	G	D	G	0.134	-0.372	0.848	-0.439	0.661	25	G	G	D	G	0.135	-1.196	0.956	-1.252	0.211
25	G	G	W	A	0.241	0.030	0.709	0.042	0.966	25	G	G	W	A	0.237	-1.666	0.832	-2.004	0.045
25	G	G	W	G	0.053	2.445	1.368	1.787	0.074	25	G	G	W	G	0.055	1.813	1.480	1.225	0.221
25	*	*	*	*	0.003	3.408	6.805	0.501	0.617	25	*	*	*	*	0.003	2.861	7.518	0.381	0.704
25	A	G	W	A	0.259	NA	NA	NA	NA	25	A	G	W	A	0.259	NA	NA	NA	NA
26	A	W	A	G	0.035	-1.587	1.240	-1.280	0.201	26	A	W	A	G	0.035	0.774	1.390	0.557	0.578
26	G	D	A	C	0.180	-0.315	0.651	-0.483	0.629	26	G	D	A	C	0.182	-0.294	0.723	-0.407	0.684
26	G	D	A	G	0.071	-0.021	1.022	-0.021	0.983	26	G	D	A	G	0.070	0.055	1.174	0.047	0.963
26	G	D	G	G	0.135	-0.077	0.751	-0.103	0.918	26	G	D	G	G	0.137	-0.057	0.837	-0.068	0.946
26	G	W	G	G	0.072	0.077	1.008	0.077	0.939	26	G	W	G	G	0.072	1.500	1.118	1.342	0.180
26	*	*	*	*	0.008	-1.610	2.881	-0.559	0.577	26	*	*	*	*	0.007	6.890	3.377	2.040	0.042
26	G	W	A	G	0.499	NA	NA	NA	NA	26	G	W	A	G	0.497	NA	NA	NA	NA
27	D	A	C	C	0.181	-0.225	0.651	-0.345	0.730	27	D	A	C	C	0.182	-0.320	0.721	-0.443	0.658
27	D	A	G	C	0.071	0.113	1.019	0.111	0.912	27	D	A	G	C	0.070	0.064	1.171	0.054	0.957
27	D	G	G	C	0.135	0.016	0.751	0.021	0.983	27	D	G	G	C	0.137	-0.080	0.836	-0.096	0.923
27	W	A	G	A	0.026	-0.514	1.541	-0.334	0.739	27	W	A	G	A	0.026	1.153	1.736	0.665	0.507
27	W	G	G	C	0.073	0.236	1.004	0.235	0.814	27	W	G	G	C	0.073	1.467	1.113	1.318	0.188
27	*	*	*	*	0.007	-2.025	2.886	-0.702	0.483	27	*	*	*	*	0.006	8.123	3.379	2.404	0.016
27	W	A	G	C	0.508	NA	NA	NA	NA	27	W	A	G	C	0.506	NA	NA	NA	NA
28	A	C	C	C	0.185	-0.393	0.684	-0.574	0.566	28	A	C	C	C	0.186	0.092	0.764	0.121	0.904
28	A	G	A	C	0.026	-0.649	1.555	-0.417	0.677	28	A	G	A	C	0.026	1.310	1.759	0.745	0.457
28	A	G	C	C	0.251	-0.222	0.633	-0.351	0.726	28	A	G	C	C	0.252	0.643	0.708	0.908	0.364
28	G	G	C	G	0.206	-0.036	0.680	-0.053	0.957	28	G	G	C	G	0.209	0.657	0.764	0.860	0.390
28	*	*	*	*	0.004	-2.672	6.417	-0.416	0.677	28	*	*	*	*	0.004	11.204	7.103	1.577	0.115
28	A	G	C	G	0.329	NA	NA	NA	NA	28	A	G	C	G	0.324	NA	NA	NA	NA
29	C	C	C	T	0.184	-0.430	0.643	-0.668	0.504	29	C	C	C	T	0.185	-0.322	0.714	-0.452	0.652
29	G	A	C	T	0.026	-0.767	1.538	-0.499	0.618	29	G	A	C	T	0.025	0.881	1.731	0.509	0.611
29	G	C	C	T	0.253	-0.321	0.588	-0.547	0.585	29	G	C	C	T	0.253	0.294	0.657	0.447	0.655
29	G	C	G	G	0.034	-1.479	1.266	-1.168	0.243	29	G	C	G	G	0.034	-1.410	1.447	-0.974	0.330
29	*	*	*	*	0.002	-5.780	6.368	-0.908	0.364	29	*	*	*	*	0.002	24.357	7.315	3.330	0.001
29	G	C	G	T	0.503	NA	NA	NA	NA	29	G	C	G	T	0.501	NA	NA	NA	NA
30	A	C	T	A	0.025	-0.761	1.542	-0.493	0.622	30	A	C	T	A	0.025	0.524	1.740	0.301	0.764
30	C	C	T	A	0.437	-0.405	0.496	-0.816	0.415	30	C	C	T	A	0.439	-0.234	0.558	-0.419	0.675
30	C	G	G	A	0.034	-1.510	1.271	-1.188	0.235	30	C	G	G	A	0.034	-1.576	1.431	-1.101	0.271
30	C	G	T	G	0.027	-0.755	1.479	-0.510	0.610	30	C	G	T	G	0.027	-3.873	1.694	-2.287	0.022
30	C	G	T	A	0.477	NA	NA	NA	NA	30	C	G	T	A	0.475	NA	NA	NA	NA
31	G	G	A	C	0.034	-1.045	1.252	-0.835	0.404	31	G	G	A	C	0.034	-1.434	1.410	-1.016	0.310
31	G	T	A	C	0.427	0.517	0.505	1.025	0.306	31	G	T	A	C	0.428	0.095	0.568	0.166	0.868

Table B1.31. Continued

							ApoA1											ApoB	
Window	loc.1	loc.2	loc.3	loc.4	hap.freq	coef	se	t.stat	pval	Window	loc.1	loc.2	loc.3	loc.4	hap.freq	coef	se	t.stat	pval
31	G	T	A	T	0.049	0.067	1.090	0.061	0.951	31	G	T	A	T	0.047	1.160	1.250	0.928	0.353
31	G	T	G	C	0.027	-0.317	1.479	-0.215	0.830	31	G	T	G	C	0.027	-3.646	1.689	-2.159	0.031
31	C	T	A	C	0.463	NA	NA	NA	NA	31	C	T	A	C	0.465	NA	NA	NA	NA
32	G	A	C	W	0.032	-1.346	1.272	-1.058	0.290	32	G	A	C	W	0.033	-1.528	1.421	-1.076	0.282
32	T	A	C	D	0.148	-0.128	0.665	-0.193	0.847	32	T	A	C	D	0.149	-0.112	0.754	-0.148	0.882
32	T	A	T	W	0.048	-0.213	1.094	-0.195	0.846	32	T	A	T	W	0.046	1.043	1.251	0.834	0.405
32	T	G	C	W	0.027	-0.589	1.472	-0.400	0.689	32	T	G	C	W	0.026	-3.748	1.683	-2.226	0.026
32	T	A	C	W	0.744	NA	NA	NA	NA	32	T	A	C	W	0.744	NA	NA	NA	NA
33	A	C	D	A	0.150	-0.286	0.684	-0.419	0.676	33	A	C	D	A	0.151	0.122	0.773	0.157	0.875
33	A	C	W	A	0.261	-0.716	0.572	-1.253	0.211	33	A	C	W	A	0.262	0.618	0.652	0.948	0.344
33	A	T	W	C	0.049	-0.259	1.084	-0.239	0.811	33	A	T	W	C	0.047	1.254	1.247	1.006	0.315
33	G	C	W	A	0.025	-0.896	1.572	-0.570	0.569	33	G	C	W	A	0.026	-3.426	1.731	-1.979	0.048
33	*	*	*	*	0.002	1.111	8.020	0.139	0.890	33	A	C	W	C	0.513	NA	NA	NA	NA
33	A	C	W	C	0.513	NA	NA	NA	NA	34	C	D	A	A	0.151	0.143	0.776	0.184	0.854
34	C	D	A	A	0.150	-0.292	0.686	-0.426	0.670	34	C	W	A	A	0.262	0.643	0.654	0.983	0.326
34	C	W	A	A	0.260	-0.681	0.573	-1.188	0.235	34	C	W	A	G	0.026	-3.181	1.736	-1.832	0.067
34	C	W	A	G	0.025	-0.835	1.559	-0.535	0.592	34	T	W	C	A	0.047	1.265	1.249	1.012	0.312
34	T	W	C	A	0.049	-0.261	1.086	-0.240	0.810	34	C	W	C	A	0.513	NA	NA	NA	NA
34	*	*	*	*	0.002	1.214	7.805	0.156	0.876	35	D	A	A	T	0.151	0.187	0.769	0.243	0.808
34	C	W	C	A	0.513	NA	NA	NA	NA	35	W	A	A	T	0.262	0.661	0.649	1.019	0.309
35	D	A	A	T	0.150	-0.299	0.682	-0.438	0.662	35	W	A	G	T	0.026	-3.127	1.728	-1.810	0.071
35	W	A	A	T	0.260	-0.679	0.570	-1.191	0.234	35	W	C	A	C	0.020	3.909	1.937	2.018	0.044
35	W	A	G	T	0.025	-0.846	1.551	-0.546	0.586	35	W	C	A	T	0.541	NA	NA	NA	NA
35	W	C	A	C	0.021	-0.764	1.653	-0.462	0.644	36	A	A	T	C	0.413	0.483	0.557	0.868	0.386
35	*	*	*	*	0.002	1.270	8.188	0.155	0.877	36	A	G	T	C	0.026	-3.113	1.700	-1.831	0.068
35	W	C	A	T	0.541	NA	NA	NA	NA	36	C	A	C	C	0.020	3.926	1.939	2.024	0.043
36	A	A	T	C	0.410	-0.559	0.493	-1.134	0.257	36	C	A	T	A	0.019	-0.408	2.071	-0.197	0.844
36	A	G	T	C	0.026	-1.102	1.506	-0.731	0.465	36	C	A	T	C	0.522	NA	NA	NA	NA
36	C	A	C	C	0.021	-0.814	1.651	-0.493	0.622	37	A	C	C	G	0.018	3.455	2.087	1.656	0.098
36	C	A	T	A	0.020	1.049	1.757	0.597	0.551	37	A	T	A	G	0.018	-0.488	2.139	-0.228	0.820
36	C	A	T	C	0.522	NA	NA	NA	NA	37	A	T	C	A	0.098	-0.153	0.905	-0.169	0.866
37	A	C	C	G	0.019	-0.079	1.798	-0.044	0.965	37	G	T	C	G	0.026	-3.385	1.681	-2.014	0.044
37	A	T	A	G	0.018	2.301	1.853	1.241	0.215	37	*	*	*	*	0.003	3.492	6.991	0.500	0.618
37	A	T	C	A	0.096	-0.187	0.802	-0.233	0.816	37	A	T	C	G	0.837	NA	NA	NA	NA
37	G	T	C	G	0.027	-0.418	1.465	-0.285	0.775	38	C	C	G	G	0.018	3.963	2.087	1.899	0.058
37	*	*	*	*	0.004	-3.403	5.509	-0.618	0.537	38	T	A	G	G	0.017	-0.175	2.165	-0.081	0.936
37	A	T	C	G	0.836	NA	NA	NA	NA	38	T	C	A	G	0.096	0.049	0.912	0.053	0.957
38	C	C	G	G	0.019	-0.163	1.823	-0.089	0.929	38	T	C	G	C	0.019	-0.065	1.833	-0.036	0.972
38	T	A	G	G	0.018	2.233	1.863	1.199	0.231	38	*	*	*	*	0.005	0.394	5.311	0.074	0.941
38	T	C	A	G	0.095	-0.170	0.809	-0.210	0.833	38	T	C	G	G	0.845	NA	NA	NA	NA
38	T	C	G	C	0.018	-1.340	1.643	-0.815	0.415	39	A	G	G	W	0.017	-0.383	2.220	-0.173	0.863
38	*	*	*	*	0.006	-2.564	4.151	-0.618	0.537	39	C	A	G	W	0.098	-0.128	0.904	-0.142	0.887
38	T	C	G	G	0.845	NA	NA	NA	NA	39	C	G	C	W	0.019	-0.374	1.799	-0.208	0.836
39	A	G	G	W	0.019	1.923	1.793	1.073	0.284	39	C	G	G	I	0.081	-2.145	1.006	-2.132	0.033
39	C	A	G	W	0.097	-0.051	0.796	-0.064	0.949	39	*	*	*	*	0.003	-2.904	5.831	-0.498	0.619
39	C	G	C	W	0.019	-1.143	1.616	-0.707	0.480	39	C	G	G	W	0.782	NA	NA	NA	NA
39	C	G	G	I	0.082	1.678	0.880	1.906	0.057	40	A	G	W	A	0.098	-0.392	0.918	-0.426	0.670
39	*	*	*	*	0.002	-1.384	5.904	-0.234	0.815	40	G	C	W	A	0.020	-0.607	1.777	-0.342	0.733
39	C	G	G	W	0.781	NA	NA	NA	NA	40	G	G	I	A	0.081	-2.103	1.003	-2.096	0.036
40	A	G	W	A	0.096	-0.068	0.811	-0.083	0.934	40	G	G	W	G	0.052	0.011	1.207	0.009	0.992
40	G	C	W	A	0.018	-1.601	1.692	-0.946	0.344	40	*	*	*	*	0.004	7.380	7.604	0.971	0.332
40	G	G	I	A	0.082	1.648	0.887	1.857	0.064	40	G	G	W	A	0.745	NA	NA	NA	NA
40	G	G	W	G	0.055	0.013	1.040	0.013	0.990	41	C	W	A	G	0.020	-0.459	1.776	-0.258	0.796
40	*	*	*	*	0.004	0.484	0.115	4.199	0.000	41	G	I	A	G	0.082	-1.985	1.000	-1.985	0.048
40	G	G	W	A	0.745	NA	NA	NA	NA	41	G	W	A	T	0.039	1.261	1.363	0.925	0.355
41	C	W	A	G	0.019	-1.475	1.620	-0.910	0.363	41	G	W	G	G	0.055	0.530	1.136	0.466	0.641
41	G	I	A	G	0.082	1.701	0.886	1.919	0.055	41	G	W	A	G	0.804	NA	NA	NA	NA
41	G	W	A	T	0.040	1.118	1.173	0.953	0.341	42	I	A	G	C	0.080	-1.689	1.007	-1.677	0.094
41	G	W	G	G	0.057	0.020	0.997	0.020	0.984	42	W	A	G	T	0.022	-0.338	1.891	-0.179	0.858
41	G	W	A	G	0.800	NA	NA	NA	NA	42	W	A	T	C	0.039	1.260	1.357	0.929	0.353
42	I	A	G	C	0.081	1.697	0.897	1.893	0.059	42	W	G	G	C	0.056	0.639	1.133	0.564	0.573
42	W	A	G	T	0.022	1.435	1.661	0.864	0.388	42	*	*	*	*	0.001	-23.261	NA	NA	NA
42	W	A	T	C	0.040	1.261	1.174	1.074	0.283	42	W	A	G	C	0.802	NA	NA	NA	NA
42	W	G	G	C	0.058	0.201	0.986	0.204	0.839	43	A	G	C	A	0.427	-0.836	0.574	-1.457	0.146

Table B1.31. Continued

							ApoA1											ApoB	
Window	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**	**Window**	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**
42	*	*	*	*	0.002	7.058	7.112	0.992	0.321	43	A	G	T	A	0.022	-1.619	1.863	-0.869	0.385
42	W	A	G	C	0.797	NA	NA	NA	NA	43	A	T	C	G	0.039	1.150	1.379	0.834	0.405
43	A	G	C	A	0.426	0.046	0.517	0.089	0.929	43	G	G	C	A	0.056	0.275	1.158	0.238	0.812
43	A	G	T	A	0.024	1.700	1.601	1.062	0.289	43	A	G	C	G	0.455	NA	NA	NA	NA
43	A	T	C	G	0.040	1.016	1.193	0.851	0.395	44	G	C	A	A	0.034	1.898	1.449	1.311	0.190
43	G	G	C	A	0.058	0.040	1.015	0.039	0.969	44	G	C	A	G	0.448	-0.925	0.567	-1.633	0.103
43	A	G	C	G	0.452	NA	NA	NA	NA	44	G	T	A	G	0.023	-1.664	1.876	-0.887	0.375
44	G	C	A	A	0.035	-0.869	1.265	-0.687	0.492	44	T	C	G	G	0.039	1.124	1.374	0.818	0.413
44	G	C	A	G	0.448	0.112	0.513	0.218	0.827	44	G	C	G	G	0.456	NA	NA	NA	NA
44	G	T	A	G	0.024	1.680	1.602	1.049	0.295	45	C	A	A	A	0.035	1.927	1.577	1.222	0.222
44	T	C	G	G	0.041	1.015	1.194	0.850	0.396	45	C	A	G	A	0.090	-2.496	1.049	-2.380	0.018
44	G	C	G	G	0.453	NA	NA	NA	NA	45	C	A	G	T	0.352	-0.632	0.610	-1.036	0.301
45	C	A	A	A	0.036	0.731	1.358	0.538	0.591	45	C	G	G	T	0.071	0.250	1.129	0.221	0.825
45	C	A	G	A	0.090	0.657	0.929	0.708	0.479	45	T	A	G	A	0.023	-1.924	1.899	-1.013	0.311
45	C	A	G	T	0.350	0.315	0.539	0.584	0.560	45	*	*	*	*	0.002	2.322	6.818	0.341	0.734
45	C	G	G	T	0.072	2.531	0.993	2.548	0.011	45	C	G	G	A	0.428	NA	NA	NA	NA
45	T	A	G	A	0.024	1.971	1.586	1.242	0.214	46	A	A	A	G	0.035	2.102	1.557	1.350	0.177
45	*	*	*	*	0.002	-9.790	5.412	-1.809	0.071	46	A	G	A	G	0.113	-2.095	0.910	-2.303	0.022
45	C	G	G	A	0.425	NA	NA	NA	NA	46	A	G	T	A	0.351	-0.609	0.610	-0.999	0.318
46	A	A	A	G	0.037	-0.075	1.334	-0.056	0.955	46	G	G	T	G	0.074	0.675	1.049	0.643	0.520
46	A	G	A	G	0.114	0.415	0.801	0.518	0.605	46	*	*	*	*	0.001	2.119	7.619	0.278	0.781
46	A	G	T	A	0.350	0.395	0.541	0.730	0.466	46	G	G	A	G	0.425	NA	NA	NA	NA
46	G	G	T	G	0.076	1.437	0.911	1.576	0.115	47	A	A	G	C	0.030	3.747	1.790	2.093	0.037
46	*	*	*	*	0.001	-6.481	6.522	-0.994	0.321	47	G	A	G	A	0.069	1.234	1.159	1.065	0.287
46	G	G	A	G	0.422	NA	NA	NA	NA	47	G	T	A	A	0.012	-2.971	3.118	-0.953	0.341
47	A	A	G	C	0.032	0.785	1.455	0.540	0.590	47	G	T	A	C	0.337	0.125	0.615	0.203	0.839
47	G	A	G	A	0.071	0.747	0.997	0.749	0.454	47	G	T	G	A	0.024	1.447	1.899	0.762	0.446
47	G	T	A	A	0.011	-6.778	2.817	-2.406	0.016	47	G	T	G	C	0.050	1.181	1.339	0.882	0.378
47	G	T	A	C	0.338	0.650	0.533	1.220	0.223	47	*	*	*	*	0.004	-4.249	7.283	-0.583	0.560
47	G	T	G	A	0.023	0.397	1.787	0.222	0.824	47	G	A	G	C	0.474	NA	NA	NA	NA
47	G	T	G	C	0.052	2.419	1.150	2.104	0.036	48	A	G	A	G	0.072	0.636	1.134	0.561	0.575
47	*	*	*	*	0.004	-8.813	5.860	-1.504	0.133	48	A	G	C	A	0.204	0.520	0.728	0.714	0.475
47	G	A	G	C	0.470	NA	NA	NA	NA	48	A	G	C	G	0.297	0.100	0.663	0.151	0.880
48	A	G	A	G	0.073	0.002	0.998	0.002	0.998	48	T	A	A	G	0.011	-1.896	3.242	-0.585	0.559
48	A	G	C	A	0.203	-0.316	0.647	-0.488	0.626	48	T	G	A	G	0.023	1.868	1.991	0.938	0.348
48	A	G	C	G	0.297	-0.697	0.582	-1.198	0.231	48	T	G	C	G	0.051	1.046	1.349	0.776	0.438
48	T	A	A	G	0.011	-7.138	2.648	-2.696	0.007	48	*	*	*	*	0.001	25.295	NA	NA	NA
48	T	G	A	G	0.023	-0.779	1.767	-0.441	0.659	48	T	A	C	G	0.340	NA	NA	NA	NA
48	T	G	C	G	0.052	1.847	1.177	1.569	0.117	49	A	A	G	C	0.011	-0.144	3.094	-0.046	0.963
48	*	*	*	*	0.001	8.254	8.830	0.935	0.350	49	G	A	G	C	0.095	0.867	0.977	0.887	0.375
48	T	A	C	G	0.339	NA	NA	NA	NA	49	G	C	A	C	0.206	0.670	0.729	0.919	0.358
49	A	A	G	C	0.011	-6.573	2.747	-2.393	0.017	49	G	C	G	A	0.097	0.274	0.988	0.277	0.782
49	G	A	G	C	0.096	-0.338	0.866	-0.390	0.696	49	G	C	G	C	0.246	0.291	0.713	0.408	0.684
49	G	C	A	C	0.204	-0.289	0.650	-0.445	0.657	49	*	*	*	*	0.002	10.507	0.233	45.167	0.000
49	G	C	G	A	0.095	-0.393	0.890	-0.441	0.659	49	A	C	G	C	0.342	NA	NA	NA	NA
49	G	C	G	C	0.249	-0.187	0.632	-0.295	0.768	50	A	G	C	A	0.106	0.724	0.883	0.820	0.413
49	*	*	*	*	0.003	6.866	6.401	1.073	0.284	50	C	A	C	A	0.205	0.745	0.658	1.133	0.258
49	A	C	G	C	0.342	NA	NA	NA	NA	50	C	G	A	A	0.098	0.298	0.941	0.317	0.751
50	A	G	C	A	0.107	-0.560	0.790	-0.709	0.479	50	C	G	C	G	0.022	1.822	1.850	0.985	0.325
50	C	A	C	A	0.204	-0.037	0.595	-0.063	0.950	50	C	G	C	A	0.568	NA	NA	NA	NA
50	C	G	A	A	0.097	-0.010	0.844	-0.011	0.991	51	A	C	A	G	0.206	0.708	0.722	0.980	0.327
50	C	G	C	G	0.024	0.728	1.545	0.471	0.638	51	G	A	A	G	0.097	0.367	0.982	0.374	0.708
50	C	G	C	A	0.569	NA	NA	NA	NA	51	G	C	A	G	0.315	0.548	0.652	0.840	0.401
51	A	C	A	G	0.204	-0.010	0.649	-0.016	0.987	51	G	C	G	G	0.022	1.958	1.877	1.043	0.297
51	G	A	A	G	0.095	-0.006	0.877	-0.007	0.995	51	*	*	*	*	0.002	9.289	0.000	1.67E+16	0.000
51	G	C	A	G	0.318	-0.001	0.578	-0.002	0.999	51	G	C	A	T	0.358	NA	NA	NA	NA
51	G	C	G	G	0.024	0.797	1.566	0.509	0.611	52	A	A	G	T	0.096	-0.059	0.970	-0.061	0.951
51	*	*	*	*	0.002	5.845	6.879	0.850	0.396	52	C	A	T	C	0.133	-0.314	0.832	-0.377	0.706
51	G	C	A	T	0.357	NA	NA	NA	NA	52	C	A	T	T	0.223	-0.602	0.685	-0.879	0.379
52	A	A	G	T	0.095	0.079	0.872	0.090	0.928	52	C	G	G	T	0.022	1.437	1.863	0.771	0.441
52	C	A	T	C	0.134	-0.816	0.737	-1.108	0.268	52	*	*	*	*	0.001	-8.307	9.212	-0.902	0.367
52	C	A	T	T	0.222	0.522	0.609	0.857	0.391	52	C	A	G	T	0.524	NA	NA	NA	NA
52	C	G	G	T	0.024	0.789	1.550	0.509	0.611	53	A	T	C	C	0.133	-0.263	0.820	-0.320	0.749
52	*	*	*	*	0.001	3.666	10.600	0.346	0.730	53	A	T	T	C	0.224	-0.807	0.664	-1.215	0.225

Table B1.31. Continued

ApoA1										ApoB									
Window	loc.1	loc.2	loc.3	loc.4	hap.freq	coef	se	t.stat	pval	Window	loc.1	loc.2	loc.3	loc.4	hap.freq	coef	se	t.stat	pval
52	C	A	G	T	0.524	NA	NA	NA	NA	53	G	G	T	C	0.022	1.493	1.846	0.809	0.419
53	A	T	C	C	0.134	-0.809	0.726	-1.114	0.265	53	*	*	*	*	0.001	17.816	7.235	2.463	0.014
53	A	T	T	C	0.222	0.518	0.590	0.878	0.380	53	A	G	T	C	0.620	NA	NA	NA	NA
53	G	G	T	C	0.024	0.774	1.534	0.504	0.614	54	G	T	C	C	0.018	-0.553	1.886	-0.293	0.769
53	*	*	*	*	0.001	0.699	6.418	0.109	0.913	54	T	C	C	T	0.132	-0.459	0.822	-0.558	0.577
53	A	G	T	C	0.619	NA	NA	NA	NA	54	T	T	C	T	0.223	-0.850	0.664	-1.278	0.201
54	G	T	C	C	0.018	-0.904	1.613	-0.561	0.575	54	*	*	*	*	0.002	19.446	7.214	2.696	0.007
54	T	C	C	T	0.134	-0.882	0.728	-1.212	0.226	54	G	T	C	T	0.624	NA	NA	NA	NA
54	T	T	C	T	0.222	0.459	0.593	0.773	0.440	55	C	C	T	A	0.132	-0.536	0.818	-0.656	0.512
54	*	*	*	*	0.001	0.643	6.433	0.100	0.920	55	T	C	C	A	0.018	-0.675	1.880	-0.359	0.720
54	G	T	C	T	0.624	NA	NA	NA	NA	55	T	C	T	C	0.127	-1.809	0.791	-2.285	0.023
55	C	C	T	A	0.134	-0.881	0.730	-1.208	0.227	55	*	*	*	*	0.002	19.055	7.089	2.688	0.007
55	T	C	C	A	0.018	-0.942	1.617	-0.582	0.560	55	T	C	T	A	0.720	NA	NA	NA	NA
55	T	C	T	C	0.129	0.512	0.699	0.732	0.464	56	C	C	A	G	0.019	0.310	1.800	0.172	0.863
55	*	*	*	*	0.001	0.827	6.392	0.129	0.897	56	C	T	C	G	0.127	-1.847	0.779	-2.371	0.018
55	T	C	T	A	0.717	NA	NA	NA	NA	56	*	*	*	*	0.002	19.425	7.083	2.742	0.006
56	C	C	A	G	0.018	-0.773	1.611	-0.480	0.632	56	C	T	A	G	0.852	NA	NA	NA	NA
56	C	T	C	G	0.129	0.779	0.687	1.134	0.257	57	C	A	G	G	0.019	0.271	1.811	0.149	0.881
56	*	*	*	*	0.002	-4.421	6.410	-0.690	0.491	57	T	A	G	A	0.034	-0.184	1.433	-0.128	0.898
56	C	T	A	G	0.851	NA	NA	NA	NA	57	T	C	G	G	0.128	-1.576	0.775	-2.032	0.042
57	C	A	G	G	0.018	-0.734	1.614	-0.455	0.649	57	T	A	G	G	0.819	NA	NA	NA	NA
57	T	A	G	A	0.034	0.281	1.260	0.223	0.824	58	A	G	A	C	0.034	-0.170	1.433	-0.118	0.906
57	T	C	G	G	0.130	0.784	0.682	1.150	0.250	58	C	G	G	C	0.036	0.019	1.508	0.013	0.990
57	T	A	G	G	0.816	NA	NA	NA	NA	58	C	G	G	T	0.094	-2.027	0.909	-2.231	0.026
58	A	G	A	C	0.034	0.303	1.259	0.241	0.810	58	A	G	G	C	0.836	NA	NA	NA	NA
58	C	G	G	C	0.038	0.495	1.258	0.393	0.694	59	G	A	C	A	0.034	-0.013	1.437	-0.009	0.993
58	C	G	G	T	0.094	0.900	0.806	1.117	0.264	59	G	G	C	G	0.110	0.850	0.857	0.992	0.322
58	A	G	G	C	0.833	NA	NA	NA	NA	59	G	G	T	A	0.090	-1.250	0.960	-1.302	0.193
59	G	A	C	A	0.034	0.437	1.257	0.347	0.728	59	G	G	C	A	0.765	NA	NA	NA	NA
59	G	G	C	G	0.112	1.056	0.754	1.401	0.162	60	A	C	A	G	0.034	-0.015	1.439	-0.010	0.992
59	G	G	T	A	0.090	1.455	0.841	1.730	0.084	60	G	C	A	A	0.096	-0.152	0.881	-0.172	0.863
59	G	G	C	A	0.762	NA	NA	NA	NA	60	G	C	G	G	0.110	0.878	0.861	1.019	0.308
60	A	C	A	G	0.034	0.463	1.260	0.368	0.713	60	G	T	A	G	0.090	-1.234	0.963	-1.282	0.200
60	G	C	A	A	0.097	0.204	0.776	0.263	0.792	60	G	C	A	G	0.670	NA	NA	NA	NA
60	G	C	G	G	0.112	1.081	0.757	1.428	0.154	61	C	A	A	A	0.096	-0.175	0.880	-0.199	0.842
60	G	T	A	G	0.090	1.463	0.844	1.734	0.083	61	C	G	G	A	0.110	0.822	0.860	0.956	0.340
60	G	C	A	G	0.666	NA	NA	NA	NA	61	T	A	G	A	0.090	-1.277	0.962	-1.328	0.185
61	C	A	A	A	0.097	0.167	0.775	0.215	0.830	61	*	*	*	*	0.009	-2.661	2.799	-0.951	0.342
61	C	G	G	A	0.112	1.000	0.755	1.325	0.186	61	C	A	G	A	0.694	NA	NA	NA	NA
61	T	A	G	A	0.090	1.389	0.841	1.651	0.099	62	A	A	A	G	0.096	-0.051	0.878	-0.058	0.953
61	*	*	*	*	0.009	-2.859	2.460	-1.162	0.246	62	G	G	A	G	0.110	1.021	0.853	1.197	0.232
61	C	A	G	A	0.691	NA	NA	NA	NA	62	*	*	*	*	0.014	-0.915	2.336	-0.392	0.695
62	A	A	A	G	0.097	-0.004	0.773	-0.005	0.996	62	A	G	A	G	0.780	NA	NA	NA	NA
62	G	G	A	G	0.112	0.795	0.748	1.063	0.288	63	A	A	G	G	0.095	-0.346	0.880	-0.394	0.694
62	*	*	*	*	0.014	-3.646	2.043	-1.784	0.075	63	*	*	*	*	0.015	0.272	2.238	0.122	0.903
62	A	G	A	G	0.777	NA	NA	NA	NA	63	G	A	G	G	0.890	NA	NA	NA	NA
63	A	A	G	G	0.095	-0.126	0.775	-0.162	0.871	64	A	G	G	C	0.040	1.007	1.381	0.729	0.466
63	*	*	*	*	0.015	-3.237	1.963	-1.649	0.100	64	*	*	*	*	0.015	0.408	2.259	0.181	0.857
63	G	A	G	G	0.890	NA	NA	NA	NA	64	A	G	G	T	0.945	NA	NA	NA	NA
64	A	G	G	C	0.038	-0.673	1.247	-0.540	0.589	65	G	G	C	C	0.041	1.111	1.372	0.810	0.418
64	*	*	*	*	0.015	-3.248	1.925	-1.688	0.092	65	G	G	T	A	0.096	-0.044	0.894	-0.050	0.960
64	A	G	G	T	0.946	NA	NA	NA	NA	65	*	*	*	*	0.006	5.026	3.464	1.451	0.147
65	G	G	C	C	0.039	-0.650	1.236	-0.526	0.599	65	G	G	T	C	0.857	NA	NA	NA	NA
65	G	G	T	A	0.097	-0.337	0.785	-0.430	0.668	66	G	C	C	C	0.042	1.340	1.352	0.991	0.322
65	*	*	*	*	0.006	-3.222	3.047	-1.058	0.291	66	G	T	A	C	0.096	-0.117	0.899	-0.130	0.896
65	G	G	T	C	0.858	NA	NA	NA	NA	66	G	T	C	G	0.065	-0.154	1.072	-0.144	0.886
66	G	C	C	C	0.041	-0.850	1.214	-0.700	0.484	66	*	*	*	*	0.002	13.667	7.266	1.881	0.060
66	G	T	A	C	0.096	-0.305	0.791	-0.386	0.700	66	G	T	C	C	0.795	NA	NA	NA	NA
66	G	T	C	G	0.064	-0.011	0.941	-0.012	0.991	67	C	C	C	C	0.042	1.515	1.361	1.114	0.266
66	*	*	*	*	0.002	1.221	6.440	0.190	0.850	67	T	A	C	C	0.096	0.116	0.899	0.129	0.897
66	G	T	C	C	0.797	NA	NA	NA	NA	67	T	C	C	T	0.132	1.276	0.813	1.570	0.117
67	C	C	C	C	0.041	-0.708	1.221	-0.580	0.562	67	T	C	G	C	0.066	0.060	1.070	0.056	0.955
67	T	A	C	C	0.097	-0.193	0.792	-0.244	0.808	67	T	C	C	C	0.664	NA	NA	NA	NA
67	T	C	C	T	0.135	0.883	0.707	1.248	0.212	68	A	C	C	A	0.096	0.279	0.923	0.302	0.763

Table B1.31. Continued

							ApoA1										ApoB		
Window	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**	**Window**	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**
67	T	C	G	C	0.065	0.088	0.936	0.094	0.925	68	C	C	C	G	0.246	0.787	0.672	1.172	0.242
67	T	C	C	C	0.662	NA	NA	NA	NA	68	C	C	T	A	0.132	1.485	0.848	1.751	0.080
68	A	C	C	A	0.097	-0.145	0.815	-0.178	0.859	68	C	G	C	A	0.067	0.201	1.095	0.184	0.854
68	C	C	C	G	0.246	0.011	0.594	0.018	0.985	68	C	C	C	A	0.459	NA	NA	NA	NA
68	C	C	T	A	0.135	0.941	0.738	1.276	0.202	69	C	C	A	T	0.064	1.477	1.174	1.258	0.209
68	C	G	C	A	0.066	0.120	0.955	0.126	0.900	69	C	C	G	T	0.248	0.800	0.657	1.218	0.224
68	C	C	C	A	0.456	NA	NA	NA	NA	69	C	T	A	C	0.132	1.596	0.842	1.895	0.058
69	C	C	A	T	0.064	-1.500	1.028	-1.459	0.145	69	G	C	A	T	0.066	0.113	1.088	0.104	0.917
69	C	C	G	T	0.247	-0.172	0.581	-0.297	0.767	69	*	*	*	*	0.002	2.338	7.231	0.323	0.747
69	C	T	A	C	0.136	0.766	0.731	1.048	0.295	69	C	C	A	C	0.487	NA	NA	NA	NA
69	G	C	A	T	0.065	-0.108	0.962	-0.112	0.911	70	C	A	C	T	0.142	-1.596	0.905	-1.765	0.078
69	*	*	*	*	0.002	-4.448	6.314	-0.704	0.481	70	C	A	T	A	0.105	0.364	0.993	0.367	0.714
69	C	C	A	C	0.486	NA	NA	NA	NA	70	C	A	T	T	0.025	-1.082	2.061	-0.525	0.600
70	C	A	C	T	0.144	0.765	0.756	1.012	0.312	70	C	G	T	T	0.248	0.356	0.705	0.504	0.614
70	C	A	T	A	0.104	-0.490	0.865	-0.566	0.571	70	T	A	C	T	0.132	1.062	0.882	1.203	0.229
70	C	A	T	T	0.025	-0.916	1.798	-0.510	0.610	70	*	*	*	*	0.002	-2.408	0.000	-5.96E+14	0.000
70	C	G	T	T	0.247	0.032	0.621	0.052	0.959	70	C	A	C	A	0.346	NA	NA	NA	NA
70	T	A	C	T	0.135	0.999	0.767	1.303	0.193	71	A	C	T	C	0.274	-0.347	0.750	-0.463	0.643
70	*	*	*	*	0.002	-4.590	0.000	-1.05E+16	0.000	71	A	T	A	C	0.105	0.235	1.036	0.227	0.821
70	C	A	C	A	0.343	NA	NA	NA	NA	71	A	T	T	C	0.026	-0.274	2.183	-0.125	0.900
71	A	C	T	C	0.280	0.949	0.620	1.531	0.126	71	G	T	T	C	0.228	0.250	0.725	0.345	0.730
71	A	T	A	C	0.104	-0.245	0.878	-0.279	0.780	71	G	T	T	T	0.019	1.298	1.884	0.689	0.491
71	A	T	T	C	0.025	-1.458	1.832	-0.796	0.426	71	*	*	*	*	0.002	-2.504	NA	NA	NA
71	G	T	T	C	0.228	-0.155	0.632	-0.245	0.806	71	A	C	A	C	0.347	NA	NA	NA	NA
71	G	T	T	T	0.019	3.018	1.675	1.802	0.072	72	C	A	C	C	0.150	1.165	0.915	1.273	0.204
71	*	*	*	*	0.002	-4.481	NA	NA	NA	72	C	A	C	T	0.195	0.681	0.925	0.736	0.462
71	A	C	A	C	0.343	NA	NA	NA	NA	72	T	A	C	T	0.106	0.331	1.016	0.326	0.744
72	C	A	C	C	0.149	-0.330	0.783	-0.421	0.674	72	T	T	C	T	0.254	1.046	0.843	1.242	0.215
72	C	A	C	T	0.194	-0.896	0.759	-1.181	0.238	72	T	T	T	T	0.019	1.794	1.939	0.925	0.355
72	T	A	C	T	0.104	-1.463	0.874	-1.674	0.095	72	*	*	*	*	0.002	2.887	NA	NA	NA
72	T	T	C	T	0.255	-0.895	0.703	-1.272	0.204	72	C	T	C	T	0.274	NA	NA	NA	NA
72	T	T	T	T	0.018	1.969	1.724	1.142	0.254	73	A	C	C	T	0.149	0.596	0.807	0.739	0.460
72	*	*	*	*	0.002	3.092	0.000	1.09E+16	0.000	73	A	C	T	C	0.011	-5.145	2.670	-1.927	0.054
72	C	T	C	T	0.279	NA	NA	NA	NA	73	A	C	T	T	0.291	0.246	0.632	0.389	0.698
73	A	C	C	T	0.147	0.089	0.705	0.126	0.900	73	T	T	T	T	0.018	1.239	1.936	0.640	0.522
73	A	C	T	C	0.011	-1.043	2.328	-0.448	0.654	73	*	*	*	*	0.002	2.499	7.796	0.321	0.749
73	A	C	T	T	0.288	-0.660	0.539	-1.225	0.221	73	T	C	T	T	0.529	NA	NA	NA	NA
73	T	T	T	T	0.017	2.325	1.736	1.340	0.181	74	C	C	T	T	0.153	0.064	0.755	0.084	0.933
73	*	*	*	*	0.002	4.644	6.397	0.726	0.468	74	C	T	C	C	0.010	-5.446	2.679	-2.033	0.042
73	T	C	T	T	0.535	NA	NA	NA	NA	74	T	T	T	C	0.018	1.174	1.908	0.615	0.539
74	C	C	T	T	0.152	0.292	0.671	0.435	0.663	74	*	*	*	*	0.005	1.845	4.274	0.432	0.666
74	C	T	C	C	0.011	-0.939	2.317	-0.405	0.686	74	C	T	T	C	0.813	NA	NA	NA	NA
74	T	T	T	C	0.018	2.900	1.642	1.767	0.078	75	C	T	T	T	0.153	0.520	0.796	0.653	0.514
74	*	*	*	*	0.005	-4.992	3.652	-1.367	0.172	75	T	C	C	G	0.011	-4.523	2.628	-1.721	0.086
74	C	T	T	C	0.814	NA	NA	NA	NA	75	T	T	C	G	0.390	0.883	0.582	1.518	0.129
75	C	T	T	T	0.152	-0.071	0.708	-0.101	0.920	75	*	*	*	*	0.005	-0.040	4.445	-0.009	0.993
75	T	C	C	G	0.011	-1.268	2.310	-0.549	0.583	75	T	T	C	T	0.441	NA	NA	NA	NA
75	T	T	C	G	0.390	-0.856	0.511	-1.674	0.095	76	C	C	G	G	0.011	-5.390	2.615	-2.061	0.040
75	*	*	*	*	0.005	-6.142	3.808	-1.613	0.107	76	T	C	T	A	0.290	-0.136	0.643	-0.212	0.832
75	T	T	C	T	0.443	NA	NA	NA	NA	76	T	C	T	G	0.155	-1.900	0.801	-2.372	0.018
76	C	C	G	G	0.011	-0.443	2.308	-0.192	0.848	76	T	T	T	A	0.155	-0.331	0.813	-0.407	0.684
76	T	C	T	A	0.291	0.773	0.568	1.362	0.174	76	*	*	*	*	0.003	-2.406	5.149	-0.467	0.640
76	T	C	T	G	0.155	0.686	0.704	0.974	0.330	76	T	C	G	G	0.386	NA	NA	NA	NA
76	T	T	T	A	0.154	0.684	0.728	0.939	0.348	77	C	G	G	A	0.047	-0.383	1.506	-0.254	0.799
76	*	*	*	*	0.003	-5.462	4.487	-1.217	0.224	77	C	T	A	A	0.120	0.584	0.932	0.626	0.531
76	T	C	G	G	0.386	NA	NA	NA	NA	77	C	T	A	G	0.171	-0.461	0.795	-0.580	0.562
77	C	G	G	A	0.048	-0.187	1.391	-0.135	0.893	77	C	T	G	A	0.011	-1.066	3.169	-0.336	0.737
77	C	T	A	A	0.118	0.640	0.829	0.772	0.440	77	C	T	G	G	0.143	-1.828	0.855	-2.137	0.033
77	C	T	A	G	0.174	0.785	0.709	1.108	0.268	77	T	T	A	A	0.150	-0.201	0.838	-0.240	0.810
77	C	T	G	G	0.144	0.839	0.768	1.091	0.276	77	*	*	*	*	0.008	0.726	3.592	0.202	0.840
77	T	T	A	A	0.149	0.727	0.754	0.964	0.335	77	C	G	G	G	0.350	NA	NA	NA	NA
77	*	*	*	*	0.018	-1.767	2.502	-0.706	0.480	78	G	G	A	G	0.047	-0.580	1.539	-0.377	0.706
77	C	G	G	G	0.349	NA	NA	NA	NA	78	G	G	G	A	0.043	1.307	1.332	0.981	0.327
78	G	G	A	G	0.046	0.326	1.409	0.232	0.817	78	T	A	A	G	0.268	0.306	0.727	0.421	0.674

Table B1.31. Continued

							ApoA1											ApoB	
Window	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**	**Window**	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**
78	G	G	G	A	0.040	-0.697	1.268	-0.550	0.583	78	T	A	G	G	0.178	-0.291	0.814	-0.358	0.721
78	T	A	A	G	0.265	0.534	0.648	0.823	0.411	78	T	G	A	G	0.011	-0.769	3.050	-0.252	0.801
78	T	A	G	G	0.180	0.731	0.721	1.014	0.311	78	T	G	G	G	0.143	-1.641	0.884	-1.856	0.064
78	T	G	A	G	0.009	-0.129	3.527	-0.037	0.971	78	*	*	*	*	0.003	-2.065	5.210	-0.396	0.692
78	T	G	G	G	0.145	0.628	0.781	0.804	0.422	78	G	G	G	G	0.307	NA	NA	NA	NA
78	*	*	*	*	0.005	-10.847	4.084	-2.656	0.008	79	A	G	G	A	0.147	-0.376	0.918	-0.409	0.682
78	G	G	G	G	0.309	NA	NA	NA	NA	79	A	G	G	G	0.029	-2.217	1.900	-1.167	0.244
79	A	G	G	A	0.150	-0.539	0.798	-0.676	0.500	79	G	A	G	G	0.057	-0.805	1.373	-0.586	0.558
79	A	G	G	G	0.028	2.642	1.642	1.609	0.108	79	G	G	A	A	0.042	1.280	1.364	0.939	0.348
79	G	A	G	G	0.055	-0.272	1.312	-0.207	0.836	79	G	G	G	A	0.252	-0.961	0.755	-1.274	0.203
79	G	G	A	A	0.040	-1.329	1.294	-1.027	0.305	79	G	G	G	G	0.201	-0.581	0.804	-0.723	0.470
79	G	G	G	A	0.253	0.196	0.662	0.297	0.767	79	*	*	*	*	0.002	-0.946	9.059	-0.104	0.917
79	G	G	G	G	0.203	-1.044	0.703	-1.486	0.138	79	A	A	G	G	0.271	NA	NA	NA	NA
79	*	*	*	*	0.003	-12.200	5.820	-2.096	0.036	80	A	G	G	W	0.327	0.642	0.635	1.012	0.312
79	A	A	G	G	0.268	NA	NA	NA	NA	80	G	A	A	W	0.042	1.966	1.329	1.479	0.139
80	A	G	G	W	0.325	-0.262	0.560	-0.468	0.640	80	G	G	A	D	0.019	1.490	2.015	0.739	0.460
80	G	A	A	W	0.040	-2.087	1.202	-1.737	0.083	80	G	G	G	W	0.230	0.048	0.701	0.068	0.946
80	G	G	A	D	0.018	-0.879	1.830	-0.480	0.631	80	*	*	*	*	0.002	2.214	0.022	100.522	0.000
80	G	G	G	W	0.231	-0.672	0.615	-1.092	0.275	80	G	G	A	W	0.379	NA	NA	NA	NA
80	*	*	*	*	0.002	0.013	8.698	0.001	0.999	81	A	A	W	T	0.042	1.675	1.303	1.285	0.199
80	G	G	A	W	0.384	NA	NA	NA	NA	81	G	A	D	A	0.019	1.226	2.003	0.612	0.541
81	A	A	W	T	0.041	-1.615	1.169	-1.383	0.167	81	G	A	W	A	0.204	-0.636	0.684	-0.931	0.352
81	G	A	D	A	0.018	-0.371	1.823	-0.204	0.839	81	G	A	W	T	0.172	0.307	0.755	0.406	0.685
81	G	A	W	A	0.206	0.612	0.603	1.014	0.311	81	*	*	*	*	0.002	-4.675	0.000	-9.23E+15	0.000
81	G	A	W	T	0.174	0.244	0.666	0.366	0.714	81	G	G	W	T	0.560	NA	NA	NA	NA
81	*	*	*	*	0.002	-1.128	0.000	-2.48E+15	0.000	82	A	D	A	T	0.019	1.168	2.019	0.578	0.563
81	G	G	W	T	0.558	NA	NA	NA	NA	82	A	W	A	T	0.204	-0.687	0.689	-0.997	0.319
82	A	D	A	T	0.018	-0.295	1.828	-0.161	0.872	82	A	W	T	G	0.064	0.451	1.099	0.410	0.682
82	A	W	A	T	0.206	0.659	0.606	1.089	0.277	82	A	W	T	T	0.150	0.701	0.811	0.865	0.388
82	A	W	T	G	0.062	-0.976	0.992	-0.983	0.326	82	*	*	*	*	0.002	-4.487	NA	NA	NA
82	A	W	T	T	0.153	0.237	0.709	0.335	0.738	82	G	W	T	T	0.561	NA	NA	NA	NA
82	*	*	*	*	0.002	-1.079	0.000	-6.74E+14	0.000	83	D	A	T	T	0.019	1.269	2.023	0.627	0.531
82	G	W	T	T	0.559	NA	NA	NA	NA	83	W	A	T	T	0.205	-0.588	0.726	-0.810	0.418
83	D	A	T	T	0.018	-0.276	1.821	-0.152	0.879	83	W	T	G	A	0.065	0.502	1.111	0.452	0.651
83	W	A	T	T	0.207	0.652	0.631	1.034	0.302	83	W	T	T	T	0.298	0.349	0.650	0.537	0.592
83	W	T	G	A	0.063	-0.974	0.997	-0.977	0.329	83	W	T	T	A	0.413	NA	NA	NA	NA
83	W	T	T	T	0.299	0.125	0.566	0.222	0.825	84	A	T	T	G	0.224	-0.816	0.762	-1.071	0.285
83	W	T	T	A	0.412	NA	NA	NA	NA	84	T	G	A	G	0.065	0.144	1.141	0.126	0.900
84	A	T	T	G	0.225	0.489	0.662	0.739	0.460	84	T	T	A	A	0.149	0.157	0.861	0.183	0.855
84	T	G	A	G	0.063	-1.049	1.023	-1.026	0.305	84	T	T	A	G	0.263	-0.557	0.726	-0.767	0.443
84	T	T	A	A	0.147	-0.040	0.759	-0.052	0.958	84	T	T	T	G	0.299	NA	NA	NA	NA
84	T	T	A	G	0.264	-0.129	0.629	-0.205	0.837	85	G	A	G	C	0.018	2.216	2.020	1.097	0.273
84	T	T	T	G	0.300	NA	NA	NA	NA	85	G	A	G	T	0.047	-0.353	1.267	-0.279	0.781
85	G	A	G	C	0.018	-1.778	1.784	-0.996	0.319	85	T	A	A	C	0.149	0.446	0.806	0.553	0.580
85	G	A	G	T	0.045	-1.054	1.156	-0.912	0.362	85	T	A	G	C	0.262	-0.183	0.641	-0.285	0.775
85	T	A	A	C	0.147	-0.223	0.711	-0.313	0.754	85	T	T	G	C	0.524	NA	NA	NA	NA
85	T	A	G	C	0.264	-0.325	0.553	-0.588	0.557	86	A	A	C	A	0.149	0.449	0.806	0.558	0.577
85	T	T	G	C	0.526	NA	NA	NA	NA	86	A	G	C	A	0.261	-0.178	0.641	-0.278	0.781
86	A	A	C	A	0.147	-0.227	0.711	-0.319	0.750	86	A	G	C	G	0.019	2.155	1.981	1.088	0.277
86	A	G	C	A	0.263	-0.343	0.554	-0.620	0.536	86	A	G	T	G	0.047	-0.367	1.267	-0.290	0.772
86	A	G	C	G	0.019	-1.409	1.756	-0.802	0.423	86	T	G	C	A	0.524	NA	NA	NA	NA
86	A	G	T	G	0.045	-1.098	1.158	-0.949	0.343	87	A	C	A	A	0.148	0.476	0.782	0.608	0.543
86	T	G	C	A	0.526	NA	NA	NA	NA	87	G	C	A	T	0.016	-1.239	2.023	-0.612	0.541
87	A	C	A	A	0.146	-0.187	0.691	-0.270	0.787	87	G	C	G	A	0.019	2.173	1.981	1.097	0.273
87	G	C	A	T	0.016	-2.519	1.781	-1.414	0.158	87	G	T	G	A	0.047	-0.333	1.252	-0.266	0.790
87	G	C	G	A	0.019	-1.389	1.755	-0.791	0.429	87	G	C	A	A	0.770	NA	NA	NA	NA
87	G	T	G	A	0.045	-1.034	1.145	-0.903	0.367	88	C	A	T	C	0.016	-1.329	2.018	-0.659	0.510
87	G	C	A	A	0.774	NA	NA	NA	NA	88	C	G	A	G	0.019	2.103	1.978	1.063	0.288
88	C	A	T	C	0.016	-2.516	1.782	-1.412	0.158	88	T	G	A	G	0.047	-0.424	1.242	-0.341	0.733
88	C	G	A	G	0.019	-1.332	1.750	-0.761	0.447	88	C	A	A	C	0.918	NA	NA	NA	NA
88	T	G	A	G	0.044	-0.987	1.135	-0.870	0.385	89	A	A	C	T	0.374	0.089	0.564	0.158	0.874
88	C	A	A	C	0.920	NA	NA	NA	NA	89	A	T	C	C	0.016	-1.303	2.031	-0.642	0.521
89	A	A	C	T	0.374	-0.474	0.494	-0.960	0.337	89	G	A	G	T	0.066	0.317	1.081	0.293	0.770
89	A	T	C	C	0.016	-2.669	1.784	-1.496	0.135	89	A	A	C	C	0.544	NA	NA	NA	NA

Table B1.31. Continued

ApoA1										ApoB									
Window	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**	**Window**	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**
89	G	A	G	T	0.064	-1.263	0.973	-1.297	0.195	90	A	C	C	G	0.067	0.703	1.140	0.616	0.538
89	A	A	C	C	0.546	NA	NA	NA	NA	90	A	C	T	G	0.373	0.017	0.577	0.030	0.976
90	A	C	C	G	0.067	-0.603	0.989	-0.609	0.543	90	A	G	T	G	0.066	-0.061	1.105	-0.056	0.956
90	A	C	T	G	0.373	-0.619	0.507	-1.219	0.223	90	T	C	C	A	0.016	-1.260	2.042	-0.617	0.537
90	A	G	T	G	0.064	-1.460	0.975	-1.497	0.135	90	A	C	C	A	0.477	NA	NA	NA	NA
90	T	C	C	A	0.016	-2.822	1.791	-1.576	0.116	91	C	C	G	T	0.067	0.623	1.139	0.547	0.585
90	A	C	C	A	0.479	NA	NA	NA	NA	91	C	T	G	C	0.253	-0.176	0.647	-0.273	0.785
91	C	C	G	T	0.067	-0.407	0.990	-0.411	0.681	91	C	T	G	T	0.119	0.615	0.890	0.691	0.490
91	C	T	G	C	0.254	-0.498	0.566	-0.880	0.379	91	G	T	G	C	0.066	-0.050	1.104	-0.045	0.964
91	C	T	G	T	0.118	-0.613	0.776	-0.790	0.429	91	*	*	*	*	0.002	-3.241	7.448	-0.435	0.664
91	G	T	G	C	0.064	-1.417	0.972	-1.457	0.146	91	C	C	A	T	0.493	NA	NA	NA	NA
91	*	*	*	*	0.002	-8.785	6.677	-1.316	0.189	92	C	G	T	G	0.067	0.608	1.139	0.533	0.594
91	C	C	A	T	0.495	NA	NA	NA	NA	92	T	G	C	A	0.063	0.378	1.106	0.342	0.733
92	C	G	T	G	0.067	-0.416	0.989	-0.421	0.674	92	T	G	C	G	0.256	-0.277	0.640	-0.432	0.666
92	T	G	C	A	0.061	-1.574	0.995	-1.582	0.114	92	T	G	T	G	0.119	0.608	0.890	0.683	0.495
92	T	G	C	G	0.257	-0.479	0.562	-0.853	0.394	92	*	*	*	*	0.002	-3.258	7.471	-0.436	0.663
92	T	G	T	G	0.118	-0.602	0.776	-0.775	0.438	92	C	A	T	G	0.493	NA	NA	NA	NA
92	*	*	*	*	0.002	-8.772	6.678	-1.314	0.189	93	G	C	A	G	0.065	0.335	1.088	0.308	0.758
92	C	A	T	G	0.495	NA	NA	NA	NA	93	G	C	G	A	0.253	-0.238	0.643	-0.369	0.712
93	G	C	A	G	0.063	-1.362	0.980	-1.389	0.165	93	G	T	G	A	0.186	0.607	0.740	0.821	0.412
93	G	C	G	A	0.254	-0.514	0.565	-0.909	0.363	93	A	T	G	A	0.495	NA	NA	NA	NA
93	G	T	G	A	0.185	-0.533	0.647	-0.823	0.410	94	C	A	G	T	0.065	0.338	1.072	0.315	0.753
93	A	T	G	A	0.497	NA	NA	NA	NA	94	C	G	A	T	0.251	-0.136	0.626	-0.218	0.828
94	C	A	G	T	0.063	-1.139	0.968	-1.177	0.239	94	T	G	A	G	0.026	0.730	1.790	0.408	0.684
94	C	G	A	T	0.252	-0.255	0.547	-0.466	0.642	94	T	G	A	T	0.658	NA	NA	NA	NA
94	T	G	A	G	0.026	-0.692	1.555	-0.445	0.656	95	A	G	T	G	0.065	0.273	1.088	0.251	0.802
94	T	G	A	T	0.658	NA	NA	NA	NA	95	G	A	G	G	0.026	0.547	1.807	0.303	0.762
95	A	G	T	G	0.063	-0.991	0.984	-1.008	0.314	95	G	A	T	T	0.362	-0.187	0.587	-0.319	0.750
95	G	A	G	G	0.026	-0.566	1.563	-0.362	0.717	95	G	A	T	G	0.547	NA	NA	NA	NA
95	G	A	T	T	0.362	0.248	0.518	0.478	0.633	96	A	G	G	G	0.026	0.569	1.806	0.315	0.753
95	G	A	T	G	0.549	NA	NA	NA	NA	96	A	T	G	A	0.067	-0.024	1.085	-0.022	0.982
96	A	G	G	G	0.026	-0.546	1.567	-0.349	0.727	96	A	T	T	G	0.362	-0.233	0.601	-0.388	0.698
96	A	T	G	A	0.067	0.138	0.959	0.144	0.886	96	G	T	G	G	0.063	-0.135	1.107	-0.122	0.903
96	A	T	T	G	0.362	0.255	0.529	0.482	0.630	96	A	T	G	G	0.482	NA	NA	NA	NA
96	G	T	G	G	0.061	-1.017	0.997	-1.020	0.308	97	G	G	G	A	0.027	0.921	1.761	0.523	0.601
96	A	T	G	G	0.484	NA	NA	NA	NA	97	T	G	A	G	0.067	0.033	1.082	0.030	0.976
97	G	G	G	A	0.027	-0.497	1.529	-0.325	0.745	97	T	G	G	A	0.076	0.210	1.043	0.202	0.840
97	T	G	A	G	0.067	0.272	0.957	0.284	0.777	97	T	T	G	G	0.362	-0.176	0.599	-0.293	0.769
97	T	G	G	A	0.075	0.253	0.917	0.276	0.783	97	T	G	G	G	0.469	NA	NA	NA	NA
97	T	T	G	G	0.362	0.407	0.529	0.769	0.442	98	G	A	G	G	0.067	0.032	1.077	0.030	0.976
97	T	G	G	G	0.470	NA	NA	NA	NA	98	G	G	A	A	0.104	0.697	0.908	0.767	0.443
98	G	A	G	G	0.067	0.274	0.956	0.286	0.775	98	T	G	G	G	0.362	-0.146	0.598	-0.244	0.807
98	G	G	A	A	0.103	-0.034	0.806	-0.042	0.966	98	G	G	G	G	0.467	NA	NA	NA	NA
98	T	G	G	G	0.362	0.393	0.530	0.742	0.459	99	A	G	G	G	0.066	0.172	1.072	0.160	0.873
98	G	G	G	G	0.468	NA	NA	NA	NA	99	G	A	A	G	0.103	0.840	0.890	0.944	0.345
99	A	G	G	G	0.065	0.190	0.985	0.193	0.847	99	G	G	G	A	0.020	1.202	1.843	0.652	0.515
99	G	A	A	G	0.101	-0.145	0.803	-0.181	0.857	99	*	*	*	*	0.002	-2.546	0.000	-4.83E+15	0.000
99	G	G	G	A	0.020	-1.962	1.609	-1.220	0.223	99	G	G	G	G	0.810	NA	NA	NA	NA
99	*	*	*	*	0.003	-4.301	7.662	-0.561	0.575	100	A	A	G	C	0.104	0.776	0.889	0.872	0.383
99	G	G	G	G	0.812	NA	NA	NA	NA	100	G	G	A	C	0.018	1.224	1.897	0.645	0.519
100	A	A	G	C	0.103	-0.113	0.788	-0.143	0.886	100	G	G	G	T	0.041	-0.021	1.328	-0.016	0.988
100	G	G	A	C	0.018	-1.750	1.669	-1.048	0.295	100	*	*	*	*	0.002	-0.542	8.033	-0.067	0.946
100	G	G	G	T	0.041	1.825	1.166	1.565	0.118	100	G	G	G	C	0.834	NA	NA	NA	NA
100	*	*	*	*	0.002	-3.644	7.041	-0.518	0.605	101	A	G	C	G	0.103	0.662	0.911	0.727	0.467
100	G	G	G	C	0.835	NA	NA	NA	NA	101	G	A	C	G	0.019	1.147	1.880	0.610	0.542
101	A	G	C	G	0.101	-0.184	0.802	-0.230	0.818	101	G	G	C	A	0.169	-0.062	0.723	-0.086	0.931
101	G	A	C	G	0.019	-1.993	1.643	-1.213	0.226	101	G	G	T	A	0.043	-0.179	1.320	-0.136	0.892
101	G	G	C	A	0.168	-0.714	0.634	-1.125	0.261	101	G	G	C	G	0.666	NA	NA	NA	NA
101	G	G	T	A	0.042	1.669	1.162	1.436	0.151	102	A	C	G	G	0.019	1.139	1.881	0.606	0.545
101	G	G	C	G	0.668	NA	NA	NA	NA	102	G	C	A	G	0.169	-0.076	0.717	-0.106	0.916
102	A	C	G	G	0.019	-1.815	1.656	-1.096	0.273	102	G	C	G	A	0.031	1.217	1.502	0.811	0.418
102	G	C	A	G	0.168	-0.643	0.629	-1.022	0.307	102	G	T	A	G	0.042	-0.230	1.315	-0.175	0.861
102	G	C	G	A	0.030	1.012	1.331	0.760	0.447	102	*	*	*	*	0.001	0.161	8.659	0.019	0.985
102	G	T	A	G	0.042	1.787	1.161	1.539	0.124	102	G	C	G	G	0.738	NA	NA	NA	NA

Table B1.31. Continued

ApoA1										ApoB									
Window	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**	**Window**	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**
102	*	*	*	*	0.001	-4.949	7.523	-0.658	0.511	103	C	A	G	A	0.138	0.651	0.847	0.768	0.443
102	G	C	G	G	0.740	NA	NA	NA	NA	103	C	A	G	C	0.031	-4.323	1.957	-2.209	0.027
103	C	A	G	A	0.134	-1.226	0.760	-1.615	0.107	103	C	G	A	C	0.031	1.114	1.503	0.741	0.459
103	C	A	G	C	0.034	0.472	1.529	0.309	0.758	103	C	G	G	C	0.237	-0.278	0.677	-0.412	0.681
103	C	G	A	C	0.030	0.823	1.337	0.616	0.538	103	T	A	G	C	0.043	-0.192	1.288	-0.149	0.882
103	C	G	G	C	0.236	-0.958	0.588	-1.629	0.104	103	C	G	G	A	0.519	NA	NA	NA	NA
103	T	A	G	C	0.043	1.384	1.147	1.207	0.228	104	A	G	A	A	0.139	-0.130	0.983	-0.133	0.895
103	C	G	G	A	0.522	NA	NA	NA	NA	104	A	G	C	A	0.072	-1.069	1.203	-0.889	0.374
104	A	G	A	A	0.136	-1.129	0.848	-1.331	0.184	104	G	A	C	A	0.031	0.848	1.536	0.552	0.581
104	A	G	C	A	0.074	0.485	1.027	0.472	0.637	104	G	G	A	T	0.203	-0.276	0.793	-0.348	0.728
104	G	A	C	A	0.030	0.693	1.360	0.509	0.611	104	G	G	C	A	0.237	-0.965	0.796	-1.212	0.226
104	G	G	A	T	0.202	-0.550	0.691	-0.795	0.427	104	*	*	*	*	0.002	-0.077	7.004	-0.011	0.991
104	G	G	C	A	0.237	-1.019	0.673	-1.515	0.130	104	G	G	A	A	0.315	NA	NA	NA	NA
104	*	*	*	*	0.002	-0.942	6.271	-0.150	0.881	105	A	C	A	A	0.031	1.083	1.520	0.713	0.476
104	G	G	A	A	0.318	NA	NA	NA	NA	105	G	A	A	G	0.081	1.003	1.048	0.957	0.339
105	A	C	A	A	0.030	1.137	1.355	0.839	0.402	105	G	A	T	A	0.203	-0.025	0.749	-0.033	0.974
105	G	A	A	G	0.079	0.849	0.953	0.891	0.373	105	G	C	A	A	0.301	-0.632	0.662	-0.955	0.340
105	G	A	T	A	0.201	-0.026	0.662	-0.039	0.969	105	*	*	*	*	0.009	-5.010	3.635	-1.378	0.169
105	G	C	A	A	0.302	-0.079	0.588	-0.134	0.893	105	G	A	A	A	0.376	NA	NA	NA	NA
105	*	*	*	*	0.010	-3.974	3.391	-1.172	0.242	106	A	A	G	G	0.080	1.060	1.047	1.013	0.312
105	G	A	A	A	0.378	NA	NA	NA	NA	106	A	T	A	G	0.203	0.040	0.749	0.053	0.957
106	A	A	G	G	0.079	0.870	0.952	0.914	0.361	106	C	A	A	A	0.042	-1.759	1.434	-1.227	0.220
106	A	T	A	G	0.201	0.033	0.663	0.049	0.961	106	C	A	A	G	0.291	-0.289	0.661	-0.436	0.663
106	C	A	A	A	0.043	-0.602	1.237	-0.487	0.627	106	*	*	*	*	0.009	-5.627	3.897	-1.444	0.149
106	C	A	A	G	0.291	0.167	0.590	0.283	0.777	106	A	A	A	G	0.375	NA	NA	NA	NA
106	*	*	*	*	0.010	-4.054	3.506	-1.156	0.248	107	A	A	A	T	0.042	-1.720	1.408	-1.221	0.222
106	A	A	A	G	0.376	NA	NA	NA	NA	107	A	A	G	C	0.049	1.538	1.296	1.186	0.236
107	A	A	A	T	0.044	-0.741	1.193	-0.621	0.535	107	A	G	G	T	0.087	0.851	0.955	0.891	0.373
107	A	A	G	C	0.048	-1.090	1.140	-0.956	0.339	107	T	A	G	T	0.200	0.448	0.693	0.647	0.518
107	A	G	G	T	0.087	0.388	0.832	0.466	0.642	107	*	*	*	*	0.005	-8.311	5.904	-1.408	0.160
107	T	A	G	T	0.200	0.089	0.608	0.146	0.884	107	A	A	G	T	0.617	NA	NA	NA	NA
107	*	*	*	*	0.003	-13.312	7.999	-1.664	0.096	108	A	A	T	A	0.041	-2.045	1.448	-1.413	0.158
107	A	A	G	T	0.619	NA	NA	NA	NA	108	A	G	C	A	0.050	0.682	1.201	0.568	0.570
108	A	A	T	A	0.041	-0.762	1.241	-0.614	0.539	108	G	G	T	G	0.080	0.567	0.948	0.598	0.550
108	A	G	C	A	0.048	-1.673	1.083	-1.545	0.123	108	*	*	*	*	0.011	0.635	3.012	0.211	0.833
108	G	G	T	G	0.079	-0.015	0.842	-0.017	0.986	108	A	G	T	A	0.818	NA	NA	NA	NA
108	*	*	*	*	0.011	0.226	2.560	0.088	0.930	109	A	T	A	G	0.041	-2.376	1.423	-1.669	0.095
108	A	G	T	A	0.821	NA	NA	NA	NA	109	G	C	A	G	0.050	0.516	1.197	0.431	0.667
109	A	T	A	G	0.042	-0.779	1.225	-0.636	0.525	109	G	T	A	A	0.015	-2.486	2.181	-1.140	0.255
109	G	C	A	G	0.049	-1.746	1.082	-1.613	0.107	109	G	T	G	G	0.078	0.849	0.990	0.858	0.391
109	G	T	A	A	0.014	-2.023	2.012	-1.005	0.315	109	*	*	*	*	0.002	7.052	7.437	0.948	0.343
109	G	T	G	G	0.076	-0.104	0.885	-0.117	0.907	109	G	T	A	G	0.814	NA	NA	NA	NA
109	*	*	*	*	0.002	1.111	8.684	0.128	0.898	110	C	A	G	G	0.052	0.879	1.167	0.754	0.451
109	G	T	A	G	0.817	NA	NA	NA	NA	110	T	A	A	G	0.014	-2.205	2.236	-0.986	0.324
110	C	A	G	G	0.050	-1.632	1.061	-1.539	0.124	110	T	A	G	A	0.019	1.426	1.965	0.726	0.468
110	T	A	A	G	0.014	-1.872	2.008	-0.932	0.352	110	T	G	G	G	0.077	0.997	1.000	0.997	0.319
110	T	A	G	A	0.019	2.026	1.725	1.174	0.241	110	T	A	G	G	0.837	NA	NA	NA	NA
110	T	G	G	G	0.076	0.011	0.885	0.013	0.990	111	A	A	G	A	0.015	-2.402	2.213	-1.085	0.278
110	T	A	G	G	0.840	NA	NA	NA	NA	111	A	G	A	A	0.019	1.331	1.967	0.676	0.499
111	A	A	G	A	0.015	-1.355	1.982	-0.684	0.494	111	A	G	G	G	0.171	-0.217	0.712	-0.305	0.761
111	A	G	A	A	0.018	2.424	1.726	1.405	0.161	111	G	G	G	A	0.077	0.870	1.003	0.867	0.386
111	A	G	G	G	0.170	1.392	0.625	2.227	0.026	111	A	G	G	A	0.718	NA	NA	NA	NA
111	G	G	G	A	0.077	0.359	0.884	0.406	0.685	112	A	G	A	G	0.014	-2.094	2.255	-0.928	0.353
111	A	G	G	A	0.720	NA	NA	NA	NA	112	G	A	A	G	0.017	2.631	2.073	1.269	0.205
112	A	G	A	G	0.015	-1.283	1.919	-0.668	0.504	112	G	G	G	G	0.117	-0.489	0.841	-0.582	0.561
112	G	A	A	G	0.018	2.046	1.782	1.148	0.251	112	G	G	G	T	0.067	0.917	1.115	0.823	0.411
112	G	G	G	G	0.118	1.822	0.733	2.485	0.013	112	*	*	*	*	0.004	-8.678	7.498	-1.157	0.248
112	G	G	G	T	0.068	-0.113	0.941	-0.120	0.905	112	G	G	A	G	0.781	NA	NA	NA	NA
112	*	*	*	*	0.002	8.417	0.006	1475.339	0.000	113	A	A	G	C	0.018	1.143	1.962	0.583	0.560
112	G	G	A	G	0.779	NA	NA	NA	NA	113	G	A	G	T	0.216	-0.576	0.667	-0.863	0.388
113	A	A	G	C	0.018	2.159	1.763	1.225	0.221	113	G	G	G	C	0.118	-0.638	0.863	-0.739	0.460
113	G	A	G	T	0.217	-0.337	0.585	-0.576	0.565	113	G	G	T	C	0.068	0.234	1.127	0.208	0.835
113	G	G	G	C	0.118	1.747	0.750	2.329	0.020	113	*	*	*	*	0.002	4.315	8.695	0.496	0.620
113	G	G	T	C	0.068	-0.309	0.978	-0.316	0.752	113	G	A	G	C	0.577	NA	NA	NA	NA

Table B1.31. Continued

ApoA1										ApoB									
Window	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**	**Window**	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**
113	*	*	*	*	0.002	8.169	6.854	1.192	0.234	114	A	G	C	A	0.113	1.281	0.891	1.437	0.151
113	G	A	G	C	0.576	NA	NA	NA	NA	114	A	G	T	A	0.198	-0.423	0.703	-0.601	0.548
114	A	G	C	A	0.114	0.506	0.772	0.655	0.513	114	A	G	T	G	0.018	-0.698	2.152	-0.324	0.746
114	A	G	T	A	0.200	-0.172	0.617	-0.278	0.781	114	G	G	C	G	0.119	-0.424	0.870	-0.488	0.626
114	A	G	T	G	0.018	-2.552	1.831	-1.394	0.164	114	G	T	C	G	0.068	0.493	1.137	0.433	0.665
114	G	G	C	G	0.119	1.756	0.759	2.313	0.021	114	*	*	*	*	0.002	4.118	8.559	0.481	0.631
114	G	T	C	G	0.068	-0.210	0.986	-0.213	0.831	114	A	G	C	G	0.482	NA	NA	NA	NA
114	*	*	*	*	0.002	7.289	6.990	1.043	0.297	115	G	C	A	G	0.112	1.284	0.884	1.453	0.147
114	A	G	C	G	0.480	NA	NA	NA	NA	115	G	C	G	A	0.012	-2.351	2.528	-0.930	0.353
115	G	C	A	G	0.113	0.118	0.769	0.154	0.878	115	G	T	A	G	0.199	-0.348	0.685	-0.508	0.611
115	G	C	G	A	0.011	-2.907	2.288	-1.270	0.204	115	G	T	G	G	0.018	-0.682	2.148	-0.317	0.751
115	G	T	A	G	0.200	-0.587	0.602	-0.975	0.330	115	T	C	G	A	0.070	0.638	1.121	0.569	0.569
115	G	T	G	G	0.018	-2.849	1.842	-1.546	0.122	115	*	*	*	*	0.001	-4.581	9.726	-0.471	0.638
115	T	C	G	A	0.070	-0.362	0.962	-0.377	0.707	115	G	C	G	G	0.587	NA	NA	NA	NA
115	*	*	*	*	0.001	4.135	0.019	214.393	0.000	116	C	A	G	T	0.113	1.230	0.899	1.368	0.172
115	G	C	G	G	0.586	NA	NA	NA	NA	116	C	G	A	T	0.081	0.116	1.050	0.111	0.912
116	C	A	G	T	0.114	0.436	0.777	0.562	0.575	116	C	G	G	C	0.117	-0.382	0.874	-0.437	0.662
116	C	G	A	T	0.080	-0.188	0.919	-0.204	0.838	116	T	A	G	T	0.199	-0.414	0.709	-0.583	0.560
116	C	G	G	C	0.117	1.723	0.767	2.247	0.025	116	T	G	G	T	0.018	-0.788	2.159	-0.365	0.715
116	T	A	G	T	0.200	-0.103	0.622	-0.165	0.869	116	*	*	*	*	0.001	-1.279	7.371	-0.174	0.862
116	T	G	G	T	0.018	-2.618	1.832	-1.429	0.153	116	C	G	G	T	0.471	NA	NA	NA	NA
116	*	*	*	*	0.001	-10.034	6.430	-1.560	0.119	117	A	G	T	G	0.312	0.309	0.628	0.491	0.623
116	C	G	G	T	0.470	NA	NA	NA	NA	117	G	A	T	G	0.079	0.109	1.141	0.095	0.924
117	A	G	T	G	0.314	0.284	0.541	0.526	0.599	117	G	G	C	G	0.115	-0.248	0.934	-0.265	0.791
117	G	A	T	G	0.079	0.178	0.936	0.190	0.849	117	G	G	T	A	0.045	1.309	1.265	1.035	0.301
117	G	G	C	G	0.116	1.939	0.777	2.494	0.013	117	*	*	*	*	0.003	2.783	10.361	0.269	0.788
117	G	G	T	A	0.044	1.294	1.136	1.139	0.255	117	G	G	T	G	0.445	NA	NA	NA	NA
117	*	*	*	*	0.002	-9.011	6.440	-1.399	0.162	118	A	T	G	A	0.017	-4.349	2.326	-1.870	0.062
117	G	G	T	G	0.444	NA	NA	NA	NA	118	A	T	G	G	0.063	1.659	1.208	1.373	0.170
118	A	T	G	A	0.015	-1.424	2.554	-0.558	0.577	118	G	C	G	G	0.118	-0.247	0.850	-0.290	0.772
118	A	T	G	G	0.066	0.206	1.049	0.196	0.845	118	G	T	A	G	0.043	1.437	1.309	1.097	0.273
118	G	C	G	G	0.118	1.863	0.750	2.484	0.013	118	G	T	G	A	0.160	1.205	0.765	1.574	0.116
118	G	T	A	G	0.044	1.165	1.110	1.050	0.294	118	G	T	G	G	0.597	NA	NA	NA	NA
118	G	T	G	A	0.160	0.844	0.698	1.209	0.227	119	C	G	G	C	0.115	-0.345	0.897	-0.385	0.700
118	G	T	G	G	0.597	NA	NA	NA	NA	119	T	A	G	C	0.045	1.055	1.281	0.823	0.411
119	C	G	G	C	0.115	1.877	0.788	2.383	0.017	119	T	G	A	G	0.177	0.273	0.766	0.356	0.722
119	T	A	G	C	0.044	0.927	1.131	0.820	0.413	119	T	G	G	C	0.260	-0.412	0.675	-0.610	0.542
119	T	G	A	G	0.176	0.418	0.669	0.625	0.532	119	*	*	*	*	0.003	-4.393	6.491	-0.677	0.499
119	T	G	G	C	0.260	-0.445	0.591	-0.752	0.452	119	T	G	G	G	0.400	NA	NA	NA	NA
119	*	*	*	*	0.003	-8.927	6.043	-1.477	0.140	120	A	G	C	G	0.044	1.385	1.278	1.084	0.279
119	T	G	G	G	0.402	NA	NA	NA	NA	120	G	A	G	G	0.178	0.628	0.756	0.831	0.407
120	A	G	C	G	0.043	0.545	1.132	0.481	0.631	120	G	G	G	A	0.318	0.340	0.629	0.540	0.589
120	G	A	G	G	0.176	0.138	0.665	0.207	0.836	120	G	G	G	G	0.082	1.044	1.093	0.955	0.340
120	G	G	G	A	0.320	-0.330	0.552	-0.598	0.550	120	*	*	*	*	0.001	5.042	0.007	739.332	0.000
120	G	G	G	G	0.082	0.042	0.937	0.045	0.964	120	G	G	C	G	0.378	NA	NA	NA	NA
120	*	*	*	*	0.001	8.886	0.000	1.89E+16	0.000	121	A	G	G	G	0.177	0.494	0.745	0.663	0.507
120	G	G	C	G	0.378	NA	NA	NA	NA	121	G	G	A	G	0.015	1.298	2.232	0.582	0.561
121	A	G	G	G	0.176	0.108	0.656	0.165	0.869	121	G	G	A	T	0.303	0.189	0.624	0.302	0.762
121	G	G	A	G	0.015	-2.336	1.935	-1.207	0.228	121	G	G	G	G	0.080	0.912	1.092	0.834	0.404
121	G	G	A	T	0.305	-0.195	0.550	-0.356	0.722	121	*	*	*	*	0.002	-4.789	6.207	-0.772	0.441
121	G	G	G	G	0.080	0.057	0.942	0.060	0.952	121	G	C	G	G	0.423	NA	NA	NA	NA
121	*	*	*	*	0.002	-2.633	5.441	-0.484	0.629	122	C	G	G	A	0.031	2.181	1.512	1.443	0.150
121	G	C	G	G	0.422	NA	NA	NA	NA	122	G	A	G	G	0.015	1.632	2.211	0.738	0.461
122	C	G	G	A	0.030	1.334	1.354	0.985	0.325	122	G	A	T	G	0.303	0.331	0.636	0.521	0.602
122	G	A	G	G	0.015	-2.131	1.939	-1.099	0.272	122	G	G	G	G	0.260	0.695	0.677	1.027	0.305
122	G	A	T	G	0.305	-0.099	0.560	-0.176	0.860	122	*	*	*	*	0.002	-4.775	7.481	-0.638	0.524
122	G	G	G	G	0.258	0.149	0.593	0.251	0.802	122	C	G	G	G	0.390	NA	NA	NA	NA
122	*	*	*	*	0.002	-2.120	6.707	-0.316	0.752	123	A	G	G	C	0.014	1.454	2.277	0.638	0.523
122	C	G	G	G	0.390	NA	NA	NA	NA	123	A	T	G	C	0.125	0.527	0.827	0.638	0.524
123	A	G	G	C	0.014	-2.530	1.974	-1.282	0.200	123	A	T	G	T	0.179	-0.364	0.700	-0.521	0.603
123	A	T	G	C	0.125	0.626	0.724	0.864	0.388	123	G	G	A	C	0.031	1.917	1.497	1.281	0.201
123	A	T	G	T	0.181	-0.852	0.616	-1.382	0.167	123	G	G	G	T	0.012	-2.524	2.624	-0.962	0.336
123	G	G	A	C	0.030	1.193	1.336	0.893	0.372	123	*	*	*	*	0.003	-3.547	7.232	-0.490	0.624
123	G	G	G	T	0.011	-2.967	2.383	-1.245	0.214	123	G	G	G	C	0.637	NA	NA	NA	NA

Table B1.31. Continued

ApoA1										ApoB									
Window	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**	**Window**	**loc.1**	**loc.2**	**loc.3**	**loc.4**	**hap.freq**	**coef**	**se**	**t.stat**	**pval**
123	*	*	*	*	0.003	0.229	6.434	0.036	0.972	124	G	A	C	A	0.032	1.577	1.466	1.076	0.282
123	G	G	G	C	0.636	NA	NA	NA	NA	124	G	G	T	A	0.013	-2.367	2.526	-0.937	0.349
124	G	A	C	A	0.032	1.113	1.303	0.855	0.393	124	T	G	C	A	0.126	0.772	0.835	0.925	0.355
124	G	G	T	A	0.013	-2.256	2.316	-0.974	0.330	124	T	G	T	A	0.180	-0.434	0.697	-0.623	0.533
124	T	G	C	A	0.127	0.706	0.735	0.960	0.337	124	*	*	*	*	0.003	-5.541	5.365	-1.033	0.302
124	T	G	T	A	0.182	-0.905	0.613	-1.476	0.140	124	G	G	C	A	0.646	NA	NA	NA	NA
124	*	*	*	*	0.003	-8.539	4.031	-2.119	0.034	125	A	C	A	C	0.032	1.358	1.465	0.927	0.354
124	G	G	C	A	0.644	NA	NA	NA	NA	125	G	C	A	G	0.026	-1.002	1.691	-0.593	0.553
125	A	C	A	C	0.032	0.957	1.299	0.736	0.462	125	G	T	A	C	0.193	-0.733	0.673	-1.089	0.277
125	G	C	A	G	0.027	-0.750	1.440	-0.521	0.603	125	*	*	*	*	0.003	-5.678	6.033	-0.941	0.347
125	G	T	A	C	0.194	-1.145	0.593	-1.930	0.054	125	G	C	A	C	0.746	NA	NA	NA	NA
125	*	*	*	*	0.003	-8.689	4.476	-1.941	0.053	126	C	A	C	C	0.131	-1.019	0.880	-1.159	0.247
125	G	C	A	C	0.744	NA	NA	NA	NA	126	C	A	G	T	0.025	-1.389	1.733	-0.802	0.423
126	C	A	C	C	0.133	-0.244	0.715	-0.341	0.733	126	T	A	C	C	0.016	-0.559	3.241	-0.172	0.863
126	C	A	G	T	0.027	-0.758	1.460	-0.519	0.604	126	T	A	C	T	0.177	-1.022	0.776	-1.318	0.188
126	T	A	C	C	0.015	0.349	2.365	0.147	0.883	126	*	*	*	*	0.004	-5.630	6.132	-0.918	0.359
126	T	A	C	T	0.178	-1.361	0.654	-2.080	0.038	126	C	A	C	T	0.648	NA	NA	NA	NA
126	*	*	*	*	0.004	-8.068	4.353	-1.853	0.064	127	A	C	C	A	0.147	-0.754	0.763	-0.988	0.323
126	C	A	C	T	0.643	NA	NA	NA	NA	127	A	C	T	G	0.025	-1.033	1.646	-0.628	0.530
127	A	C	C	A	0.149	0.065	0.652	0.100	0.920	127	A	G	T	A	0.026	-1.104	1.681	-0.657	0.512
127	A	C	T	G	0.024	-1.831	1.475	-1.241	0.215	127	*	*	*	*	0.003	-5.949	6.095	-0.976	0.329
127	A	G	T	A	0.027	-0.574	1.429	-0.402	0.688	127	A	C	T	A	0.799	NA	NA	NA	NA
127	*	*	*	*	0.004	-8.265	4.974	-1.662	0.097	128	C	C	A	G	0.026	-7.059	2.161	-3.267	0.001
127	A	C	T	A	0.796	NA	NA	NA	NA	128	C	C	A	T	0.125	0.476	0.859	0.554	0.579
128	C	C	A	G	0.028	-0.375	1.716	-0.219	0.827	128	C	T	A	G	0.167	0.378	0.751	0.504	0.615
128	C	C	A	T	0.126	-0.011	0.745	-0.015	0.988	128	C	T	G	T	0.025	-1.088	1.629	-0.668	0.504
128	C	T	A	G	0.162	0.349	0.666	0.525	0.600	128	G	T	A	T	0.024	-2.558	1.750	-1.462	0.144
128	C	T	G	T	0.025	-2.042	1.458	-1.401	0.162	128	*	*	*	*	0.002	16.577	7.692	2.155	0.031
128	G	T	A	T	0.024	-1.186	1.596	-0.743	0.458	128	C	T	A	T	0.631	NA	NA	NA	NA
128	*	*	*	*	0.004	4.037	6.028	0.670	0.503										
128	C	T	A	T	0.632	NA	NA	NA	NA										

APPENDIX B2. Supplementary figure for *CETP* gene resequencing and association analyses

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AATGTTCAGA GTAGGCAATC CCATAGAGAC AGAAAGCACA TTTATGGTTG 50   | REPEAT
CCAGGAGCTG GGAAAGGGCA GGATGGGGAA TGACTGTTTA TTGGATGTGG 100
GGCTCTATTT TGGGGTGATG AGAATGTTCT GGAATTAAAT TCATGGCTGC 150    p.109-[T/G]
ATAACACTGT GAACATACTA AATGCCCCTG AATTGTACAC TTTAAAATGG 200    p.163/ rs13332526-[A/G]; p.187/rs148562851-[A/G]
TTAAAGTGGC AAGTTTTCAT TAAGCAGTAA ATTAAATTCT ACTACAATTT 250  | p.220/rs12447924-[T/C];p.240/rs12720918-[T/C]
TAAAAAGACT AAAAAATAAT TTAAAAAAAG ATTAAATGAG ATAACGCAAA 300  | p.266/rs13332571-[A/G];p.273delA/rs36229491;p.296-[G/A]
AAAGCATTAT CTCGAAAATA CAGCTGATAT TAGTATAATT CTTACTAAGT 350
TTTAAGAGTC TAAGGTGCAG GATTCTAAGT TTAAAGGGAT AGGCTCTTTT 400
GGTTTTTTGG TTTAGTTATT TGGTTTTTTT TTTTAATCCA TTATCCCCAC 450
CCTTGGGAGG CCCCCAGCAC CCAGTCTGCA CTAGAGGATG GGGCCCACCT 500    p.452-[C/A]
CCCTTTTCTC TCCAGGCCCA GCCACTGACC ACCAGTACCC TGGCCAGGGG 550    p.546-[A/C]
CACCCTCGGT CATTGCCCTC CGTGGCCCAA GGAAGGGAAC AGAAACAACA 600  | p.557/rs17231506-[C/T]
GCCAAGAAGA CAATAGCCGC CGGGAAGTCC TCACATTTCT GGAGAAATAG 650
AGCCCATTAA TGAATGAAGT TCCTCCAGCC TGATCGGAGG ACGGGGTGCT 700
GGGGAGGCCT GGGCTAAAGG GCTCACCTCC AGCCCCCACC CTGGCAGGGC 750
CGATGGTACA TGCTCACTCA GTGAGGGGGC TCCAGAGGTC TGTGGGTACG 800
AACCCAAGGG CTGGTGCCCA GGGGCAATCA GCTTATGTCT CTGAGCCTTG 850  | p.848/rs12708968-[T/C]
GGAAACAGTG AGGGTCAGCC CGGCTCCCCA CGTGCTTCTG GGCAGCTTTG 900  | p.870/rs13338602-[C/G]
GTATTGGAGC AGGTGCAAAC TCGGGACTAG GGCAGGACCC CCTGAGAGGC 950  | p.923/rs4783961-[A/G]; p.950/rs146122874-[C/T]
GACTGAGCAA GGCCATCCCG ACTCATGTTT CCTTGGCCCT GCCCGGGGCA 1000
CAGCATCCTG CCCACATCCC TGCAGCCCTG GCTCCTTCCT AGGGGCTCTG 1050 | p.1019/rs17245715-[C/T]
AGGAGGCAGC ACTTGGCCAT CTGGTCACAG TTGCTGCAGG GCAGTTCTTG 1100   p.1067/rs4783962-[C/T]
GCCCCAGCTG TAGGTAAAGT ACTGTATGTT GTAATTTTTT GAAAGATAAC 1150
ACGTTCACAC AACTCAGAAT TGAAATGCCA CAGACATTCC CCCTCGTCCG 1200 | p.1153/rs17237883-[G/A]; p.1189/rs114856405-[C/A]
CCCCTTTCCC CCGGATACCC AGTTTCTCCC GGAGGCAGCC AATGATCTCA 1250
GAGGCTGTAT ACCCCCCCAG AGTTATTTTA TGCATATCAA GGAAAGTCTA 1300 | p.1263/rs1800776-[C/A]; p.1265/rs1800775-[C/A]
CATAGAGGAC TGTTTCTGGG GTACCCAGAT GCAGCGTCAA ATGCCATGGA 1350 | REPEAT
ATACTACAGT GAGGACATTA TCCTTTCAAG CTTTCAAATC AGAGCAAGGG 1400
AAAGGTCGAT GCTAGAGTTT CTCTAGCACC CATGAAGCCC TCTCCCTTTT 1450
TCTACTGAGT TTTACTTTAC AGGCAACAGC AGGCTTCAAG CTTGGGGTCA 1500
TTGTCGGGCA ACAGTATCTG GCAAGAATTC AATGTCTTTT TCTCATAGTC 1550
ATTGTATTTT GGCCTCTTTC TATTTATGGC AACTGAGAGA GAAAGCTTAT 1600
TCCTAGATAT ATGTATTTAA GTAAAAAATA AATGAATTCA TGGAAACATA 1650
TTAAGCAATT ATCCAGATAA CATAAGGGAT GGCAAAAATG GTGCAGATGG 1700
TGGAGGGGAG ACAAGTAGAA GTTGGGGTGC TCTTGTTGAA TGTCTGGCTC 1750
TGAACTCTAG AGGAGGCCGC AGGGGCTGGG CAGGAAGGAG GTGAATCTCT 1800 | Exon 1 | UTR
GGGGCCAGGA AGACCCTGCT GCCCGGAAGA GCCTCATGTT CCGTGGGGGC 1850
TGGGCGGACA TACATATACG GGCTCCAGGC TGAACGGCTC GGGCCACTTA 1900 | p.1856/rs17231520-[G/A]
CACACCACTG CCTGATAACC ATGCTGGCTG CCACAGTCCT GACCCTGGCC 1950   p.1937/rs34119551-[T/A]
                       M  L  A   A  T  V  L  T  L  A   10
CTGCTGGGCA ATGCCCATGC CTGCTCCAAA GGCACCTCGC ACGAGGCAGG 2000 | p.1964/rs34065661-[C/G]; p.1986/rs5884-[C/A]
 L  L  G   N  A  H  A   C  S  K   G  T  S   H  E  A  G 27
CATCGTGTGC CGCATCACCA AGCCTGCCCT CCTGGTGTGT AAGTATCAGT 2050
  I  V  C   R  I  T   K  P  A  L   L  V                39
GCATCTGTCT GCCCTGCCAG GGGTCTTTTC ATGGACACCC ACTATGCCAG 2100   p.2089/rs34680782-[C/A]
GAGCCTCCCT GGCCTGAAGC CAGCCCTGAA GCCGGCTGCC ACACTAGCCC 2150 | p.2133/rs17231534-[C/A]
AGAGAGAGGA GTGCCCTGGG AGGGAGATGG GCTGAGCGGA GCTGTCATCA 2200 | p.2187/rs3816117-[C/T]
CCCCCTCCTG ACCTCGCCTT CAAGGTCAAG TTCTTTGGTG AGAAGGTCCT 2250 | p.2240/rs711752-[G/A]
AGCTGCATTG CAAACAGCCA GGTATAGGGA TTTGTGTTTG TCTGAGACCC 2300
AGAATCACTG GGGTTCGAGT TAGGGTTCAG ATCTGAGCCA GGTTAGGGGG 2350 | p.2308/rs5030708-[G/T]; p.2317/rs708272-[G/A]
TTGAGTCAGG GGGTAAAGAT TAGGAGGTTG GTGTATATTT GGTGTTGGGG 2400
GTCACTCTAT GGCCAAAGTC AGGGGTTGCC ATGAGCTCAG GTGACGGAGG 2450 | REPEAT
CTCCATCACT GACTGTTGTG TGACTTTGGC CAGCTCCCCT GCCCTCTCTG 2500
GGCCTCAGTC TCTTGCTCAA TATAATAAGG GTATAGGGAG GCTAAATGAT 2550
ACAATTTCTA AAATAGAGTA TCGCCAAGTT CAAAAGCCAG AATTATAGAC 2600
CCCCAGGACT ACAGACAGTG TCACAGCATC GTCTGGGTGA GGCTAGGGTT 2650
AGTGTGCGGC TGGGCTCAGG GCTGCCCCAT TTGCTAGGAT CGTGGGGTTC 2700   p.2676del2/rs34145065; p.2678/rs34620476-[C/A]; p.2692/rs60195610-[G/A]
CCATGTGTCA GGATCCAGAG GCTAGGGTAT GATCAGGATC TCTAGCTGGG 2750   p.2736/rs59008849-[G/T]
GTCAGGGTCA GAGCTCTCTG TGTCCCCTAG AATTGCCATC AACCTTAAAC 2800
CCAGAGGGAG GCCCAGTCCA ACCCCTCAGC TTTAAGACCT GCTGGGAGCC 2850
TCATCTCAGA GAGGCTGAGT CATGGCCAAG GCCAGTTGGG GGTGGGAGCA 2900
GGGGGCTTGG TGTGGGCCTG CAGCCCCTCA TCCACTGCCC TCCCCTCTAG 2950
                                                       39
TGAACCACGA GACTGCCAAG GTGATCCAGA CCGCCTTCCA GCGAGCCAGC 3000 | Exon 2
L  N  H  E   T  A  K   V  I  Q   T  A  F  Q   R  A  S  56
TACCCAGATA TCACGGGCGA GAAGGCCATG ATGCTCCTTG GCCAAGTCAA 3050
 Y  P  D   I  T  G  E   K  A  M   M  L  L   G  Q  V  K 73
GTATGGGTTG CACAAGTGAG TCGGGCCTCG GGTGTGACCA GGCTGGGGGT 3100
  Y  G  L   H  N                                       78
AGGGAGGCGG GAGGAACAGC CTGGGGCTTG CCCCCAGCCC ACAGGGAGGA 3150 | p.3101/rs9935228-[A/G]
AAGGCAGCAG CTGGGGGACT CAGGTCTCTC CCCTTGATTT GGAACCAGAG 3200   p.3153-[G/A]
CCTGACACCT TCCCTACCCC CACCCTCCAT CCCCTGGTGC CCTGGGGGGA 3250
TTTATTGGAG TGTATCAACC TCTCCAACAG CCCCTCTAAG AGTCAGGCTT 3300   p.3262/rs1864163-[G/A]
CAAAGGGTCC TTTCCCACTG CCCTGGGAAG ATGGAGGTCT TATTTCGGGG 3350   p.3347/rs75313088-[G/A]
TGAATGGGGG GTAGGGTAGA AAAATCTCAA ACAAAATAAG TATTTTTTTA 3400 | p.3381delA/rs5817083;p.3399/rs4587963-[T/A]
AAAAATGTAT AAATGTTGTT TTCTTATAGT ACAGACAGGT CTTGCTATGT 3450 | REPEAT p.3412-[A/G]
TGGCCAGGTT GGTCTTGAAC TCTTGGCTTA GCCAGTCCCC CACCCCAAGC 3500
CTAAAATTAG TATCTTGACT TTATTTGGGA TGATGGTAAC AGTCAAGGGT 3550
CGGTTGTGGG CCAGGTGCTT TTACAAACAA TATCCTCACC TTTATCATAT 3600 | p.3581/rs4369653-[T/C]
ATTTTTTTCT TTCTTGTTTT TCATTTTTTG AGACAGAGTC TCCCTCTGTC 3650 | REPEAT
ACTTAGGCTG GAGTGCAGTG GCACAATCTC AGCTCGTTGC AACCTCCGTC 3700 | p.3686/rs7194225-[G/C]
TCTGGGTTCA AGGAATTTTC GTGCCTCAGC CTCCAGAGTA GCTGGAATTA 3750
CAGGCACACG TCACCACATC CGCGTAATTT TTGTATTTTT AGTAGAGATG 3800
GGGTTTCATC ATGTTGGCCA GACTGGTCTC CAACTCCTGA CCTCAAGTGA 3850   p.3803_3804InsG
TCCGCCCACC TCAGTCTCCC GAAGTGCTGG GGTTACAGGC GTGAGCCACC 3900   p.3854-[G/T]
ACGCCTGGCC CTTTATCTAT CTTAATCTTT ATTTTATTTA TTTATTTATT 3950 | REPEAT p.3918-[T/A]
TATTTATTTA TTTATTTATT TATTTATTTA TTTATTGAGA TGGAGTCTCT 4000
CACTGTCACC CAGGCTGGAG TGCAGTGGCA CGATCTCAGC TCACTGCAAC 4050
CTCCACCTCC CGGGTTCAAG ACGTTCTCCT GCCTCAGCCT CCCTAGTAGC 4100
TGGGATTACA GGTGCCCACC ACCACGCCCG GCTAATTTTT GTATTCTTAG 4150
TAGAGACGGG GTTTCACCAT GTTGACCTGG TTGGTCTTAA ACTCCTGACC 4200
TCAAGTGATC CACCCGCCTC GGCCTCCCAA AGTCCTGGGA TTGCAGGCGT 4250
GAGCCACAGC GTCCGGCCTA TCTTAATCTT TATCATATAT TTTAGCCTCT 4300   p.4299/rs114908369-[C/A]
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CGGAAACAGG AGCCGATAGA GGTTTAGCAG CCTGGCGGAG CTCATGTGCA 4400
AACTCAGCTC AGTATCGGAA ACTCAGCCAC CTTCATGGCA CCTCAGGCTG 4450
CCCTGGAGCC TGGGTCCCGG TCTGTGTGTC GGTCTGAGGC CCCAAGGGTG 4500
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CTCCTCCCCG GCCCTGCTAA ACACGCTCCC CAGGGGTGGT CTCTGCTACC 4600   p.4559-[C/T]
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GCTAGCGGGT GCTGTGGGGC GTCCCAGGTC TCGCGCAGCC ACGCCCTCTG 4750
TGTGACCTTG GGCTTCAGTT TAGGCTTCTG TAAAAGAGAA TAATGGGCAA 4800 | p.4791/rs12720906-[G/C] | REPEAT
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GAGGATTACC TCAGCCAGGG TTCAAGACCA CCTGTCTCTA TAAAAAATTT 4900
AAAAATTAGC TGGGCATGGT GGTGCGTGCC TGCAGTCCCA GCTACTCAGG 4950 | p.4948/rs12720926-[A/G]
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AATGCTATCC TAGACCTATG TGTTGCAAGA GGTCAGACAT GGCAAAAGCG 5100
TTGAGAAGTT AAAGAAATAG TATCCTTAAT AAATCAGCAA TAATTCAGTA 5150   p.5130/rs116604371-[T/A]
AGACCAGACT GCCATAGACT AGATGTCATA GTCATTAATA TATAACTGTT 5200 | NOT SCANNED
ATCCCAAACG TATATGAGTG GGGTAGAAAT AAAATATGAT TGGCCATAAC 5250   p.5209-[C/T];p.5215delT/rs35585922
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AACAGACCGG GAAAGCCAGA TATATGTGGA TTCTCCTTGC TGGGCACAGT 5400 | REPEAT p.5358/rs11508026-[C/T];p.5375/rs80296794-[T/C]; p.5383delC/rs71383212
GTGTCATAGT GGCTTATAAT ATGGGATTTG GAGTGGGATG GACCCAGGAT 5450
CAAATTCCCT TCTACTGAGG TTTTCTGAAG CCACATAAGC TGTCTGAGCC 5500
ATTTCTGTCT CAGTTCAGTG GGTACAGCAA TAGTGACTAC CTCGTGGGTA 5550
GCTGTGAGGA TTAAACCAGG AAATGTGTAT AAACTCTAAG CACAGTGCCT 5600   p.5593/rs112236143-[C/A]
GCCACACAGC ATGTGTTTGG TACGTGATGG CCGCTTCTAT TGTGTCATAT 5650
TCCATGTGCT CAAGCCGGGC CCTGGGGGAG AGTTCAGCAA GGGTAGAGGG 5700
ATATGAGAGT GAATGTGGCC CACTGGCCTC CCTGCCTGCA GTCTCTCCTC 5750
TCTGATCCTT GCTTCCTAAG GGTCTTCACT GAGCCCCACC TCTGACCAAG 5800
TCCCCGGCGG CACAGGCAGC ACAGATCCTC TGCTGTACCT ACACCAAGAC 5850 | p.5808/rs17237946-[C/T] ; p.5810delG/rs17231569
CCCAGGGCCA ACGCTTCTCC CATTGTGCAG CTCCACCTCT GCCCCCGGGG 5900
CCTAGCTGAG GCCTCCTCCA AGCTGAGCCA CCTACTATCT TCCAAACTCC 5950 | REPEAT
CACCCTCCAT CTGGTGTCAC CTCCTCCCGG AAGCCCTCTG TATCAGTTTC 6000 | p.5979/rs708273-[G/A]; p.5990/rs17231583-[G/C]
CTGTTTTCTG CCATAAAAAA AATCACTCCA AGTTTAGTGG CTTAACATGA 6050   p.6022_6023InsA/rs142058276(inserted in Ref. seq)
CACAAGTTTA CCATTTTACA GTTTAAAAGG CTAGAAGTCC ACCATGGCCC 6100
TCCCTGAGCT AAGATCAAGC TGTCAGCAGA ACCAGATTCC TTCTGGGGGC 6150
TATAGGGGAG AATTAATTCC CTCGCTTTCT GCAGCTTCTA GAGGCTTCCC 6200 |
CCATTCCTTG GCTTCCCTCC ATCTACTTTT ATTTAGGGCG AGGGAAGCTT 6250 | p.6221/rs17231590-[A/G]; p.6239/rs17237953-[C/A] | REPEAT
CCTGCTCTGA CTTTCTCATT TATGGTATTC TCCCCTGCTT TCCAGCAGCT 6300   p.6251/rs35619327-[C/T]
GTGATTGTCC CAAGTCCTGT CCTCTGGTTC TCTAGGCCAG AAAAACTATG 6350 | p.6314/rs820299-[A/G]
ATCTACCAGA GCTCAAGAAC TTGAAAGGGC CTTTTCCCAC TGTCCCTTCT 6400   p.6361-[G/C]
CACAGTGAGA GCCGGAGCCC AGCTTCGTGC TAGAATCTGT GAAAATGGAG 6450 | p.6427/rs17237967-[G/A]
AAATGCACCC TGTGCTGTTC TCTTCCTCCA CCCGGCATCT CCCCTGCAGC 6500
CCGGCTGGGT TTTTTTGTTT GTTTGTTTGT GGGTTTTTTT GTTTTTTTGT 6550 | REPEAT
TTGTTTTTGA GACAGAGTTT TGCACTTGTC GCCCAGGCTG GAGTGCAATG 6600
GCACGATCTC GACTCACTGC AACTTCTGCC TCCTGGGTTC AAGCGATTCT 6650
CCTGCCTCAA CCTCCCGAGC AGCTGGAACC ACAAGCATAT GCCACCACTC 6700
CCGGCTAATC TTTTTTTTTT TTTTTATGCA TTTTTAGTAG AGATGGGGTT 6750   p.6725/rs8045855-[A/T]
TCACCATGCT GGCCAGGCTG GTCTCGAACT CCTGACCTCA GATGATCCAC 6800
CTGCCTCGGC CTTCCAAAGT GCTGGGATTA TAGGCGTGAG CCACGGCCTG 6850
GCCCAGTCTG ACTGTTTTCA CTTACTCTCT AATGTCTCAG GTAGTGTTTA 6900 | REPEAT
TTGTATTCTG TGCGGAGGTC AAGAATTTAG TCATCCAAGG AGGTTAGTGT 6950 | p.6914/rs12720922-[G/A]
ATTAGGAGCT TACGCAACTA TTACCAGAAG AGACTCCACT CAAAAATTTG 7000
GTACGTGGCT GGGCGCAGTG GCTCAAACCT ATAATCCCAG CACTTTGGGA 7050 | REPEAT
GGCCGAGGCG GGCAGATCAC CTGAGGTCAG GAGTTCAAGA CCAGCCTGGC 7100
CAACATGGTG AAACCTATCT CTATTAAAAG TACAAAATTA GCTGGGCATG 7150 |
ATGGTGCATG CCCATAATCT CAGCTACTTG GGAGGCCAAG GCAGGAGAAT 7200
CACTGAACCC AGGAGGTGGA GACTGCAGTG AGCTGAGATT GCCCGCTGCA 7250 |
CTCCAGCCTG GGCAGCAAGA GCAAAATTCT GTCACACACA CAAACAAACA 7300 |
AACAAACAAA AAAAACGGGT TGGGCATGGT GGCTCATGCC TGTAACCCCA 7350 | REPEAT
ACACTTTGGG AGGCTGAGGT GGGGGAATCA CCTGAGGTCA GGAGTTCAAG 7400
ACCAGCCTGG CAACATGGTG AAACCCCCTC TCTACTAAAA GTACAAAAAT 7450
TAGCTGGATG TCGTGGCGGG AGCCTGTAAT TTCAGCTACT AGGGAGGCTG 7500
AGGCAGGAGA ATCACTTGAA CCCAGGAGGC AGAGGTTGCA GTGAGCCGAG 7550
ATCGTGCCAC TGCACTCCAG CCTGAGCAAC AGAGCCAGAC TCAGTCTCAA 7600
AAAAAAAAAA AAAAACAATG GTATGAGCTT TAAATTTCTG TAGAACTGAA 7650 |
AGAGGATTGG AGATTGTAGT AGGGTCTAAT TCTAAATTAG AGCATTTAGA 7700
ATAATGTGGA GTCTGGTCAA CATAGTGAGA CCCCCCCAAT CTGCACAAAA 7750 | NOT SCANNED | REPEAT
AAGACAAAAA TTAGCCAGGC AGTGTTGGTG CATGCCTGTG GTCCCAGCTA 7800
TTCCAGAGGC TGAGGCAGGA AGATCGTTGG AATTCGAGGC TGCAGTGAAC 7850
TGTGATTACA CAACTGCACT CTGGCCTGGG CAACAGAGAG CCACCCTATC 7900
TCAAACAAGA AAGAACAAAC TAAAAAAAAA AAAAGAAGAA GAAGAATTTG 7950
GAGCAATCTA GTTGTTTCCT ATACCAGAAG TCTTTGCCAA TCTATTTTTT 8000
TTTAATTTTA TTTTTAATTT TTGTGAGTAC ATAGTAGGAG TATATATTTA 8050 | REPEAT
TGGGGTACAT GAGAGTACAT AGTAGGAGTA TATATTTATG GGGTACATGA 8100 | REPEAT
GATGTTTTGA TATAGACCTG CAACGTTTTG TCAATCTATT TTTTTTTTGG 8150 | REPEAT
CGACAGTCTT GCTCTGTTGC CCAGGCTGGA GTGTAATGGC GCGATCTCAG 8200
CTCACTGCAA CTTCCGCCTC GTGGGTTCAG GCTATTCTCC TGCCTTAGCC 8250
TCCAAACTAG CTGGGACTAC AGACGCCCAC CATCATGCCC GGTTAATTTT 8300
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GAACTCCTGA CCTCAGGTGA TCTGCCCTCC TCGGCCTCCC AAAGTGCTAG 8400
GATTACAGGT GTGAGCCACC ACGCTGGCCC ACCAACCTAT TTTTGATCTA 8450
ACTTTACCTC TGGTGGTGTA TTGATACTCT TCCGAATCAA TTTTCACCCT 8500
TCTTCATATA CCATTTACAT TTCTAAGAAT TTGTCCATTT CATTTCATCT 8550 | REPEAT
AGTTAACCTC ATTTGTTGAC ATACAATTGT TCGTAGTATT CTCTCATAAT 8600
TCCTTTTATT TCTGTAAGAC TGGTAATAAT GGCCTTGCTT TTATTTCTGT 8650
TTTTAGTAAT TTGAGTCTTC TTCTTTTTTT TTTTTTTTGC CAGTGTAGCT 8700 | p.8695/rs9926440-[G/C]; p.8698/rs192306644-[G/C]
AAAGGTTTGT TGATTTTGTT GATCTTTTGG AAAAACCAGC TATTGTTTTC 8750 | p.8742/rs12720863-[A/G]
ACCGATTGTT GTTGTTGTTC TATTATTTCA TTCATAGGCA CTAAGATCCT 8800 | p.8764/rs9939224-[G/T]
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CAAGTTCCAT AAGGTGGAAA GTTTGATTAT TGAGTTGAGA TCTTTCTCTT 8900
TTTTAAAGAT AGGCATTTCT AGATATAAAT CTCCCTGTGA GCACGGTTCC 8950 | REPEAT
CTCCATCTTC AGCACACCAG GGTTGACTCT CTCCGGGCGT TCTTCCCTGG 9000
TCACCTCTCC CCTTCCTCTC CTCTTCTGCC TCCTCTTCCA CTTTTCGGTA 9050
CCCTGTGATT GTATTGGGAC CACCCAGATA ACCTAGGATC ATCTCCCCAC 9100   p.9075/rs60531466-[C/T]
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TGAGTGTGGT ACCCAGGGTT TGACATGTTG GGTAACATAT TTGCAGGTTC 9200 | p.9178/rs11076174-[T/C]
TGTGGATTAG GAGGACATTT TGGGGGCCAT GATTCTATCT TCCACCCTCG 9250
CCTAGACAAA ATTGGAGGCT CACTCCTTGG GCTCCCTGGA TGACCCCCAA 9300   p.9282/rs13306230-[C/A]
CATCCTTCCT CACTTCCATT CCTTCCCAGC ATCCAGATCA GCCACTTGTC 9350 | Exon 3
                                  I  Q  I   S  H  L  S 85
CATCGCCAGC AGCCAGGTGG AGCTGGTGGA AGCCAAGTCC ATTGATGTCT 9400
  I  A  S   S  Q  V   E  L  V  E   A  K  S   I  D  V   101
CCATTCAGAA CGTGTCTGTG GTCTTCAAGG GGACCCTGAA GTATGGCTAC 9450
S  I  Q  N   V  S  V   V  F  K   G  T  L  K   Y  G  Y  118
ACCACTGCCT GGTGGTAAGC ATTCCTGTCA GCTGATGCCC CATGCCCTGG 9500 | p.9493/rs12708971-[T/C]
 T  T  A   W  W                                        123
CCCTCTCTGG GCTGGAGGGC TGAATGAGGG TCCTGGGTCC TTGGCTCTTT 9550
CCAGGCTGGG TATTGATCAG TCCATTGACT TCGAGATCGA CTCTGCCATT 9600 | Exon 4
      L  G   I  D  Q   S  I  D   F  E  I  D   S  A  I  138
GACCTCCAGA TCAACACACA GCTGAGTATG TGTCAAGCGT CCTCTGGGGA 9650
 D  L  Q   I  N  T  Q   L                              146
AGTGGGAGCT GGACTCCAGG GCTTGGCCTC AGCAGAGGGG GAGGTTGTGC 9700   p.9670/rs60896367-[T/C]; p.9693/rs35752722-[G/A]
AGGCAGAGGG TTCTGGGGCC ACCAAAGGAG GCCCAGCCTG GGAAGTTTGC 9750
AGGGTTGGGG ACCCCAGAGC TGGCCAAGCT CTTGACTGGC CTGGGCAGCA 9800 | p.9755/rs891141-[T/G];
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CCTGCAGCCT GTGACTCTGG TAGAGTGCGG ACCGATGCCC CTGACTGCTA 9900 | Exon 5 p.9878/rs34716057-[C/T]
       T   C  D  S  G   R  V  R   T  D  A   P  D  C  Y 161
CCTGTCTTTC CATAAGCTGC TCCTGCATCT CCAAGGGGAG CGAGAGTAAG 9950
  L  S  F   H  K  L   L  L  H  L   Q  G  E   R  E      176
TACACCACCC TGTGGCCCCC ATTCCTGCTC GTGCCCATCC TGTTAGTGTG 10000
TCCACGGCCC CCTCCAGGCT CAACCCCACA CAGGGCATGC TTGTGGGTGG 10050  p.10009/rs891142-[C/T]; p.10012/rs891143-[C/T]
CCAAACCTGA GGGCAGCAAT ACCTTCAGTG GGGTCACTTC CTACCCCCTC 10100
CCATCAATAC ACCCTCAAAG GCTGGAAACA ACAATAACCA ACAGCTAGTA 10150 | REPEAT
ACTAACAGCT ATTAAGAACT TGCTGTGTGC AAAGCACTAT TCCAAGCCCT 10200
TTTCATGAAT TAATTGATTT TGTCCTTAAA ACCAACCCTA GGATATAGAT 10250
TCTGTTATCA TCCCCTTTTT ACATATGGGT AAACTGAGTC ACAGAGAGGT 10300
TAGAAAGGAA AAGCTCATAT CTACGGAGTG CATCCTGCAT TCCAAGCACC 10350
ACACTAACTC AGAGATAAAA CTCTAGCCAA GCTAAGTAAC TTGCTGAGGA 10400 | REPEAT
CACACAACTC GCCACTAAGG GATGGGAGTA GGATTTGAAC CCAGCATTCT 10450
CTGACCCCAG AAGCTGAGTT CCTAGATACT TTACTCTCCT GCTTCCCAGG 10500 | p.10459/rs139040281-[C/T];p.10491/rs12720861-[G/A]
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CCCCATTGCA CAGAGGAAGA TAACAAGGTT TGGAGAGTCC CTAGTCATGT 10600
TACCAATGCC AAACCTGGAA GGCAGAAGGG AACTGGTGGG TGGGGTCTGG 10650
AGAGGAGCCC TCTATTCAGG CCATTTTCTG ACTCTGGAGC AGACGGATAC 10700 | p.10694/rs12720860-[C/T]
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ATGTATGAAT TTGGACTCTA GACACGTTCT CGTGTGTGTG ACAGGTGTGA 10750
GCGTCACAGG AGCTGGGCCC TCCCGAGGAA TTCTGGGATG GTGCCACAGT 10800 | p.10775-[G/A];p.10779/rs12720862-[A/G]
TAATTCTTGG GTCTGAGGCT CCGTGTTCTC AGCTGCAAAA TGGGAGTGAT 10850 | REPEAT
AATTCTTACT TCCTGAGCTA CAAGAGTCAG GGCCAACAGA GCCATGAACG 10900
GTGCCTGGTA CACACTAGGC GCTCCATGGA TGCACAGGAC TGGTCAGGGG 10950 | p.10921/rs7205804-[G/A];p.10924/rs139040281-[C/T]; p.10934/rs12708973-[A/G]; p.10943/rs148134355-[G/A]
CTCATTGTGG TGCTTGCTGC CTTCAGGCCT GGGTGGATCA AGCAGCTGTT 11000 | Exon 6 p.10983/rs34611098-[G/A]
                              P   G  W  I   K  Q  L  F 184
CACAAATTTC ATCTCCTTCA CCCTGAAGCT GGTCCTGAAG GGACAGGTGA 11050
  T  N  F   I  S  F   T  L  K  L   V  L  K   G  Q      199
GTGAGGCTGG CTGACTCCCT GTGGTCCAGG GCCATGCCAG GAGGCTGGAT 11100
CCCTTTCCTC CCTGCCTTTC CCTGAGAAGG TGCCACTCCC ACCTTCTCCA 11150
TGTGGCCAGT CCCCTGTGCC GGTCCCCAGC ACTGCCACCA CCACGCAGCT 11200  p.11194/rs34523084-[C/T]
GGAAGGAGGC ACTGCCTCTG GCCTCCTTTC CTGCCTGGAA AGCACCTGCT 11250
CTGTCTGCCC CAGATCTGCA AAGAGATCAA CGTCATCTCT AACATCATGG 11300 | Exon 7
               I  C   K  E  I  N   V  I  S   N  I  M   211
CCGATTTTGT CCAGACAAGG GCTGGTGAGT GCGTTTCTGT CTGCATGCCT 11350 | p.11332/rs1532625-[C/T]
A  D  F  V   Q  T  R   A                               219
CAGAAGACAG CAGTGGGAGC CAGAAAGCCA CCTGCTGCAC TATGTGGCCT 11400
TGGGACTGTC ACTCTTCCTG TCTAGGTCCC ATGGGCTCTA TCTGGCTCTG 11450   p.11433-[G/A]
ACACTTGATG ATTAGTTATG AGCATACTTT GGCAAATCTC TGCCCCTTTG 11500 | p.11456/rs12720925-[T/C]
GGCTGCAGCC TCACAAGCTG TGTGGCGTTG GGCAAGTCTA TAGAACTCAG 11550 | p.11510/rs1532624-[C/A]
GACAAATGGG TGATTAAGTC CAAGAGGACT CCAAGATTCT CCTGGAAGTA 11600   p.11581/rs12708974-[C/T]
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GACAGACAGA CTTGGGAAAA GAGAGAATGA AAAAGTGCCA CACCCCTCCC 11800 | p.11793/rs117040820-[C/T];p.11795/rs12720871-[C/G]
CGCACACCCA GGTCCCACTT TACAGAGGGG AACACTGAGG CTGGAGGGTT 11850
GGGTAGCTGT GTGGATGCAG GGGAGCGGTG ACTCAGGGCA ATTCCCCCAT 11900
CCTGAGGCCC TGCGTTGATC TTTTCCTCCT GCAGCCAGCA TCCTTTCAGA 11950 | p.11913/rs12720872-[C/T] | Exon 8
                                     A  S   I  L  S  D 225
TGGAGACATT GGGGTGGACA TTTCCCTGAC AGGTGATCCC GTCATCACAG 12000
  G  D  I   G  V  D   I  S  L  T   G  D  P   V  I  T   241
CCTCCTACCT GGAGTCCCAT CACAAGGTAG GAGTTGTGGG AGGGTGGGGC 12050
A  S  Y  L   E  S  H   H  K                            250
AGGGCCCAGC TTCCCCAGGG GAGTTGGTCC TTTTTTGTGC TCTGACAACC 12100
CCGTCCCCCA GCTTCAACCT TATGGCAGCC AAGAGTCCTG GGGCGCTCCT 12150 | p.12103/rs12720873-[G/A]; p.12123-[T/A]
CCTCATTCCT GATGCTCCTC CGCATTCCTG ATGCTGCGAG GAGGGCAGGC 12200   p.12178/rs148654654-[C/T]
CACAGCGACG TGCCCCTGAC CCCTCTCTGC AGGCACCAGG GCTGCCCACT 12250
ACAAGGATCC CAGCAAAGCA CCAGCTCCTT CCTAGAGGGC TTATTCGGCT 12300   p.12281-[C/T]
TCTGTCATCC TCTACAGCAG TGGATTGTGG CCCCCCCCCA GGGGGTACTG 12350   p.12331delC/rs67114203; p.12336C>T>A
ACAAAAGCTT TGGACCCTCT ATTACTTAGG ATATAGATTT CTGTAACAAA 12400 | REPEAT
GAAATCCGAA ATAATAGCTG CTTAAACACA ATAAACAGTT ATTTCCCTCT 12450   p.12409/rs11076175-[A/G]
GTTGCGTTCT GAGCATCTGC AGCCCCGCGG GATCAGGAGG CTGCAGGGTG 12500
TCAGGCACGC AGGCCCCTTC CACGTGTTCT CAGCCAGCCC CAGGCATGAC 12550 | NOT SCANNED
CTCATCCCAG GGTCCTGGCT GACTGGCCTG ACCACCACAC CCACTCTGCT 12600 | REPEAT
CACAGCCCGT TGGCCTGAAC CTGATCGCAG GACCCCACCC TAGCTGCAAG 12650   p.12621/rs7499892-[C/T]; p.12627/rs146562593-[G/A]
GGAAACTGAG GAATTTATTT CAGCTAAATA TTGAGACCAG CTAAAAGTTA 12700
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TTCAGAGGTT CATGGCCACT CCTGAAGCCT GTTCACAACC CATGGGCTGG 12850
ATGATCTAGT GGGGCGGGGG ACTGGGCAGC AGCTTGTTTT CCTGATTTTG 12900   p.12860/rs289713-[T/A];
GCCTCCAGGA GCCGATGGTC AATGGACTGC CCTCTGCAGG GGCAGGGCTG 12950   p.12913/rs191754368-[C/T]
GTGGTCAGCT GGGGCGGGGT GGGAGCTGGA GGTCCGTGGT CACCAGCTGC 13000   p.12970/rs182480194-[T/A]; p.12981/rs146782017-[G/A]
CCTGACTAAT GTCGTTACTT GAATATAACC CTGTGAAGGC AGGAACCACG 13050 | REPEAT
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CTTTCCTCAG TTTCCCCATC TGCACTCTGG GCTGAATGCT GGGGCTCCTC 13200
CCAATCTCCC TGAAGCTGGA CCTGAGCCCA GTAGGGACAC ACAGGGTCCA 13250   p.13223/rs9930761-[T/C];
GCCAGCGTCC TGGCTTCCTC CAGGGTCATT TCATCTACAA GAATGTCTCA 13300 | Exon 9 p.13279/rs35878799-[T/C]
                          G  H   F  I  Y  K   N  V  S  259
GAGGACCTCC CCCTCCCCAC CTTCTCGCCC ACACTGCTGG GGGACTCCCG 13350   p.13327/rs28381707-[G/T]
 E  D  L   P  L  P  T   F  S  P   T  L  L   G  D  S  R 276
CATGCTGTAC TTCTGGTTCT CTGAGCGAGT CTTCCACTCG CTGGCCAAGG 13400 | p.13384/rs5883-[C/T]
  M  L  Y   F  W  F   S  E  R  V   F  H  S   L  A  K   292
TAGCTTTCCA GGATGGCCGC CTCATGCTCA GCCTGATGGG AGACGAGTTC 13450
V  A  F  Q   D  G  R   L  M  L   S  L  M  G   D  E  F  309
AAGGTGAGTG GGTGGGGCTG GGCTGCTAGG GAATCCAGAT GGCATGTGGT 13500 | p.13477/rs11076176-[T/G]; p.13482/rs289714-[A/G]
 K                                                     310
ATGTGTGTGT GTGCACACGC ATGGGGAGGA GGGAGGAAAC TCGGAAACTT 13550
GGTGGTGGGC AAAAGAACTA AGCTGGAGCA ATAGCAGTGA AGTCCAGACT 13600 | REPEAT
GGGCACAGTG GCTCACACCT GTAATCCCAA TCCTTTGGGA AGCTGAGATG 13650 | p.13641/rs158477-[G/A] | REPEAT
TAGCAGGACG AACCGCAGAC AAAACTCCTC AGACACTGAG TTAAAGAAGG 13700   p.13683 /rs11644475-[A/G]
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GAGCTCTCCG AGTGAGCAAT TCCTGTCCCT TTTAAGGGCT CACAACTCTA 13800 | p.13765/rs158478-[A/C]
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ATAAAACAAT ATAAAACAAT ATGAGAGGGT CTGTCTCTCT TCTCTCAGAG 14150 | REPEAT
ACAGGAGGGT CCCTGGAGGC CAGGAGTTCA AGACCAGCCT GGGCAACATG 14200 | p.14192/rs12720892-[G/A]
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CACGTAGTAA CTGTGCATTA AATATAAGTT GATATTAGTC TTACATTTAT 14550 | p.14539/rs289715-[T/A]
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CTGTGCTTGT CATTGAACTC ATGAGGAAAC TGAGGCCCAC AGAGGGGAAG 14800 | REPEAT
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GCCAGGCCTC CAGCCGGGAC AGGGGTTCCC TGTTCCACAC CCTGCCCAGA 14900
GCATCTCACA TGTTGTCTGG GAGGTTGGGA GTTGCGTCTG AGGAGGGGTC 14950
CAGTCCTTGA AACTGCCCTT GGTCCCTGCG AAGTTTTCTT CTGAGGAGTG 15000
GACTTTACTC CACCCACCCT CCAACTTCCT CATTTCTTTT CAGGCAGTGC 15050 | Exon 10
                                                A  V   312
TGGAGACCTG GGGCTTCAAC ACCAACCAGG AAATCTTCCA AGAGGTAACT 15100
L  E  T  W   G  F  N   T  N  Q   E  I  F  Q   E        327
GCCCCCTGCC CCTGTGTGGG GTTTATCTCA CGTACCCCAA TCCTGCTCTG 15150
GCTTCAAGAG CCCCCACACA GCCAATAACA CCACCAATGG CAACAATTAT 15200 | REPEAT p.15196/rs116351574-[A/G]
AACAGCGAAC ACAGCTCCTA CTCGGTTGTT CGGCATGGAG TGAAGCACTT 15250 | p.15226/rs2303789-[T/G]; p.15231/rs12720877-[C/T] p.15232/rs13306232-[G/C];
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GGGTTTGAGC CCAGCTCTAT TGCCCCCAAA GATAAGGCTC CATTCCCTGC 15400
TCCATTACCC AGGCATAGGG ACTTGTAGGG GGCTGGAACC CCAGGATCAA 15450 | p.15407/rs289716-[A/T]; p.15419/rs289717-[G/A]
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TGTCTACCTT CCACTTCCCT CTCCACACAC AACCTGCTTA CCAGAGAGCT 15800 | p.15800/rs736274-[T/A]
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CAGAGGACGG TCCCTCTTCC CTTCTGAACT CAGGCCGTCC AGCCTTCCCC 15950 | p.15913/rs12720937-[C/G] | REPEAT
GGCTCTGTGA TGTCTCTCTC CCTGCACATA CACAACTCAC AATATTGGGC 16000 | p.15963/rs289718-[T/C] | p.15972/rs289719-[C/T]
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CCCAGGCTAC CATTATCTCT AGTGGGGACC CATCTGTAGC TCCCGGTGGG 16150 | NOT SCANNED p.16146/rs112205272-[G/A]; p.16148/ /rs72771489-[G/A]
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AACAATCTTT TCAAGAAATA AAACTGGTCA TTCACCTGCC TGCTTAAAGC 16250
CGGTGTAGGA TACAGGCTAA ACGCTCTCCC ATGGCCTCCA GGGCCCTGCA 16300   p.16263/rs56208677-[C/T]
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TGAGCCACAG CACCCAGCCC ATCAGCTCTG GAAATTTCTT CATCACTCTC 16600 | REPEAT p.16598-[C/T]
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TTCCATGAGA CACACGTTGG GCCATCTCAT TCCATTTTCC GTGTCTCTTA 16700
GTTGCTCTGT CGTGTTTTCC ATCTCTTTTA TCTCTATCCT AAATTCTGGA 16750   p.16709/rs151104194-[G/C]
TAGTTTCTTC AAGTATCTTT TTAGTTCATT AATTCTTTTT ACAGCTGTGT 16800
CTTATTTGTT TACTTACCCA CTGAGATTTT CATTTTATTT TATTTAATTA 16850
ATTAATTTAT TTATTTTTGA GACAGAGTCT CGCTCTTGTT CCCCAGGCTG 16900 | REPEAT | p.16859/rs11860407-[A/G]
GAGTGCAGTG GCGCAATCTC AGCTCACTGC AACCTACGCC TCCTGTGTTC 16950 | p.16935/rs12720901-[T/A]
AAGCAATTCT CGTGCCTCAG CCTCCCGAGT GGCTGGGGTT ACAGGGGTGC 17000 | p.16979/rs1968905-[G/T]
ACCACTGTGC CCAGCTCATT TTTTTGTATT TTTAGTAGAG ACGGGGTTTC 17050 | p.17025/rs12720897-[T/G]
ACCATGTTGG CCAGGCTGGT CTTGACCTCC TGACCTCAAA TGATCCTCCT 17100
GCCTCAGCCT CCCAAAGTGC CGGGATTACA GGTGTGAGCT CCCGCACCCC 17150
GCCGGCCCTT TCTTTCTTTT GAGCTGAGCT ATGTATTTAA TGAAACCTTT 17200 | p.17154/rs12720903-[G/A]
TCTTGTGTAT CCAGCGGTTC AGTGGTTTCT TGGGGCATGT GATCTCCTTG 17250 | p.17216/rs4784744-[G/A]
AGCCCAGTCC CACAGGCTGT AATCGAAGGT CCTCAGGCCA CACTCCCCAG 17300 | p.17274/rs12720898 -[C/T] | REPEAT
CCCCGCTGGC TGCCTGCGCA TTCCTTATCT TGGCCATGTT CCTTCCACAG 17350
GGCTCTTGTC CACACTGTCC CCTCTGCCAG AATGGTTTGC CCTCCCCCAT 17400
GCCATCTGCT CCTCCTCCTG CCACCTCAGG GAAGGCCTCT CCCACCTCCC 17450
TGACTAGGTC AGGTCCCCTC GTGCCACAGC CTGGTGTGTC TCTCCTTTAA 17500 | p.17483/rs291044-[G/A]
ATACTCCTCA GCTGCAGTTT TACGTTCTGT TCTGGGATGC CCTGGAAAAT 17550
GCTGGGCTCC TGCAGATATG GCCCGCAGCT CCTGCGCTCT CTGCTGCTCT 17600   p.17575/rs114486472-[G/A]
ATCCCCACCC CTAGCCCAGC TGCTACAGCA GCTTCCCTCG GAGGGTTACC 17650 | REPEAT
ATGCAGTAGG TCCTGTTCTA AGCTCTTTCC ACAGATTATC TCATTCCATC 17700
CTCAGGACAA CCCTATGAGG TAGGATCTAT GATTATCCCC ATTTTACAGA 17750   p.17740-[C/T]
TGAGGAAAGT GAGGCCCAGA AGGCTAAGTG AAGGCATCCT CAGCACATCC 17800
TGAGAGAGGA GTTCAGGGTA GGAATAGCTT CACTAGCACA CAGATGAGAA 17850 | REPEAT
ACTGAGGCCC AGAGAGGACA AGAGTCCTAA TTTGCACAGC CTGGGGCCTG 17900   p.17860/rs8053613-[C/T]; p.17875/rs34337891-[T/C]
GGCACTACCC CGAGCTACTT CCTTTTCCCC AGCCCTGGGG CCCGGAGCCA 17950   p.17918/rs34426213-[C/T]
GCTTTGTCCT TCCCATCTCC GAGGGCATGG ACTGCTGCTG CCCTGATGGG 18000   p.17970/rs891144-[C/T]
CCCCTGTCCT GGCCATGGGA CCCCTGTCTT CCACAGGTTG TCGGCGGCTT 18050 | Exon 11
                                       V   V  G  G  F 332
CCCCAGCCAG GCCCAAGTCA CCGTCCACTG CCTCAAGATG CCCAAGATCT 18100
  P  S  Q   A  Q   V  T  V  H  C   L  K  M   P  K  I  348
CCTGCCAAAA CAAGGGAGTC GTGGTCAATT CTTCAGTGAT GGTGAAATTC 18150
S  C  Q  N   K  G  V   V  V  N   S  S  V  M   V  K  F 365
CTCTTTCCAC GCCCAGACCA GCAACATTCT GTAGCTTACA CATTTGAAGA 18200
 L  F  P   R  P  D  Q   Q  H  S   V  A  Y   T  F  E  E 382
GGTGAGGCGG GTGCAGGGAG AGGTGGTGGT GGGGGAACCT GACTCACATA 18250
                                                      382
TGGGCCGCAG AGGGCAGGGG CCTGGGGGTC TCTGAAGCCT CCAGATCCTT 18300   p.18256/rs28381709-[C/A]
CTCACCACCT CTGCTGGCAC TGGTTGTCTC TTGCACATGG CTCCTTACAA 18350
TCAAAATCAC ATCATGCAAG TAACGAGGGG GTACACACGT GGTTTCCACA 18400 | p.18388/rs12708979-[C/T] REPEAT
GCTTAGGTAA TATTTCTCT CTTTTCTTAT TTTTATTTTT TTTAGAGACA 18450 | p.18413/rs12708980-[T/G]
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ACTGCAGCCT CGAATCCTGG GCTCGAGTGA TCCTCCCACC TCAGCCCTCC 18550
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CAAACTCCTG GCCTCAAGCA ATTCTCCTGC CTTGGCCTCC TAAGTTGCTG 18700   p.18663-[C/T]; p.18678-[T/G]; p.18689-[C/T]
GGGTTATAGG CATGAGCCAC CATGCCAAGC ATATGTTCTT TCATTCTTAT 18750 | p.18717/rs143024882-[C/A]; p.18733/rs291043-[A/G]| REPEAT p.18746-[C/T]
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TCACTGTGTT GCCCAGGCTG GAGTGCGGTG GCACAATCTC GGCTCACTAC 18850
AACCTCTGCC TCCCAGGTTC CAGCGATTCT CATGCCTCAG CCTCCCAGGT 18900
AGCTGGGATT ACAGGCATGC GCTACCACGC CTGACTAATT TTTTGTATTT 18950 | p.18921/rs17239354-[G/A]
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GGTTTCAAGT GATCTGCCCG CCTCAGCCTC CCAAAGTGCT GGGATTACAG 19050 |
GCATGAGCCA CCACGCCCAG CCAATATTCT CCTCCTTAAG CTGAGCAGTG 19100
GACAATGGTG TTTATTACCC GAGTCCACAA CCCTTTATTC ATTAGGGCCA 19150 | REPEAT
CAAGGGTTTC CAAATTCAGA ACTTCTGTGA ATTTGTAAAA GTAGTATAGT 19200
GTATAGACAC TGGATATATT GCAGAACACC CCAATAGGGT GTGGGGTGGC 19250
ACCCCACAAT CAATTCTCCT CAAATGCCTC AATTGGCATT TCTCCTCATA 19300
TGAAGCAAGA TAAATACCAT ACATAGCTTC CTAGACAATG GCCAGGTTTT 19350   p.19317-[C/T]
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TATAATTACA AATAAGGAAT TAAGAATCAG TATTATCTTT AATGCTCCTT 19450
AGAATATCTT CAATTTTTTT TTTTTGAGAC AGAGTCTCAC TCTGTCACCC 19500 | REPEAT
AGGCTGGAGT GCAGTGGTGC AATCTCGGCT CACTGCAACC TCCACCTTCC 19550   p.19519/rs146251160-[G/A]
TGGTTCAAGC GATTCGCGTG CCTCAGCCTC CCCAGTAGCT AGCTGGCACT 19600 | p.19561/rs12708981-[G/A]
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ACCAGGTTGG CCAGGCCAGT TTCAAAGTCC TGACCTCCAG TGATCCACCT 19700 | p.19700/rs12720857-[T/C]
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GCCAATATTT CTTAATACAT TAAGAACTAA AGACAAGAGC GATACAATCA 19800   p.19757-[A/G]; p.19789/rs74678905-[G/A]
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ACCCCCTTCT CCAGGGGCCT TCGATGTGGT GACTGGGTGC ATTTCCTTCT 19900 | p.19872/rs148807012-[C/T]; p.19881/rs17238225-[G/T]
GGTGCTTTGT TATTTTTAAA TAAATTTTTT ATCTTGGAGT AACTTTATAT 19950 | REPEAT
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TTCCCGCTTT GTCCACATCT TACATAACCA TGCTACAGTG TCATAGCGGA 20050
GAGATTAACA TTGGTGCATG ACTGTTAACC AAACTCTAAA CTTTATTTGA 20100   p.20072/rs80180245-[C/T]
ATCTCCCCAG TTTTTCCACT GATGATACCC TTTTTCTTTT CCAAGATCTG 20150
ATCCAGGATA GCACATTGTA TTTAGCCGTT CTTTTTTGTT GTTGTTTGTT 20200
TGTTTGTTTG TCTGTTTGTT TCTGCCCAGG CTGGAGTGCA GCGGTGATCC 20250 | REPEAT
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TAGAGACAGG GTTTTGCCAC ATTGCCCAAG CTGGTCTCAA ATCCCTGGGC 20350
TCAGGTGATC CTCCCACCTT GGCCTCCCAA AGTGTTGGGA TTATAGGCAT 20400 | p.20354/rs12447620-[G/A]; p.20374/rs17231869-[C/T]
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GTATTACTTT CCTTTTCATT TTTCTGTTTT ATTCCTTTTG GCTTTCTCAT 20500 | p.20457/rs12708984-[C/T]
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CTGAAACATT GAGCATTTGT TAAAAAAAAG AATTATTCGG CCGGGCACGG 20600 | p.20551/rs115390156-[C/A]; p.20593-[G/A]
TGGCTCACGC CTGTAATCCC AGCACTTTGA GAGGCTGAGG TGGGCGGATC 20650   p.20624-[A/G]; p.20641/rs189327489-[T/C]; p.20645/rs12708985-[C/T]
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CCTAGCTACT TGGGAGGCTG AGGTAGGACA ATCGCTTGAA CCTGGGACGT 20800
GGAGGTTGCA GTGAGCTGAG ATCGTGCCAC TGCCCTCCAG CCTGGGCAAC 20850   p.20804-[G/A]; p.20844/rs13331688-[G/A]
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CTCTCTGCTT CGGGAAGAGC CCTGGCTCAC AGCAAATTTG GTTTCTCTCC 21100   Exon 12
CCAGGATATC GTGACTACCG TCCAGGCCTC CTATTCTAAG AAAAAGCTCT 21150 | p.21111/rs34855278-[G/A]; p.21119/rs7192120-[C>T>G]; p.21126/rs5880-[G/C]
     D  I   V  T  T   V  Q  A  S   Y  S  K   K  K  L  397
TCTTAAGCCT CTTGGATTTC CAGTATGTGC TGCAGAGAAG AGAGGGGGCG 21200
F  L  S  L   L  D  F   Q                              405
GTCAACTCCG CAAACCTCTC CCTGGCCCCT TGGAGTCAGG CACAGGGCGG 21250
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GGGCCCAATG GAGGGTCAAA TTATCATCGC TTTTTTATTT CAGGATTACA 21600 | Exon 13 p.21579/rs7196174-[G/T]; p.21580/rs1800774-[C/T]
                                                 I  T  407
CCAAAGACTG TTTCCAACTT GACTGAGGTA GGTAGTCTTG GATAGACTGG 21650
 P  K  T   V  S  N  L   T  E                           416
GGGAAATAAG TCCTGTGGGA CCTCCTGCCT TAAAGAAAGC AGGCGGAGGG 21700
CCCTAAAGGA AATCAGGCAA CCAGACCAAA AGAATGTGGA CCAGGTGGTC 21750
CATGCTGTGT CTCTTGTGAC CCTTCTTCTC CCTGCCATGT CTTTTGGGAG 21800   p.21760/rs78603009-[T/C]
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TTTTTTCACG GATGGGCATG AGGATGAATG CTTGTCCAGG CCGTGCAGCA 22050
TCTGCCTTGT GGGTCACTTC TGTGCTCCAG GGAGGACTCA CCATGGGCAT 22100
TTGATTGGCA GAGCAGCTCC GAGTCCATCC AGAGCTTCCT GCAGTCAATG 22150 | Exon 14 | p.22127/rs5882-[A/G]
             S  S  S   E  S  I   Q  S  F  L   Q  S  M  429
ATCACCGCTG TGGGCATCCC TGAGGTCATG TCTCGTAAGT GTGGGCTGGA 22200 | p.22162/rs5886-[G/A]
 I  T  A   V  G  I  P   E  V  M   S                    440
GGGGAAACTG GGTGCCGAGG CTGACAGAGC TTCCCATTTC ACCTTGTGGG 22250
CCCTTCCCAG GCAGAGCTTC AGGTGCCCCT CTTCCCAGTC ATTGATACTT 22300
AGCGGTCCTG GCCCCCTTTC CTCTCCCTGC TGGTGGTATT GCACGCCAAT 22350 | p.22327/rs111379440-[C/T];p.22337/rs8045701-[T/C]; p.22349/rs12720882-[A/G]
GACTCGGCCA GATGCCCAGA CCCCTGTTCT TGGTTTACCT GCAGAATATT 22400 |
ATCTTTGCCA CCCCGCGGGA TGGCTCAACC CACTTTCAGG ATGCAGGTCT 22450
CCTAATAGCA ACCTGATATA GCAGAAAGAC CCCTGGGCTG GGAGTCTGAG 22500 | REPEAT  | p.22480/rs12598103-[C/G]
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GAATGATCCT AGTGGGGTGT CTTGGCATCT CTTGGCCTCA TTTTCCCCAT 22850 | REPEAT
CTGAACCATG AAGCTAAAAC TAGGGGATGT GGATTAAATG GTTCCTACAA 22900   p.22888delA
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TCTTCCTCAT CCTCAGAAGC ACTTGCTCAC TCTGCTAAAT CAAAGTGAAA 23150
CGCATGTTTA CAGAATATTG GTCCAAAAGG GTCTCAGCAT CTCCCACTAC 23200   p.23152/rs150048432-[G/A]
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                       R  L  E   V  V  F  T   A  L  M  450
AACAGCAAAG GCGTGAGCCT CTTCGACATC ATCAACCCTG AGATTATCAC 23350
 N  S  K   G  V  S  L   F  D  I   I  N  P   E  I  I  T 467
TCGAGATGTG AGTACAAAGC CCCCCTCACC AGCCCCTGTT CCTGGGGAGA 23400   p.23353/rs1800777-[G/A]
R  D                                                 469
GAGGCCCAGA CAGGATTCCT GGGGTGACTG GGGGCTGTTG GGGAGACAGA 23450
CAGAGGGGCC TCTACCAGCT TGGCTCCCTC CTGGTGGCCT GGGAGTCAGC 23500
CCAGCTCACC CCTCTCTCCT ACTGCCCCTC CCTTCAGGGC TTCCTGCTGC 23550 | p.23508/rs289741-[A/G] | Exon 16
                                         G   F  L  L   473
TGCAGATGGA CTTTGGCTTC CCTGAGCACC TGCTGGTGGA TTTCCTCCAG 23600
L  Q  M  D   F  G  F   P  E  H   L  L  V  D   F  L  Q  490
AGCTTGAGCT AGAAGTCTCC AAGGAGGTCG GGATGGGGCT TGTAGCAGAA 23650 | UTR
 S  L  S                                               493
GGCAAGCACC AGGCTCACAG CTGGAACCCT GGTGTCTCCT CCAGCGTGGT 23700 | p.23696/rs1801706-[G/A]
GGAAGTTGGG TTAGGAGTAC GGAGATGGAG ATTGGCTCCC AACTCCTCCC 23750
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CAGTGCCGTC CACCTCTTTT CAGCCCTTCC AAGGCAGCTG CCCCCAAACC 23900   p.23858-[G/A]
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GACTCACGAT CCTCCCTGAT CAGGTCCCTG GATACCTTCC AAATTTATCC 24000
CCTTTAACCC AGCACTCTCC TTGTCTGACC AGCTTCCTGC AGGAGCTGTC 24050
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GACCAGGGCT TCAGATCCTG AGGATGGTGG GAGGGTAAGG GGCCCTCAGA 24150   p.24136/rs289744-[T/G]
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GCTCACCTTT TTTTTTTTTT TTTTTTTGAG ACGGAGTCTC TCTGTGACCC 24300 | REPEAT p.24258/rs76732052-[T/G]
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TTTCACCATG TTGGCCAGGC TGGTCTCGAA CTCCTGACCT GCAGTGATCC 24500 | p.24499/rs12720875-[C/T]
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CTCATACCTC TGCTCTCTTT AAAATAGCCA ATCGGAATTA GCTTAGACCG 24900 | p.24881/rs114646974-[A/G]; p.24889/rs112039804-[T/A]; p.24899/rs138161274-[C/G]
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CTCAAGCTAC AATACAAAAA GTTTCTTCCA ACCCTCTCAG TCTTGGAAGG 25250 | p.25217/rs76500832-[A/G]; p.25218/rs12720916-[A/G]
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TAGCCAATTG AGACGGGAGG AAGCGCAGCA AGATGCTGGC TAGTGCAAGG 25350 | REPEAT
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TGAGCCAGGT TT
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Appendix B2 Figure 1. *CETP* Annotated FASTA Sequence. The color FASTA representation of the *CETP* annotated reference sequence was adapted and modified from the SeattleSNPs database (http://pga.gs.washington.edu). The color code for the reference sequence is as follows: green for UTR, grey for introns, black for exons, purple for repeat region. The variants identified in this study also listed in dbSNP build 131 are shown with refSNP ID; common variants for both population are shown in red, unique variants for NHWs are shown in blue and for African blacks in black. The flanking bases for insertions and deleted bases for deletions were highlighting in yellow.

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